User Manual

Leksell GammaPlan®

Online Reference Manual

Document ID: 1550593 Rev. 01
Publication date: 2020-04-07
Language: English

Acknowledgment of other trademarks

Elekta acknowledges the trademarks and registered trademarks of other manufacturers that we use in this document.

Referenced documents

Elekta does not supply all the documents that we refer to in this document with the equipment. Elekta reserves the right to make the decision on which of the documents we supply with the equipment.

Contact information

PRODUCT MANUFACTURING and SUPPORT CENTER – NEUROSURGERY

ELEKTA INSTRUMENT AB

Kungstensgatan 18

Box 7593

SE-103 93 Stockholm

Sweden

Tel +46 8 587 254 00

Fax +46 8 587 255 00

CE 0413

TECHNICAL SUPPORT

Contact your local Elekta representative for technical support

Table of Contents

— Blank page —

List of Figures and Tables

— Blank page —

1 Safety and regulatory information

— Blank page —

1.1 Intended use

Leksell GammaPlan® is a computer-based system designed for Leksell Gamma Knife® treatment planning.

1.2 Use of the equipment

This equipment is intended to be installed and used only in accordance with the safety procedures given within this document for the purpose for which it was designed. Nothing stated in this document reduces the user's professional responsibilities for sound judgement and best practice.

Installation and use of this equipment is subject to the law in the jurisdictions in which the equipment is being used. Users shall only install and use the equipment in such ways that do not conflict with applicable laws or regulations which have the force of law.

Use of the equipment for purposes other than those intended and expressly stated by the manufacturer, as well as incorrect use or operation, may relieve the manufacturer or his agent from all or some of the responsibility for resultant non-compliance, damage or injury.

Note: *In the United States, federal law restricts this device to sale, distribution and use by, or on order of, a licensed physician.*

1.3 Compliance of the equipment with international standards

This product is designed to comply with the requirements of the Medical Device Directive 93/42/EEC.

The product is CE marked.

Leksell GammaPlan® complies with the following safety standard:

- EN62083:2009 Medical electrical equipment – Requirements for the safety of radiotherapy treatment planning systems

1.4 Recommendations for training

Users of the software shall have received adequate training on its safe and effective use before attempting to work with it.

Training requirements may vary from country to country. The user shall ensure that training is received in accordance with local laws or regulations that have the force of law. Information on training is available from Elekta or your local Elekta® representative.

1.5 Important safety instructions

Elekta® products are designed to meet stringent safety standards. Every reasonable precaution has been taken during manufacture to safeguard the health and safety of persons who will operate this equipment.

All medical electrical equipment requires proper installation, operation and maintenance, particularly with regard to safety.

It is vital that the user reads, understands, and where applicable strictly observes all safety directions, warnings, cautions, notes and safety markings within this manual, on all other product documentation, release notes delivered with the software media pack and on the equipment.

WARNING 1.1

Never attempt to remove, modify or override any switches, interlocks, or other safety device on this equipment. Interfering with such safety devices could lead to death or serious injury.

This product should be installed and commissioned by Elekta® personnel or other qualified maintenance personnel approved in writing by Elekta.

The system in whole or in part may not be modified in any way without the prior written approval of Elekta.

1.5.1 Conventions for warnings, cautions, and notes

The following are samples of how warnings, cautions and notes appear throughout this document. The text within the samples explains their meaning.

WARNING 1.2

Warnings are directions which, if ignored, could constitute a health hazard, cause fatal or serious injury, or lead to clinical mistreatment.

CAUTION 1.1

Cautions are directions which, if ignored, could cause damage to the equipment described in this manual, and/or any other equipment or goods, and/or could cause environmental damage.

Note: *Notes provide advice and highlight unusual points. A note can also be part of an instruction.*

1.5.2 Warning labels found on the equipment

The following warning label may be found on the equipment:

Warning label		Indicates a specific warning if displayed in conjunction with warning text. Instructs the user to refer to the product documentation if displayed without warning text.

1.5.3 Symbols found in the software

The following symbols are found in the software:

	Name and address of manufacturer
	CE Marking
	For provision and use only at a licensed physician's direction and under medical supervision
⚠	Attention, consult accompanying documentation
	General warning sign

1.5.4 Extended symbol glossary

For more information about symbols on Product Labels, see SYMBOL GLOSSARY EXTENDED (77700544) on the Elekta website: **http://www.elekta.com/services/supportplus**. The glossary lists contain applicable standards, symbol reference codes and symbol meanings, for example.

1.6 Safety precautions

1.6.1 Safety precautions for the compatibility of the equipment

Equipment described in this document shall only be used in combination with other equipment or components if these are expressly recognized by Elekta as approved and compatible. Consult Elekta for advice on compatibility with the equipment before using any equipment not supplied by Elekta.

The use of accessories, transducers and cables other than those specified by Elekta may result in increased emissions or decreased immunity of the equipment.

Changes or additions to the equipment must only be performed by persons expressly authorized to do so by Elekta. Such changes must comply with best engineering practice and all applicable laws, and regulations that have the force of law within the jurisdiction.

WARNING 1.3

Changes, additions or maintenance to the equipment performed by persons without appropriate qualifications and training, and/or the use of unapproved spare parts, may lead to serious injury and/or damage to the equipment, as well as making the warranty void.

1.6.1.1 The export and import function of patient files in Leksell GammaPlan®

The export and import function of patient files in Leksell GammaPlan® can only be used to transfer treatment planning data between different Leksell GammaPlan® workstations.

1.6.2 Safety precautions for operation of the equipment

Do not use the equipment for any application until you are sure that the procedures for care and maintenance have been satisfactorily completed.

In normal operation, the software needs no maintenance other than:

- regular backup of images and patient data
- occasional checks that the hard disk of the workstation is not full.

In both cases, this is a task for the system administrator. See the *Treatment Planning System Administrator Tool, Online Reference Manual*.

WARNING 1.4

If any part of the equipment is known or suspected to be defective or incorrectly adjusted, DO NOT USE the equipment until a repair has been made by Elekta. Use with defective or incorrectly adjusted components or systems could expose the users and/or the patient to radiation and other safety hazards. This could lead to injury or to clinical mistreatment.

1.6.3 Final disposal of the equipment

Prior to disposal, always contact Elekta for advice.

The term final disposal means disposal of the equipment, or any part of the equipment, in such a way that the equipment or part can no longer be used for its intended purpose(s).

Never dispose of Elekta® products in the domestic waste stream.

Disposal must always be executed in an environmentally sensitive manner that complies with all local and international regulations and laws. Materials hazardous to human health and the environment must be separately removed and disposed of through competent, licensed facilities. The remaining material may be recycled where facilities and local regulations permit.

WARNING 1.5

Incorrect handling or disposal of hazardous material may cause death, serious injury and environmental damage.

1.6.4 Product lifetime

Product lifetime is not applicable for software.

2 Introduction

— Blank page —

2.1 Function of this document

This document is the Online Reference Manual for Leksell GammaPlan® and can be accessed on screen from the **Help** menu.

This document is intended to assist users in the safe and effective operation and maintenance of the equipment described. The user includes the body with authority over the equipment and those persons who actually handle the equipment.

Before attempting to work with this equipment, the user must:

- Thoroughly read and completely understand this document.
- Keep this document with the equipment for easy access.

The most extensive configuration is described within this document, including the maximum number of options and accessories. Not every function, option or accessory described may have been purchased or licensed by the user.

2.2 Intended audience

This document is written for trained users of Leksell GammaPlan® and Elekta® field service personnel.

2.3 Structure of this document

The information in this document has a defined structure. The structure helps the user to find the information it contains more easily. The information comes in the following chapters:

- Safety and regulatory information
- Introduction
- Product description
- Getting started
- Using Leksell GammaPlan®
- Appendix with product specifications (where applicable).

2.4 Leksell GammaPlan® version

This manual is valid for Leksell GammaPlan® version 11.3 with any service packs installed.

2.5 Examples and illustrations

If the examples in this document refer to patients, physicists, or hospitals by name, then they are not the names of real persons or hospitals. If an example uses the name of a real person or hospital, it is accidental.

Illustrations in this document show the equipment as present. Differences may occur compared to previous models and versions of the equipment. Such differences in the illustrations are of aestethic character and not functional.

2.6 Disclaimer

- Elekta assumes no liability for use of this document if any unauthorized changes to the content or format have been made.
- Every care has been taken to ensure the accuracy of the information in this document. However, Elekta assumes no responsibility or liability for errors, inaccuracies, or omissions that may appear in this document.
- Elekta reserves the right to change the product without further notice to improve reliability, function or design.
- This document is provided without warranty of any kind, either implied or expressed, including, but not limited to, the implied warranties of merchantability and fitness for a particular purpose.
- If you find any errors in the software operation, contact your Elekta® service representative.

2.7 Related documentation

This manual forms part of the accompanying documentation for this product. The other document in the set is:

- *Treatment Planning System Administrator Tool, Online Reference Manual*.

The following Elekta manuals describe other products related to Leksell GammaPlan® that are referenced in this manual:

- *Leksell Gamma Knife® Icon™, Instructions for Use*
- *Leksell Gamma Knife® Perfexion™, Instructions for Use*
- *Leksell Gamma Knife®, Instructions for Use, various models*
- *Leksell® Vantage™ Stereotactic System, Instructions for Use*
- *Leksell Stereotactic System®, Instructions for Use*.

2.8 Positional references on the computer screen

Unless stated to the contrary, positions and directions such as left, right, upper, lower, clockwise, and counterclockwise are given with respect to the computer screen when viewed from the front.

2.9 Positional references in patient images

Patient images displayed on the screen may be rotated or reversed. Always observe the actual direction given in the image reference.

2.10 Conventions for text formats

Convention	Usage
Menu > Item	Denotes a sequential selection from a menu and submenu, e.g. **File > Open**, or **View > Toolbars > Standard**
<Key>	Denotes a keyboard key, e.g. <Return> or <Ctrl>
<Key>+<Key>	Denotes keys to be pressed simultaneously, e.g. <Shift>+<Tab>
<Key>, <Key>	Denotes keys to be pressed in sequence, e.g. <Home>, <Enter>
`Name\Name\Name`	Denotes a path to a specific file location

2.11 User definitions

Term	Definition
Authorized person	A person specifically authorized by the authority controlling the use of the equipment.
Qualified person	A person legally permitted to work on, and operate, the equipment in the jurisdiction in which the equipment is being used.
User	The body which has authority over the equipment and the person who actually uses the equipment.

2.12 Glossary of terms

Term	Definition
Anatomical image	An image of the anatomy of a patient. An anatomical image may be acquired by magnetic resonance imagery (MRI), by computed tomography (CT), or by common X-ray technology (angiograms). An anatomical image is represented in a view.
Anterior commissure	The most anterior junction of axons connecting the hemispheres of the brain. Defines the intercommissural line together with the posterior commissure. Notice that the intercommissural line refines the definition of the position of the anterior commissure when used as a point landmark. When abbreviated in the literature, the anterior commissure is referred to as C. a., Cm.a, or CA, while the abbreviation AC is being used throughout the AtlasSpace® documentation.
Atlas contour	An atlas structure outline on a single plane of a contour-based atlas. An atlas contour is defined by its outline, its position, and its depth range (defining the extent of the contour orthogonal to its plane).
Atlas contour plane	A single plane of contours in the Schaltenbrand-Wahren atlas. An atlas contour plane may contain any number of atlas contours.
Atlas contour projection	An atlas contour as projected to a given viewing plane.
Atlas registration	Any transformation between an atlas coordinate system and a patient coordinate system.

Term	Definition
Atlas structure	A named, anatomical or functional structure outlined in the brain atlas. An atlas structure has both a full name as well as an abbreviated name.
Atlas structure cut	A two-dimensional, visual representation of an atlas structure in a single viewing plane.
Brain atlas	A patient-neutral map of anatomical and functional structures in the brain. A brain atlas generally, and especially in the context of AtlasSpace®, comprises a number of two-dimensional planes of contours.
Convolution	Convolution is an algorithm for dose calculation with heterogeneity correction that is commonly used.
Coordinate frame	Leksell® Vantage™ Head Frame, or Leksell® Coordinate Frame G, or Extend™ Frame.
Depth range	The range perpendicular to an atlas contour within which the contour is valid.
Examination	Patient data and one or more treatment plans.
Exploration point	The current point of interest at which all non-locked views are centered. Locked views remain centered at the point of exploration that was effective upon locking the view.
Functional target	A functional target is a landmark defined by a functional targeting formula and is defined in a coordinate system based on the intercommissural registration.
Intercommissural distance	The distance between the anterior commissure and the posterior commissure.
Intercommissural line	The shortest line segment between the opposing surfaces of the anterior commissure and the posterior commissure.
Intercommissural plane	The plane that contains the intercommissural line and is orthogonal to the midsagittal plane.
Intercommissural registration	A transformation between the Leksell® Coordinate System and the patient coordinate system. This transformation is defined by the positions of the anterior commissure, the posterior commissure, and the midline reference point as they are defined in the Leksell® Coordinate System.
Invalid atlas registration	An atlas registration that has not been accepted by the user. When the atlas registration is invalid, AtlasSpace® disallows the use of much of the atlas functionality.
Leksell® Coordinate System	The coordinate system defined by the Leksell® stereotactic frame.
Leksell Gamma Knife®	The term is applicable for all models of Leksell Gamma Knife® if not otherwise specified: • Leksell Gamma Knife® Icon™ • Leksell Gamma Knife® Perfexion™ • Leksell Gamma Knife® B • Leksell Gamma Knife® C

Term	Definition
	• Leksell Gamma Knife® 4 • Leksell Gamma Knife® 4C
Locked view	A view whose exploration point and orientation have been locked.
Midsagittal plane	The vertical symmetry plane of the brain that divides the brain into its hemispheres.
Midline reference point	Any point in the midsaggittal plane that is superior or inferior to the intercommissural line. The abbreviation MR is being used throughout the AtlasSpace® documentation to refer to the midline reference point.
Monte Carlo	Monte Carlo simulation is a statistical procedure used to model probabilistic systems and establish the probability for a variety of outcomes.
MOSAIQ®	MOSAIQ® is Elekta's image-enabled oncology EMR with fully integrated business features such as scheduling, billing, and management reporting and analysis.
Patient file	The collection of anatomical images and treatment planning data prepared for treatment or follow up of a single individual. Specifically, the data prepared for a single examination of a single patient. A patient file includes the components of a treatment plan.
Planar view	A view that displays a single two-dimensional reconstruction of the anatomical images of the patient.
Posterior commissure	The most posterior junction of axons connecting the hemispheres of the brain. Defines the intercommissural line together with the anterior commissure. Notice that the intercommissural line refines the definition of the position of the posterior commissure when used as a point landmark. When abbreviated in the literature, the posterior commissure is referred to as C.p., Cm.p or CP, while the abbreviation PC is being used throughout the system documentation.
Structure display set	A named set of shown atlas structures. A structure display set is available within the context of any patient file and can be recalled to show a frequently used set of atlas structures.
Talairach grid	A three-dimensional grid defined by the standard Talairach landmarks; the anterior commissure, the posterior commissure, the midline reference point, the most superior point of the parietal cortex, the most inferior point of the temporal cortex, the most anterior point of the frontal cortex, the most posterior point of the occipital cortex, and the most lateral points of the parietotemporal cortices. The grid is aligned with the axes of an intrinsic coordinate system.
Talairach proportional grid	See Talairach grid.
Talairach registration	A continuous, piece wise linear atlas registration, defined by the Talairach proportional grid system as it is defined in the atlas coordinate system and by the Talairach proportional grid system as it is defined in the patient coordinate system.

Term	Definition
Target	A target is a cube enclosing the target volume. A prescription dose is applied to the target according to the lesion(s) inside.
Shield	A logical concept used when protecting tissue from radiation; physically the protection is realized by replacing collimators with plugs in the collimator helmet of Leksell Gamma Knife® 4, Leksell Gamma Knife® 4C, Leksell Gamma Knife® C and Leksell Gamma Knife® B. (Note: Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ use dynamic shaping to protect critical anatomical structures.)
Shot	A spherical volume where the radiation from multiple collimators is concentrated.
Treatment	The administration of a prescribed procedure or part thereof, for therapeutic purposes.
Treatment plan	A specification of a treatment; appears in two forms: • a treatment data file for Leksell Gamma Knife® • a treatment protocol for printout.
Treatment protocol	A printout of treatment data.
Valid atlas registration	An atlas registration that has been explicitly accepted by the user. When the atlas registration is valid, the system allows all the functionality of the atlas to be used.
View	A window to a part of a view plane and represented on the computer screen by a window. A view may be either planar or three-dimensional.
View plane	A plane in three-dimensional space onto which anatomical images, atlas structures, and other treatment planning elements have been projected.
Volume	A limited space which you define (draw) during the planning of the treatment.
Workspace	A collection of screen windows.

2.13 Abbreviations and acronyms

Abbreviation	Definition
AC	Anterior Commissure
AI	Angiographic Image
APS	Automatic Positioning System™
CBCT	Cone Beam Computerized Tomography
CE	Conformité Européenne
CT	Computerized Tomography
DICOM	Digital Imaging and Communications in Medicine
DICOM RT	An extension of DICOM for radiation therapy
EMR	Electronic Medical Records

Abbreviation	Definition
ID	Identity
IFU	Instructions For Use
MOSAIQ	MOSAIQ Oncology Information System (Elekta software)
MR	Magnetic Resonance or Midline Reference (when used in commissure point context)
N/A	Not Applicable
PACS	Picture Archiving and Communication System
PC	Posterior Commissure
PDF	Portable Document Format
PET	Positron Emission Tomography
QA	Quality Assurance
TMR	Tissue Maximum Ratio
TERMA	Total Energy Released in MAtter
TPS	Treatment Planning System
USB	Universal Serial Bus

— Blank page —

3 Product description

— Blank page —

3.1 Introduction to Leksell GammaPlan®

3.1.1 Description of Leksell GammaPlan®

Leksell GammaPlan® is a powerful, computer-based treatment planning system specifically designed for the simulation and planning of stereotactic Leksell Gamma Knife® radiosurgery based on tomographic and projectional images.

The basis of treatment planning is the acquisition and processing of digital images by a computer workstation running the treatment planning application software. The program is capable of handling a range of different imaging modalities. Images from tomographic sources such as Computer Tomography (CT), Magnetic Resonance (MR) and Positron Emission Tomography (PET) scanners can be used as well as projectional images from angiograms (AI). This allows the direct comparison between vascular structures in projectional images and tissue structures in CT and MR.

Digital images can be imported into the system via the computer network.

The treatment planning application has the ability to plan a patient's treatment protocol based on a single target or multiple targets.

The basic elements of treatment planning are:

- defining the cranial target or targets
- devising the configuration of the collimators to be used during treatment
- determining the parameters of the radiation shots to be delivered by Leksell Gamma Knife®.

WARNING 3.1

Examples of the treatment parameter values shown throughout this manual are for demonstration purposes only. They are not intended to represent actual values and must not be used as a basis for treatment planning.

3.1.2 Description of the software environment

The treatment planning application uses a graphical environment of menus, windows and dialogs. You communicate with the software by using the keyboard, mouse and color display screen of the workstation. Information is presented on the screen, and you select the required function from the displayed menus and dialogs.

This document is readily accessible online and provides full instructions about the system and describes the purpose of each available function.

Note: *Certain functions described in this manual may not have been installed on your system but are available as optional features. Consult the Sales Department of your Elekta® office for further details.*

3.1.3 Description of Leksell Gamma Knife®

Having ascertained the target it is necessary for a physician to devise an appropriate treatment plan. Surgery is achieved by delivering a prescribed dose as one or more shots of ionizing radiation to the exact position of the lesion.

In this manual six (6) types of Leksell Gamma Knife® are mentioned:

- Leksell Gamma Knife® Icon™ (not illustrated)
- Leksell Gamma Knife® Perfexion™, see **Figure 3.1** on page 36
- Leksell Gamma Knife® 4C, see **Figure 3.2** on page 37
- Leksell Gamma Knife® 4 (not illustrated)
- Leksell Gamma Knife® C (not illustrated)
- Leksell Gamma Knife® B (not illustrated).

For more information about each type of Leksell Gamma Knife®, see the respective *Instructions for Use*.

The main characteristic of Leksell Gamma Knife® as a radiosurgical instrument is its simplicity. There are few moving parts, and therefore inherent features are safety, stability, accuracy, reliability, and reproducibility. This radiosurgery technique has proved successful in many years of application. Nevertheless, radiosurgery remains a precise science that requires sophisticated planning which is achieved by the treatment planning application.

When the patient's images have been plotted, the treatment planning application is used as a sophisticated tool for planning radiosurgical treatment with Leksell Gamma Knife®. The software algorithms provide accurate calculations that support the treatment planning phase.

It should be noted that the purpose of the treatment planning application is explicitly to calculate and present the various parameters of a treatment protocol. The software does not have direct control of Leksell Gamma Knife® during radiosurgery.

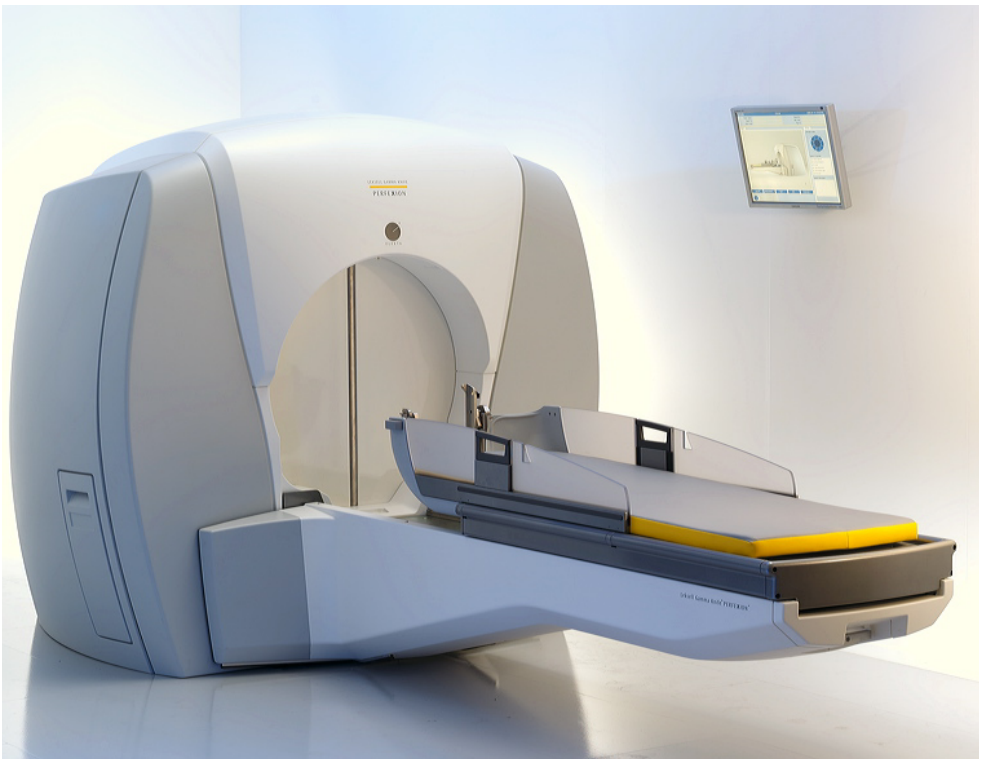


Figure 3.1 Leksell Gamma Knife® Perfexion™

Figure 3.2 Leksell Gamma Knife® 4C

3.1.4 Basis for treatment planning

Detailed graphic images of the patient's head form the basis for treatment planning. The images can be obtained by employing one or more scanning techniques: CT, MR, PET, and/or angiograms (X-ray films).

As part of the imaging process, it is essential to provide exact points of reference by means of which the shape and position of the targets can be ascertained with respect to the patient’s skull. Moreover, during the subsequent radiosurgery session, the head of the patient must be entirely immobilized to maintain the accuracy of the shots.

3.1.4.1 Stereotactic reference

There are two different procedures to get stereotactic reference:

- Use an indicator box during image acquisition
- Use the CBCT (Leksell Gamma Knife® Icon™ only).

Stereotactic reference from indicators

Indicators are available for CT, MR and X-ray imaging. The purpose of the indicator is to impose reference fiducials on the images during image acquisition.

The indicator is mounted on the Leksell® Coordinate Frame or the Extend™ Frame and can not be used separately.

For more information about indicators, refer to *Leksell Stereotactic System®, Instructions for Use*.

Related Links:

Alignment of tomographic images on page 57

Tomographic fiducials and fiducial markers on page 59

Stereotactic reference from CBCT

When the CBCT is used for image acquisition, no external reference is necessary. The CBCT is an integrated part of the Leksell Gamma Knife® Icon™ and the whole system is calibrated to use the same spatial reference.

3.1.4.2 Description of the fixation systems

To keep the head of the patient immobilized, the following fixation systems are used:

- Leksell® Coordinate Frame G
- Leksell® Vantage™ Head Frame
- Mask fixation setup.

Note: *Support for Extend™ Frame System is discontinued. Functionality related to Extend™ Frame System is only included in this manual for the sake of handling patient files with Extend™ Frame System originating from a previous version of the system.*

Description of Leksell® Coordinate Frame G

Leksell® Coordinate Frame G provides the mechanical interface to the docking device of the treatment equipment. It is rectangular with engraved, scaled rulers. It is affixed to the head by means of screws and rigid corner posts and thereby prevents intra-operative coordinate frame displacement.

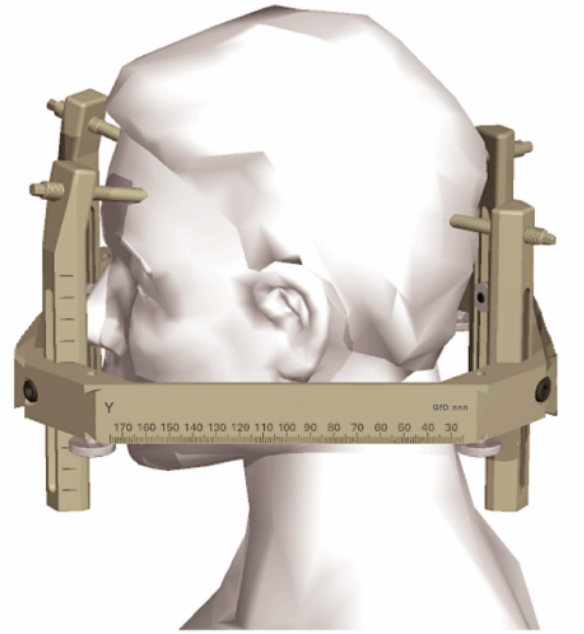


Figure 3.3 Leksell® Coordinate Frame G

Leksell® Coordinate Frame is a component of Leksell Stereotactic System®. See the *Leksell Stereotactic System®, Instructions for use* for more information.

Description of the Leksell® Vantage™ Head Frame

Leksell® Vantage™ Head Frame is the mechanical interface to the docking device of the treatment equipment. It is attached to the patient's head with fixation pins, and thereby prevents intra-operative coordinate frame displacement. The frame has an open space in front of the face area. It has three interface areas on which different tools and accessories are attached.

The frame has eight holes for the fixation pins. Normally the four outer holes are used, but if needed, for example to avoid bone flaps, the inner holes can be used.

Figure 3.4 Leksell® Vantage™ Head Frame attached to the head of the patient

Leksell® Vantage™ Head Frame is a component of Leksell® Vantage™ Stereotactic System. See the *Leksell® Vantage™ Stereotactic System, Instructions for use* for more information.

Description of the mask fixation setup

The mask fixation setup includes a thermoplastic mask, a head cushion and also a mask adapter that provides the mechanical interface to the docking device of the treatment equipment. To provide a fixation, both the mask and the head cushion are carefully shaped after the patient's head and then hardened.

The patient's head can be removed from the fixation and re-fitted at the same position. This means that the mask fixation setup can be used for fractionated treatments over an entire treatment period. The mask fixation is a separately licensed feature.

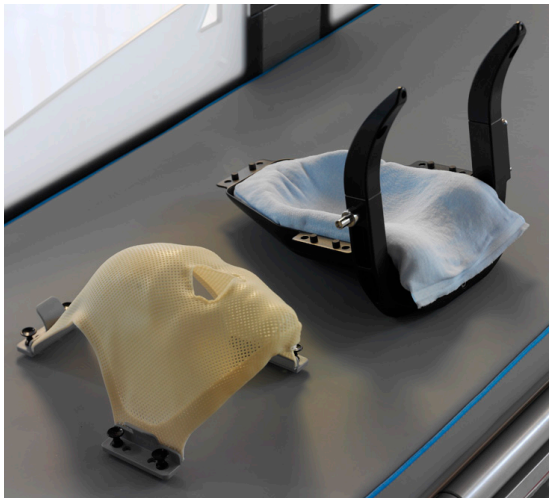


Figure 3.5 Mask fixation setup

For more information about the mask fixation setup, see *Leksell Gamma Knife® Icon™ Instructions for Use*.

3.1.4.3 Description of Leksell® Coordinate System

Leksell® Coordinate Frame is the basis for Leksell Stereotactic System®. The coordinate scales are engraved on Leksell® Coordinate Frame G.

The origo of Leksell® Coordinate System (the point where X, Y and Z are numerically zero) is located outside the coordinate frame at a point that is superior, lateral and posterior to the coordinate frame on the patient's right side. See the figure below, which also shows the left L, right R, posterior P, and anterior A sides of the coordinate frame and patient.

The coordinate scales are graduated in millimeters and conform with the X, Y and Z directions used in CT and MR scanning.

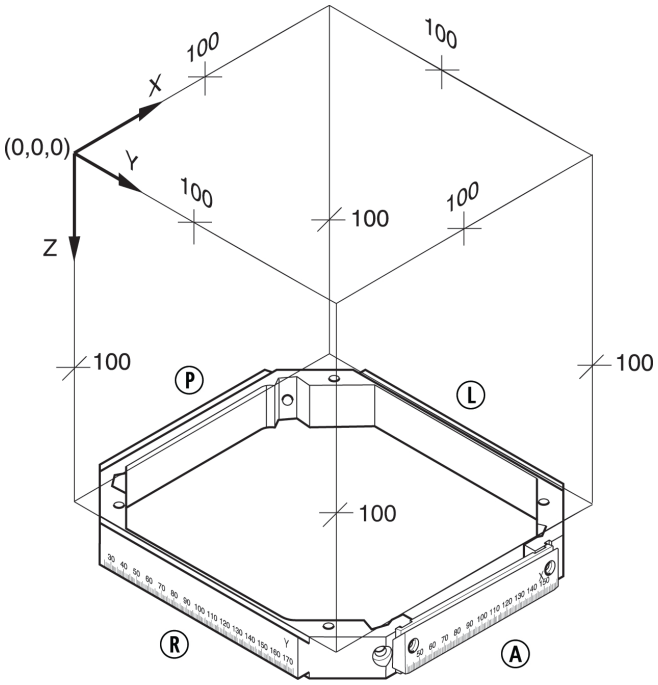


Figure 3.6 Leksell® Coordinate System

3.1.5 Compatibility with MOSAIQ®

Leksell GammaPlan®, as well as Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™, can be connected to MOSAIQ®. The connection allows the LGK treatment system (including Leksell GammaPlan®) to exchange treatment information such as treatment plans, treatment records, protocols etc. with MOSAIQ®, pre and post treatment.

The Treatment Planning System Administrator Tool application is used to configure and test the Leksell GammaPlan® connection to MOSAIQ®.

MOSAIQ® is a dedicated oncology information system that streamlines the entire medical oncology or radiation oncology workflow from the first diagnosis and staging, through planning, treatment and long-term follow-up.

4 Getting started

— Blank page —

4.1 Introductory tasks

4.1.1 Starting and exiting

4.1.1.1 Starting

1 If the workstation is not powered up, switch on peripherals first and then the workstation as described in the workstation user manuals.
2 Enter user name and password when requested.
3 Click on the treatment planning application icon on the Desktop taskbar to start the application.

The treatment planning application desktop opens.

4 Use the menus to access patient files and start treatment planning.

4.1.1.2 Exiting

1 From the **Patient** menu, select **Exit**.

The Exit dialog opens.

2 Confirm in the **Question** dialog box.

All work is automatically saved while working and when exiting the treatment planning application.

4.1.2 Locking the planning session

1 To lock the planning session, choose **Lock Session** from the main menu on the Desktop taskbar or press <CTRL>+<ALT>+<L>.

4.1.3 Logging out

Note: *Make sure the treatment planning application has been exited before logging out.*

1 To log out from the workstation, choose **Logout** from the main menu on the Desktop taskbar or press <CTRL>+<ALT>+<DELETE>.

4.1.4 Shutting down

After exiting the treatment planning application, the workstation remains running.

1 Consult the system administrator before attempting to shut down the system. Other users may be logged in and be using the system.
2 Shut down the primary workstation if and only if all secondary workstations have been shut down.

4.1.5 Unlocking the screen

Besides the system security protocols provided by the operating system, the workstation has an additional security feature. When no keyboard entries or mouse movements have occurred for a period of time, the screen is automatically locked.

In this event the Locked dialog opens and no further activity can take place until you unlock the system.

1 To unlock the screen, type in your password and click **Unlock**.

4.1.6 Setting up user preferences

The treatment planning application allows you to customize certain features to meet your personal requirements. Your choices are loaded automatically when you start the application. You can select the default conditions for radiation shots, the default reference isodose level, round-off values, and other parameters.

By default the treatment planning application operates in the interactive exploration mode. This means that, as you adjust the point-of-exploration in a workspace window, the images in the other workspace windows track this movement and move simultaneously.

1 To open the User Preferences dialog, select **Preferences** in the **Patient** menu.

2 Set up your personal user preferencies.

3 To close the User Preferences dialog and save the changes, click **OK**.

4.2 Understanding the interface

4.2.1 Graphical user interface

A typical treatment planning application display is shown in the figure below.

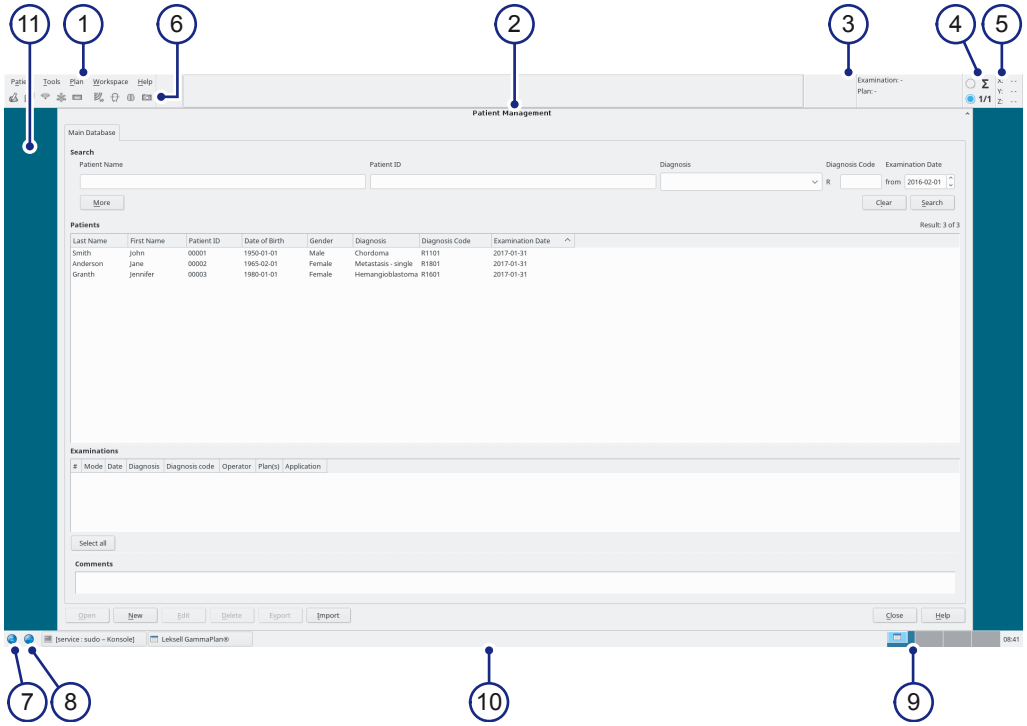


Figure 4.1 Example of a treatment planning application screen with a workspace and an open dialog

(1)	Treatment planning application menu bar	(7)	Desktop menu
(2)	Dialog; Patient Management	(8)	Application icon: Leksell GammaPlan®
(3)	Examination mode	(9)	Desktops available
(4)	Target mode	(10)	Desktop taskbar
(5)	Point-of-Exploration coordinates	(11)	Workspace
(6)	Toolbar		

4.2.1.1 Study icons

The image studies in a patient's file are represented by study icons. A separate icon for each study available in the patient's file appears beside the menu bar when you open the file.

The studies are sorted by date into tabs.

Related Links:

Study icons on page 80

4.2.1.2 Target mode

Target mode is chosen in the treatment planning application menu bar using the radio buttons **Σ** and **1/1** respectively.

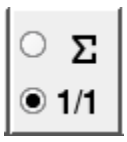


Figure 4.2 Radio buttons for target mode selection

All targets mode - **Σ** - is used when evaluating the total effect of a complete treatment plan, since this reflects the actual total dose that the patient will be exposed to. All shots in all targets will contribute to the isodose curves shown. The dose unit used in All targets mode is absolute dose in Gray (Gy).

When All targets mode is selected, the color of this part of the treatment planning application menu bar changes to yellow.

In **Single target** mode - **1/1** -, only shots from the selected target contribute to the isodose curves shown. The dose unit used in Single target mode is % of the dose in the reference point for the target according to the point dose calculation.

4.2.1.3 Point-of-exploration coordinates

The Point-of-Exploration Coordinates field gives the Leksell® coordinates of the current position of the images. The coordinates change interactively as the point-of-exploration is adjusted.

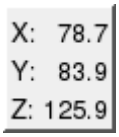


Figure 4.3 The Point-of-Exploration Coordinates field

4.2.1.4 Workspace

Workspaces are the means by which the treatment planning application displays the patient's image studies. A workspace consists of a number of windows containing the different images of the open study. Treatment planning is performed by working with the images in a workspace.

4.2.1.5 Toolbar

The Toolbar provides quick access to certain tools and commands. It is displayed when the program has started up and remains active during the session. The Toolbar contains accelerator buttons which provide a shortcut to certain frequently used commands.

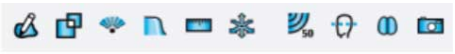


Figure 4.4 Treatment planning application toolbar

Accelerator buttons

The accelerator buttons provide shortcuts to certain frequently used commands. Click on the accelerator button to activate the specified command:


Regions & Volumes button


Target button


Shot button


Dose evaluation button


Clearance button

Measure button

Isodose button: toggles display of isodose curves on and off.

AC-PC alignment button: align images to the AC-PC line.

Brain Atlas button: toggles display of atlas structures on and off.

Snapshot button

4.2.1.6 Dialog controls

Dialogs contain one or more special items known collectively as dialog controls. They are:

- lists
- text fields
- push buttons
- radio buttons
- check boxes
- drop down lists

4.2.1.7 Push buttons

There are a number of push buttons that appear regularly in many dialogs. They have the following general functions:

Apply	Confirms that the contents of a dialog are correct. All settings and entries that you made in the dialog are saved. The dialog is not closed.
Cancel	Closes a dialog without saving any changes that you have made in the dialog.
Close	Closes the dialog. Typically this button is used in an information dialog where there is nothing to be saved.
Delete	Removes a selected object. For example, you can delete a patient file, an image study, a workspace, a region or a volume.
Edit	When you click this button another dialog usually opens to allow you to edit the information as desired.
Help	Opens the Leksell GammaPlan® Online Reference Manual (this document).
New	Used to add a new object to the treatment plan. For example, you can add a new workspace, a volume etc. When you click this button, another dialog usually opens to allow you to name the new object.
OK	Confirms that the contents of a dialog are correct. All settings and entries that you made in the dialog are saved and the dialog is closed.

	This button is also an affirmative response to prompts and other information dialogs.
Print	Initiates the printing of a selected item on hardcopy. Typically this push button allows you to print the patient's treatment protocol, geometric measurements, snapshots etc.

Default push button

One of the push buttons in a dialog is defined as the default button, and you can use the <Return> key on the keyboard to press it.

The default button is recognized by a thicker border than other buttons.

4.2.2 Main Menu

The treatment planning application contains the following menus:

- Patient
- Tools
- Plan
- Workspace
- Help

4.2.2.1 Menu commands

The commands in each menu are grouped according to usage. In the **Plan** menu the commands are listed in the suggested order of execution.

Grayed out commands

Buttons and other features may be grayed out when they are disabled or not applicable, for example, until specific treatment parameters have been set up.

4.2.2.2 Patient menu

The **Patient** menu includes the following alternatives:

- **Patient Management**
- **Import DICOM**
- **Import Examination**
- **Import Log**
- **Request CBCT** (Leksell Gamma Knife® Icon™ only)
  - **Stand Alone**
- **Export Protocol**
- **Export DICOM**
- **Print**
- **DICOM Configuration**
- **Preferences**
- **Exit**

The first step in the treatment planning procedure for a new patient is to create a patient file and enter the patient's demographic and radiological details. Once a patient file has been created you can:

- edit the patient data
- add new radiological examination results to the patient file
- import new image studies into the patient file and delete old ones.

Patient Management

When you choose **Patient Management** in the **Patient** menu, the Patient Management dialog opens.

From here you can:

- create a new patient file
- open an existing patient file
- change an existing patient file
- add new radiological examination data
- delete patient files
- export patient files to a USB mass storage device
- import patient files from a USB mass storage device.

Import DICOM

When you choose **Import DICOM** in the **Patient** menu, the DICOM Import dialog opens.

From this dialog, you can import DICOM images or structure sets pushed from a radiological device (MR, CT, PET scanner, PACS) to the DICOM INBOX.

You can also select the remote DICOM server to import the images or structure sets.

Import Examination

This command opens the Select Examination to Import dialog.

The import examination functionality makes it possible to transfer information, for example images, between radiological examinations for the same patient. The functionality is used when doing re-treatment.

Import log for Leksell Gamma Knife® C, 4 and 4C

Once a treatment is completed, treatment log files can be exported from the operator console of Leksell Gamma Knife® C, 4 and 4C. The log files are automatically imported into the treatment planning application via the serial communications line, or by a USB memory stick.

Related Links:

Import of the treatment log file on page 299

Request CBCT

Select Request CBCT > Stand Alone to request a CBCT scan from Leksell Gamma Knife® Icon™.

Export protocol for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™

The treatment planning application transfers the treatment plan to a treatment plan database common to the treatment planning application and Leksell Gamma Knife®. The database can store any number of treatment plans to be imported and executed by Leksell Gamma Knife®.

When using MOSAIQ® to schedule a treatment and exchange treatment information, the actual treatment plan used for treatment is always the one that is stored in the treatment plan database.

Related Links:

Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™: Exporting the treatment protocol on page 296

Export protocol for Leksell Gamma Knife® C, 4 and 4C

The treatment planning application exports the treatment plan to Leksell Gamma Knife® C, 4 and 4C.

Related Links:

Leksell Gamma Knife® C, 4 and 4C: Exporting the treatment protocol on page 298

Export DICOM

This command allows you to export DICOM RT structure sets and dose from the system.

Print

This command allows you to print:

- protocols
- geometric and statistical measurement data
- patient images
- snapshots of the workspace

DICOM Configuration

This command opens the Configure DICOM Server dialog, where you;

- configure the AET for Leksell GammaPlan® on the specific workstation
- add/edit/delete external DICOM server entries
- set the external DICOM server to use by default in the Import DICOM dialog.

If the workstation AET has not been configured it will not be possible to modify the list of external DICOM servers or to import from or export to remote DICOM servers.

Related Links:

DICOM server configuration on page 302

Preferences

The treatment planning application allows customization of certain features to meet personal requirements. The chosen preferences are loaded automatically when you log in.

Related Links:

Setting up user preferences on page 44

Exit

The **Exit** command closes the treatment planning application and saves all data.

4.2.2.3 Tools menu

From the **Tools** menu you can:

- create and manipulate anatomical volumes and the regions within them
- perform geometric and dosimetric measurements
- take digital snapshots of the display screen
- define the patient's skull boundary by grayscale segmentation
- check for clearance between the coordinate frame and the Leksell Gamma Knife® parts
- create blank image studies for lesion projection from other images
- enter Treatment mode

The **Tools** menu includes the following alternatives:

- **Volumes**
- **Measure**
- **Dose Evaluation**
- **Snapshot**
- **Segment**
- **Clearance**
- **Create Study**
- **Treatment Mode**

Volumes

This command allows you to delineate volumes of interest. An image study must first be defined and displayed in a workspace before regions of interest can be created or changed.

Volumes can be denoted as:

- the target
- an area of high risk
- an anatomical object

all of which can be visualized during treatment planning.

You can also measure the size of a volume by using the **Measure** command in the **Tools** menu.

When working with volumes you can:

- add a new volume to the patient's image studies
- draw the regions of interest within a volume – can be done manually or semi-automatically
- adjust the regions of interest within existing volumes
- delete regions of interest from a volume
- adjust the parameters of existing volumes
- delete volumes from the patient's image studies.

Related Links:

Regions and volumes on page 154

Measure

The measurement tools are used to perform dose and geometric measurements of volumes, lines, and points.

Related Links:

Performing measurements on page 270

Dose Evaluation

Use the **Dose Evaluation** tool to review the planned dose.

Related Links:

Dose Evaluation on page 279

Snapshot

The **Snapshot** feature allows you to capture snapshots of the computer screen with its open workspace. The snapshots are stored with the patient file and can be viewed, printed and saved to a USB device.

Related Links:

Printing snapshots on page 288

Snapshots on page 300

Segment

The **Segment** tool is used to adjust the image grayscale threshold so that the boundary of the patient's skull becomes clearly visible in all 3D views of the open images. This is particularly useful for enhancing Cut Box images.

Related Links:

Segmenting the skull for visualization in 3D-views on page 142

Clearance for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™

The treatment planning application does not allow to place a shot at a position that does not have clearance between the fixation or the patient's head and the radiation unit.

Related Links:

Clearance on page 237

Clearance for Leksell Gamma Knife® B, C, 4 and 4C

Before approving a treatment plan, perform a check to identify shot positions that may not have clearance between the collimator helmet and the coordinate frame, posts and screws or the patient's skull.

Create Study

For tomographic image studies, the program reconstructs two image studies in the other directions. For example, if the original study is axial, the program reconstructs image studies in the coronal and sagittal directions also.

If a patient file has angiographic image studies only, you can create a blank tomographic study into which certain graphics can be projected and examined in three dimensions. The blank study consists of 200 axial images spaced at intervals of 1 mm apart. The **Create Study** command is

used to obtain coronal, sagittal and axial reconstructions of an empty image stack of angiographic images.

By using the blank study you can explore the target, volumes, and the isodose contours of the irradiation scheme in the third dimension against a black background. In most cases, reconstructed image studies can be used for treatment planning in the same way as the original study, but there are some restrictions. It is not possible to pre-plan or to enter treatment mode without an original tomographic image study.

Related Links:

Creating a blank study on page 141

Treatment Mode

During a Leksell Gamma Knife® Icon™ treatment, you can do the treatment delivery evaluation only if Leksell GammaPlan® is in treatment mode.

Related Links:

Treatment delivery evaluation for Leksell Gamma Knife® Icon™ on page 268

4.2.2.4 Plan menu

The **Plan** menu commands are the main tools for treatment planning. Here you set up and arrange the shots for the treatment plan. You also enter details of the patient's skull shape, the coordinate frame configuration, position the target, select the target prescription dose and plot isodose contours.

For Leksell Gamma Knife® B, C, 4 and 4C, you can also arrange the plugging and set up the treatment.

The **Plan** menu includes the following alternatives:

- **Fixation configuration**
- **Skull definition**
  - **Images**
  - **Measurements**
  - **Simulated skull**
- **Electron Density**
- **New Plan**
- **Copy Plan**
- **Edit Plan**
- **Plans**
- **AC-PC Line**
- **Brain Atlas**
- **Functional Targets**
- **Target**
- **Isodose**
- **Shot**
- **Shot Summary**
- **Plug**, Leksell Gamma Knife® B, C, 4 and 4C only

- **Setup Treatment**, Leksell Gamma Knife® C, 4 and 4C only
- **Approve**
- **Re-plan**

Fixation configuration

Depending on Leksell Gamma Knife® model, there are different fixations available for use:

- Leksell® Coordinate Frame G, available for all models
- Leksell® Vantage™ Head Frame, available for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™
- Mask, only available for Leksell Gamma Knife® Icon™.

Note: *Support for Extend™ Frame System is discontinued. Functionality related to Extend™ Frame System is only included in this manual for the sake of handling patient files with Extend™ Frame System originating from a previous version of the system.*

Skull definition

There are three ways to define the patient's skull shape: using simulated values; using the skull scaling instrument and manually entering measured values; or using CT or MR image segmentation. CT or MR image segmentation is required when planning a treatment using mask fixation.

Electron Density

This command allows you to define the Electron Density to be used for calculating dose using the Convolution dose algorithm by selecting a CT image study.

New Plan

This command allows you to create a new treatment plan.

Copy Plan

This command allows you to copy an existing plan and modify it to create a new treatment plan.

Edit Plan

This command allows you to edit an existing treatment plan.

Plans

This command opens an overview of all plans in the examination. Here you can create, edit, copy, and delete plans.

AC-PC Line

This command allows you to place the anterior and posterior commisures. The AC-PC line formed by the anterior and posterior commisures can then be used to place functional targets.

Brain Atlas

This command allows you to define an atlas registration and handle atlas structures in the views.

Functional Targets

This command allows you to define functional targets based on the AC-PC line.

Target

To be able to create an irradiation scheme for a lesion you need to use the Target dialog to add a target covering that lesion. A target defines a cube where shots can be placed. The Target dialog is also used to prescribe dose to lesion(s) inside the target cube.

Isodose

Isodose contours represent the sum dose distribution resulting from all shot placements. You can select the isodose contours that you want to display, and update them.

Shot

You use the **Shot** command to create the patient's irradiation scheme on images.

Related Links:

Creation of the irradiation scheme on page 205

Shot Summary

The Shot Summary dialog shows an overview of the shots and their parameters.

Plug

This feature is only valid for Leksell Gamma Knife® B, C, 4 and 4C.

Create plug patterns for shots to protect critical anatomical structures.

Related Links:

Protection of critical structures using plug patterns on page 230

Setup Treatment

This feature is only valid for Leksell Gamma Knife® C, 4 and 4C.

Setup treatment data comprises the process of preparing the treatment data for printing and exporting. Shots are automatically organized into runs suitable for treatment with or without the automatic positioning system. The shot attributes can also be adjusted manually.

Approve

Approve the selected treatment plan.

Related Links:

Approving a treatment plan on page 250

Re-plan

This feature is available if the treatment plan is in Approved, Printed, or Exported state.

To re-plan a treatment plan, select **Re-plan**.

4.2.2.5 Workspace menu

The treatment planning application is supplied with certain predefined workspaces that will accommodate most treatment planning requirements:

- **Standard**
- **Multi Target**
- **Multi Poster**
- **Cut View**
- **Angio**
- **Print**

It is possible to create custom workspace layouts to satisfy individual preferences for image display and manipulation, or to meet the needs of a particular patient. The created workspaces will be available for other users too.

In addition to the predefined workspaces mentioned above, the Workspace menu includes the following alternatives:

- **Edit**
- **Clear**

The **Edit** alternative opens a dialog allowing modification of existing workspaces and creation of new workspaces.

The **Clear** command closes any open workspace.

Related Links:

Creating workspaces on page 144

4.2.2.6 Help menu

The **Help** menu contains the following two items:

- **On Application**
- **On Version**

On Application opens the Online Reference Manual, and **On Version** displays the version of the treatment planning application.

4.2.3 Tomographic images

Treatment planning in the treatment planning application is achieved by working with computerized images of the patient's skull. Tomographic images are acquired by taking MR and/or CT scans of the brain, resulting in digital images that can be imported into, and manipulated by, the program.

4.2.3.1 Image directions

The field of view of one tomographic image is known as a slice. Each image represents a slice of the patient's brain acquired from a single MR or CT scan. A complete examination of the patient's brain is made possible by taking a series of slices, one above the other (or side-by-side).

Image slices have depth (thickness) and are taken at certain intervals along the axis perpendicular to the image plane. Image depth and the intervals between images are determined during the scanning process.

All the slices in a set of sequential images acquired during MR or CT scanning are always taken in the same direction with respect to the patient's skull.

For MR images any one of three directions is commonly used:

- sagittal
- coronal
- axial.

CT scanners most commonly produce only axial images. However, some may also produce sagittal and coronal images.

Image orientations

When an image is displayed in a workspace, its orientation with respect to the patient's position is always indicated by two green letters. One letter appears at the top of the image and the other letter is on the left side of the image:

- R indicates the patient's right side
- A indicates the patient's anterior
- S indicates the patient's superior

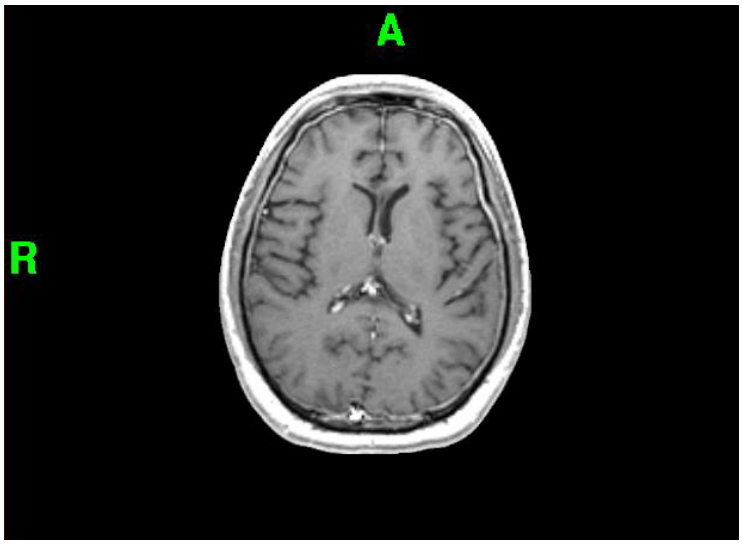


Figure 4.5 Orientation indicators on an axial image

4.2.4 Tomographic image acquisition using indicator box

Leksell Stereotactic System® includes an attachment that fits to the bed of the scanner. This supports the patient's head, holds the coordinate frame firmly in place and minimizes inadvertent movement of the head during MR and/or CT scanning.

Refer to *Leksell Stereotactic System®, Instructions for Use* for details of the scanner attachments.

WARNING 4.1

When acquiring CT images you must ensure that there is no gantry tilt. Images with gantry tilt must not be used for treatment planning with the treatment planning application or subsequent Leksell Gamma Knife® surgery.

WARNING 4.2

When acquiring tomographic images you must ensure that the images are equidistant. Non-equidistant images must not be used for treatment planning with the treatment planning application or subsequent Leksell Gamma Knife® surgery.

4.2.4.1 Alignment of tomographic images

A special MR or CT indicator box must be attached to the coordinate frame prior to scanning. The purpose of the indicator is to impose the fiducials on to the acquired images. The fiducials are subsequently used to define the images within the treatment planning application.

Tomographic indicator box

A CT indicator box for a Leksell® Coordinate Frame G treatment has a Z-shaped fiducial (F) frame embedded within each panel. The fiducial frames are manufactured from a high contrast copper material. This is illustrated in **Figure 4.6**.

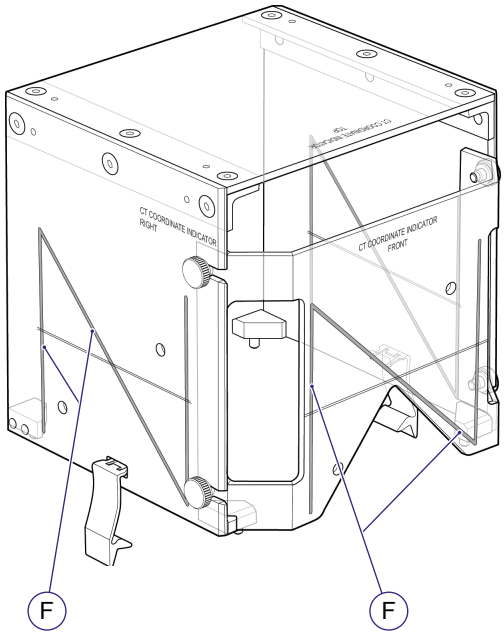


Figure 4.6 CT Indicator box

The design of an MR Indicator box for a Leksell® Coordinate Frame G treatment is different from that of a CT indicator box to accommodate the requirements of the imaging process.

In MR Indicator boxes the fiducials (F) consist of a Z-shaped cavity filled with copper sulfate. This is illustrated in **Figure 4.7**.

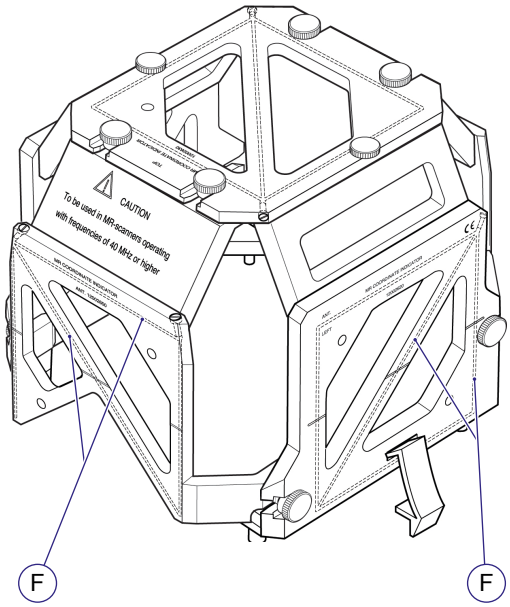


Figure 4.7 MR Indicator box

The coordinates provided by the fiducials can be determined manually or automatically by the treatment planning application. This is known as defining the images. Refer to the Leksell Stereotactic System®, *Instructions for Use*.

4.2.4.2 Tomographic fiducials and fiducial markers

Tomographic image studies consist of images that were acquired with the aid of Leksell Stereotactic System®. The images in these studies include the fiducials that were imposed on the images during tomographic scanning. They appear as white dots on the image.

For the purposes of study definition, the treatment planning application superimposes at least two sets of fiducial markers on the images. Each set consists of three red circles linked by a dotted red line. There is a fiducial marker (red circle) corresponding to each fiducial (white dot).

If a third set of fiducials was included on the images during scanning, you can add another set of fiducial markers horizontally across the top of the image. This set of fiducial markers is known as the third plate.

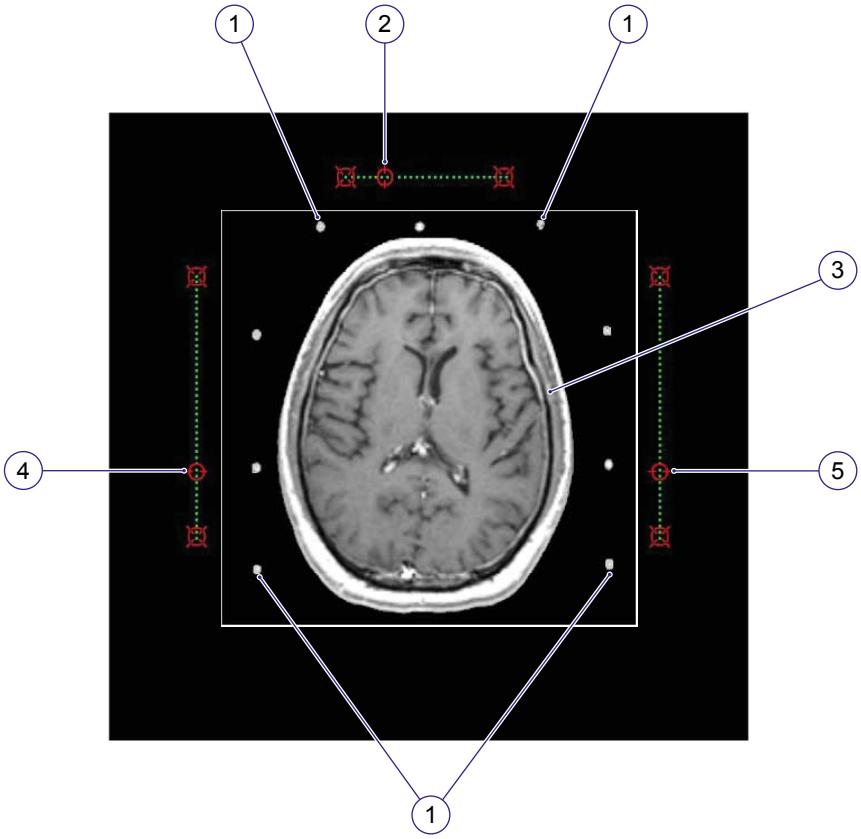


Figure 4.8 Tomographic Fiducials and Markers

(1) Fiducials
(2) Third plate markers
(3) Image
(4) Right fiducial markers
(5) Left fiducial markers

4.2.4.3 Image sources for stereotactic localization

Care must be taken when determining coordinates since individual imaging sources may be subject to geometrical distortion. The nature of the distortion and the likelihood of its occurrence depend upon the type of image source that has been used and how it was set up. In any event you must measure and verify potential distortion to ensure that they are within acceptable limits.

Tomographic image distortion

Magnetic resonance imaging produces images by coding static and time-varying electromagnetic fields within the head of the patient. The magnetic fields are not subject to linear measurement

and therefore some geometric distortion of the image may occur. Geometric distortion of as much as 5 mm have been observed in certain systems.

Distortion in MR images may also result from:

- the direction and position of the slice
- different pulse sequences
- the different magnetic susceptibilities of individual patients
- the magnetic signature of the scanner environment.

You must also give consideration to the presence of magnetic objects such as surgical clips or implanted devices. These can cause further distortion up to a range of 1 cm.

WARNING 4.3

As a fundamental design requirement the treatment planning application never corrects, or attempts to correct, distortions in the patient's images.

WARNING 4.4

To minimize the likelihood of distortion in magnetic resonance images it is imperative that operational units should devise and maintain standard procedures for stereotactic localization.

The geometrical distortions inherent in the procedures should be measured with a water phantom and periodically recorded in order to ascertain that such distortions remain within acceptable tolerance limits.

It is important also that only non-magnetic materials are used with MR imaging and it is strongly recommended that only parts provided by the coordinate frame manufacturer are used for stereotactic MR imaging procedures.

4.2.4.4 Acquiring MR and CT images

The exact procedure for acquiring MR and CT images depends upon the type of scanner in use. The following guidelines are offered for consideration when acquiring MR or CT images for the treatment planning application. These statements must be read in conjunction with the instructions provided by the manufacturer of the scanner and are not intended to replace, supersede or overrule any such information.

1 If Leksell® Coordinate Frame and the associated MR Indicator or CT Indicator are in use, ensure that the coordinate frame has been correctly applied to the patient and that the indicator is properly attached to the coordinate frame.

Instructions on fitting the instrument are given in the *Leksell Stereotactic System®, Instructions for Use*.

2 If the MR or CT scanner attachment is in use, ensure that the attachment has been correctly fitted to the bed of the scanner and that, when introducing the patient, the coordinate frame is properly secured to the scanner attachment.

Instructions are provided in the *Leksell Stereotactic System®, Instructions for Use*.

3 Always ensure that all fiducials are included on the scanned images.

4 Always ensure that the images in a study are taken at a slice thickness sufficient to support subsequent treatment planning and surgery:

a The thickness of the image slices must be such that all areas of anatomical and diagnostic interest are included with sufficient detail in the image studies.

b The thickness of the image slices and the distance between slices should be the same.

5 Always adhere to the operating instructions and observe all hazard notices provided by the manufacturer of the scanner.

4.2.5 Tomographic image acquisition using Leksell Gamma Knife® Icon™ CBCT

This section is valid only for Leksell Gamma Knife® Icon™.

With Leksell Gamma Knife® Icon™, you can acquire stereotactic CT images using Cone Beam Computerized Tomography (CBCT). The CBCT scanner is an integrated part of Leksell Gamma Knife® Icon™ and the whole system is calibrated to use the same spatial reference. Therefore, no external references such as fiducials are needed.

4.2.6 Angiographic images

As well as tomographic images, the treatment planning application commonly utilizes angiographic images for treatment planning. They are particularly useful for visualizing the cardio-vascular system within the brain.

Note: *Angiographic images cannot be used in a treatment plan for the mask fixation setup.*

Angiographic images are also acquired by using Leksell® Coordinate Frame with a special AI indicator attached. This imposes the inner and outer fiducials necessary for subsequent image definition in the treatment planning application.

The fiducials are made of high-density material that is clearly visible on angiograms. Each plate has four fiducials shaped as either crosses or plus signs. A fifth fiducial is placed on the patient's left on the frontal plate and on the patient's anterior on the left plate, see figure below. These extra fiducials show the direction in which the image was taken.

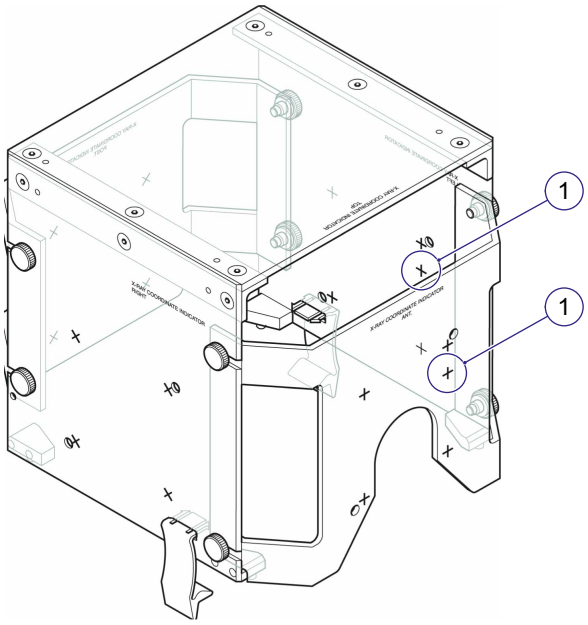


Figure 4.9 X-ray indicator with markers

(1) Extra fiducial markers

Note: *As can be seen in the figure, indicator box plates have either plus sign fiducials or cross fiducials.*

4.2.6.1 Angiographic projections

Angiographic images are projections through the entire skull in one direction – as distinct from single tomographic image slices which have thickness. Images may be acquired using film, image intensifier or flat detector systems.

Two basic angiographic projections are used:

- frontal – corresponds to the coronal slice direction of tomographic images
- lateral – corresponds to the sagittal slice direction of tomographic images.

Each projection can be acquired with the x-ray tube on each side of the patient:

- frontal: anterior and posterior x-ray tube position
- lateral: right and left x-ray tube position.

Among these four acquisitions, radiological units are most often configured with the x-ray tube:

- on the patient’s right side on the lateral stand
- on the patient's posterior side on the frontal stand.

Producing images with the x-ray tube on the patient’s left side is atypical, and doing it with the x-ray tube on the patient’s anterior side is extremely unusual.

4.2.6.2 Image visualization requirements

Since an acquired image can be viewed from both sides, the visualization requirements below must be fulfilled and verified when defining images.

The application must display:

- frontal projections from the patient’s anterior side (patient’s left side to the right)
- lateral projections from the patient’s left (patient’s anterior/nose to the left).

With digital images, the orientation is determined by the radiological software.

Use anatomical structures or a lead marker to differentiate frontal projections from lateral projections.

WARNING 4.5

If the patient orientation cannot be extracted from the image when importing angiographic images, the treatment planning application will assume that the image has standard orientation. For frontal images, the application assumes that the patient's left is to the right in the image and the patient's superior is up in the image. For lateral images the assumption is that the patient's anterior is to the left and the patient's superior is up in the image.

4.2.6.3 Usual acquisitions

Frontal projection, anterior film

The x-ray source is at the patient’s posterior and the film at the patient’s anterior:

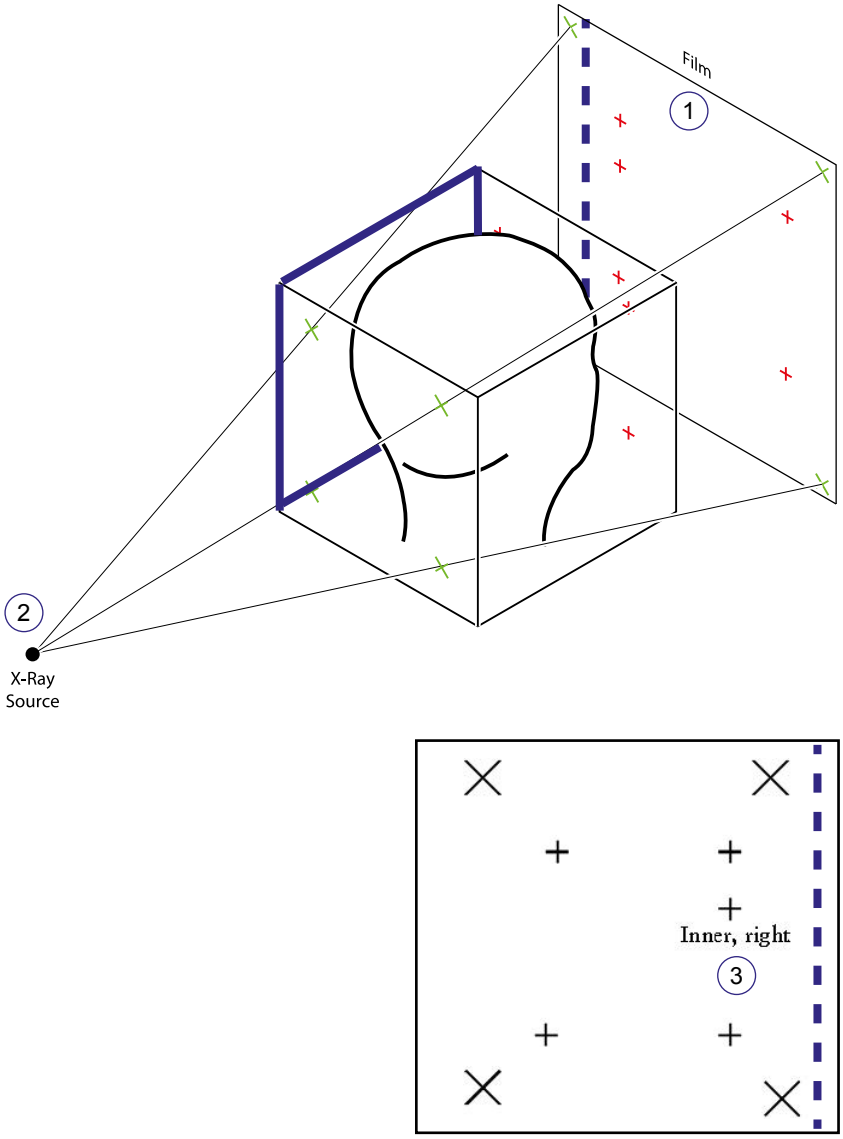


Figure 4.10 Frontal angiographic projection using anterior film

(1) Film

(2) X-Ray Source

(3) Inner, right

Note: *During definition, check that patient's left side is to the right and that the extra fiducial is to the right and aligned with the inner fiducials!*

Lateral projection, left film

The x-ray source is at the patient's right and the film at the patient's left:

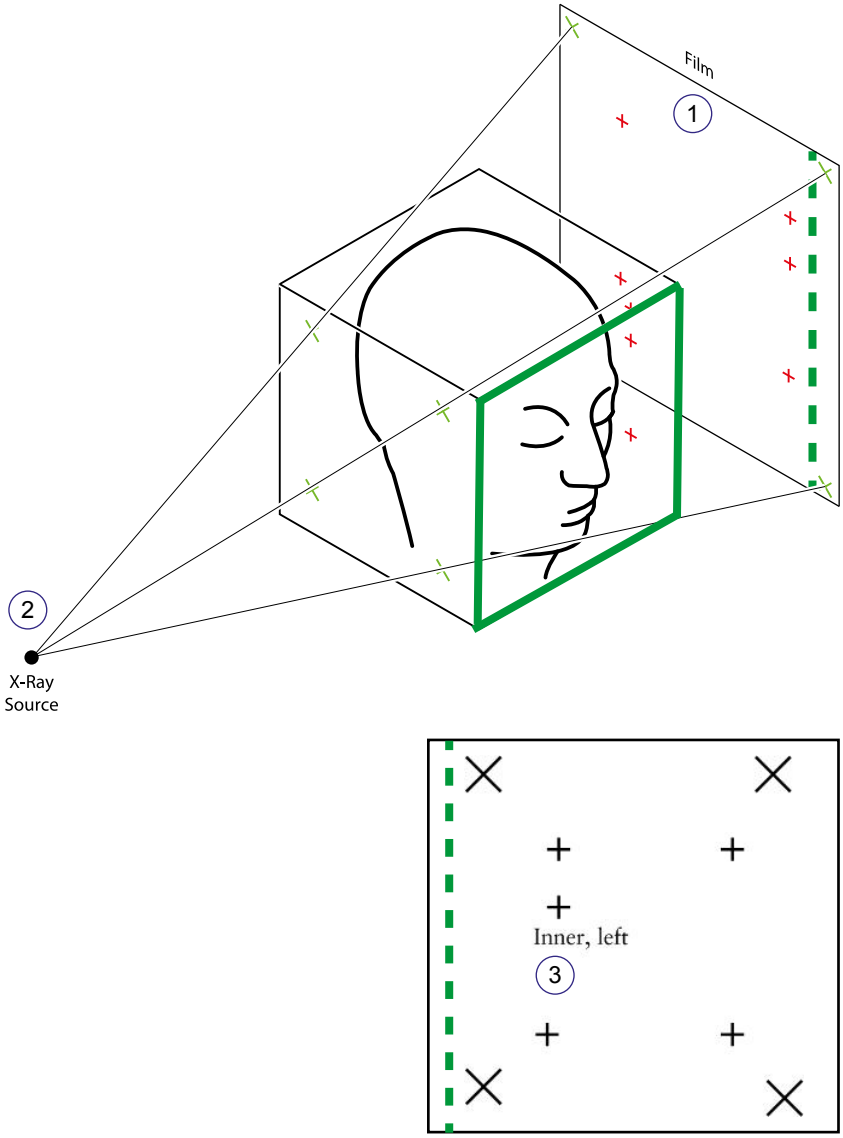


Figure 4.11 Lateral angiographic projection using left film

(1) Film

(2) X-Ray Source

(3) Inner, left

Note: *During definition, check that patient's anterior (or nose) is to the left and that the extra fiducial is to the left and aligned with the inner fiducials!*

4.2.6.4 Less common acquisitions

Frontal projection, posterior Film

The x-ray source is at the patient's anterior and the film is at the patient's posterior:

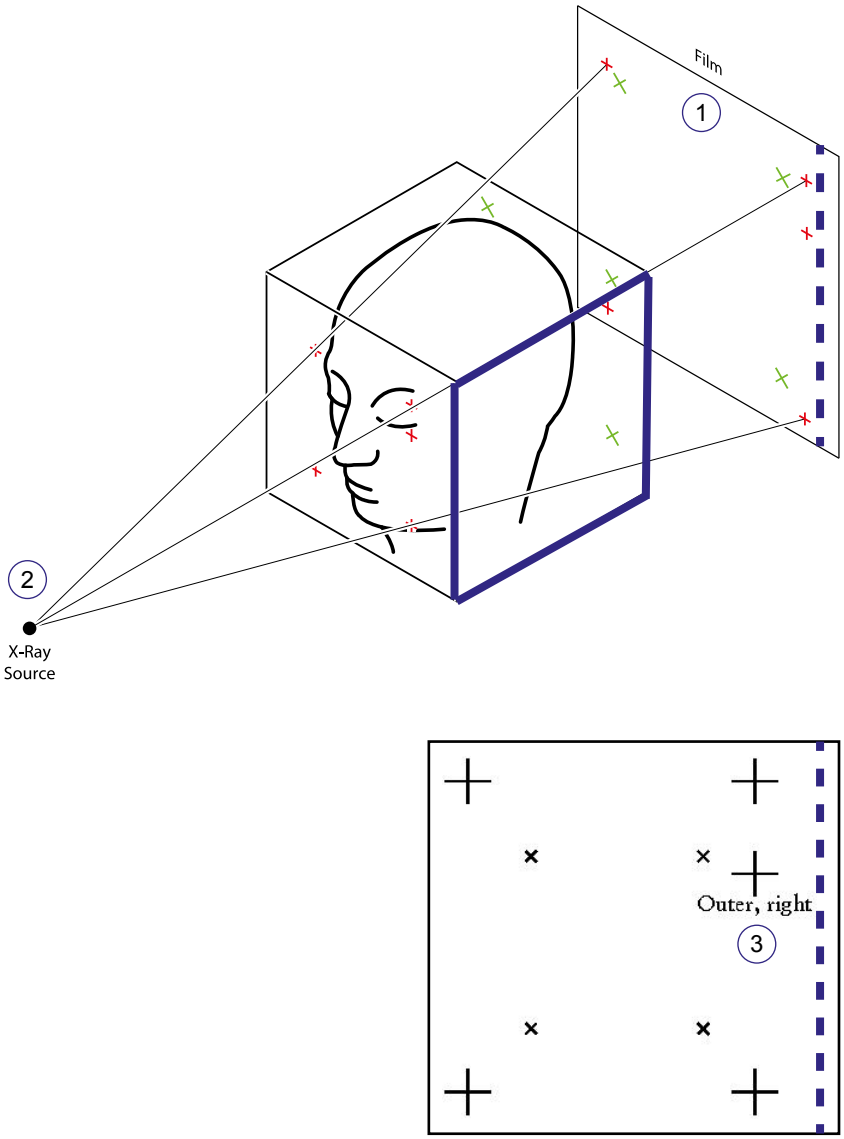


Figure 4.12 Frontal angiographic projection using posterior film

(1) Film

(2) X-Ray Source

(3) Outer, right

Note: *During definition, check that patient's left side is to the right and that the extra fiducial is to the right and aligned with the outer fiducials!*

Lateral projection, Right Film

The x-ray source is at the patient's left and the film at the patient's right:

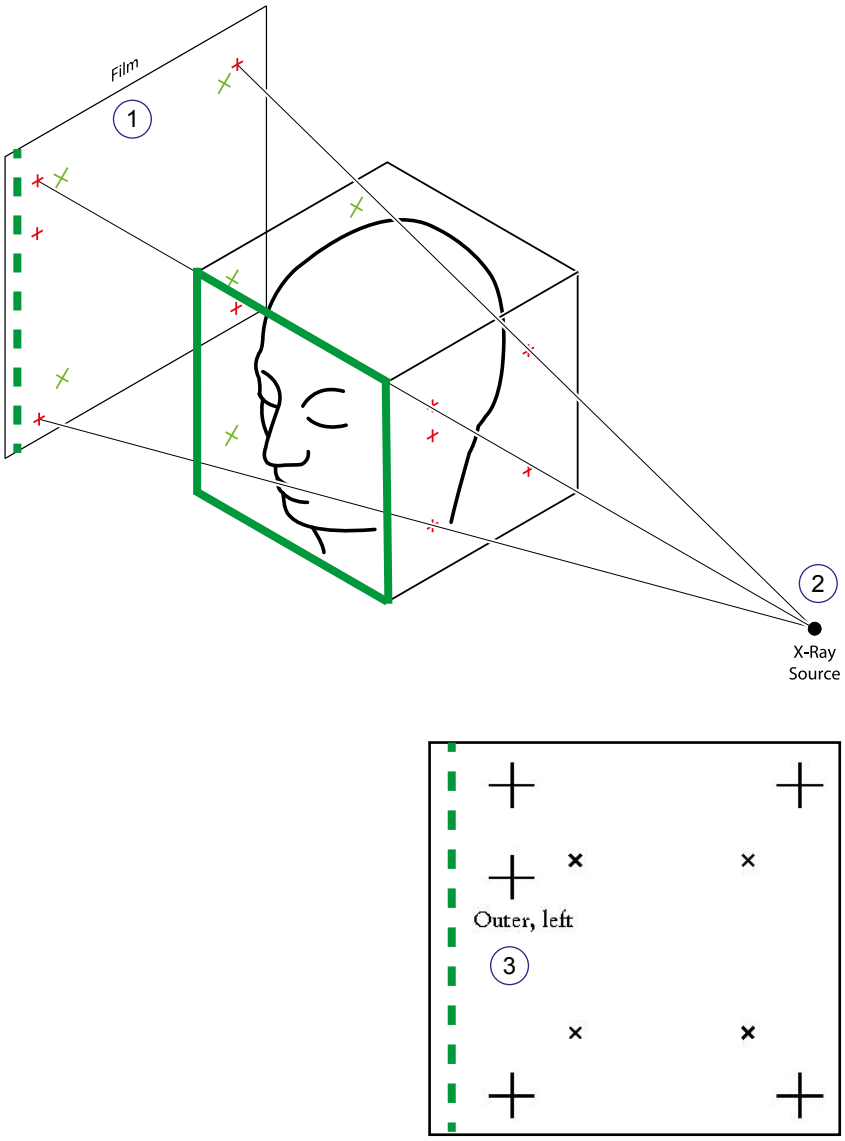


Figure 4.13 Lateral angiographic projection using right film

(1) Film

(2) X-Ray Source

(3) Outer, left

Note: *During definition, check that patient's anterior (or nose) is to the left and that the extra fiducial is to the left and aligned with the outer fiducials!*

4.2.6.5 Example of incorrect visualization orientation: flipped image

An image is defined as flipped if the visualization requirements are not respected. If information about the patient orientation is not included in the digital image header, flipped images could accidentally be defined in an incorrect orientation (lateral instead of frontal or vice-versa). This issue must be avoided by checking the image orientation based on anatomical structures or orientation markers.

A flipped image of a **frontal projection, posterior film** may in theory be incorrectly defined as a **lateral projection, right film:**

WARNING 4.6

To avoid mistreatment by the use of flipped images, always make sure that imported images have the correct orientation. Also be careful never to define frontal images as lateral or lateral images as frontal.

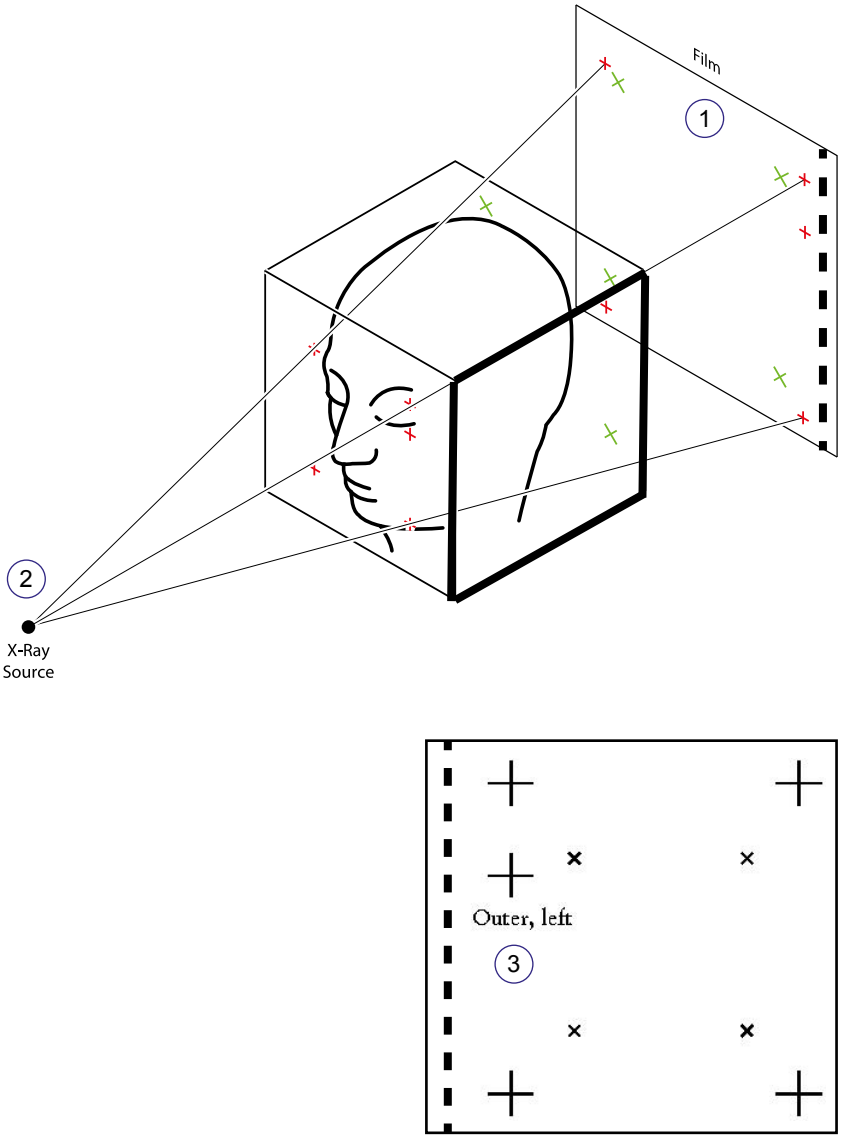


Figure 4.14 The flipped frontal projection could be erroneously defined as a lateral projection

(1) Film

(2) X-Ray Source

(3) Outer, left

4.2.6.6 Observation conventions

As can be seen in the figures, the convention is to look at frontal projections from the patient's anterior side, whether the film is anterior or posterior. By the same convention, lateral projections are looked at from the patients left.

As an example, the angiographic fiducial system for a frontal projection is shown below.

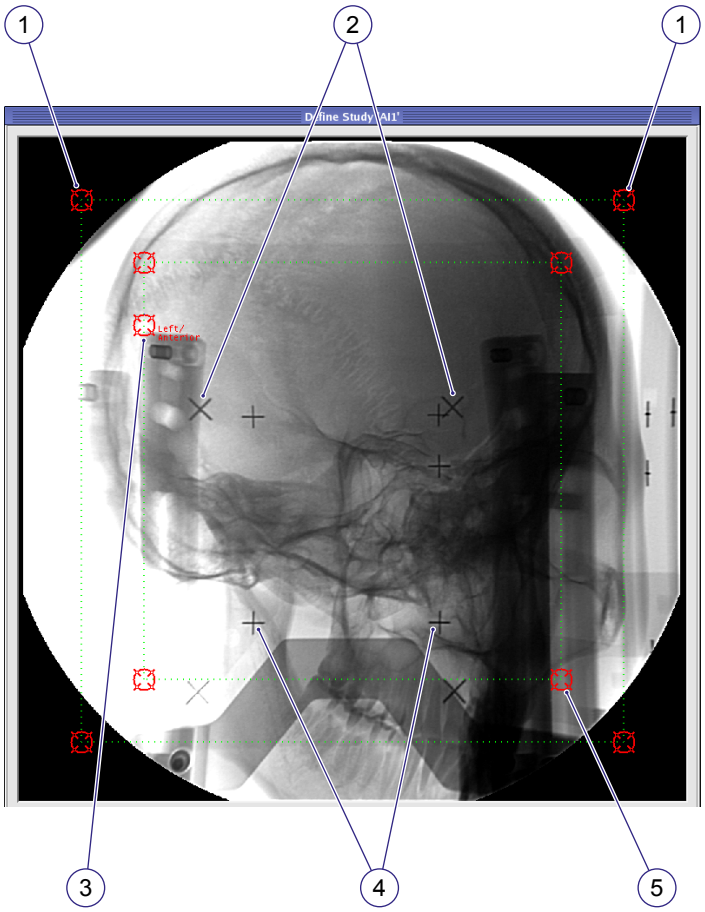


Figure 4.15 Angiographic fiducials and markers

(1) Outer Fiducial Marker

(2) Outer Fiducials (nearest x-ray source)

(3) Patient's Positional Marker

(4) Inner Fiducials (furthest from x-ray source)

(5) Inner Fiducial Marker

4.2.6.7 Acquiring angiographic images

The exact procedure for acquiring angiographic images depends upon the type of radiological equipment in use. The following guidelines are offered for consideration when acquiring angiographic images for the treatment planning application. These statements must be read in conjunction with the instructions provided by the manufacturer of the radiological equipment and are not intended to replace, supersede or overrule any such information.

Note: *Multi-frame angiographic images are not supported by the treatment planning application.*

1 If Leksell® Coordinate Frame and the associated AI Indicator are in use, ensure that the coordinate frame has been correctly applied to the patient and that the indicator is properly attached to the coordinate frame.

   Instructions on fitting the instrument is given in the series of handbooks for Leksell Stereotactic System®.

2 If the AI equipment attachment is in use, ensure that the attachment has been correctly fitted to the bed of the equipment and that, when introducing the patient, the coordinate frame is properly secured to the AI equipment attachment.

   Instructions are provided in the series of handbooks for Leksell Stereotactic System®.

3 Always ensure that all fiducials are included on the acquired images.

4 It is advisable to position the AI indicator perpendicular to the source to detector direction.

5 It is advisable to use lead marker to differentiate frontal from lateral projections.

6 Always adhere to the operating instructions and observe all hazard notices provided by the manufacturer of the scanner.

4.2.7 Digital subtraction angiograms

The distortion resulting from digital subtraction angiograms (DSA) primarily derives from the image intensifier and the video system.

If subtracted angiograms are to be used, to avoid subtraction of the fiducials it may be necessary to amplify them by moving the mask a few pixels (pixel shift).

WARNING 4.7

It is strongly recommended that only clinically distortion-free images should be used for stereotactic therapeutic applications such as Leksell Gamma Knife® surgery.

4.2.8 Conventional X-ray and angiography

Distortion should not result from direct projection of the coordinate frame markers to x-ray film. However, source to surface distances (SSD) and magnification ratios should be taken into account when determining the precision of the markers.

WARNING 4.8

A poorly-defined lesion can result in a wholly inaccurate treatment plan.

To achieve the highest accuracy, always ensure that the outline of the lesion is clearly visible on the frontal and lateral AI images before importing them into the treatment planning application.

4.2.9 Image studies

When you create a new patient file, the sets of digital images that you import into the treatment planning application are stored in an image repository. The images for the patient are accessed from the repository when you open the patient's file.

An image study in the treatment planning application consists of a set of tomographic images or a single angiographic image. Imported tomographic images originating from one DICOM image

series must have the same orientation (sagittal, coronal or axial), and are sorted in the direction perpendicular to the image plane (X, Y or Z).

4.2.9.1 Image coordinates

To ensure accurate computer processing and subsequent treatment planning, the treatment planning application must compile the images of a study in their correct sequence. For this purpose each image is identified in terms of its Leksell® coordinate value.

The figure below shows the way in which Leksell® stereotactic coordinates are imposed on an image study. The point-of-origin of the Leksell® coordinates is superior/ right/posterior with respect to the patient. At this point in stereotactic space, the X, Y, and Z coordinates all have the value 0 mm.

An image study need not be exactly aligned with the Leksell® coordinates. As a result of the image definition phase, the treatment planning application calculates the orientation of the image study.

For each image in a study, the program calculates and displays the slice position, which is defined as follows:

- Sagittal study: Leksell® X coordinate of the image center
- Coronal study: Leksell® Y coordinate of the image center
- Axial study: Leksell® Z coordinate of the image center

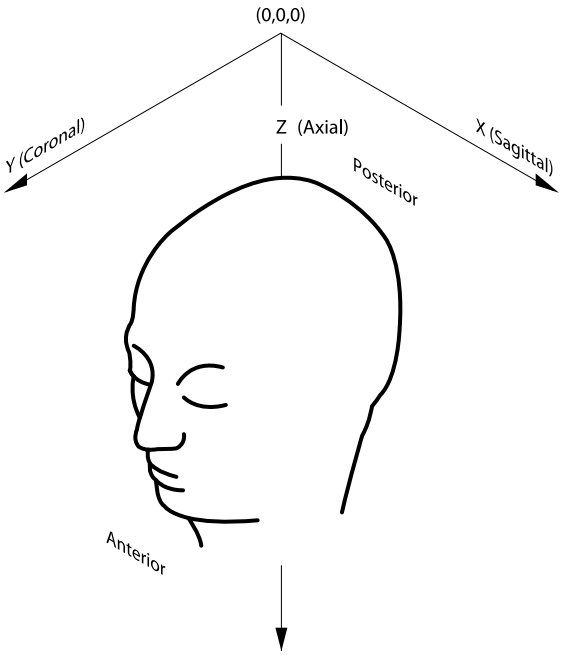


Figure 4.16 Image study with Leksell® Stereotactic Coordinates imposed

Sagittal images

Each image in a sagittal study is identified by the Leksell® X coordinate of the central point in the image. The X coordinate value of a sagittal image increases as the image slice is positioned further away from the Leksell® point-of-origin towards the patient's left side, along the X axis.

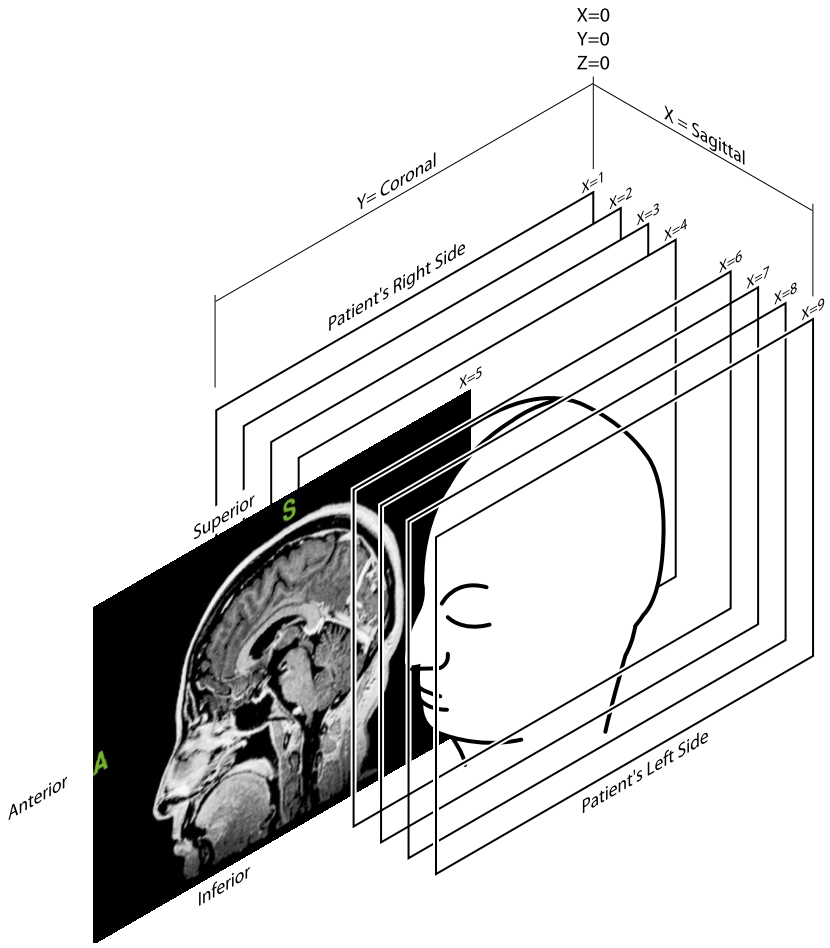


Figure 4.17 Sagittal image coordinates

Coronal images

Each image in a coronal study is identified by the Leksell® Y coordinate of the central point in the image. The Y coordinate value of a coronal image increases as the image slice is positioned further away from the Leksell® point-of-origin towards the patient's anterior, along the Y axis.

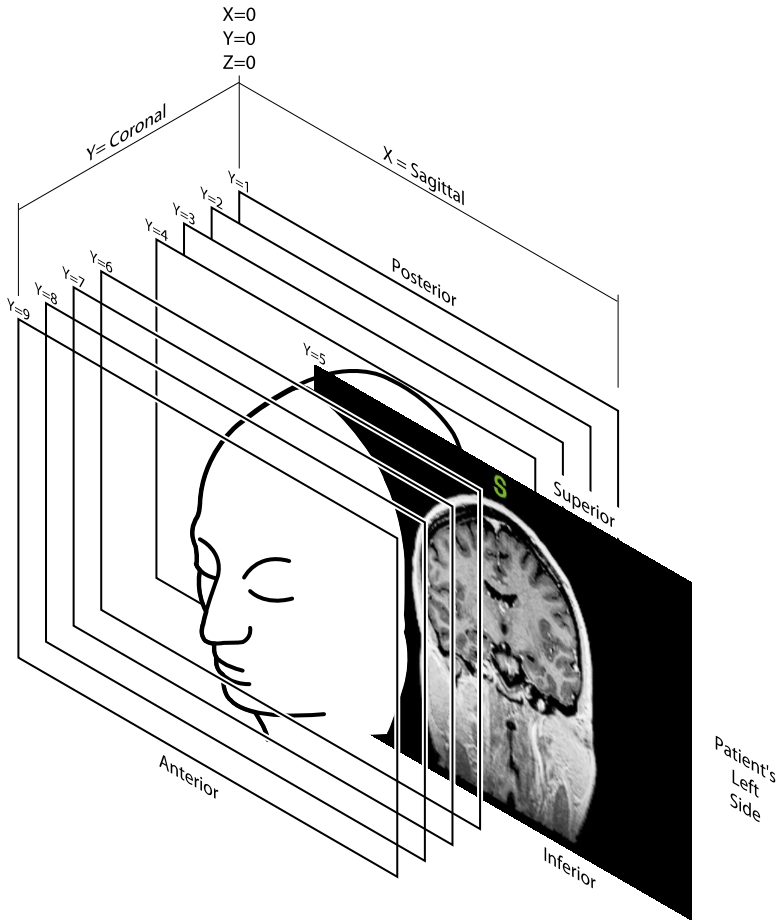


Figure 4.18 Coronal image coordinates

Axial images

Each image in an axial study is identified by the Leksell® Z coordinate of the central point in the image. The Z coordinate value of an axial image increases as the image slice is positioned further away from the Leksell® point-of-origin towards the patient's inferior, along the Z axis.

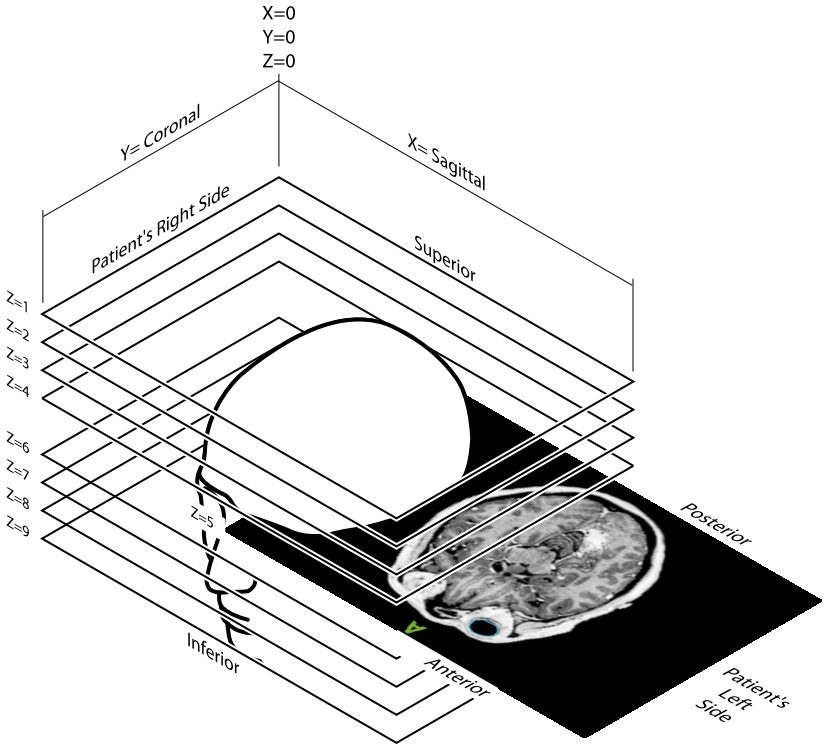


Figure 4.19 Axial image coordinates

4.2.9.2 Description of how image studies are used by Leksell GammaPlan®

The importance of the image study concept in the treatment planning application cannot be over-emphasized. It not only provides the mechanism for viewing images on screen but is also the means by which treatment planning takes place.

Consider an image study as a matrix consisting of an imaginary cube in stereotactic space. Within this matrix the treatment planning application executes the software processes that permit you to work with the computerized images.

The images in the windows of a treatment planning application workspace are obtained from one or more image studies. By extracting the necessary data from a study matrix, the program automatically reconstructs and displays all the images that you require.

You can affect the visualization of image data in the views by moving the exploration point and by changing zoom and level settings, for example. This also affects corresponding graphics such as shot, shield, region and volume projections and isodose curves.

In the study fusion function two separate studies are blended. This **Fuse** command creates a third (fused) study consisting of data calculated from the matrices of the two registered studies allowing you to emphasize areas of particular anatomic interest on the fused images.

Shots, shields, plugs, contours, regions and volumes plotted on the two studies are automatically projected on the fused study and can be manipulated there in stereotactic space. See the figure below.

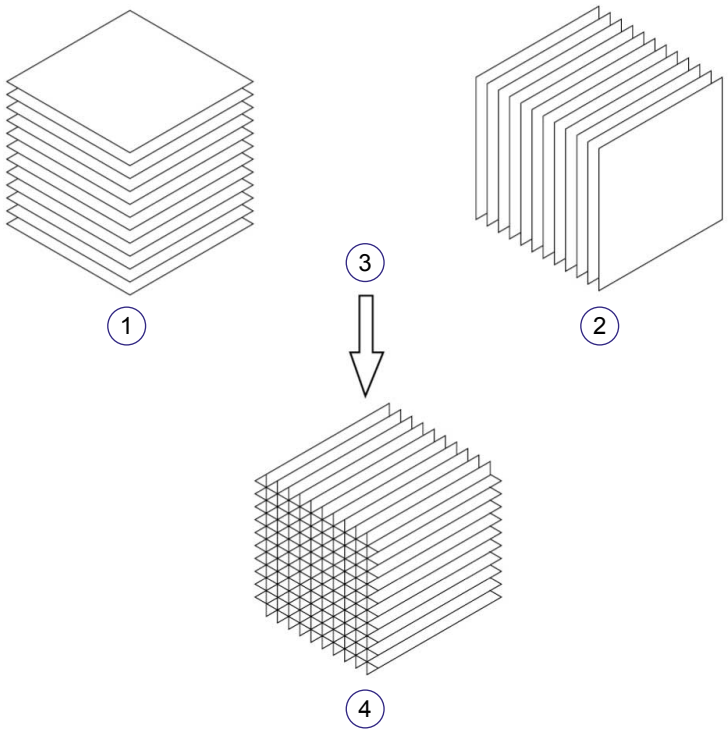


Figure 4.20 The concept of fused studies

(1) MR Axial Study
(2) MR Sagittal Study
(3) Fuse Studies
(4) Fused Study

Related Links:

Fuse studies on page 137

4.2.9.3 Reconstructed images

As well as the original image studies that have been imported into the treatment planning application, the program automatically reconstructs images in directions other than those of the original studies. In other words the data in the matrix of the original image study are used to calculate image studies and single image views in other directions.

Reconstructed three-dimensional views

In addition to automatically reconstructed image studies, the treatment planning application uses the data in the original study matrix to reconstruct special three-dimensional views of images.

These views can be displayed in two different three-dimensional views:

- Open Book
- Cut Box

The Open Book and Cut Box views are affected by the segmentation of the skull boundary.

Open Book view

An Open Book view is composed from axial, coronal and/or sagittal images overlaid on each other at the point of intersection of the image planes. You can select and deselect the images that will appear in the Open Book.

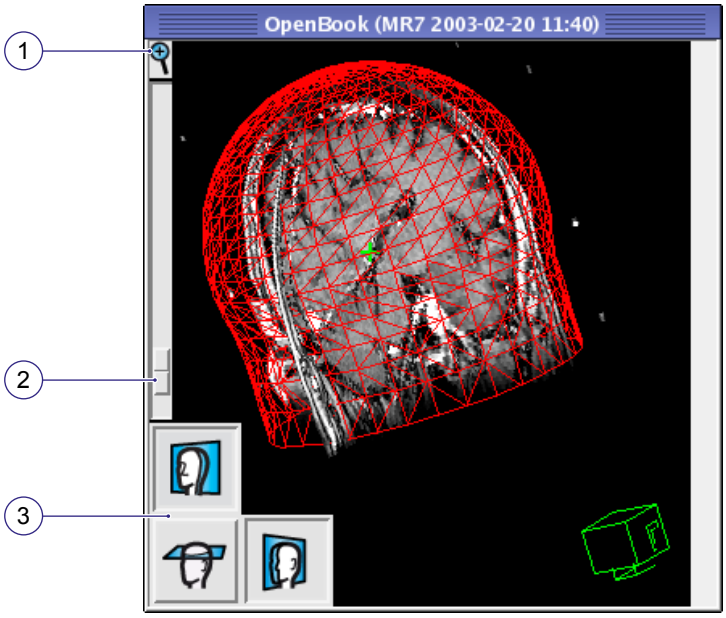


Figure 4.21 Open Book view

(1) Reset Zoom Button

(2) Zoom Slider Bar

(3) View Icons

The reset button restores the zoom factor of the Open Book to its initial value.

Using the view icons, you choose the images that appear in the Open Book.

Cut Box view

A Cut Box view is constructed from axial, coronal, and/or sagittal images overlaid on a rendered surface image of the patient's skull. The images cut into the skull at the point of intersection of the image planes, thus simulating an interior view of the brain.

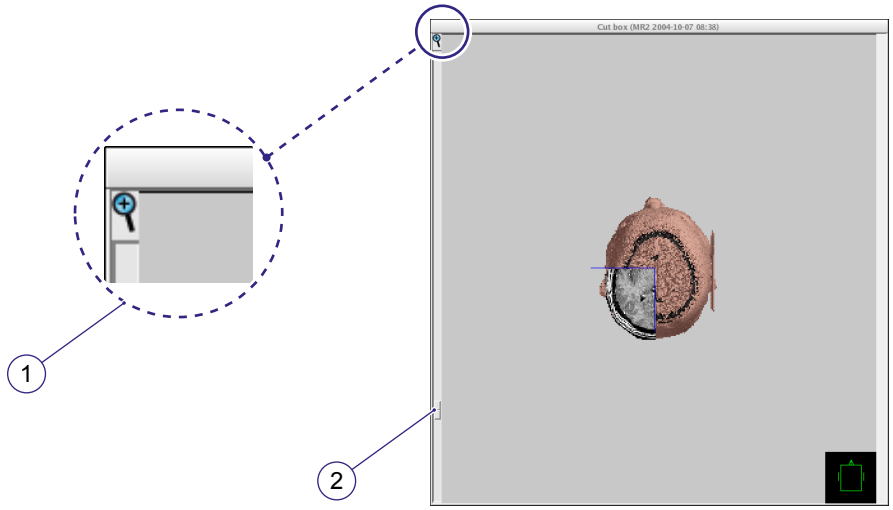


Figure 4.22 Cut Box view

(1) Reset Zoom Button

(2) Zoom Slider Bar

The Reset Zoom button (1) is used to restore the zoom factor of the Cut Box to its initial value after zooming using the Zoom Slider Bar (2).

4.2.9.4 Angiographic image studies

Angiographic image studies differ from tomographic studies in that the treatment planning application handles each separate angiographic image as a single image study: therefore an angiographic study contains one image only. However, for the program to construct a useful stack containing corresponding fiducials, at least two angiographic studies must be used: one frontal and one lateral.

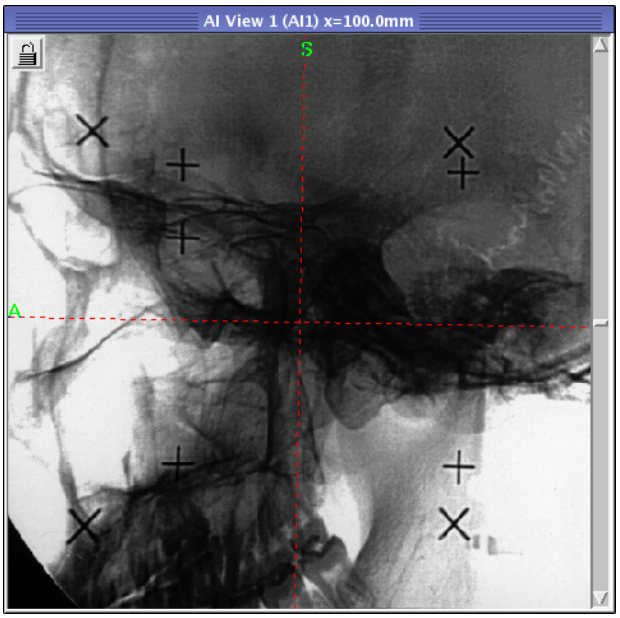


Figure 4.23 Angiographic image in the treatment planning application

4.2.10 ColorPET™

The optional software ColorPET™ is used for visualizing PET image studies using color encoding. More exactly, the ColorPET™ license makes PET studies available in the treatment planning application and allows for visualizing them using color encoding in preparation for subsequent treatment planning.

4.2.10.1 Acquiring PET images

The exact procedure for acquiring PET images depends upon the type of scanner in use. The following guidelines are offered for consideration when acquiring PET images for the treatment planning application. These statements must be read in conjunction with the instructions provided by the manufacturer of the scanner and are not intended to replace, supersede or overrule any such information.

1. Immobilize the patient's head to minimize inadvertent movement of the head during scanning.
2. Always ensure that the PET images in a study are acquired such that all areas of anatomical and diagnostic interest are included with sufficient detail in the image studies.
3. Always adhere to the operating instructions and observe all hazard notices provided by the manufacturer of the scanner.

Note: *Dynamic PET studies are not supported by the treatment planning application.*

4.2.10.2 Color Definitions

There are three pre-defined color maps offered in the system:

Hotmetal

Rainbow

Stern

The software maps 256 colors from the pre-defined color map to an image study.

WARNING 4.9

The visualization of anatomical features in a color-mapped image may differ significantly from the original image study leading to misjudging color-mapped images.

WARNING 4.10

The visualization of the dose distribution curves and user defined volumes may coincide with the colors applied to an image study by the selected color map leading to misinterpretation of the dose distribution.

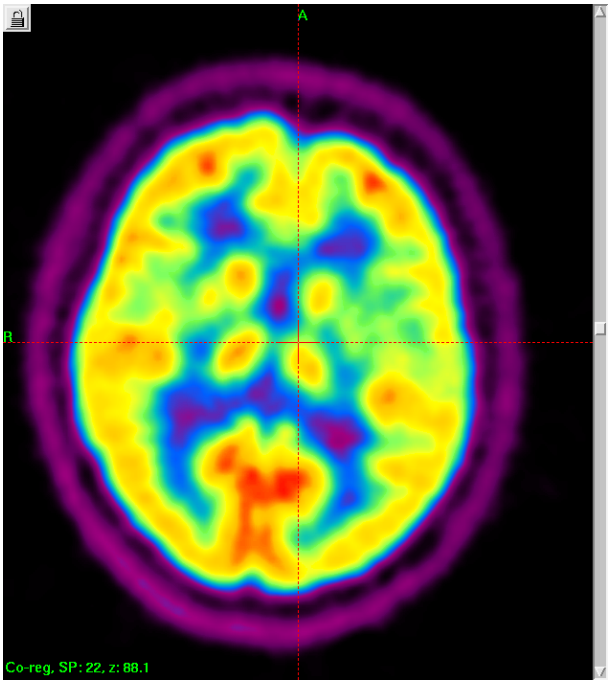


Figure 4.24 A ColorPET™ image with the color map Rainbow selected

4.2.10.3 Using Color Maps

Available color maps are listed in the drop down menu of each image study. Only one color map for each image study can be active at a time.

To activate a color map:

1 In the drop down menu of an image study, select **Colormap** and then the preferred color map.

The color map will now be applied to all 2D views in workspaces, the Level dialog and the Define dialog, visualizing the image study. The 3D workspace views will not be color encoded though. The name of the color map is indicated by that the color map is checked in the drop down menu for the image study.

WARNING 4.11

It is the responsibility of the user to verify that a color map is clinically appropriate to avoid misinterpretation of color maps. This may depend on the type of PET scanner that is used, the image acquisition protocol and the clinical task at hand.

2 Adjust the brightness/contrast settings to enhance visualization of particular areas of interest. The settings affect the colorization and changes the way color-encoded anatomy is displayed.

Related Links:

Setting grayscale during treatment planning on page 113

4.2.11 Description of the workspace concept

Workspaces are the means by which the treatment planning application presents the patient's image studies for treatment planning purposes. A workspace consists of one or more windows, each of which displays an original or reconstructed image from one study.

During treatment planning, shots, shields, isodose contours, regions, and volumes are plotted and visualized on the images in the workspace windows.

A workspace window can contain:

- an original image study
- the image studies that have been reconstructed in the other directions
- a three-dimensional reconstruction
- a fused image study.

All windows except the three-dimensional views include a lock icon in the top-left corner. This allows you to lock the image in the window so that it does not move as you adjust the point-of-exploration. In addition, image information, such as the slice number and coordinate, are given in green text at the bottom left corner of the window.

The number of windows that appear in a workspace, and the contents of each window, are determined when the workspace is configured.

The workspaces are shared with other users.

The treatment planning application is supplied with a number of predefined workspaces and includes an editing facility that allows you to customize workspaces. The figure shows a typical workspace containing the images from a MR study.

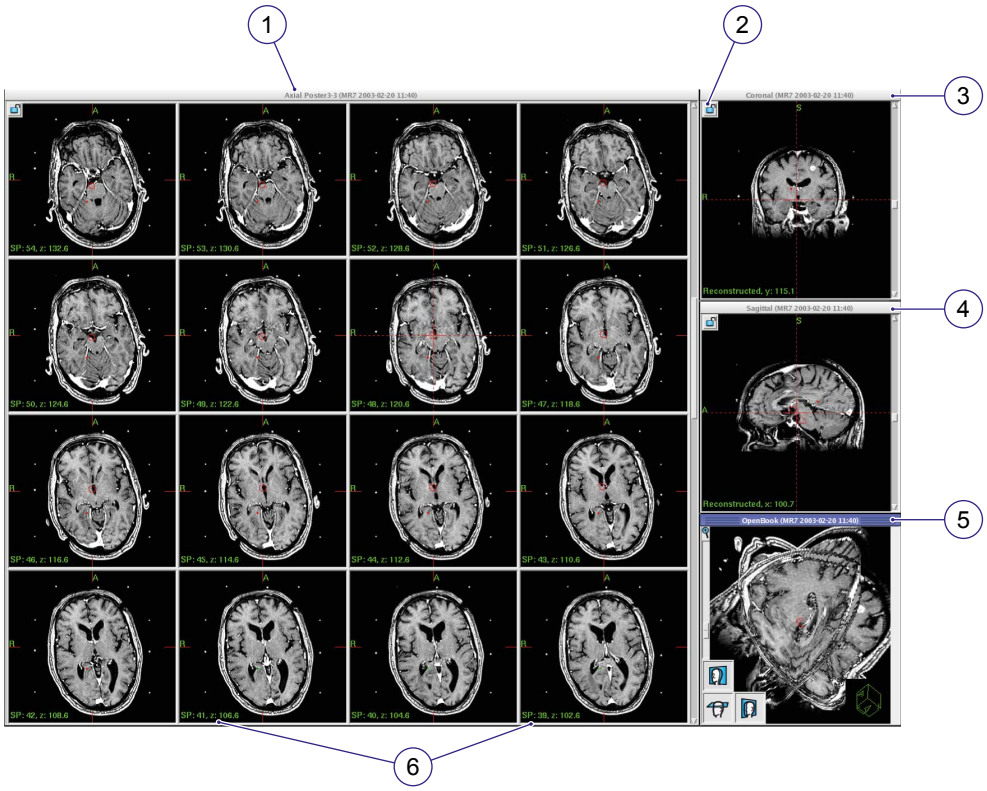


Figure 4.25 Typical workspace with MR images

(1) Axial Poster
(2) Lock Icon
(3) Single Coronal Image
(4) Single Sagittal Image
(5) Open Book Reconstruction
(6) Image information

4.2.11.1 Workspace managing dialogs

You can create and modify workspaces by using workspace managing dialogs obtained in sequence from the **Edit** command in the **Workspace** menu. The design can be adjusted as required, and you can delete workspaces as you wish.

The **Workspace** menu is dynamic in that it contains a separate item for each workspace that you have created. Initially, the menu contains the **Edit** and **Clear** commands and the items representing predefined workspaces. When you design a new workspace it is automatically listed as an item in the menu.

Related Links:

Creating workspaces on page 144

4.2.12 Graphics

A number of graphical objects and symbols are utilized to enhance the usability of the treatment planning application, including:

- icons
- isodose contours
- shots

- shields
- point-of-exploration
- regions and volumes
- measurements (lines and points).

4.2.12.1 Icons

Icons are graphical symbols that represent various objects in the treatment planning application. The accelerator buttons in the Toolbar and the workspace window locking symbol are examples of icons. In addition there are study icons and view icons.

Study icons

Study icons are graphical representations of the patient's image studies. When you open a patient's file, the menu bar displays a separate icon for each image study in the file.

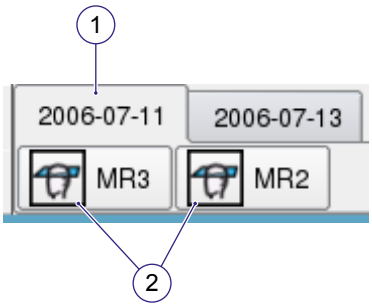


Figure 4.26 Study icons on the menu bar

(1) Image study date tab

(2) Study icons


A defined axial study.


A defined coronal study.


A frontal angiographic study with the film posterior to the patient.


A frontal angiographic study with the film anterior to the patient.


A lateral angiographic study with the film left of the patient.


A lateral angiographic study with the film right of the patient.


A blank tomographic study.


A study that has not yet been defined or co-registered.

A co-registered axial study.

A co-registered coronal study.

A co-registered sagittal study.

Handling the study icon menu and dialog

There is a drop-down menu and a dialog associated with each study icon. This drop-down menu provides quick access to the commands available for handling the study.

1 To obtain the menu, click on the study icon.

Figure 4.27 The study icon

The study icon menu includes the following alternatives:

- **View**
- **Level**
- **Edit**
- **DICOM Attributes**
- **Define Stereotactic Reference**
- **Define Pre-plan Reference**
- **Co-register**
- **Fuse**
- **Colormap**
- **Delete**

2 To view information about the study, place the mouse pointer on the study icon without clicking.

You see the name of the study together with patient information and information about how the study was obtained and defined. The figure below shows an example of the displayed study information.

Name: MR2

Date & time: 2004-10-07 08:38

MR, Axial orientation

Patient Id: 001

Patient Name: Name

Number of images: 144

Stereotactic definition

Mean definition error: 0.5 mm

3 To hide the information, move the mouse pointer away from the study icon.

View icons

View icons are used for representing image view in a workspace. View icons appear in certain dialogs such as the Workspace Editor and the Add Window dialog. In addition they are included in three-dimensional workspace windows, to allow you to select and de-select the images in the 3D view.


Axial poster view.


Coronal poster view.


Sagittal poster view.


Single axial view.


Single coronal view.


Single sagittal view.


Cut Box view.


Open Book view.


Angiographic view.

4.2.12.2 Shot graphics

The irradiation scheme is created by placing shots on the patient's images. You position a shot by clicking on the image at the point where the center of the shot is to be located. If necessary, adjust thereafter the shot coordinates and finally set the shot to confirm the shot position.

- When you first place a shot, and before it is set, the shot is represented by a red shape. The shape emanates from the center of the shot and represents the default 50% isodose level contributed by this shot alone.
- The isodose level can be selected in the User preferences dialog.

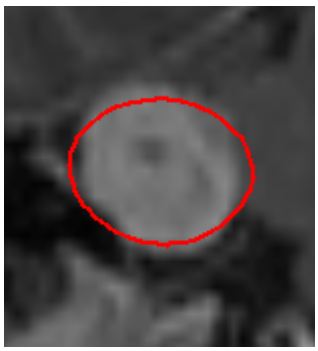


Figure 4.28 Shot graphic before the shot is set

- When the shot is set, a small red circle enclosing the shot number is displayed at the shot center position.

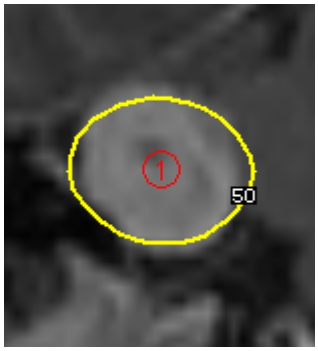


Figure 4.29 Shot graphic after the shot is set

4.2.12.3 Shield graphics

This section is only applicable for Leksell Gamma Knife® B, C, 4 and 4C.

Note: *Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ use user defined risk zones to protect critical anatomical structures.*

To modify the irradiation scheme and protect critical anatomical structures, you create collimator plug patterns by placing shields on the patient's images. A shield is a sphere of 2 mm, 10 mm or 20 mm in diameter, represented by a circle on the images. You position them by using the Plug Editor.

You place a shield by first selecting the shield button of the required diameter and then using the left mouse button to place and move the shield into position on an image.

Plug Editor buttons:

	A shield of 2 mm in diameter.
	A shield of 10 mm in diameter.
	A shield of 20 mm in diameter.

When you place a shield in an image, it is plotted as a magenta circle of 2 mm or 10 mm or 20 mm in diameter. Unselected shields are visualized with blue color.

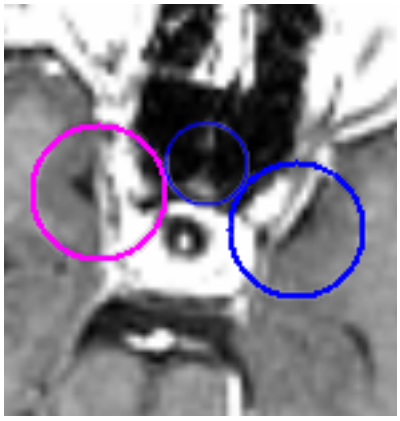


Figure 4.30 Shield graphics on an image

Related Links:

Protection of critical structures using plug patterns on page 230

4.2.12.4 Isodose contours

Isodose contours represent the irradiation scheme that you devise by placing radiation shots on the patient's images.

The isodose contours are plotted when at least one shot has been placed, and they appear as colored curves on the images.

You choose the isodose levels that you want to work with by using the Display Isodose dialog. The selected isodose contour is always plotted in yellow: the other isodose contours are drawn in green. The isodose level of each contour is given at a convenient point along the curve.

You can switch the isodose contours on and off by using the **Isodose** accelerator button in the Toolbar.

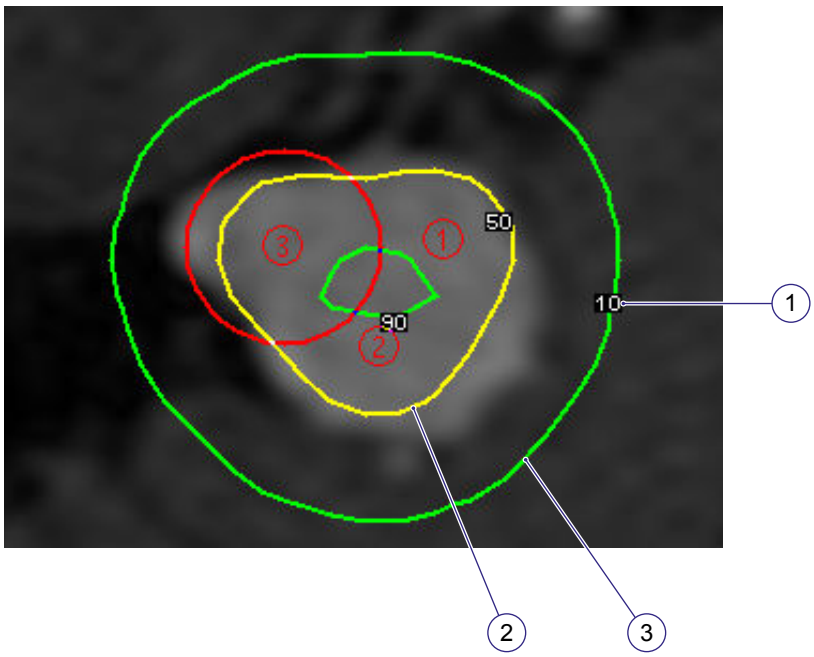


Figure 4.31 Isodose contours on an image

(1)	Isodose Level
(2)	Selected Isodose Contour (50% in this example)
(3)	Ordinary Isodose Contour

Related Links:

Configuring the isodose display on page 203

4.2.12.5 Point-of-exploration

You explore the patient's images in the windows of a workspace by moving the point-of-exploration to the part of the image that you want to examine. The point-of-exploration consists of vertical and horizontal cross-wires colored red. They extend the full height and width of the image respectively.

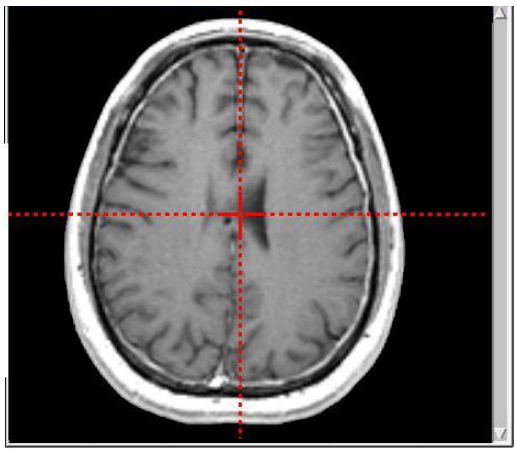


Figure 4.32 Point-of-exploration

Related Links:

Study exploration on page 150

4.2.12.6 Region and volume graphics

The treatment planning application includes features that allow you to plot two-dimensional regions of interest and three-dimensional volumes on the patient's images. These plots can then be projected on to all open images.

Related Links:

Regions and volumes on page 154

Region of interest plots

You draw regions of interest on an image by using the mouse pointer like a pen, or by using semi-automatic segmentation. The region is outlined on the image in one of fourteen colors that you can select.

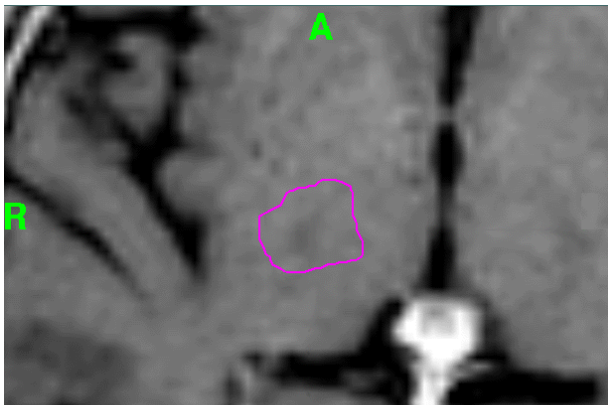


Figure 4.33 Region of interest plotted on image

A region of interest can be projected as a template onto other images in the workspace. In this case it appears as a dotted outline in the selected color.

Graphical presentation of volumes

Three-dimensional volumes are constructed from the regions of interest that you draw on the patient's images. Volumes can be projected on to open images in one of nine selected colors. In addition you can select one of four rendered forms in which the volume will be shown. These are:

- wire – the object is displayed as a wireframe of original contours
- mesh – the object is displayed as a wireframe of original contours with interconnecting triangles
- solid – an opaque object
- transparent – a translucent object.

The figures below illustrate the forms in which a volume can be displayed.

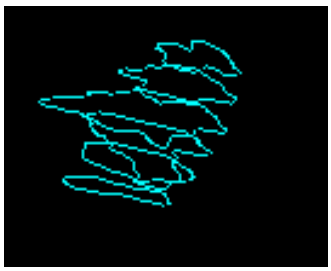


Figure 4.34 Volume shown as wire

Figure 4.35 Volume shown as mesh

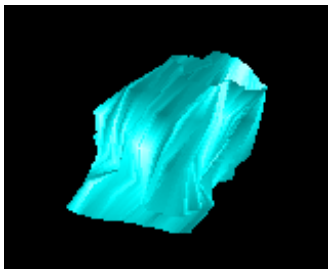


Figure 4.36 Volume shown as solid

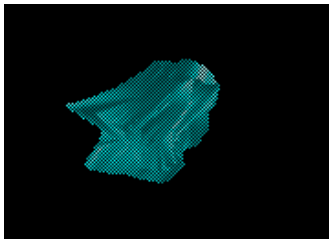


Figure 4.37 Volume shown as transparent

4.2.12.7 Graphical presentation of the AC-PC Line

The AC-PC Line connects the anterior and posterior commissural points. The AC-PC Line is used as a reference point when plotting target formulae on the patient's image study. An example of an image slice displaying the AC-PC Line is below:

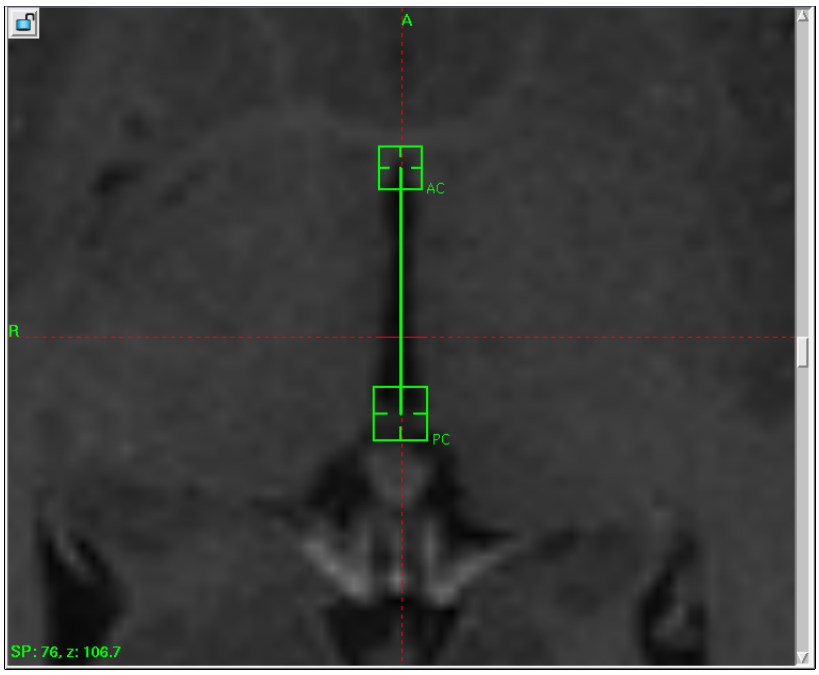


Figure 4.38 Image study displaying the AC-PC Line

AC, PC and MR Markers and Points

AC, PC and MR markers are used to indicate and adjust the AC, PC and MR points that have been plotted on an image study. When you place an AC or PC marker on a patient's image, the marker appears as a small green square and the center of the square defines its position. When you place an MR marker on a patients image, the marker appears as a smaller green square and the center of the square defines its position.

Note: *The Midline Reference (MR) point shall be placed in the midsagittal plane superior to the intercommissural line.*

4.2.12.8 Functional targets markers

Functional target markers are used to indicate and adjust the positions of the targets that have been calculated from the functional target formulas. The functional targets appear in the images as small green crosses.

Figure 4.39 Functional target marker

5 Using Leksell GammaPlan

— Blank page —

5.1 Quality of input data

The quality of the treatment plan is critically dependent of the quality of the input data. Any irregularities or uncertainties about input data units, identification, or quality of any other nature must be thoroughly investigated before the data are used.

5.2 Working with patient files

5.2.1 Patient files

For each patient there must be a dedicated patient file consisting of:

- demographic information about the patient
- information about the patient's radiological examination(s)
- the patient's image studies.

The patient's demographic and radiological data are stored in the treatment planning application patient database, and the image studies are loaded into the image repository. When you open a patient file, the associated patient data and image studies are read from the database and repository.

The first step in the treatment planning procedure for a new patient is to create a patient file and enter the patient's demographic and radiological details. The images for the new patient file can then be imported via the computer network. Once a patient file has been created you can:

- edit the patient data
- add new radiological examination results to the patient file
- import new image studies into the patient file and delete old ones
- archive the patient files and delete files no longer used.

5.2.2 Accessing the patient database

The patient database is accessed from the Patient Management dialog.

To open the Patient Management dialog, do as follows:

1 In the **Patient** menu, select **Patient Management**.

5.2.2.1 Description of the Patient Management dialog

The Patient Management dialog consists of three parts: Search pane (1), a pane with patients and examinations table including a comments field (2), and a button pane (3).

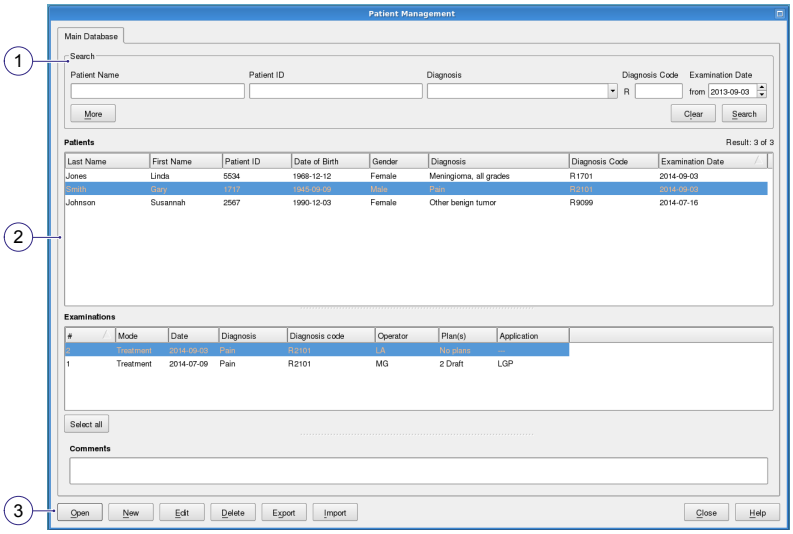


Figure 5.1 The Patient Management dialog

(1) Search pane

(2) Patients and examinations pane

(3) Button pane

By default, only patients with examinations registered during the last 12 months are displayed. You can list patients with older examinations by entering a new Examination Date and perform a search.

The number of found patients as well as the total number of patients are displayed above the Patients pane (at the right).

If a patient file is already open when you open the dialog, it is highlighted in the list using red/orange text.

The panes can be resized to accommodate to your needs.

Searching the patient database

The patient management dialog offers a number of search criteria that you can combine to perform searches among the patients in the database. To perform a search, do as follows:

1 Enter the search criteria.

To display further search criteria, click **More**. To hide them again, click **Less**.

To clear all search fields and perform a search using the default settings, click **Clear**.

2 Click **Search**.

3 To sort the list on any column, click the corresponding column header.

A second click reverses the sorting order.

Note: *By default, if a patient has gone through several examinations, the **Patients** list shows the latest examination, even if your search was matched by one of the earlier ones. For example, if you search for patients with a Metastasis Single diagnosis and one of them was diagnosed with Glial Tumor in the latest examination, the Diagnosis column will show Glial Tumor, since this is the latest diagnosis.*

Available functions in the Patient Management dialog

From the Patient Management dialog you can:

- create a new patient file
- open an existing patient file

- change an existing patient file
- add new radiological examination data
- delete radiological examination data and patient files
- export patient files to a USB mass storage device
- import patient files from a USB mass storage device.

5.2.2.2 Creating a new patient file

With the Patient Management dialog in view:

1 Click **New**.

The New Entry dialog opens.

Note: *If a patient is loaded or marked in the Patient Management dialog you will be given the option to create a new examination for this patient. Otherwise, the New Patient dialog opens.*

2 Select the **Create a new patient** radio button.

3 Click **OK**.

The New Patient dialog opens.

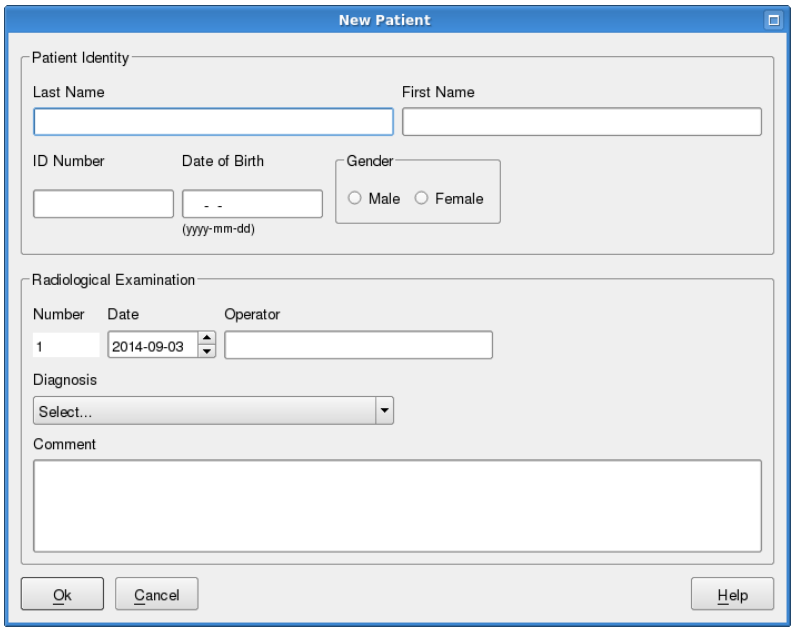


Figure 5.2 The New Patient dialog

The **Patient Identity** fields are mandatory and must be completed first – you cannot proceed further until all fields are filled in. Move between the fields by pressing the <Tab> key or by clicking.

4 Type the patient's last name.

5 Type the patient's first name.

6 Type the patient's identification number allocated by your hospital.

7 Type the patient's date of birth using the **ISO** format:

a enter the year as a 4-digit number (e.g. **1940**)

b enter the month as a 2-digit number (e.g. **09**)

c enter the day as a 2-digit number (e.g. **09**)

8 Indicate the patient's gender by selecting the appropriate check box.

Complete the **Radiological Examination** fields – mandatory:

9 Click in the **Date** field and type the date on which the radiological examination took place.

10 Type your name in the **Operator** field.

11 Click on the **Diagnosis** drop-down list and select the one that best describes the patient's condition.

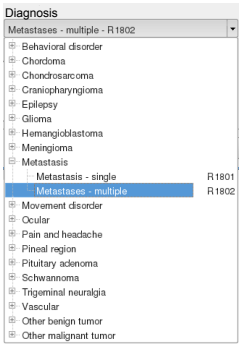


Figure 5.3 Selecting diagnosis

Hint: you can navigate through the diagnosis list by using the keyboard (cycle through diagnoses based on first letter, navigate tree with arrow keys, expand collapse using Space, select using Enter).

12 If you want the patient's file to include any brief notes, click in the **Comments** field and type in your remarks.

13 To save the new patient file, click on **Ok**.

The New Patient dialog closes. The patient's data is saved in the database.

The new patient file can now be accessed from the Patients list in the Patient Management dialog. The next step is to import the patient's image studies.

Note: *You must select **New Plan** in the **Plan** menu and make a new treatment plan before you can start planning.*

Related Links:

Importing the patient's images on page 101

5.2.2.3 Opening a patient file

To begin treatment planning the patient's file must first be open. All patient files are accessed from the Patient Management dialog, where the **Patients** list shows all the files presently stored in the treatment planning application patient database.

1 In the **Patient** menu, select **Patient Management**.

The Patient Management dialog opens.

2 Scroll through the **Patients** list until the patient file is visible, or perform a new search.

3 Select the patient to be opened.

The patient's details appear in the **Radiological Examination** list and the **Comments** field.

4 If there is more than one radiological examination in the patient's file, scroll through the **Radiological Examinations** list to find the required examination.

5 Select the radiological examination that is to be opened, and click **Open** (or double-click on the examination in the list).

For each image study that has been prepared for this patient, there is a separate study icon on the menu bar.

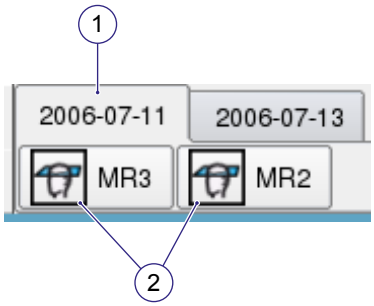


Figure 5.4 Study icon

(1) Image study date tab

(2) Study icons

You can use the study icons to work with the patient's images.

Note: *Only one patient file can be open at a time. If you open a patient file when another file is already open, the previously opened file is automatically closed. Any changes that you have made to the file are saved before it is closed.*

5.2.2.4 Editing a patient file

The information in an existing patient file can be changed, for example, if a new radiological examination has been performed. As always, you must first open the existing file from the Patient Management dialog.

1 In the **Patient** menu, select **Patient Management**.

The Patient Management dialog opens.

2 Scroll through the **Patients** list to find the required patient file, or perform a new search.

3 Select the patient file to be opened.

4 Click **Edit**.

The Edit Patient dialog opens. Its fields contain the existing patient data.

5 Click on the fields or drop-down lists where information is to be edited.

6 Type new information or select a different option, as required.

7 Click **Ok**.

The patient file is updated in the patient database and the Edit Patient dialog closes.

5.2.2.5 Adding a new radiological examination

An important feature of the treatment planning application is that data from more than one radiological examination can be included in a patient file.

For example, having treated a patient and after a period of convalescence, a new radiological examination can be performed to monitor the progress. The new radiological data can be added to the existing patient file. Then you can compare the new and old data by opening one examination and then the other.

1 In the **Patient** menu choose **Patient Management**.

The Patient Management dialog opens.

2 Scroll through the **Patients** list to find the required patient file.

3 Select the patient file to be extended.

4 Click **New**.

The New Entry dialog opens where you can add radiological data to the selected patient file.

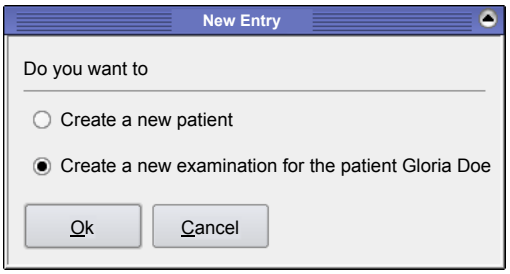


Figure 5.5 The New Entry dialog

5 Select the **Create a new examination** radio button.

6 Click **OK**.

The Edit Patient dialog opens with the new radiological examination number in the **Number** field.

7 Click in the **Date** field and enter the date (using the appropriate date format) on which the new radiological examination was performed.

8 Enter your name in the **Operator** field.

9 Click on the **Diagnosis** drop-down list and select the diagnosis of the patient's condition. Unless the patient has been diagnosed as having a new condition, this selection should be the same as that identified in previous radiological examinations.

10 Click **Ok**.

The Edit Patient dialog closes. The new radiological data are saved in the database and appear in the Patient Management dialog when the patient file is next opened.

Note: *You must select New Plan in the Plan menu and make a new treatment plan before you can start planning.*

5.2.2.6 Deleting a radiological examination

You can delete unwanted radiological examinations from a patient's file.

1 In the **Patient** menu, select **Patient Management**:

The Patient Management dialog opens.

2 Scroll through the **Patients** list to find the desired patient file.

3 Select the patient file.

All the radiological examinations in the patient file are in the **Examinations** list.

4 Scroll through the **Examinations** list to find the desired examination.

5 Select the examination that is to be deleted and click **Delete**.

Make sure that this is the record you want to delete.

A confirmation dialog opens.

6 Click **OK**.

The selected radiological examination is deleted from the patient file and is removed from the **Examinations** list.

Note: *If dose delivery for an examination is started, it is not possible to delete the examination. This is valid for treatment plans for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™.*

5.2.2.7 Closing a patient file

In the treatment planning application there is no explicit command that permits you to close a patient file. For the purposes of patient safety only one patient file can be open at a time. Consequently, if you open a patient file while another patient file is already open, then the previously opened file is automatically saved and then closed.

1 To automatically close an open patient file and save all data, use the **Exit** command.

5.2.2.8 Deleting a patient file

To delete a patient file from the treatment planning application, delete all the patient's examinations, one at a time.

Related Links:

Deleting a radiological examination on page 98

5.2.2.9 Exporting a patient file

You can export a patient file from the treatment planning application to a USB (mass storage) device.

Note: *For safety reasons, it is not possible to export a patient file for examinations with a treatment plan in state approved, or printed, i.e. the treatment plan has been approved but not yet exported.*

1 Connect a USB device to the workstation.

2 In the **Patient** menu, select **Patient Management**.

The Patient Management dialog opens.

3 Scroll through the **Patients** list to find the desired patient file.

4 Select the patient file and one ore more of its examinations.

5 Optionally select **Anonymize file** to remove all patient identifiers from the exported file, including the identifiers of the DICOM images.

A randomized patient id will be assigned to the exported patient file.

6 Click **Export**.

7 Enter a file name. Supported characters are [a-z][A-Z][0-9][Space . /]. Unsupported characters will be removed from the name.

8 Click **OK**.

The patient file and examinations are now copied to the USB device.

9 Disconnect the USB device.

5.2.2.10 Importing patient files

You can import patient files available on a USB (mass storage) device to the treatment planning application.

1 Connect a USB device to the workstation.

2 In the **Patient** menu, select **Patient Management**.

The Patient Management dialog opens.

3 Click **Import**. The Import Patients dialog opens.

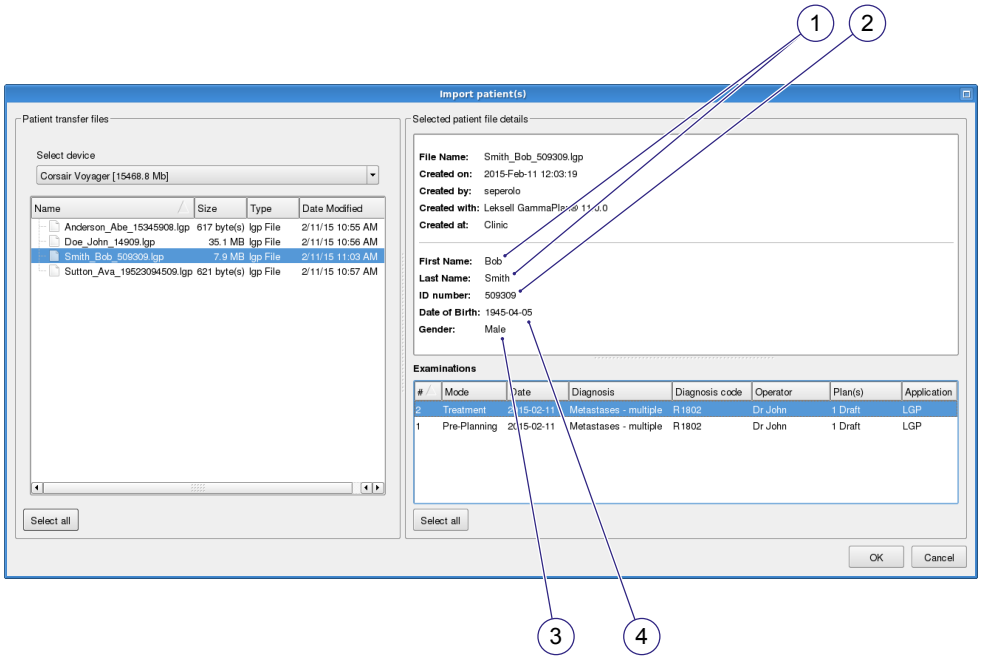


Figure 5.6 The Import Patients dialog

4 Scroll through the list of files to find the desired patient files.

5 Select the patient files.

6 Click **OK**. The patient files are now copied from the USB device.

- Imported examinations that have a patient name (1), ID (2), gender (3) and birth date (4) that are identical to an existing patient file in the treatment application are added to that patient file.
- For examinations where just the ID (2), gender (3) and birth date (4) are identical to an existing patient file in the treatment planning application you have the choice to either add the examinations to the existing patient file, create a new patient file or cancel the import of this patient file.
- For patient files containing images with identities that conflict with existing images in the treatment planning application you will be asked to either cancel the import of this patient file or let the imported examination use the existing images.
- If a patient file contains treatment plans that conflict with treatment plans that already exist in the database it is not possible to import the patient file.

7 Review the resulting log for the patient file import and then click **Close**.

8 Disconnect the USB device.

5.3 DICOM import and export

5.3.1 Prerequisites for DICOM import and export

The conformance to the DICOM standards is specified in *DICOM Conformance Statement* for Leksell GammaPlan®. This document is available at www.elekta.com.

If the workstation AET has not been configured it will not be possible to modify the list of external DICOM servers or to import from or export to remote DICOM servers. This manual describes the following ways to configure the DICOM server:

- configure the AET for Leksell GammaPlan® on the specific workstation
- add/edit/delete external DICOM server entries
- set the external DICOM server to use by default in the Import DICOM dialog.

Related Links:

DICOM server configuration on page 302

5.3.2 Importing the patient's images

Once you have created a new patient file, the next step in the treatment planning workflow is to import the patient's images to the treatment planning application.

1 You can import patient images in two different ways:

- Import images from the local DICOM INBOX
- Import images from a remote DICOM server

Note: *The "Import images from a remote DICOM server" functionality is only available if the system is licensed for remote DICOM Query and Retrieve functionality.*

Related Links:

Importing images from the local DICOM INBOX on page 103

Importing images from a remote DICOM server on page 104

5.3.2.1 Description of the DICOM import dialog

To open the DICOM import dialog, select **Import DICOM** in the **Patient** menu.

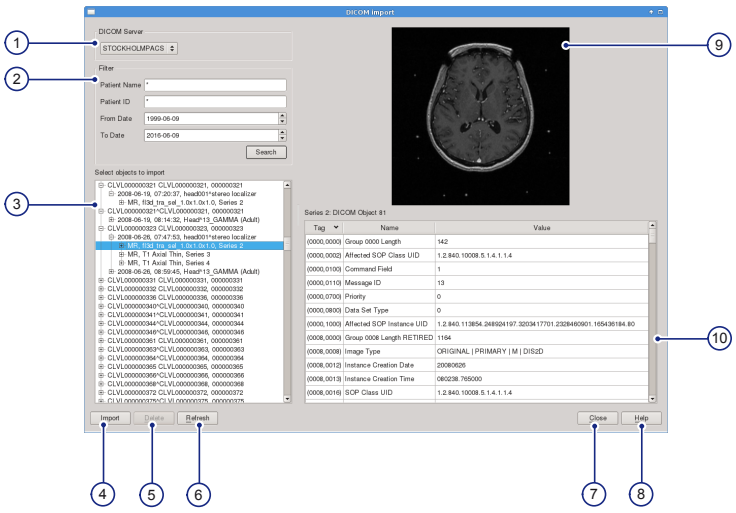


Figure 5.7 The DICOM import dialog

(1)	**DICOM Server** frame	(6)	**Refresh** button
(2)	**Filter** frame	(7)	**Close** button
(3)	**Select objects to import** frame	(8)	**Help** button
(4)	**Import** button	(9)	**Image Preview** frame
(5)	**Delete** button	(10)	**DICOM Attribute list** frame

The **DICOM Server** frame contains a drop-down list to select the server from which to import the patient file(s).

The **Filter** frame is only available when a remote server is selected. It contains fields for entering search criteria:

- **Patient Name** - case sensitive and possible to search on part of the name. Wild cards such as * can be entered. Some language specific letters are not possible to search on. Any non-ASCII characters are automatically replaced by the wild card character “?”.
- **Patient ID** - fill in the patient ID. (See below about wild cards.)
- **From Date** and **To Date** - in the format YYYY-MM-DD.

The entered search criteria in the filter frame are remembered until a new examination is loaded upon which the search criteria are reset to the following:

- Patient name: *
- Patient ID: the ID of the patient in the database.
- From date: today’s date.
- To date: today’s date.

In the **Filter** frame, it is possible to use wild card matching when searching for DICOM objects for patients on a remote DICOM PACS.

When using “*” in the Patient Name and/or Patient ID field, sequences of characters will be matched.

When using “?” in the Patient Name and/or Patient ID field a single character will be matched. This matching is case sensitive for the patient’s ID. For the patient’s name the matching can either be case sensitive or insensitive. This is different for different PACS servers. Information about this can be found in the DICOM conformance statement for the different servers.

In the **Select objects to import** frame, the object list displays the available patient files, in chronological order, on the selected server. The list is automatically updated for the INBOX server. To update the list for a remote DICOM server, click on the Refresh button.

The **DICOM Attribute list** displays the DICOM tags from the object or series that currently is selected in the **Select objects to import** frame. The **Image preview** displays the corresponding image if the selected object is of a supported image modality.

The following push buttons are available in the DICOM import dialog:

- **Import** button - click this button to import a selected file from the object list.
- **Delete** button - click this button to delete the selected file from the object list.
- **Refresh** button - click this button to send a query to the server and update the displayed data.
- **Close** button - click this button to close the dialog.
- **Help** button - click this button to open the *Online Reference Manual*.

5.3.2.2 Importing images from the local DICOM INBOX

Perform the following steps to import images:

1 Select **Import DICOM** from the **Patient** menu.

The **DICOM import** dialog opens.

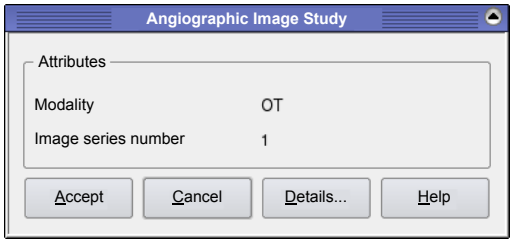
2 In the DICOM Server frame, select **INBOX** from the drop-down list to choose the DICOM INBOX. (If the system is licensed for remote DICOM Query and Retrieve functionality, the DICOM Server selection is by default set to the configured server.)

The object list shows all available DICOM studies sorted in chronological order under their respective patient.

3 Expand to series level, select the series that you wish to import and click **Import**.

You cannot import objects from higher levels in the list (patient or image study). Only one image series can be selected for import at the time. If you wish to import several image series, repeat the steps below until all images are imported.

4 This step differs depending on the type of images to be imported, see table below:

Instructions for tomographic images	Instructions for angiographic images
The Tomographic Image Study dialog opens. The images in the image study are compared to a visualization model. The visualization model is defined as having: – images of the same size – square pixels, all of the same size – equidistantly spaced images – images with the same orientation – images whose corners are aligned along a line perpendicular to the image plane – images with no gantry tilt. The deviation from the visualization model, if any, is shown together with image study attributes such as modality, number of slices etc; see above. You can display more detailed information by clicking on the **More** button. Any calculated characteristic (Deviation from visualization model, Gap or Overlap) that exceeds a preset limit is marked with a deviating color. Image studies are rejected if the deviation from the visualization model exceeds 1 mm.	The Angiographic Image Study dialog opens. 

5 Click **Details** to open the detailed information dialog.

The DICOM tags of the first selected image in the image study are presented.

6 If the Calculated characteristics are satisfying, click **Accept** to continue the import. Otherwise, interrupt with **Cancel**.

7 Give the study a name that is unique within the examination. Click **OK**.

8 When you are done importing images, close the DICOM Import dialog with **Close** and return to the workspace.

Related Links:

Description of the DICOM import dialog on page 101

Error, warning and notification messages at image import on page 352

Viewing details

The **DICOM Attribute list** and **Image Preview** are updated when the user selects a new series or object from the list. If several objects are selected, the DICOM attributes for the first selected object are presented (without some attributes, for example private attributes). When selecting a series the details and preview for the middle image in the series are displayed.

Refreshing the list in the DICOM import dialog

If the system receives new DICOM objects while the DICOM Import dialog is open, these will not appear in the list automatically.

1 To update the list with any new data, click on **Refresh**.

Deleting images from the DICOM INBOX

The storage for incoming DICOM data, the DICOM INBOX, is limited to 5 GB. When new incoming DICOM data cause the DICOM INBOX to exceed this limit the least recently accessed image series is automatically deleted.

To manually delete objects from the DICOM INBOX:

1 In the displayed list, select the image series or DICOM object to be deleted and click on the **Delete** button.

Deleted objects are removed from the list view.

WARNING 5.1

Some patients may have a number of successive treatment plans devised in the treatment planning application. In this case the patient's image studies from earlier planning sessions will remain in the image repository. Image studies from previous treatment planning sessions may be valuable for the purposes of clinical comparisons but they must not be used in the current planning session, or the new plan will be based on obsolete images. To prevent the use of obsolete images, define a new radiological examination in the patient's file for each successive set of image studies.

5.3.2.3 Importing images from a remote DICOM server

Prerequisites

Before images can be retrieved from the remote DICOM server, the connection must be configured.

Note: *This functionality is only available if the system is licensed for remote DICOM Query and Retrieve functionality.*

1 Select **Import DICOM** from the **Patient** menu.

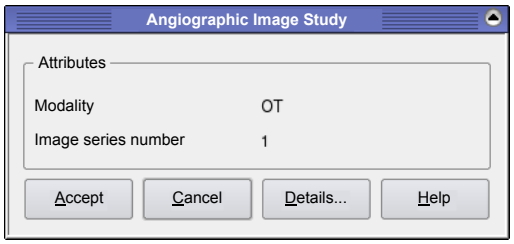
The **DICOM import** dialog opens.

– The configured remote DICOM server is diplayed by default in the DICOM Server frame.
– The object list shows all available DICOM studies sorted in chronological order under their respective patient.

2 Expand to series level, select the series that you wish to import and click **Import**.

You cannot import objects from higher levels in the list (patient or image study). Only one image series can be selected for import at the time. If you wish to import several image series, repeat the steps below until all images are imported.

3 This step differs depending on the type of images to be imported, see table below:

Instructions for tomographic images	Instructions for angiographic images
The Tomographic Image Study dialog opens. The images in the image study are compared to a visualization model. The visualization model is defined as having: – images of the same size – square pixels, all of the same size – equidistantly spaced images – images with the same orientation – images whose corners are aligned along a line perpendicular to the image plane – images with no gantry tilt. The deviation from the visualization model, if any, is shown together with image study attributes such as modality, number of slices etc; see above. You can display more detailed information by clicking on the **More** button. Any calculated characteristic (Deviation from visualization model, Gap or Overlap) that exceeds a preset limit is marked with a deviating color. Image studies are rejected if the deviation from the visualization model exceeds 1 mm.	The Angiographic Image Study dialog opens. 

4 Click **Details** to open the detailed information dialog.

The DICOM tags of the first selected image in the image study are presented.

5 If the Calculated characteristics are satisfying, click **Accept** to continue the import. Otherwise, interrupt with **Cancel**.

6 Give the study a name that is unique within the examination. Click **OK**.

7 When you are done importing images, close the DICOM Import dialog with **Close** and return to the workspace.

Related Links:

DICOM server configuration on page 302

Description of the DICOM import dialog on page 101

Sending a query to a DICOM server

1 Specify the query in the **Filter** frame (note that the search criteria is case sensitive) in order to limit the results of the query:

- Patient Name - a substring of the patient name (DICOM tag (0010,0010)).
- Patient ID - the patient ID (DICOM tag (0010,0020)).
- From Date and To Date - a time interval filtering the study dates (DICOM tag (0008,0020))

2 To send a query to the selected DICOM server, click on the **Refresh** button in the DICOM import dialog.

The result is displayed in the list in the bottom of the dialog.

Note: *The exact behaviour of the query depends on the implementation on the server side.*

5.3.2.4 Conflicts when importing images

The system internally uses the SOP Instance UIDs of the DICOM images to identify them. According to the DICOM standard, the SOP Instance UID of a DICOM image shall be unique. Despite that, situations may occur when different images have the same SOP Instance UID. A conflict can arise if an image selected for import and an image already stored in the system have the same SOP Instance UID and if the two images despite this are not identical.

The system will then display a warning and a list of the attributes that differ between the images already stored in the system and the images being imported and ask for a confirmation. If the warning and the differences are confirmed, the system will use the already stored images instead of the images selected for import. The system will never overwrite an image that has previously been imported.

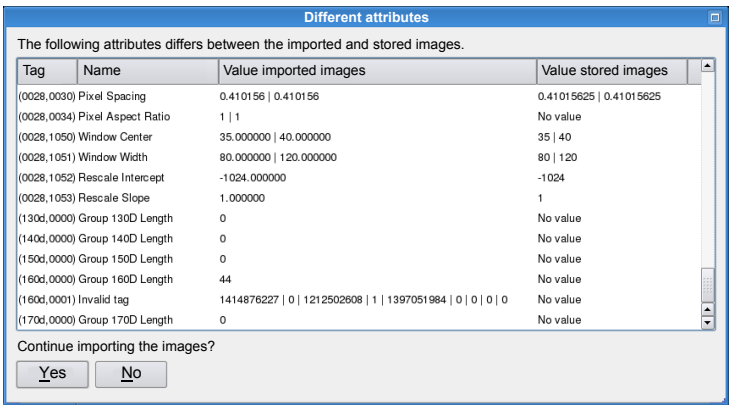


Figure 5.8 The Different attributes dialog

5.3.3 Importing the DICOM objects stored on external media

DICOM objects stored on external media (CD or USB storage device) can be imported using an application that can be reached from the Desktop menu on the taskbar. All DICOM files stored on the media will be sent to the treatment planning application DICOM inbox.

Note: *The media must not contain more than 50 DICOM studies due to the limitation of maximum 50 DICOM studies in the DICOM inbox.*

1 Insert the media with the DICOM objects.

2 Start the application by selecting **Import DICOM objects from external media** (1) in the Desktop menu on the taskbar (2).

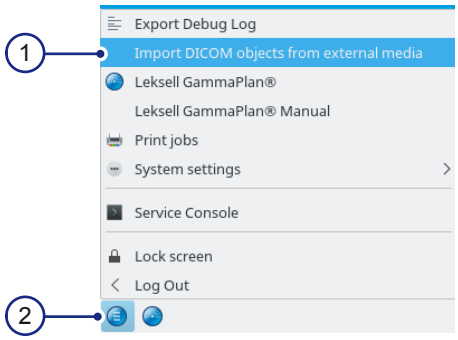


*Figure 5.9 Selecting **Import DICOM objects from external media** in the Desktop menu*

3 In the drop-down list, select the media with the DICOM objects and click **OK**.

A dialog window opens.

4 Click **Yes** to start the import.

The DICOM objects on the media are read by the DICOM import application. This step might take some minutes. A progress bar is displayed during the subsequent object transfer, enabling the user to stop the transfer preventing more objects to be sent. When the transfer is finished, the number of objects sent, skipped, and failed to be sent is presented. All DICOM objects from the media are now stored in the treatment planning application DICOM inbox.

5 Eject the media.

6 Follow the instructions in this manual to import the patient's images into an examination or to import DICOM RT structure sets.

Related Links:

Importing the patient's images on page 101

Importing DICOM RT structure sets on page 107

5.3.4 Importing DICOM RT structure sets

Prerequisites

Before importing the structure set, you must import the image study in which the regions were drawn. The contours in the ROIs must be closed and planar and drawn in the image planes of the image study.

Note: *DICOM RT functionality is only available if licensed.*

A structure set contains a number of regions of interest (ROIs), that will be converted to volumes and show up in the Regions and Volumes dialog.

To import a structure set, perform the following steps:

1 From the **Patient** menu, choose **Import DICOM**.

The DICOM Import dialog opens. The list shows all available DICOM studies sorted in chronological order under their respective patient.

2 Expand to series level.

The structure sets will show up in the list with modality RTSTRUCT. When selecting the RTSTRUCT the DICOM tags of the object are shown in the **DICOM Attribute list**.

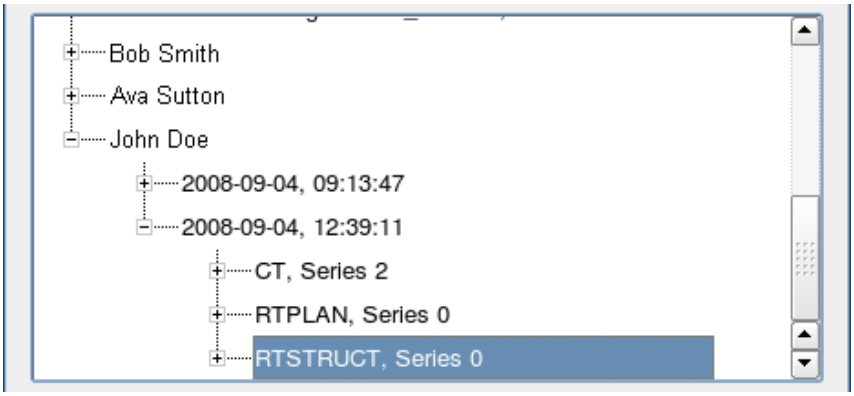


Figure 5.10 The DICOM Import dialog

WARNING 5.2

The 3D shape of created, modified, or imported volumes must be reviewed in a 3D view before being used for treatment plan evaluation.

3 Select the structure set to import and click **Import**.

The data are imported and saved with the examination. The imported volumes can be viewed and edited in the Regions and Volume dialog.

4 Repeat steps 2 to 3 if more structure sets are to be imported, otherwise click on **Close** to close the DICOM import dialog.

Note: *If the image study in which the structure set is drawn differs from the visualization model, the accuracy of the imported data may be degraded. A warning will be shown if the difference exceeds 0.1 mm.*

Related Links:

Importing the patient's images on page 101

Regions and volumes on page 154

Tomographic image validation visualization model on page 351

5.3.5 Description of the export of DICOM RT data

Note: *DICOM RT functionality is only available if licensed.*

This section describes how to export plans, dose and structure sets in DICOM RT format from the application. It is possible to export the data both to a USB device and via the network to a remote DICOM server.

- The exported plan, exported dose and the exported structure sets are always exported in the context of a tomographic image study providing a reference coordinate system for the objects.
- Dose is exported as a DICOM RT Dose object, containing a grid of absolute dose values. The axes of the grid are aligned with the reference image study and the resolution of the grid can be selected when exporting. Also, the skull volume is automatically included in the structure set.

Note: *The dose in the grid aligned with the reference image study is linearly interpolated from the treatment plan dose grid for the selected resolution and dose algorithm. The exported aligned dose grid will therefore normally not contain the maximum dose as seen within Leksell GammaPlan®.*

- Plans are exported as DICOM RT Plan objects where the Shots are represented by entries in the beam sequence of the plan.
- Volumes defined in the Regions and Volumes tool can be exported as a DICOM RT Structure Set. The volumes are reconstructed in the image planes of the reference image study. This means that the same contours are exported as the ones shown when viewing the volume in the reference image study in the views of a workspace.

5.3.5.1 Description of the DICOM Export dialog

The DICOM Export dialog provides the user interface to export data to the DICOM server or to a USB storage.

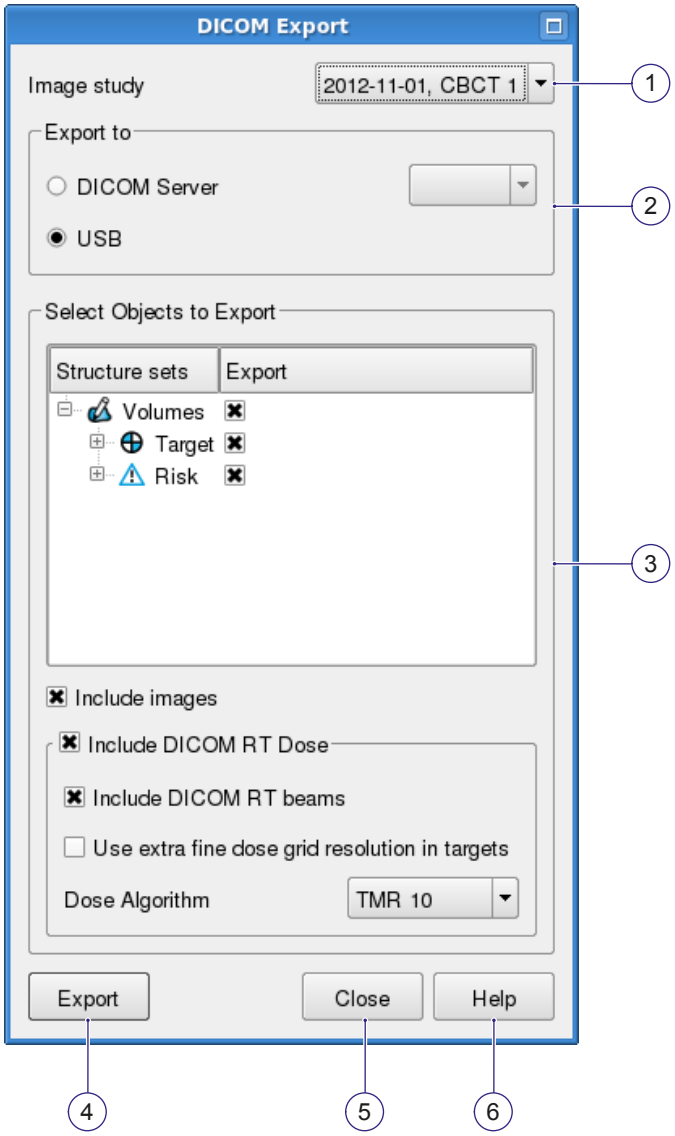


Figure 5.11 The DICOM Export dialog

(1) **Image study** selection

(2) **Export to** frame

(3) **Select Objects to Export** frame

(4) **Export** button

(5) **Close** button

(6) **Help** button

From the **Image study** drop-down list (1), you select the image study to use as reference.

In the **Export to** frame (2) you select the destination for the export. The objects can either be exported to a configured **DICOM Server** from the drop-down list or to a **USB** device.

The objects list in the **Select Objects to Export** frame (3) contains the volumes that are possible to export.

- The objects list is split into two columns: **Structure sets** and **Export**.
- The objects are shown in a hierarchical list - when an item in the tree is selected or unselected, the items below it will be selected or unselected too. The items above it will be updated to indicate whether none, some or all objects below are selected.

- Only volumes drawn in tomographic image studies are possible to export and the image study must be defined.
- A structure set object will be created containing the volumes whose check box is marked in the Export column (if any).

The **Select Objects to Export** frame also contains:

- Check boxes for:
  - **Include Images** - mark the check box to export the images reference with the DICOM RT objects.
  - **Include Dicom RT Dose** - mark the check box to include the dose with the DICOM RT objects. The skull volume will be exported as a DICOM RT structure set if DICOM RT dose is exported.
  - **Include Dicom RT beams** - mark the check box to include the RT beams with the DICOM RT objects. (This option is selectable due to the fact that some systems require DICOM RT beams, and some systems prefer without, because it simplifies the necessary configuration in the other system.)
  - **Use extra fine dose grid resolution in targets** - mark the check box to use extra fine dose grid resolution in the targets.
- A drop-down list for selecting **Dose Algorithm** - select the dose algorithm to be used for the dose calculations.

The **DICOM Export** dialog also contains these push buttons:

- **Export** button - click this button to export the data.
- **Close** button - click this button to close the dialog.
- **Help** button - click this button to open the *Online Reference Manual*.

5.3.5.2 Exporting DICOM RT objects

1. In the **Patient** menu, select **Export DICOM**.

   The DICOM Export dialog opens.
2. Select the image study to use as reference.
3. In the **Export to** frame, select the destination for the export:
   - To export the data to a remote DICOM server, select the **DICOM Server**.
   - To export the data to a USB device, select **USB** and connect the USB device.
4. To export the images reference with the DICOM RT objects, select the check box **Include images**.
5. To include the dose with the DICOM RT objects, select the check box **Include Dicom RT Dose**.

   If this check box is not selected, the alternatives within the frame will be grayed-out and not possible to select.
6. To include the RT beams with the DICOM RT objects, select the check box **Include Dicom RT beams**.
7. To use extra fine dose grid in targets, select the check box **Use extra fine dose grid resolution in targets**.
8. Select the dose algorithm to be used for dose calculations.
9. Click **Export** to export the data.

Note: *Depending on chosen dose grid resolution and dose algorithm, the dose calculations performed during export can be very time-consuming. You may start a new instance of the application in another desktop to perform other tasks while waiting for the export to finish.*

Note: *If the image study differs from the visualization model, the accuracy of the exported data may be degraded. A warning will be shown if the difference exceeds 0.1 mm.*

Related Links:

Introduction to mathematical modeling on page 309

Tomographic image validation visualization model on page 351

5.4 Requesting CBCT images

To request a CBCT scan from Leksell Gamma Knife® Icon™, do as follows:

1 From the **Patient** menu, select **Request CBCT > Stand Alone**.

The **CBCT request is pending** icon appears in the menu bar. When the CBCT scan is completed by the Leksell Gamma Knife® Icon™ operator, the icon is changed to an ordinary image study icon.

Figure 5.12 The CBCT request is pending icon

5.5 Working with image studies

5.5.1 Study grayscale

The grayscale of the images can be set and adjusted:

- by selecting **Level** in the image study icon drop-down menu when defining the image study
- when viewing images on screen during treatment planning.

5.5.1.1 Description of grayscale settings in the Level dialog or when defining the study

In the Level dialog, or during the study definition, you set the base grayscale level of the images in the study. You use grayscale controls in the Level or Define Study dialog to obtain a setting that provides optimum visibility of fiducials, markers and anatomical features:

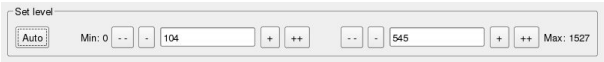


Figure 5.13 Grayscale adjustment during study definition

The left and right values define, respectively, the lowest and highest luminosity values that will be kept in the images. Your aim is to reduce the image dynamics as much as possible, to allow the remaining grayscale levels to be well separated when displayed on screen. You try to cut off the parts of the spectrum that do not contain any information. In other words, you should try and

find values that are as close to each other as possible, without losing important features in the images.

This setting applies to all image slices in the study.

Note: *The application automatically attempts to find the best settings for brightness and contrast when an image study is imported. The settings can still be adjusted as seen fit. Pressing "Auto" reverts to the automatic settings.*

5.5.1.2 Setting grayscale during treatment planning

During treatment planning you can further adjust the grayscale setting by using the mouse. Note that the grayscale is reset to the settings from the Level dialog when a workspace is reopened.

1. To change the brightness setting, hold down the keyboard <Ctrl> key and the right mouse button, and move the mouse up and down.
2. To change the contrast setting, hold down the keyboard <Ctrl> key and the middle mouse button, and move the mouse up and down.

5.5.2 Tomographic study definition

When you open a patient's image study for the first time, you must define the study. Study definition is the procedure in which you inform the treatment planning application of the relative positions of the images in a study and confirm that the quality of the images is acceptable. For CBCT images, you just have to confirm an automatic definition. Other tomographic images are defined by aligning the fiducial markers generated in the treatment planning application with the fiducials imposed on the image during acquisition.

Note: *Before you start planning treatment, the patient's image studies must have been defined.*

5.5.2.1 Defining a CBCT study from Leksell Gamma Knife® Icon™

A CBCT study from Leksell Gamma Knife® Icon™ is stereotactically localized by default and, therefore, study definition using fiducials is not applicable. You only have to confirm that you want to define the study.

1. Open the patient's file, and the radiological examination that contains the study that you want to define.
2. Click on the icon of the study that you want to define and select **Define Stereotactic Reference**.

   The Confirm Definition dialog opens.
3. Verify the date and time of the study and click **Yes** to define the CBCT study.

   The study is defined, and no further action is needed.

5.5.2.2 Tomographic study definition based on fiducials

Note: *Tomographic image studies containing non square images cannot be used for fiducial based definition.*

For tomographic image studies you define the slices in the original study. The overall tomographic procedure is summarized in the figure below.

You define an image by aligning the fiducial markers generated in the treatment planning application with the fiducials imposed on the image during acquisition.

When you have defined the original image slices in a study, the program automatically makes available reconstructed slices in the two other image directions. For example, if the original study contains axial image slices then the program reconstructs the study in the coronal and sagittal directions and requires you to confirm the definition and quality of these images.

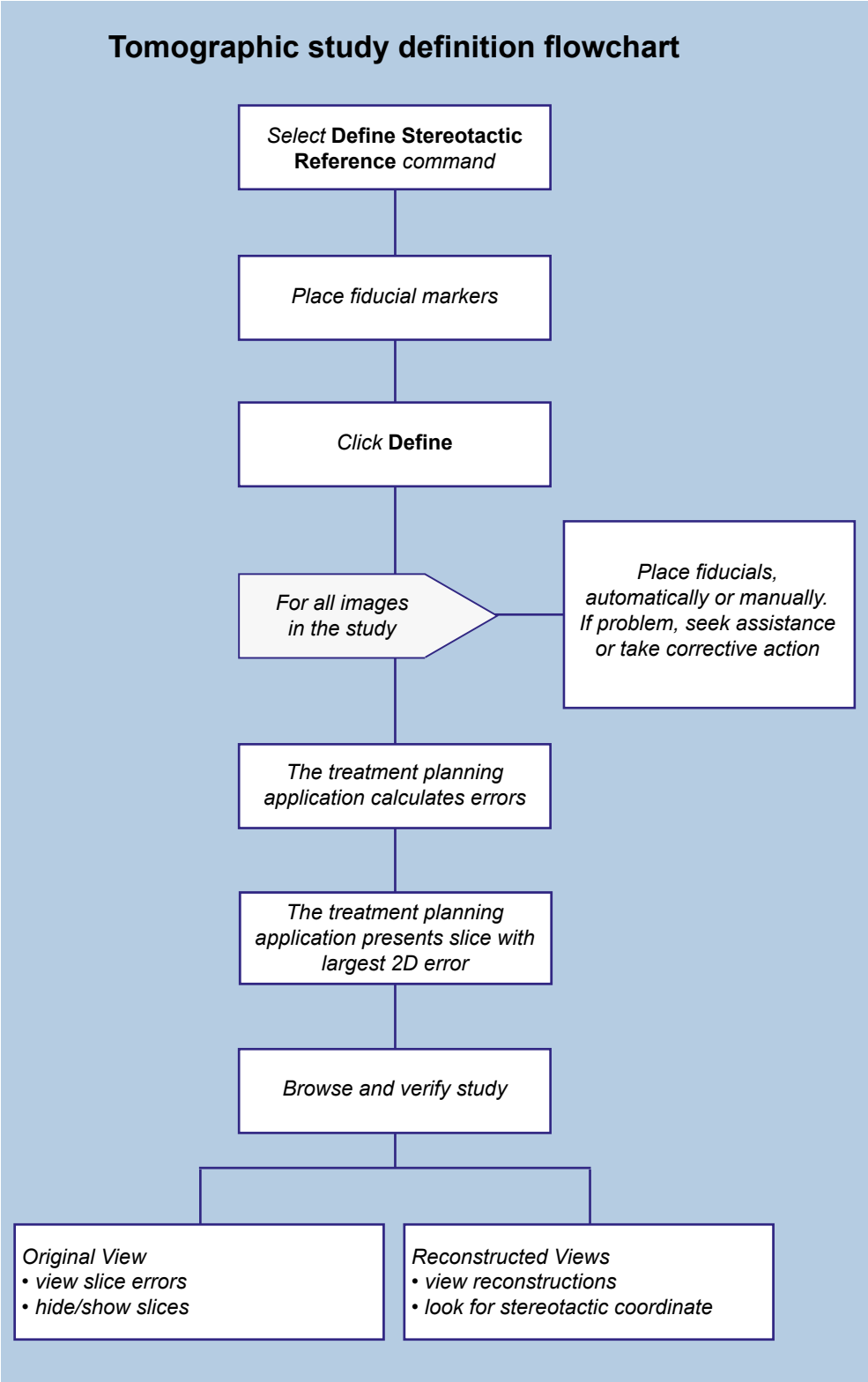


Figure 5.14 The workflow of tomographic study definition

Preparations when defining a tomographic study automatically

Before you define the study, do the following preparations.

1 Open the patient's file, and the radiological examination that contains the tomographic study that you want to define.

2 Click on the icon of the study that you want to define and select **Define Stereotactic Reference**.

The Define Study dialog opens. It displays the first image to be defined. The image slice number (1) is shown in the bottom right corner of the image.

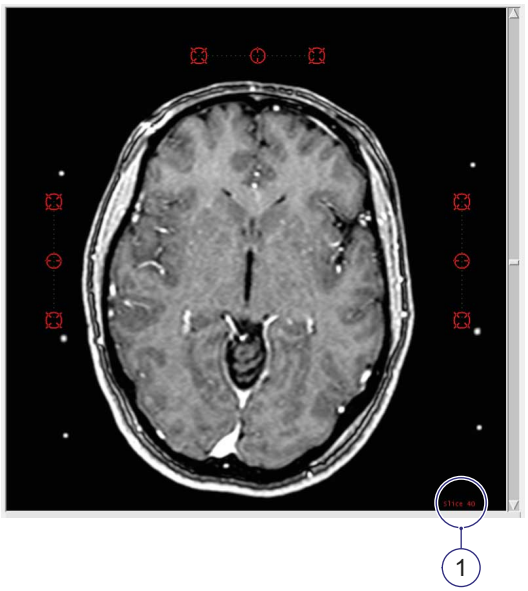


Figure 5.15 Image study displayed in the Define Study dialog

When defining a tomographic study automatically, you are usually required to define only one image slice in the original study. By default, the image slice at the center of the study is displayed first, but you can start the definition process at any suitable slice.

3 If you want to change image slice, use the vertical scroll bar in the Define Study dialog.

Note: *If you attempt to define images taken at the periphery of the indicator (where the fiducials may not be clearly distinct), a dialog will open. It offers you the option to include or exclude the slice(s) preceding the one at which you start.*

4 To inform the treatment planning application that the tomographic study is to be defined automatically, ensure that **Define manually** is not selected.

Figure 5.16 Define manually not selected in the Define Study dialog

5 If the patient's images have a third set of fiducials, use the option **Use third plate** to minimize the uncertainty of the study definition.

Note: *The third plate is used for verification only and not for calculating the study geometry.*

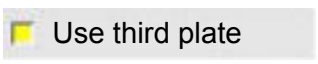


Figure 5.17 Use third plate selected in the Define Study dialog

6 If necessary, use the **Set Level** step fields to adjust the image grayscale so that the fiducials and markers are clearly visible.

Figure 5.18 Set Level step fields in the Define Study dialog

Note: *If necessary during treatment planning, you can readjust the image grayscale in the same way by using the **Level** command in the study icon menu.*

Postrequisites

When you have completed this task, define the original study.

Related Links:

Description of grayscale settings in the Level dialog or when defining the study on page 112

Defining the original study automatically

Prerequisites

Before defining the original study, you must select a study to be defined, select the definition parameters, select an image slice for definition, and set the image grayscale.

Observe that the marker automatically snaps into position over the fiducial. The color of the marker changes to green when it is correctly positioned.

WARNING 5.3

The color of a fiducial marker changes to green whenever it is positioned over a bright spot, irrespective of whether the marker is aligned to the correct (corresponding) fiducial or to other image structures or noise.

Note: *The automatic snap facility is enabled when you use the left button of the mouse. To prevent the marker from snapping to an unwanted object, use the center button of the mouse instead. This disables the snap facility.*

1 Drag the top left fiducial marker to the top left fiducial on the image.

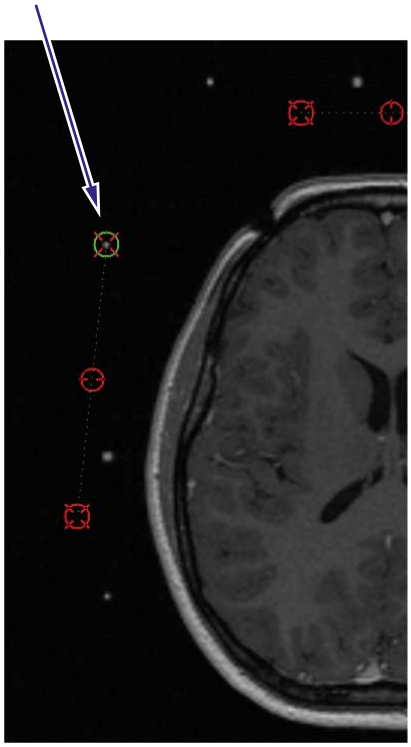


Figure 5.19 Dragging the top left fiducial marker to the top left fiducial

2 Now drag the bottom left fiducial marker to the bottom left fiducial.

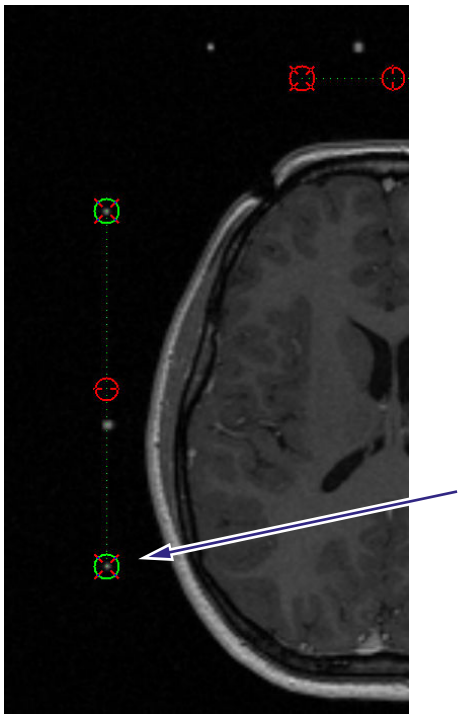


Figure 5.20 Dragging the bottom left fiducial marker to the bottom left fiducial

3 Drag the center left fiducial marker to the center left fiducial.

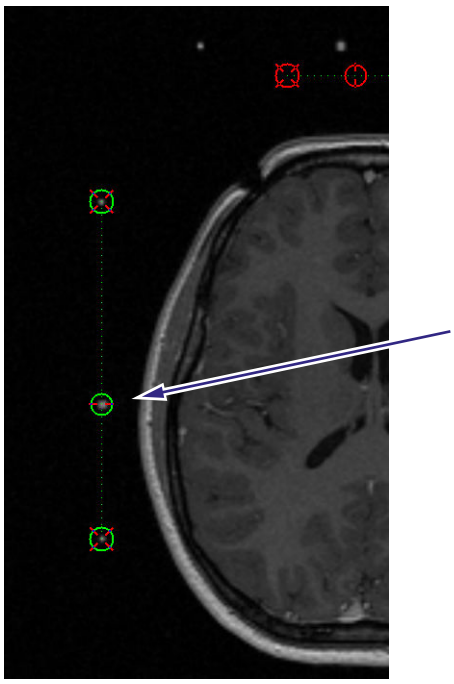


Figure 5.21 Dragging the center left fiducial marker to the center left fiducial

The fiducials and markers on the left side of the image are now aligned.

4 Repeat steps **1** to **3** and align the markers with the fiducials on the right side of the image.

5 If you checked **Use Third Plate** when selecting the definition parameters earlier, position the left third plate marker over the left fiducial.

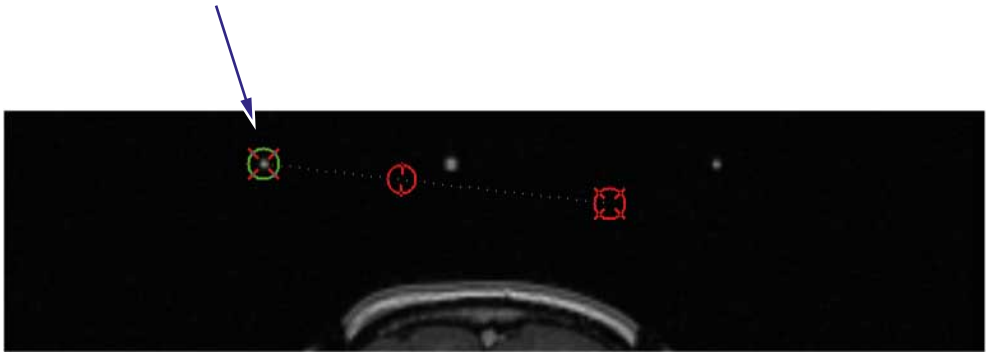


Figure 5.22 Positioning the left third plate marker over the left fiducial

6 Position the right third plate marker over the right fiducial.

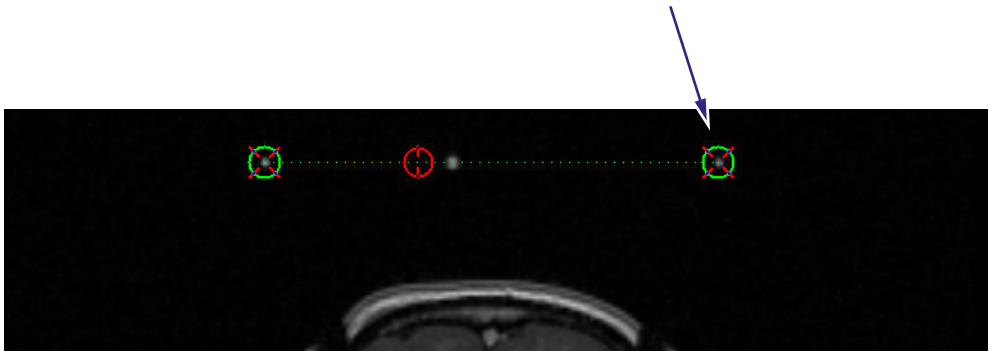


Figure 5.23 Positioning the right third plate marker over the right fiducial

7 Position the center third plate marker over the center fiducial.

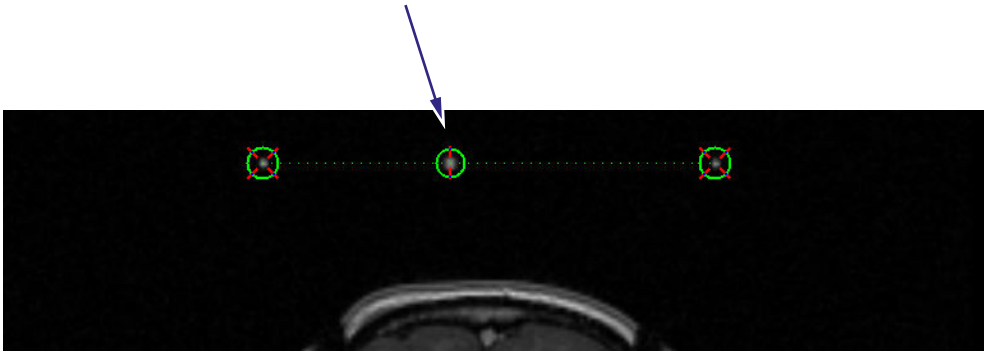


Figure 5.24 Positioning the center third plate marker over the center fiducial

When you have finished aligning all the markers, the image should resemble the figure below.

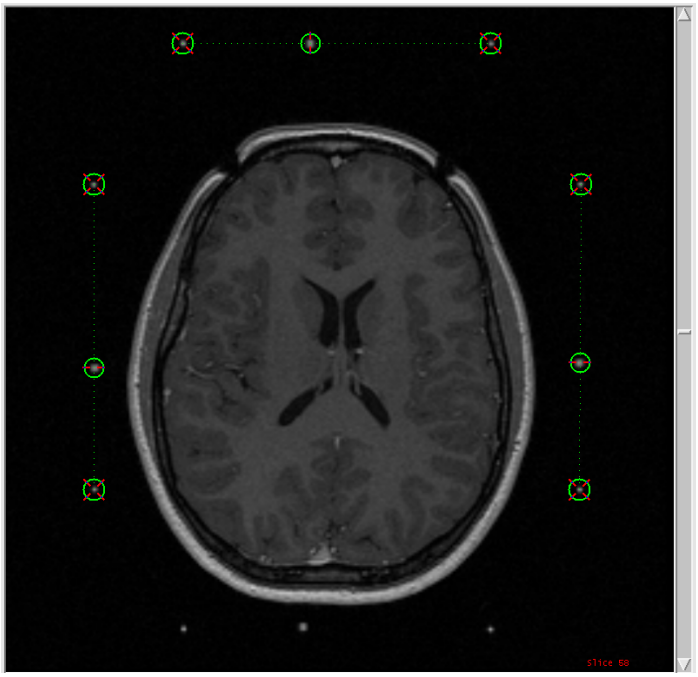


Figure 5.25 All fiducial markers aligned

Note: *The fiducial markers can be aligned in any order.*

8 When you are satisfied with the fiducial/marker alignment, click **Define**.

The program now executes geometrical consistency checks. If no errors are detected, then the study is defined and the settings for this image slice are stored. Based on the fiducial definition, the treatment planning application automatically searches for fiducials in the remaining slices of the study.

If the program detects an error in the image slices or the markers during study definition, then an appropriate dialog opens.

The slices are rapidly displayed in sequence. The fiducial markers are automatically placed on the fiducials of all succeeding slices. Consequently, the side markers track the fiducials up or down the image, and the third plate markers move across the image. (The direction of this movement depends on the order of the image slices as assigned by the scanner.)

The progress of the automatic definition procedure is also indicated by the movement of the slider in the vertical scroll bar.

If there are any images outside the indicator box, the following dialog will appear.

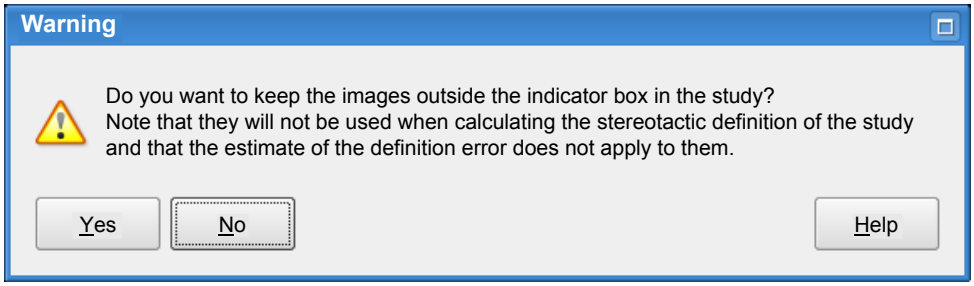


Figure 5.26 Warning dialog about images outside the indicator box

9 To include the images in the study, click **Yes**. To hide the images, click **No**.

It is important to note that the estimate of the definition error does not apply to the images outside the indicator box.

Postrequisites

After defining the original study, you must verify the definition result.

Verifying the result of an automatic study definition

Prerequisites

Before verifying the definition result, you must define the original study.

When the entire study has been defined, an information dialog opens. It states the mean and maximum errors in fiducial placement. These error values are an estimate of the accuracy of fiducial/fiducial marker correlation throughout the study.

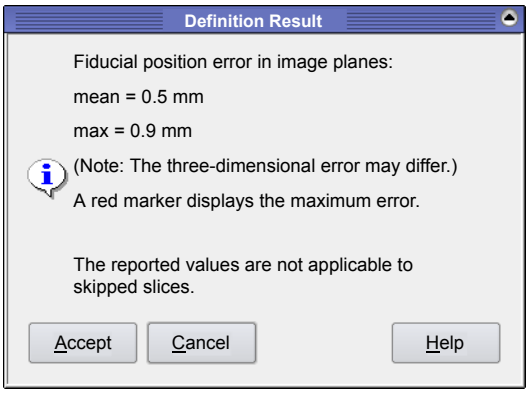


Figure 5.27 The Definition Result dialog

The image slice with the largest error value is automatically displayed in the Define Study dialog. The fiducial marker with the largest error on that slice is indicated by a red circle. In addition the maximum fiducial error is shown in red in the bottom right corner of the image.

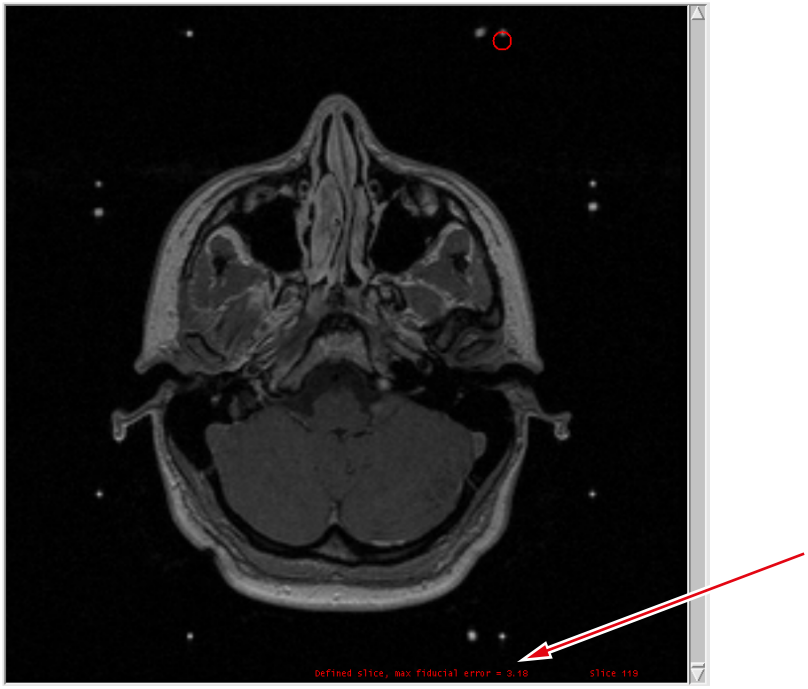


Figure 5.28 The image slice with the largest error value

1 If the accuracy is unacceptable, click **Cancel**.

   In this event you must repeat the entire definition procedure until an acceptable accuracy is achieved. Alternatively you can attempt to define the study manually.

2 If the accuracy is acceptable, click **Accept**.

   The View Study dialog opens.

3 Check the other image slices in the study. The maximum error in each image is indicated by a red circle.

Note: *If you excluded any image slices from the definition procedure then all the fiducial markers on these images will be marked by a red circle to show that they have not been defined.*

Note: *Error values do not necessarily indicate an unusable study, although a high value usually means that the study is of poor quality.*

Initially the **Log Window** field of the View Study dialog shows the definition status of the original study. For example:

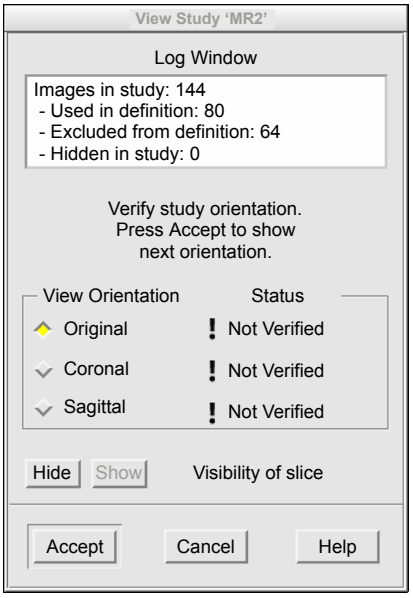


Figure 5.29 Definition status of the original study, Not Verified

4 If you are satisfied with the definition of the original study, in the View Study dialog click **Accept**.

The **Log Window** then shows that the original study is **OK** and the original study is shown as **ACCEPTED** in the **View Orientation/Status** field. For example:

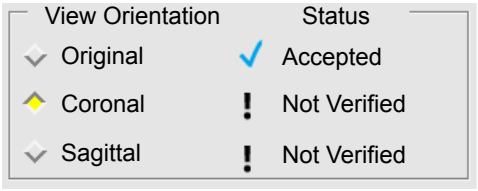


Figure 5.30 Definition status of the original study, Accepted

Postrequisites

After verifying the definition result, you must define the reconstructed studies.

Description of estimated error of the fiducial marker positions

The error in fiducial marker position can be measured in each two-dimensional image plane only. Hence, any occurring three-dimensional errors like shifts and rotations are not included in the individual error estimates.

The ability to detect and measure three-dimensional shifts and rotations increases with the distance between the first and the last image used when defining an image study. As a rule of thumb, a stack height of at least 5 cm gives a reasonable agreement between 2D and 3D errors. If the image stack is less than 5 cm, you get an information message.

To minimize any uncertainty further, check the option **Use third plate** (if applicable) at the beginning of the image study definition process.

Related Links:

Recommendations for tomographic image acquisition on page 367

Defining the reconstructed studies

Prerequisites

Before defining the reconstructed studies, you must verify the definition result from the original study.

When the original study is accepted, you can examine and accept the two reconstructed image studies that derive from the original study.

1 Ensure that View Orientation of the reconstructed study that you want to define next is selected:

Figure 5.31 View Orientation selected, Coronal

The first image slice in that reconstructed study appears in the Define Study dialog.

2 Use the vertical scroll bar in the Define Study dialog to examine each image slice in turn. Visually inspect the positions of the fiducial markers and the fiducials on the images.

3 When examining the fiducials and markers, check the overall quality of each image also.

4 When you are satisfied that the reconstructed study is properly defined, in the View Study dialog click **Accept**.

The **Status** of that view orientation is now shown as **ACCEPTED** and the third **View Orientation** button is automatically selected.

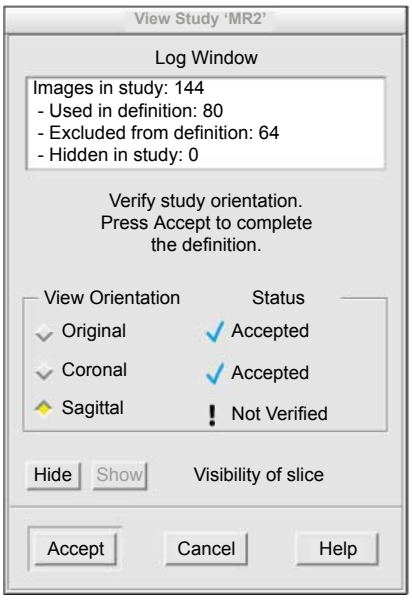


Figure 5.32 Definition status of the original and one reconstructed study, Accepted

5 Verify the images in the third reconstructed study as described in steps **1** , **2** and **3** above.

6 In the View Study dialog click **Accept**.

7 Click **OK**.

8 All open dialogs close.

This concludes the automatic definition of a tomographic image study.

Defining a tomographic study manually

Instead of automatically defining a tomographic study, you can manually define each image slice in the study. Typically you would use this technique if the automatic definition procedure persists in placing a fiducial marker at an incorrect location such as an earlobe, or on image noise. You can also attempt to manually define a study if the automatic definition process returns excessive error values.

1 Click on the icon of the study that you want to define and select **Define Stereotactic Reference**.

The Define Study dialog opens.

2 Select **Define manually**.

3 If the patient's images have a third set of fiducials the option **Use third plate** may be used to minimize the uncertainty of the study definition.

4 Use the scroll bar to select the first image slice to be defined. You can start at any suitable slice – it need not be the first slice in the study.

5 Use the step buttons in the **Set Level** area to adjust the image grayscale so that the fiducials and markers become clearly visible.

The grayscale levels in the displayed image slice will be adjusted to your settings.

6 Align the fiducial markers and the fiducials in the image slice.

7 When you are satisfied with the fiducial/marker alignment click **Define**.

8 If the manual definition is not started on the first image, the following dialog will appear.

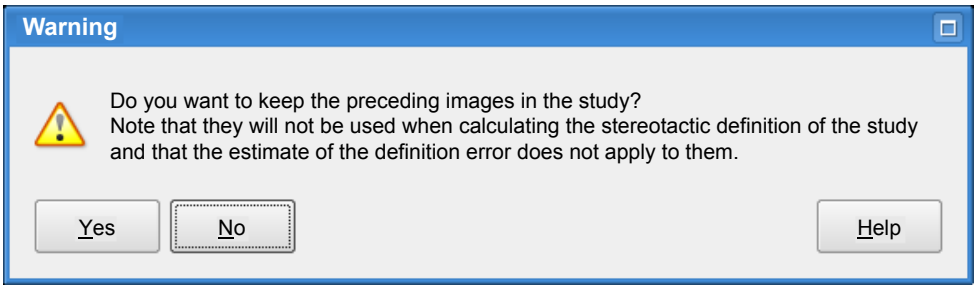


Figure 5.33 Warning about including images

By clicking **Yes** in the dialog, the images preceding the selected one will be included in the study. By clicking **No**, the images will be hidden. It is important to note that the estimate of the definition error does not apply to these images, i.e. the images not included in the definition.

9 The Slice Options dialog opens.

10 Check the overall quality of the image slice.

11 Are both the image quality and the fiducial/marker alignment acceptable?

– If Yes, click **Accept**.

The Slice Options dialog closes.

– If No, click **Next**.

The Slice Options dialog closes. This image slice is not included in the mathematical calculations of the study definition procedure but the image slice remains in the study.

12 When the Slice Options dialog closes, the treatment planning application automatically displays the next image in the Define Study dialog. The slice number is given in the bottom left corner of the image. Repeat steps **6** to **12** for each image.

13 When you have defined all the images that you require, in the Slice Options dialog click **Done**.

A Warning dialog opens.

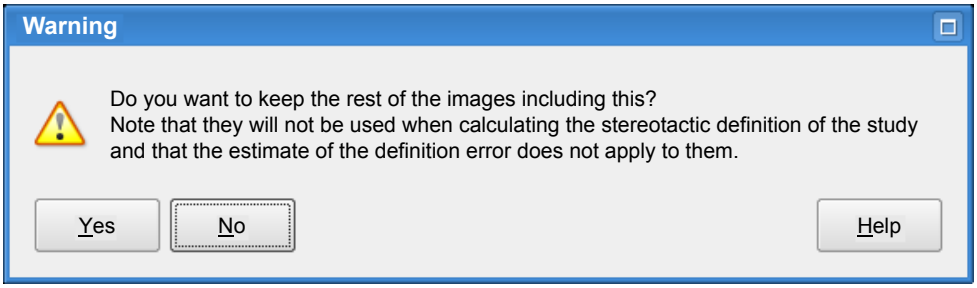


Figure 5.34 Warning about including images

By clicking **Yes** in the dialog, the rest of the images will be included in the study. By clicking **No**, the images will be hidden. It is important to note that the estimate of the definition error does not apply to these images, i.e. the images not included in the definition.

14 When the entire study has been defined, an information dialog opens. If the accuracy is acceptable, click **Accept**.

The View Study dialog opens.

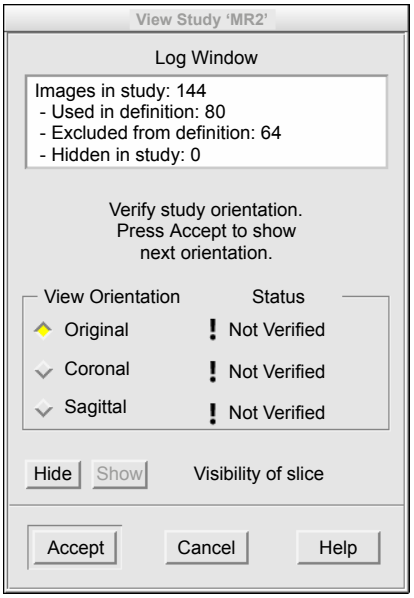


Figure 5.35 The View Study dialog

15 Are you satisfied with the definition of the original study?

– If Yes, click **Accept**.

The **Log Window** shows that the original study is **OK** and the original study is shown as **ACCEPTED** in the **View Orientation/Status** field.

– If No, click **Cancel**.

In this case you must repeat the manual definition procedure until you achieve an acceptable degree of accuracy.

16 Examine and accept the two reconstructed image studies that derive from the original study.

This concludes the manual definition of a tomographic image study. You can manually define any other tomographic image studies of the patient in the same way.

Related Links:

Defining the reconstructed studies on page 122

Description of grayscale settings in the Level dialog or when defining the study on page 112

Error conditions during study definition

When defining image studies there are several circumstances under which the treatment planning application may display warning dialogs. These dialogs are self-explanatory and typically they occur if:

- the fiducial markers have not been properly aligned to the correct fiducial
- the mean/maximum error is unacceptable
- an image slice is distorted
- during scanning an image was not fully enclosed by the indicator box.

WARNING 5.4

The treatment planning application does not compensate for distorted or misaligned images. Such images shall not be used for treatment planning or subsequent surgery.

Individual image slices that are not of acceptable quality and slices that do not include useful anatomical detail can be omitted from the automatic or manual definition procedure and/or hidden from view.

When defining an image study it is critical to ensure that each image slice is of an acceptable visual quality and is not excessively distorted. Slices that do not meet these criteria can be skipped or hidden during the definition procedure.

Quality control: skipping image slices

When the treatment planning application detects a distorted image slice you are offered the option to include the slice in the study definition or to skip the slice. If you decide to skip an image slice, then that slice is excluded from all calculations of the study geometry and therefore has no effect on the final accuracy of the definition.

1 To skip an image during the study definition procedure, in the Slice Options dialog click **Next**.

Note: *Skipped slices are not deleted from their study - they are merely excluded from all mathematical processing associated with the study. They can be included in the mathematical calculations by repeating the definition procedure and choosing not to skip these images.*

Quality control: hiding image slices

During the definition procedure you can choose to hide an image slice that is of unacceptable quality or has no anatomical interest. In this event the slice is no longer displayed in the Define Study dialog or when the study is subsequently opened in a workspace. Instead, a blank space occupies that slice's position in all views. Hidden slices are also excluded from the calculations of study geometry and have no effect on the definition procedure.

1 To hide an image during the study definition procedure, in the View Study dialog click **Hide**.

2 To restore a hidden image, in the View Study dialog click **Show**.

Note: *Hidden slices are not deleted from their study – they are merely not shown. They can be restored to view.*

5.5.3 Co-registration of a study with ImageMerge™

An image study that has been acquired without stereotactic reference can be co-registered to another image study and be used for treatment planning in that way. Co-registration can be done with the optional software ImageMerge™.

ImageMerge™ provides functionality for registering image studies as well as for verifying the accuracy of the resulting co-registration.

Image studies that have been co-registered to stereotactic image studies can be used like any other stereotactic study in the treatment planning application. Only image studies in the same examination can be co-registered.

The automatic co-registration is based on an algorithm that matches mutual information in the images. By design, the co-registration does not alter the shape or form of the images to compensate for distorted images. If both images have the same frame of reference, this may optionally be used to register the images.

5.5.3.1 Important considerations when coregistering a study with ImageMerge™

The software does not validate if co-registered images can be used or not. You must visually verify and validate the co-registration in all orientations before allowing the image study to be used for treatment planning purposes.

Image study recommendations when co-registering a study

To get the best co-registration in the treatment planning application, recommendations about slice distance, overlap, and orientation have to be followed.

The recommendations for image acquisition, given in this manual, shall be followed.

WARNING 5.5

Defects or distortions in images may result in inaccuracies or invalid co-registration. The treatment planning application does not compensate for distorted or defective images. Such images must not be used for co-registration.

Related Links:

Tomographic image acquisition using indicator box on page 57

Tomographic image acquisition using Leksell Gamma Knife® Icon™ CBCT on page 61

Recommendations for slice distances of the two image studies

To be able to verify the correctness of a registration, the image studies need to cover some easily distinguishable anatomical structures that are common to both the co-registered and the reference image study. It is important that these anatomical structures, or anatomical landmarks, are not only contained in the image studies but also clearly distinguishable. Adjust the slice distance accordingly.

Recommendations for overlap between the two studies

The image studies do not have to be completely overlapping. But for the registration to succeed, it is recommended that 1000 cm^3 of the image study volume is the same for the two studies. In general, the registration gets more accurate and is easier to verify with a larger overlap.

WARNING 5.6

Co-registration of not sufficiently overlapping or non-overlapping image studies may result in invalid or inaccurate co-registration.

Recommendations for different orientations in the two studies

The treatment planning application allows for co-registering image studies of different orientations. However, the result of such a co-registration is often hard to verify, especially when slice distances are large. This needs to be considered when acquiring images of different orientations to be co-registered.

The same reasoning as on image overlap applies in the case of co-registering image studies of different orientations. That is, 1000 cm^3 of the image study volume needs to be the same for the two studies. To facilitate the verification process, assure that the image studies contain anatomical structures that are common to both image studies for the verification.

5.5.3.2 Co-registration procedure

A co-registration includes the following steps:

1 Open the co-registration dialog.

2 Select the reference study.

3 If preferred, define a region of interest.

4 Do the registration:

If	Then
The two image studies are acquired using the same frame of reference	Select same frame of reference registration
The two image studies do not have the same frame of reference	**1** If needed, do a manual co-registration **2** Run automatic co-registration

5 Review and approve the registration.

Opening the co-registration dialog

1 Click on the image study icon of the target study and select **Co-register** from the drop-down menu.

The co-registration dialog opens and the selected study name is presented.

Description of the co-registration dialog

The co-registration dialog consists of a workspace, and controls for handling studies, views, and registration to the right of the workspace.

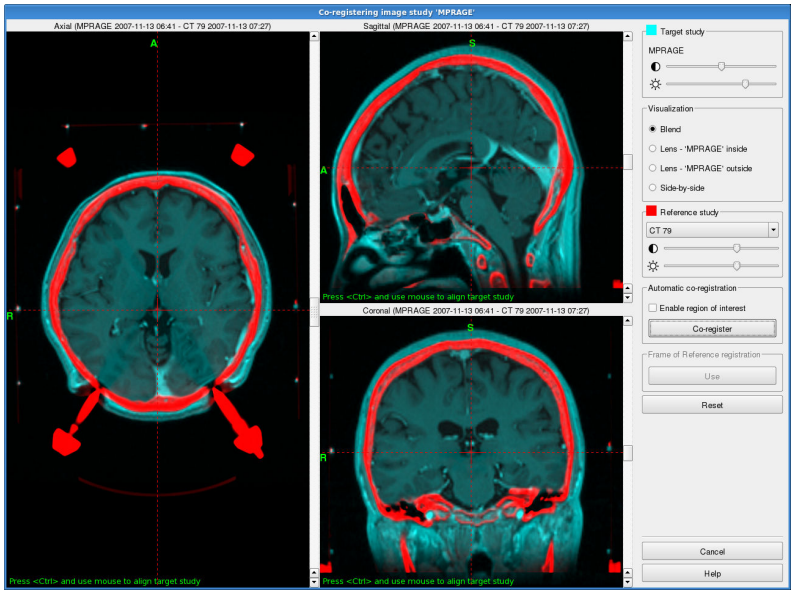


Figure 5.36 The co-registration dialog

The images of the target study and the reference study are displayed in the workspace. The way they are displayed, is selected in the **Visualization** frame. All images contain orientation information.

Exploring the images in the workspace

The following methods for study exploration are available in the workspace:

- To move the exploration cross, move the mouse over it, press the left mouse button and drag the cross with the mouse while keeping the left mouse button pressed down.

  All 2D views are updated so that they show image planes intersecting at the position of the exploration cross.
- To zoom, press the right mouse button in a view and move the cursor downwards for zooming in and upwards for zooming out.
- To select a slice, use the mouse scroll wheel or move the scroll bar at the right of the window.

  The exploration cross is moved to the selected slice and the other 2D views are updated accordingly.

Description of the visualization modes

The visualization frame in the co-registration dialog contains radio buttons for selecting the visualization mode to use in the image study views. The visualization modes are:

- **Blend**
- **Lens**
- **Side-by-side**

The workspace of the **Blend** and **Lens** modes has three windows. The original images of the target study are displayed in the left window, and the two other windows display reconstructed images of the study in perpendicular orientations.

Select **Blend** to display the target study and the reference study in different coloring on top of each other in the views. The colors used for the target and reference studies are displayed in the image study frames. The colors used can be cycled by clicking the color fields next to the image study name. This mode allows you to verify the match of the studies in the entire view.

Select **Lens** to display one of the studies inside a moveable lens in the view, and the other outside. You can select to display the target study inside or outside the lens. These modes allow you to verify the match of the studies on a detailed level in the studies. You can navigate to anatomical landmarks and verify that the result is correct, and also zoom in the views to visualize anatomical details in the image studies.

Select **Side-by-side** to display the different orientations of the target study and the reference study in six separate windows. The axial, sagittal and coronal views of the target study are displayed in the first row, and the corresponding views of the reference study are displayed in the second row.

Exploring the studies in the Lens visualization mode in the co-registration dialog

In the **Lens** visualization mode, you can navigate to anatomical landmarks and verify that the result is correct, and also zoom in the views to visualize anatomical details in the image studies:

- To move the lens, press the left mouse button when the cursor is inside the lens and move the cursor.

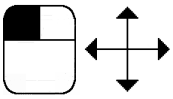


Figure 5.37 Moving the lens

- To resize the lens, press the right mouse button when the cursor is inside the lens and move the cursor upwards for a smaller lens, and downwards for a larger lens.

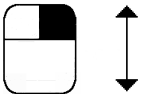


Figure 5.38 Resizing the lens

Note: *Pan and zoom in the windows are disabled when the cursor is inside the lens.*

Related Links:

Description of the co-registration dialog on page 128

Description of the visualization modes on page 129

Adjusting brightness and contrast of a study

1 To adjust brightness and contrast of a study, use the two slider bars in the study frame.

Note: *The contrast and brightness settings do not affect the automatic co-registration. The settings only affect the visibility on the screen.*

Related Links:

Description of the co-registration dialog on page 128

Selecting the reference study

1 In the **Reference study** frame, select a reference study among the defined studies in the examination in the drop-down selection list.

The views display slices of both the study to co-register, which is called the target study, and the reference study. In the **Blend** and **Lens** visualization modes, the center of the reference study is positioned at the center of the target study.

Note: *It is possible to use both stereotactic studies and previously co-registered studies as reference.*

Related Links:

Description of the co-registration dialog on page 128

Defining a region of interest

Optionally, a region of interest in the selected image study can be defined and used by the automatic co-registration. By default, the whole image study is considered when doing the automatic registration, but if a region of interest is defined, only the part of the image study that is inside the region is considered. Defining a region of interest can be useful to exclude parts of the image studies containing distortion or parts that differs for some other reason, for example

that the neck is in a different position. It is still important to include a large part of the anatomy for the best co-registration result.

To define a region of interest, do the following:

1 Select **Enable region of interest** in the **Automatic co-registration** frame.

The region of interest is shown in turquoise in the views.

2 Resize the region of interest by dragging the borders using the left mouse button.

3 Move the whole region of interest by pressing down the <Shift> key and dragging the region using the left mouse button.

Related Links:

Description of the co-registration dialog on page 128

Registering images using same frame of reference

The target study and the reference study have the same frame of reference if they, for example, are acquired using the same multi-modality scanner.

WARNING 5.7

It is not a guarantee for good alignment that two image studies have the same frame of reference. You always have to carefully review the registration.

1 In the **Frame of Reference registration** frame, click **Use**.

When the registration is finished, the workspace shows the aligned images, and the **Review registration** frame is displayed.

Postrequisites

When the registration is finished, you must review and approve it.

Related Links:

Reviewing and approving a co-registration on page 132

Running automatic co-registration

1 Press the **Co-register** button in the **Automatic co-registration** frame.

During automatic co-registration, a progress dialog opens.

The position of the target study in the windows is updated throughout the process, displaying how the target study and the reference study are aligned.

The time used for automatic co-registration depends on the image quality and the size of the image studies to be registered.

When the co-registration is finished, the progress dialog is closed, the co-registration workspace shows the aligned images, and the **Review registration** frame is displayed.

Note: *The search space for the automatic registration limits rotations to 30 degrees and translations to 5 cm. If the starting position differs more than this from the optimal position, you may need to align the images manually before running automatic co-registration.*

Postrequisites

When the co-registration is finished, you must review and approve it.

Related Links:

Reviewing and approving a co-registration on page 132

Aligning images manually on page 132

Aligning images manually

A manual alignment of the images can improve the chances for the automatic co-registration to succeed if the images are misaligned. It is recommended that manual alignment is done using the 'Blend' visualization mode.

1 Press and hold down the <Ctrl> key on the keyboard and align the target and reference study by holding down the left or right mouse button and moving the mouse.

   a Holding down the left mouse button and moving the mouse translates the reference study accordingly.

   b Holding down the right mouse button and moving the mouse rotates the reference study.

2 Exploring and zooming in the view can be done without the <Ctrl> key pressed.

Reviewing and approving a co-registration

1 In the **Review registration** frame, select the study you want to use for reviewing the co-registration.

   If the reference study is previously co-registered to other studies, or if there are other stereotactically defined studies, it is possible to select those studies too. This means that you can review the registration to multiple studies, not only to the reference study.

WARNING 5.8

Significant anatomical discrepancies, such as excessive tumor growth or other malformations, between the study to co-register and the reference study may result in invalid or inaccurate automatic registration.

WARNING 5.9

Co-registration of intrinsically significantly different image modalities may result in invalid or inaccurate automatic registration due to insufficient mutual information.

2 Carefully review the co-registration using the methods described in this manual. Use the different visualization modes and adjust the brightness and contrast of the studies if needed.

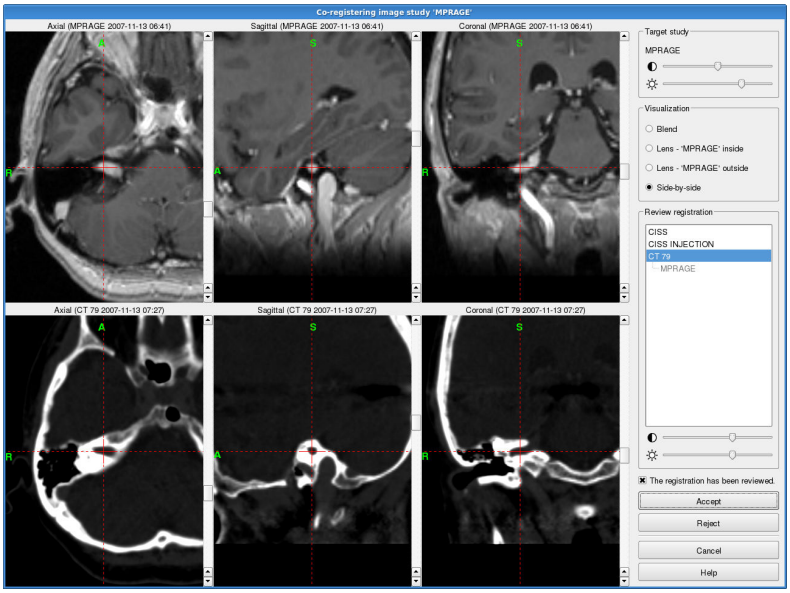


Figure 5.39 Visualization mode Side-by-side

3 If you want to review the target study against another available study, repeat step **1** to **2**

4 Accept or reject the co-registration:

- If the co-registration is of sufficient quality, select the **The registration has been reviewed** check box and click **Accept**.
- If you want to reject the co-registration, click **Reject**.

If the co-registration was accepted, the co-registration dialog closes. If the co-registration was rejected, the dialog remains open and you can start a new co-registration.

Related Links:

Exploring the images in the workspace on page 128

Exploring the studies in the Lens visualization mode in the co-registration dialog on page 129

Description of the visualization modes on page 129

Aligning images using fusion

Non-stereotactic images can be aligned outside the co-registration dialog, using the fusion function.

Related Links:

Using fusion to align images in Workspace views on page 139

5.5.4 Angiographic study definition

An angiographic image study consists of a single projectional image only: it does not contain multiple image slices. To define an angiographic study it is merely necessary to align the treatment planning application fiducial markers with the fiducials on the image, and place the patient's positional marker.

5.5.4.1 Defining an angiographic study

Angiographic image studies can only be defined manually. There is no automatic definition function.

1 Import the patient's angiographic image studies.

2 Click on the icon of the first study that you want to define and select **Define Stereotactic Reference**.

The Define Study dialog opens. It contains the angiographic image to be defined, superimposed with fiducial markers.

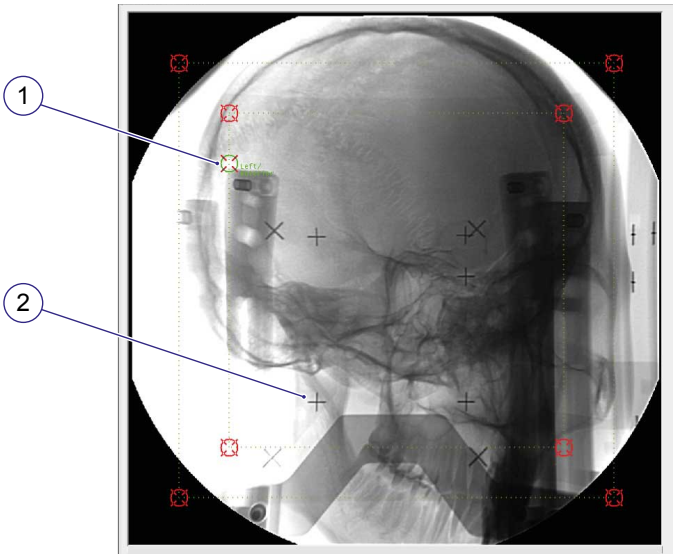


Figure 5.40 Image and fiducial markers

(1) Positional Marker

(2) Positional Fiducial

3 To make the fiducials and markers clearly visible, use the step buttons in the **Set Level** area to adjust the image grayscale.

Note: *If necessary during treatment planning, you can readjust the image grayscale in the same way by using the **Level** command in the study icon menu.*

4 Align the inner and outer sets of fiducial markers with the corresponding fiducials on the image. You can drag them in any order.

Click on the positional marker and drag it to the fifth inner fiducial.

When all markers have been correctly positioned the image should resemble the figure below.

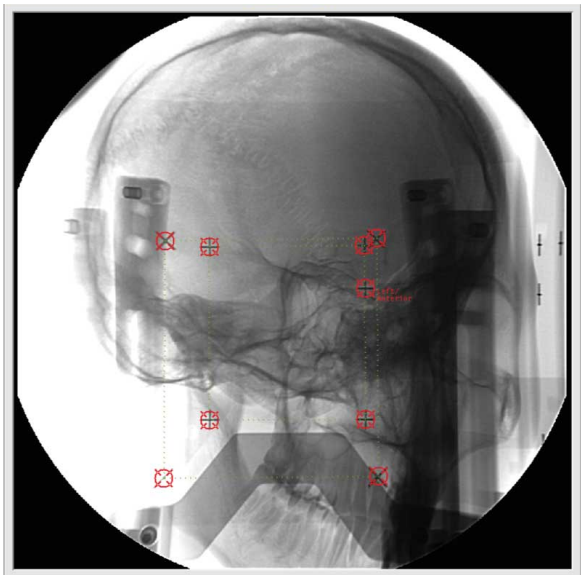


Figure 5.41 Markers correctly positioned

5 When you are satisfied with the fiducial and marker alignment, click **Define**.

The AI Orientation dialog opens.

6 Select the appropriate direction and orientation option. See figure below.

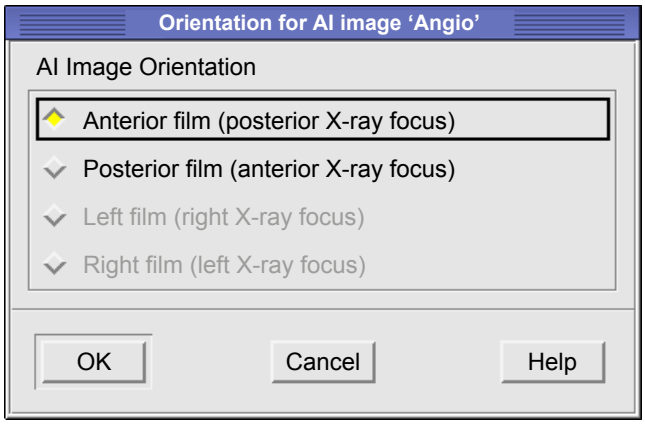


Figure 5.42 Orientation for AI image 'Angio'

7 Click **OK**.

The AI Orientation dialog closes. The treatment planning application now executes geometrical consistency checks. If no errors are detected, then the study is defined and the settings are stored.

An information dialog opens. It gives the accuracy of the fiducial markers.

8 If you are satisfied with the accuracy of the fiducial markers, click **Accept**.

The positional fiducial and a rectagonal frame, with corners aligned to a set of four fiducials, are projected in red onto the image, and an information dialog opens, presenting the location of the coordinate of the coordinate frame.

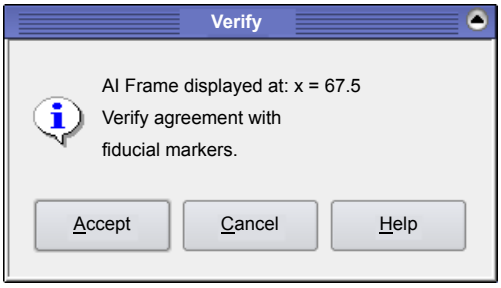


Figure 5.43 The Verify dialog

9 If you are satisfied with the accuracy of this projection, click **Accept**.

The coordinate frame is moved so that its corners align to the other set of fiducials and another information dialog gives the new coordinate of the coordinate frame.

10 If you are satisfied with the accuracy of this projection, click **Accept**.

The study is defined. The Define Study dialog and the information dialog close.

Go to step **12** .

11 If the accuracy of the fiducial markers or the coordinate frame is unacceptable, click **Cancel**.

In this event you must repeat the entire definition procedure until a satisfactory alignment is achieved.

12 You can now define the other angiographic projection (frontal or lateral) and any other images in the set as described in **2** to **11** .

Related Links:

Description of grayscale settings in the Level dialog or when defining the study on page 112

5.5.5 Opening an image study

When you have fully defined the patient's image studies you can open the images in a treatment planning application workspace.

1 Click on the icon of the study that you want to open and choose **View**.

When the information dialog closes the selected image study opens in a workspace as shown in the following example. You can now work with the opened image study.

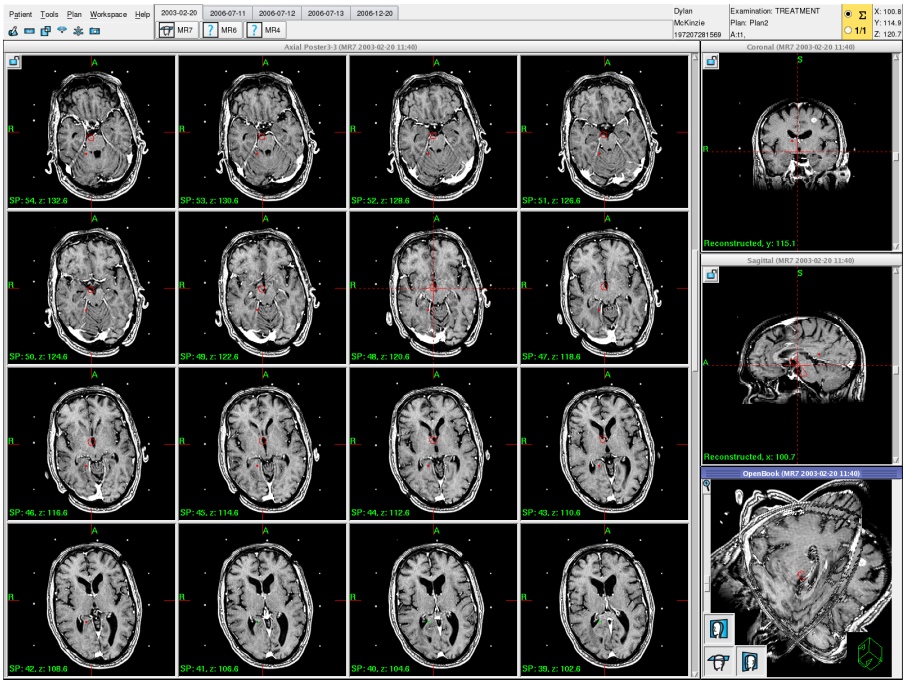


Figure 5.44 Treatment planning application workspace

In the treatment planning application, workspaces are independent of the studies displayed. The first time that you view a study in a new patient file, the workspace that opens is the first in the list of workspaces in the **Workspace** menu. You can use that workspace or view the study in another workspace by selecting a different workspace from the **Workspace** menu.

5.5.5.1 Opening other image studies

If the patient has more than one image study you can view another study in the open workspace.

1 Drag and drop the study icon palette on to one of the workspace windows by using the center button of the mouse.

5.5.6 Fuse studies

You can fuse (blend) two defined studies so that anatomical structures can be clearly visualized by enhancing the best features of both studies. This is done by setting maximum or minimum grayscale values, by mixing the studies, or by subtracting the characteristics of one study from the other. The two studies are known as the Reference study and the Target study.

5.5.6.1 Adding a new fused study

In the treatment planning application there are two methods of adding a fused study to the patient's treatment plan.

- Using the **Fuse** command
- Dragging and dropping the icons on the menu bar, using the center button of the mouse. This is the quickest method for fusing a pair of registered studies.

1 To open the Fuse studies dialog and select studies, obey one of these procedures.

Options	Description
Use the Fuse command	**1** From the drop-down menu of the study, select **Fuse**. The Fuse studies dialog opens. **2** Type a name for the new fused study in the name dialog. The **Reference study** text field shows the name of the image study you selected in the previous step. **3** The **Target study** drop-down menu lists all the registered studies that can be fused with the **Reference study**. Select the study that you want to fuse. ***Note:*** *The name of the **Reference study** is not included in the **Target study** list since a study cannot be fused to itself.*
Drag and drop the icons on the menu bar	**1** With the center button of the mouse, click on the icon that represents the **Target study**, drag it over the icon that represents the **Reference study**, then release the mouse button. The Fuse Studies dialog opens. It contains an item for the new fused study. The button is already configured with the **Reference study** and **Target study** that you selected.

2 From the **Fusion Function** drop-down list, select one of the options for image fusion. See table below.

Max Value	The images in the fused study will be reconstructed from the maximum grayscale values of the Reference study and the Target study.
Min Value	The images in the fused study will be reconstructed from the minimum grayscale values of the Reference study and the Target study.
Mix	The mix selection control becomes visible.

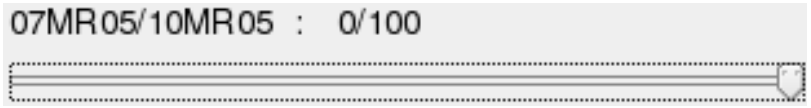


Figure 5.45 The mix selection control

Use the scroll bar to adjust the grayscale percentage of the Reference study with respect to the Target study. The images in the fused study will be reconstructed from the values that you set.

If the grayscale of the Target study is to be predominant, move the slider to the right.

If the grayscale of the Reference study is to be predominant, move the slider to the left.

If you select the **Subtract** option, the images in the fused study will be reconstructed by subtracting the grayscale values of the Target study from those of the Reference study.

3 To close the dialog without applying any changes, click **Cancel**. If you wish to apply the settings without closing the dialog, click **Apply**. To show the fused study in a workspace, click **View**. To subsequently close the dialog and keep the applied settings, click **OK**.

An icon for the new fused study appears on the menu bar. You can now work with the fused study in the same way as with all other studies.

5.5.6.2 Opening a fused study

1 To view the fused study in a workspace, select **View** from the drop-down menu of the fused study.

The fused study opens in a workspace.

5.5.6.3 Editing a fused study

1 From the drop-down menu of the fused study, choose **Edit**.

The Fuse Studies dialog opens. It is now possible to change the name and the fusion parameters for the fused study.

5.5.6.4 Deleting a fused study

1 From the drop-down menu of the fused study, choose **Delete**.

When you confirm the deletion, the fused study is removed from the list in the Fuse Studies dialog, and its icon is removed from the menu bar.

5.5.7 Using fusion to align images in Workspace views

This section deals with alignment of non-stereotactic images using the fusion function outside the co-registration dialog.

In the treatment planning application, images are displayed in the original image slice orientation. This orientation is normally not the same for two studies, which can make it difficult to compare the co-registered study to the reference study outside the co-registration dialog, see the screen shot below.

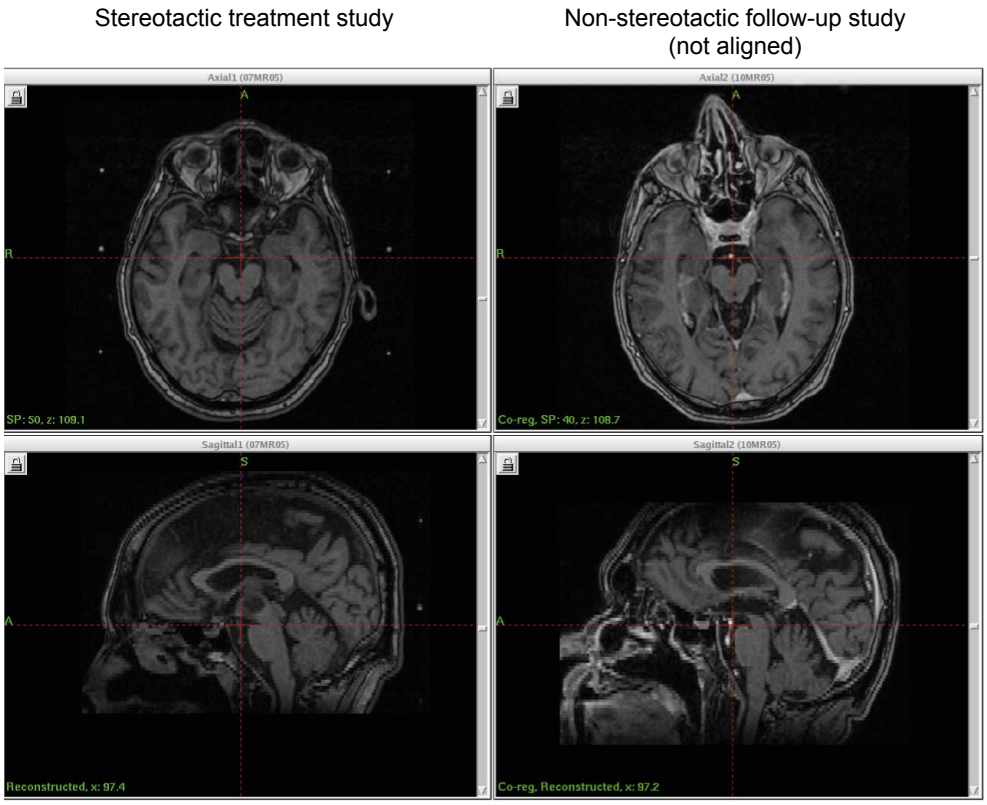


Figure 5.46 Stereotactic treatment study compared to non-stereotactic follow-up study

Using the fusion function, it is possible to align co-registered non-stereotactic images with reference images.

1 To align the co-registered non-stereotactic images with the reference images:

a Create a new fused study with the reference images as Reference study (1) and the co-registered images as Target study (2).

b Select the Mix fusion function with a value of 0/100.

The fused study will show the non-stereotactic image data, but aligned according to the stereotactic reference images, see the screen shot below.

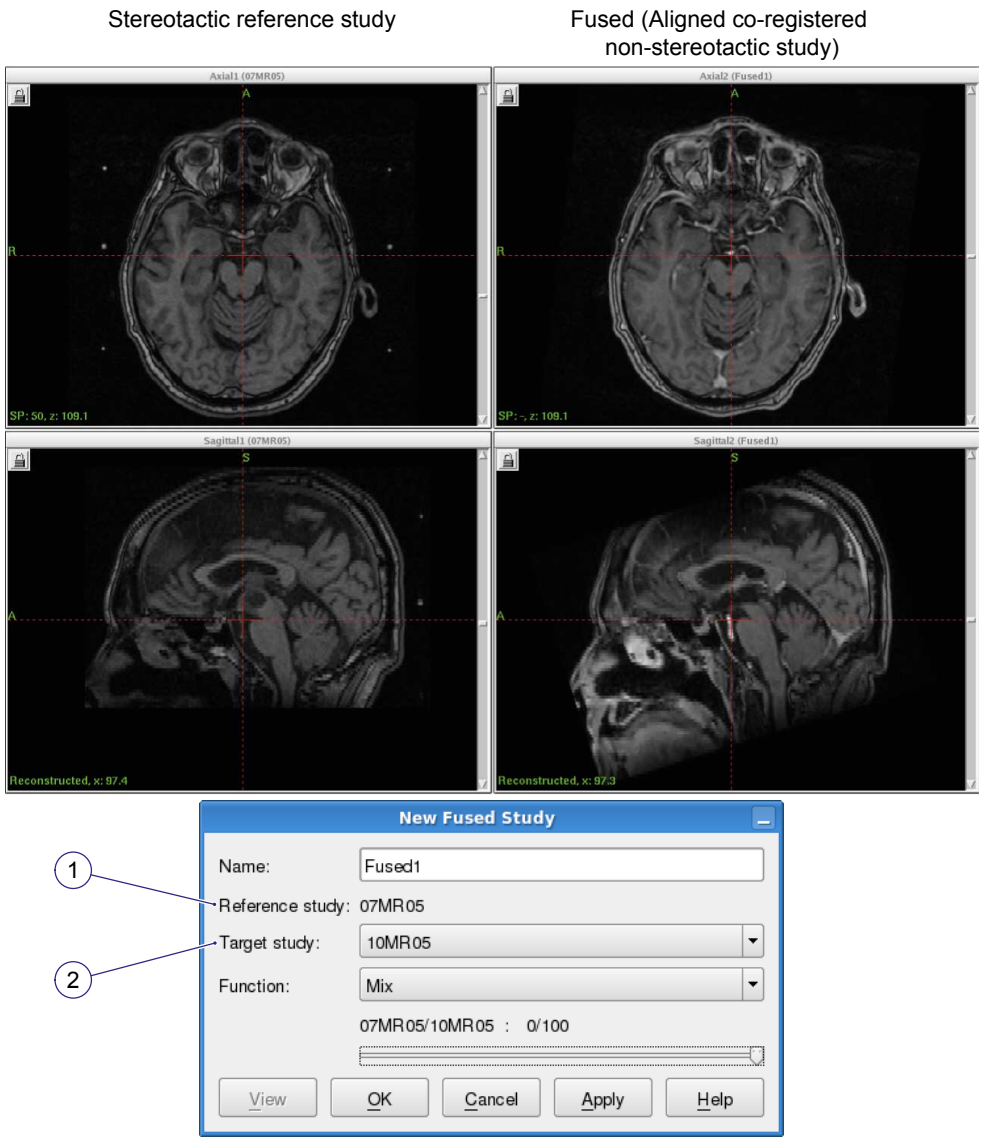


Figure 5.47 Co-registered non-stereotactic study aligned with stereotactic reference study

Note: *It is also possible to align the reference images with the co-registered non-stereotactic images, in a similar way.*

5.5.8 Creating a blank study

If a patient file has angiographic image studies only, you can create a blank tomographic study into which certain graphics can be projected and examined in three dimensions. The blank study consists of 200 axial images spaced at intervals of 1 mm apart.

By using the blank study you can explore the target, volumes, and the isodose contours of the irradiation scheme in the third dimension against a black background.

1 From the **Tools** menu choose **Create Study**.

A blank study icon appears on the menu bar.

2 Click on the blank study icon and choose **View**.

The blank study opens in the active workspace.

You can now see the projected graphics in the image windows of the workspace and you can manipulate the images in the normal manner.

5.5.9 Editing the name of an image study

1 Click on the icon of the study that you want to edit and choose **Edit**.

The image study dialog opens.

2 Enter a new name in the **Name** field of the image study dialog.

3 Click **OK**.

5.5.10 Deleting an image study

1 Click on the icon of the study that you want to remove and choose **Delete**.

A confirmation dialog opens. It prompts you to confirm that this image study is to be deleted.

2 Click **OK**.

The selected image study is permanently deleted from the treatment planning application and the dialogs are closed. The study icon is cleared from the menu bar.

5.5.11 Segmenting the skull for visualization in 3D-views

For the application to be able to visualize the skull boundary in 3D-views, it needs to know the grayscale threshold corresponding to the transition between air and tissue. The segmentation tool affects the 3D views, Open Book and especially Cut Box. All values below the selected threshold (areas displayed in blue while adjusting the threshold) will appear transparent in the 3D-views. It is important to use a proper threshold when doing this segmentation so that the correct areas are displayed as transparent.

1 With the patient file and radiological examination selected, open the image study that you intend to use.

2 From the **Tools** menu choose **Segment**.

The Segment by Threshold dialog opens.

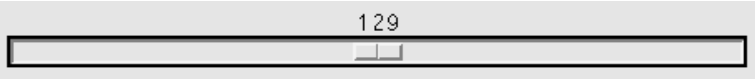


Figure 5.48 Segment threshold

3 Adjust the scroll bar until a red color wash covers the patient's skull, and random grays outside the head have a minimum red color wash. The outside of the head should have a blue color wash.

4 To close the Segment by Threshold dialog, click **OK**.

5.6 Workspaces

A workspace is the way you arrange different kinds of images on the screen to make your work comfortable and efficient.

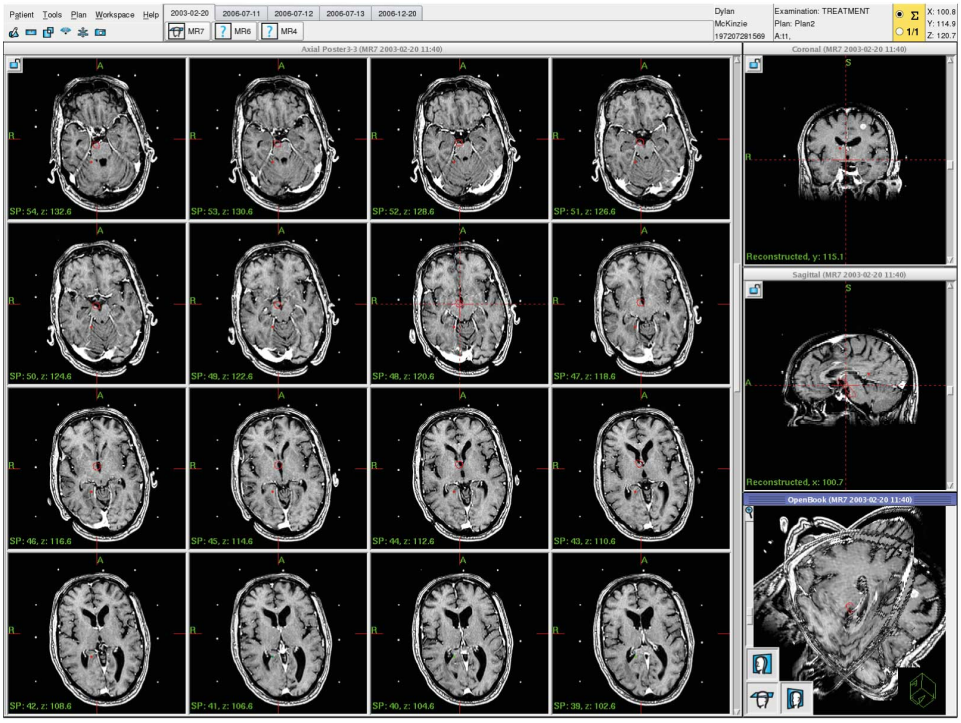


Figure 5.49 Example of a workspace in the treatment planning application

5.6.1 Opening workspaces

All the predefined and user-defined workspaces that are available for a patient are listed in the **Workspace** menu when you open the patient's file.

There are two ways of opening an existing workspace:

- from the **Workspace** menu
- from a study icon menu.

5.6.1.1 Opening a workspace from the workspace menu

1 Click on the **Workspace** menu.

The menu lists the available workspaces.

2 Select a workspace. For example, if you want to open the predefined standard workspace, select **Standard**.

The selected workspace opens. It contains images from the study that was last used for this patient.

You can now work with these images or, if more than one study is available for this patient, you can open another image study in the workspace.

5.6.1.2 Opening a workspace from a study icon menu

1 Click on the icon of the study that you intend to use and, from the drop-down menu, choose **View**.

The selected study opens in the first workspace listed in the **Workspace** menu.

5.6.2 Moving between workspaces and studies

1 If more than one workspace is available for the patient, use the **Workspace** menu commands to switch between the workspaces.

The point-of-exploration remains unchanged when you move from one workspace to another.

2 If more than one image study is available for the patient, grab the study icon with the middle mouse button and drop it into the desired window to open another study in the selected workspace.

5.6.3 Closing workspaces

In the treatment planning application only one workspace can be open at a time.

1 The previously open workspace is automatically closed when you do one of the following:

- Open a new workspace while an other is already in use.
- Open a new patient file.
- Select the **Exit** command in the **Patient** menu.

2 To close a workspace without opening another workspace or a new patient file, choose **Clear** from the **Workspace** menu.

5.6.4 Creating workspaces

The treatment planning application is supplied with predefined workspaces that will accommodate most treatment planning requirements. However, you can create your own workspace layouts to satisfy individual preferences for image display and manipulation, or to meet the needs of a particular patient. Note that the workspace layouts are common for all the users of the system, so a created workspace layout will be available for other users too.

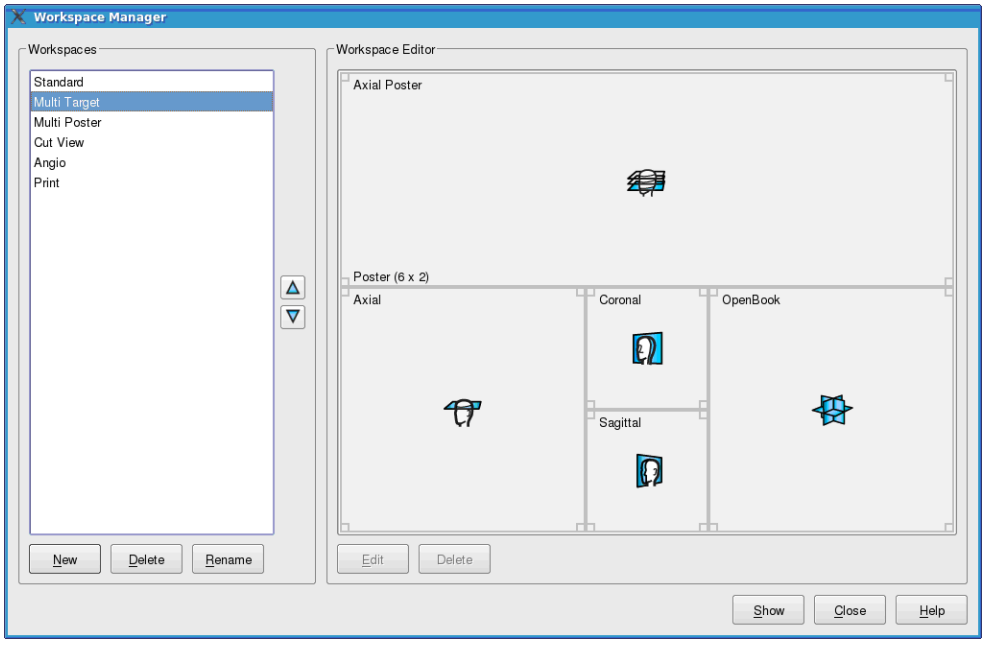


Figure 5.50 The Workspace Manager

You can create tomographic and/or angiographic workspaces. The steps needed to create a new workspace are:

1 Add a new workspace to the **Workspace Manager**.
2 Set the position and size of the first window of the workspace in the **Workspace Editor**.
3 Use the **New Window** dialog to:
   – choose the way in which images will be displayed in the first window
   – choose the type of images that the first window will contain
   – adjust the initial zoom setting for the images in the first window.
4 Repeat step **3** for all other windows that you place in the new workspace.

5.6.4.1 Adding and configuring a tomographic workspace

A tomographic workspace presents image studies in a way that allows you to explore the patient's anatomy at any point on a tomographic image. The predefined **Standard** workspace is intended for this purpose but you can also create tomographic workspaces of your own.

Adding a new tomographic workspace

1 From the **Workspace** menu choose **Edit**.

   The Workspace Manager opens.
2 Click on **New**.

   The New Workspace dialog opens.
3 Type an appropriate label for the new workspace into the **Name** field. For example:

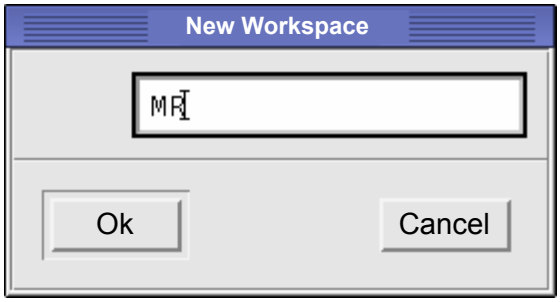


Figure 5.51 Typing a label for the new workspace

4 Click on **OK**.

   The New Workspace dialog closes and a blank Workspace Editor opens.

Positioning a workspace window

1 In the **Screen Layout** field, click at the point where you want to position the top, left corner of the first window. Drag the mouse until the window is of the size and shape that you want. Then release the mouse button. Observe that the window requires a minimum size.

   When you release the mouse button the New Window dialog opens. The New Window dialog is used to configure the new workspace window.

Creating a poster window

A poster window is a window that displays an array of the images in a study simultaneously. A scroll bar allows you to view all images in the window.

1 In the **Window type** field of the New Window dialog, click on the appropriate icon for the study that will be displayed in the poster window.

Figure 5.52 Selecting window type

2 In the **Name** field, type a name for the new poster window. Alternatively, you can use the default name provided by the program when you select the window type.

3 Adjust the zoom setting for the images that will appear in the new window.

Note: *When using the workspace you can adjust the zoom factor by pressing and holding the right mouse button while moving the mouse.*

4 When you are satisfied with the new poster window, click on **Ok**.

The New Window dialog closes, and a representation of the new window appears in the Workspace Editor.

Creating a single window

A single window is a window that displays all the images in a study one-by-one. A scroll bar allows you to view each image in turn.

1 In the **Window type** field of New Window dialog, click on the appropriate icon for the study that will be displayed in the single window.

Figure 5.53 Selecting window type

2 Click in the **Name** field and type a suitable name for the new window. Alternatively, you can use the default name provided by the program when you select the window type.

3 Adjust the zoom setting for the images that will appear in the new single window.

Note: *When using the workspace you can adjust the zoom factor by pressing and holding the right mouse button while moving the mouse.*

4 When you are satisfied with the new single window, click on **Ok**.

The New Window dialog closes, and a representation of the new single window appears in the Workspace Editor.

Creating a 3D window

A 3D window displays a three-dimensional reconstruction of the original image study. It is recommended that a workspace should contain only one Cut Box and/or one Open Book window.

1 Select type of window:

– If the 3D window is to display an Open Book reconstruction, click on the Open Book icon in the Window type field of the New Window dialog.

Figure 5.54 Window type Open Book

– If the 3D window is to display a Cut Box reconstruction, click on the Cut Box icon.

Figure 5.55 Window type Cut Box

2 Click in the **Name** field and type a suitable name for the new window. Alternatively you can use the default name provided by the program when you select the window type.

3 Adjust the zoom setting for the reconstruction that will appear in the new 3D window.

4 When you are satisfied with the new 3D window click on **Ok**.

The New Window dialog closes and a representation of the new 3D window appears in the Workspace Editor.

Creating an angiographic window

An angiographic window presents angiographic image studies in a way that allows you to explore the patient's arteriovenous anatomy in stereotactic space. The predefined **Angio** workspace supplied with the treatment planning application is intended for this purpose but you can also create customized angiographic workspaces.

1 Click on the Angio Image icon in the **Window type** field of the New Window dialog.

Figure 5.56 Window type Angio Image

2 Adjust the zoom setting for the image that will appear in the new angiographic window.

Note: *When using the workspace you can adjust the zoom factor by pressing and holding the right mouse button while moving the mouse.*

3 When you are satisfied with the configuration of the angiographic window, click on **Ok**.

The New Window dialog closes and a representation of the new angiographic window appears in the Workspace Editor.

4 Position and configure any other angiographic windows that you want to have in the new workspace as described in steps **1** to **3** .

Viewing the new workspace

1 When the workspace is configured, in the Workspace Editor click on **Show**.

The Workspace Editor closes and the newly created workspace opens. Each window of the workspace will contain one or more images from, or a reconstruction of, the currently open image study.

The example below shows a tomographic workspace containing single axial, coronal and sagittal windows and a Cut Box.

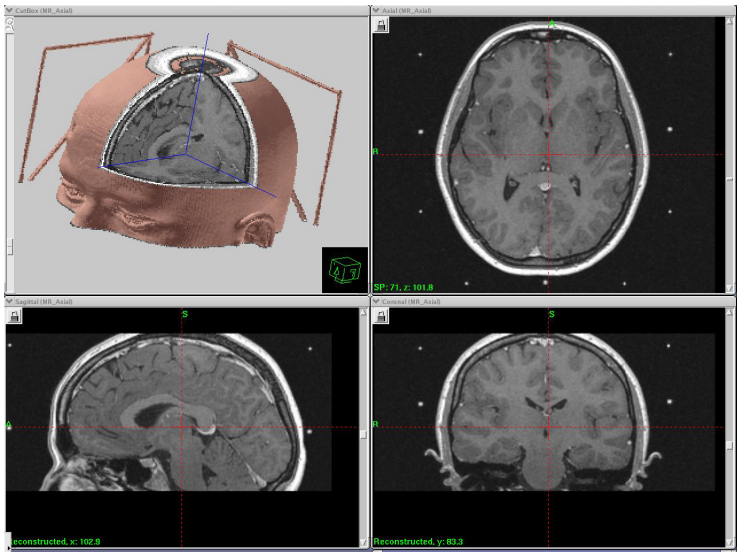


Figure 5.57 Viewing the new workspace

5.6.5 Adjusting workspaces

You can adjust the configuration of any workspace. Note that all users of the system share the same set of workspace layouts, so any adjustments will affect other users too.

5.6.5.1 Selecting a workspace for editing

1. With a patient file open, choose **Edit** from the **Workspace** menu.

   The Workspace Manager opens.
2. Select the workspace that you want to adjust.

   The windows of the selected workspace are shown in the **Workspace Editor** frame.

5.6.5.2 Changing the configuration of a workspace window

1. In the Workspace Editor frame of the Workspace Manager window, double-click on the window that you want to edit or click once on the window and then on **Edit**.

   The Edit Window dialog opens. It is similar to the New Window dialog and shows the present settings of the selected window.
2. Change any of the parameters of the window.
3. When you are satisfied with the new window layout click on **Ok**.

   The Edit Window dialog closes.
4. If desired, you can now adjust the parameters of other windows of the workspace in the same way.
5. When you have fully reconfigured the workspace, in the Workspace Manager, click on **Show**.

   The Workspace Manager closes and the edited workspace opens. You can now view the changes that you made.

5.6.5.3 Repositioning and resizing a workspace window

You can adjust the size of any window in a workspace and/or move it to a new position on the workspace.

1 Open the Workspace Editor as described in this manual.
2 To resize a window in the Workspace Editor, drag a corner until the window is of the size and shape that you require.
3 To reposition a window in the Workspace Editor, click in the window and drag it to a new position.
4 When you have resized and/or repositioned the windows of a workspace, click on **Show**.

   The Workspace Manager closes and the edited workspace opens.

Related Links:

Selecting a workspace for editing on page 148

5.6.5.4 Deleting a workspace window

You can permanently delete a window from a workspace.

1 Open the Workspace Editor as described in this manual.
2 In the Workspace Editor, click on the window that you want to remove and then click on **Delete** and confirm.

   The window is removed from the Workspace Editor.
3 Click on **Close**.

Related Links:

Selecting a workspace for editing on page 148

5.6.5.5 Reordering workspaces

You can change the sequence in which workspaces are shown in the **Workspace** menu.

1 Select the workspace to move in the Workspace Manager as described in this manual.
2 Use the up/down arrows to move the selected workspace up/down in the list of workspaces.
3 Click on **Close** to close the Workspace Manager.

Related Links:

Selecting a workspace for editing on page 148

5.6.6 Deleting a workspace

You can permanently delete any workspace from the treatment planning application. Note that all users of the system share the same set of workspace layouts, so deleting a workspace layout will delete it for the other users too.

1 From the **Workspace** menu choose **Edit**.

   The Workspace Manager opens.
2 Select the workspace that you want to delete.
3 Click on **Delete** and confirm.

   The selected workspace is permanently deleted. Its name is no longer presented in the **Workspace** menu and it is not listed in the Workspace Manager.
4 To close the Workspace Manager click on **Close**.

5.7 Image exploration

The facilities available in the treatment planning application for the handling and manipulation of the image studies are displayed in the workspaces.

5.7.1 Study exploration

The technique of examining the images in workspace windows is called “Study Exploration”. You can explore studies in any of the defined workspaces.

You can explore the images in a treatment planning application workspace by manipulating a cross-hair cursor known as the point-of-exploration. The point-of-exploration is always displayed in all windows of a workspace. It is a thin red cross that extends to the edges of each window.

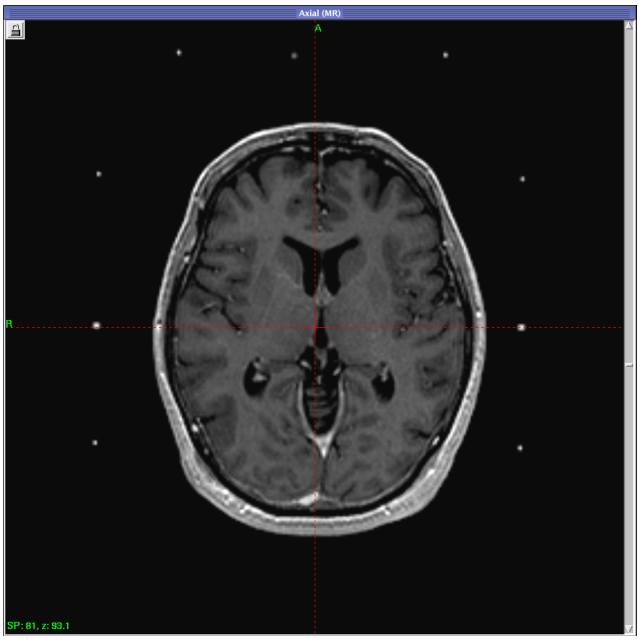


Figure 5.58 Point-of-exploration

5.7.1.1 Zooming

- To zoom in all images on the screen, press the right mouse button and move the cursor downwards to zoom in, and upwards to zoom out.
- To zoom in one image, click on the corresponding window and press down the <Shift> key while zooming as described above.

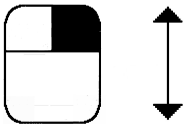


Figure 5.59 Mouse zoom

5.7.1.2 Moving the point-of-exploration

1 On the image that you want to explore, click at the intersection of the cross or one of the lines of the point-of-exploration.

The point-of-exploration momentarily changes color to green.

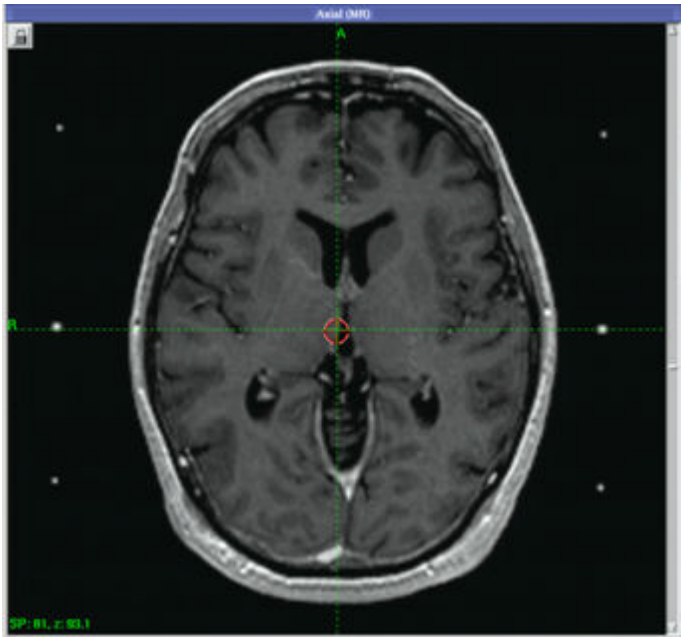


Figure 5.60 Intersection of the point-of-exploration lines

2 Drag the point or line to the position that you want to explore on the image.

When you release the mouse button, the active image moves to keep the point-of-exploration at the center of the image window. This movement is tracked in all other workspace windows.

3 Release the mouse button when the point-of-exploration is at the desired position on the image.

For example, in the image below, the point-of-exploration has been moved to the left.

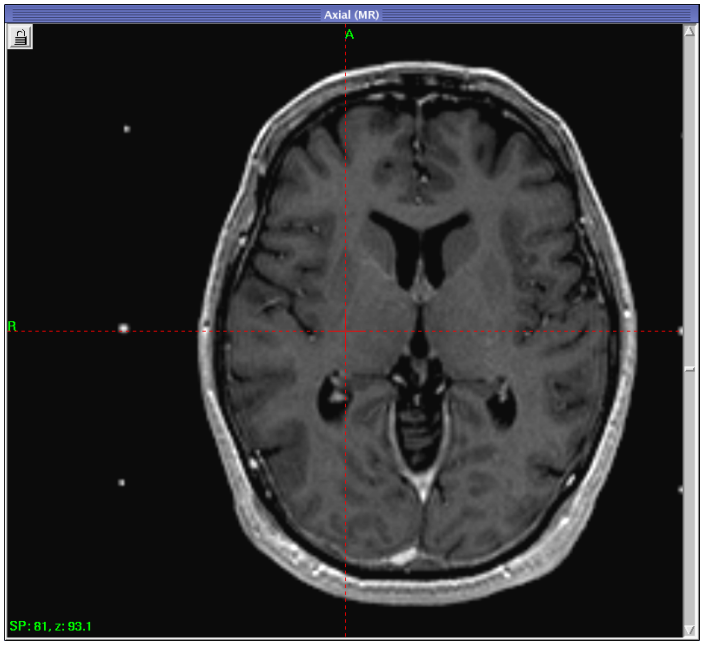


Figure 5.61 Moved point-of-exploration

Note: *In poster windows the point-of-exploration consists of unbroken lines only in the image that is on the same plane as the point-of-exploration. In other poster images the point-of-exploration consists of broken lines only. You can still move the point-of-exploration in the other poster windows by clicking and dragging on the broken lines.*

5.7.1.3 Locking a window

You can lock the images in axial, sagittal, coronal, poster, and angio workspace windows so that the image does not simultaneously track the movement of the point-of-exploration. You cannot lock 3D windows.

1 Click on the lock icon in the window that you want to lock.

The image remains immobile as you adjust the point-of-exploration.

Figure 5.62 Lock icon

2 To unlock the window, click on the window lock icon again.

The image in the window is now automatically adjusted to center on the new point-of-exploration.

Note: *As you lock and unlock one window in an angiographic workspace, the window containing the other projection is locked/unlocked also.*

5.7.1.4 Exploration of cut box and open book images

In addition to moving the point-of-exploration, you can manipulate the images in a Cut Box or Open Book window to explore anatomical structures.

Manipulating 3D images

1 Click anywhere in a Cut Box or Open Book window on a workspace and drag with the mouse.

The three-dimensional image tracks the movement of the mouse and can be rotated to obtain the optimum view by using the left and center mouse buttons.

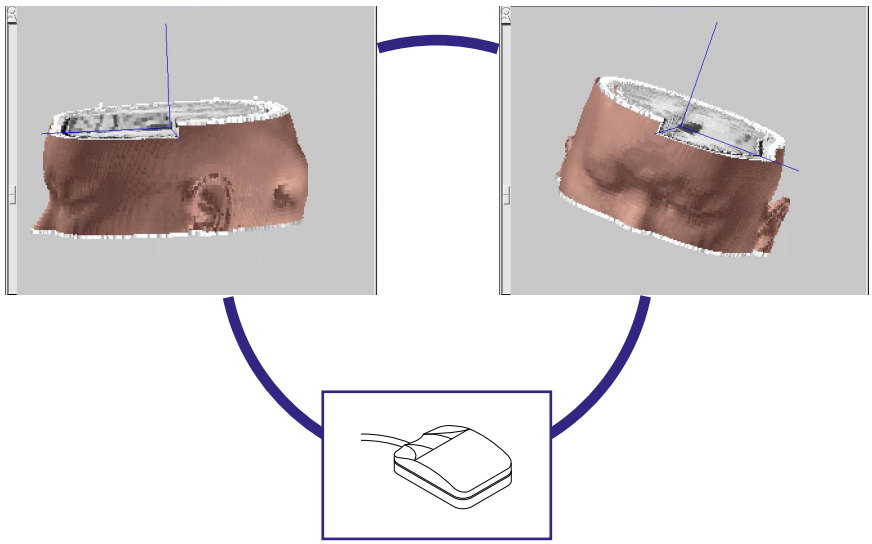


Figure 5.63 3D image manipulation

Exploring single images in an Open Book

An Open Book window always contains axial, coronal, and sagittal icons that are used to display and remove reconstructed images in the Open Book window.

1 To include an axial image in an Open Book, click on the corresponding icon (1) in the Open Book window:

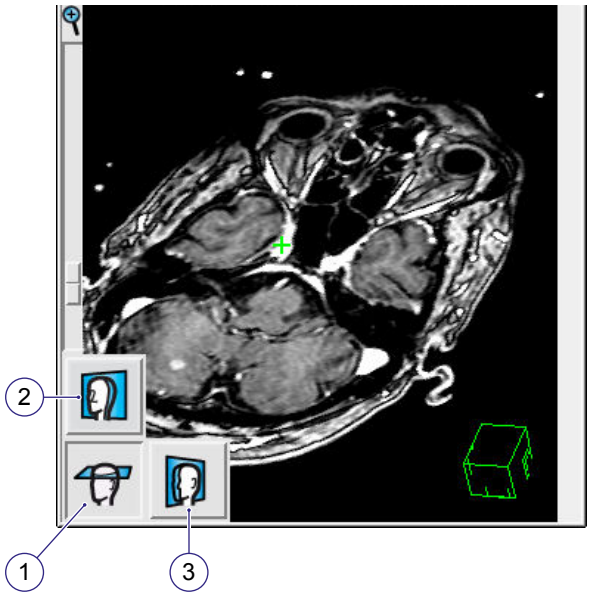


Figure 5.64 Open book with an axial image

2 To exclude the axial image from the Open Book, click on the corresponding icon (1) again.

3 Include and exclude coronal and sagittal images by clicking the corresponding icons (2) and (3), respectively.

An Open Book view with all three image directions included resembles the figure below.

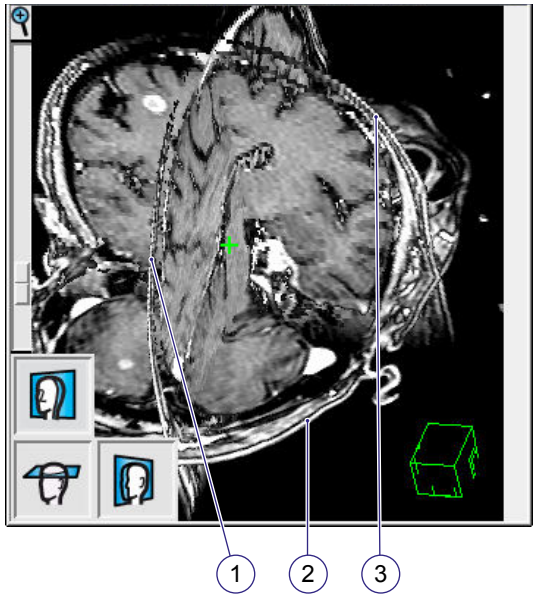


Figure 5.65 Open Book view with all three image directions

(1) Sagittal slice

(2) Axial slice

(3) Coronal slice

Exploring a volume in an Open Book

If you have created and displayed a volume or another anatomical object by using the **Regions & Volumes** command, you can examine the volume alone by removing all the single images from an Open Book.

1 Deselect all the image icons in the Open Book window.

The single images are cleared from the Open Book.

2 Rotate the volume by clicking in the Open Book window and dragging with the mouse.

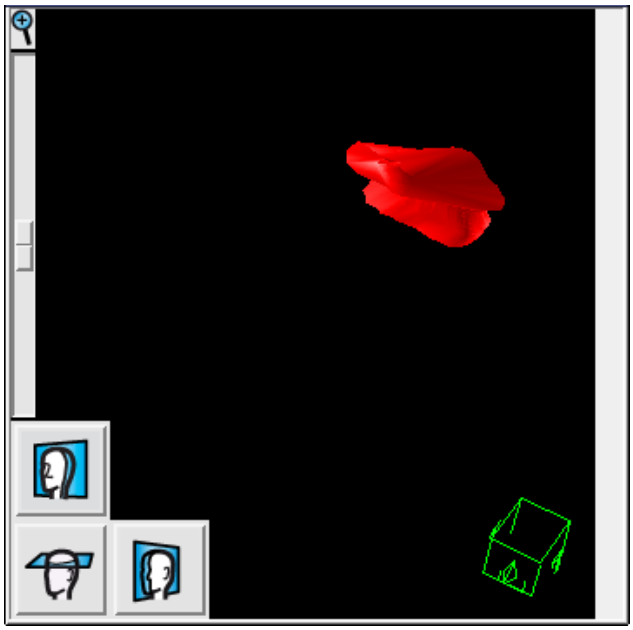


Figure 5.66 Volume rotation in the Open Book window

5.8 Regions and volumes

The **Volumes** command in the **Tools** menu allows you to draw anatomical regions of interest (ROI) on open images, and define three-dimensional volumes from the ROI that you draw.

You can draw ROI in the axial, sagittal or coronal workspace windows, but each ROI must be drawn in the same image orientation and image study. The resulting three-dimensional volume can be viewed in all image orientations and image studies in the workspace.

WARNING 5.10

The 3D shape of created, modified, or imported volumes must be reviewed in a 3D view before being used for treatment plan evaluation.

Volumes can be denoted as:

- target-volumes
- an area of high risk
- an anatomical object

All volume types can be visualized and used for treatment planning and for examining purposes.

5.8.1 Creating a new volume

1 On the menu bar, click **Plan**, then click **Tools** > **Volumes**.

You can also click the **Regions & Volumes** button on the toolbar.

The **Regions & Volumes** dialog box is displayed.

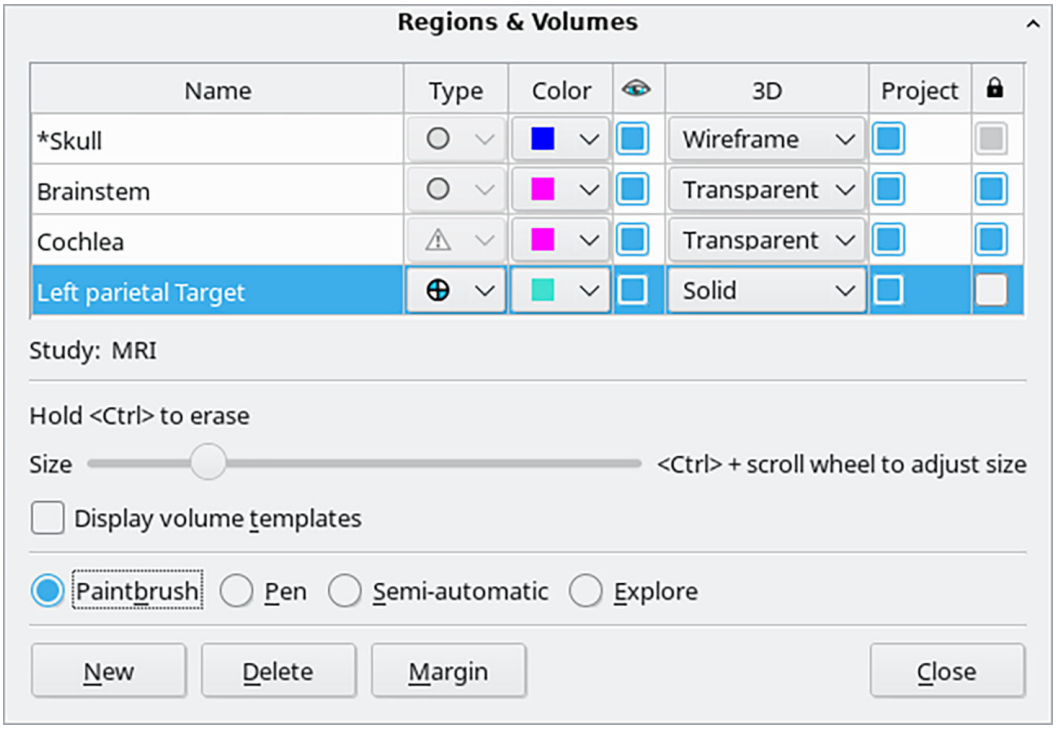


Figure 5.67 The Regions & Volumes dialog box

2 Click **New**.

The **Edit Volume** dialog box is displayed.

3 Type a name for the new volume.

Note: *A volume name can only be used for one volume, two volumes cannot have the same name.*

4 In the **Type** box, select **Object**, **Risk** or **Target**.

5 In the **Color** box select a display color for the new volume and regions.

6 In the **Lock** box, select or clear for editing. You can also edit a volume by selecting the volume and then selecting a drawing tool.

Related Links:

Drawing regions of interest on page 155

5.8.2 Drawing regions of interest

When you have established the basic characteristics of a volume, you can draw the regions of interest from which the three-dimensional volume is constructed.

1 In the **Regions & Volumes** dialog box, select the name of the target volume to edit.

2 Click the workspace of the image study.

3 With the **Explore** tool selected, find an image where you want to draw a region.

4 Select a drawing tool: **Semi-automatic**, **Pen** or **Paintbrush**.

The drawn regions are displayed as solid outlines in the selected color on the image. The volume containing the region is calculated by the software. The study used for drawing the ROI is displayed in the Regions & Volumes dialog box.

Note: *It may not be necessary to draw regions on all images since the three-dimensional volume is created from the drawn regions. Interpolated regions between drawn regions for a volume, are displayed with a dashed line.*

5 Use the vertical scroll bar of the workspace window, or, use mouse scroll-wheel to display the next image where you want to draw a region for the volume. You can also use the Exploration tool to find an image where you want to draw.

6 Click **Display volume templates** to display the closest drawn region outside the volume extents as a template for further drawing.

7 Do the steps again to draw as many regions on as many images as necessary.

5.8.2.1 Drawing regions using the paintbrush tool

1 In the **Regions & Volumes** dialog box, select the name of the target volume to edit.

2 Select the **Paintbrush** tool.

3 Move the **Size** slider to adjust the size of the paintbrush tool.

You can also press CTRL + wheel button to adjust the size.

Note: *Use the right mouse button to zoom in the image view to draw small regions with the paintbrush tool.*

4 With the left mouse button, click a starting point. Move the mouse while you hold down the left mouse button to draw the region outline. Release the button to stop drawing.

If there is a hole within the region it is automatically removed when you draw around it

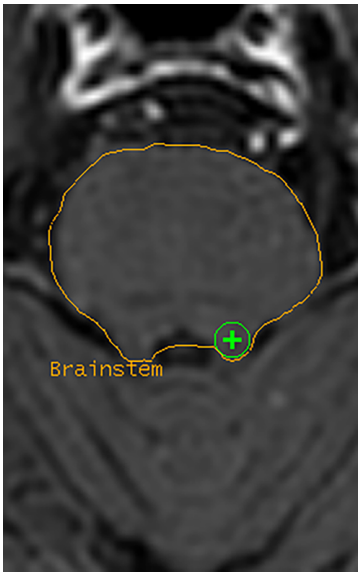
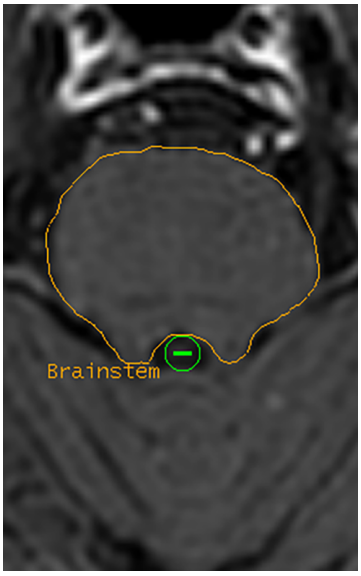


Figure 5.68 Drawing a region with the paintbrush tool

– Click the **Paintbrush** tool to add parts to a closed region. Both drawn and interpolated regions can be edited.

– Click the CTRL + **Paintbrush** to erase a part of a region. You can erase an entire region with the tool.

Erasing parts of a region with the paintbrush tool.



The region is displayed as a solid outline in the selected color in the image. The volume containing the region is calculated by the software.

5 Do the steps again to draw regions on the necessary images.

5.8.2.2 Drawing regions using the pen tool

1 In the **Regions & Volumes** dialog box, select the name of the target volume to edit.

2 Select the **Pen** tool.

3 With the left mouse button, click a starting point for the region. Move the mouse while you hold down the left mouse button to draw the region outline.

You can also use the left mouse button and click a polygon shape around the region.

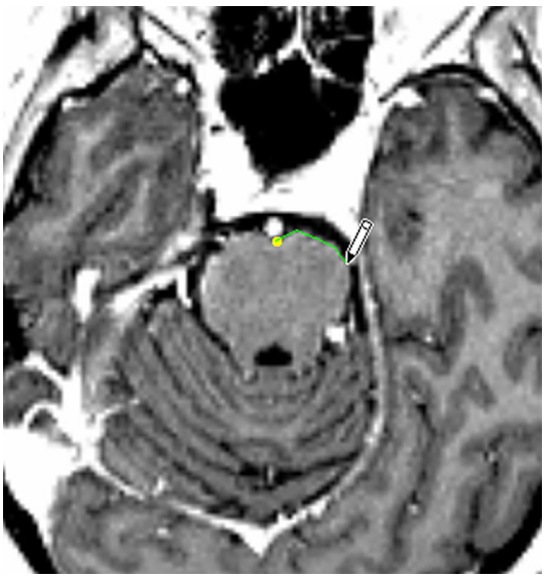


Figure 5.69 Outlining the region

– To erase a line: draw the line again in the opposite direction. You can also use the center mouse button to delete single points of the line.

– To cancel a drawn region before the outline is closed: Scroll, up or down, to the next slice and then back again, and the non-closed outline disappears.

4 With the **Pen** tool, click on the starting point to close the drawn region.

The new region is displayed as a solid outline in the selected color on the image. The volume containing the region is calculated by the software.

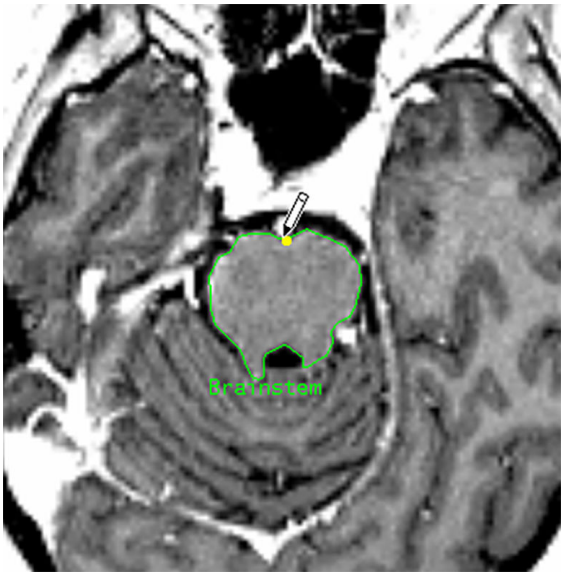


Figure 5.70 Closing the region

5 To edit a drawn region, click a point of the outline and draw a new line.

6 Do the steps again to draw as many regions on as many images as necessary.

5.8.2.3 Drawing regions using the semi-automatic segmentation tool

Drawing regions with the Semi-automatic segmentation tool is a technique that uses the gray level contrast between a lesion area, such as a tumor, and the surrounding tissue. It is particularly useful for outlining complex objects with high contrast in the images.

1 In the **Regions & Volumes** dialog box, select the name of the target volume to edit.

2 Select the **Semi-automatic** tool.

3 Move the slider until the red color includes the region in gray that you want to include.

– To show the red color, point to the slider and hold down the mouse button.

– The left side of the slider shows the darkest gray level included in the segmentation.

– The right side of the slider shows the brightest gray level included in the segmentation.

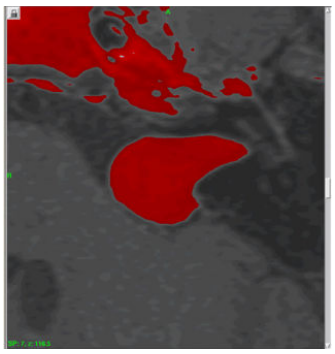


Figure 5.71 The red color shows the defined region

4 When the region is defined, click in the center of the region with the **Pen**tool, and drag outwards until the region is enclosed by a green circle. Release the mouse button.

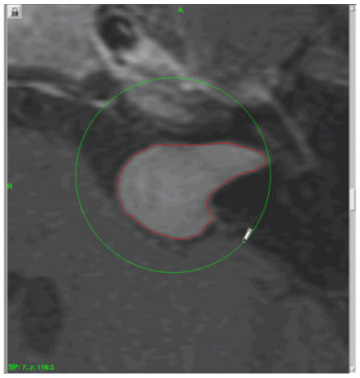


Figure 5.72 Enclosed region

5.8.3 Visualizing volumes

1 In the **Regions & Volumes** dialog box, double-click a row to center the workspace view on the target.

The volume is centered in the axial, coronal, sagittal and 3D image views.

2 In the **Color** box, select a color for displaying the volume and regions.

3 In the **3D** box, select visual appearance:

- **Wireframe**
- **Mesh**
- **Solid**
- **Transparent**

4 Select or clear the **Display** box to display the volume in the workspace view or not.

5 Select or clear the **Project** box to show the volume on other imaeg views in the workspace. Volumes are shown in all image views by default.

5.8.4 Editing volumes

1 In the **Regions & Volumes** dialog box, select the volume.

2 Click a volume name to edit. Type a new volume name.

Note: *A volume name can only be used for one volume, two volumes cannot have the same name.*

3 To change a volume type, click the volume and then in the **Type** box, select **Object**, **Risk** or **Target**.

4 To modify, add or remove ROI for the selected volume, select a tool: **Semi-automatic**, **Pen** or **Paintbrush**.

Note: *For adjusting drawn and interpolated regions, it is recommended to use the **Paintbrush** tool.*

5.8.5 Adding a margin to a volume

1 From the **Tools** menu select **Volumes**, or click on the **Regions & Volumes** button.

Figure 5.73 The Regions & Volumes button

The **Regions & Volumes** dialog opens.

2 Select the volume to add margin to.

3 Click **Margin**.

The Add Margin dialog opens.

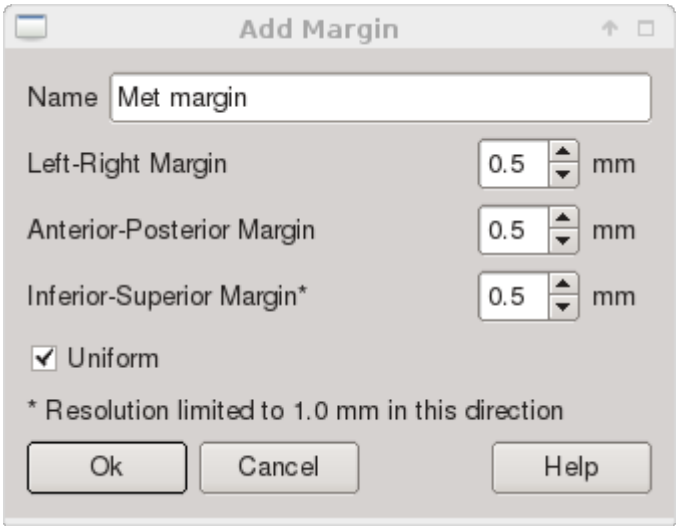


Figure 5.74 The Add Margin dialog

4 Type an appropriate name for the new volume.

Note: *You cannot have more than one volume with the same name.*

5 Select the desired margin.

Note: *Put a check mark in the **Uniform** box to select the same margin for all directions. In the direction normal to the contours, the margin can only be applied in steps of the image slice distance in the normal direction. This resolution is shown in the dialog and the normal direction is marked with an asterisk.*

6 Click **Ok**.

The new volume with the added margin inherits all properties from the original volume. The type of the original volume is set to **Object**.

Note: *If the treatment plan is in any other state than **Draft**, and the original volume is of type **Target**, the original volume will still be of type **Target** and the new volume is set to **Object**.*

WARNING 5.11

The 3D shape of margin volumes must be reviewed in a 3D view before being used for treatment plan evaluation.

Related Links:

Treatment planning states **on page 248**

5.8.6 Deleting a volume

1. Open the Regions & Volumes dialog.
2. Select the volume to be deleted.
3. Click **Delete** and confirm by clicking **Ok**.

   The selected volume is cleared from all images and deleted from the Regions & Volumes dialog.
4. To close the Regions & Volumes dialog, click **Close** or the **Regions & Volumes** button.

Figure 5.75 The Regions & Volumes button

5.9 AtlasSpace®

5.9.1 About AtlasSpace®

5.9.1.1 AtlasSpace® overview

AtlasSpace® is an electronic brain atlas that is derived from the *Atlas for Stereotaxy of the Human Brain* by Schaltenbrand and Wahren. AtlasSpace® is an optional feature.

AtlasSpace® uses three microseries of the Schaltenbrand and Wahren brain atlas, in axial, coronal, and sagittal direction. The three microseries are digitized and extended to include the two hemispheres. They are also co-registered together. Therefore, they can be put on anatomical images of a patient in the three orientations at the same time.

The 3D Talairach proportional grid system is specified by eight anatomical landmarks. The grid system is used to initially align AtlasSpace® to the anatomical images of the patient. Use local anatomical landmarks that you can see clearly to better align AtlasSpace® to the anatomical images in the target area.

Each one of the structures has a contour and a label. This makes it possible to turn each one of the structures on and off at a time. You can divide structures into groups that show only the necessary contours for different procedures.

Restrictions for AtlasSpace®

As AtlasSpace® is derived from the Schaltenbrand-Wahren brain atlas, it has the same restrictions.

- The sagittal and axial microseries are made from the same brain, which makes them co-registered from the start. The coronal microseries is made from a different brain. The accuracy of the co-registration of the orthogonal microseries is related to the accuracy of the AC-PC distances. These distances do not agree in the different microseries of the Schaltenbrand-Wahren atlas, which decreases the accuracy. To decrease this effect, use the same procedure to make the definition of the AC and PC points in the anatomical images of the patient as in the Schaltenbrand-Wahren brain atlas. The intercommissural line must go through the center of AC and PC. Make the definition of the AC point on the most posterior part of the anterior commissure. Make the definition of the PC point on the most anterior part of the posterior commissure.
- The axial microseries of the Schaltenbrand-Wahren atlas is tilted 7 degrees compared to the AC-PC line, which also decreases the accuracy. To decrease this effect, AtlasSpace® makes sure that the exploration point always maps correctly to the contours in the three orthogonal views.
- A different restriction is that the Talairach proportional grid system does a linear size change of the Schaltenbrand-Wahren brain atlas. It does not adjust the width of the third ventricle, for example. This is adjusted in AtlasSpace® since it uses local anatomical landmarks near the target structure to increases the accuracy when targets are specified.

Differences between the paper atlas and the digital atlas

When the initial paper atlas and the digital atlas are compared, a number of problems are found.

- There are contours in the Schaltenbrand-Wahren digital atlas that have incorrect name or the name of a different structure. There are contours that have different shapes than in the paper atlas.
- There are contours on the borders of the slices that are included in the Schaltenbrand-Wahren digital atlas but continue on the outer side of the slices in the paper atlas.
- There are contours that are not included in the paper atlas but are included in the Schaltenbrand-Wahren digital atlas.
- There are contours and structures in the paper atlas that are not included in the Schaltenbrand-Wahren digital atlas version.
- Some structures in the initial Schaltenbrand-Wahren paper atlas have a text label only and no contour in some slices. These labels without contours are not shown in the views in AtlasSpace®. But the structures are included in the list of atlas structures.

Related Links:

Contour labels on page 377

Differences in contours on page 377

5.9.1.2 Atlas registration

AtlasSpace® works independently to the patient. It must therefore be connected to an image study specified to a patient before the atlas can be used for treatment planning. This results in a change of coordinates from the Leksell® Coordinate System, which is specified to the patient, to the atlas coordinate system.

Atlas coordinate system

Atlas registration is derived from the eight standard landmarks of the Talairach proportional grid system and one more landmark — the midline reference point:

- Anterior commissure (AC)
- Posterior commissure (PC)

- Midline reference point (MR)
- Highest point of the parietal cortex
- Lowest point of the temporal cortex
- Most anterior point of the frontal cortex
- Most posterior point of the occipital cortex
- Most lateral point of the parietotemporal cortex (left)
- Most lateral point of the parietotemporal cortex (right).

Initial registration

To make the atlas agree with the images of the patient, it is necessary that the registration procedure has a point to start at. Therefore the AtlasSpace® automatically does an initial registration the first time it is used with a patient file.

The initial atlas registration, which is derived only from the AC and PC points, does not have sufficient accuracy for full treatment planning. It is therefore necessary to tune the registration against the eight standard landmarks of the Talairach proportional grid system and/or atlas structures. This is the function of the atlas registration.

5.9.1.3 Atlas structures

Atlas structures are specified anatomical areas in the database of AtlasSpace®. The atlas structures are shown as contours with different colors put on images in a plane that is orthogonal to the atlas coordinate system. Atlas structures can all be switched on or off, or selected structures can be put in display sets.

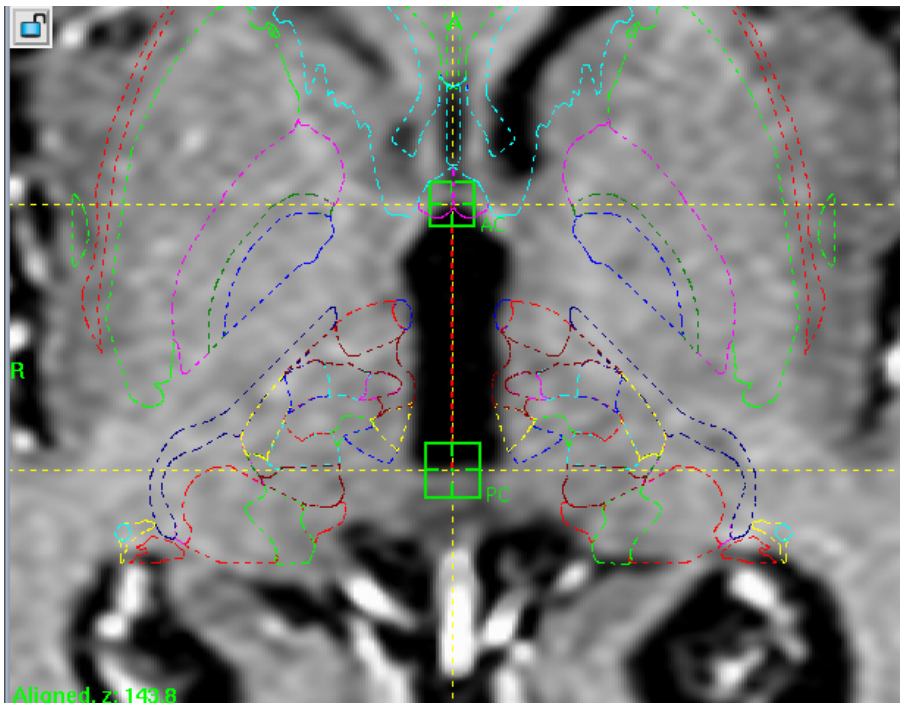


Figure 5.76 Atlas structures in an image of a patient

The atlas structures function includes an interactive labeling feature. This feature lets you read the name of each structure on images of the patient.

5.9.2 AtlasSpace® user interface

5.9.2.1 The Brain Atlas dialog box

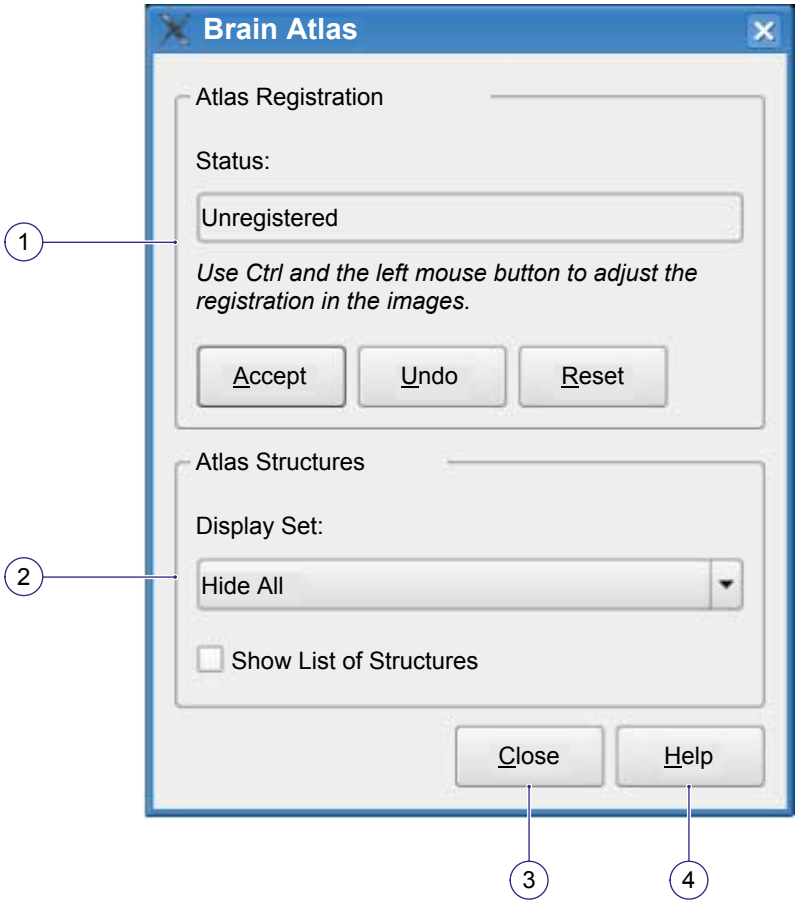


Figure 5.77 The Brain Atlas dialog box

(1) **Atlas Registration** frame
(2) **Atlas Structures** frame
(3) **Close** button
(4) **Help** button

The Brain Atlas dialog box contains the following:

- **Atlas Registration** frame
- **Atlas Structures** frame
- **Close** button: Click this button to close the dialog box.
- **Help** button: Click this button to open the *Online Reference Manual*.

Related Links:

The Atlas Registration frame on page 165

The Atlas Structures frame on page 166

Opening the Brain Atlas dialog box

1 To open the Brain Atlas dialog box, select **Brain Atlas** in the **Plan** menu.

The Atlas Registration frame

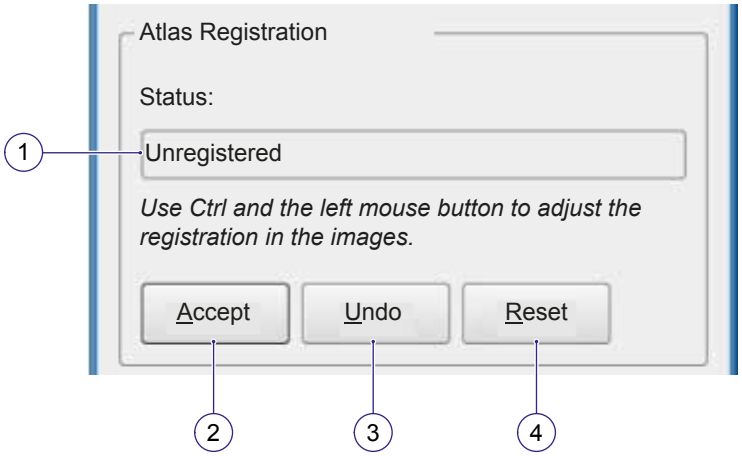


Figure 5.78 The Atlas Registration frame

(1) **Status** field

(2) **Accept** button

(3) **Undo** button

(4) **Reset** button

The Atlas Registration frame contains the following:

- **Status** field: This field shows the current status of the atlas registration. The status is “Unregistered” if the atlas is not connected to the patient images. When the atlas registration is accepted, the status changes to “Registered”.
- **Accept** button: Click this button to do a validation of the atlas registration. This function makes sure that you accept the locations of atlas structures and landmarks.
- **Undo** button: Click this button to go back to the last accepted registration. If no registration was accepted before, the button is not active. When the patient file is released, information about the last accepted registration is gone.
- **Reset** button: Click this button to set the atlas registration to the initial (default) atlas registration derived from the AC-PC position.

Using the Atlas Registration frame

1 Use the features in the **Atlas Registration** frame to make AtlasSpace® synchronized with the AC, PC and MR points. These points make up the intercommissural line of the images of the patient.

The Atlas Structures frame

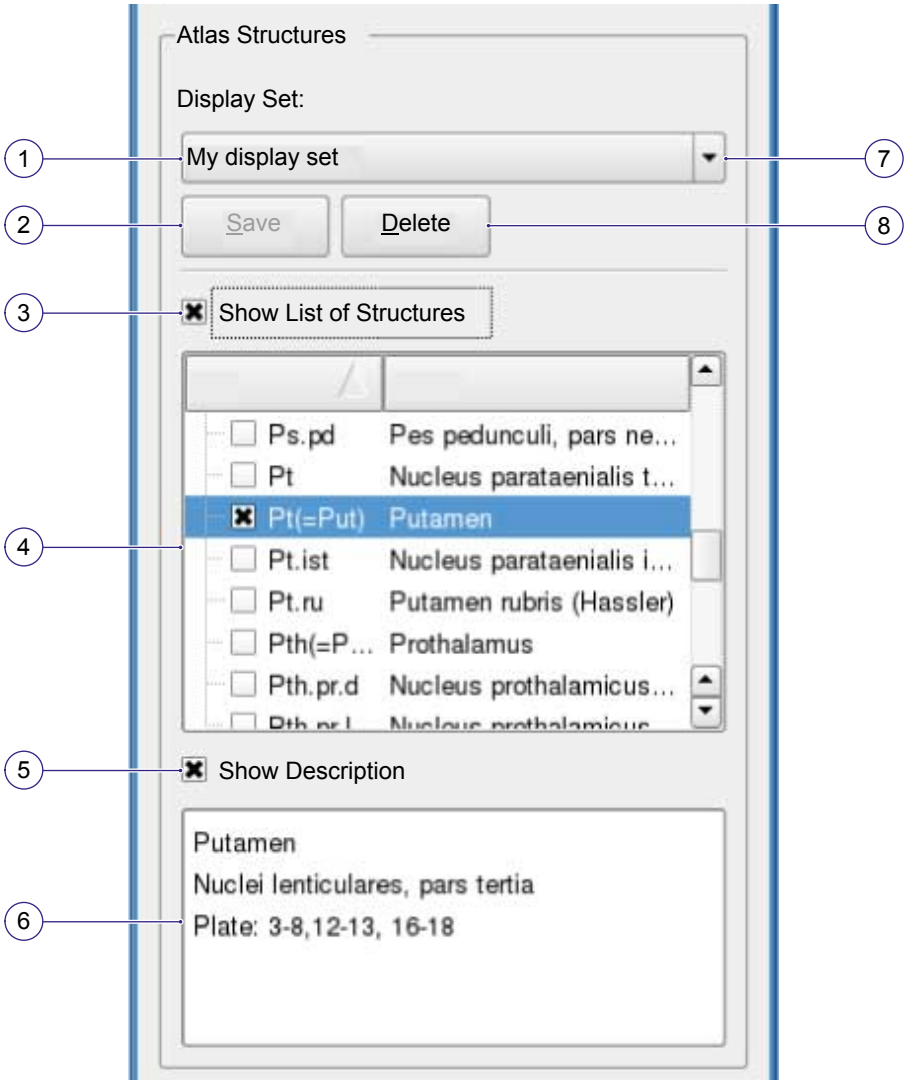


Figure 5.79 The Atlas Structures frame

(1) **Display Set** field

(2) **Save** button

(3) **Show List of Structures** check box

(4) Structure list

(5) **Show Description** check box

(6) Description field

(7) **Display Set** drop list

(8) **Delete** button

The Atlas Structures frame contains the following:

- **Display Set**: A display set is a saved set of selections of check boxes in the Structure list. To select all check boxes, select the applicable display set from the **Display Set** drop list. The **Display Set** field shows the name of a display set, which is selected from a drop list. The list includes predefined display sets and user-defined display sets. It is put in date sequence, with the newest display set at the end of the list.

Display set	Description
Predefined	The **Display Set** drop list includes two display sets predefined by the program: – **Hide All** - no structures are shown on the images of the patient. This alternative is selected by default if no display set is available for the patient examination. – **Show All** - all structures in the Schaltenbrand-Wahren atlas are shown on the images of the patient. The **Display Set** field is empty if you try to change a predefined display set.
User-defined	User-defined display sets are display selections that you make and keep in the database.

  If you change the selection of check boxes in the Structure list for a selected display set, the name of the display set is then possible to change.

- **Save** button: Click this button to save the current display selection as a display set. The button is active if changes were made to the selection and a correct display set name was typed.
- **Delete** button: Click this button to erase the display set that is shown in the **Display Set** field. The button is not active if no display set is selected. It is not possible to erase predefined display sets.
- **Show List of Structures** check box: Use this check box to show or not show the Structure list.
- Structure list: This list shows all the available structures and their display status. If an alternative name for a structure is available, it is also shown in the list. The structures in the Structure list are put in alphabetic sequence. Only one structure at a time can be selected. To change the sequence of the Structure list, click in the column headers.

  The list has two columns:

  – The **Tag** column shows an abbreviation for each structure. The same abbreviation is used as in the Schaltenbrand-Wahren atlas. A check box controls if the structure is shown or not.

  – The **Name** column shows the full name of the structure.

  When a check box is selected, the related structure is shown on the images of the open patient. The check boxes related to possible alternative names of the structure are also selected automatically.

  The display selection of a structure is saved in the database. It is automatically used when that patient file is opened.

  When a structure in the list is selected, its contours are selected in the views for some seconds.

  When a structure in the list is double-clicked, the exploration cross in the views is adjusted to the center of the structure.

- **Show Description** check box: Use this check box to show or not show the Description field.
- Description field: This field shows the full name of the selected structure in the Structure list. The Description field also contains other descriptions from the atlas database and shows the initial plates that contain the structure.

Using the Atlas Structures frame

1 Use the features in the **Atlas Structures** frame to show known anatomical structures that are selected from the AtlasSpace® database. It is possible to show a selection of atlas structures. It is also possible to make user-defined display sets which gives the display selection of all the structures in the set.

5.9.3 Atlas registration

5.9.3.1 Prerequisites for making an atlas registration

To make the explanation in this section easier:

- The image studies of the patient must be defined and opened in an applicable workspace.
- The intercommissural line must be specified.

WARNING 5.12

This manual does not explain the criteria that can be applied to ascertain the validity of a treatment protocol. It describes the use of the functions available in AtlasSpace® to assist during the evaluation of treatment planning information.

Only fully-trained neurosurgeons should perform this evaluation.

WARNING 5.13

AtlasSpace® does not compensate for distorted or misaligned images. Such images must not be used for treatment planning.

WARNING 5.14

The AC-PC distances are not consistent in the different microseries of Schaltenbrand-Wahren atlas, resulting in some inaccuracy.

The axial microseries of the Schaltenbrand-Wahren atlas is tilted 7 degrees with respect to the AC-PC line, resulting in some inaccuracy.

The Talairach proportional grid system scales the Schaltenbrand-Wahren atlas linearly, not compensating for individual variations.

WARNING 5.15

The accuracy of the image study produced for treatment planning will be affected if the distance between slices is excessive.

WARNING 5.16

When choosing the patient's images that are to be used with AtlasSpace®, ensure that the anatomical target(s) and all appropriate anatomical landmarks are clearly visible on the image(s).

Do not use images on which significant anatomical features are missing or indistinct, otherwise you could devise an incorrect treatment plan that is hazardous to the patient.

5.9.3.2 Making an atlas registration

WARNING 5.17

Exercise care during atlas registration and thoroughly evaluate the atlas registration prior to using the atlas as the basis of a treatment plan.

Ensure that all anatomical landmarks are clearly visible on the patient's images.

Ensure that the atlas is accurately registered with the patient's images and is accepted when correct in all respects.

Once the registration has been accepted, take care not to inadvertently move the registration, and check that the registration has not been intentionally or accidentally adjusted by another user.

To make and accept the first atlas registration for the patient, perform the following steps:

1 Select **Plan** > **Brain Atlas** to start the atlas registration.

The Brain Atlas dialog box opens.

The patient images align to the intercommissural line and the Talairach grid appears on all patient images.

The grid has broken yellow lines to show that the atlas registration is not accepted at this time.

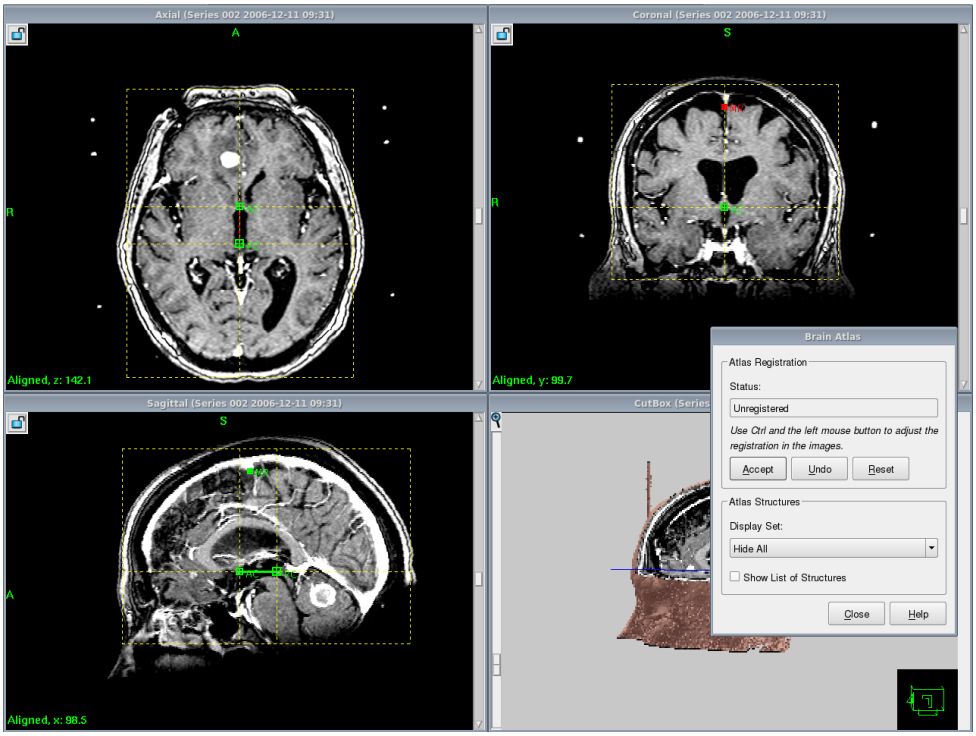


Figure 5.80 Images in a workspace that shows the Talairach grid as broken yellow lines

2 Make sure that you can see the full skull clearly in the images in the workspace. In applicable images, perform the following steps simultaneously:

a Press down the <Ctrl> key.

b Drag the sides of the Talairach grid until they align with the eight standard landmarks in the images of the patient.

The pointer does not have to be on a line of the Talairach grid before you start to drag. If there is an atlas contour below the pointer, it will move with the pointer.

Note: *If the pointer is near one of the inner lines of the Talairach grid when you start to drag, the outer lines of the Talairach grid could move very quickly.*

To make the atlas registration easier, use the procedure that follows:

a Put the cross hair exploration point on the AC point in all open views.

b Give the definition of the Anterior/Posterior position in the axial view.

c Put the other landmarks in position. Start with Inferior/Superior in the coronal view.

d To put Left/Right independently in the axial view, drag the middle section of the registration grid.

e Use the sagittal view to do a verification of the Anterior/Posterior and Inferior/Superior position of the Talairach grid.

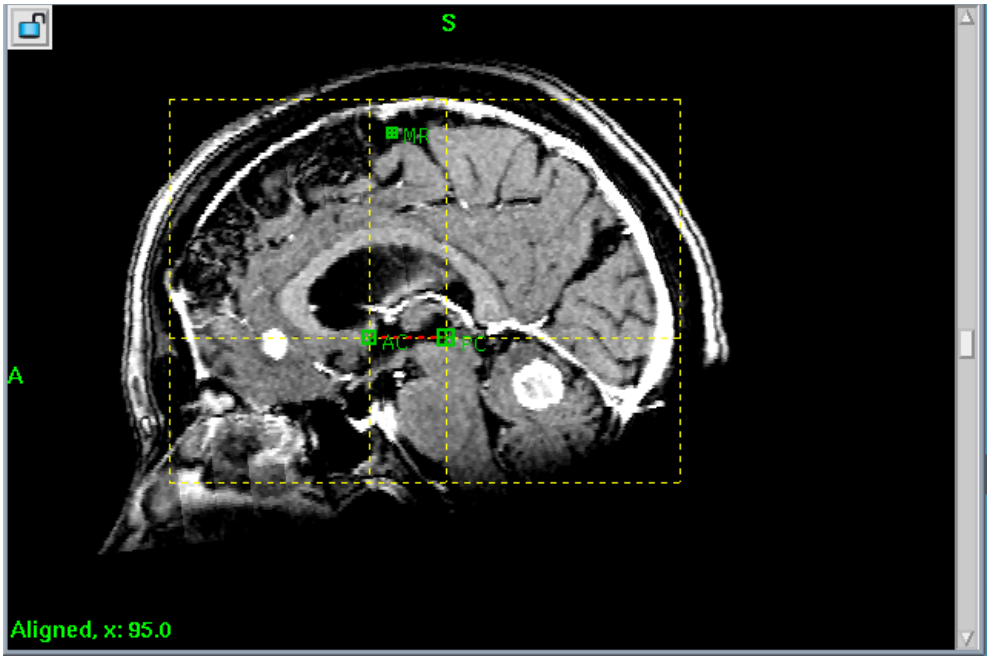


Figure 5.81 Verifying the position of the Talairach grid

3 Carefully examine the agreement between the Talairach grid and the images of the patient.

4 Make sure that the atlas registration is correct. To accept the atlas registration, click **Accept**.

When the atlas registration is accepted, the Talairach grid is shown with solid lines, see figure below.

It is possible to remove an unsatisfactory atlas registration and get the initial (not approved) registration that agrees with the positions of AC, PC and MR while their definitions are kept.

a As an alternative to accept the atlas registration, click **Reset**. The atlas registration is immediately rejected and the Talairach grid is changed from solid to broken lines.

b Do the registration procedure again. Start at **2** .

During an atlas registration, it is possible to go back to a registration that was accepted before.

a As an alternative to accept the atlas registration, click **Undo**. The atlas registration is set to the condition that was before the Brain Atlas dialog box was opened.

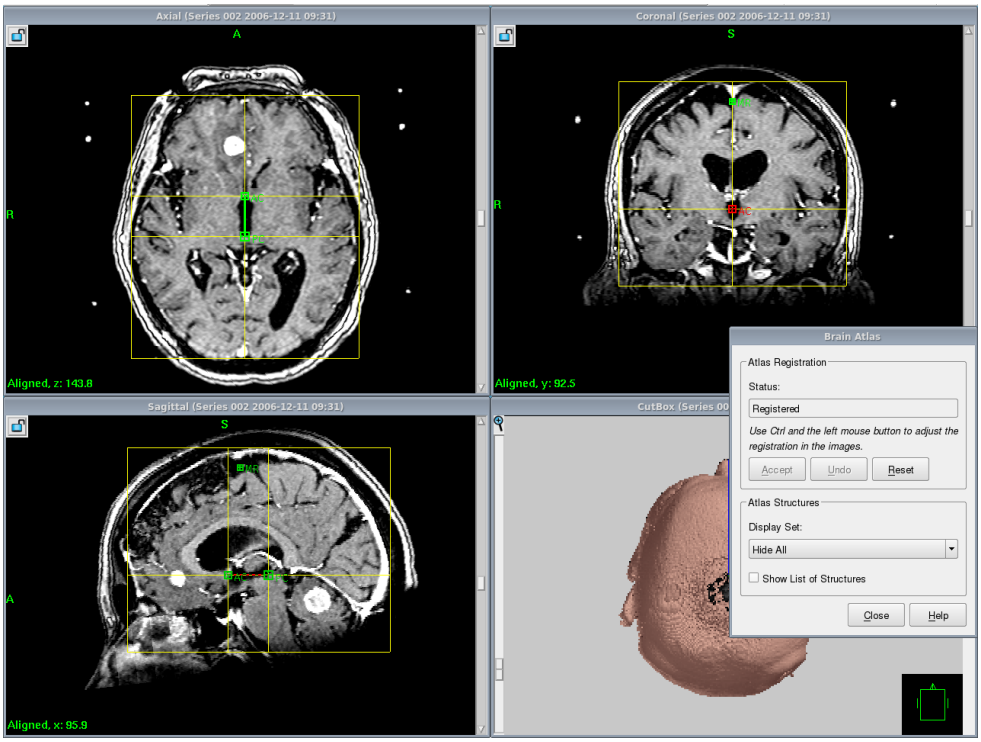


Figure 5.82 Talairach grid shown with solid lines when the registration is accepted

5 Click **Close**.

The Brain Atlas dialog box closes and the Talairach grid is removed from the images of the patient.

The patient examination contains a correct atlas registration at this time.

5.9.3.3 Adjusting an atlas registration

To align atlas structures better to anatomical landmarks, it is possible to adjust an atlas registration that was specified before. The prerequisites for this are the same as those for the initial atlas registration.

1 Select **Plan** > **Brain Atlas** to start the atlas registration.

The Brain Atlas dialog box opens.

The Talairach grid appears in all patient images. The registration is approved and therefore the grid has solid lines.

Atlas structures that were switched on are shown in the images of the patient.

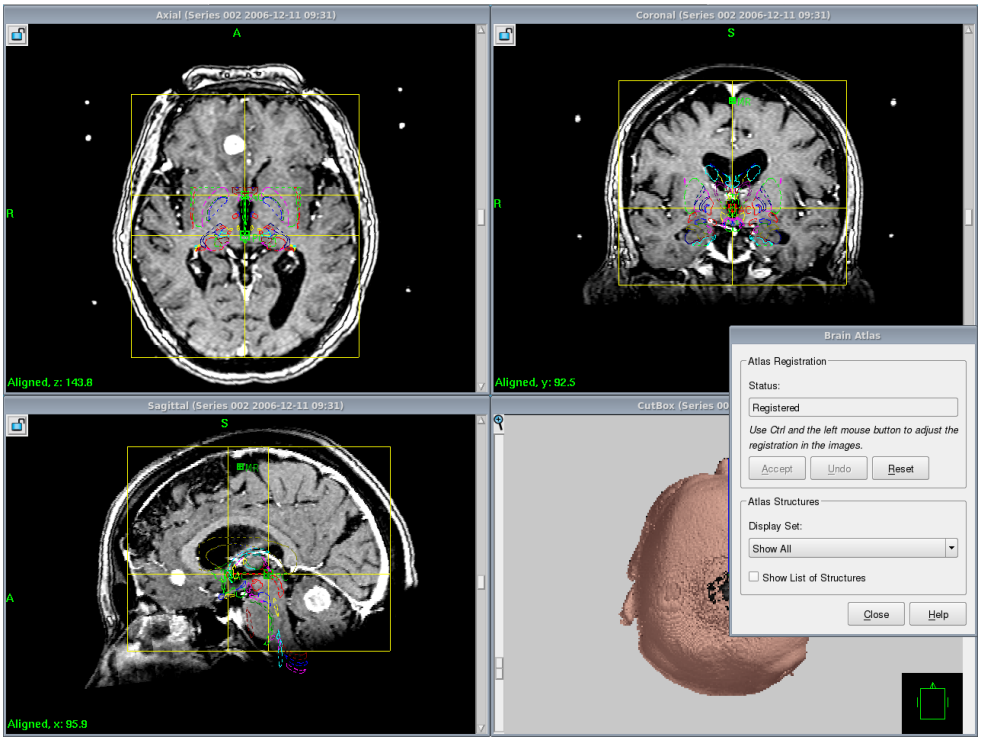


Figure 5.83 Atlas registration adjustment

2 To get good views of the region of interest, move the point-of-exploration to the target area. Then increase the size of the region in the applicable images.

WARNING 5.18

Ensure that you have selected the correct atlas contour(s) for the patient and the treatment plan, otherwise you could devise an incorrect treatment plan that is hazardous to the patient.

Use the interactive labeling feature to identify the contour of interest. Make sure that the contour of interest is clearly visible and, if necessary, clear all unwanted structures and contours from the patient's images.

3 Display one or more atlas structures.

4 Carefully examine the agreement between the atlas contours and local anatomical landmarks in the images of the patient.

5 Hold down the <Ctrl> key and drag the selected structures to align to the image anatomically.

The atlas registration is rejected and the Talairach grid is changed from solid to broken lines.

6 Make sure that the atlas registration is correct. To accept the atlas registration, click **Accept**.

The Talairach grid is shown with solid lines in the images of the patient.

7 Click **Close**.

The Brain Atlas dialog box is closed and the Talairach grid is removed from the images of the patient.

The patient examination contains the updated atlas registration at this time.

Related Links:

The Brain Atlas dialog box on page 164

The Atlas Structures frame on page 166

Showing atlas structures on page 174

5.9.3.4 Rejected registration

An Atlas registration is rejected if:

- The registration is removed with the **Reset** button
- The AC, PC, MR or Talairach grid is moved during registration
- The Brain Atlas dialog box is closed before registration is complete.

Do the registration procedure again to make a correct atlas registration.

Related Links:

Making an atlas registration **on page 169**

5.9.4 Atlas structures

5.9.4.1 Prerequisites for viewing atlas structures

To make the explanation in this section easier:

- An image study of a patient must be open in an applicable workspace.
- The images must be aligned to the intercommissural line.
- A successful atlas registration is made.

WARNING 5.19

The atlas contour database may contain inconsistencies and inaccuracies introduced by the process of digitizing the original atlas.

Related Links:

Making an atlas registration **on page 169**

5.9.4.2 Showing atlas structures

To show atlas structures in the images of the patient, perform the following steps:

1 Select **Plan** > **Brain Atlas**.

The Brain Atlas dialog box opens.

2 Select the **Show List of Structures** check box to show the list of atlas structures.

3 Click the **Display Set** list to open one of the predefined display sets or one of the user-defined display set.

Note: *It is possible to save user-defined sets of structures in the **Display Set** list.*

4 To show an atlas structure, select the check box adjacent to the name of the structure in the **Structure** list.

If a contour of the selected structure is sufficiently near a viewing plane in one of the images of the patient, the contour will be put on the image of the patient.

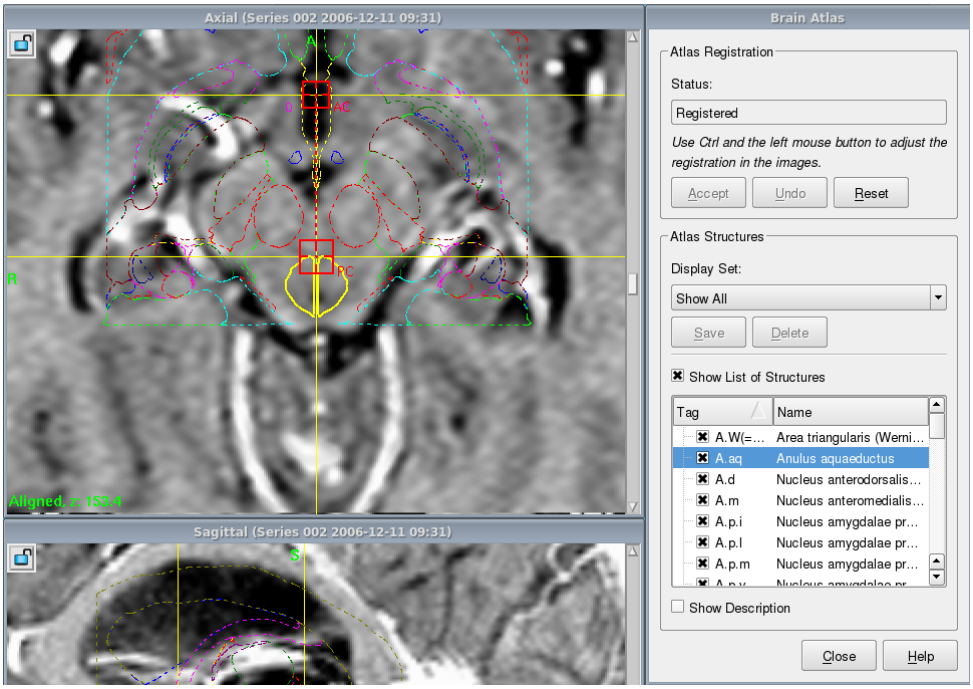


Figure 5.84 Atlas registration display

5 To close the Brain Atlas dialog box, click **Close**.

The display selection (show/not show) for each atlas structure is saved in the database.

Related Links:

The Brain Atlas dialog box on page 164

The Atlas Structures frame on page 166

Saving a display set of atlas structures on page 175

5.9.4.3 Saving a display set of atlas structures

To make and save user-defined display sets of atlas structures, perform the following steps:

1 Select **Plan** > **Brain Atlas**.

The Brain Atlas dialog box opens.

2 Select the **Show List of Structures** check box to show the list of atlas structures.

3 Select check boxes of the necessary structures.

4 Type an applicable name in the **Display Set** field.

5 Click **Save**.

Note: *If the name is used before, a confirmation dialog box appears. Click **Yes** or **No** to continue. If you click **No**, you will go back to **4** .*

Related Links:

The Brain Atlas dialog box on page 164

The Atlas Structures frame on page 166

5.9.4.4 Changing a display set of atlas structures

To change and save user-defined display sets of atlas structures, perform the following steps:

1 Select **Plan** > **Brain Atlas**.

The Brain Atlas dialog box opens.

2 Select the **Show List of Structures** check box to show the list of atlas structures.

3 Click the **Display Set** drop-down list and select the name of the display set that you want to change.

4 Select and clear the check boxes of the necessary structures.

The display set name becomes possible to change.

5 Type an applicable name in the **Display Set** field.

6 Click **Save**.

Note: *If the name is used before, a confirmation dialog box appears. Click **Yes** or **No** to continue. If you click **No**, you will go back to* **5** *.*

Related Links:

The Brain Atlas dialog box on page 164

The Atlas Structures frame on page 166

5.9.4.5 Erasing a display set of atlas structures

To erase user-defined display sets that are saved in the system, perform the following steps:

1 Select **Plan** > **Brain Atlas**.

The Brain Atlas dialog box opens.

2 Click the **Display Set** drop-down list and select the name of the display set to be erased.

A confirmation dialog box opens.

3 Click **Yes** to erase the selected display set.

The dialog box closes and the selected list is erased from the display set list.

Related Links:

The Brain Atlas dialog box on page 164

The Atlas Structures frame on page 166

5.10 Treatment planning preparations

5.10.1 Description of the skull scaling instrument

Note: *This section is valid only for Leksell® Coordinate Frame G.*

For the purposes of treatment planning, it is first necessary to define the boundary of the patient's skull in the Leksell® stereotactic space. This can be done either automatically from CT or MR images (in which case this section can be skipped) or manually by doing manual

measurements and recordings of the distance between the center of Leksell® stereotactic space and certain significant points on the outer boundary of the patient's skull.

When doing manual measurements, the obtained data is entered into the treatment planning application, where it is essential for dose calculations, shot clearance calculations, and the generation of a three-dimensional skull model.

The Skull Scaling Instrument and Leksell® Coordinate Frame are used to take skull measurements. These instruments are part of the stereotactic equipment delivered with Leksell Gamma Knife®.

Note: *For more information see the Skull Scaling Instrument, Instructions for Use and Leksell Stereotactic System®, Instructions for Use.*

The skull scaling instrument is a partial sphere made of transparent plastic. It is placed on top of the coordinate frame attached on the patient's head.

The surface of the instrument contains 24 circular holes. The top radius hole is labelled **0** and is used to obtain the patient's **Top Radius** measurement.

The other 23 holes are arranged in eight longitudinal columns, with lateral rings designated **A**, **B**, **C**, and **D**. Each hole is labelled with a unique number within the range **A1** to **D8**. Not all points on the skull require a measurement hole because the treatment planning application interpolates certain points automatically. Some positional numbers in the A1 to D8 range are therefore not used.

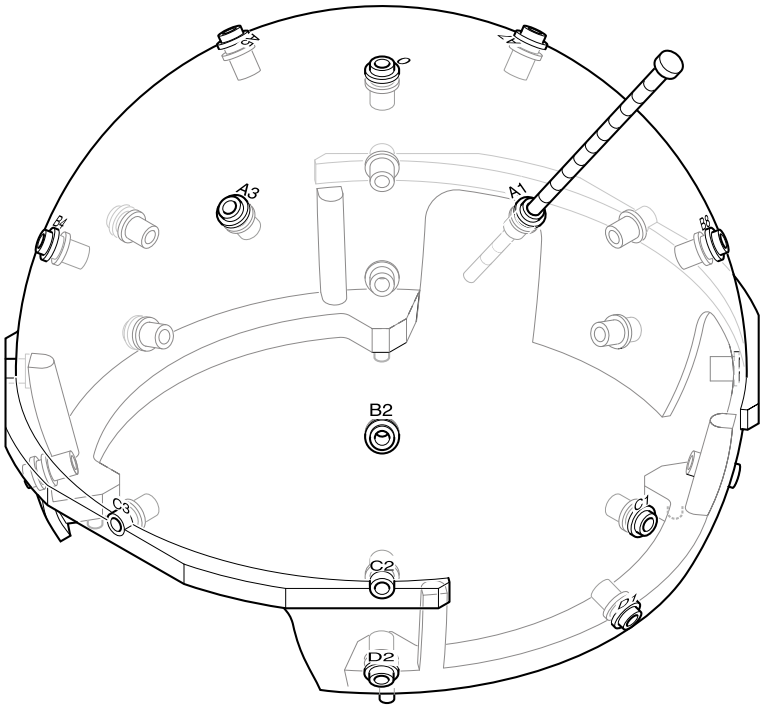


Figure 5.85 Skull scaling instrument

Skull measurements are made by inserting a ruler into the holes in the sphere to make contact with the patient's skull. The ruler is marked with a scale graduated in millimeters. This scale represents a reverse value, being the distance from the center of the Leksell® stereotactic space to the outer surface of the patient's head at the point of measurement.

5.10.1.1 Description of the skull and coordinate frame measurements protocol

Note: *This section is valid only for Leksell® Coordinate Frame G.*

Use the supplied protocols to print copies as needed.

The *Skull and Leksell® Coordinate Frame G measurements protocol* contains four subsections:

- Skull measurements
- Frame cap fits (not applicable for Leksell Gamma Knife® B, C, 4 and 4C)
- Front piece
- Frame configuration

Skull measurements

The values obtained from the skull scaling instrument are to be recorded in the Skull measurements section of the protocol. These measurements are then entered into the Skull dialog presented by the treatment planning application prior to placing shots.

The skull measurement table in the protocol contains 33 fields in total; namely the **Top radius** field and fields **A1** to **D8**. The shaded fields in the table represent interpolated values.

Frame cap fits

This section is not applicable for Leksell Gamma Knife® B, C, 4 and 4C.

Select Yes or No to record if the frame cap fits or not.

Front piece

Select the applicable front piece used in the procedure.

Frame configuration

Measure and record the actual coordinate frame configuration.

Related Links:

Skull and Leksell® Coordinate Frame G measurements protocol on page 361

5.10.2 Measuring the patient's skull

Prerequisites

This section is valid only for Leksell® Coordinate Frame G.

Note: *It is not necessary to measure the patient's skull if CT or MR images will be used to automatically define the skull.*

WARNING 5.20

When taking skull measurements the tip of the measuring probe must come into contact with, but must not penetrate, the patient's scalp or skin. The probe must therefore pass through head hair and facial hair, otherwise it may result in inaccurate measurements.

WARNING 5.21

Exercise extreme caution when taking skull measurements in close proximity to the patient's eyes and ears. The tip of the probe must not penetrate these organs, otherwise the patient could sustain severe injury. Instead, place the tip of the probe at the point that approximates the continued curvature of the skull at the eyes and ears.

1 For instructions on how to measure the patient's skull with Leksell® Coordinate Frame fitted, refer to the *Skull Scaling Instrument, Instructions for Use*.

5.10.3 Measuring posts and screws

Prerequisites

This section is valid only for Leksell® Coordinate Frame G.

Measure the post and screws using the following procedure. Record the post types and the measured values in the *Skull and Leksell® Coordinate Frame G measurements protocol* included in this manual.

1 Record the type of front piece and posts used for each position in the post type fields.

Note: *If using the slotted front piece, determine the post offset by using the post locking screw center as a reference and enter the scale value corresponding to a thought vertical line from the screw mid point and the scale on the slotted front piece. See figure below.*

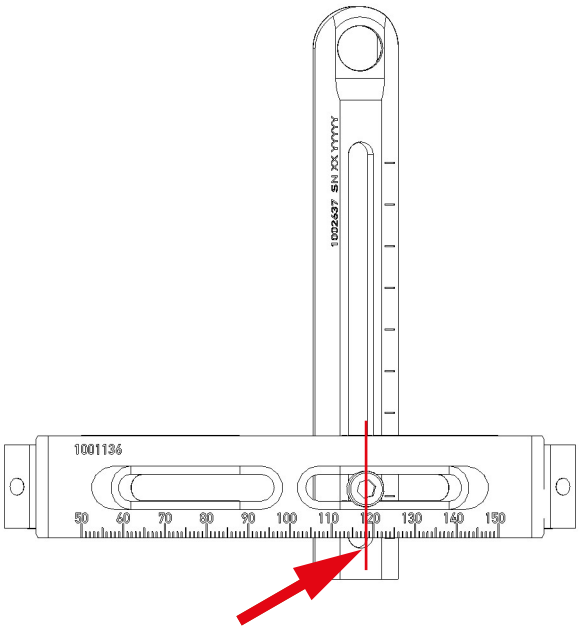


Figure 5.86 Slotted front piece

2 Using a vernier caliper, measure and record the height of each of the four corner posts of Leksell® Coordinate Frame. The height is defined as the perpendicular distance, that is, along the Z-axis in Leksell® Coordinate System, from the upper edge of the coordinate frame to the top of the post (in mm). Record the measured value in the **Superior** field in the protocol for each post.

3 Using a vernier caliper, measure and note how far each post protrudes below the coordinate frame, from the lower edge of the coordinate frame to the bottom of the post (in mm). Record the measured value in the **Inferior** field in the protocol for each post. For curved posts, only the number of the attachment hole is necessary.

Note: *If you are uncertain about which hole is used, verify by comparing the measured height with the corresponding height given in the menu.*

4 Using a vernier caliper, measure and note the length of the fixating screw in each post. The length is defined as the distance that the screw protrudes from the post (in mm). Record this value in the **Screw** field in the protocol for each post.

Note:

For Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™, the measurements acquired in the steps above may be noted and included in the treatment plan even if the frame cap fits.

In certain cases, a treatment position may not be reachable using the pre-defined frame cap geometry. In these cases, the measured values may then allow sufficient clearance for the intended treatment position.

If uncertain, measure the values as indicated in the steps above and note them on the Skull and Leksell® Coordinate Frame G measurements protocol, even if the frame cap fits.

Related Links:

Skull and Leksell® Coordinate Frame G measurements protocol on page 361

5.10.4 Using the frame cap

Prerequisites

This section is valid only for Leksell® Coordinate Frame G combined with either Leksell Gamma Knife® Perfexion™ or Leksell Gamma Knife® Icon™.

The frame cap is intended as a quick measurement tool to facilitate a smooth workflow with Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™. The frame cap has a known and fixed geometry used by the treatment planning application when estimating clearance. Treatment plans where the frame cap is used instead of detailed measurements will not need a clearance check prior to treatment.

Note:

For more information of the Frame Cap see Leksell Gamma Knife® Perfexion™ Instructions for Use or Leksell Gamma Knife® Icon™ Instructions for Use.

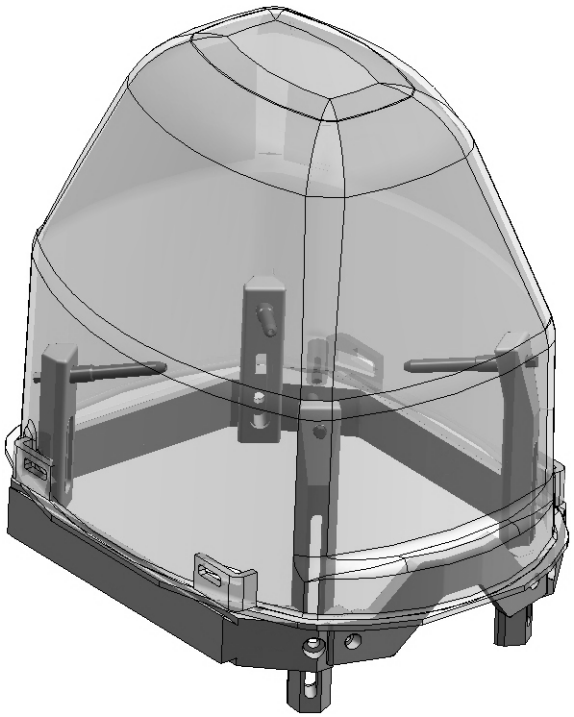


Figure 5.87 The frame cap fitted to the coordinate frame

CAUTION 5.1

Do not force the frame cap onto the coordinate frame; it should fit easily.

1. Test if the frame cap fits by carefully placing it on top of the patient's head. The frame cap has locating pins fitting to corresponding holes in the top of the coordinate frame. When performing the test, make sure the locating pins are fully seated in the corresponding holes in the coordinate frame.
2. If the frame cap does not fit, this may be due to protruding screws, posts or the patient skull. A treatment plan can still be devised but post configuration and measurements will have to be recorded and entered in the treatment planning application.
3. Record if the frame cap fits or not in the *Skull and Leksell® Coordinate Frame G measurements protocol*.

Related Links:

Skull and Leksell® Coordinate Frame G measurements protocol on page 361

5.11 Treatment planning tools for Leksell Gamma Knife®

5.11.1 Prerequisites for making a treatment plan

Perform the following steps before devising a treatment plan:

- Configure the user preferences (optional).
- Create the patient's file and import the tomographic and/or angiographic images.
- Prepare the patient's image studies for treatment planning.
- Leksell® Coordinate Frame G only: Fill out the *Skull and Leksell® Coordinate Frame G measurements protocol*, or make sure that the frame cap fits.

- Configure any special workspaces that you may need (optional).
- Outline the lesion on the patient's images.

5.11.2 Fixation configuration

Depending on Leksell Gamma Knife® model, there are different fixations available for use:

- Leksell® Coordinate Frame G, available for all models
- Leksell® Vantage™ Head Frame, available for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™
- Mask, only available for Leksell Gamma Knife® Icon™.

Note: *Support for Extend™ Frame System is discontinued. Functionality related to Extend™ Frame System is only included in this manual for the sake of handling patient files with Extend™ Frame System originating from a previous version of the system.*

5.11.2.1 Defining fixation Leksell® Coordinate Frame G

Defining fixation coordinate frame when frame cap fits

Prerequisites

This section is valid only for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™.

This procedure is applicable if the frame cap fits over the coordinate frame and the patient's head, as recorded in the *Skull and Leksell® Coordinate Frame G measurements protocol*, included in this manual. Perform the following steps to enter the coordinate frame configuration into the treatment planning application:

1 From the **Plan** menu, select **Fixation configuration**.

The Fixation configuration dialog opens.

2 Select **Leksell® Coordinate Frame G**.

3 Select **Frame cap fits**.

4 Select **Reviewed for plan approval** to show that the fixation configuration has been reviewed and can be used for treatment.

5 Click **Save** to confirm the fixation configuration.

Related Links:

Skull and Leksell® Coordinate Frame G measurements protocol on page 361

Defining fixation coordinate frame using measurements

This procedure defines the coordinate frame according to the measurements recorded in the *Skull and Leksell® Coordinate Frame G measurements protocol*, included in this manual. Obey these steps to enter the coordinate frame configuration into the treatment planning application:

1 From the **Plan** menu, select **Fixation configuration**.

The Fixation configuration dialog opens.

2 Select **Leksell® Coordinate Frame G**.

3 Select **Use measurements**.

The dialog is extended with fields to enter measuring values for posts and screws.

Note: *When using both frame cap and measured values, also select **Frame cap fits**.*

WARNING 5.22

It is essential for the clearance calculation in Leksell GammaPlan® that the posts configuration in the Treatment Planning System Administrator Tool is done correctly. If not, this could lead to interference with the radiation unit during treatment.

WARNING 5.23

Take caution that you specify the correct coordinate frame parts used. This includes the front piece, posts and screws. This is essential information for the clearance calculations executed in the treatment planning application. Incorrect information may cause interference with the radiation unit during the treatment.

WARNING 5.24

It is essential that only posts that are configured for the system are used. The use of posts that the system is not configured for may cause interference with the radiation unit during the treatment, leading to patient injury.

4 Select the correct front piece and select the correct post type from the list for each of the four positions and enter the measured values in the corresponding text fields. Only the posts configured as present at your specific site will be available to select.

5 Select **Reviewed for plan approval** to show that the fixation configuration has been reviewed and can be used for treatment.

6 Click **Save** to confirm the fixation configuration.

Related Links:

Measuring posts and screws on page 179

Skull and Leksell® Coordinate Frame G measurements protocol on page 361

Defining fixation coordinate frame using simulated frame measurements

You can simulate a common Leksell® Coordinate Frame G configuration and allow a treatment plan to be devised.

1 From the **Plan** menu, select **Fixation configuration**.

The Fixation configuration dialog opens.

2 Select **Leksell® Coordinate Frame G**.

3 To simulate a coordinate frame configuration, select **Simulate frame**.

It will not be possible to edit the coordinate frame configuration until the **Simulate frame** checkbox is turned off.

Note: *A treatment plan devised using the simulated coordinate frame configuration will not be possible to approve.*

Note: *Clearance results and possible indications of needed clearance checks are likely to change when the actual coordinate frame configuration is entered.*

4 Click **Save** to confirm the fixation configuration.

5.11.2.2 Defining fixation Leksell® Vantage™ Head Frame

Prerequisites

This section is valid only for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™.

To define the fixation configuration, obey these steps:

1. From the **Plan** menu, select **Fixation configuration**.

   The Fixation configuration dialog opens.
2. Select **Leksell® Vantage™ Head Frame**.
3. Select **Reviewed for plan approval** to show that the fixation configuration has been reviewed and can be used for treatment.
4. Click **Save** to confirm the fixation configuration.

5.11.2.3 Defining fixation mask

Prerequisites

This section is valid only for Leksell Gamma Knife® Icon™.

To define the fixation configuration, obey these steps:

1. From the **Plan** menu, select **Fixation configuration**.

   The Fixation configuration dialog opens.
2. Select **Mask**.
3. Select **Reviewed for plan approval** to show that the fixation configuration has been reviewed and can be used for treatment.
4. Click **Save** to confirm the fixation configuration.

5.11.3 Defining the skull shape

5.11.3.1 Prerequisites for defining the skull shape using CT or MR images

The skull shape can be generated from CT or MR images. It is recommended that the images cover the whole head.

Note: *For best results, the fixation configuration should be defined before the skull shape as the skull shape generation takes the fixation configuration into account.*

5.11.3.2 Defining the skull shape using CT or MR images

After the appropriate CT or MR images have been imported and defined, do the following:

1. From the **Plan** menu, select **Skull definition** > **Images**.

   The Skull Definition dialog opens.

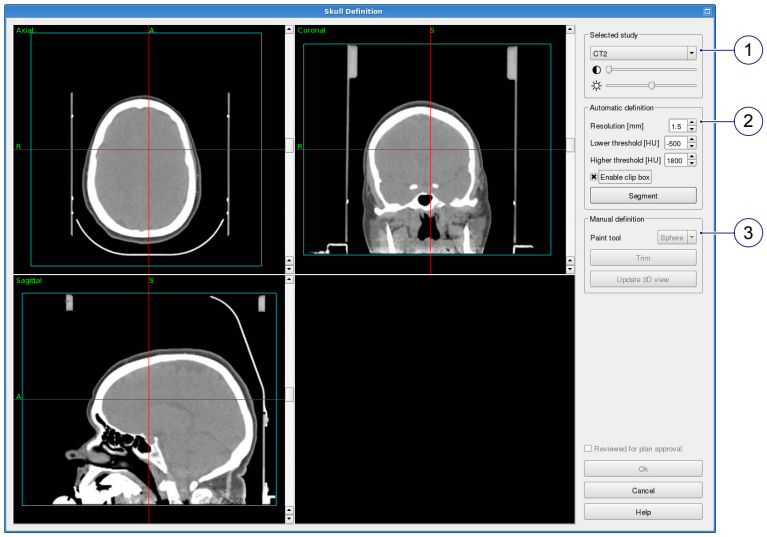


Figure 5.88 The Skull Definition dialog showing the selected image study

(1) **Selected study** frame

(2) **Automatic definition** frame

(3) **Manual definition** frame

2 Select the image study that shall be used for the skull definition among the defined image studies in the **Selected study** frame.

The selected study is shown in an axial, coronal and sagittal 2D view in the dialog.

3 In the **Automatic definition** frame, select the necessary resolution in mm to make the skull shape. The **Lower threshold** and **Higher threshold** are only applicable to CT images. They give the range of image values (in Hounsfield Units) to include in the automatic skull definition.

Note: *If the automatic skull definition results in an irregular skull contour with holes, it can help to increase the **Higher threshold**. If the automatic skull definition results in a skull contour that include unwanted frame details etc., it can help to increase the **Lower threshold** and/or decrease the **Higher threshold**.*

Note: *An unsatisfactory segmentation result can be the result of an unsatisfactorily calibrated CT scanner. It is important to use a correctly calibrated scanner with the Convolution dose algorithm. The default values of [-500HU, 1800HU] must include soft tissue and bone on a calibrated CT scanner.*

4 If applicable, select **Enable clip box** and adjust the boundaries of the box.

5 Click **Segment** to start the automatic skull shape definition.

The process may take several seconds, depending on the selected resolution. When the process is finished, the skull contour is shown in the 2D views and the skull shape is shown in 3D in the lower right view.

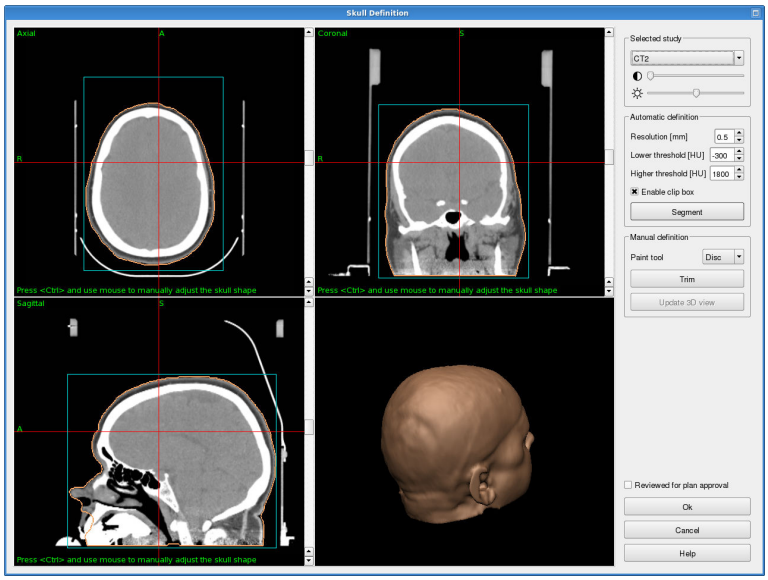


Figure 5.89 The Skull Definition dialog showing the skull shape in 3D

Related Links:

Using the clip box when defining the skull shape on page 186

Using the clip box when defining the skull shape

When you define the skull shape from images, you can select to exclude all information outside a specified volume. Typically, this is done to exclude the fixation from the skull shape.

1. In the **Automatic definition** frame in the **Skull Definition** dialog, select **Enable clip box**.

   A turquoise square appears in the 2D views.
2. Press the left mouse button and drag the borders of the clip box in the views, so that the box contains only the volume of interest.
3. To move the whole clip box, press the <Shift> key and drag the clip box using the left mouse button.

Related Links:

Defining the skull shape using CT or MR images on page 184

5.11.3.3 Verifying the skull shape using CT or MR images

Carefully verify that the skull contour agrees with the images everywhere. The following methods can be used to explore the images and verify the skull shape:

1. To move the exploration cross, move the mouse over it, press the left mouse button and drag the cross with the mouse while keeping the left mouse button pressed down.

   All 2D views are updated so that they show image planes intersecting at the position of the exploration cross.
2. To pan, press the left mouse button in a view and move the cursor.
3. To zoom, press the right mouse button in a view and move the cursor downwards for zooming in and upwards for zooming out.

4 To select a slice, use the mouse scroll wheel or move the scroll bar at the right of the window.

The exploration cross is moved to the selected slice and the other 2D views are updated accordingly.

5 To compare with another image study, select it in the **Selected study** frame.

5.11.3.4 Adjusting the skull shape using CT or MR images

Sometimes, the skull shape cannot be defined completely automatically and manual adjustments are necessary. This may happen if the images are distorted or contain artifacts.

1 In the **Manual definition** frame, select the shape of the paint tool, Sphere or Disc. The Disc-shaped paint tool will only paint in the current image. The Sphere shaped tool will paint in the adjacent images too.

2 Press and hold down the <Ctrl> key to activate the paint tool.

The cursor shape is changed to a green circle when moving it over one of the 2D views.

3 To change the size of the paint tool, press the right mouse button and move the mouse up or left to make the paint tool smaller and down or right to make it bigger (still with the <Ctrl> key pressed down). The size can also be changed with the mouse scroll wheel.

4 To erase a part of the skull shape, press the left mouse button outside the skull contour and move the paint tool towards the contour while keeping the mouse button pressed down.

5 To enlarge the skull shape, press the left mouse button inside the skull contour and move the paint tool towards the contour while keeping the mouse button pressed down.

6 The 3D view is not updated automatically after the manual adjustments. To update the view, click the **Update 3D view** button.

7 If the manual modifications above have disconnected parts from the skull shape (for example parts of the coordinate frame or indicator box that should not be included), click the **Trim** button in the **Manual definition** frame to remove them. The 3D view updates automatically.

5.11.3.5 Canceling the skull shape definition process

1 Click the **Cancel** button to cancel the skull definition process at any time.

Canceling leaves the skull shape as it was when the Skull Definition dialog opened.

5.11.3.6 Approving the skull shape derived from CT or MR images

After the skull shape has been carefully verified and its contour matches the images, it is ready for approval.

1 Select **Reviewed for plan approval** to show that the skull shape has been reviewed and can be used for treatment.

2 Click **Ok** to approve the skull shape.

The image views are adjusted to show the most inferior plane of the segmented skull shape, and the **Inferior plane** confirmation dialog appears.

3 Click **Ok** to confirm that the most inferior part of the segmented skull shape covers the patient anatomy displayed in the image.

If	Then
The system finds that the reconstructed skull shape is incomplete in one or several directions:	The **Incomplete skull** confirmation dialog appears. It has a check box for each incomplete direction. **1** Select the check box(es) and click **Ok** to confirm that the patient's anatomy agrees with the reconstructed skull shape in those directions. The **Approving skull shape** confirmation dialog appears.
The skull shape is complete:	The **Approving skull shape** confirmation dialog appears.

4 Click **Ok** to confirm that the reconstructed skull shape matches the image data in all views.

The Skull Definition dialog closes and the skull shape can now be used for treatment planning.

WARNING 5.25

Verify that the skull shape matches the images. An incorrectly defined skull shape may result in inaccurate dose calculations and may affect clearance results.

Using an incomplete skull shape can result in an overestimation of dose and missing clearance indications.

Note: *When the skull shape has been approved, a region-based representation of the skull is generated and shows up in the Regions-&-Volumes dialog. This region-based representation is only used for visualization and is the one that is shown in the views in a workspace. Note that this representation may differ slightly from the skull shape as it was defined in the Skull Definition dialog. However, the dose calculation and clearance estimation functions use the skull shape exactly as it was defined. To review the exact definition of the skull shape, open the Skull Definition dialog again.*

5.11.3.7 Defining the skull shape using skull measurements

Prerequisites

This section is only valid for Leksell® Coordinate Frame G.

After measuring the geometry of the patient's skull, the obtained measurements must be entered into the treatment planning application.

1 Open the patient's file and radiological examination.

2 From the **Plan** menu, select **Skull definition** > **Measurements**.

The Skull dialog opens.

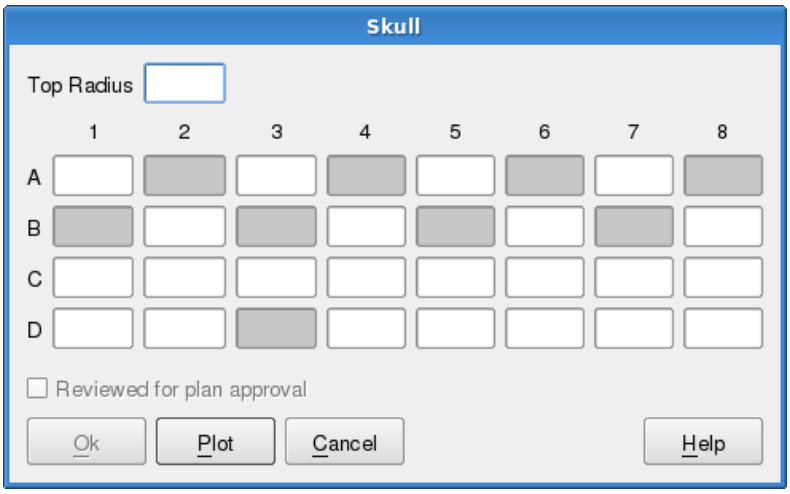


Figure 5.90 The empty Skull dialog

3 Click in the **Top Radius** field and enter the value that you previously recorded in the corresponding field of the skull measurement table.

4 Proceed to the fields in the Skull dialog and enter the patient's measurements into the respective fields. The fields can be completed in any order, and you can use the <Tab> key to move from one field to the next.

Note: *Fields **A2**, **A4**, **A6**, **A8**, **B1**, **B3**, **B5**, **B7** and **D3** contain the interpolated values calculated by the treatment planning application. You cannot enter new values into these fields or adjust the interpolated values in them.*

When you have completed the fields of the Skull dialog it should resemble the following:

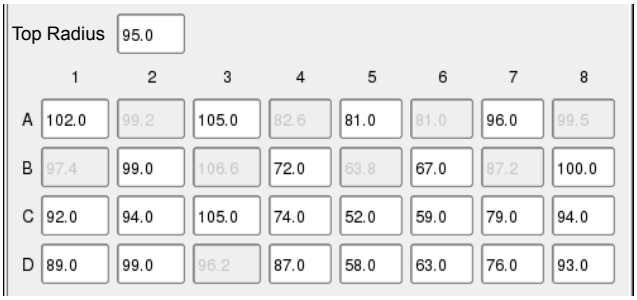


Figure 5.91 The completed Skull dialog

Postrequisites

When you have entered all values, confirm the skull shape as described in this manual.

5.11.3.8 Confirming the skull shape using skull measurements

Prerequisites

This section is only valid for Leksell® Coordinate Frame G.

1 To view the shape of the patient's skull in three-dimensions, click **Plot**.

The Skull Plot opens.

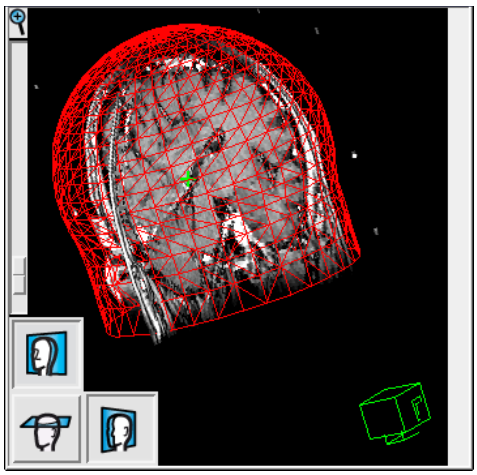


Figure 5.92 The Skull Plot

2 To explore the model, click anywhere in the Skull Plot window and drag the mouse so that the image rotates to the position that you want.

   The model and all superimposed graphics move as you move the mouse. The image orientation is indicated by the green box head in the lower right corner.

3 Move the slider of the scroll bar upwards to zoom into the image and explore in detail. Move the slide bar downwards to zoom out.

4 Toggle the view icons to clear and display the corresponding image slices in the Skull Plot.

5 Visually examine the shape of the model and compare it with that of the patient. Make sure that the model accurately reflects the shape of the patient's skull.

6 When you are certain that the skull measurements are correct, select the **Reviewed for plan approval** check box in the Skull dialog.

7 Click **Ok** to approve the skull shape.

   The Skull dialog and the Skull Plot dialog close.

WARNING 5.26

Verify that the skull measurements are correctly recorded. An incorrectly defined skull shape may result in inaccurate dose calculations and may affect clearance results.

5.11.3.9 Defining the skull shape using simulated values for skull measurements

You can use simulated values for the skull measurements if these are not available when starting treatment planning. The simulated values may also be used for training or demonstration purposes. It is not possible to approve a treatment plan when simulating the skull measurements.

1 From the **Plan** menu, select **Skull definition** > **Simulated skull**.

   The Simulated Skull dialog opens. The default radius of the simulated skull is 80.0 mm.

2 If needed, edit the radius of the simulated skull.

3 To view the shape of the simulated skull in 3D, click **Plot**.

4 Click **OK** to accept the simulated skull shape definition.

5.11.4 Defining the electron density

5.11.4.1 Prerequisites for defining the electron density

In order to use the Convolution dose algorithm, the electron density of the patients anatomy must be defined from CT images.

It is necessary that the Convolution dose algorithm gets information about the electron densities of the tissues which the beams go through. The CT calibration is used to calculate the electron densities from the Hounsfield numbers in the CT study.

WARNING 5.27

It is essential that a correct CT calibration is used for the correctness of dose calculations using the Convolution dose algorithm.

The CT image study used to get the information about electron densities must include the vertex and the sides of the head. It is strongly recommended that the images at least reach down to Z = 167 in the Leksell® Coordinate System (the upper edge of the stereotactic frame, if that fixation is used). The image study must be a defined stereotactic study or a study co-registered to a defined stereotactic study.

Note: *For Leksell® Coordinate Frame G, use Reusable Fixation Screws to decrease possible image distortions, for example "streaking artifacts". For more information about Reusable Fixation Screws, refer to Leksell Stereotactic System®, Instructions for Use.*

5.11.4.2 Defining the electron density

After the appropriate CT images have been imported and defined, and a skull shape has been defined using CT or MR images, do as follows:

1 From the **Plan** menu, select **Electron Density**.

The Electron Density dialog opens.

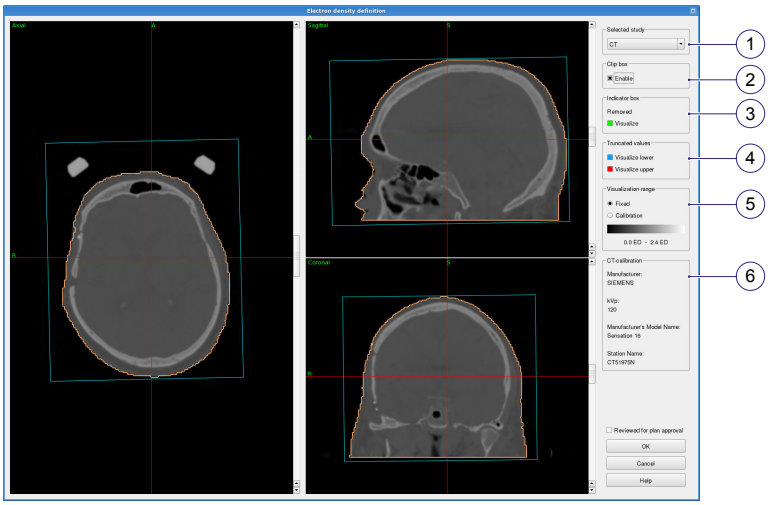


Figure 5.93 The Electron density definition dialog

(1) **Selected study** frame
(2) **Clip box** frame
(3) **Indicator Box** frame
(4) **Truncated values** frame
(5) **Visualization Range** frame
(6) **CT-calibration** frame

2 Select the CT image study that shall be used for the electron density definition among the defined image studies in the **Selected study** frame. (If the electron density has already been defined, the used study is marked as (Defined) in the study selection.)

If a uniquely matching CT calibration is found, the electron density defined from the selected study is immediately shown in the axial, coronal, and sagittal views.

If several CT calibrations match the selected image study, possibly due to missing DICOM attribute values for Manufacturer, Kvp, Manufacturer's Model Name, and Station Name, you are prompted with a dialog that allows you to select from the partially matching CT calibrations manually. Once a matching CT calibration has been selected, the electron density defined from the selected study is shown in an axial, coronal and sagittal view.

Note: *If the selected study contains Hounsfield values that are either below (or above) the applicable CT calibration range, you have the option of either having these values truncated to an electron density value of 0.0 (or the highest electron density value in the CT calibration range) or selecting another study.*

3 If there is an indicator box in the images, the system automatically removes it. This is to prevent unwanted effects on dose calculations since the indicator box is not attached to the frame during treatment. If needed, use the check box in the **Indicator Box** frame to visualize the indicator box.

Note: *The application does not try to remove the indicator box (if any) if the study has not been stereotactically defined.*

4 If needed, adjust the size and placement of the clip box.
5 Select the **Reviewed for plan approval** check box.
6 Click **OK**.

Related Links:

Using the clip box when defining the electron density on page 192

Using the clip box when defining the electron density

When you define the electron density, you can select to exclude all information outside a specified volume. Typically, this is done to exclude parts of the CT scanner or fixation that will not be present at the treatment. Everything that is outside the clip box is considered to be air when the electron density is calculated. This means that the area outside the clip box is assigned an electron density value of 0.0 and attenuates no dose.

The clip box in the Electron density definition dialog is enabled by default. It is shown as a turquoise square in the 2D views. The default size of the clip box is that it covers the skull shape. If needed, you can adjust the size and placement of the clip box, but it is not possible to make it smaller than the skull shape. The patient anatomy must be included in the electron density calculation.

1 Press the left mouse button and drag the borders of the clip box in the views, so that the box contains only the volume of interest.
2 If you want to remove the clip box, deselect **Enable** in the **Clip box** frame.

Note: *Without a clip box, the entire extent of the electron density will be accounted for in convolution dose calculations.*

Related Links:

Defining the electron density on page 191

5.11.4.3 Verifying the electron density

Carefully review the electron density regarding completeness, image quality and imaging artifacts that may affect dose calculations using the Convolution dose algorithm. The following tools can be used in the review:

1 Use the toggle buttons in the **Truncated values** frame to select regions with values outside the specified CT calibration range, which therefore have been truncated. Truncated regions with values below the specified CT calibration range are visualized in blue. These regions are assigned a relative electron density of 0.0 (corresponding to vacuum). Truncated regions with values above the specified CT calibration range are visualized in red. These regions are assigned the highest relative electron density in the specified CT calibration range. Make sure that the electron density does not contain large truncated regions since these are an indication that the CT calibration used is not sufficient.

Note: *The occurrence of truncated electron density values may be an indication of either a poor CT calibration or imaging artifacts.*

2 In the **Visualization range** frame you can select to show relative electron density values as:

- **Fixed** - grey levels in the fixed range [0.0, 2.4] (approximately covering all materials with relative electron densities between air and aluminium), or
- **Calibration** - grey levels that include all relative electron density values in the calculated CT calibration.

Note: *If the calculated CT calibration contains relative electron density values that are larger than 2.4, the Fixed range can give an improved visual contrast for usual tissue. But it will not be possible to visually distinguish relative electron density values higher than 2.4. To distinguish all relative electron density values in the CT calibration range, you must then select the Calibration visualization range.*

3 In the **CT calibration** frame the attribute values used for identifying the CT calibration are displayed.

4 Explore the images in the workspace using the mouse.

Exploring the images in the electron density definition workspace

The following methods for study exploration are available in the workspace:

- To move the exploration cross, move the mouse over it, press the left mouse button and drag the cross with the mouse while keeping the left mouse button pressed down.

  All 2D views are updated so that they show image planes intersecting at the position of the exploration cross.
- To pan, press the left mouse button in a view and move the cursor.

- To zoom, press the right mouse button in a view and move the cursor downwards for zooming in and upwards for zooming out.
- To select a slice, use the mouse scroll wheel or move the scroll bar at the right of the window.

  The exploration cross is moved to the selected slice and the other 2D views are updated accordingly.

5.11.4.4 Canceling the definition process

1 Click **Cancel** to cancel the electron density definition process at any time. Canceling leaves the electron density as it was when the **Electron Density** dialog was opened.

5.11.4.5 Approving the electron density

After the electron density definition has been carefully verified, it is ready for approval.

1 Select the **Reviewed for plan approval** check box.
2 Click **OK** to approve the electron density. If the electron density does not cover the entire segmented skull, an error message appears, and the electron density cannot be approved.

WARNING 5.28

Using distorted or otherwise unrepresentative CT images for defining the electron density may result in inaccurate dose calculations when using the Convolution dose algorithm.

Note: *If the skull shape, frame configuration or any of the images used in the electron density definition changes, the electron density will be invalidated and have to be redefined.*

3 Click **Confirm** to confirm that the electron density is adequate for dose calculations with the Convolution dose algorithm. The Electron Density definition dialog closes and the electron density is used for dose calculations with the Convolution dose algorithm.

Related Links:

Convolution dose algorithm on page 318

5.11.5 Creating a treatment plan

1 From the **Plan** menu, select **New Plan**.

The New Treatment Plan dialog opens.

2 Type an appropriate name for the new treatment plan and enter a comment if desired.
3 If multiple Leksell Gamma Knife® units are available, select the correct one.
4 Select the **Dose algorithm** to be used for dose calculations in the treatment plan:

- TMR 10 - An updated version of the TMR Classic dose algorithm.
- Convolution - A dose algorithm with heterogeneity correction (optional software). Only available if the electron density of the patient's anatomy has been defined.

Note: *The TMR Classic dose algorithm is used for treatment plans made in Leksell GammaPlan® 9 and earlier versions. This dose algorithm is not available for new treatment plans.*

5 If it is applicable, select the **Use extra fine dose grid resolution in targets** check box.

This option gives a dose grid resolution of 0.5 mm at the expense of poorer system responsiveness. It should only be used when the default grid resolution of 1.0 mm is insufficient.

The treatment plan dose grid is set up to cover as much of the skull as possible without containing grid points where dose cannot be reliably calculated with respect to the dose algorithm used.

Note: *For treatment plans made in Leksell GammaPlan® 10 or earlier, the **Use extra fine dose grid resolution in targets** check box is enabled if the treatment plan contained a single target with resolution finer than 1.0 mm.*

6 Click **OK**.

The dialog closes and the Treatment Plans dialog is updated to include the new treatment plan.

Note: *When creating a new treatment plan, the system automatically creates targets that enclose all volumes of type **Target**.*

Related Links:

TMR dose algorithms on page 311

Convolution dose algorithm on page 318

Treatment plan dose grid on page 324

5.11.6 Target definition

The irradiation scheme defined by a treatment plan in Leksell GammaPlan® is based on the definition of one or more targets, inside which shots can be placed. Our recommendation is to create one target for each lesion to be treated. By creating one target for each lesion, the treatment planning application lets you work with each target independently.

The maximum number of targets in one treatment plan is 52 for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™. For the other Leksell Gamma Knife® models the maximum number is 26. However, it is possible to treat more than 52 or 26 lesions by gathering several lesions per target.

When creating a new treatment plan, the system automatically creates targets that enclose all volumes of type **Target**. If the number of targets is more than the maximum number, no targets are automatically created.

All target centers must be inside the skull boundaries, but there are no limitations on how targets can be placed inside the skull. It is allowed to define overlapping targets.

When dose and isodose have been prescribed to all targets, Leksell GammaPlan® automatically calculates a weight for each target that affects the dose delivered by the shots in each target. This concept allows you to focus on the selected target only.

Note: *The target cube is aligned with the treatment plan dose grid and not with Leksell® Coordinate System.*

5.11.6.1 Target mode

Target mode is chosen in the treatment planning application menu bar using the radio buttons **Σ** and **1/1** respectively.

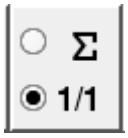


Figure 5.94 Radio buttons for target mode selection

All targets mode - **Σ** - is used when evaluating the total effect of a complete treatment plan, since this reflects the actual total dose that the patient will be exposed to. All shots in all targets will contribute to the isodose curves shown. The dose unit used in All targets mode is absolute dose in Gray (Gy).

When All targets mode is selected, the color of this part of the treatment planning application menu bar changes to yellow.

In **Single target** mode - **1/1** -, only shots from the selected target contribute to the isodose curves shown. The dose unit used in Single target mode is % of the dose in the reference point for the target according to the point dose calculation.

5.11.6.2 Creating a new target

All target management is performed in the Targets dialog. To create a new target, obey these steps:

1 From the **Plan** menu, select **Target**, or in the Toolbar click on the **Target** button.

The Targets dialog opens.

2 In the Targets dialog, click **New**.

The New Target dialog opens.

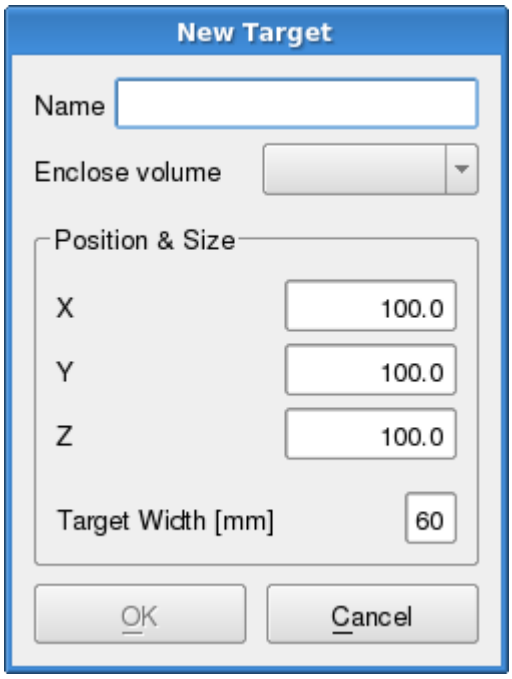


Figure 5.95 New target

3 If you have defined more volumes of type Target you may select one of these using **Enclose volume** to automatically adjust the position and grid size to enclose the selected volume. In this case the target name is set according to the volume name.

To manually define the target name, enter a descriptive name for the new target. An index A-Z is prepended to the target name, to make it unique within the treatment plan.

4 The cut between the target and the image plane is shown in all 2D-images. Position the center of the target, either by clicking/dragging in the images or by entering coordinates in the New Target window. The target center can also be positioned by double clicking in the views. The target center can be moved in views representing any orientation. Another way to change the position is to place the mouse cursor on one of the fields X,Y,Z and use the scroll wheel to adjust the current value up or down. Holding down the <Ctrl> key while scrolling slows down the change.

5 Adjust the width of the target. The value can be adjusted with the scroll wheel or entered by hand.

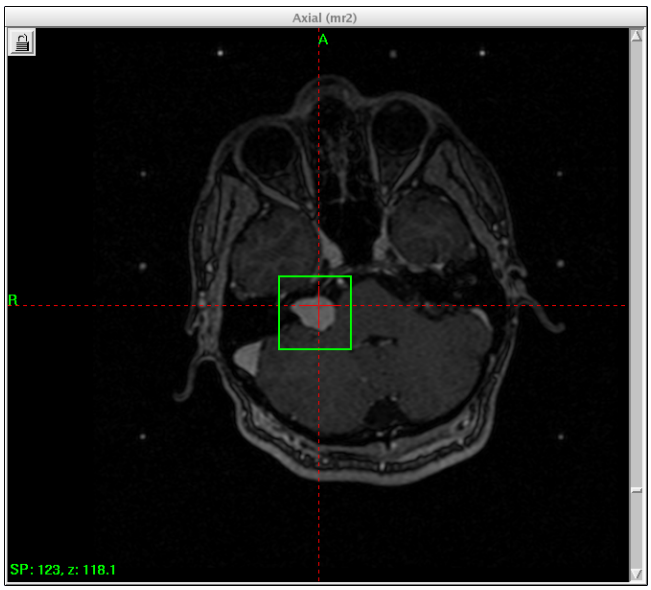


Figure 5.96 Image target

6 When satisfied, click **Ok**. The New Target dialog is closed and the new target shows up in the list in the Targets dialog.

The target list in the Targets dialog contains the following columns when using mask fixation:

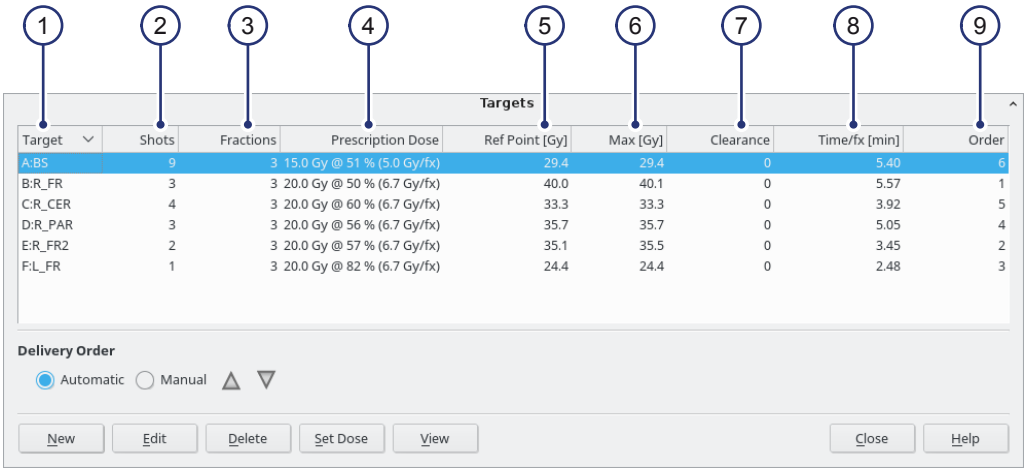


*Figure 5.97 The **Targets** dialog when using mask fixation*

(1)	**Target**	The name of the target, including the fixed index A-Z.
(2)	**Shots**	The number of shots belonging to the target.
(3)	**Fractions**	The number of fractions to use when delivering dose to the target. Note that this number is the same for all targets.

(4)	**Prescription dose**	The dose prescribed to the target.
(5)	**Ref Point [Gy]**	The actual dose delivered to the reference point of the target.
(6)	**Max [Gy]**	The maximum dose inside the target, when all shots from all targets are taken into account.
(7)	**Clearance**	The number of shots in the target that need clearance check.
(8)	**Time/fx [min]**	The total beam-on time for the shots in the target.
(9)	**Order**	The order in which the targets are delivered in each run.

The target list in the Targets dialog contains the following columns when using Leksell® Coordinate Frame G or Leksell® Vantage™ Head Frame, and Leksell Gamma Knife® Icon™ or Leksell Gamma Knife® Perfexion™:

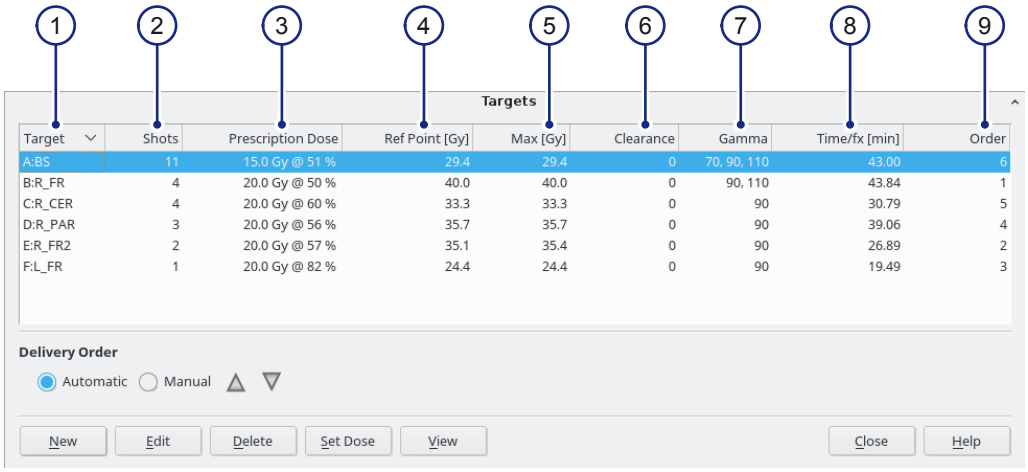


*Figure 5.98 The **Targets** dialog when using Leksell® Coordinate Frame G or Leksell® Vantage™ Head Frame, and Leksell Gamma Knife® Icon™ or Leksell Gamma Knife® Perfexion™*

(1)	**Target**	The name of the target, including the fixed index A-Z.
(2)	**Shots**	The number of shots belonging to the target.
(3)	**Prescription dose**	The dose prescribed to the target.
(4)	**Ref Point [Gy]**	The actual dose delivered to the reference point of the target.
(5)	**Max [Gy]**	The maximum dose inside the target, when all shots from all targets are taken into account.
(6)	**Clearance**	The number of shots in the target that need clearance check.
(7)	**Gamma**	The gamma angles for the shots in the target.
(8)	**Time/fx [min]**	The total beam-on time for the shots in the target.
(9)	**Order**	The order in which the targets are delivered in each run.

The target list in the Targets dialog contains the following columns when using Leksell® Coordinate Frame G, and Leksell Gamma Knife® C :

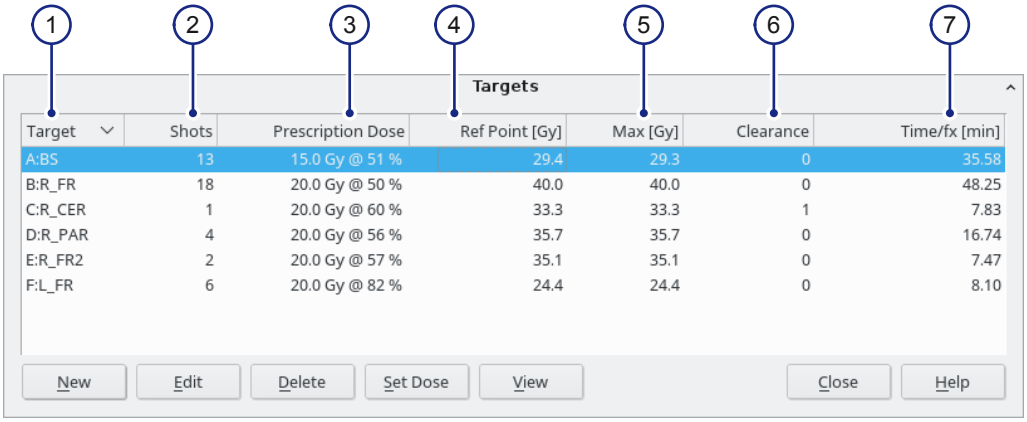


*Figure 5.99 The **Targets** dialog when using Leksell® Coordinate Frame G, and Leksell Gamma Knife® C*

(1)	**Target**	The name of the target, including the fixed index A-Z.
(2)	**Shots**	The number of shots belonging to the target.
(3)	**Prescription dose**	The dose prescribed to the target.
(4)	**Ref Point [Gy]**	The actual dose delivered to the reference point of the target.
(5)	**Max [Gy]**	The maximum dose inside the target, when all shots from all targets are taken into account.
(6)	**Clearance**	The number of shots in the target that need clearance check.
(7)	**Time/fx [min]**	The total beam-on time for the shots in the target.

If the prescription dose cannot be achieved, a red cross is displayed in the **Ref Point [Gy]** column in the list.

Note: *The dose at the reference point is calculated as a point measurement regardless of the plan dose grid. Unlike other dose measurements, the dose at the reference point is therefore not affected by the resolution and interpolation in the plan dose grid. The dose at the reference point may therefore differ from the reported max dose even though they have the same stereotactic coordinate.*

Related Links:

Failed prescription dose criteria on page 202

Target reference point on page 202

5.11.6.3 Selecting a target

1 Select the target to use in the Targets dialog, by making a selection in the target list.

The selected target is displayed in the top level menu bar (updated immediately when a new target is selected).

5.11.6.4 Centering images on a target

1 Click on **View** to center all workspace views on the selected target. Double-clicking on a target in the target list also selects the target and centers views on this target.

5.11.6.5 Editing an existing target

1 Open the Targets dialog.
2 Select the target from the list in the Targets dialog.
3 Click **Edit**. The Edit Target dialog opens.
4 Adjust the target parameters. Click **Ok** to apply the changes and close the dialog or click **Apply** to apply the changes and leave the dialog open. If **Cancel** is pressed, changes since the latest click on **Apply** are ignored.

5.11.6.6 Deleting a target

1 Open the Targets dialog.
2 In the target list, select the target that is to be deleted, and click **Delete**.
3 A confirmation dialog is shown and after accepting the deletion, the selected target is deleted from the treatment plan. If the target contains shots, the confirmation dialog informs you that all shots belonging to the selected target will be deleted.
4 Repeat steps **2** to **3** for all targets that are to be deleted.
5 Click **Exit**.

The Targets dialog closes.

5.11.6.7 Manually changing the target delivery order

Note: *This is only applicable for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™.*

Target delivery order mode is by default set to automatic delivery order. When automatic delivery order is selected the target delivery order is optimized aiming for the shortest path length between targets.

To manually change the target delivery order:

1 From the **Plan** menu, select **Target**, or in the Toolbar click the Target button.

The **Targets** dialog opens.

2 Select the **Manual** radio button.
3 Select a target in the list and click the up/down arrow buttons to change the order of the targets in the list.

The list is automatically sorted by the **Order** column. To sort the list by another column, click the column title.

If you add a new target when manual delivery order is selected, the new target is added last in the order. If you delete a target when manual delivery order is selected, the order of the remaining targets is adjusted.

Note: *It is only possible to adjust the delivery order of targets within a run. The order of runs is selected manually on the Leksell Gamma Knife® at the time of treatment.*

To go back to automatic delivery order, click the **Automatic** radio button. The target delivery order is then optimized aiming for the shortest path length again.

5.11.6.8 Prescribing dose to a target

WARNING 5.29

Different countries may use different units to quantify the absorbed dose. The treatment planning application uses the Gray (SI unit Gy), which must not be confused with cGy or rad.

Before a treatment plan can be used for treatment, each target shall be assigned the desired prescription dose and isodose. The dose can be prescribed whether or not shots have been placed in the target. If no shots have been added, it is normally not possible to achieve the prescription dose. If the prescribed dose cannot be achieved, a red cross appears in the **Ref Point [Gy]** column in the target list. To prescribe or change the dose to an existing target, obey the following steps:

1 From the **Plan** menu, select **Target**, or in the Toolbar click the **Target** button.

The Target dialog opens.

2 In the target list, select the target to which a dose is to be prescribed, and click **Set Dose**.

The Set Target Prescription Dose dialog opens.

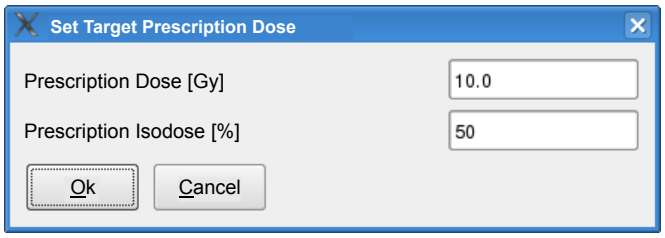


Figure 5.100 The Set Target Prescription Dose dialog when using Leksell® Coordinate Frame G or Leksell® Vantage™ Head Frame

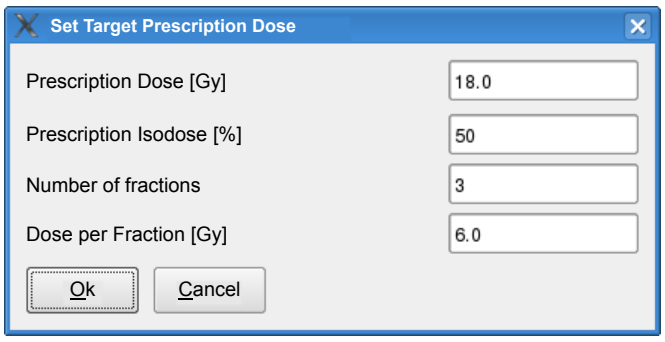


Figure 5.101 The Set Target Prescription Dose dialog when using mask fixation

3 Enter the desired dose prescription. The scroll wheel can be used to adjust the values. Holding down the <Ctrl> key while scrolling speeds up the change.

Note that when you plan a fractionated treatment, there are two options: either the prescription dose and number of fractions can be specified and the dose per fraction will be automatically calculated, or the dose per fraction and number of fractions can be specified and the total prescription dose will be automatically calculated.

4 Click **Ok**.

The dialog closes and the target list information is updated.

WARNING 5.30

Convolution integrates the effect of tissue heterogeneities when calculating dose, whereas TMR assumes the head to be of water equivalent tissue. As a consequence, the equivalent dose prescription levels for Convolution are different from dose prescription levels established using the TMR dose algorithm.

Recommendations when prescribing dose to a target when using Convolution

For each patient, the user is advised to compare new treatment plans based on the Convolution dose algorithm to equivalent plans using TMR 10 dose algorithm during a transition period. The aim is to find the dose prescription using Convolution, which gives approximately the same shot times and total beam-on time, given that the TMR 10 dose algorithm provides the clinically proven dose prescription.

Comparisons of dose algorithms can be made by doing dose measurements.

Physicist users can decide the dose algorithms that can be used for plan approval. For details refer to *TPSAdm Online Reference Manual*.

Related Links:

Performing measurements on page 270

Target reference point

The reference point of the target is set to the point that gets the maximum dose when only shots belonging to that target are taken into account. How this maximum dose point is determined depends on the prescription isodose level.

Reference point for normal dose prescription

For a normal dose prescription (prescription isodose level not set to 100%), the maximum dose point is searched for in the treatment plan dose grid.

Reference point for max dose prescription

For a max dose prescription (isodose prescription is set to 100%), it is the actual max dose that is the prescription criteria. Therefore a special search for the max dose point with a very fine resolution of 0.25 mm is performed. Note that this means that for a target with max dose prescription, the reference point isn't necessarily a treatment plan dose grid point.

Related Links:

Treatment plan dose grid on page 324

Failed prescription dose criteria

In some exceptional situations, it is not possible to achieve the dose prescribed to one or more targets. If two targets are located close to each other and one of the targets is given a much higher prescription dose than the other, it might be impossible to meet the prescription dose criteria for the smaller target.

In the example shown below, target “small” is treated with one 4 mm shot and the closely located target “large” is treated with one 16 mm shot.

As you can see from the isodose curves, the dose from the shot in target “large” is quite high also inside target “small”.

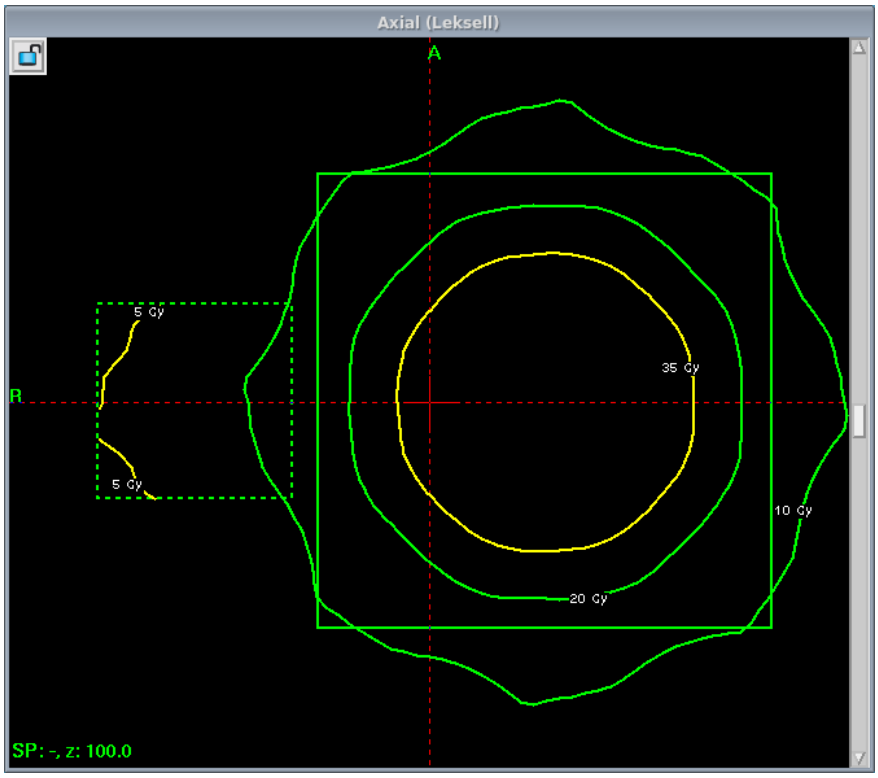


Figure 5.102 Total dose from both targets

Hypothetically, if a high dose is prescribed to target “large”, compared with the dose prescribed to target “small”, it is not possible to achieve the high dose in target “large” without exceeding the prescription dose in target “small”. The wanted reference point dose in target “small” is 1.7 Gy, but with the contribution from target “large” the reference point dose is already 11.1 Gy. See figure below.

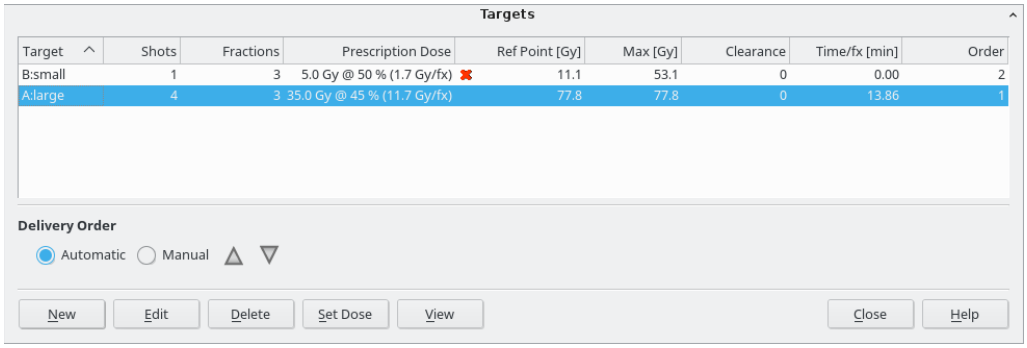


Figure 5.103 The prescribed dose for target “small” cannot be achieved

5.11.7 Configuring the isodose display

1 With the patient's file, radiological examination, and image study open, select **Isodose** from the **Plan** menu.

The Display Isodose dialog opens.

2 Type the values corresponding to the isodose contours that you want to display.

– For **Single Target (1/1)** mode, click in the **Target dose relative level(s) [%]** field (1).

– For **All Targets (Σ)** mode, click in the **Absolute level(s) [Gy]** field (2).

Each value must be separated by a space character. See figure below.

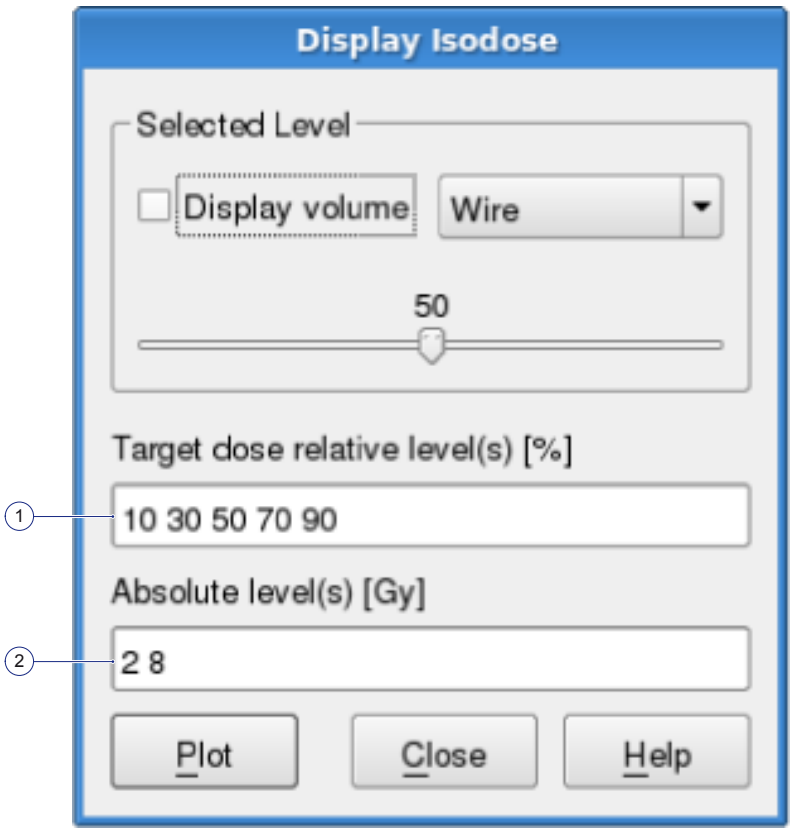


Figure 5.104 The Display Isodose dialog

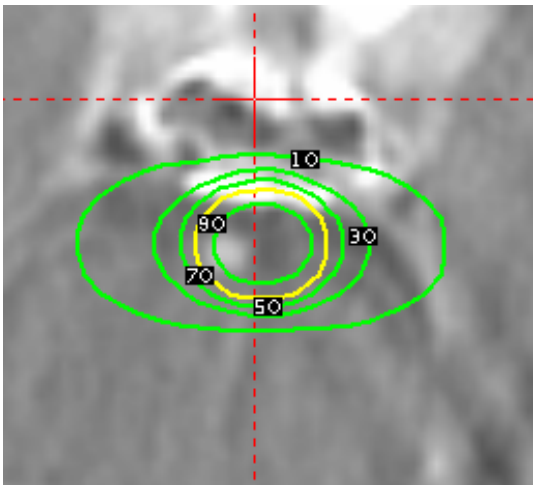
3 The scroll bar sets the **Selected Level**, that is, an isodose level that is displayed in yellow color on the image. If necessary, adjust the scroll bar to a different reference isodose level.

If the prescription isodose has been set, it is possible to change the selected isodose level temporarily only by keeping the left mouse button pressed while moving the **Selected level** slider.

4 If you want to display the reference isodose as a volume in three-dimensional windows, select **Display volume**. Also select the display texture for the reference isodose volume, for example, **Wire**.

5 To save the isodose settings in readiness for shot placement, click **Plot**.

If you have already placed at least one shot, the selected isodose contours will appear on the patient's images.



The isodose contours are updated automatically as new shots are placed or an existing irradiation scheme is modified.

6 To close the Display Isodose dialog, click **Close**.

Related Links:

Single target or All targets on page 270

Target mode on page 45

5.11.8 Creation of the irradiation scheme

When the lesions have been outlined and the general treatment planning parameters have been set up, you can position the radiation shots on the patient's images. Manual shots are placed by clicking at the required point on an image or by stipulating the Leksell® coordinates at the center of the shots. Shots may be placed automatically using Dose Optimization or Inverse Planning. For Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™, an automatic protection of critical structures or risk zones can be applied to dynamically shape the irradiation scheme.

In image studies shots can be placed on one or more image slices. A shot marker extends 3 mm in all directions and is therefore automatically projected onto all other image slices within range of the center of the shot. For example, if a shot is placed on an axial slice with the coordinate Z = 100 mm, then it also appears and can be adjusted on all image slices between the coordinates Z = 97 mm and Z = 103 mm.

All shots must be placed within the targets. You are not allowed to place shots outside the skull or outside the system boundaries.

For Leksell Gamma Knife® B, C, 4, and 4C, the maximum number of shots in a treatment plan is 50. For Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™, it is 500.

Related Links:

Automatically creating an irradiation scheme using Dose Optimization on page 216

Automatically creating an irradiation scheme using Inverse Planning on page 219

Protection of critical structures using Dynamic Shaping on page 226

5.11.8.1 Manually creating the irradiation scheme

1 Open an image study in a workspace and select the image which best displays the first lesion.

2 Adjust the point-of-exploration and use the interactive **Zoom** and **Level** controls to obtain the optimal view of the lesion area.

3 From the **Plan** menu, select **Shot**, or in the Toolbar click the Shot icon.

The Shot dialog opens.

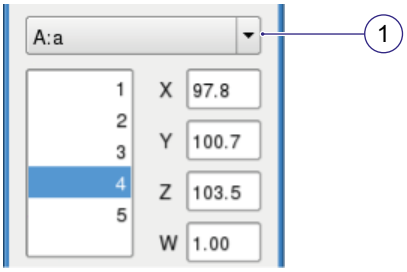


Figure 5.105 The Shot dialog

When more than one target have been added to the treatment plan, the currently selected target is displayed in the target drop-down menu (1).

Selecting a target

1 To change the target in which a shot is to be placed, click on the target drop-down menu and choose a target. Upon selecting a target, the point of exploration is automatically changed to the position of the selected target.

2 For Leksell Gamma Knife® models C, 4, 4C and B only, select **Position**:

- If the first shot to be delivered to the patient is in the supine position, do not change the patient position setting. The **Supine** option is selected by default.
- If the first shot to be delivered to the patient is in the prone position, select **Prone** from the **Position** drop-down list.

Adding the first shot with the mouse

1 Add the first shot by clicking on the lesion at the point where the center of the shot is to be located. A red shape is plotted on the image, it emanates from the center of the shot.

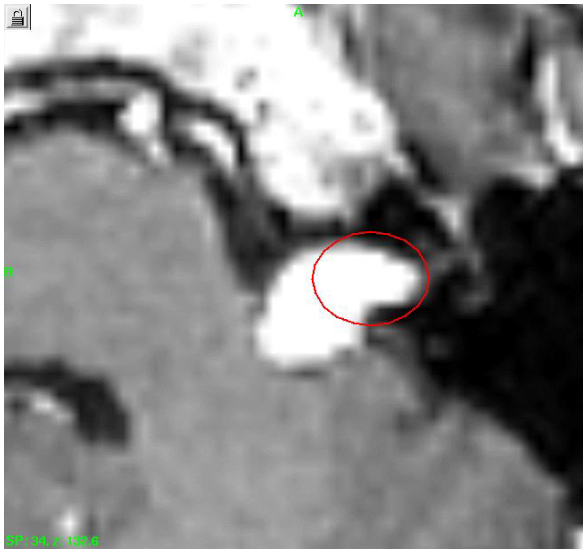


Figure 5.106 Adding the first shot

The red shape represents the default isodose level contributed by this shot alone. The displayed isodose level represents the value previously chosen in the **Selected Level** field of the User Preferences dialog.

In addition, the **X**, **Y**, and **Z** fields in the Shot dialog show the Leksell® coordinates at the center of the shot.

Note: *The point of the origin of the Leksell® coordinates is the superior, posterior, right-hand side of the patient's head.*

Adding the first shot with the keyboard

1 Add the first shot by stipulating its center coordinates in the Shot dialog:

a Click in the **X** field and type the required X coordinate of the center of the shot.

b Go to the **Y** field and type the required Y coordinate of the center of the shot.

c Go to the **Z** field and type the required Z coordinate of the center of the shot.

You can change the value in a coordinate field with the **Up** and **Down** arrows on the keyboard or with the mouse scroll wheel.

Note: *You can move from one coordinate field to another by clicking with the mouse or by using the <Tab> key.*

The default isodose contour of the shot is plotted as a red shape on the image as previously described.

2 When you are satisfied with the position of the first shot, click **Set**. As the shot is set, the treatment planning application calculates the isodose distribution of the total radiation scheme from the contributions made by all the shots that have so far been set. In the example below, only the first shot has been placed and therefore the isodose contours originate from that shot.

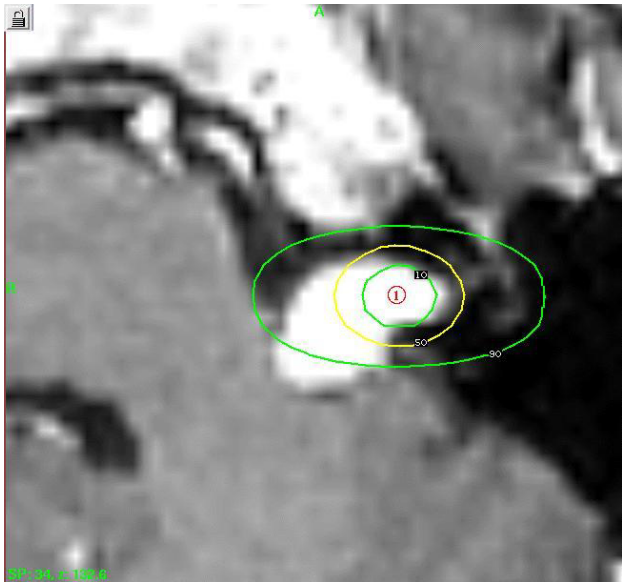


Figure 5.107 Isodose contours

- The shot number is shown in a small red circle at the center of the shot.
- The isodose contours emanate from the center of the shot.
- There is one isodose contour for each level previously selected in the Display Isodose dialog.
- The selected reference isodose level is plotted in yellow and its level is marked on the contour.
- The other isodoses are plotted in green and each level is marked on its contour.

Related Links:

Configuring the isodose display on page 203

Adding more shots

When you have set the first shot, the list of shots in the Shot dialog automatically shows shot number 2 ready for placement. All shot defaults now apply also to the second shot.

1 Add the second shot similarly to the first one. You can place this shot on the same image slice as the first shot, or on a different image within the target.

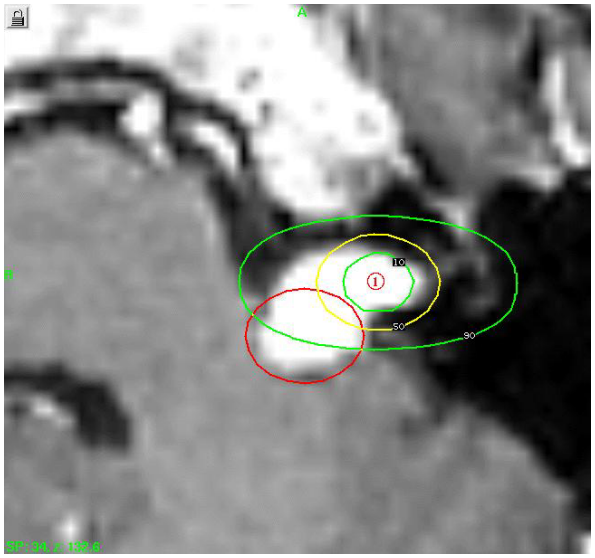


Figure 5.108 Placing the second shot

2 When you are satisfied with the position of the second shot, click **Set**.

The treatment planning application now displays the new dose distribution based on the contributions from both shots.

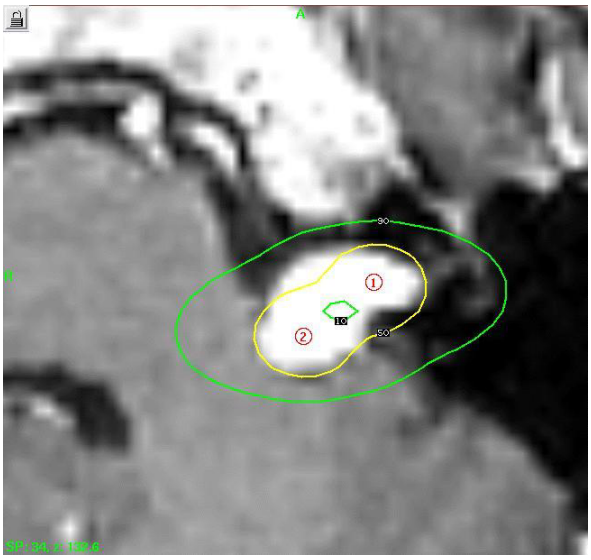


Figure 5.109 Dose distribution based on two shots

3 Add subsequent shots in the same way. You can place these shots on any image slice within the target.

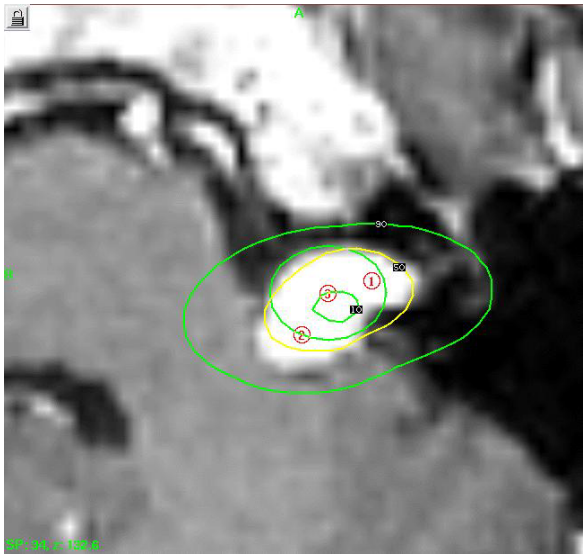


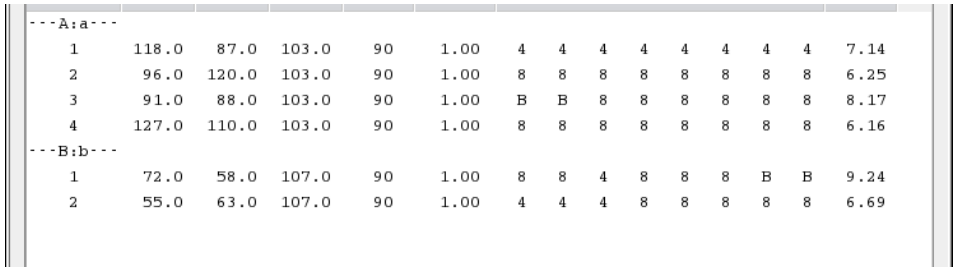
Figure 5.110 Adding more shots

Checking the shot data

You can rapidly examine the data for each shot that you have placed.

1 From the **Plan** menu, select **Shot Summary**.

The Shot Summary dialog opens.



---A:a---													
1	118.0	87.0	103.0	90	1.00	4	4	4	4	4	4	4	7.14
2	96.0	120.0	103.0	90	1.00	8	8	8	8	8	8	8	6.25
3	91.0	88.0	103.0	90	1.00	B	B	8	8	8	8	8	8.17
4	127.0	110.0	103.0	90	1.00	8	8	8	8	8	8	8	6.16
---B:b---													
1	72.0	58.0	107.0	90	1.00	8	8	4	8	8	8	B	B	9.24
2	55.0	63.0	107.0	90	1.00	4	4	4	8	8	8	8	8	6.69

Figure 5.111 The Shot Summary dialog

In the Shot Summary dialog, the shots are listed in the same order as those in the Shot dialog.

Note: *You can refer to the Shot Summary dialog at any time during treatment planning. Some users may prefer to open the dialog when starting shot placement and keep it open throughout. Others may prefer to open and close the dialog as needed.*

5.11.8.2 Adjustment of shots in images

When you have added a sufficient number of shots to the patient's treatment plan you should examine the dose distribution and adjust the parameters of the individual shots to ensure that the isodose contours fit the profile of the target as closely as possible.

Adjusting the position of a shot

With the Shot dialog open and the appropriate target selected:

1 In the list of shots, click on the number of the shot that is to be adjusted.

The shape representing the selected isodose level contour of the selected shot is plotted in red on the images within range of the contour.

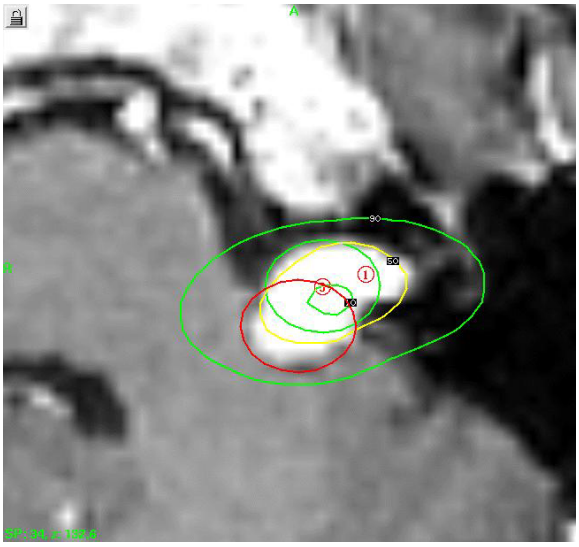


Figure 5.112 Selected shot plotted in red

2 Click on the red shape in the image slice that best displays the shot and drag the shot to the new position.

Alternatively, you can fine-tune the position of the shot by adjusting one or more of its coordinates directly in the **X**, **Y**, and **Z** fields in the Shot dialog. This can be done with the **Up** and **Down** arrows on the keyboard or with the mouse scroll wheel. You can also enter the numbers directly by using the keyboard numeric pad.

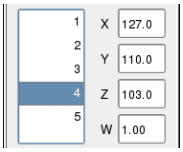


Figure 5.113 The Shot dialog

3 Apply the changes by clicking **Set**. If you select another shot number, without clicking **Set**, the changes will not be saved.

Adjusting the gamma angle of a shot

Prerequisites

This section is only valid for Leksell® Coordinate Frame G and Leksell® Vantage™ Head Frame.

By adjusting the gamma angle of an individual shot you can change the dose distribution in the image planes. With the appropriate target and shot number selected in the Shots dialog:

1 Set the gamma angle.

– For Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™, click in the gamma angle field, marked **G**, and select one of the three gamma angles available. See figure below.

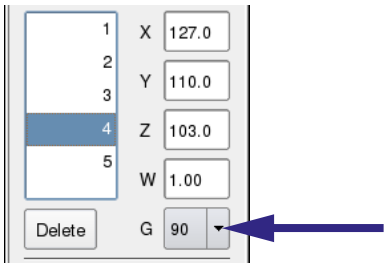


Figure 5.114 Gamma angle field, Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™

– For Leksell Gamma Knife® models C, 4, 4C and B, click in the gamma angle field, marked **G**, to define the angle. Use the up and down arrows or the scroll wheel to adjust the angle to the next available APS angle. Use the keyboard to enter arbitrary angle for trunnions. See figure below. This is only valid for Leksell® Coordinate Frame G.

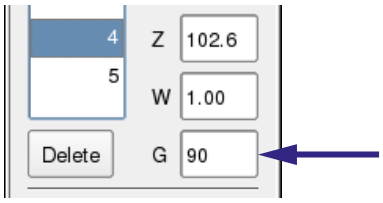


Figure 5.115 Gamma angle field, Leksell Gamma Knife® models C, 4, 4C and B

2 View the revised isodose curves and, if necessary, adjust the other parameters of the selected shot.

3 Click **Set** to apply the changes. If you select another shot number, without clicking **Set**, the changes will not be saved.

Note: *Shots with the same gamma angle will be grouped as one run. Using more than one gamma angle will thus result in several runs.*

Adjusting the weight of a shot

By adjusting the weight of an individual shot you effectively change the duration of the shot. With the appropriate target and shot number selected:

1 Position the cursor over the weight field in the Shot dialog, marked **W**, or simply click in the weight field. Example:

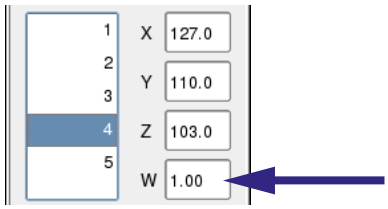


*Figure 5.116 The **Weight** field*

2 Adjust the weight using the mouse scroll wheel or use the up and down arrows if the cursor is positioned in the weight field. Holding down the <Ctrl> key slows down the change.

3 View the revised isodose curves and, if necessary, adjust the other parameters of the selected shot.

4 Apply the changes by clicking **Set**. If you select another shot number, without clicking **Set**, the changes will not be saved.

Changing the collimator setup for a uniform shot

Prerequisites

This section is valid only for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™.

Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ uses eight sectors individually controlled to form a shot. The sectors can all be set to have the same collimator size, resulting in a uniform shot. To change the size of a shot:

1 Select the shot in the list of shots (or place a new shot by having the bottom, non-placed shot in the list of shots selected).

2 Select the desired shot size by clicking on the collimator size buttons in the Shot dialog.

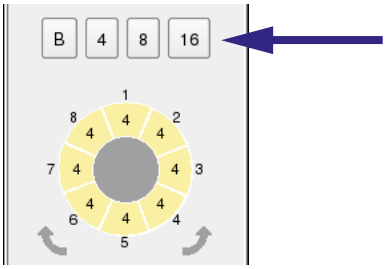


Figure 5.117 Collimator size buttons

The circular collimator graph changes to a uniform shot with the selected collimator size for all sectors. The red isodose preview shape in the image changes to the corresponding size.

3 Click **Set** to apply the collimator size to the selected shot. This change can also be applied to a multiple selection of shots.

Changing the collimator setup for a composite shot

Prerequisites

This section is valid only for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™.

As sectors are individually controlled, a shot can also have different collimator sizes for the different sectors. This results in a non-uniform or composite shot. A composite shot can be shaped either manually or automatically. To manually place a composite shot, or to manually change a uniform shot to a composite shot:

1 Select the shot in the list of shots (or place a new shot by having the bottom, non-placed shot in the list of shots selected).

2 Change the collimator setup for an individual collimator by:

   a Placing the cursor over a collimator in the collimator graph and use the scroll wheel to increase or decrease the collimator size. Choosing a **B** means that this collimator will be blocked and thus will not contribute to the dose distribution. Note how the red isodose preview in the image changes shape.

   b Right-click on any of the collimator size buttons. Note how the cursor changes to a pen with a collimator size indicator. Use the pen and the right mouse button to paint the collimator graph with the selected size. Note how the red isodose preview in the image changes shape. Turn off the pen by left-clicking anywhere in the collimator graph area of the Shot dialog.

Related Links:

Protection of critical structures using Dynamic Shaping on page 226

Changing the collimator size for a shot

Prerequisites

This section is valid only for Leksell Gamma Knife® models C, 4, 4C and B.

You can increase or decrease the area of an individual shot by selecting a different collimator helmet to be fitted to the patient when the shot is delivered. With the appropriate target and shot number selected:

1 Click on the **Helmet** drop-down menu and select a different collimator size.

2 View the revised isodose curves and, if necessary, adjust the other parameters of the selected shot.

Changing the plug pattern for a shot

Prerequisites

This section is valid only for Leksell Gamma Knife® models C, 4, 4C and B.

If collimator plug patterns have already been devised you can modify the influence of an individual shot by selecting a different plug pattern for the helmet. With the appropriate target and shot number selected:

1 Click on the **Plug** drop-down menu and select a different plug pattern.
2 View the revised isodose curves and, if necessary, adjust the other parameters of the selected shot.

Changing the patient's position for a shot

Prerequisites

This section is valid only for Leksell Gamma Knife® models C, 4, 4C and B.

You may be able to optimize the effect of an individual shot by selecting an alternative position for the patient to assume when the shot is delivered. With the appropriate target and shot number selected:

1 Click on the **Position** drop-down menu and choose a different position for the patient (**Supine**, **Prone**).
2 View the revised isodose curves and, if necessary, adjust the other parameters of the selected shot.

Applying changes to a shot

1 When you are satisfied with all parameters of a shot, click **Set**. If you select another shot number, without clicking **Set**, the changes will not be saved.

The Use TMR 10 check box

Figure 5.118 ***Use TMR 10*** *check box*

If the **Use TMR 10** check box in the Shot dialog box is selected, the dose algorithm for the plan is temporarily changed to TMR 10, while working in the Shot dialog box. The check box is available in plans with the Convolution dose algorithm (optional software) to enable the operation of Inverse Planning (optional software) and Real time update (optional software). When you close the Shot dialog box, the dose algorithm for the plan goes back to Convolution.

The Real time update check box

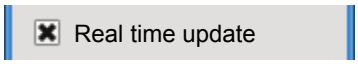


Figure 5.119 ***Real time update*** *check box*

If the **Real time update** (optional software) check box in the Shot dialog is selected, the isodoses in the images will be updated in real time as the shot is modified. If the check box is not selected, the isodoses will update when the mouse button is released or when clicking **Set**.

The Outline all shots check box

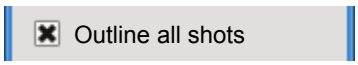


Figure 5.120 ***Outline all shots*** *check box*

If the **Outline all shots** (optional software) check box in the Shot dialog is selected, outlines for all shots will be shown in the images in red for the selected shot and in blue for all other shots. The outline of a shot represents the default isodose level contributed by the shot alone. The displayed isodose level represents the value previously chosen in the **Selected Level** field of the User Preferences dialog.

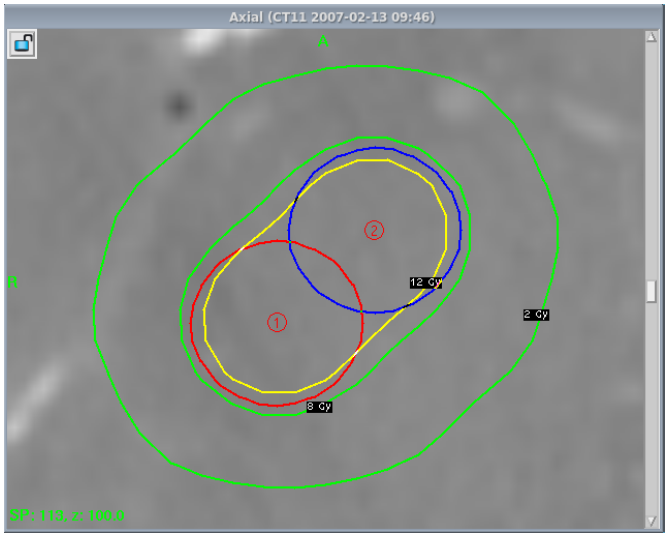


Figure 5.121 Outline all shots

The values of automatic optimization terms

In the lower part of the Shot dialog box the current values for the terms used in the automatic optimization of shots are shown (if applicable).

Related Links:

Definition of the objective function and terms used in optimization on page 225

5.11.8.3 Shot manipulation techniques

When placing and adjusting shots there are several useful techniques that can be employed to enhance the shot manipulation procedures.

Selecting several shots

You can select several shots in the Shots dialog and apply a change to all selected shots at once.

1. Do a multiple selection of shots by clicking and dragging with the mouse in the list of shots or select all shots within the current target by pressing <Ctrl>+<A>.
2. Select a group of shots by using the <Ctrl> key and click on the shots to be selected, or by using <Ctrl>+<Shift> and clicking on the shots to be selected.

Using the mouse scroll wheel

The mouse scroll wheel can be used for several tasks in the Shot dialog.

1. Position the mouse cursor over the **X**, **Y** or **Z** fields and use the wheel to increase or decrease the respective Leksell® coordinate. Holding down the <Ctrl> key on the keyboard accelerates the change.
2. You can also change the collimator size for a sector by positioning the cursor over a sector and scrolling the mouse scroll wheel up and down.

Undoing the latest changes to a shot

You can remove the effect of the latest changes to a shot immediately.

1 With the Shot dialog open and the appropriate target selected, click **Undo**. The status of the selected shot or shots will be restored to that which prevailed before the **Set** button was last clicked. You can now re-adjust the shot parameters as required and then click **Set** again.

Moving a shot to another image slice

If a shot has been placed in one image slice and you want to rapidly move it to another slice:

1 In the list of shots, click on the number of the shot to be moved.

2 Double-click on the image slice to which the shot is to be moved.

The center of the shot is transferred from the first image and placed at the point where you clicked in the second image.

If the first image is within the range of the reference isodose (the red shape) then the contour of the shot will be plotted in both images.

If the first image is not within the range of the reference isodose then the contour will be deleted from the first image and plotted in the second image.

Adjusting multiple shots for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™

1 Select several shots in the Shot dialog.

- The **X**, **Y**, and **Z** fields in the Shot dialog are cleared. When you adjust the multiple shots, these fields contain the distance of movement of the shot centers. They do not show the coordinates of the individual shots.
- The weight field contains the factor by which the weight factor of all shots is adjusted. It does not show the weight factor of the individual shots.
- Blank fields indicate that no change should be applied when pressing **Set**.
- The circular collimator graph indicates sectors that have the same setting for all shots by its size and color. Sectors that do not have the same setting for all shots are shown in white color with no size indication.

2 Re-position all the selected shots by adjusting the values in the **X**, **Y**, and **Z** fields by using the keyboard arrows or the mouse scroll wheel.

- As you adjust the shot positions, the center of each shot moves in the direction and by the distance that you enter into the coordinate fields.

3 Adjust the weight factor for all shots by using the keyboard arrows or the mouse scroll wheel.

4 Change the gamma angle for all shots by using the keyboard arrows or the mouse scroll wheel. This step is applicable for Leksell® Coordinate Frame G and Leksell® Vantage™ Head Frame only.

5 Change collimator setup for all shots by using the collimator buttons or the mouse scroll wheel.

- Sectors shown in white will not be changed.

6 Click **Set** to apply the change to all shots.

Adjusting multiple shots for Leksell Gamma Knife® models C, 4, 4C and B

1 Select several shots in the Shot dialog.

- The **X**, **Y**, and **Z** fields in the Shot dialog are cleared. When you adjust the multiple shots, these fields contain the distance of movement of the shot centers. They do not show the coordinates of the individual shots.
- The weight field contains the factor by which the weight factor of all shots is adjusted. It does not show the weight factor of the individual shots.
- Blank fields indicate that no change should be applied when pressing **Set**.
- The drop down menus for **Helmet**, **Plug** and **Position**, indicates equal settings amongst the selected shots by showing this value. Parameters that do not have the same setting for all shots are indicated using a blank selection.

2 Re-position all the selected shots by adjusting the values in the **X**, **Y**, and **Z** fields by using the keyboard arrows or the mouse scroll wheel.

- As you adjust the shot positions, the center of each shot moves in the direction and by the distance that you enter into the coordinate fields.

3 Adjust the weight factor for all shots by using the keyboard arrows or the mouse scroll wheel.

4 Change the gamma angle for all shots by using the keyboard arrows or the mouse scroll wheel.

5 Change the collimator size for all shots by selecting the size in the **Helmet** drop-down menu.

6 Change the plug pattern for all shots by selecting the plug pattern from the **Plug** drop-down menu.

7 Change the patient position for all shots by selecting the position from the **Position** drop down menu.

Deleting shots

You can delete one or more shots from the patient's treatment plan.

1 In the Shot dialog, select the shot in the shot list and click **Delete** or press <Delete> on the keyboard.

The selected shot is deleted from the patient’s treatment plan. The shot data are removed from the Shot Summary dialog and all graphics pertaining to the shot are cleared from the patient's images.

Selecting shots on the fly

1 Select a shot by holding down <Ctrl> and move the mouse marker over the shot position while pressing the right mouse button. Release the mouse button and the shot is selected.

5.11.8.4 Automatically creating an irradiation scheme using Dose Optimization

Note: *This section, including subsections is only valid for the Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™.*

The optional function, Dose Optimization, is an inverse planning tool for automatically creating an irradiation scheme for one or more targets through optimization. The optimization is controlled by specification of dose constraints for targets and risk zones, together with priorities for minimizing the overall low dose and beam-on-time.

Optimization times are typically less than a minute thanks to a fast and robust optimization method using linear programming and a convex formulation of the optimization problem. Refer to appendix *Dose Optimization Algorithm* for a detailed description of the method. It is therefore possible to create alternative plans with different priorities and objectives to find the most clinically appropriate plan.

The Dose Optimization function can be used in combination with, and as a complement to, the other available dose planning tools in Leksell GammaPlan®.

Related Links:

Creation of the irradiation scheme on page 205

Prerequisites for automatically creating an irradiation scheme using Dose Optimization

- Applicable volumes of type **Target** and **Risk** are outlined
- A plan with targets enclosing volumes of type **Target** is created

Automatically creating an irradiation scheme using Dose Optimization

1 On the menu bar, click **Plan** > **Dose Optimization**.

You can also click the **Dose Optimization** button on the toolbar.

The Dose Optimization dialog box is displayed.

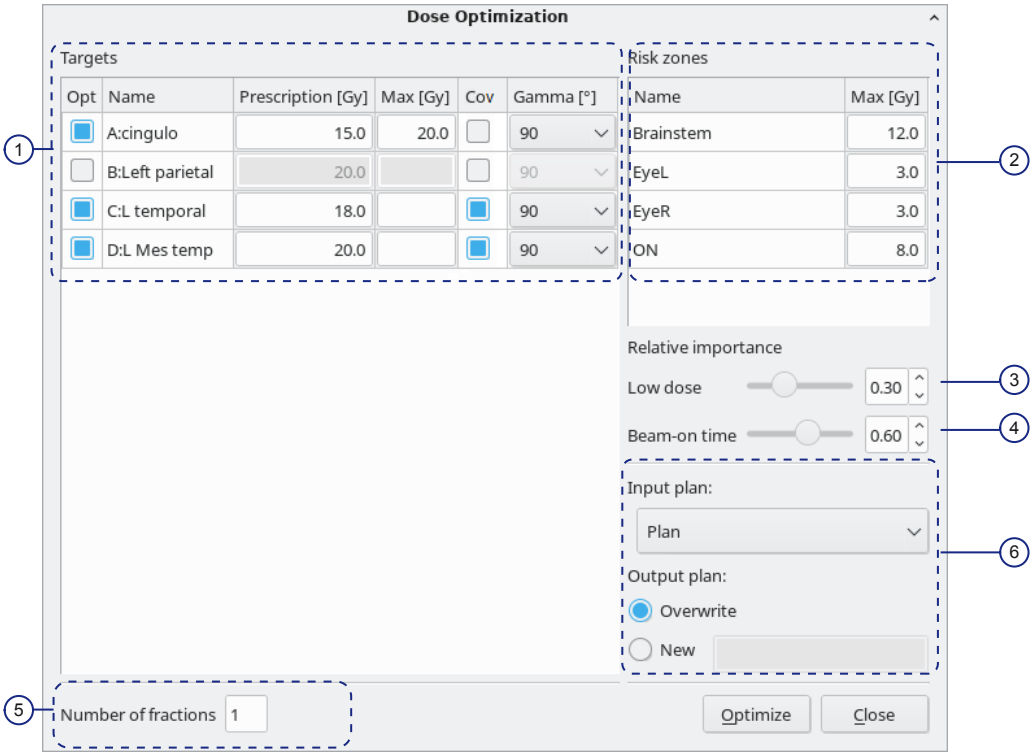


Figure 5.122 Dose Optimization dialog box showing functional areas

(1)	The **Targets** area lists all targets enclosing volumes of type **Target** and is used to control the dose to these in the optimization	(2)	The **Risk zones** area lists all volumes of type **Risk** and is used to control the dose to these in the optimization
(3)	The **Low dose** slider is used to set the relative importance of minimizing the overall low dose volume to surrounding tissue outside targets in the optimization	(4)	The **Beam-on-time** slider is used to set the relative importance of minimizing the beam-on time in the optimization
(5)	**Number of fractions** for the optimized plan (only applicable for mask fixation)	(6)	Selection of **Input plan** and **Output plan** for the optimization

Note: *Double-click a target name or a risk organ name to center the workspace views on that object.*

2 Select the **Input plan** to choose the overall plan parameters for the optimization (i.e. targets, dose grid resolution, dose algorithm, and Gamma Knife configuration). If optimization has previously been performed for the selected input plan, the optimization settings are set according to the previous optimization. By default, the current plan is selected as the input plan.

3 In the **Targets** area, use the **Opt** check box to select the targets that should be included in the optimization. All targets that have not had their shots or prescription isodose adjusted outside Dose Optimization are included in the optimization by default. Although all targets are normally included in the optimization, partial optimization makes it possible to combine optimization with other dose planning tools, and to perform optimization with different priorities for different targets. Targets that are not included in the optimization are left unchanged and their dose contribution is not taken into account in the optimization.

Note: *Click the **Opt** column header to quickly toggle selection of all targets for optimization.*

4 Set the **Prescription [Gy]** dose for each target. The optimization aims to cover 95% (or more) of each target with the prescription dose and at the same time keep the dose outside the targets to a minimum.

Note: *If needed, it is possible to fine-tune coverage and selectivity for a target by manually adjusting the isodose prescription level after optimization.*

5 If needed, set **Max [Gy]** dose for targets to optionally limit the maximum dose and thereby achieve a more homogenuous dose within targets.

Note: *A more homogeneous dose to the target typically increases the overall dose outside the target. Due to the heterogenuous nature of Gamma Knife dosimetry it is not feasible to achieve fully homogenuous doses with maintained target coverage. The lowest allowed Max dose is therefore limited to 4/3 of the Prescription dose for the target.*

6 If needed, use the **Cov** check box to optionally increase the target coverage to 99% (or more) in the optimization, at the price of more dose outside the target.

Note: *A small portion of risk zones may receive a dose exceeding the specified max dose when target coverage is prioritized in the optimization.*

7 When optimizing a plan for frame based fixation, **Gamma [°]** angle can be selected per target.

8 When optimizing a plan for mask fixation, set the **Number of fractions** for the plan.

9 In the **Risk zones** area, set the **Max [Gy]** dose for risk zones to optionally limit the maximum dose to the risk zone.

Note: *A small portion of risk zones may receive a dose exceeding the specified max dose due to limited sampling resolution in the optimization.*

10 Use the **Low dose** slider to set the relative importance of minimizing the overall low dose volume to surrounding tissue outside targets in the optimization. The slider can be adjusted from 0.0 (not important) to 1.0 (very important).

Note: *A reduction of overall low dose to surrounding tissue typically results in longer beam-on-time.*

11 Use the **Beam-on-time** slider to set the relative importance of minimizing the beam-on-time in the optimization. The slider can be adjusted from 0.0 (long time) to 1.0 (short time).

Note: *A reduction of beam-on-time typically result in an increase of the overall dose outside targets.*

12 Specify **Output plan** to choose the destination for the optimization result:

- Select **Overwrite** to save the optimization result in the selected Input plan. This is the default selection.
- Select **New** to save the optimization result in a new plan. This allows for easily creating alternative plans with different optimization objectives or priorities. The default name of the new plan is the name of the input plan with a suffix.

13 Click **Optimize** to start the automatic dose optimization.

A progress bar is displayed during the optimization. When the optimization is done, the **Dose Evaluation** dialog opens and display the resulting plan for evaluation.

Note: *Click the **Dose Optimization** and **Dose Evaluation** buttons on the toolbar to quickly switch between the two functions.*

Note: *Plans created with the Dose Optimization function need to be evaluated by the user in the same way as manually created plan.*

5.11.8.5 Automatically creating an irradiation scheme using Inverse Planning

An automatic irradiation scheme may be produced using the Leksell GammaPlan® Inverse Planning (optional software). With the patient's file and radiological examination open, and the lesions outlined as volumes of type Target do:

1 From the **Plan** menu select **Shot**, or in the Toolbar click on the Shot button.

The Shot dialog opens.

2 To select the target in which the shots should be placed, click on the target drop-down menu and choose a target.

3 Click **Fill** to automatically position shots in the lesion according to the prescription isodose level for the selected target.

Note: *Skip this step if there is already a sufficient number of shots in the target.*

4 Click **Optimize** to automatically optimize the shots according to the current objective function. During optimization the Optimization progress dialog displays the current objective function value (1), number of iterations (2), and the estimated values for the individual metrics included in the objective function (3). The isodose curves in the views are updated regularly during optimization.

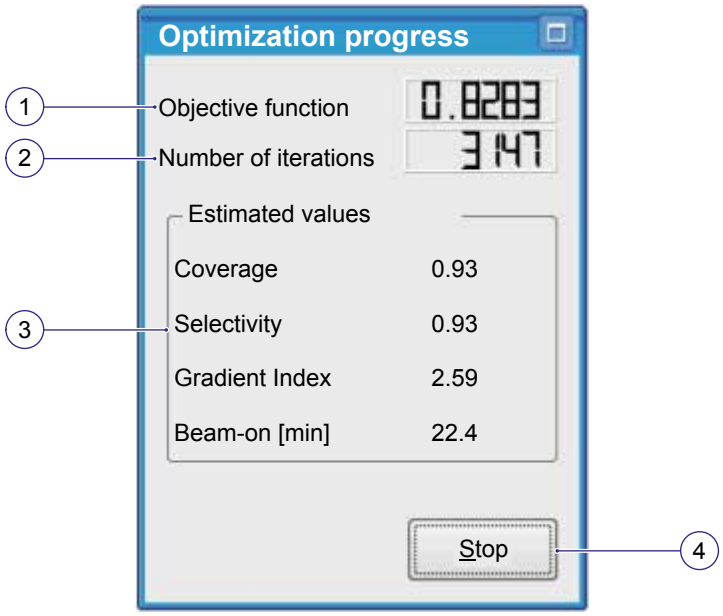


Figure 5.123 Optimization progress

Note: *When the optimization is in progress the Shot dialog is disabled.*

5 The optimization continues until the **Stop** button (4) is clicked.

The isodose curves in the views and the metrics in the Shot dialog are updated.

Note: *Plans created using Inverse Planning needs to be evaluated by the user in the same manner as manually created plans.*

Note: *The automatic optimization of shots is well suited for a highly interactive workflow where it is combined with manual placement and adjustment of shots.*

Note: *The isodose curves shown during optimization are based on the simplified dose calculation model. When optimization is stopped, the isodose curves are updated. This can cause a small shift in the curves.*

Related Links:

Creation of the irradiation scheme on page 205

Controlling the automatic optimization of shots on page 223

Definition of the objective function and terms used in optimization on page 225

Controlling the automatic positioning of shots for Leksell Gamma Knife® models C, 4, 4C and B on page 222

Controlling the automatic positioning of shots for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ on page 220

Controlling the automatic positioning of shots for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™

The manner in which shots are automatically placed when pressing **Fill** is dependant upon the targets volume, the prescribed isodose, and existing shots in the target. In addition, there are some ways of controlling the process itself.

With the Shot dialog open, perform the following steps:

1 Click **IP settings**, and select the **Fill** tab (1) to review the settings for automatic shot placement.

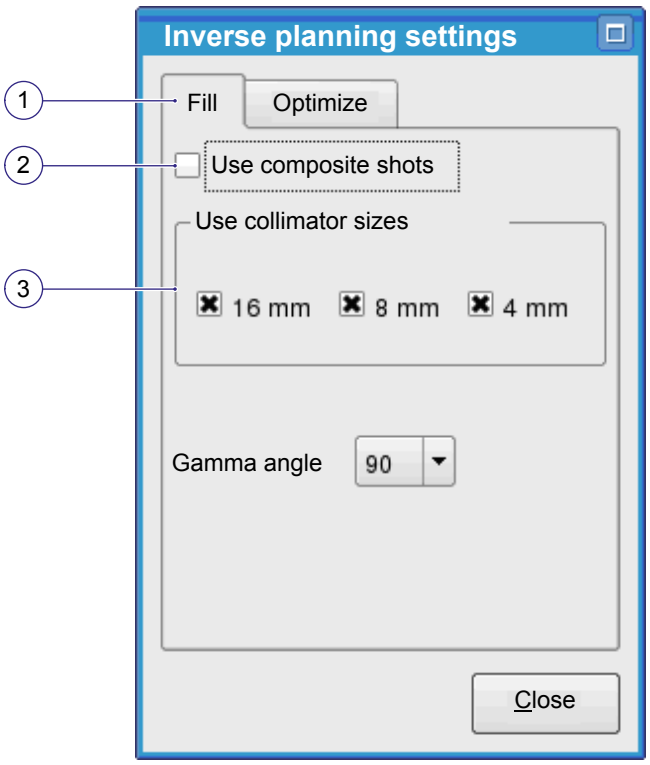


Figure 5.124 Inverse planning settings

2 Use the check box **Use composite shots** (2) to select whether the automatic shot placement should use composite shots or not.

3 If composite shots are not used for automatic shot placement the check boxes for 16, 8 and 4 mm collimator sizes in the **Use collimator sizes** frame (3) can be used to select the allowed collimator sizes.

4 If composite shots are used for automatic shot placement the slider **Collimator sizes** (4) can be used for prioritizing between large (5) and small (6) collimator sizes.

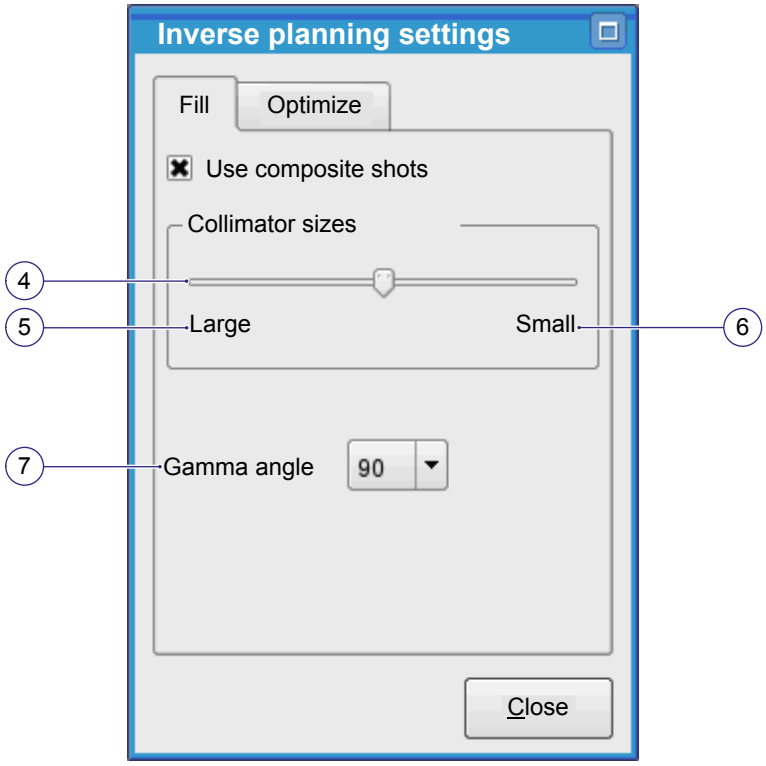


Figure 5.125 Inverse planning settings - Use composite shots

5 Use the **Gamma angle** selection (7) to choose the gamma angle of automatically placed shots.

Controlling the automatic positioning of shots for Leksell Gamma Knife® models C, 4, 4C and B

The manner in which shots are automatically placed is dependant upon the targets volume, the prescribed isodose, and existing shots in the target. In addition to this there are some ways of controlling the process itself. With the Shot dialog open do as follows:

1 Click on the **IP settings** button, and select the **Fill** tab (1) to review the settings for automatic shot placement.

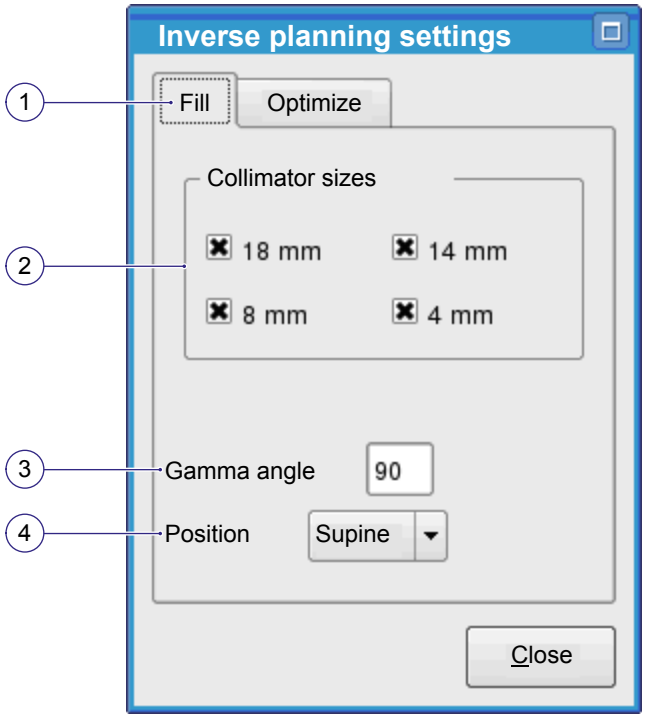


Figure 5.126 Inverse planning settings for automatic shot placement

2 Use the check boxes for 18, 14, 8 and 4 mm collimator sizes in the **Collimator sizes** frame (2) to select the allowed collimator sizes.

3 Use the **Gamma angle** selection (3) to choose the gamma angle of automatically placed shots.

4 Use the **Position** selection (4) to choose if automatically placed shots should be **Prone** or **Supine**.

Controlling the automatic optimization of shots

The automatic optimization of shots performed by pressing the **Optimize** button optimizes the position, weight, and collimator configuration of all the shots in the target according to an objective function that allows for prioritizing between coverage and selectivity, as well as penalizing poor gradient index and long beam-on times.

With the Shot dialog open, perform the following steps:

1 Click **IP settings** and select the **Optimize** tab (1) to review the optimization settings.

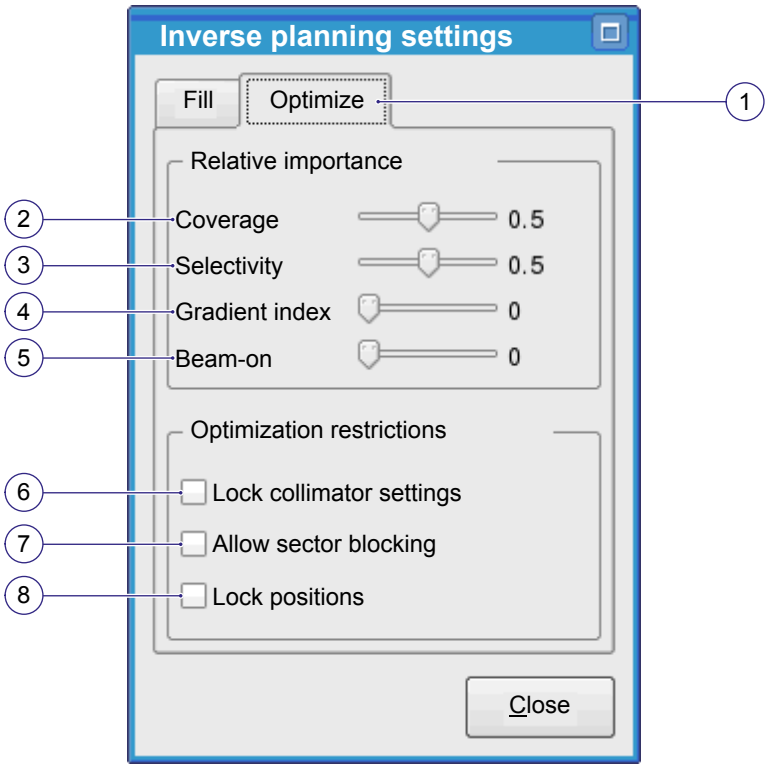


Figure 5.127 Inverse planning settings - Optimize

2 Adjust the optimization settings as follows:

a Use the **Coverage** (2) and **Selectivity** (3) sliders to adjust their relative importance in the optimization. By default, coverage and selectivity are assigned equal weight.

b Use the **Gradient index** slider (4) to adjust the relative importance of a low gradient index (indicating a steep dose fall-off). If the slider is at 0.0, gradient index is not considered in the optimization.

c Use the **Beam-on** slider (5) to adjust the relative importance of short beam-on time. If the slider is at 0.0, beam-on time is not considered in the optimization.

d Check the **Lock collimator settings** check box (6) to prevent the optimizer from changing the collimator setup for any shots during optimization. By default, the optimizer is allowed to change collimator settings for shots.

e Check the **Allow sector blocking** check box (7) to allow the optimizer to block individual sectors of a shot during optimization. By default, the optimizer is not allowed to block sectors. This check box is available only for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™.

f Check the **Lock positions** check box (8) to prevent the optimizer from changing the positions of shots during optimization. By default, the optimizer is allowed to change the position of shots.

Note: *The automatic optimization of shots does not change the number of shots in the target, but shots that do not contribute to the optimization may get a weight close to 0.*

Note: *Although it is possible to optimize shots for a high prescription isodose, in order to achieve a more homogenous dose, the result will typically come at the prize of poorer conformity and gradient index.*

Related Links:

Definition of the objective function and terms used in optimization on page 225

Definition of the objective function and terms used in optimization

The automatic optimization of shots is achieved by maximizing the value of an objective function that include the following terms:

- Coverage is defined as the proportion of the target volume (TV) that is covered by the prescription isodose volume (PIV), that is, Volume(PIV∩TV) / Volume(TV).
- Selectivity is defined as the proportion of the prescription isodose volume (PIV) that is inside the target volume (TV), that is, Volume(PIV∩TV) / Volume(PIV).

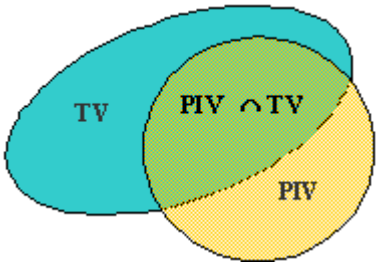


Figure 5.128 Target volume and prescription isodose volume

- Gradient Index is defined as the quotient between the half-prescription isodose volume size and the prescription isodose volume size, that is, Volume($PIV_{25\%}$) / Volume($PIV_{50\%}$) if the planning isodose is 50%. Gradient index is commonly used to quantify the steepness of the dose fall-off.
- Beam-on time is defined as the sum of the shot times for all shots in the target.

The objective function is defined as:

$$\frac{Coverage^{c} \cdot Selectivity^{1-c} + a \cdot Grad + b \cdot Time}{1 + a + b}$$

The user defined weights a, b, and c in the objective function allow for weighing the relative importance of coverage, selectivity, gradient index, and beam-on time in the optimization. Note that with a setting of a = b = 0 and c = 0.5 the objective functions equal a well established index used to quantify conformity.

The term Grad in the objective function is defined as:

$$Grad = \frac{GI_{max} - GI}{GI_{max} - GI_{min}}$$

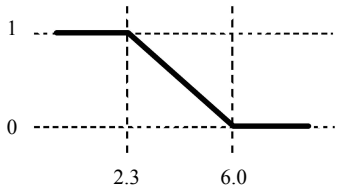


Figure 5.129 Grad graph

GI_{max} = 6

GI_{min} = 2.3

Grad(< 2.3) = 1

Grad(> 6) = 0

The term Time in the objective function is defined as:

Time = kT + m

Time(T_{ref} /4) = 1

Time($3T_{ref}$/2) = 0

where T_{ref} is the beam-on time for the shots before optimization.

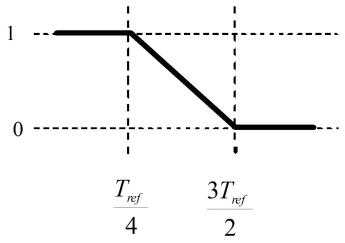


Figure 5.130 Time graph

5.11.8.6 Protection of critical structures using Dynamic Shaping

Note: *This section, including subsections, is valid only for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™.*

Critical anatomical structures in the vicinity of the lesion can be protected by using the Dynamic Shaping function in the treatment planning application.

The sector setup proposed by the Dynamic Shaping function can still be manually modified and can thus serve as a proposal or can be accepted as is.

Related Links:

Creation of the irradiation scheme on page 205

Regions and volumes on page 154

Dynamically shaping an existing group of shots to protect a critical structure

1 Select the shot distribution you want to dynamically shape to minimize the dose given to a critical structure. This is typically all shots within a target close to the critical structure, but you may select some of the shots in the target or only one single shot.

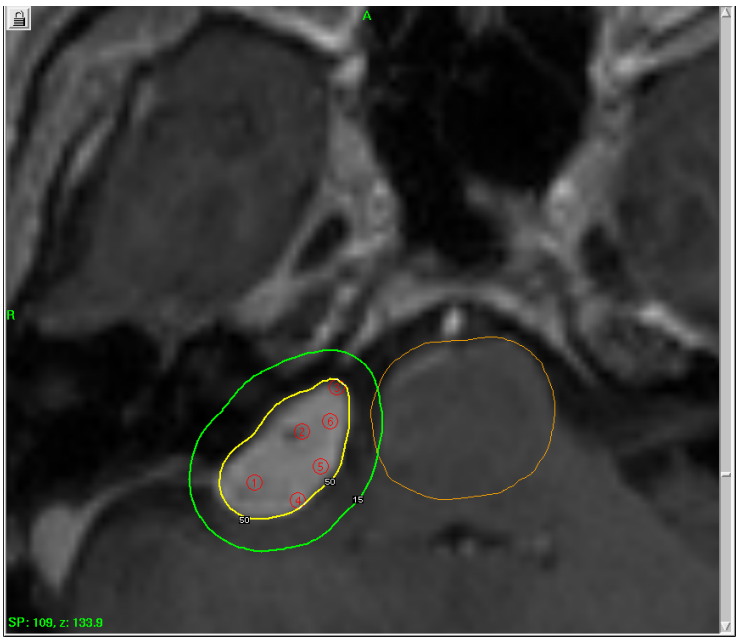


Figure 5.131 Dynamic shaping

Note in the image how the isodoses resulting from the group of shots indicate that the critical structure may receive a too high dose if this treatment plan was to be executed.

2 Set the sensitivity of the Dynamic Shaping function by clicking on the numbered **Dynamic shaping** sensitivity buttons (**1**–**4**) in the Shot dialog.

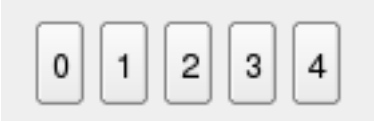


Figure 5.132 Dynamic shaping buttons

The button **0** disables Dynamic Shaping (no sectors blocked due to Dynamic Shaping). Button **1** represents minimum sensitivity (a few sectors may be blocked). Button **4** represents maximum sensitivity (more sectors may be blocked).

3 Clicking on any of the **Dynamic shaping** sensitivity buttons (**1**–**4**) invokes the Dynamic shaping functionality.

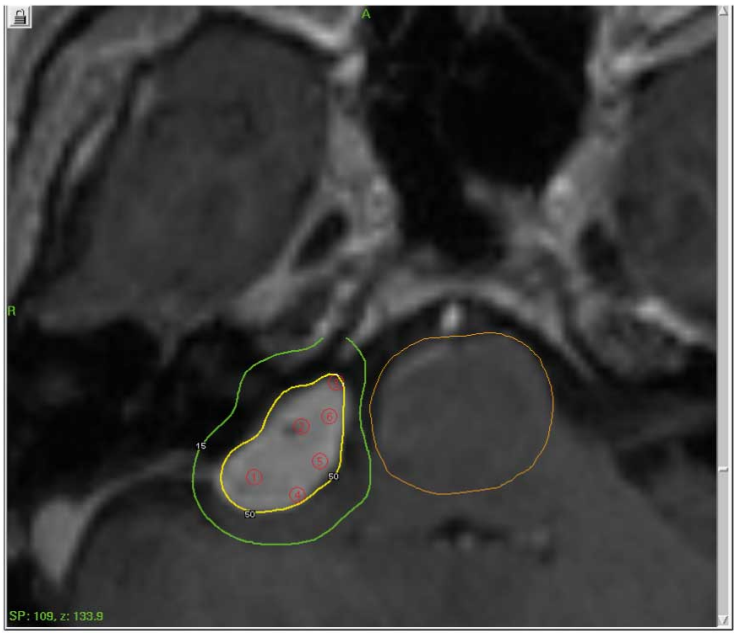


Figure 5.133 Dynamic shaping - blocked sectors

In the image, note how Dynamic Shaping has blocked sectors giving a dose distribution that better follows the critical structure boundary.

4 Any sectors blocked by Dynamic Shaping are indicated in the collimator graph in the Shot dialog with diagonal stripes. This means that the sector is blocked and will not give any contribution to the resulting dose. The original size of the now blocked collimator is visible under the diagonal stripes.

5 All shots can be examined to see which sectors have been blocked by Dynamic Shaping. All, a few or none of the shots may have been affected.

6 If you want to revert to the previous collimator setup, click on the **0** button.

7 The sensitivity of the Dynamic Shaping function can be altered, which will result in a new collimator setup. Note that this may open previously automatically blocked sectors or close more sectors, depending on the change of sensitivity.

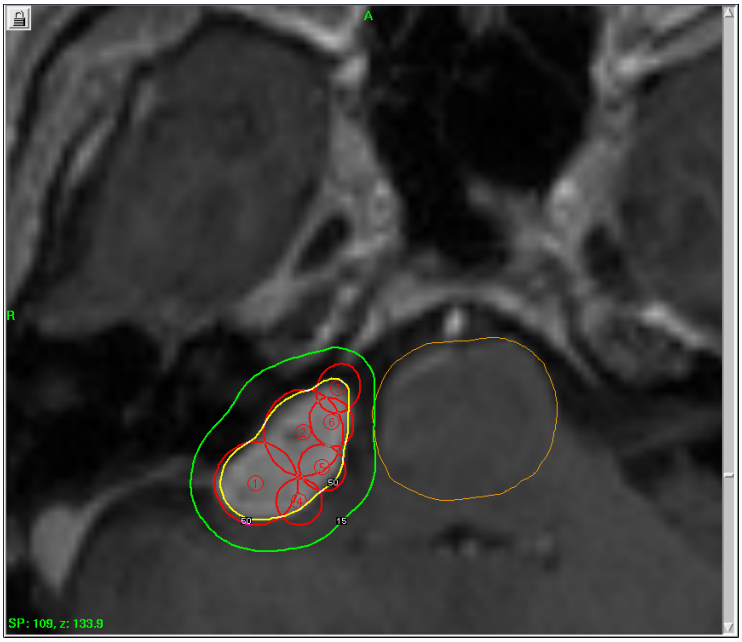


Figure 5.134 Dynamic shaping

Note in the image that when sensitivity is decreased, the isodoses change to intrude more into the critical sector.

Placing dynamically shaped shots

1. First, outline a critical structure, or risk zone, and make sure the volume you outline in the patient images is marked as a risk zone.
2. To place a dynamically shaped shot directly, use any of the **Dynamic shaping** sensitivity buttons (**1**–**4**) instead of set. This means that the Dynamic Shaping function is directly applied to the shot as it is set.
3. Press **Set** to append a new shot to the list of shots.

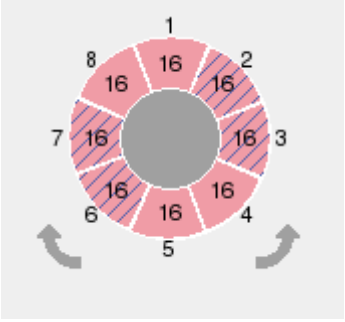
Related Links:

Regions and volumes on page 154

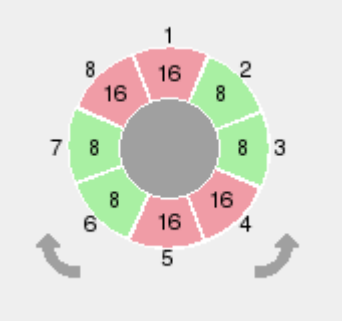
Fine-tuning dynamically shaped shots

You may want to fine-tune a dynamically shaped shot distribution. For instance, a uniform shot with a 16 mm collimator size after Dynamic Shaping may result in a shot with some of the 16 mm sectors automatically blocked. Lower collimator sizes may be allowed to iterate a shot setting to get the maximum allowed collimator sizes.

1. Select the shot you want to modify in the list of shots.
2. Note the sectors that the Dynamic Shaping function has blocked automatically.

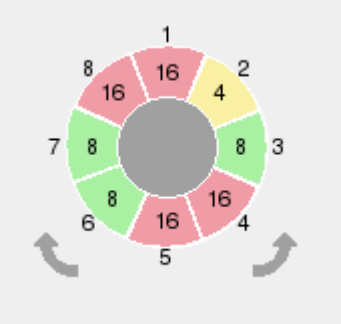


3 Set the blocked sectors to **8 mm** by using the mouse scroll wheel or by right-clicking on the collimator size buttons and “painting” the collimators you want to modify.



4 Click on the same **Dynamic Shaping** button. The Dynamic Shaping function may allow some of the 8 mm sectors in this example and block others, depending on the nature of the risk zone.

5 Try the 4 mm setting for the remaining sectors by following the procedure in step **3** .



6 Click on the same **Dynamic Shaping** button to try the new setting.

This will result in an optimally shaped composite shot. Any sectors still marked as blocked will be blocked throughout the treatment.

Overriding dynamically shaped shots

1 Select the shot you want to modify in the list of shots.
2 Open an automatically blocked sector by selecting the desired collimator size using the mouse scroll wheel or by painting.
3 Click **Set** to apply the setting to the shot.

5.11.8.7 Protection of critical structures using plug patterns

Note: *This section, including subsections, is valid only for Leksell Gamma Knife® models C, 4, 4C and B.*

Critical anatomical structures in the vicinity of the lesion are protected by placing shields over the affected areas on the patient's images. This creates a plug pattern which modifies the irradiation scheme.

The treatment planning application creates plug patterns automatically, based on the shot/shield configuration that you devise. You can also create new patterns manually by using a blank template. Alternatively, you can manually create templates for common patterns, which can be edited on a patient-by-patient basis.

Note: *It may be useful to open the Shot Summary dialog while creating plug patterns. You will be able to see the automatic calculation of shot data as you work.*

The number of plugs that can be used in a plug pattern are controlled by the user-adjustable limit set in the User Preferences dialog. The number of plugs must be within the range of 1 to 167. The default value is 33 plugs.

Creating a plug pattern automatically

To create a plug pattern automatically, do the following steps, described in this manual:

1 Open the plug editor
2 Select the automatic shielding function
3 Position the shields
4 Inspect the plug pattern
5 Superimpose plug patterns
6 If applicable, adjust the positions of the shields
7 If applicable, delete shields.

Opening the plug editor

With the patient's file and radiological examination open:

1 Open an image study in a suitable workspace and select the image which best displays the areas in which shields are to be placed.
2 Adjust the point-of-exploration and use the interactive **Zoom** and **Level** controls to obtain the optimal view of the image areas.
3 From the **Plan** menu choose **Plug**.

The Plug Editor opens.

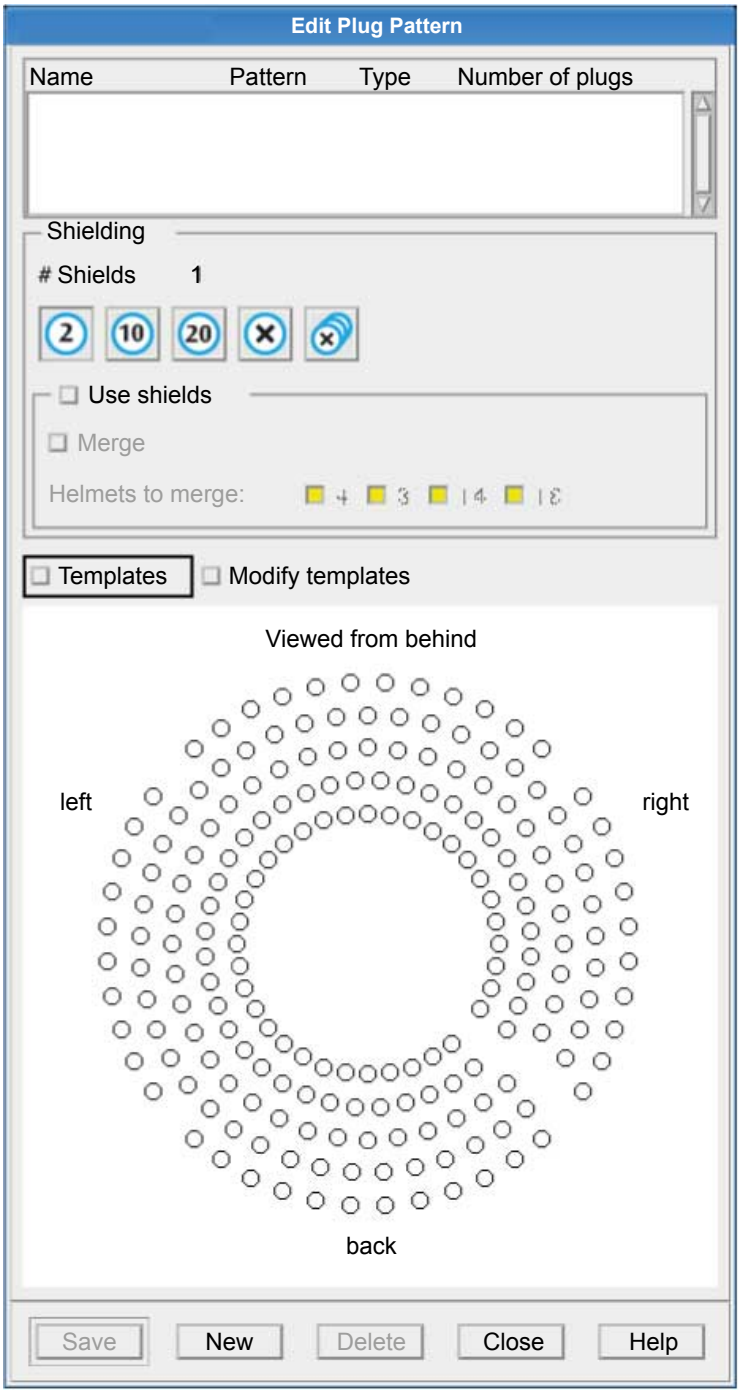


Figure 5.135 The Plug Editor

If any plug patterns already exist for this patient they are shown in the list of plug patterns. Otherwise the list is blank.

Selecting the automatic shielding function

1 Select **Use shields**.

As you position the shields, the program automatically generates a plug pattern for each existing shot and all new shots to be placed.

Positioning the shields

1 Click on the shield button representing the shield size you want to use.

Figure 5.136 A shield button representing the shield size 20 mm

2 Use the left mouse button to place the shield in the image by clicking in the area that you want to protect.

The shield is plotted as a circle on the image.

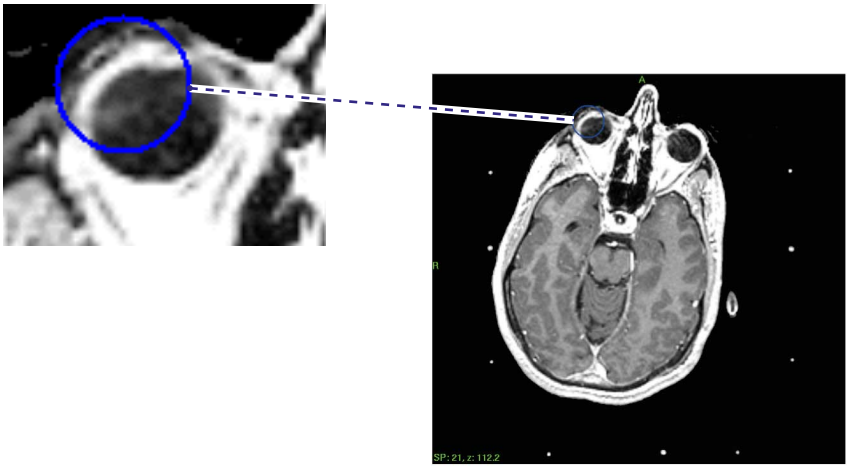


Figure 5.137 The shield is plotted as a circle

The plug pattern resulting from this shield is generated automatically and shown in the list of plug patterns.

Figure 5.138 The plug pattern is shown in the list

3 Repeat steps **1** and **2** and place other shields on the images to create the isodose profile that you require. You can switch between 2 mm, 10 mm and 20 mm shields as necessary.

Inspecting the plug pattern

1 Select an automatic plug pattern by name from the list of plug patterns.

The selected plug pattern is filled in on the plug pattern view.

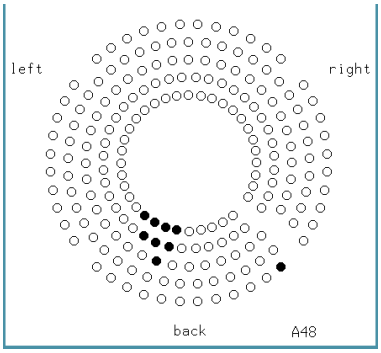


Figure 5.139 The selected plug pattern

2 To inspect any other automatic plug pattern, select it in the list

Superimposing plug patterns

When you are satisfied with the automatically generated plug patterns for each shot, you can superimpose the plug patterns for all shots that have the same collimator size and belong to the same target.

1 Select the **Helmets to merge** check boxes.

This results in a single plug pattern for each helmet used in each target.

2 Click on **Merge**.

The program calculates the merged plug patterns, applies them to the shots and recalculates the treatment plan.

The list pf plug patterns now shows a separate plug pattern for each helmet size. In practice, the 4 mm and 8 mm helmets are plugged less frequently than the 14 mm and 18 mm helmets.

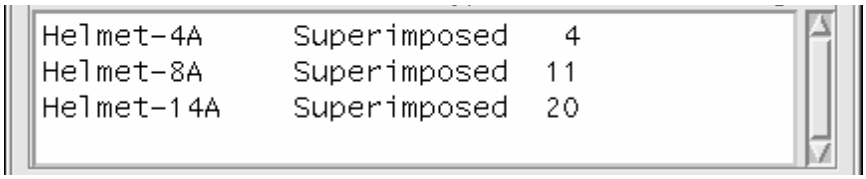


Figure 5.140 The list pf plug patterns

3 You can now select a superimposed plug pattern and view it.

Adjusting shields

1 If necessary, adjust the position of a shield by clicking on its circle and dragging it to a new position on the image with the left or middle mouse button.

Deleting shields

You can delete one or more shields from the treatment plan.

1 Select the shield that you want to delete by moving the mouse pointer over its circle without clicking.

The color of the shield graphic changes to magenta.

2 Click on this icon.

Figure 5.141 Deleting one shield

The shield is cleared from the patient's images. The treatment plan is automatically recalculated.

3 To delete all shields click on this icon.

Figure 5.142 Deleting all shields

Creating a plug pattern manually

Although the automatic shielding facility is the easiest method of creating plug patterns, you can also generate patterns manually. For example this might be done if the lesion is close to the skull boundary and you want to plug certain radiation sources close to the skin.

1 Open the Plug Editor.

2 Click **New**.

The New Pattern dialog opens.

3 Type a suitable name for the new manual plug pattern. Example:

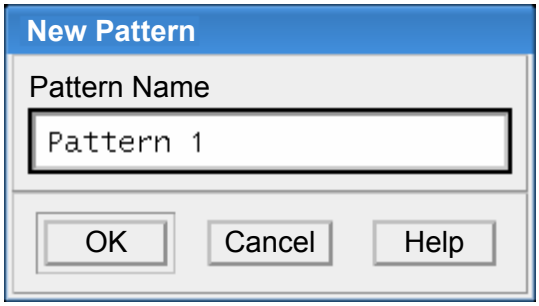


Figure 5.143 Typing a name for the new plug pattern

4 Click **OK**.

The New Pattern dialog closes and the list of plug patterns now includes the new manual plug pattern.

5 To plug collimator channels manually, click in the corresponding circle of the blank plug template.

The circle is filled in black. For example

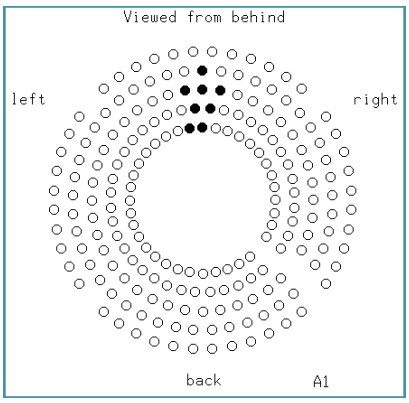


Figure 5.144 Collimator channels plugged manually

6 To plug a number of adjacent channels, click and drag across the area of the channels.

7 If you plug a collimator channel in error, click in the corresponding circle again to unplug the channel.

8 When you have completed the manual plug pattern, click **Save**.

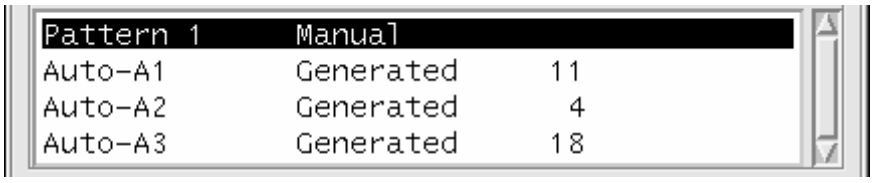


Figure 5.145 The list of plug patterns

9 To apply the manual plug pattern to a shot you must change the plug pattern option for the shot as described in this manual.

Related Links:

Changing the plug pattern for a shot on page 213

Creating a plug template

You can denote a manually-created plug pattern as a template that can be modified and used for other patients who require a similar plug configuration.

1 Open the Plug Editor.
2 Ascertain that the **Modify templates** check box is selected.
3 Prepare to create a manual plug pattern as described in this manual.
4 Now the option **Save as template** will be available. Make sure that this option is selected, see the figure below.

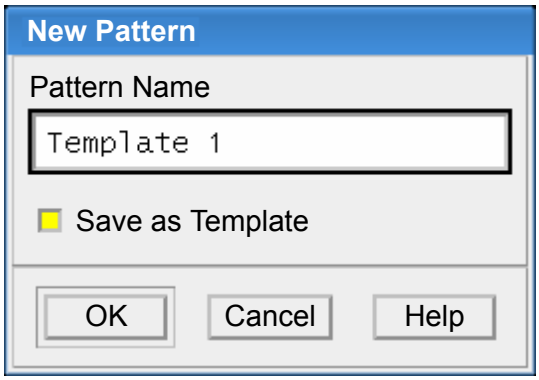


Figure 5.146 Select to save the pattern as a template

5 Name the template, plug the required collimator channels and save the template as described in this manual.

Using a plug template

For safety reasons you cannot directly apply a plug pattern designated as a template to a shot in any treatment plan. Instead you must first check the template and modify it as necessary.

1 Open the Plug Editor.

   A blank plug pattern is displayed in the Plug Editor.
2 Select the **Templates** check box in the dialog.
3 Select the template that you require from the list of plug patterns.

   The selected template is filled in on the blank plug pattern.
4 Examine the template and, if necessary, modify it by selecting the **Modify templates** check box and then plugging different collimator channels as described in this manual.
5 Click **New**.

   The New Pattern dialog opens.
6 Type a suitable name for the plug pattern but do not select the **Save as Template** check box.
7 Click **OK**.

   The New Pattern dialog closes.
8 Click **Save**.

   The list of plug patterns now includes the new manual plug pattern derived from the template.
9 To apply this plug pattern to a shot, you must change the plug pattern option for the shot as described in this manual.

Related Links:

Changing the plug pattern for a shot on page 213

5.11.8.8 Prone shot coordinates

Note: *This section is valid only for Leksell Gamma Knife® models C, 4, 4C and B.*

A single treatment session may include shots that are administered to the patient in the supine position, and other shots delivered in the prone position.

In the prone position the orientation of the patient is effectively reversed. To obtain the correct Leksell Gamma Knife® settings for a prone shot, the treatment planning application must therefore mirror the X coordinate for the treatment protocol from the X coordinate of the shot center on the images.

5.11.9 Clearance

The treatment planning application automatically calculates clearance for each shot as it is set or placed. The clearance status for set shots may change if the stereotactic definition is altered. For Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™, a treatment plan cannot be approved if it contains shot positions that are outside the Leksell Gamma Knife® range (reachability of the patient positioning system), or shot positions with potential collision risk outside the Clearance Check Tool (CCT) range.

If using the frame cap (only applicable for Leksell® Coordinate Frame G combined with Leksell Gamma Knife® Perfexion™ or Leksell Gamma Knife® Icon™), a shot without clearance may be reachable if you enter the detailed measured values of post height and screw protrusion.

5.11.9.1 Checking the clearance of the set shots

1 Open the patient's file and radiological examination.
2 From the **Tools** menu select **Clearance**, or from the Toolbar click the **Clearance** button.

Figure 5.147 The Clearance button

The Clearance dialog opens.
3 Study the information in the Clearance dialog, as described in this manual.
4 Click **Close** to deactivate the dialog.

Related Links:

Description of the Clearance dialog on page 238

Description of the Clearance dialog

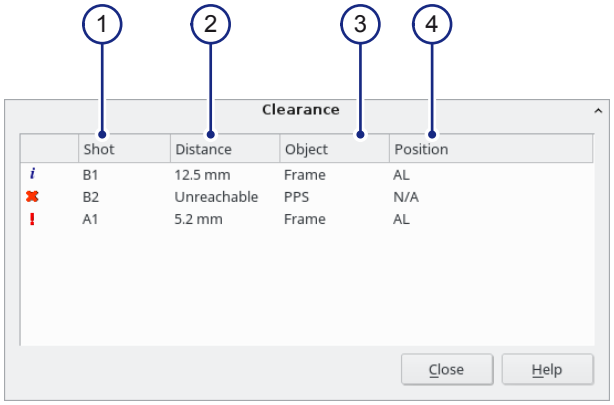


Figure 5.148 The Clearance dialog

(1) **Shot**

(2) **Distance**

(3) **Object**

(4) **Position**

The columns in the **Clearance** dialog shows the folllowing information:

- The signs in the first column indicates:

Sign	Description
(!)	The shot position needs clearance check prior to the treatment
(X)	The shot position is outside of the Leksell Gamma Knife® range, or has a potentional collision risk outside the Clearance Check Tool (CCT) range
(i)	The shot is clear but close (≤ 20 mm)

  If the treatment planning application estimates that a clearance check is necessary, this is indicated on the patient's treatment protocol. The intention with the (i) is to tell the user to inform the patient about treatment positions that have little clearance.

- The **Distance** column shows the smallest estimated distance between the radiation unit and the patient and/or any part of the coordinate frame. Negative values indicate that the program has estimated that the position has no clearance by the specified distance, whereas positive values indicate the estimated margin.

  In case of Leksell Gamma Knife® models C, 4, 4C, or B, the **Distance** column shows the smallest estimated distance between the collimator helmet and the patient, and/or any part of the coordinate frame.

- The **Object** and **Position** columns indicate the object providing the least clearance and its position.

  Definition of the abbreviations in the **Position** column:

  – **A**: Anterior
  – **P**: Posterior
  – **L**: Left
  – **R**: Right

- The content of the list is updated when the patient’s skull measurements are updated, when the coordinate frame configuration is updated, and when shots are defined/re-defined.

Note: *The clearance distances are shown with one decimal. This means that a clearance distance presented as 12.0 mm can be slightly smaller, or slightly larger, than 12.0 mm.*

5.11.9.2 Clearance limits for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ with Leksell® Coordinate Frame G

When using detailed measured values, the treatment planning application enforces two separate limits for clearance check:

- **Clearance from coordinate frame assembly**
  - **5 mm from the coordinate frame, or frame adapter**

    A shot position with clearance less than 5 mm to the frame base, or the frame adapter, will cause the treatment planning application to indicate that this shot position needs clearance check prior to the treatment.
  - **12 mm from the posts or screws**

    A shot position with clearance less than 12 mm to any post, or screw, will cause the treatment planning application to indicate that this shot position needs clearance check prior to the treatment.
- **Clearance from patient's head**
  - **10 mm from patient's head** (skull defined from measurements)

    If the skull was defined using the skull scaling measurements, a shot position with clearance less than 10 mm to the patient's head will cause the treatment planning application to indicate that this shot position needs clearance check prior to the treatment.
  - **5 mm from patient's head** (skull defined from images)

    If the skull was defined by CT, or MR, a shot position with clearance less than 5 mm to the patient's head will cause the treatment planning application to indicate that this shot position needs clearance check prior to the treatment.

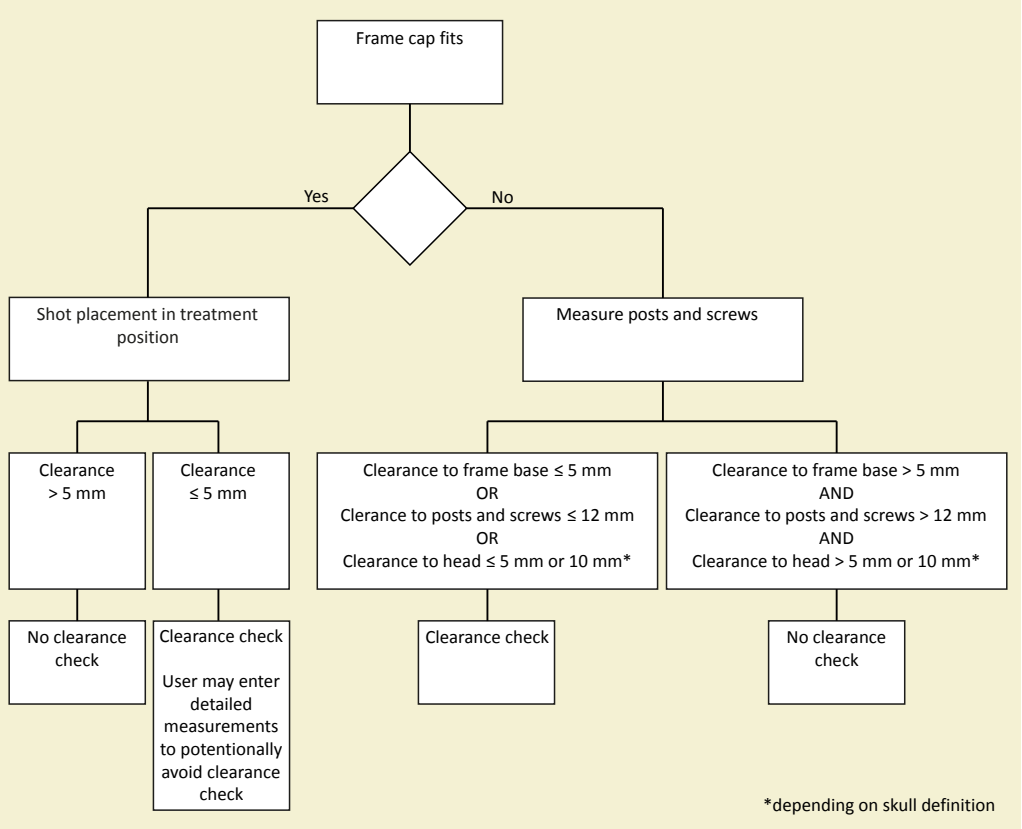


Figure 5.149 Clearance limits flowchart

Note: *In extreme cases, a clearance check can be required because of potential collisions with more than one object. In these cases only one indication will be presented to the user. It is of vital importance that the clearance check is performed in such way that all protruding objects are taken into account. In effect, this means that a complete circle should always be performed with the clearance check tool before accepting the clearance check results and commencing treatment.*

If using both frame cap and detailed measured values, the treatment planning application will automatically choose the case giving the most clearance. This means, for example, that if a post or screw is estimated to give less than 12 mm clearance (which would indicate the need for a clearance check) but the frame cap fits, the treatment planning application will not indicate the need for clearance check prior to the treatment.

When using the frame cap, the treatment planning application will indicate in the Clearance dialog if a treatment position brings the patients head or the coordinate frame assembly close to the radiation unit. This does not imply that a clearance check is needed. The information can be used as an indication that the patient may be informed that he or she will pass closely to the radiation unit during treatment but that there is no need to be alarmed.

WARNING 5.31

Use the Clearance function with care. Clearance is modeled with a limited resolution and the possibility of errors exist when defining the skull and fixation.

5.11.9.3 Clearance limits for Leksell Gamma Knife® Icon™ with mask fixation

- **No clearance**
  - **7 mm or less outside the Clearance Check Tool range**

    A shot cannot be placed at coordinates not providing clearance.
- **Clearance from Mask fixation**
  - **3 mm from Mask fixation**

    A shot position with clearance less than 3 mm to the mask fixation will cause the treatment planning application to indicate that this shot position needs clearance check prior to the treatment.
- **Clearance from patient's head**
  - **18 mm from patient's head**

    A shot position with clearance less than 18 mm to the patient's head will cause the treatment planning application to indicate that this shot position needs clearance check prior to the treatment.

Note: *In extreme cases a clearance check can be required because of potential collisions with more than one object. In these cases only one indication will be presented to the user. It is of vital importance that the clearance check is performed in such way that all protruding objects are taken into account. In effect, this means that a complete circle shall always be performed with the clearance check tool before accepting the clearance check results and commencing treatment.*

WARNING 5.32

Use the Clearance function with care. Clearance is modeled with a limited resolution and the possibility of errors exist when defining the skull and fixation.

5.11.9.4 Clearance limits for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ with Vantage Head Frame

- **No clearance**
  - **7 mm or less outside the Clearance Check Tool range**

    A shot cannot be placed at coordinates not providing clearance.
- **Clearance from Vantage assembly**
  - **5 mm from the Vantage Head frame, or frame adapter**

    A shot position with clearance less than 5 mm to the Vantage Head frame, or frame adapter, will cause the treatment planning application to indicate that this shot position needs clearance check prior to the treatment.
- **Clearance from patient's head**
  - **5 mm from patient's head**

    A shot position with clearance less than 5 mm to the patient's head will cause the treatment planning application to indicate that this shot position needs clearance check prior to the treatment.

Note: *In extreme cases a clearance check can be required because of potential collisions with more than one object. In these cases only one indication will be presented to the user. It is of vital importance that the clearance check is performed in such way that all protruding objects are taken into account. In effect, this means that a complete circle shall always be performed with the clearance check tool before accepting the clearance check results and commencing treatment.*

WARNING 5.33

Use the Clearance function with care. Clearance is modeled with a limited resolution and the possibility of errors exist when defining the skull and fixation.

5.11.10 Setup of treatment data

Note: *This section, including subsections, is applicable only to treatment planning for Leksell Gamma Knife® C, 4 and 4C configured with Automatic Positioning System™.*

Setup treatment data comprises the process of preparing the treatment data for printing and exporting. Shots are automatically organized into runs suitable for treatment with or without the automatic positioning system, as well as manual adjustment of shot attributes in order to optimize the treatment for patient comfort and/or convenience. The treatment preparation includes:

- sorting all shots into runs based on certain criteria, where all shots have the same:
  - collimator size
  - plug pattern
  - target
  - gamma angle
  - patient position
  - docking mode.

  In addition to these criteria, the following user adjustable criteria allows for further optimizing of the runs in order to improve patient comfort and safety within the system-defined limits:
  - the maximum number of shots in a single run
  - the maximum APS z coordinate for the docking position.

  Furthermore, the following criteria are considered, but are not user-adjustable:
  - a maximum distance of 20 mm from the center of the run in the x and y directions of the APS
  - a maximum (three-dimensional) distance of 50 mm between two consecutive shots.
- manually adjusting individual shots or groups of shots to rearrange the runs
- manually adjusting the gamma angle and docking mode of individual shots or groups of shots
- manually removing shots from the clearance check to be performed by the system.

Note: *Whenever a shot is moved, its gamma angle changed, or a new shot is added, the shot is checked for a potential collision. A shot or docking position is considered to cause a potential collision if the estimated distance to collision is below 12 mm. If a collision is detected, the shot is appended to the clearance check.*

Note: *A shot run may be split into multiple shot runs because of potential collisions at the docking position. This problem may be resolved by setting a lower maximum APS z coordinate for the docking position in the Options tab in the Setup treatment dialog.*

5.11.10.1 Setting up treatment data

1. Open the patient's file.
2. Ascertain that there is only one treatment plan in which shots have been placed.
3. From the **Plan** menu, select **Setup Treatment**.

   The Setup Treatment dialog opens.

Description of the Setup Treatment dialog

The Setup Treatment dialog provides three buttons, **Results**, **Check**, and **Options**, which provide access to task-specific panels in the dialog.

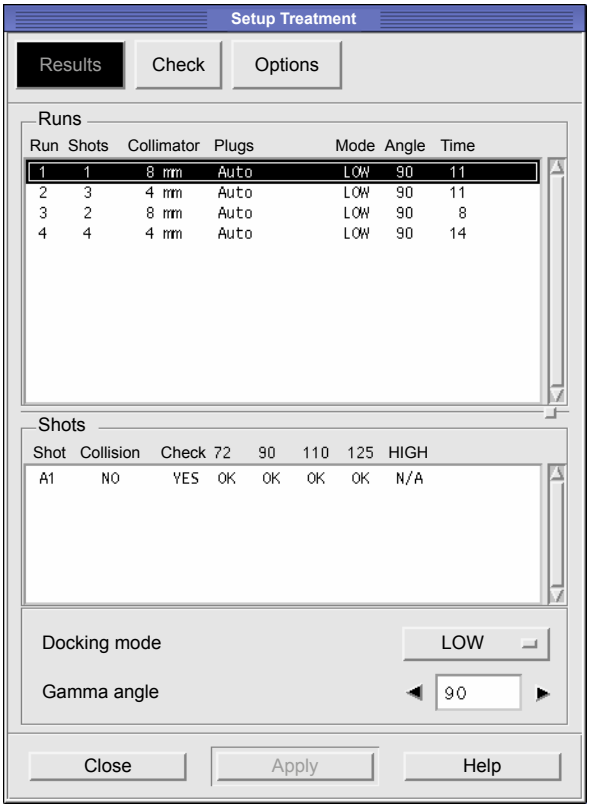


Figure 5.150 The Setup Treatment dialog with the Results panel selected

The **Runs** field of the **Results** panel provides summary data relating to all runs to be performed. It includes the run, the number of shots, collimator size, the name of the plug pattern (if applicable), docking mode (high, low or trunnion), gamma angle and time.

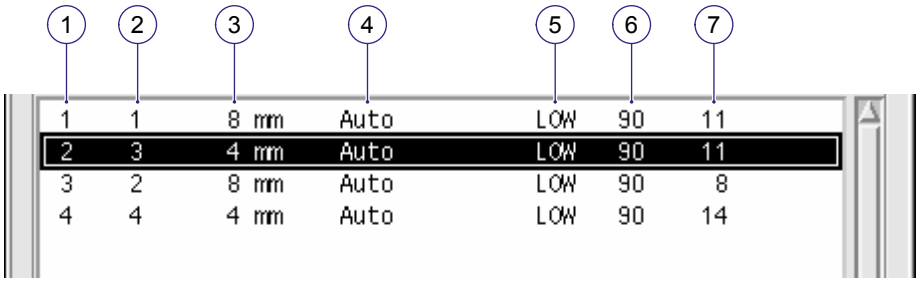


Figure 5.151 The Runs field of the Results panel

(1) Run
(2) Shots
(3) Collimator
(4) Plug
(5) Mode
(6) Angle
(7) Time

The **Time** column in the Runs field provides the estimated total time in minutes necessary to apply a run, including the time taken to open and close the radiation unit, the number of shots in a run, the time taken to move to or from the defocus position, the transportation time between shots, and the total irradiation time.

Note: *If any run is considered to present a potential problem, such as collisions by one or more shots belonging to a run, the run will be marked with an asterisk (e.g. 6*).*

The **Shots** field of the **Results** panel provides all shot information relating to the currently selected run.

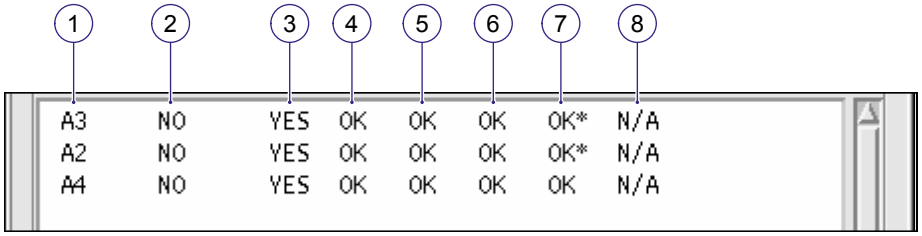


Figure 5.152 The Shots field of the Result panel

(1) Shot
(2) Collision
(3) Check
(4) 72
(5) 90
(6) 110
(7) 125
(8) HIGH

Note: *Only one run can be selected for display at any one time.*

The columns 72, 90, 110, 125 and HIGH indicate the availability of a given combination of gamma angle and docking mode:

- OK – no collision, reachable
- OK* – collision, reachable
- N/A – no collision, not reachable
- N/A* – collision, not reachable.

The **Editor** field of the **Results** panel allows you to change the docking position and/or the gamma angle of individual shots, groups of shots or complete runs.

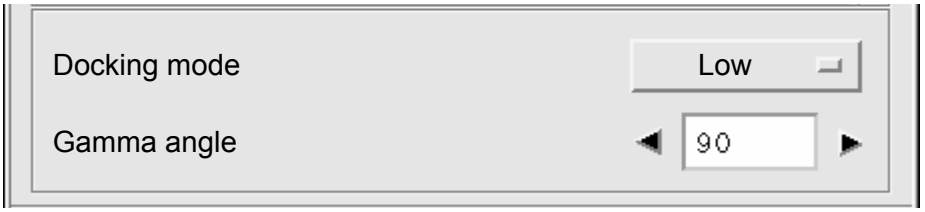


Figure 5.153 The Editor field of the Results panel

The **Check** panel displays a list of shots that the program has determined will pose a potential collision and are therefore appended to a clearance check to be performed prior to treatment.

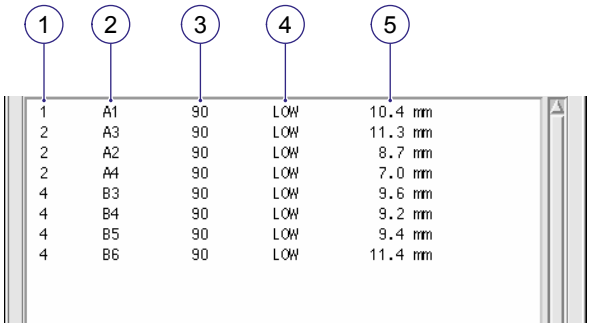


Figure 5.154 The Check panel

(1) Run
(2) Shot
(3) Gamma
(4) Docking
(5) Collision

In the **Options** panel, you can adjust maximum distances and maximum number of shots.

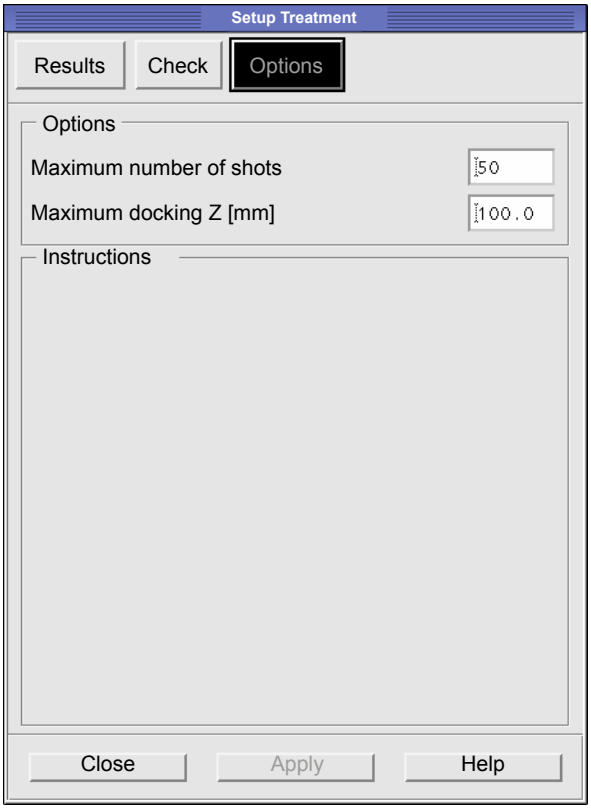


Figure 5.155 The Options panel

The **Instructions** field in the Options panel provides error information if a value entered into a field exceeds the range permitted by the treatment planning application.

Using the Results panel

1. To view a summary of the treatment plan or to modify the gamma angle and/or docking position of individual shots or complete runs, click **Results** in the Setup Treatment dialog.
2. To display additional information relating to a particular run in the **Shots** and **Editor** fields, select a run in the **Runs** field.
3. Select shot, shots or run to be edited:
   - To edit a single shot, select a run in the **Runs** field and a shot in the **Shots** field.
   - To edit multiple shots in a single run, select a run in the **Runs** field and click on the shots in the **Shots** field. All changes made in the **Editor** field will be applied to all the selected shots.
   - To edit an entire run, select a run in the **Runs** field and ensure that no shots are selected in the **Shots** field. All changes made in the **Editor** field will be applied to the entire run.

Note: *Whenever you select a run or multiple shots, changes will only be applied to those shots that are reachable within the given gamma angle/docking mode combination.*

4. To change the **Docking mode** for the selected shot, shots or run, choose **Trunnions**, or **High** or **Low**.
5. To change the **Gamma angle** of the selected shot, shots or run, use the arrows on each side of the field to increase or decrease the gamma angle.

   When a Low docking mode is selected the arrows allow you to select one of four angles 72, 90, 110 and 125. For trunnion shots you can select the Gamma angle field and type the required angle or use the arrows to increase or decrease the angle in one degree steps.

Note: *Shots with a high docking position can only be applied at a gamma angle of 90°. The **Gamma angle** field and arrow buttons therefore remain disabled (grayed-out) when a **High** docking mode is selected and will always display 90°.*

6 To implement all changes to the selected shot, shots or run, click **Apply**.

Note: *The **Apply** button remains disabled (grayed-out) until a change has been made in the **Editor** field. No changes are applied until you click **Apply**.*

Using the Check panel

1 To view and/or remove shots that are considered by the treatment planning application as potential collisions, click **Check** in the Setup treatment dialog.

The Check panel is displayed.

2 To remove a shot from the clearance check, select the required shot and click **Remove**.

3 If you have accidently removed a shot or you require the program to perform an additional collision detection check, click **Reset**.

4 To implement all changes to the Check panel, click **Apply**.

Using the Options panel

1 To adjust the maximum number of shots in a run, the distance from a collision, and the optimization method, click **Options** in the Setup Treatment dialog.

The Options panel is displayed.

2 For Leksell Gamma Knife® B, C, 4 and 4C, the maximum number of shots must be within the range 1 to 50. To change this value, click in the **Max number of shots** field and type the required value.

3 The maximum APS z coordinate for the docking position must be within the range 58 to 138 mm. To change the distance, click in the **Maximum docking Z [mm]** field and type the required value.

4 To implement all changes in the **Options** panel, click **Apply**.

5 To close the Setup Treatment dialog, click **Close**.

5.11.11 Evaluation of the results

Evaluation of the information obtained from a treatment planning session is a crucial step and requires special clinical expertise. Part of the evaluation process may involve the statistical analysis and measurement of dose related information within the displayed patient images.

For the purpose of statistical analysis there are point, line, area and volume, as well as dose volume histogram measurement facilities provided in the treatment planning application. In addition you can use the clearance check.

The following tools might be useful:

- The Measurements dialog
- The Dose Evaluation dialog

WARNING 5.34

This manual does not explain the criteria that can be applied to ascertain the validity of a treatment protocol. It describes the use of the functions available in the treatment planning application to assist during the evaluation of treatment planning information.

Only fully-trained neurosurgeons, medical physicists, neuroradiologists and radiation oncologists should perform this evaluation.

Related Links:

Measuring a point on page 271

Measuring a line on page 272

Measuring a 90° line on page 275

Measuring a volume on page 276

Plotting histograms on page 277

Dose Evaluation on page 52

5.11.12 Treatment planning states

The treatment plan state describes how far the plan has been completed. The progress of the work is divided into the following steps:

- Draft - the treatment plan is prepared.
- Approved - the treatment plan is approved for treatment.
- Printed - the treatment plan has been printed onto a treatment protocol.
- Exported - the treatment plan has been exported to Leksell Gamma Knife® for treatment.
- Rejected - the treatment plan has been rejected. This state is applicable only to plans that were rejected in Leksell GammaPlan® version 10 or earlier.

Note: *A treatment plan for Leksell Gamma Knife® B does not contain the state Printed.*

The progress is described in the figure below.

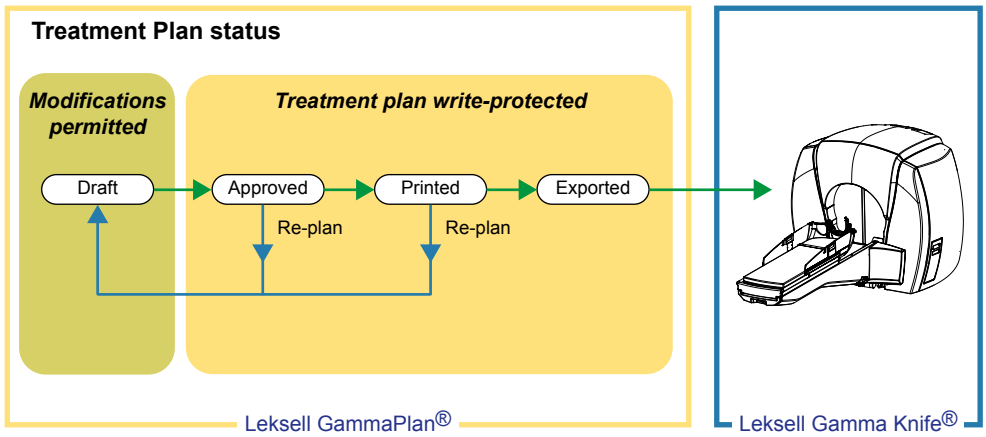


Figure 5.156 The treatment plan status

In any state other than **Draft**, the treatment plan is read-only. This means (where applicable) that targets and shots cannot be added or edited, possible clearance check indications cannot be

addressed, plug patterns cannot be added or edited, docking mode cannot be changed, and the maximum number of shots and maximum Z-coordinate for docking cannot be changed.

In addition, the following cannot be changed:

- Existing image study definitions and co-registrations
- Fixation configuration
- Skull shape
- Electron density
- Regions and type of existing volumes (new volumes can be created and changed)

Only one treatment plan in the radiological examination may be in **Approved**, **Printed** or **Exported** state at a time. For Approved or Printed plans you can do Re-plan to get back to the Draft state. You can also re-plan an Exported plan, but this will result in a new examination, leaving the original examination and plan intact.

Treatment plans that have been converted from Leksell GammaPlan® versions 4.x/5.x/4C have the treatment plan state **Converted**. By design, a treatment plan in state **Converted** cannot change state.

Related Links:

Introduction to re-planning on page 263

5.11.13 Alternative treatment plans

While planning a patient's treatment protocol you can create alternative treatment plans before choosing one of them. The treatment planning application allows you to create a new treatment plan, copy and make alterations to an existing treatment plan, rename a treatment plan and finally select the treatment plan that is to be used for patient treatment.

5.11.13.1 Creating a new treatment plan

Create a new treatment plan as described in this manual.

Related Links:

Creating a treatment plan on page 194

5.11.13.2 Copying an existing treatment plan

1 From the **Plan** menu, choose **Copy Plan**.

The Copy Treatment Plan dialog opens.

2 Type an appropriate name for the treatment plan and enter a comment if desired.

3 If other radiation units are available, the Leksell Gamma Knife® unit can be changed.

Note: *It is possible to change to another Leksell Gamma Knife® only if it is of the same type as the one for which the original plan was created.*

4 Change the **Dose algorithm** for the treatment plan if necessary.

5 Optionally select **Use extra fine dose grid resolution in targets**.

6 Click **OK**.

The dialog closes and the Treatment Plans dialog is updated to include the new treatment plan.

5.11.13.3 Editing a treatment plan

1 From the **Plan** menu, select **Edit Plan**.

The Edit Treatment Plan dialog opens.

Note: *The name and radiation unit of the treatment plan can only be changed when the plan is in state Draft. Comments are not state-dependant and can be changed when needed.*

2 Type an appropriate name for the treatment plan and a comment if desired.

3 If other radiation units are available, the Leksell Gamma Knife® unit can be changed.

Note: *It is possible to change to another Leksell Gamma Knife® only if it is of the same type as the one for which the original plan was created.*

4 If necessary, change the **Dose algorithm** for the treatment plan.

5 Optionally select **Use extra fine dose grid resolution in targets**.

6 Click **OK**.

The dialog closes and the Treatment Plans dialog is updated to include the renamed treatment plan.

5.11.13.4 Approving a treatment plan

1 From the **Plan** menu, select **Plans**.

The Treatment Plans dialog opens.

2 Select the treatment plan that is to be approved and select **Approve** from the **Plan** menu. The treatment plan must be in Draft state, and no other plan in the examination can be in state Approved, Printed, or Exported.

The **Approve Treatment Plan** dialog opens and shows information about the plan. The dose algorithm and the maximum dose in the plan are displayed. For each target, this information is shown: number of shots, prescription dose, and max dose. For a fractionated treatment, number of fractions and dose per fraction are also displayed.

If the current examination contains previously delivered dose, the **Approve Treatment Plan** dialog also informs about this and warn about taking these into account when prescribing the dose.

If previousoly delivered dose exist for the patient in another examination but is not imported to the current examination, the **Approve Treatment Plan** dialog informs about this.

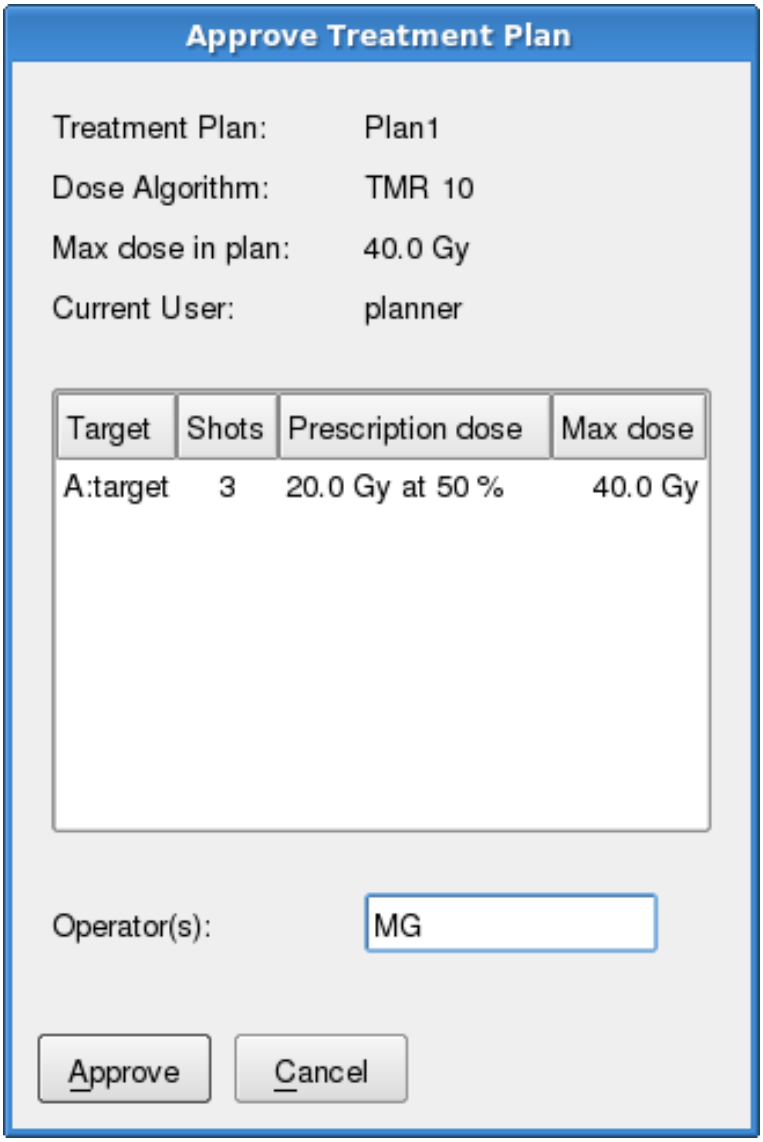


Figure 5.157 Approve Treatment Plan dialog for a non-fractionated treatment (Leksell Gamma Knife® Perfexion™)

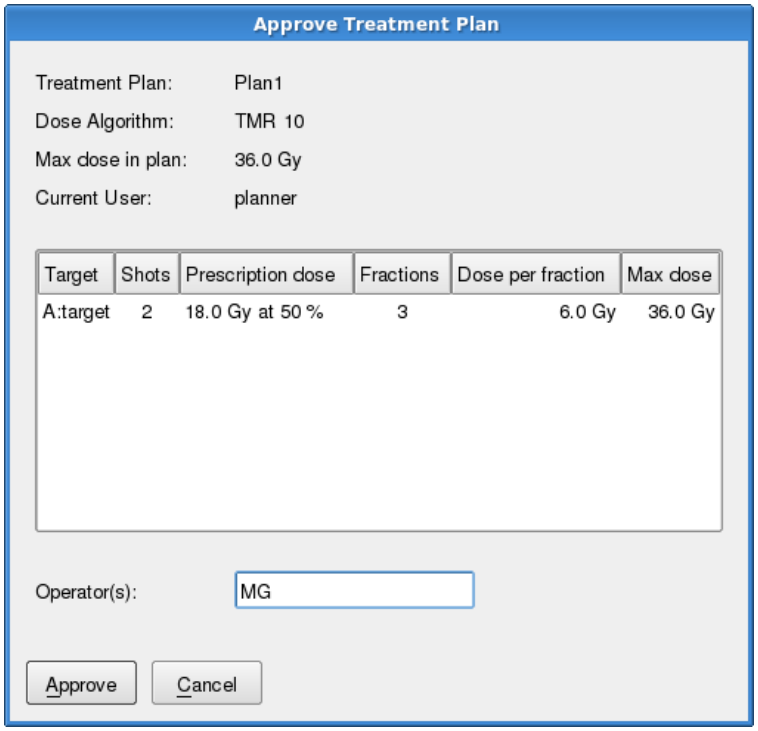


Figure 5.158 Approve Treatment Plan dialog for a fractionated treatment

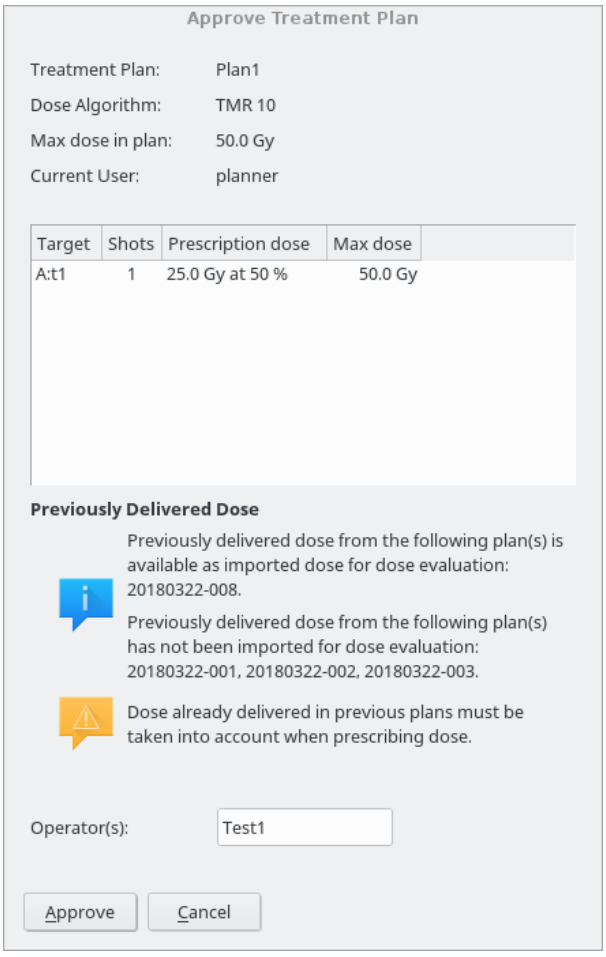


Figure 5.159 Approve Treatment Plan dialog when previous delivered dose is available

3 Enter the operator name.

4 If the Leksell Gamma Knife® unit is model B, C, 4 or 4C, enter the treatment date.

5 To accept the treatment plan for patient treatment, click **Approve**.

Note: *When approving a treatment plan, you will be informed if the plan contains any shots with weight **0** or any shots with all sectors closed. These shots will be removed from the treatment plan as they will not contribute to the delivered dose.*

Note: *A treatment plan with a dose algorithm that has not been approved for treatments by a site physicist cannot be approved.*

5.11.13.5 Deleting a treatment plan

1 Select a treatment plan and click **Delete**.

2 Confirm the deletion in the dialog that opens.

The **Delete** button is enabled if the selected treatment plan is in the Draft or Rejected state, and otherwise disabled.

5.11.14 Defining the AC-PC Line

The AC-PC Line is a specified line in the patient's brain which connects the anterior and posterior commissural points. Once this line has been identified, formulae for functional targets can be plotted using the line as a reference point.

Note: *For all AC-PC Line dialogs, the abbreviation MR stands for Midline Reference.*

1 Open the patient's file.

2 View the image studies in which you intend to plot the line.

3 From the **Plan** Menu choose **AC-PC Line**.

4 The AC-PC Line dialog opens.

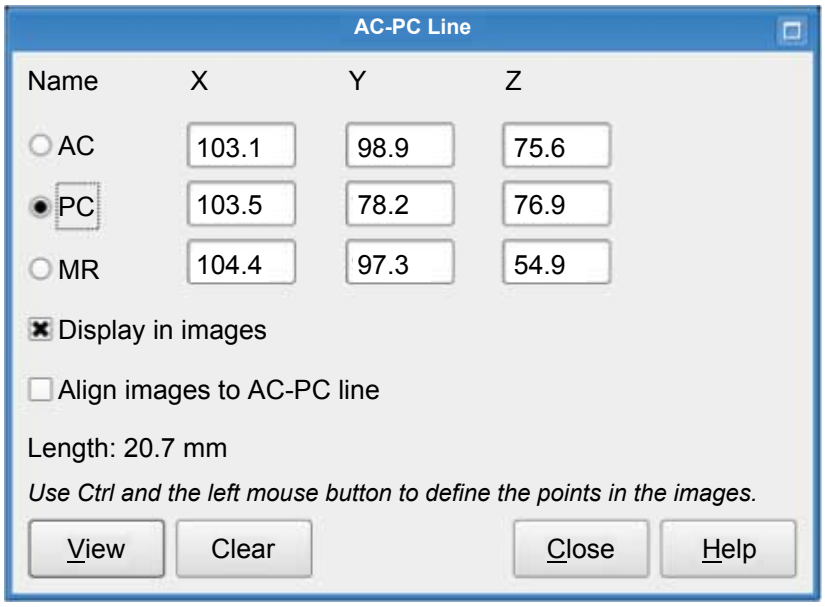


Figure 5.160 The AC-PC Line dialog

5 Click on the **AC** tick box to activate it. Press and hold down <Ctrl>. On the image study click and drag to locate the AC point. The AC point appears in the images as a green square. The center of the square defines the position of the AC point.

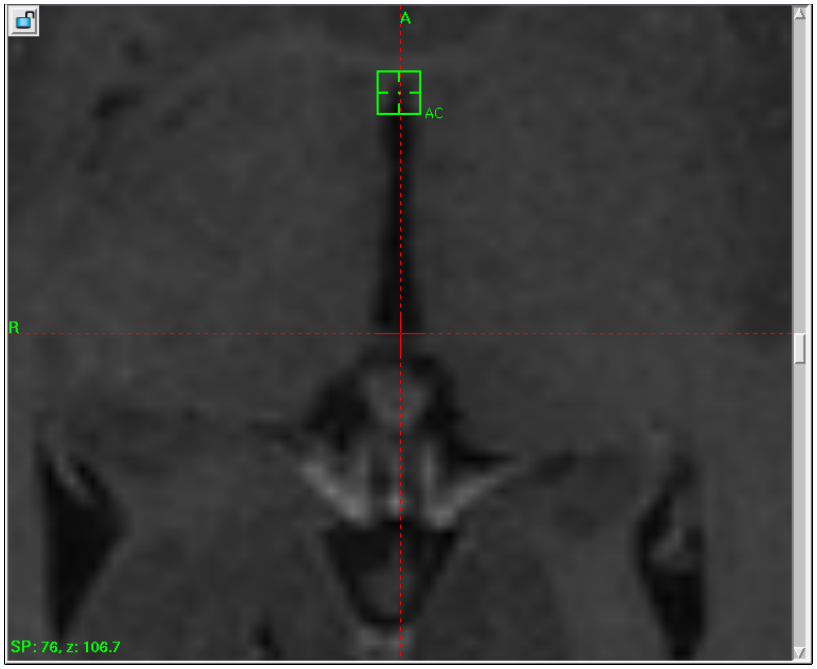


Figure 5.161 The AC point

6 The **AC** button displays the coordinates of the AC point.

Figure 5.162 The AC button

7 Click on the **PC** tick box to activate it. Press and hold down <Ctrl>. On the image study click and drag to locate the PC point. The PC point appears in the images as a green square. The center of the square defines the position of the PC point.

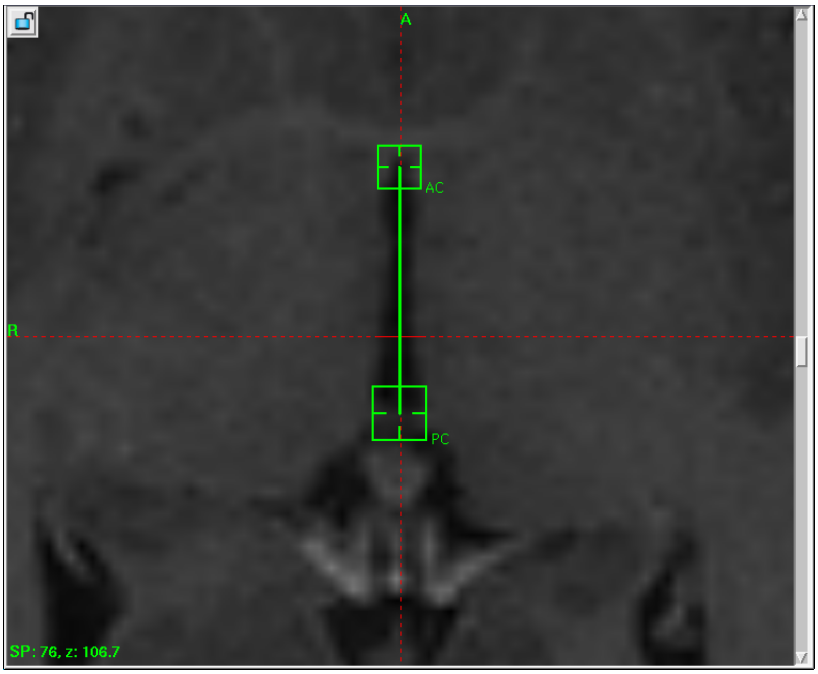


Figure 5.163 The PC point

8 The PC button displays the coordinates of the PC point.

Figure 5.164 The PC button

The MR point defines the midline reference point. It determines the tilt correction needed with respect to how the coordinate frame is mounted.

9 Click on the **MR** point button to activate it. Press and hold down <Ctrl>. On the image study, click and drag to locate the MR point on the sagittal midline above or below the AC-PC line. The MR point appears in the images as a green square. The center of the MR point defines the position of the MR point.

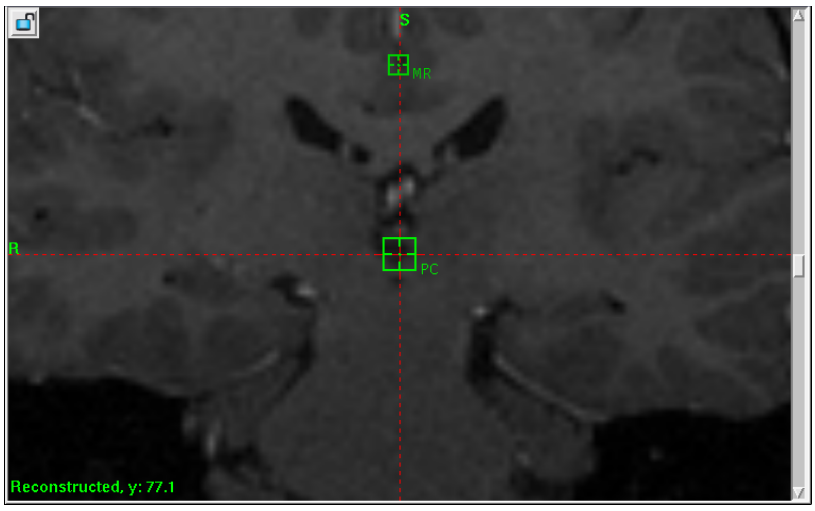


Figure 5.165 The MR point

10 The **MR** point button displays the coordinates of the MR point.

Figure 5.166 The MR point button

The AC-PC Line dialog displays the length of the intercommissural line. The length is shown only after the AC and PC points have been defined.

11 Toggle the **Display in images** button, located in the center of the dialog, to display the line in all images.

12 Select the **Align images to AC-PC line** check box to align all open images to the plane defined by the AC-PC-MR points. This correlates the images to the orientation of common brain atlases and compensates for tilt when mounting the coordinate frame.

13 Click **View**. The images are centered around the selected point.

5.11.14.1 Moving a point to another location

1 Open the AC-PC dialog.

2 Select the point to be set.

3 Click **View** (the images center around the selected point).

4 Press and hold down <Ctrl>. Drag the point to the required location.

5.11.14.2 Moving a point to another plane

1 Open the AC-PC dialog and click on the button of the point you want to move.

2 Go to the plane to which you want to move the point.
3 Press and hold down <Ctrl>. Double click on the point to be moved.
4 The point moves from one plane to another.

5.11.15 Functional targets

Functional targets is an optional feature. You can localize a target point based on the following attributes:

- Percentage of the length of the AC-PC Line (Anterior or Posterior from the PC point)
- Up/down or Superior/Inferior (millimeters) from the AC-PC Line
- Left/Right (millimeters) from the AC-PC Line
- Forward/Backward or Anterior/Posterior (millimeters).

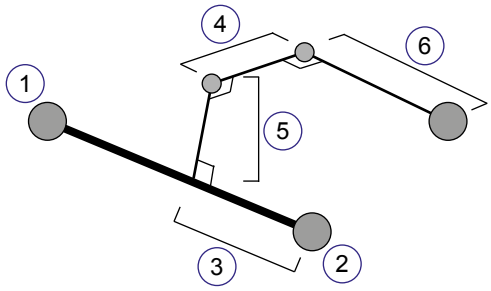


Figure 5.167 Functional target localization

(1) AC
(2) PC
(3) PC-AC%
(4) Left/right (mm)
(5) Superior/Inferior (mm)
(6) Anterior/Posterior (mm)

Several formulae can be created for each patient: each formula has a unique name. The AC point, PC point and MR point must be defined before this tool can be used.

WARNING 5.35

A functional target formula does not necessarily map the functional target exactly due to differences to the patient's anatomy.

5.11.15.1 Adding a formula

1 View the image study where the formula is to be plotted.
2 From the **Plan** menu, select **Functional Targets**. The Functional Target Formula dialog opens.

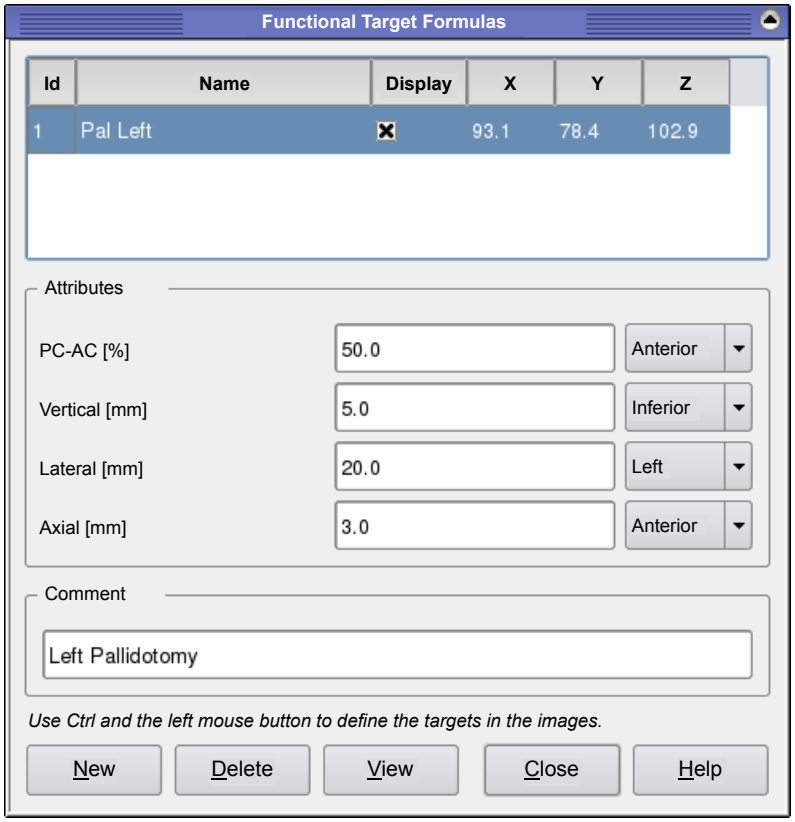


Figure 5.168 The Functional Target Formula dialog

The dialog contains all formulae which have been previously defined for the patient.

3 Click **New**.

The Add Formula dialog opens.

Figure 5.169 The Add Formula dialog

4 Type an appropriate name for the new formula. The treatment planning application adds 'Formula #' as default, where # is a sequential number. See figure below.

Figure 5.170 The Formula name field

5 Click **Ok**.

The Add Formula dialog closes and a **Formula** button appears in the Functional Target Formula dialog.

6 Type the required values and select the orientation of the four fields in the attributes section of the dialog.

7 Type any details or special comments about the target into the field located at the bottom of the dialog.

The treatment planning application automatically calculates the coordinates for the target using the values in the Functional Target Formula dialog.

The values of a formula are automatically recalculated if the formula target is grabbed and moved. Press down the <Ctrl> key and use the left mouse button to move the target.

The formulae target coordinates are automatically recalculated if the AC, PC or MR point locations are modified.

To center the images around the formula target click **View**.

Note: *The coordinates for the center point appear in the top right corner of the treatment planning application.*

Note: *No reset button is available to restore the location of the moveable target.*

Note: *The AC, PC and MR points must be defined correctly to ensure that accurate values are produced by the formula tool.*

To place an additional formula, repeat steps **2** to **7** above.

5.11.15.2 Deleting a formula

1. From the **Plan** menu, select **Functional Targets**.

   The Functional Target Formula dialog opens.

   The dialog contains all formulae which have been previously defined for the patient.
2. Select the formula that you want to delete.
3. Click **Delete**.

   A confirmation dialog opens.
4. Click **OK**.

   The formula is deleted.
5. To close the Functional Targets dialog, click **Exit**.

5.12 Leksell GammaPlan procedures

5.12.1 Treatment planning workflow

5.12.1.1 Treatment planning for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™

Typically, the workflow for treatment planning with the treatment planning application comprises the following steps:

1. Create a new patient (or a new examination for an existing patient).
2. Import one or several image series.
3. Select fixation configuration.
4. If using **Leksell® Coordinate Frame G**, supply frame cap information and/or detailed coordinate frame measurements.
5. Define stereotactic reference:
   - For Leksell Gamma Knife® Perfexion™, define the imported images based on fiducials.
   - For Leksell Gamma Knife® Icon™, either define the imported images based on fiducials, or define a CBCT study.

6 Define the skull shape.
7 Define a target volume.
8 Define any risk zones close to the lesion.
9 Create a treatment plan.
10 If needed, define the target. Targets are automatically created if all volumes of type **Target** were defined before creating the treatment plan.
11 Create the irradiation scheme using the available dose planning tools (either automatically through Dose Optimization or Inverse Planning, or manually through manual shot placement).
12 Check the clearance status of the shots.
13 Evaluate (using measurements) and approve the treatment plan when satisfied..
14 Print the treatment protocol.
15 Sign the printed treatment protocol.
16 Export the treatment plan to Leksell Gamma Knife®.

5.12.1.2 Treatment planning for Leksell Gamma Knife® B, C, 4 and 4C

Typically, the workflow for treatment planning with the treatment planning application comprises the following steps:

1 Create a new patient (or a new examination for an existing patient).
2 Import one or several image series.
3 Supply coordinate frame measurements.
4 Define the imported images.
5 Supply skull measurements or define the skull shape from images.
6 Outline a target volume.
7 Create a treatment plan.
8 If needed, define the target. Targets are automatically created if all volumes of type **Target** were defined before creating the treatment plan.
9 Place shots.
10 Set shields and generate the plug pattern.
11 Check the clearance status of the shots.
12 Approve the treatment plan (using measurements) when satisfied.
13 Print the treatment protocol.
14 Sign the printed treatment protocol.
15 Leksell Gamma Knife® C, 4 and 4C only: Export the treatment plan to Leksell Gamma Knife®.

5.12.2 Typical procedures during treatment planning

5.12.2.1 Preparations for treatment planning

1 Log in and start the treatment planning application.
2 Create a new patient, or a new examination for an existing patient.
3 Import the patient's images.
4 Define the image study in one of the following ways:
   – For Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® models B, C, 4 and 4C, define the imported images based on fiducials.

– For Leksell Gamma Knife® Icon™, either define the imported images based on fiducials (if available), or do as follows:

1 Do a CBCT scan.

2 Define the CBCT image study.

3 Co-register the imported images to the CBCT image study.

5 View the image studies.

6 If needed, adjust the image contrast and brightness.

7 Select a predefined workspace or create a preferred user-defined workspace.

8 Outline the lesion(s).

9 Outline any critical structures.

10 Define the skull shape.

5.12.2.2 Creating a treatment plan for a single target

1 Perform the Preparations for Treatment Planning procedure.

2 Create a new treatment plan.

3 If needed, define the target. Targets are automatically created if all volumes of type **Target** were defined before creating the treatment plan.

4 Define the irradiation scheme.

5 Plot the isodose configuration.

6 Check the clearance between the radiation unit/collimator helmet and to the fixation and/or to the patient's skull.

7 Prescribe dose to the target. The dose to prescribe can be determined either visually or by using the DVH method.

Related Links:

Preparations for treatment planning on page 259

Using DVH for peripheral dose definition on page 261

5.12.2.3 Creating a treatment plan for multiple targets

1 Create a treatment plan for a single target.

2 For any consecutive targets repeat the following steps:

a If needed, define the target. Targets are automatically created if all volumes of type **Target** were defined before creating the treatment plan.

b Define the irradiation scheme.

c Plot the isodose configuration.

d Check the clearance between the radiation unit/collimator helmet and to the fixation and/or to the patient's skull.

e Prescribe dose to the target. The dose to prescribe can be determined either visually or by using the DVH method.

f Toggle between **All targets/Single target** mode and visually inspect how the isodose curves change after adding a new target.

3 If necessary, change target delivery order manually.

4 Make dose volume histograms or other measurements and toggle between **All targets/ Single target** mode between measurements to assess the dose contribution from other targets on each selected target.

Related Links:

Manually changing the target delivery order **on page 200**

Creating a treatment plan for a single target **on page 260**

5.12.2.4 Using DVH for peripheral dose definition

1 Perform the Preparations for Treatment Planning procedure.
2 Create dose-volume histograms for the target and lesion volume in **Single target** mode.
3 Conclude the peripheral isodose to be used on the protocol, e.g. the peripheral isodose should cover at least 95% of the target volume.
4 Determine the volume defined by the peripheral isodose in the lesion volume DVH, V_{lesion}, and the full volume of the isodose defined in the target DVH, V_{target}.
5 The ratio of the V_{target} over V_{lesion} is a conformity index and can be used when comparing different plan alternatives and the absolute difference is the amount of normal tissue irradiated to full dose.

Related Links:

Preparations for treatment planning **on page 259**

5.12.2.5 Comparing alternative treatment plans

1 Create at least two draft treatment plans.

When comparing alternative treatment plans, remember to set the prescription dose of all targets for the plans in draft mode.
2 Perform the Using DVH for peripheral dose definition procedure for all plans.
3 For all plans, perform the **volume statistics** for the target and skull object.
4 Perform a benchmark test on all the plans by:
   a Visually inspecting the isodose curves for all plans.
   b Comparing the dose to critical structure for all plans.
   c Comparing the conformity index between all the plans.
   d Comparing the integrated dose to the skull for all plans.
   e Comparing the mean and max dose to target for all plans.
   f Comparing the number of shots and treatment times for all plans.
5 Use the different aspects of the above as a weighting factor in determining the optimal treatment for the patient.

5.12.2.6 Pre-planning with Leksell GammaPlan®

Pre-planning with Leksell GammaPlan® is available as an optional functionality, which makes it possible to bring a treatment plan to near completion using non-stereotactic image studies only. A pre-plan can be made on non-stereotactic MR, CT and PET image studies and later be transformed to the stereotactic space by associating the images to a stereotactic image study the day of surgery.

The system does not require that the non-stereotactic image studies are acquired at the day of the surgical procedure. Nor does the system require that the image studies used for pre-planning are acquired on the same day if more than one study is used. Several treatment plan alternatives (drafts) can be made in the pre-planning mode, the most suitable treatment plan can then be used at the day of the Leksell Gamma Knife® procedure.

Limitations when pre-planning with Leksell GammaPlan®

A treatment plan created when the examination is in the pre-planning mode has no stereotactic coordinates since the treatment planning is made entirely on non-stereotactic images. The coordinates indicated when in the pre-planning mode are not Leksell® coordinates, they are to be seen as temporary coordinates used only during pre-planning.

The dose calculation in the pre-planning mode is an approximation based on the preliminary alignment and definition of the patient anatomy.

A treatment plan created when the examination is in the pre-planning mode can not be approved for treatment. Protocols can be printed and will contain any targets and shots added, including their temporary coordinates.

Pre-planning procedure

To do a pre-plan, obey these steps:

1 Create an examination.

2 Select fixation.

3 Import one or several non-stereotactic image studies (MR, CT or PET) to the examination.

4 Select an image study to be the pre-plan reference. To open the Pre-plan Reference dialog, select **Define Pre-plan Reference** from the study icon drop-down menu.

Note: *The pre-plan will use this image study as a reference. All treatment plan objects and any co-registered image studies will refer to this image study. It is therefore important to choose the most suitable non-stereotactic image study available as the pre-plan reference with regards to quality and size.*

5 Align the image study to the fixation.

6 Define the skull shape, either from images or using a simulated skull.

7 Create a treatment plan.

Note: *It is not possible to approve the treatment plan when the examination is in pre-planning mode.*

Note: *All coordinates are preliminary during pre-planning. New coordinates will be given to treatment plan objects once the pre-plan reference study is co-registered to a stereotactic study.*

Description of the Pre-Plan Reference dialog

The **Align image study to fixation** dialog consists of:

- A workspace with three windows, that show the sagittal, coronal, and axial views of the head and the fixation in grayscale.
- The **Study** frame, where you can adjust the contrast and brightness of the images.
- The **Fixation** frame, where you can see what kind of fixation that was previously selected for the examination.
- The buttons **Accept**, **Reset**, **Cancel**, and **Help**.

Aligning an image study to the fixation

Before making a treatment plan based on non-stereotactic images, you can align the image study to the fixation in the **Align image study to fixation** dialog.

1 From the study icon menu, select **Define Pre-plan Reference**.

The **Align image study to fixation** dialog opens.

2 If needed, adjust the contrast and brightness of the study to improve the visibility.

3 Press and hold down <Ctrl> and use the left mouse key to move the image study and align it to the fixation in all three directions.

4 Press and hold down <Ctrl> and use the right mouse key to rotate the image study.

5 If you want to return to the starting position, click **Reset**.

6 Repeat step **3** , **4** , and **5** as applicable until the study is correctly aligned.

7 Click **Accept**.

The **Align image study to fixation** dialog closes.

Adding a stereotactic reference to a pre-plan

1 Import a stereotactic reference study to the pre-plan examination.

2 Define the stereotactic reference study using **Define Stereotactic Reference**.

The co-registration dialog opens.

3 Co-register the study used in the pre-plan with the stereotactic reference study.

If there are any issues for approval of the plan, a dialog box appears. Click **Ok** to close this dialog box.

WARNING 5.36

The stereotactic image study may differ significantly from the non-stereotactic image studies used during pre-planning. Any treatment plan objects defined during pre-planning such as targets, shots, AC-PC definition, functional targets, volumes etc. should be evaluated and if necessary modified after changing the stereotactic localization.

The examination mode has now changed from Pre-Planning to Treatment. It is possible to approve and export the treatment plan, and use it for a Leksell Gamma Knife® procedure.

5.12.2.7 Re-planning with Leksell GammaPlan®

Introduction to re-planning

It is possible to re-plan a plan after it has been approved in order to apply changes that have been proposed after approval. Dose that has been delivered (if any) will be stored for future review.

The reasons for re-planning may differ, including changed fixation and stereotactic localization, or adjustments of the plan and its dose prescription. Re-planning can be done for both fractionated and non-fractionated (single session) plans.

When re-planning an already exported plan, isodose volumes are added to the new plan describing the prescribed isodoses for the original plan. If dose has been delivered, the delivered dose is added to the new plan in the form of imported dose which can be viewed in the dose evaluation dialog.

Note: *Re-planning cannot be done if the treatment has already been re-planned.*

Note: *Re-planning cannot be done if the treatment has already been re-treated.*

Description of the Re-plan dialog

The **Re-plan** dialog is identical to the Copy Plan dialog with the addition of Re-plan options.

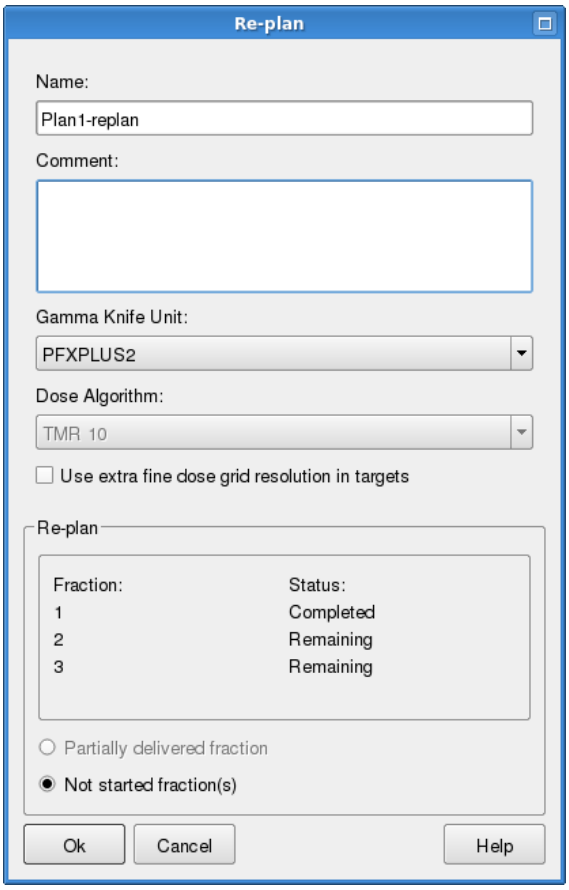


Figure 5.171 The Re-plan dialog

The dialog contains options to decide the starting point for the modifiable plan created by the re-plan operation. These options include change of **Name**, **Comment**, **Gamma Knife Unit**, **Dose Algorithm** and **Use extra fine dose grid resolution in targets**. The **Re-plan** frame of the dialog contains information and choices of what parts or fractions of the planned delivery that will be transferred to the new plan. The available choices differ depending on the state and number of fractions of the plan when the re-plan dialog was opened.

Re-planning procedure

To do re-planning, obey these steps:

1. Open the treatment plan that is to be re-planned (if it is not already open).
2. From the **Plan** menu, select **Re-plan**.

   If the plan has been exported and not completed, a dialog opens, saying that no dose may be delivered from this treatment plan after it has been re-planned. Click **Yes**.

   The Re-plan dialog opens.
3. Optionally change the name of the new treatment plan and add a comment.
4. Optionally change the **Gamma Knife Unit** if enabled.
5. Optionally change **Dose Algorithm** if enabled.
6. Optionally check **Use extra fine dose grid resolution in targets**.
7. Review the fraction statuses and select one of the available options in the **Re-plan** frame.

Note: *The Re-plan frame is not applicable and therefore not present for non-exported plans.*

8 Click **Ok**.

The dialog closes. A modified copy of the original plan in state Draft is created according to the parameters specified in the Re-plan dialog. Note that the examination mode will be Pre-planning and that the fixation and stereotactic reference must be defined again before the plan can be evaluated and approved.

The plan is now ready for modifications and subsequent approval.

Re-planning an exported plan

Re-planning an exported plan will open a new examination with a modified copy of the original plan. The differences come from the options chosen in the Re-plan dialog. The original exported plan will still be available for review in the original examination. The new examination will hold a reference to the plan that was re-planned. Any delivered dose will be available as imported dose in the new examination. The dose can be viewed in the Dose Evaluation dialog, as described in this manual.

The Re-plan dialog shows the status of each fraction in the plan. The statuses are:

- **Remaining** – fraction has not been started.
- **Partial** – fraction has been started but not completed.
- **Completed** – fraction is complete. No more dose remains to be delivered.
- **Discarded** – fraction has been manually discarded on the treatment unit.

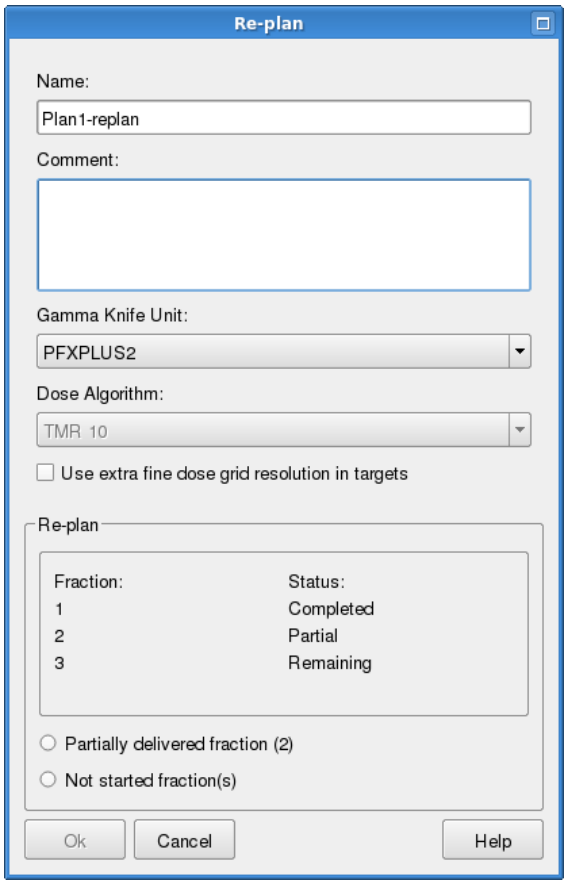


Figure 5.172 Example of fraction status

The **Re-plan** frame in the Re-plan dialog holds alternatives for the starting point of the new plan. Depending on the status of the fractions, different options will be shown.

Re-plan alternative	Description of the created plan
Entire plan	Re-plan the entire plan. The created plan will be a copy of the entire original plan.
Add fraction(s)	Re-plan to add fractions. The created plan will be a copy of the entire original plan, allowing the planner to choose and modify the number of fractions before approval of the new plan.
Not started fraction(s)	Re-plan all remaining fractions. The created plan will be a copy of the original plan, with the dose prescription altered to only contain the remaining fractions.
Partially delivered fraction (X)	Re-plan a partially delivered fraction (only). The created plan will only contain the remainder of the partially delivered fraction (indicated within the parenthesis). This may be useful for completing a fraction were plan changes are needed.

Note: *If no dose has been delivered from treatment, all fractions will have status Remaining and no dose will be imported to the new examination when re-planning.*

Note: *For Leksell Gamma Knife® B, C, 4 and 4C, re-planning is limited to re-plan of entire plans, and imported dose will not be available in the created plan.*

Related Links:

Dose Evaluation on page 52

Re-planning an approved but not yet exported plan

If the planner realizes that an approved plan requires modification, re-planning can be done. Re-planning the non-exported plan will revert the plan to state Draft to allow modifications. Therefore, no new plan or examination will be created.

Volumes representing planned dose from previous treatments

The volumes representing the dose from previous treatments correspond to the prescribed isodose volume for the respective targets in a previous treatment plan.

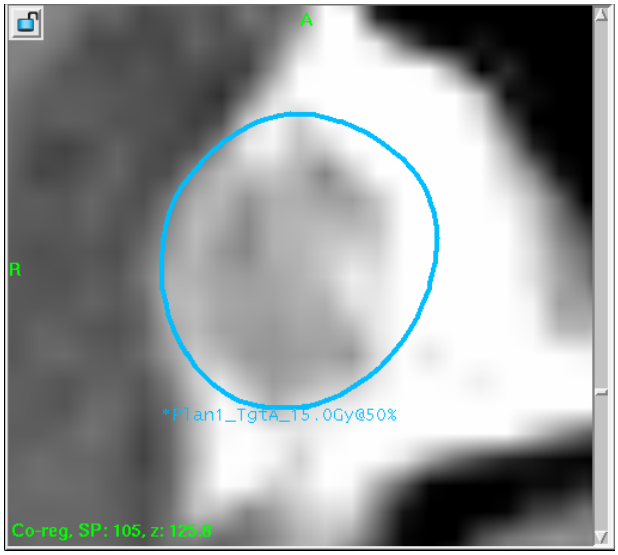


Figure 5.173 Volume representing dose from previous treatment

The names of the volumes indicate the name of the exported treatment plan they come from (first six letters), the target index, the prescribed dose and the prescribed isodose level. To give an example, the volume ***Plan1_TgtA_15.0Gy@50%** corresponds to target A in the plan “Plan1”, to which 15 Gy has been prescribed to the 50% isodose. This special type of volumes representing dose is indicated with an isodose icon in the Regions & Volumes dialog.

Figure 5.174 The isodose icon

WARNING 5.37

If a prescribed isodose volume from the previous treatment is small, and the image study has thick image slices, the generated isodose volume may not be visible when projecting it on the new patient images. Carefully review the isodose volumes in the Regions and Volumes dialog before planning the new treatment.

5.12.2.8 Re-treatment with Leksell GammaPlan®

It is possible to do a re-treatment based on a previous examination for the same patient. This is done by importing information from a previous examination into the current treatment planning examination. Previous delivered dose will be available as imported dose in the current treatment planning examination, and can be viewed in the **Dose Evaluation** dialog. The treatment plan is imported into the current examination as volumes representing the prescribed dose for each target.

Imported volumes are indicated in the user interface with the date of the examination they were imported from. Imported volumes of type Target are changed to volumes of type Object in the new examination.

Stereotactic image studies used in the previous treatment are available to be used for reference, but they cannot be defined as a stereotactic reference since they represent an earlier fixation. They can however be co-registered to new stereotactic image studies.

Note: *If the names of the imported images or volumes conflict with the existing names in the current examination, the system will assign them new names.*

Note: *You cannot import examination for re-treatment if the treatment has remaining dose delivery. It is recommended to use Re-planning in these situations.*

Note: *You cannot import examination for re-treatment if previously delivered dose has already been imported to another examination.*

Note: *You cannot import examination for re-treatment if the treatment has already been re-planned.*

Doing a re-treatment

To do a re-treatment:

1. Create a new examination for the previously treated patient.
2. Import one or several image studies to the new examination.
3. Define the stereotactic image studies.
4. Define the skull values and the fixation.

5 To import the previous treatment examination, select **Import Examination** from the **Patient** menu.

The **Select Examination to Import** dialog opens. There may be several treatment examinations for one patient. All examinations for the patient are listed in the dialog.

6 Select the treatment examination to import.

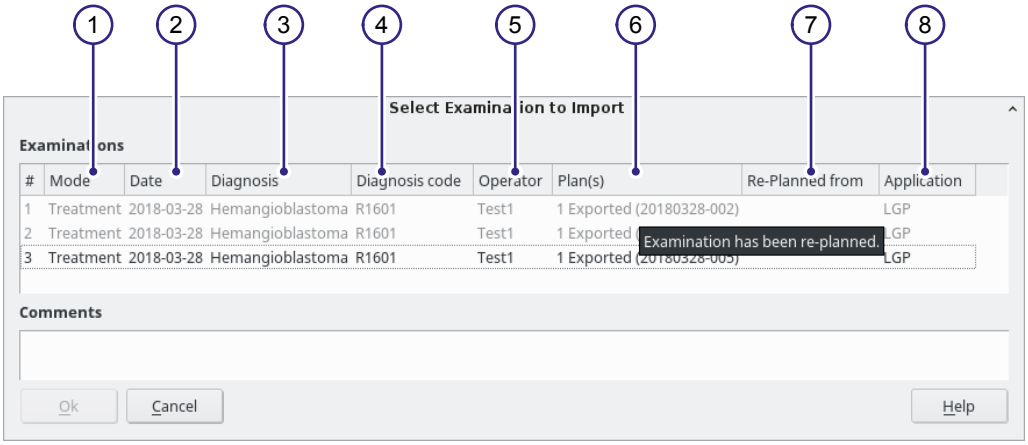


Figure 5.175 Select Examination to Import dialog

(1) **Mode**
(2) **Date**
(3) **Diagnosis**
(4) **Diagnosis code**
(5) **Operator**
(6) **Plan(s)**
(7) **Re-planned from**
(8) **Application**

Not all examinations are possible to import. If the examination is not possible to import it is not selectable, and a tool tip explains the reason why.

7 If several stereotactic image studies were used in the previous treatment, dialog opens with the image studies. Select which image study to co-register to the current stereotactic image studies.

If only one stereotactic image study is available in the previous treatment, this is chosen automatically.

When the examination and image study is selected, the co-registration window opens.

8 Co-register the image studies.

The previous delivered examination is imported to the new treatment examination.

9 Create a new treatment plan.

Related Links:

Dose Evaluation on page 279

Volumes representing planned dose from previous treatments on page 266

5.12.3 Treatment delivery evaluation for Leksell Gamma Knife® Icon™

In Treatment Mode, Leksell GammaPlan® provides the functions necessary to evaluate treatment delivery of the plan based on the current patient position from CBCT images. The treatment delivery evaluation is run as an integrated part of the treatment workflow on Leksell Gamma Knife® Icon™, and should therefore be run on a workstation located next to the Leksell Gamma Knife® Icon™ operator console.

When the CBCT images are received from Leksell Gamma Knife®, Leksell GammaPlan® starts a guided workflow.

1 Perform and review co-registration of CBCT images with plan reference images.

The system automatically recalculates dose according to the current patient position.

2 Review the dose delivery according to the current patient position compared to the planned dose.

The treatment can continue when the review has been approved.

Related Links:

Description of the Dose Evaluation dialog at treatment on page 282

Co-registration procedure on page 127

5.12.3.1 Treatment delivery evaluation for mask fixation

To find the current patient position relative the patient position used at planning, the newly acquired CBCT image is co-registered with a suitable planning reference image study.

The relative change of the patient position is presented as a geometrical rotation and translation of the Leksell® central point (100, 100, 100). This can provide valuable information about the quality and repeatability of the fixation.

For the mask fixation, the delivery of the plan is always automatically corrected according to the current patient position from CBCT images, taking both translation and rotation into account. The correction is done so that the delivery of the plan preserves the planned position of each individual shot in the patient anatomy according to the current patient position.

Delivery dose can be reviewed and compared to **Planned dose**, both in image views and through dose statistics. Delivery dose takes patient position into account for both the current fraction, and for the already delivered fractions, if any. In the delivery dose, future fractions are considered to be identical to the planned dose. Planned dose is always displayed as originally planned.

For the re-locatable mask fixation, the delivery dose must be reviewed and approved before the treatment can continue.

Related Links:

Co-registration procedure on page 127

Description of the Dose Evaluation dialog at treatment on page 282

5.12.3.2 Treatment delivery evaluation for frame based fixation

To find the current patient position relative the patient position used at planning, the newly acquired CBCT image is co-registered with a suitable planning reference image study.

The relative change of the patient position is presented as a geometrical rotation and translation of the Leksell® central point (100, 100, 100). For frame based fixation, this can provide valuable information about the quality of the fixation.

For frame based fixation, the delivery of the plan is unaffected by the current patient position from CBCT images. The review and approval of delivery dose according to the current patient position from CBCT is optional, but can be performed for QA purposes.

Delivery dose can be reviewed and compared to **Planned dose**, both in image views and through dose statistics. Delivery dose takes patient position into account. Planned dose is always displayed as originally planned.

5.13 Performing measurements

Geometric and dose measurements on the patient images can be obtained by using the **Measure** command in the Tools menu. Measurements that are made in this way can be printed.

5.13.1 Single target or All targets

Measurements and display of dose may be done for either **All targets** or **Single target**. Mode is chosen in the main menu, using the radio buttons **Σ** and **1/1** respectively.

Note: *Measurements only include dose from the currently selected treatment plan. To include dose imported from other plans, use the Dose Evaluation tool instead.*

In **Single target** mode, measurements and display of dose are performed for the selected target only and no contribution from other targets are taken into account. The dose measurement unit used is % of the dose in the reference point for the target according to the point dose calculation.

Observe that measurements and display of dose in **Single target** mode are approximations compared to **All targets** mode. **All targets** mode should be used when evaluating the total effect of a complete treatment plan, since this reflects the actual total dose that the patient will be exposed to. The dose measurement unit used for **All targets** mode is absolute dose in Gray (Gy).

In **Single target** mode, the selected target's name is shown both in the measurements on the screen and also on the printouts from measurements. For measurements performed in **All targets** mode, no target name is shown on screen or on printouts.

5.13.2 Dose statistics

The dose statistics for all measurements except point measurements are determined by linear interpolation from the dose values in the treatment plan dose grid. Point measurement dose is always calculated exactly using point dose calculations.

The results of the individual measurements that you make are displayed in the main area of the Measurements dialog. Each time a measurement is taken, the results are given as a separate item in this field. When you make line, 90° line, and histogram measurements the resulting colored curves are displayed as separate items. The measurement item shows:

- The Leksell® coordinates of the start and end points of the line
- The length of the line
- The absolute or relative maximum dose at the highest point on the curve
- The absolute or relative dose at the cursor mark on the curve
- The dose algorithm used for calculating the dose.

Measurement items can be used to indicate the origin of a result on an image. For example, by clicking on the item showing the result of a line measurement, the corresponding line is briefly displayed in a different color on the image.

If you make measurements and subsequently adjust any of the dose distribution factors (for example by re-positioning a shot or changing the target prescription dose), then the previous data is marked as obsolete. It is also marked as obsolete if you change a volume on which a measurement is based (for example by deleting a region). A dose measurement that covers points inferior of the treatment plan dose grid is marked as uncertain since the dose in that part of the anatomy is not possible to calculate.

Note: *When measuring doses, the dose algorithm set for the selected plan is used. In **All targets** mode it is possible to simultaneously measure the equivalent dose for an additional dose algorithm. The equivalent dose is the dose calculated with the additional dose algorithm that results in the same dose delivery (shot times) as the dose algorithm set for the selected plan.*

Related Links:

Dose statistics calculation on page 326

Point Dose calculation on page 310

5.13.3 Making measurements

5.13.3.1 Measuring a point

1. View the image study in which you intend to measure one or more points.
2. From the **Tools** menu select **Measure**, or in the Toolbar click the **Measure** button.

   The Measurements dialog opens.
3. Use the **Include equivalent TMR 10/Convolution** check box if available to compare with the measurements as calculated with an alternative dose algorithm.
4. Select **Point**.
5. Click on an image of interest at the point where you want to obtain the stereotactic coordinates.

   A green cross is drawn at that point in the image:

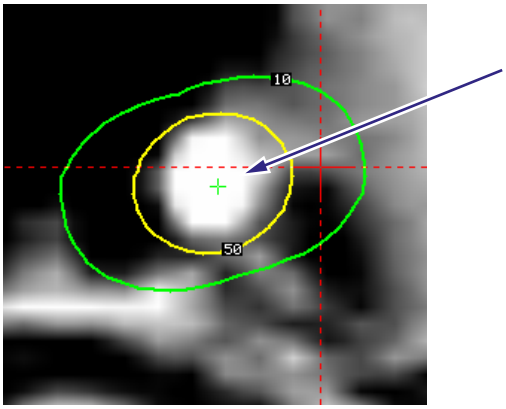


Figure 5.176 Stereotactic coordinates

The Leksell® coordinates of the point (in the order X, Y, Z) and the absolute dose (Gy) or the relative dose (%) are given on a measurement item in the Measurements dialog.

Note: *If selected, equivalent TMR 10 or Convolution dose measurements are displayed between parentheses shown with * (asterix).*

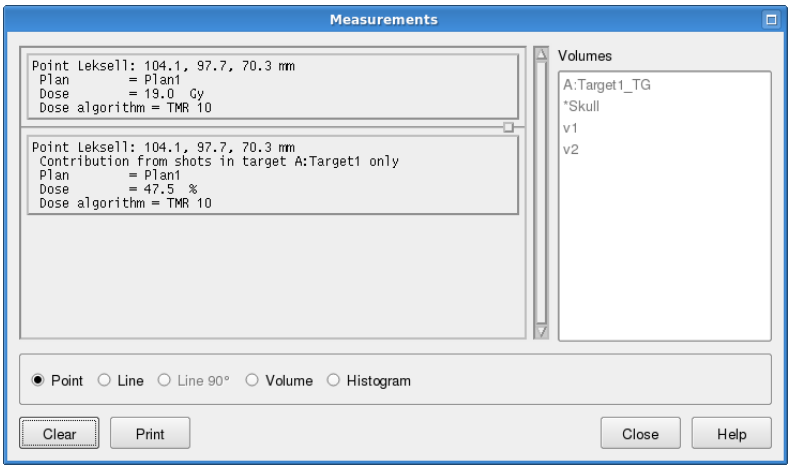


Figure 5.177 The Measurements dialog

Note: *For point measurements the dose is calculated at the exact position of the measured point regardless of the plan dose grid. Unlike other dose measurements, point measurements are therefore not affected by the resolution and interpolation in the plan dose grid.*

6 You can repeat the previous step to find the coordinates of any other point on the image. Separate measurement items give the coordinates of each point that you place.

7 If you have made a number of point measurements and you want to rapidly identify one of them, click on the measurement item for that point.

The corresponding point is momentarily highlighted in a different color in the patient's image.

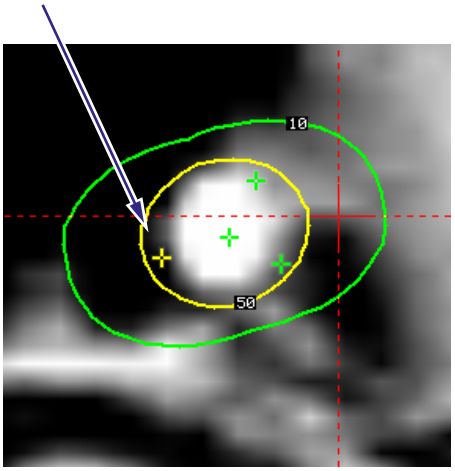


Figure 5.178 Highlighted image point

5.13.3.2 Measuring a line

Use the line measurement tool to find the coordinates of two points in a patient's image, and ascertain the distance and dose profile between them.

The measurement is continuous. If you adjust the start or end point of a line, the displayed coordinates and distance change.

1 View the image study in which you intend to measure a line.

2 From the **Tools** menu select **Measure**, or in the Toolbar click the **Measure** button.

The Measurements dialog opens.

3 Use the **Include equivalent TMR 10/Convolution** check box if available, to compare with the measurements as calculated with an alternative dose algorithm.

4 Select **Line**.

5 Click on an image of interest at the point where you want to the line measurement to start.

A small green line is drawn at the start point in the image.

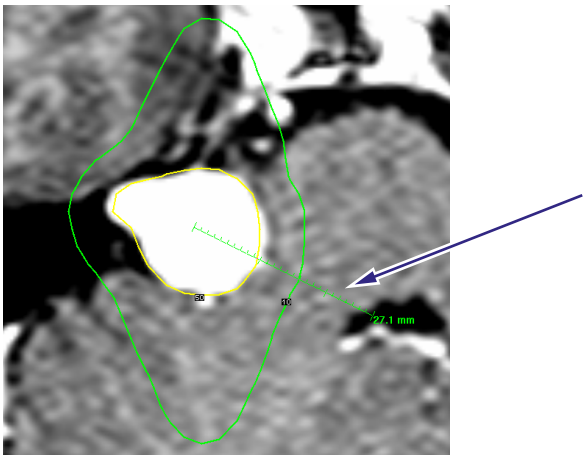


Figure 5.179 The start point of the line measurement

The coordinates of the start point (in the order X, Y, Z) are written in the Measurements dialog.

6 Click on the point where you want the line measurement to end or move the cursor to the end point.

A small green line is drawn at the end point, perpendicular to a green line which joins the start and end points.

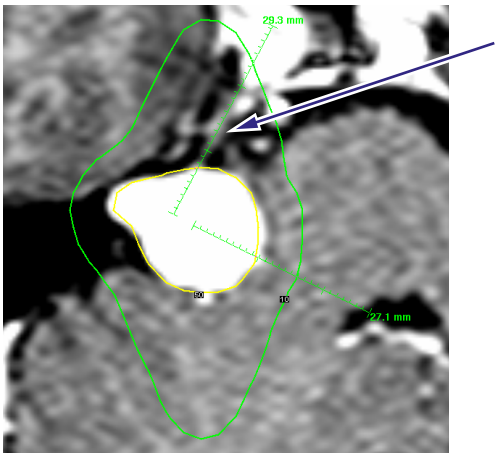


Figure 5.180 The end point of the measurement line

The absolute dose (Gy) or the relative dose (%) are given on a measurement item in the Dose Statistics Measurement dialog. The item is updated and a curve is displayed. If selected, a dashed line for the equivalent TMR 10 or Convolution dose is displayed.

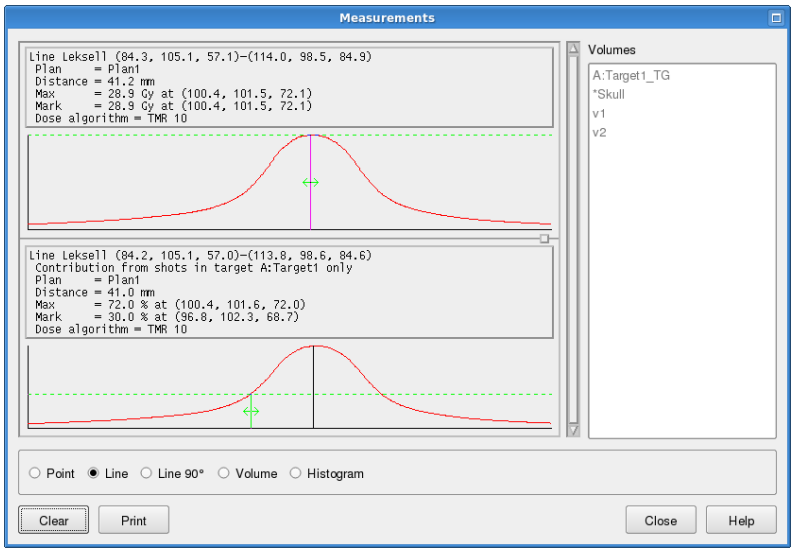


Figure 5.181 Measurement line

Line Leksell	The coordinates of both points (start X, Y, Z – end X, Y, Z)
Plan	The name of the treatment plan
Distance	The distance between the start and end points (mm)
Max	The maximum dose (in Gy or %) If selected, the maximum equivalent TMR 10 or Convolution dose (in Gy) is also displayed between parentheses shown with * (asterix).
Mark	The dose (in Gy or %) at the cursor mark on the curve If selected, the equivalent TMR 10 or Convolution dose at the pointer mark on the curve (in Gy) is displayed between parentheses shown with an * (asterix).

As you move the end point of the line, the coordinates of the point and the length of the line are updated as the point moves. This is known as continuous line/distance measurement.

7 You can repeat steps **5** and **6** to make other line measurements. Separate items in the Measurements dialog give the measured data of each line that you draw.

8 You can also examine the dose profile along the line by clicking or dragging the cursor to another position on the curve.

The measurement item shows the coordinates, the absolute dose (Gy) or the relative dose (%) at the new cursor position.

9 If you have made a number of line measurements and you want to rapidly identify one of the lines, click on the corresponding measurement item.

The selected line is highlighted in a different color in the patient's image.

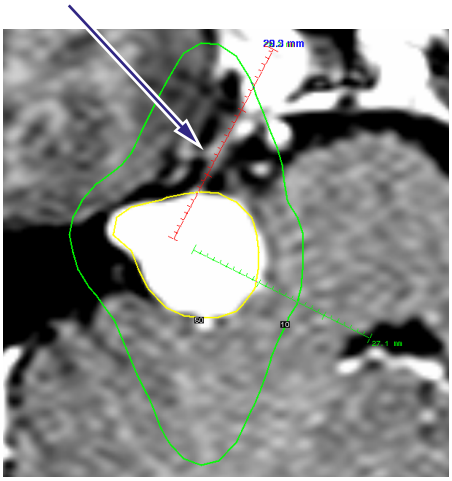


Figure 5.182 The selected measurement line

5.13.3.3 Measuring a 90° line

The **90° Line** check box is enabled only if an ordinary line measurement has been performed. It allows you to calculate the details of a line at 90° to an existing measurement line. Typically the **90° Line** tool can be used to locate a functional lesion.

This figure illustrates the principle of the 90° line measurement tool:

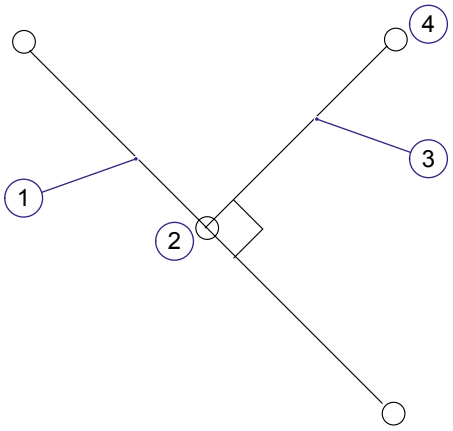


Figure 5.183 90° Line measurement

(1)	Normal Line	(3)	90° Line
(2)	START	(4)	END

1. Make a **Line** measurement as previously described.
2. Select **90° line**.
3. Click on a start point in close to the original line drawn in **1** .
4. Click on the point where the 90° line measurement is to end.

   A green line joins the end point and the start point of the 90° line, at right angles to the original measurement line.

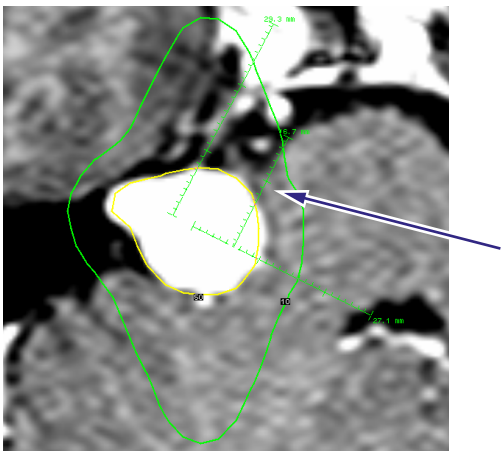


Figure 5.184 90° line measurement

A new measurement item appears in the Measurements dialog.

This measurement item gives:

- The Leksell® coordinates of both points of the 90° line (start X, Y, Z – end X, Y, Z)
- The length of the 90° line (in mm)
- The portion of the original line occupied by the 90° line. This is the distance (in mm) from the start point of the original line to the start point of the 90° line.
- The maximum dose (in Gy or %) on the 90° line
- The dose (in Gy or %) at the cursor mark on the curve.

5 As long as the end point of the 90° line has not been set, you can drag it to another position on the image, providing it remains within the span of the original measurement line.

6 The item in the Measurements dialog gives the measurement data of the new 90° line.

You can also examine the dose data at another mark on the line by adjusting the position of the cursor.

5.13.3.4 Measuring a volume

You can use the measurement tools to calculate the physical size of a defined volume and obtain dose data within it.

1 From the **Tools** menu select **Measure**, or in the Toolbar click the **Measure** button.

The Measurements dialog opens.

2 Use the **Include equivalent TMR 10/Convolution** check box if available to compare the measurements as calculated with an alternative dose algorithm.

3 Select **Volume**.

The Measurements dialog is automatically updated to include the names of all available volumes in this patient's file. In the dialog below, the measurement is done in both **All Targets** and **Single Target** mode.

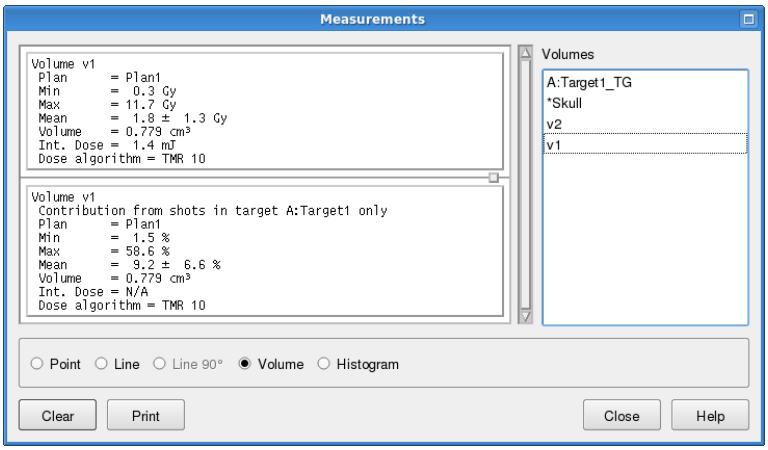


Figure 5.185 Measurement volume

4 In the **Volumes** field, click on the name of the volume that you intend to measure.

The data pertaining to the selected volume is shown on an item in the Measurements dialog.

The item gives:

- The minimum absolute (Gy) or relative (%) doses in the volume
- The maximum absolute (Gy) or relative (%) doses in the volume
- The mean absolute (Gy) or relative (%) dose and standard deviation in the volume
- The size of the selected volume (cm^3)
- The integrated dose (mJ) in the volume. Integrated dose is defined as described in this manual.

Note: *If selected, the equivalent TMR 10 or Convolution dose measurements are displayed between parentheses shown with an * (asterix).*

Note: *If the selected volume is visible in the open images, it is briefly displayed in a different color.*

Related Links:

Integral dose calculation on page 326

5.13.3.5 Plotting histograms

You can use the measurement tools to calculate and display a dose volume histogram derived from a selected volume. The histogram can be cumulative or differential.

1 From the **Tools** menu select **Measure**, or in the Toolbar click the **Measure** button.

The Measurements dialog opens.

2 Use the **Include equivalent TMR 10/Convolution** check box if available to compare the histogram as calculated with an alternative dose algorithm.

3 Select **Histogram**.

The Measurements dialog is automatically updated to include the names of all available volumes in this patient's file.

4 In the **Volumes** field, click on the name of the volume for which you intend to plot a histogram.

By default, a cumulative dose volume histogram is displayed in the Measurements dialog and the pertinent dose data is given.

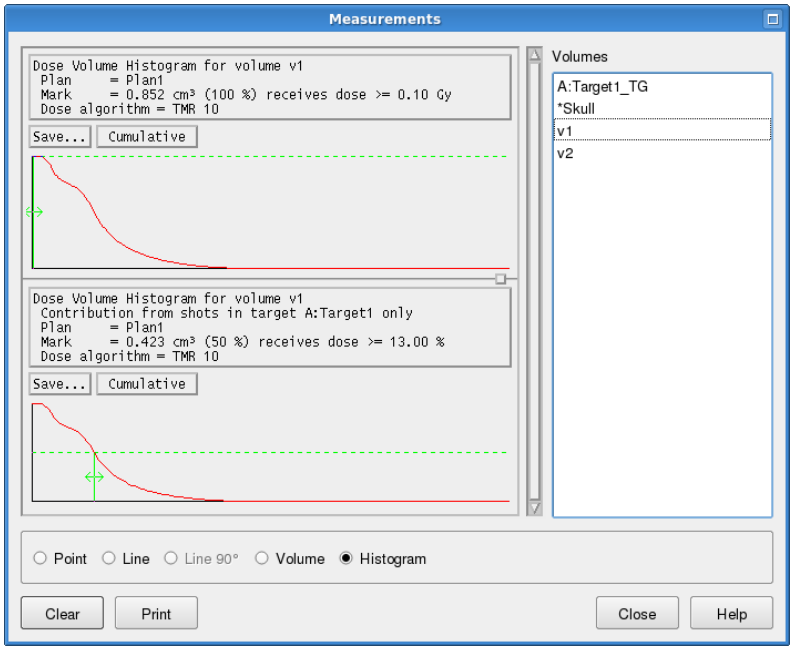


Figure 5.186 The cumulative dose volume histogram

The measurement item gives the absolute (Gy) or relative (%) dose at the cursor mark on the DVH curve. You can adjust the cursor to read dose data at other positions along the curve.

Note: *If selected, the histogram for the equivalent TMR 10 or Convolution dose is displayed with a dashed line. The equivalent TMR 10 or Convolution dose is displayed between parentheses shown with an * (asterix).*

5 To plot a differential histogram of the same volume, click the **Cumulative** button above the curve. The button changes to **Differential**.

A differential dose volume histogram is displayed in the Measurements dialog and the pertinent dose data is displayed.

Saving a histogram

To save a DVH to a USB device, perform the following steps:

1 Connect a USB device to the workstation.

2 Click **Save** for the histogram you want to save.

You can click **Save equivalent*** to save the histogram for equivalent TMR 10 or Convolution dose (if displayed).

3 The Save Dose Volume Histogram dialog opens.

4 Enter a file name.

- Supported characters are [a-z][A-Z][0-9][Space ./].
- Unsupported characters are removed from the name.

5 Click **OK**.

The histogram is now copied to the USB device.

6 Disconnect the USB device.

5.14 Dose Evaluation

The Dose Evaluation dialog provides tools for efficient evaluation of dose in image views, and through dose statistics. The Dose Evaluation dialog has two main uses:

- Evaluation of the planned dose during treatment planning.

  The Dose Evaluation dialog also allows for review of the total summed dose for the current plan including dose imported from other treatment plan(s). This is useful when re-planning a treatment, or doing a re-treatment.

- Leksell Gamma Knife® Icon™ only: Evaluation of the planned dose and the delivery dose at the time of treatment, when Leksell GammaPlan® is in Treatment mode. The delivery dose is compared to the planned dose before the dose delivery starts.

Depending on context, the available information in the Dose Evaluation dialog differs.

5.14.1 Description of the Dose Evaluation window

The **Dose Evaluation** dialog consists of a workspace to the left, and an option panel to the right.

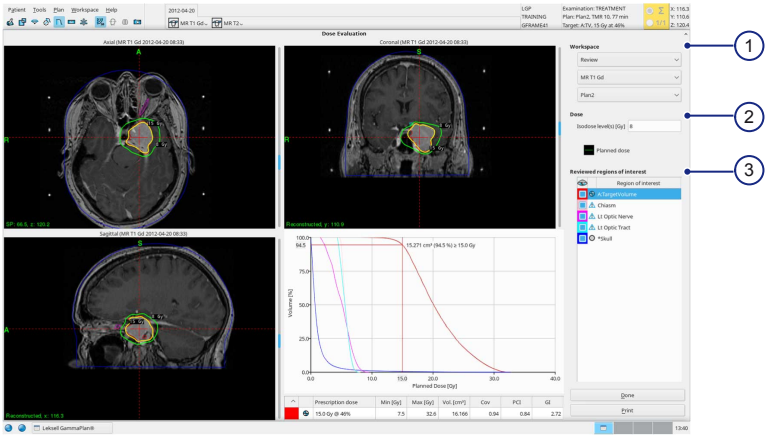


Figure 5.187 The Dose Evaluation window

In the option panel you select what to display in the workspace. The option panel contains:

- **Workspace** frame (1)
- **Dose** frame (2)
- **Reviewed Regions of interest** frame (3)

In the bottom corner there are two buttons. Click the **Done** button to exit the **Dose Evaluation** window. Click the **Print** button to take a snapshot of the window and to open the print snapshot dialog.

5.14.1.1 Description of the workspace frame

In the **Workspace** frame you select what to display in the workspace area. The available alternatives are:

- **Review** - Displays both the axial, coronal, and sagittal views of the image study, and dose statistics and DVH for the selected region of interest.
- **Single** - Displays the images of the original image study one by one.
- **Poster** - Displays an array of the images in the original study simultaneously.
- **Statistics** - Displays dose statistcs and DVHs only.

If more than one image study is available, you also select which one of the image studies to display.

If more than one plan is available, you can also change which plan that is selected.

5.14.1.2 Description of the Dose frame

In the **Dose** frame you select what dose to display in the workspace area. Depending on the context, different options are available. The following options are available for both dose evaluation for planning and dose evaluation at treatment.

- **Imported dose** - If previous delivered dose exist, you can select to add the imported dose when doing the dose evaluation. If more than one previous delivered dose exist, you can individually select which dose to add.
- **Isodose level(s) [Gy]** - Select the isodose levels to display in the workspace area.

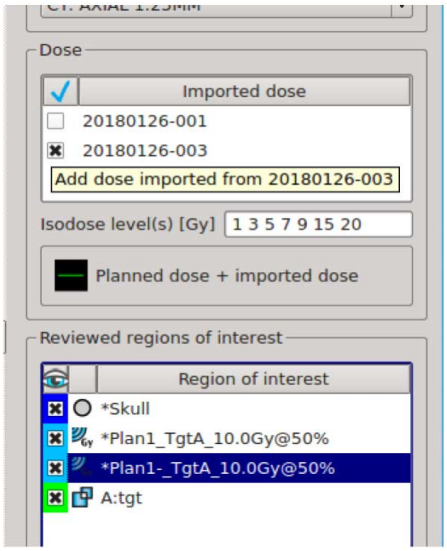


Figure 5.188 The Dose frame when previous delivered dose is available

In addition to the selected isodose levels, dose is also displayed at the mouse cursor in the image views.

Note: *Uncertain regions of the anatomy, for which the selected dose cannot be calculated completely, are indicated in red in the image views.*

5.14.1.3 Description of the Reviewed regions of interest frame

In the **Reviewed regions of interest** frame, all regions of interest (ROIs), that is, targets and outlined volumes, for the plan are listed.

Table 5.1 ROI types

Icon	Description
	Target
	Target with outlined volume
	Risk
	Object
	Treated volume

- Click the eye icon to toggle the visibility of all ROIs.

  Figure 5.189 Eye icon

- Select a ROI in the list to temporarily highlight it in the image views, and display the dose statistic for the ROI. Double-click a ROI in the list to center image views on the ROI.

The **Review** and **Statistic** workspaces contain dose statistics and DVHs for selected ROIs and dose.

In the **Statistic** workspace, both dose statistics and DVHs for all ROIs that are selected as visible are shown.

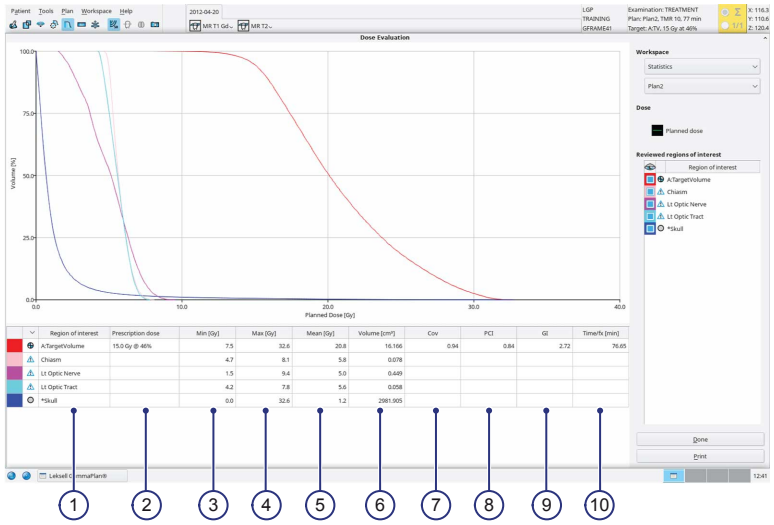


Figure 5.190 The Statistics workspace view

(1)	**Region of interest**	(6)	**Volume [cm^3]**
(2)	**Prescription dose**	(7)	**Cov** (Coverage)
(3)	**Min [Gy]**	(8)	**PCI** (Paddick Conformity Index)
(4)	**Max [Gy]**	(9)	**GI** (Gradient Index)
(5)	**Mean [Gy]**	(10)	**Time/fx [min]**

For each ROI, the dose statistics table displays:

- Color of the ROI
- Type of the ROI indicated by an icon, see **Table 5.1**
- Name of the ROI (1)
- Prescription dose for the target (only applicable to target volumes) (2)
- Minimum dose received by the ROI [Gy] (3)
- Maximum dose received by the ROI [Gy] (4)
- Mean dose received by the ROI [Gy] (5)
- Volume of the ROI [cm^3] (6)
- Coverage: the proportion of the target volume (TV) that is covered by the prescription isodose volume (PIV) = Volume(PIV∩TV) / Volume(TV). (only applicable to target volumes) (7)
- Paddick Conformity Index: (Volume(PIV∩TV))^2 / (Volume(TV)*Volume(PIV)). (only applicable to target volumes) (8)
- Gradient Index: the quotient between the half-prescription isodose volume size and the prescription isodose volume size = Volume($PIV_{0.5}$) / Volume(PIV). (only applicable to target volumes) (9)
- Beam-on time: the sum of all shot times within the ROI divided by the number of fractions set for this plan. (only applicable to target with specified prescription dose) (10).

Note: *Uncertain dose statistics are indicated in red for ROIs that contain certain points for which the selected dose cannot be completely calculated. A question mark is added before each uncertain dose value.*

Note: *Some dose statistics are specific to target volumes, and are only displayed when imported dose is not added.*

For each ROI, a cumulative dose volume histogram (DVH) graph is displayed. An interactive marker for more detailed inspection of the values in a DVH is also displayed for the ROI that is selected. Click and drag with the mouse to position the marker.

In the **Review** workspace, a subset of the dose statistices displayed in the **Statistics** workspace is displayed for the selected ROI only.

5.14.2 Description of the Dose Evaluation dialog at treatment

Note: *This section is valid only for Leksell Gamma Knife® Icon™.*

As part of the guided workflow for a Leksell Gamma Knife® Icon™ treatment, the Dose Evaluation dialog provides the functions necessary to evaluate treatment delivery of the plan based on the

current patient position from CBCT images. This section describes the functions specific to evaluating delivery dose at treatment.

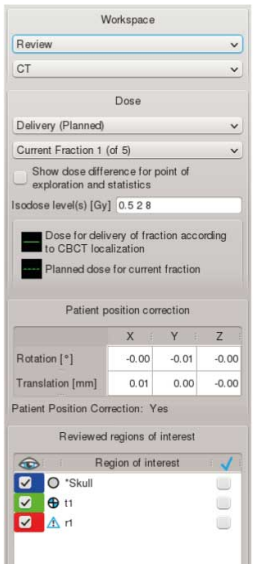


Figure 5.191 The option panel in the Dose Evaluation window at treatment

In the **Patient position correction** frame, you see information about the current patient position from CBCT images, and how this is handled by the system:

- The relative change of patient position compared to the stereotactic reference of the plan is presented as a geometrical **Rotation** (in degrees) around the Leksell® Coordinate System axes and **Translation** (in mm) of the central point at Leksell® coordinates (100, 100, 100). The rotations are applied in the order X, Y, Z and intrinsic, that is, the coordinate system rotates with each rotation.

  This relative change of patient position can be useful for evaluating the quality of the fixation.

- **Patient Position Correction** indicates if the delivery of the plan is corrected according to the current patient position from CBCT images.

  For the re-locatable mask fixation, the delivery of the plan is always automatically corrected according to the current patient position from CBCT images, taking both translations and rotations into account. The correction is done so that the delivery of the plan preserves the planned position of each individual shot in the patient anatomy according to the current patient position. See **Figure 5.192**.

  For Leksell® Coordinate Frame G and Leksell® Vantage™ Head Frame, the delivery of the plan is unaffected by the current patient position from CBCT images. See **Figure 5.193**.

- **Max shot displacement in anatomy [mm]** describes the largest positional difference for any shot due to the differences between the planned patient position and the current patient position. This is only displayed for Leksell® Coordinate Frame G and Leksell® Vantage™ Head Frame, where the delivery of the plan is not corrected according to the current patient position from CBCT images.

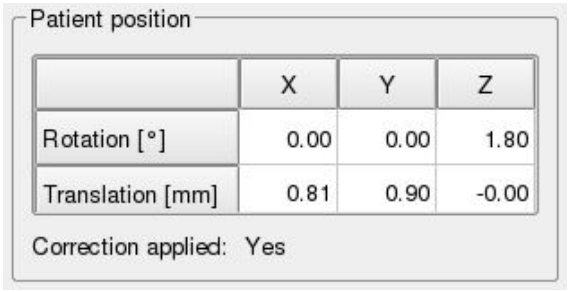


Figure 5.192 Example of Patient Position frame for mask

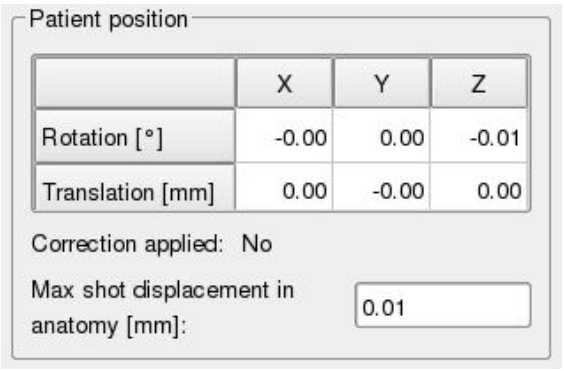


Figure 5.193 Example of Patient Position frame for Leksell® Coordinate Frame G and Leksell® Vantage™ Head Frame

In the **Dose** frame, you can select to display combinations of both planned and delivery dose in the image and statistic views:

- **Planned** dose – the planned dose without taking patient position from CBCT images into account.
- **Delivery** dose – the delivery dose taking patient position from CBCT images into account for the current fraction, and the already delivered fractions, if any. In the delivery dose, future fractions are considered to be identical to the planned dose since there is not yet any additional information of patient position for these.
- **Delivery (Planned)** dose, which means that both Delivery and Planned dose are shown simultaneously. In image views, Delivery dose is displayed in solid isodose lines, and Planned dose is displayed in dotted isodose lines. In dose statistics views, Delivery dose is presented in plain text, and the Planned dose is presented in italic text within parenthesis.
- If the **Show dose difference for point of exploration and statistics** check box is selected, the difference (subtractive) between the Delivery dose and Planned dose is displayed in the dose statistics table and at the mouse cursor in image views, instead of the absolute dose values. This option is only available when **Delivery (Planned)** dose is displayed.
- For fractionated treatments it is also possible to choose between showing only the **Current Fraction**, or the **Complete Plan**.

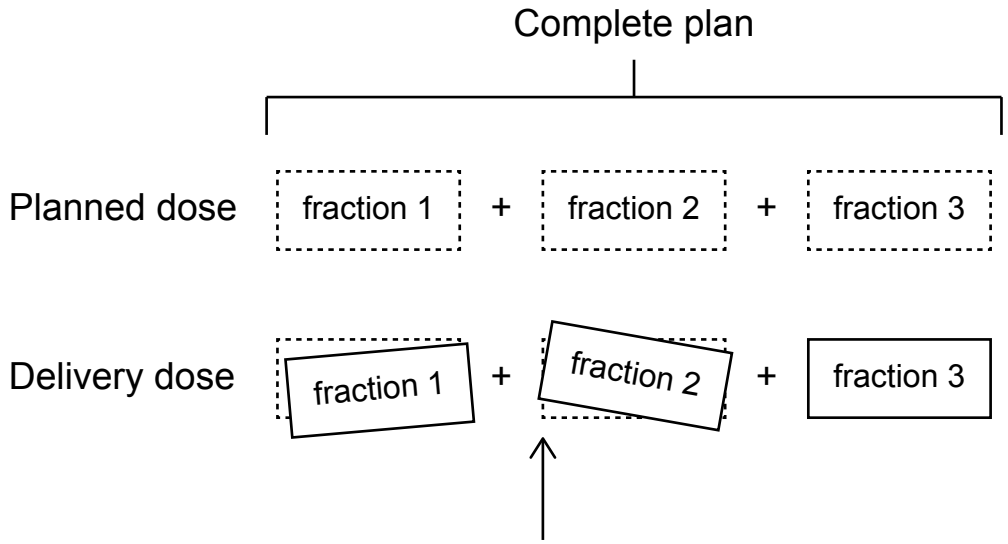


Figure 5.194 Illustration of Planned and Delivery dose at the time of evaluation of 2nd fraction (of 3)

In the **Reviewed regions of interest** frame, all regions of interest (ROI), that is, targets and outlined volumes, for the plan are listed. At dose delivery evaluation at treatment, each ROI has to be marked as reviewed in the rightmost check box for each ROI before the entire dose delivery can be approved for treatment. All ROIs can be marked as reviewed by clicking on the header for the review check box column.

5.14.2.1 Review and approval of treatment delivery

For the re-locatable mask fixation, the delivery dose must be reviewed and approved before the treatment can continue. By clicking **Accept**, the delivery evaluation is accepted, and the treatment can continue. By clicking **Reject**, the treatment delivery evaluation is rejected, and the treatment cannot continue.

For Leksell® Coordinate Frame G and Leksell® Vantage™ Head Frame, the delivery of the plan is unaffected by the current patient position from CBCT images. The review and approval of delivery dose according to the current patient position from CBCT is purely optional, but may be useful for QA purposes. By clicking **Accept**, the treatment delivery is recorded, and the delivery dose according to the current patient position will be available as delivery dose for future reference. By clicking **Reject**, the treatment delivery is ended without recording the delivery dose according to the current patient position for future reference. In both situations the treatment can continue.

5.15 Printing

5.15.1 Setting printing preferences

1 From the **Patient** menu choose **Print**.

The Print dialog opens.

- The **Page Setup** frame contains drop-down lists for selecting the paper size, the color mode, duplex mode, number of copies and a default button.
- The **Printer** frame contains a drop-down list for selecting the printer.

2 Make your selections for printer, paper size, color mode, duplex mode and number of copies.

3 To save the page setup settings as default, click **Save as default**.

Note: *The default settings for paper size and color mode are applicable when transferring printouts to MOSAIQ®.*

4 Click **Close**.

Note: *You can also change the printer selections during the various printouts.*

5.15.2 Printing from Leksell GammaPlan®

1 Open the patient's file and radiological examination.

2 From the **Patient** menu, choose **Print**.

The Print dialog opens - it contains four tabs: **Protocol**, **Measurements**, **Image**, and **Snapshots**.

By selecting the appropriate tab you can continue with printouts of the treatment protocol, measurements, images or snapshots.

Related Links:

Printing the treatment protocol on page 286

Printing measurement data on page 287

Printing images on page 287

Printing snapshots on page 288

5.15.2.1 Printing the treatment protocol

1 To print the patient's treatment protocol select the **Protocol** tab in the print dialog.

The Print dialog is updated to show the print protocol fields.

2 Use the **Include** check boxes to select the fields to be included in the printed treatment protocol. All boxes are selected by default.

3 To add any brief notes to the treatment protocol, type them into the **Comments** field.

4 To preview the protocol before printing, click **Preview**.

The preview window opens, showing the first page of the treatment protocol. Use the scroll bar to view the subsequent pages of the protocol.

5 Click **Close** in the preview window to close it.

6 If needed, change the printer preferences in the **Page Setup** and **Printer** frames.

7 When you are satisfied with the treatment protocol in all respects, click **Print**.

The treatment protocol is printed.

WARNING 5.38

The patient's treatment protocol must be approved in full by a clinical expert prior to its use in Leksell Gamma Knife® surgery.

Related Links:

Setting printing preferences on page 285

Exporting printouts to PDF on page 288

5.15.2.2 Printing measurement data

You can print the results of any dose measurements that you have taken with the **Measure** command in the **Tools** menu.

1. Open the Print dialog.
2. Choose **Measurements**.
3. The Print dialog is updated to include a list of all available measurement data (grouped by type).
4. In the **Measurement Selection** field, select the measurement data that you want to print or, to include all available measurement data, click **Select all**.
5. If you want to preview the measurement data before printing, click **Preview**.

   The preview window opens: it shows the measurement data that you have selected.

   Click **Close** in the window to close it.
6. If needed, change the printer preferences in the **Page Setup** and **Printer** frames.
7. Click **Print**.

   The measurements data are printed.

Related Links:

Setting printing preferences on page 285

Exporting printouts to PDF on page 288

5.15.2.3 Printing images

1. Open the Print dialog.
2. To print an image select the **Image** tab.

   The Print dialog is updated to include a list of all available images.
3. In the **Image Studies** field, select the image study that you want to print.
4. In the **Images** field, select the images to be printed or, to include all available images, click **Select all**.
5. To enlarge the image print, click **Large images**.
6. To include isodoses on the image printout, click **Plot Isodoses**.
7. To include volumes on the images to be printed, click **Plot Volumes**.
8. To select all images inside the dose matrices to be printed, click **Targets**.
9. To preview the image before printing, click **Preview**.
10. The preview window opens, which shows the images that you have selected.

    Click **Close** in the preview window to close it.
11. If needed, change the print preferences, or change the zoom factor of the printed images by using the scroll keys or enter the zoom factor in the **Zoom** field.
12. Click **Print**.

    The selected images are printed.

Related Links:

Setting printing preferences **on page 285**

Exporting printouts to PDF **on page 288**

5.15.2.4 Printing snapshots

You can print any snapshots that you have taken with the **Snapshot** command and/or accelerator button.

1. Open the Print dialog.
2. Choose **Snapshots**.

   The Print dialog is updated to include a list of all available snapshots.
3. In the **Select Snapshot** field, select the snapshot(s) to print.
4. To preview the snapshot(s) before printing, click **Preview**.

   The preview window opens, which shows the snapshot(s) that you have selected.

   Click **Close** in the preview window to close it.
5. If needed, change the printer preferences in the **Page Setup** and **Printer** frames.
6. Click **Print**.

   The selected snapshot(s) are printed.

Related Links:

Setting printing preferences **on page 285**

Exporting printouts to PDF **on page 288**

5.15.2.5 Exporting printouts to PDF

Instead of printing on paper, you can export the selected printout to a PDF file which is saved on an external USB device. The file name is auto-generated. LGP uses the patient identification data and constructs a file name that complies with the MOSAIQ eSCRIBE format.

1. In the **Print** dialog select what to print.
2. Click **Export** to **PDF**. The PDF Export dialog opens.
3. Click **OK** to export or click **Cancel** to abort.

5.15.3 Description of the printouts

Printouts from the treatment planning application usually occupy a number of pages, depending upon the extent of data or number of snapshots. Page breaks are automatically inserted into the printout.

The following “watermarks” are added on the printouts under the following conditions:

- **DRAFT** - The treatment plan is in Draft state.
- **EXPIRED** - The treatment plan is in Approved or Printed state, but the treatment date has expired, that is, it is not today's or tomorrow's date.
- **NOT CERTIFIED** - The changes to the Leksell Gamma Knife® configuration has not been certified, or a new, not certified Leksell Gamma Knife® configuration is used.
- **EXPORTED** - The treatment plan is in Exported state.

- **REJECTED** - The treatment plan is in Rejected state. Only applicable to plans that were rejected in Leksell GammaPlan® version 10 or earlier.
- **CONVERTED** - The treatment plan have been converted from a HP-UX version of the application and cannot be used for treatment.
- **PRE-PLANNING** - The examination is in pre-planning mode. All plan data are preliminary and non-stereotactic.

Related Links:

Converted patient files **on page 371**

5.15.3.1 Description of the printout of the treatment protocol

The printout of the treatment protocol comprises a number of fields of information, depending upon the selections made in the Print dialog. In addition, important references are given in the header and footer areas of the printout.

A treatment protocol usually contains the following fields:

- Title
- Re-plan (if applicable)
- Approval
- Gamma Knife data
- Fixation configuration data
- Treatment data
- Run data
- AC-PC Line definition (if applicable)
- Functional targets formulas (if applicable)
- Skull geometry data
- Shot dose data
- Target(s) data
- Plan and examination comments (if applicable).

Description of the Title field

This field is always present on the printout. It occupies the top part of the first page and consists of two areas.

The left side of the Title field contains the clinic name as entered in the TPS Administrator Tool. In addition, the model of Leksell Gamma Knife® and the version number of the treatment planning application are given.

The right side of the Title field contains the following data:

- the patient's name
- the patient's ID
- the diagnosis of the patient's condition
- the diagnosis code
- the Leksell Gamma Knife® unique identifier of this particular treatment plan
- the approval version
- the date of treatment (Leksell Gamma Knife® C, 4, 4C or B), or the date and time of approval (Leksell Gamma Knife® Perfexion™ or Leksell Gamma Knife® Icon™)

- the print date
- the name of the operator who devised the treatment plan
- the Leksell Gamma Knife® ID and name, entered in TPS Administrator Tool in the Leksell Gamma Knife® tab.

Description of the Re-plan field

If the treatment plan is a re-plan, the **Re-Plan** field contains the name of the original treatment plan.

Description of the Approval field

The physician must sign the **Approved for Treatment** field to denote approval of the protocol prior to the treatment.

Description of the Gamma Knife data field

The **Gamma Knife Data** field contains the following information about the Leksell Gamma Knife® unit:

- Calibration dose
- Days since calibration at approval date
- Treatment dose rate
- Output factors.

Description of the Fixation configuration field

The **Fixation Configuration** field contains information about the chosen type of fixation.

Description of the Treatment data field

The **Treatment Data** field contains one row for each target and each row has nine (9) columns:

- Name of the target
- Shots
- Prescription
- 100% [Gy]
- Max [Gy]
- X, Y, Z [mm] (one column for each)
- Width [mm]

The lower part of the **Treatment Data** field contains the following summary information:

- Number of fractions (if the treatment is fractionated)
- Total number of shots
- Treatment plan name
- Dose algorithm
- Beam-on time
- Dose grid resolution in targets

If the planned treatment is fractionated, the protocol shows treatment data both for the whole treatment and per fraction.

Description of the Run field

Note: *This section is valid only for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™.*

All shots in the irradiation scheme are grouped into one or several runs to be performed in Leksell Gamma Knife® Perfexion™ or Leksell Gamma Knife® Icon™. All shots with the same gamma angle are grouped into one run.

If you, for instance, have devised a treatment plan containing a number of shots all with gamma angle 90, they will all be grouped into the same run.

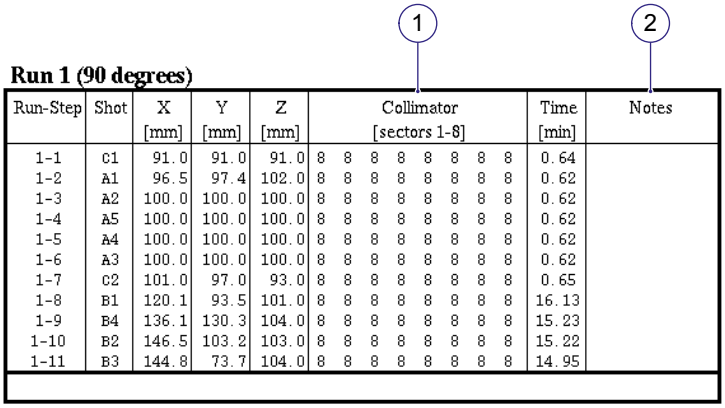


Figure 5.195 The Run field

The Collimator section (1) illustrates each shots collimator setup for the eight sectors. **B** indicates that the collimator for this treatment position is blocked, thus not contributing to the delivered dose. The Notes section (2) tells if clearance check is needed for any of the treatment positions. This is indicated by a **C** for clearance with the estimated clearance distance and position, anterior or posterior, right or left where clearance check is necessary

Description of the Shot summary field

Note: *This section is valid only for Leksell Gamma Knife® C, 4 and 4C.*

A summary containing all shots is printed with details on the treatment protocol. In the **Shot summary** the following data are printed: shot name (1), the shot's coordinates (x, y, z) (2), the gamma angle (3), the collimator size (4), the plug pattern that was used (5), shot weight (6), treatment time (7) and also a note field (8). The note field may contain clearance warning information.

The lower part of the **Shot summary** field contains significant information relating to all shots or significant information pertaining to a shot as referenced in the notes field, such as collision warnings and docking position.

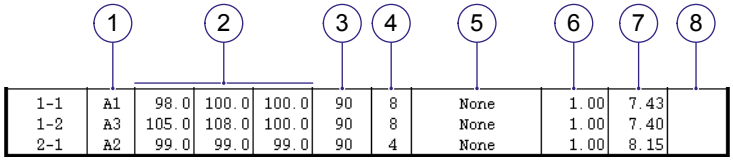


Figure 5.196 The Shot summary field

Description of the AC-PC Line definition field

The **AC-PC Line definition** field provides the coordinates of each point defined on the AC-PC Line.

The data within the **AC-PC Line definition** field are arranged in two columns:

Point

This column lists predetermined points at which treatment data are available:

- Anterior Commissure (AC)
- Posterior Commissure (PC)
- Midline Reference point (MR).

Coordinates

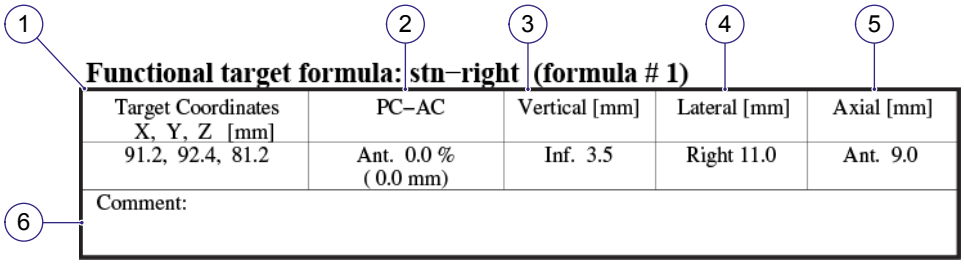
This column lists the coordinates of a point:

- X: The Leksell X coordinate in mm at the respective point.
- Y: The Leksell Y coordinate in mm at the respective point.
- Z: The Leksell Z coordinate in mm at the respective point.

There is also a **Comment** section that provides important notes.

Description of the Formula field

The **Formula** field identifies the location of the target and can be considered as comprising two parts.



Target Coordinates (1)

This column lists the coordinates of the calculated target:

- X: The Leksell X coordinate in mm at the respective point.
- Y: The Leksell Y coordinate in mm at the respective point.
- Z: The Leksell Z coordinate in mm at the respective point.

PC-AC (2)

This value is the entered percentage distance of the AC-PC line measured from the PC point in an anterior/posterior direction.

Vertical (3)

This value is the given formula value from the AC-PC line in a superior/inferior direction.

Lateral (4)

This value is the given formula value from the AC-PC line in a left/right direction.

Axial (5)

This value is the given formula value from the AC-PC line in a anterior/posterior direction.

Comments (6)

This occupies the lower part of the Formula field. It contains any notes that you may have entered on the patient's record and provides an area where you can enter handwritten notes on the protocol.

Description of the Skull Geometry field

The **Skull Geometry** field appears on the printed treatment protocol only if this option has been selected in the Include array of the Print dialog. It consists of two parts.

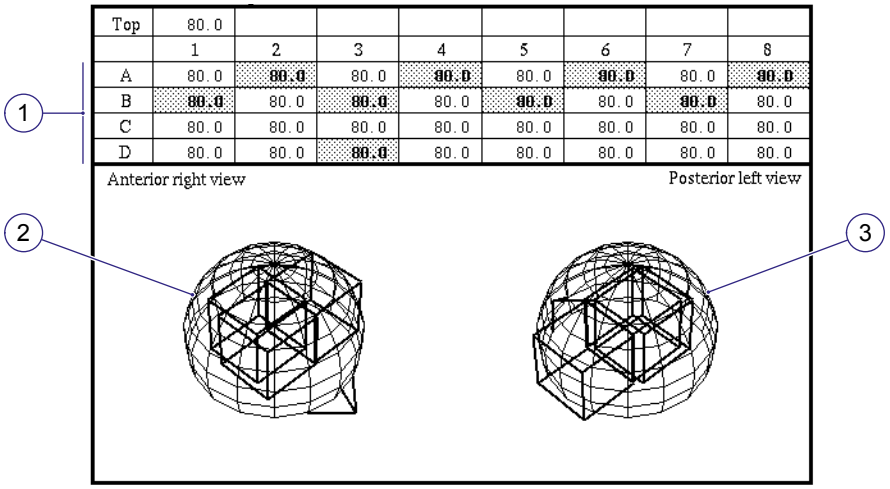


Figure 5.197 The Skull Geometry field

The upper part of the **Skull Geometry** field contains the patient's skull measurements (1), as obtained with the Skull Scaling Instrument and previously defined in the Skull dialog. In this field, the measurements given in bold typeface on a gray background are interpolated values calculated by the program, as distinct from the values that you entered. The upper part is not shown if images were used to define the skull shape.

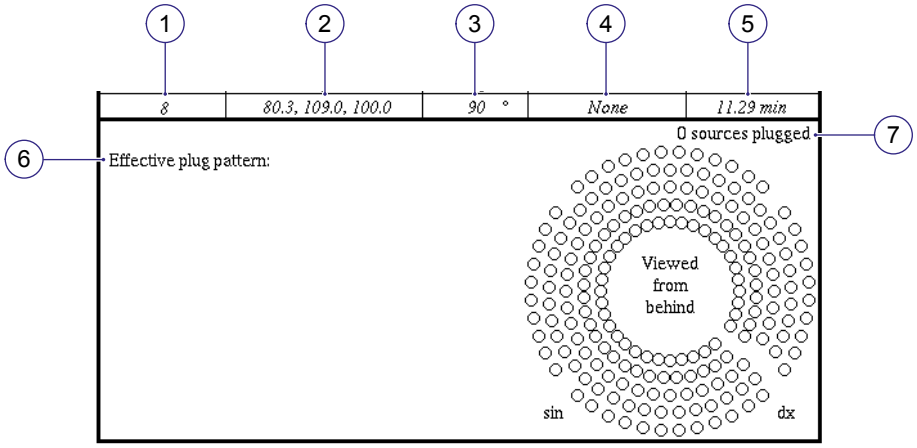
The lower part of the **Skull Geometry** field contains anterior-right (2) and posterior-left (3) wireframe representations of the patient's skull. The target(s) appears as a cube outline within the skull, and a representation of the nose is shown for orientation purposes.

Description of the Shot field

Note: *This section is valid only for Leksell Gamma Knife® B, C, 4 and 4C.*

If the **Detailed Shots** option is selected in the Include array of the Print dialog then the printed treatment protocol includes a field for each shot entitled **Run X - Step X**. (The **X** denotes variable integer values.)

The **Run X - Step X** fields contain two parts as shown below.



- The upper part of the **Run X - Step X** field is a row of columns containing:
  - **Collimator Helmet**: the diameter of the final aperture in the collimator helmet selected for the shot (1)
  - **Coordinate x, y, z**: the Leksell® coordinates of the shot, given in mm(2)
  - **Gamma Angle**: the gamma angle of the shot, given in degrees (3)
  - **Plugging**: the plug pattern used for the shot (if any) (4)
  - **Treatment Time**: the duration of the shot in minutes and decimal minutes (5)
- The lower part contains plug information.
  - Each separate radiation source that has been plugged for the shot is listed under the heading **Effective plug pattern** (6). The total number of plugged sources is given in the upper right-hand corner (7).
    - If the **Always Plug Pattern** option is selected in the Include array of the Print dialog, or if automatic lens plug patterns are in use, then the lower area also lists the plug pattern for the shot and displays a graphic of the respective collimator helmet. Plugged sources are shown as circles filled in black. Unplugged sources appear as empty circles.

Description of the Target data field

If you select the check box **Target data details**, a section with one table for each target appears. Each table has four columns.

- Column 1 contains info on what is summed up on that particular row.
- Column 2 contains shot name, except for the last row where total number of shots are shown.
- Column 3 contains dose contribution to reference point both in Gy and % of the total dose inside parentheses( ).
- Column 4 contains the distance to the reference point.

At the bottom of the table the reference point is shown. The reference point for a target is defined by the point with the max dose within the target, not taking dose contribution from shots in other targets into account.

Description of the header

A header automatically appears on all pages of the printed treatment protocol. It is located above the line at the top of the page. The header gives the clinic name and the name and version number of the treatment planning application. If the treatment protocol is approved, the approval date and time is also shown.

Description of the footer

A footer automatically appears on all pages of the printed treatment protocol. It is located below the line at the bottom of the page. The footer gives the patient's name and ID number, the page number and the total number of pages of the printout, and the date and time for printing.

5.15.3.2 Description of the printout of the measurement data

The printout of dose measurement data comprises a number of fields of information, depending on the number of separate measurements that you have made.

On the hardcopy printout, measurements always appears in the following order:

- Point measurement data
- Line and 90° line measurement data

- Volume measurement data
- Dose volume histogram measurement data.

If you have not taken a particular type of measurement, then no data is available for the printout and the corresponding field is omitted.

Related Links:

Performing measurements on page 270

Description of the Title field

This field is always present on the printout. It occupies the top part of the first page and consists of two areas.

The left side of the Title field contains the clinic name as entered in the TPS Administrator Tool. In addition, the model of Leksell Gamma Knife® and the version number of the treatment planning application are given.

The right side of the Title field contains the following data:

- the patient's name
- the patient's ID
- the diagnosis of the patient's condition
- the diagnosis code
- the print date
- the name of the operator

Description of the Points field

If included in the printout, the **Points** field shows a line of data for each point measurement that you have taken.

Description of the Line Dose field

If included in the printout, there is a **Line Dose** field for each separate line and 90° line measurement that you have taken.

A **Line Dose** field consists of two parts. The upper part is an array of six (6) columns: Point, X [mm], Y [mm], Z [mm], Distance [mm], and Dose.

The curve of dose (Gy) depending on the relative position along the line (mm) is plotted in the lower part of the **Line Dose** field. The position of the cursor mark on the curve is also shown.

Description of the Volumes field

If included in the printout, the **Volumes** field contains one row for each volumetric measurement. See figure below.

The **Volumes** field consists of the following seven (7) columns:

- Name: the name of each volume.
- Volume: the size of the volume (cm^3).
- Min: the minimum absolute dose (Gy) or minimum relative dose (%) in the volume, depending on the selected mode (Single/All Targets).
- Max: the maximum absolute dose (Gy) or maximum relative dose (%) in the volume, depending on the selected mode (Single/All Targets).
- Mean: the mean absolute dose (Gy) and its standard deviation of all voxels within the volume or the mean relative dose (%), depending on the selected mode (Single/All Targets).

- Int. Dose: the integrated dose within the volume (mJ). Integrated dose is defined as described in this manual.
- Comment: additional information, including information about the selected dose algorithm.

Related Links:

Integral dose calculation on page 326

Description of the Histogram field

There is a **Histogram** field for each DVH that you have plotted.

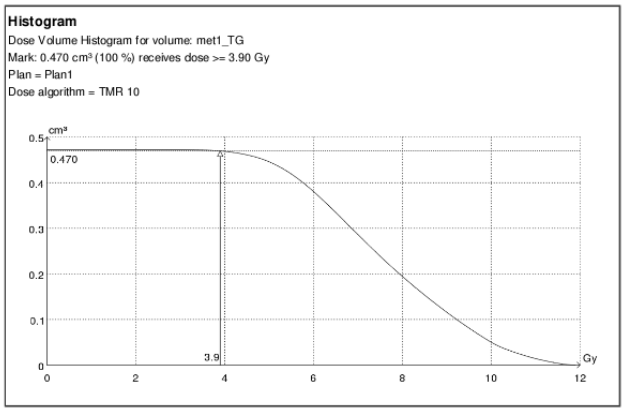


Figure 5.198 The Histogram field

The main area shows the histogram of volume (cm^3) on the y-axis and absolute dose (Gy) or relative dose (%) on the x-axis (depending on the selected mode: Single/All Targets). The position of the cursor mark on the DVH is also shown.

5.16 Export of the treatment protocol

The way of exporting the treatment plan differs depending on the model of Leksell Gamma Knife® to be used for the treatment.

5.16.1 Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™: Exporting the treatment protocol

The treatment planning application transfers the treatment plan to a treatment plan database common to the treatment planning application and Leksell Gamma Knife®. The database can store any number of treatment plans to be imported and executed by Leksell Gamma Knife®.

1 Open the patient's file and verify that the treatment plan has been printed.

2 From the **Patient** menu, select **Export Protocol**.

3 The Export Treatment Protocol dialog opens. Depending on the status of the MOSAIQ® connection it can be either a) or b):

	a) The dialog Export Treatment Protocol with MOSAIQ® enabled	b) The dialog Export Treatment Protocol with MOSAIQ® disabled
4	The operator name is preset with the user name of the person who approved the treatment plan. To change the operator name, click in the **Operator name** field and type the new name.	

5	Select an image study. The treatment protocol is exported in the context of a tomographic image study providing a reference coordinate system.	To export the treatment protocol, click **Export**.
6	Optionally edit the **Plan element prefix**. This prefix is used to make the shot names unique in MOSAIQ.	N/A
7	Make your selections in the **Select Objects to Export** frame: – **Include images**: mark the check box to include the image reference with the DICOM RT objects. – **Include Dicom RT dose**: mark the check box to include the dose with the DICOM RT objects. – Click the **Save as default** button if you wish to save the selections as default.	N/A
8	To export the treatment protocol, click **Export**.	N/A
9	If the connections to MOSAIQ® is not working properly an error message is displayed. You must select either option; retry, ignore or cancel the export of the treatment plan. – **Retry** - a new attempt to export the treatment plan is done. – **Ignore** - the connection error to MOSAIQ® is ignored and the treatment plan is exported to the treatment plan database only without updating MOSAIQ®. – **Cancel** - aborts the procedure and no treatment plan is exported.	N/A
	The treatment protocol is transferred to the treatment protocol database common to the treatment planning application and Leksell Gamma Knife® Perfexion™ or Leksell Gamma Knife® Icon™.	

In case you need to export the treatment protocol again to MOSAIQ® due to previous cancellation, perform the above steps.

Note: *The Export button remains disabled (grayed out) until the operators name has been entered into the Operator name field.*

Note: *When using MOSAIQ® to exchange treatment information, the actual treatment plan used for treatment is always the one that is stored in the treatment plan database.*

5.16.2 Leksell Gamma Knife® C, 4 and 4C: Exporting the treatment protocol

The treatment planning application exports the treatment plan via a serial line or USB device to Leksell Gamma Knife® C, 4 and 4C.

1 Open the patient's file and make verify that the treatment plan has been printed.

2 From the **Patient** menu, select **Export Protocol**.

3 The Export Treatment Protocol dialog opens. Depending on the status of the MOSAIQ® connection it can be either a) or b):

	a) The dialog Export Treatment Protocol with MOSAIQ® enabled	b) The dialog Export Treatment Protocol with MOSAIQ® disabled
4	The operator name is preset with the user name of the person who approved the treatment plan. To change the operator name, click in the **Operator name** field and type the new name.	
5	In the **Communication method** field, select the method to be used for exporting the treatment protocol: **Serial Link** or **USB**.	
6	Select an image study. The treatment protocol is exported in the context of a tomographic image study providing a reference coordinate system.	To export the treatment protocol, click **Export**
7	Optionally edit the **Plan element prefix**. This prefix is used to make the shot names unique in MOSAIQ.	N/A
8	Make your selections in the **Select Objects to Export** frame: – **Include images**: mark the check box to include the image reference with the DICOM RT objects. – **Include Dicom RT dose**: mark the check box to include the dose with the DICOM RT objects. – Click the **Save as default** button if you wish to save the selections as default.	N/A
9	To export the treatment protocol, click **Export**.	N/A
10	If the connections to MOSAIQ® is not working properly an error message is displayed. You must select either option; retry, ignore or cancel the export of the treatment plan.	N/A

	– **Retry** - a new attempt to export the treatment plan is done. – **Ignore** - the connection error to MOSAIQ® is ignored and the treatment plan is exported to the treatment plan database only without updating MOSAIQ®. – **Cancel** - aborts the procedure and no treatment plan is exported.	
	The treatment protocol is transferred to the treatment protocol database common to the treatment planning application and Leksell Gamma Knife®.	

In case you need to export the treatment protocol again to MOSAIQ® due to previous cancellation, perform the above steps.

Note: *The **Export** button remains disabled (grayed out) until the operators name has been entered into the **Operator name** field.*

Note: *When using MOSAIQ® to exchange treatment information, the actual treatment plan used for treatment is always the one that is stored in the treatment plan database.*

Note: *In case of serial line communication, if you try to export a treatment protocol before the previous treatment has resulted in an imported log file indicating a completed treatment, the treatment planning application issues a warning. Before you carry out the export, make sure that Leksell Gamma Knife®, model C, 4 or 4C is ready to receive the new treatment protocol.*

5.16.2.1 Import of the treatment log file

The treatment planning application does not currently provide a user interface for accessing this information, but it is used internally for monitoring the status of the exported treatment plans.

- The monitoring function is only used to warn if the previously exported treatment plan has not been completed upon exporting a new plan, irrespective if it is for the same or another patient.
- The information in the treatment log file does not affect the state of the original plan nor any subsequent copies of the original plan in Leksell GammaPlan®.

A log file consists of:

- demographic information about the patient (name, patient id, diagnosis, treatment date)
- comments by the operator about any problems encountered during treatment
- the result of the treatment, including completion status of each run and a detailed log of all treatment performed on the patient.

After a treatment is finished in Leksell Gamma Knife®, the treatment log file can be imported to the treatment planning application either through the serial line or by a USB device.

5.16.2.2 Import of the treatment log file over a serial line

If a serial line is connected to Leksell Gamma Knife®, the treatment log file is imported automatically to the treatment planning application.

5.16.2.3 Importing the treatment log file from a USB device

1 With the USB device with the treatment log file connected to the workstation, choose **Import Log** from the **Patient** menu.

The Import Treatment Logs dialog opens.

2 To import the treatment log file, click **Import**.

The treatment planning application processes and copies the first treatment log file found on the USB device, and then deletes this file from the USB device.

3 The process described in step **2** continues until all treatment log files stored on the USB device have been imported by the treatment planning application.

4 When importing the treatment log there are several circumstances under which error dialogs may be displayed. These are self-explanatory.

5.16.3 Leksell Gamma Knife® B: Exporting the treatment protocol

1 To export the treatment protocol for Leksell Gamma Knife® B, do a printout.

5.17 General facilities

5.17.1 Obtaining application information

1 From the Help menu, select **On Application**.

The *Leksell GammaPlan® Online Reference Manual* opens.

5.17.2 Obtaining program version information

1 From the **Help** menu choose **On Version**.

The splash screen opens. It gives details of the version of the treatment planning application that you are running.

5.17.3 Snapshots

The treatment planning application includes a feature that allows you to capture digital snapshots of the open workspace. The snapshots:

- Are stored with the examination
- Can be printed to form a permanent record of a particular treatment planning activity
- Can be saved to a USB device.

5.17.3.1 Taking a snapshot

1 With the workspace in view, click the **Snapshot** button in the Toolbar, or from the **Tools** menu, select **Snapshot**.

The Snapshot dialog opens:

Figure 5.199 The Snapshot dialog

The **Snapshot selection** field lists all snapshots that have been taken. They are listed in the order that they were taken.

2 To look at a snapshot on screen, highlight the snapshot to be viewed.

3 Click **View**.

A window opens displaying the snapshot.

4 To take a snapshot, click **Take**.

The Snapshot dialog closes and the screen is refreshed.

Note: *It is also possible to take snapshots using the Snapshot icon in the main menu, or by using keyboard shortcut <CTRL>+<P>.*

5.17.3.2 Saving a snapshot

1 Select the snapshot you would like to save to a USB device.

Note: *Only one snapshot can be saved at a time.*

2 Connect the USB device to the workstation.

3 Click **Save**.

4 Enter a file name.

a Supported characters are [a-z][A-Z][0-9][Space . /].

b Unsupported characters are removed from the name.

5 Click **OK**.

The snapshot is now copied to the USB device.

6 Disconnect the USB device.

5.17.4 Exporting the debug log

The treatment planning application allows the user to export a so-called debug log in the event of a software problem with the application. The debug log file contains the trail of events which lead up to the problem.

1 Connect a USB device to the workstation.

2 Click **Export Debug Log** on the Desktop menu on the taskbar.

The debug log is now copied to the USB device.

5.17.5 DICOM server configuration

Note: *This functionality is only available if the system is licensed for remote DICOM Query and Retrieve or DICOM RT functionality.*

In the Configure DICOM Server dialog you can:

- Configure the AET for Leksell GammaPlan®on the specific workstation,
- Add/edit/delete external DICOM server entries,
- Set the external DICOM server to use by default in the Import DICOM dialog (note that there is no default server preference for the Export DICOM dialog.

Note: *If the workstation AET has not been configured it will not be possible to add or modify the list of external DICOM servers. Also, it will not be possible to import from or export to remote DICOM servers if the workstation AET has not been configured.*

5.17.5.1 Accessing the DICOM server configuration

1 To open the configuration dialog, select **Configure DICOM** in the **Patient** menu.

The Configure DICOM Server dialog opens.

The frame **Local Application Entity Title** displays (when configured) the local AET and contains a **Configure** button.

The DICOM server frame contains the columns:

– **Default import**: Check box for marking the server that is automatically selected default when opening the DICOM Export dialog. If only the DICOM RT functionality is activated, the column and check box are not applicable and are not shown in the dialog.

– **Name**: A name identifying the server. The name shows up in the DICOM import and DICOM Export dialogs. This is only a descriptive name used within the treatment planning system - it is not needed for the actual DICOM communication.

– **AET**: The DICOM Application Entity Title to which the data is sent.

– **IP**: The IP address of the server.

– **Port**: The TCP/IP port to use for the communication.

The button frame of the dialog contains the following six push buttons:

– **New**, **Delete**, **Edit**, **Test**, **Close** and **Help**.

Configuring the local AET

1 In the Configure DICOM Server dialog, click **Configure**.

The Configure AET dialog opens.

2 Enter the local AET parameter.

3 Click **Save**

Adding a new DICOM server

1 In the Configure DICOM Server dialog, click **New**.

The DICOM server dialog opens.

2 Enter the parameters for the connection:

- **Name**: Name used to identify the DICOM server.
- **AET**: The DICOM Application Entity Title of the DICOM server.
- **IP Address**: The IP address of the DICOM server.
- **Port**: The TCP/IP port number to use for the connection.

3 Click **Ok**.

4 Click **Test** to test the connection to the server.

A DICOM C-ECHO message is sent to the server and the result of the test is displayed.

5 Click **Edit** to edit the parameters if necessary.

6 Select the check box in the **Default** column for the DICOM server that is automatically pre-selected when opening the DICOM Import dialog.

7 If the DICOM server does not support C-Get but only C-Move, it is necessary to configure the local AET, IP address and Port (50001) of the treatment planning workstation on the server side for the image import to work. The local AET is displayed at the top of the Configure DICOM Server dialog. Refer to *Configuring the local AET*. The IP address is the external router address or the IP address of an external secondary workstation.

Note: *Requirements for the AET are: A string of characters that identifies an Application Entity with leading and trailing spaces (20H) being non-significant. A value consisting solely of spaces shall not be used. Default character repertoire excluding character code 5CH (the BACKSLASH "\" in ISO-IR 6), and control characters LF, FF, CR and ESC. 16 characters maximum.*

Performing other functions

Obey the following instructions to perform other functions in the Configure DICOM Server dialog.

1 To delete a server from the list, select the applicable check box and click **Delete**.

2 To close the dialog, click **Close**.

3 To open the *Online Reference Manual*, click **Help**.

5.18 System hardware and software

5.18.1 System hardware

The hardware platform used by the treatment planning application is based on standard personal computer workstation technology.

The system can be configured for use with one or more planning workstations, see the figure below. At a Leksell Gamma Knife® Icon™ site, the primary workstation is placed in the treatment room and used during treatment. High resolution color monitors are required for the treatment planning application system. USB-connected hard disks are used as backup devices for patient data and images. Postscript printers (black and white or color) can be used for printing from the treatment planning application.

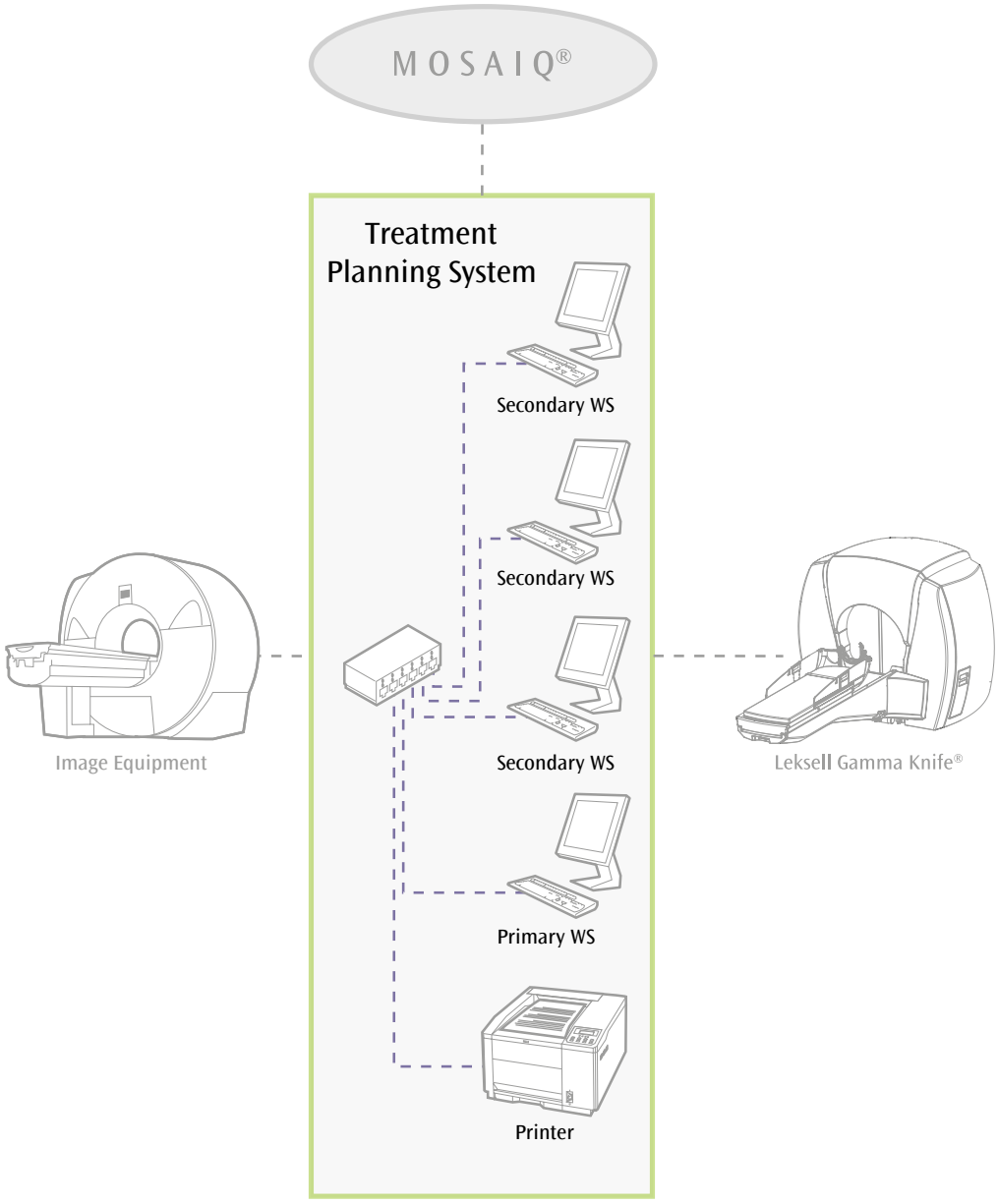


Figure 5.200 Overview of the treatment planning system: illustration with Leksell Gamma Knife® Perfexion™

The personal computer workstation is designed to operate within recommended environmental guidelines. Details of these guidelines are provided in the workstation shipping documentation that accompanies the computer on delivery.

CAUTION 5.2

Failure to maintain adequate environmental conditions may invalidate the service agreements for the personal computer workstation. It is therefore strongly recommended that these requirements be met. If necessary, obtain advice from Elekta.

5.18.2 System software

The software is based on a customized CentOS operating system adapted to be used by the treatment planning application.

5.18.2.1 Manipulation of Leksell GammaPlan® files

No user configurable files are present on the workstations. All system configuration is performed via the Treatment Planning System Administrator Tool.

WARNING 5.39

Do not amend or otherwise modify the treatment planning application software files. The configuration, naming and content of the program files delivered by Elekta are essential for the correct operation of the system. All warranties for the treatment planning application are void and Elekta will not accept responsibility for the treatment planning application if the software files are modified by users.

5.18.2.2 Software and data integrity protection

The integrity of the treatment planning application files and critical data stored in the system, such as patient data and essential system configuration data, is protected from unauthorized changes with checksum mechanisms. These mechanisms will prevent usage of applications or data that has been modified due to unauthorized changes.

— Blank page —

A Mathematical modeling

— Blank page —

1.1 Introduction to mathematical modeling

This appendix discusses the mathematical processes employed by the treatment planning application to produce diagnostic images and treatment plans. Extensive detail is given with regard to the transformation of coordinates from image sources into the internal stereotactic space within the program. The calculations that plot isodose levels and irradiation times are also discussed.

The treatment planning application includes mathematical modeling that permits users to accurately simulate and plan treatment sessions in two and three dimensions. The modeling is based on internal algorithms designed to provide rapid and reliable calculations. In addition, the algorithms facilitate the accurate transformation of magnetic resonance and computer tomography images into the treatment planning application, permitting the software to fully interact with other imaging systems.

The formulae included in this section offer an appreciation of the diagnostic and treatment software in the treatment planning application. It should be noted, however, that these calculations are integral to the program and, while the relevant source data are present, the calculations are automatically executed in software and are thus transparent to users. Nevertheless, the full calculations are given here as additional information to promote confidence when using the treatment planning application.

The treatment planning application is a software common to Leksell Gamma Knife® Perfexion™, Leksell Gamma Knife® Icon™, and Leksell Gamma Knife® B, C, 4 and 4C. From a radiophysical point of view there are many differences between the different types of treatment units and these differences by necessity imply that the dose algorithms differ. In this appendix the differences are clearly pointed out and separate sections are devoted to the more complex modeling of Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™. Also, different sections are devoted to TMR Classic and TMR 10 and the differences between them.

1.2 Coordinate systems

The algorithms employ a number of spatial coordinates that are used in the treatment planning application (X,Y,Z) and Leksell Gamma Knife® (P,Q,R), and are used to produce two and three dimensional images and provide treatment plans.

The system of coordinates illustrated in the figure below is known also as the focus system or the beam system. The coordinate axes are denoted by P, Q and R. The origin of the coordinate system is in the focus of the radiation unit. The R axis of Leksell Gamma Knife® is directed into the radiation unit along the couch, C.

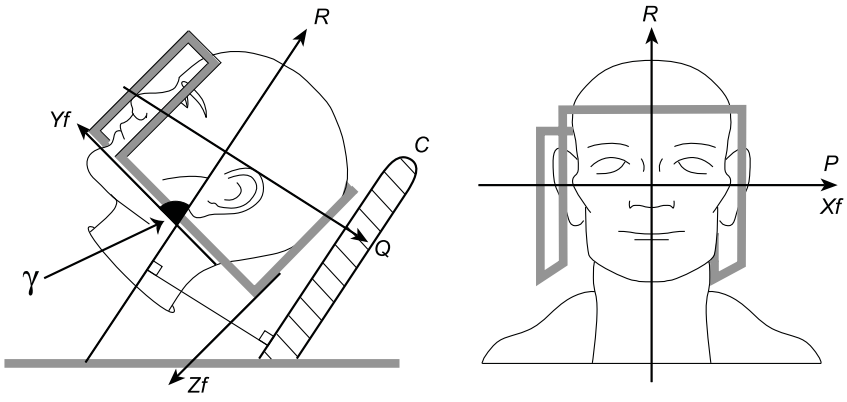


Figure 1.1 Leksell Gamma Knife® coordinates

As the left image shows in the figure above, the gamma angle is defined as the angle between the R axis and the X-Y plane of the coordinate frame. It is set mechanically when fixating the coordinate frame to the Leksell Gamma Knife® C collimator helmet or to the Leksell Gamma Knife® Perfexion™ or Leksell Gamma Knife® Icon™ coordinate frame fixation adapter.

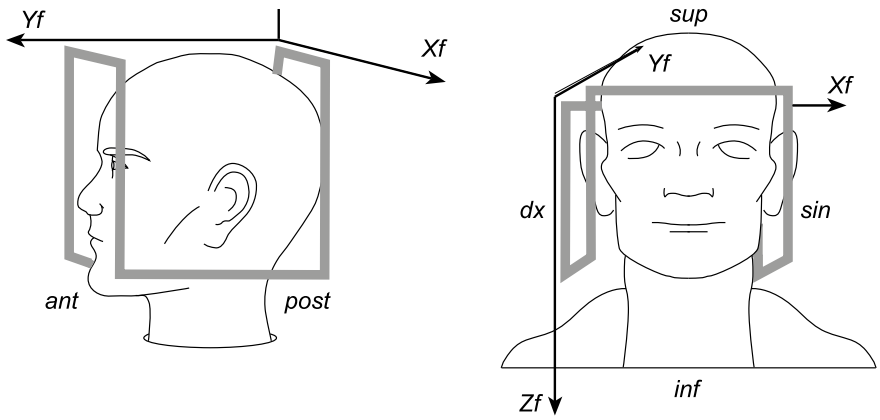


Figure 1.2 Leksell® Coordinate Frame G

The coordinate frame is denoted by coordinates Xf, Yf and Zf, see figure above. The origin of these coordinates is outside the posterior/superior right-hand corner of the coordinate frame. The center of the coordinate frame has the following coordinates:

Xf = 100, Yf = 100, Zf = 100

Related Links:

Description of Leksell® Coordinate System on page 40

1.3 Dose calculation

1.3.1 Point Dose calculation

The point dose calculations compute the total dose received at any nominated point within the three-dimensional stereotactic space.

The total dose at the nominated point is calculated by adding doses from all the sources that are not plugged. (In Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ individual sources cannot be plugged, instead entire sectors may be blocked.)

For Leksell Gamma Knife® B, C, 4 and 4C

The dose delivered from each separate cobalt-60 source is assumed to be identical. This means that the contribution to the total dose rate at the center of an 80 mm spherical water phantom is assumed to be equal for all the sources.

Thus it is possible to base calculations on measurements obtained from a single-source channel, and superimpose the dose from all other sources.

For Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™

The dose at a point is a linear superposition of the dose from all the sources.

Due to the more complex geometry of Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™, the dose from a single source at a nominated point will be dependent on the location of the source. Sources placed in the same ring are assumed to be identical, that is, their contribution to the dose rate at the center of an 80 mm spherical water phantom is equal.

Sources placed in different rings are not identical since they give different contributions to the dose rate at the center of an 80 mm spherical water phantom.

Thus a more complicated model is required to describe the dose deposition from each source.

1.3.1.1 Dose algorithms

Leksell GammaPlan® has three different dose algorithms:

- TMR Classic (not available for new treatment plans)
- TMR 10
- Convolution.

TMR is the abbreviation of Tissue Maximum Ratio. The two TMR algorithms are based on the assumption that the tissue in the head from a dosimetrical point of view can be approximated with water. Convolution is a commonly used algorithm for dose calculation in radiation therapy. The primary difference between the convolution algorithm and the TMR algorithms is that the convolution algorithm takes tissue heterogeneities in the patient into account and can model dose build-up effects near tissue boundaries.

Related Links:

TMR dose algorithms on page 311

Convolution dose algorithm on page 318

1.3.1.2 TMR dose algorithms

Dosimetry and storage of transverse dose distribution in Leksell Gamma Knife® B, C, 4 and 4C

Each type of collimator has been attached to a single source channel, and the radial dose distribution has been measured. The measurements have been made at a focal distance of 400 mm from the source, with the beam attenuated in an 80 mm spherical water phantom.

Dosimetry and storage of transverse dose distribution in Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™

Each type of collimator has been attached to a single-source channel and the dose distribution has been measured. The measurements have been made at a focal distance that is specific for the collimator. For each collimator size there are five rings and the focal distances are different for each of the rings.

In the experimental set-up, the beams have been attenuated in an 80 mm spherical water phantom where radio-sensitive films are placed, measuring the profile in a plane perpendicular to the beam. The 4 mm collimators have the sources oriented along the symmetry axes of the collimators and the profiles are therefore radial. Because of the asymmetric orientation of the source compared to the symmetry axis of the 8 mm and 16 mm collimators the profiles lack rotational symmetry and are therefore stored as two-dimensional profiles.

TMR Classic and TMR 10

The two dose calculation algorithms are based on some fundamental building blocks. Those are:

- Inverse square law
- Exponential attenuation in water
- Output factors
- Dose profiles.

The inverse square law is a consequence of the divergence of the photon flux of the beam. The number of photons passing a unit area of the beam will decrease as $1/r^2$ where r is the distance to the source.

The exponential attenuation expresses the fact that the photon flux decreases exponentially along the beam due to the interaction of photons with matter implying that the energy deposited, that is the dose, decreases exponentially along the beam.

To mathematically describe the attenuation along the beam, the virtual source focus distance and the linear virtual attenuation coefficient are introduced. These parameters are determined by a least square fitting of Monte Carlo generated deep dose profiles to the calculation model. The photon fluence field from the cobalt-60 sources is shaped in a unique way by the collimators leading to differences in dosimetric characteristics when the energy is deposited in the head of the patient. Therefore the values of the parameters in the inverse square law and exponential attenuation will be collimator size specific for Leksell Gamma Knife® C, 4 and 4C and collimator size and ring specific for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ with its more complex geometry.

The lateral spread of dose is described by the dose profile. Because of the alignment of sources with the collimator channels in Leksell Gamma Knife® C, 4 and 4C, the dose profiles will only be a function of the distance from the beam axis. In Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™, the source is aligned with the collimator channels for the 4 mm collimators. For the 8 mm and 16 mm collimators the sources are tilted compared to the collimator axis and the tilt angle depends on in which ring the source is located. The lack of rotational symmetry leads to the asymmetric profiles and the dose profiles are rather planes than profiles. In Leksell Gamma Knife® C, 4 and 4C the dose profiles are collimator size specific while in Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ the dose profiles are collimator size and ring specific.

The profiles are scaled with the depth with a single parameter denoting the scaling distance. The scaling distance, being closely correlated (but not equal) to the source focus distance, is determined by Monte Carlo simulations.

The narrower the photon beams, the smaller the deposited dose. This dependency on the field size and the dose deposition is described by output factors. The output factors are dimensionless and normalized to the largest collimator sizes. Thus every output factor is less or equal to 1.

The dose algorithm has the same overall structure for Leksell Gamma Knife® C, 4 and 4C, Leksell Gamma Knife® Perfexion™, and Leksell Gamma Knife® Icon™. More complex geometry in Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ results in more parameters than in Leksell Gamma Knife®C, 4 and 4C.

Related Links:

Dosimetry and storage of transverse dose distribution in Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ on page 311

Dosimetry and storage of transverse dose distribution in Leksell Gamma Knife® B, C, 4 and 4C on page 311

Point Dose calculation on page 310

Differences between TMR Classic and TMR 10

The physics models have been further improved in the Monte Carlo simulation code since the introduction of TMR Classic. Also the capabilities of performing more extensive simulations have increased, leading to less statistical uncertainty. Accordingly, the dose profiles as well as the parameters determining the depth dose have been updated in TMR 10.

Furthermore, in TMR 10 there is a unified description of the depth dose in the calculation algorithm for Leksell Gamma Knife® C, 4 and 4C, Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™.

Dose calculation for Leksell Gamma Knife® B, C, 4, and 4C TMR Classic

The dose contribution D_i at the point (X_{ip}, Y_{ip}, Z_{ip}) from a source i to a single isocenter is determined as shown in the figure below:

$$D_i = \dot{D}_i t$$

$$\dot{D}_i = \frac{\dot{D}_{center} \omega_{TMRcl}{}^{c} \left(\frac{d_{TMRcl,vsf}}{d_{TMRcl,vsf} - dz} \right)^2 \exp(\mu_0 (dz + (80 - d_{fei}))) P_{TMRcl}{}^{c}(d)}{201}$$

Figure 1.3 Dose calculation TMR Classic

$\dot{D}_i$	The doserate at the point (X_{ip}, Y_{ip}, Z_{ip}) from a source i
t	Irradiation time
$\dot{D}_{center}$	The dose rate is measured at the center of a 80 mm spherical water phantom with the 18 mm collimator helmet. It includes the exponential attenuation in time due to the decay of the source.
$\omega_{TMRcl}{}^{c}$	The output factor for the specific collimator size
$d_{TMRcl,vsf}$	Virtual source focus distance (where the source is modelled as a virtual point source).
$d_{scaling}$	Scaling distance (dose profile divergence distance)
dz	The distance along the beam axis from the point of focus to the intersection with the line that is perpendicular to the beam axis and connects to the point. Note that dz is positive in the direction towards the beam.
μ_0	The linear attenuation coefficient for primary cobalt energies
d_{fei}	Distance between the focus point and the skull entry point of beam i
$P_{TMRcl}{}^{c}(d)$	Transverse dose at distance d from focus (refer to the previous sub-section). The dose profile is normalized, $P_{TMRcl}{}^{c}(0) = 1$ d is related to the distance r from the point P to the main axis through: $\frac{rd_{scaling}}{d_{scaling} - dz}$

The different collimator sizes have characteristic profiles. From the formula, it can be observed that the problem of determining D_i is resolved by determining dz and d_{fei}.

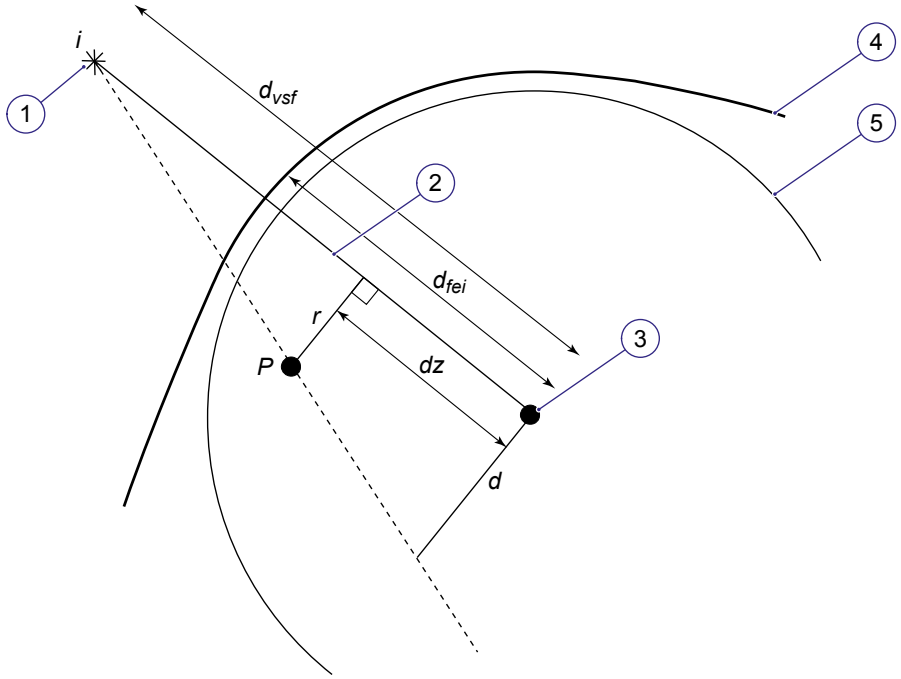


Figure 1.4 Geometry of beam i in skull

(1) Source i

(2) Entry

(3) Focus

(4) Skull boundary

(5) 80 mm spherical water phantom

Dose calculation for Leksell Gamma Knife® B, C, 4 and 4C TMR 10

One major change compared to TMR Classic is an improved description of the depth dose profiles in TMR 10. The linear virtual attenuation coefficient, ${}^{c}\alpha_{TMR10}$, is introduced to more accurately describe the attenuation of a beam along its axis. Note that it is dependent on the collimator size. Also, the numerical values of the parameters and functions are modified due to more accurate Monte Carlo simulations. This is made explicit by introducing the subscript TMR10 in the figure below.

$$D_i = \dot{D}_i t$$

$$\dot{D}_i = \frac{\dot{D}_{center}\,{}^{c}\omega_{TMR10}\left(\frac{{}^{c}d_{TMR10,vsf}}{{}^{c}d_{TMR10,vsf} - dz}\right)^2 \exp({}^{c}\mu_{TMR10}\,dz)\exp(\mu_0(80 - d_{fei}))\,{}^{c}P_{TMR10}(d)}{201}$$

Figure 1.5 Dose calculation TMR 10

$\dot{D}_i$	The doserate at the point (X_{ip}, Y_{ip}, Z_{ip}) from a source i
t	Irradiation time
$\dot{D}_{center}$	The dose rate is measured at the center of a 80 mm spherical water phantom with the 18 mm collimator helmet. It includes the exponential attenuation in time due to the decay of the source.
${}^{c}\omega_{TMR10}$	The output factor for the specific collimator size

$d_{TMR10,vsf}$	Virtual source focus distance (where the source is modelled as a virtual point source).
$d_{scaling}$	Scaling distance (dose profile divergence distance)
dz	The distance along the beam axis from the point of focus to the intersection with the line that is perpendicular to the beam axis and connects to the point. Note that dz is positive in the direction towards the beam.
μ_0	The linear attenuation co-efficient for primary cobalt energies.
$\alpha_{TMR10}{}^{c}$	The linear virtual attenuation coefficient for the specific collimator size.
d_{fei}	Distance between the focus point and the skull entry point of beam i
$P_{TMR10}{}^{c}(d)$	Transverse dose at distance d from focus (refer to the previous sub-section). The dose profile is normalized, $P_{TMR10}{}^{c}(0)=1$ d is related to the distance r from the point P to the main axis through: $\frac{rd_{scaling}}{d_{scaling}-dz}$

Dose calculation for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ TMR Classic

The general form of the expression D_i at the point (X_{ip}, Y_{ip}, Z_{ip}) from a source i to a single isocenter is similar to the expression for Leksell Gamma Knife® B, C, 4 and 4C. The important difference is that as a consequence of the more complex geometry pertaining Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™, a plethora of new parameters are introduced. Now, all model parameters will be collimator and ring specific.

To be explicit, D_i is given by the formula below.

$$D_i = \dot{D}_i t$$

$$\dot{D}_i = \frac{\dot{D}_{center}\omega_{TMRcl}{}^{c,r}\left(\frac{d_{TMRcl,vsf}{}^{c,r}}{d_{TMRcl,vsf}{}^{c,r}-dz}\right)^2 \exp(\mu_{TMRcl}{}^{c,r}(dz+80-d_{fei}))P_{TMRcl}{}^{c,r}(d,\vartheta)}{\sum_{r=1}^{5} n_r \omega_{TMRcl}{}^{c=16,r}}$$

Figure 1.6 Dose calculation TMR Classic

$\dot{D}_i$	The dose rate at the point (X_{ip}, Y_{ip}, Z_{ip}) from the source i
t	Irradiation time
$\dot{D}_{center}$	The dose rate is measured at the center of a 80 mm spherical water phantom with all the sectors having the 16 mm collimator. It includes the exponential attenuation in time due to the decay of the source.
$\omega_{TMRcl}{}^{c,r}$	The output factor for the specific collimator size and ring. It is normalized to the 16 mm collimator in the second ring.
$d_{TMRcl,vsf}{}^{c,r}$	The virtual source focus distance for the specific collimator size and ring.

dz	The distance along the beam axis from the point of focus to the intersection with the line that is perpendicular to the beam axis and connects to the point. Note that dz is positive in the direction towards the beam.
$\mu_{TMRcl}^{c,r}$	The linear virtual attenuation co-efficient specific for each collimator size and ring.
d_{fei}	Distance of the focus point from the skull entry point of beam i
$d_{TMRcl,scaling}^{c,r}$	Scaling distance (dose profile divergence distance)
$P_{TMRcl}^{c,r}(d,\vartheta)$	Transverse dose profile: d is the distance from focus. ϑ is the angle between the direction of the line extending from the source to the point P and the axis perpendicular to the beam for which ϑ = 0. The dose profile is normalized, $\max P_{TMRcl}^{c,r} = 1, \forall c, r$ d is related to the distance from the point P to the main through: $\frac{r d_{TMRcl,scaling}^{c,r}}{d_{TMRcl,scaling}^{c,r} - dz}$
n_r	Number of sources in the ring r

From the previous formula it can be observed that the problem of determining D_i is resolved by determining dz and d_{fei}.

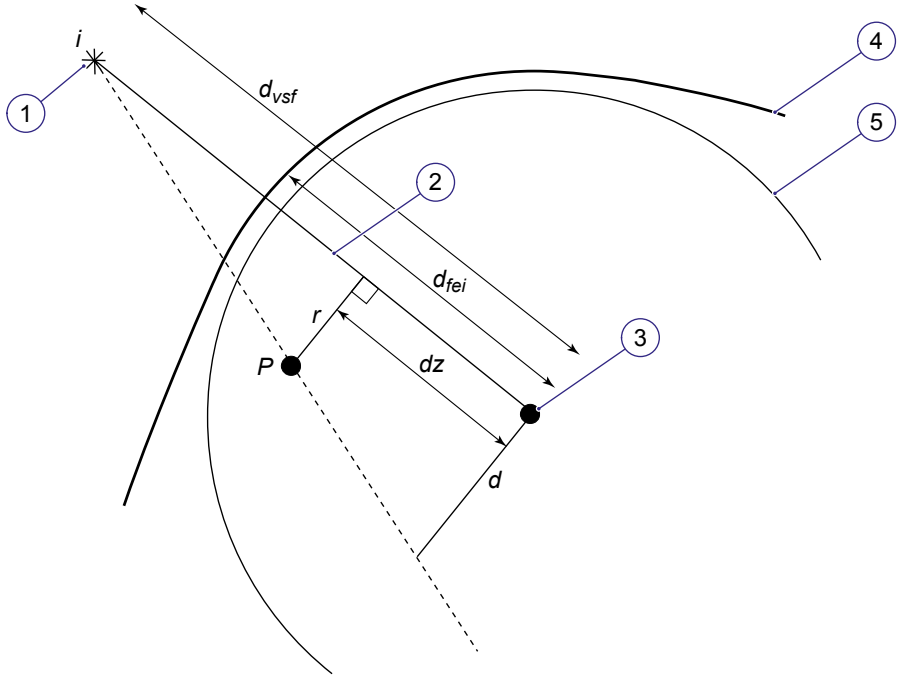


Figure 1.7 Geometry of beam i in skull

(1) Source i
(2) Entry
(3) Focus
(4) Skull boundary
(5) 80 mm spherical water phantom

The normalization in the formula above is deduced by considering the calibration of the dose rate. The calibration is performed by measuring the dose rate in the center of a 80 mm spherical water phantom with all the sectors having the 16 mm collimator set-up. To have $\dot{D}_{center}$ on the left hand side we have to divide by the sum of the dose rate contribution from all 16 mm sources which is exactly what is done in the dose calculation formula.

Dose calculation for Leksell Gamma Knife®Perfexion™ and Leksell Gamma Knife® Icon™ TMR 10

The major difference between the algorithms in TMR 10 and TMR Classic is the expression in the exponential in the dose calculation formula. In TMR Classic the attenuation of the beam is entirely determined by the linear virtual attenuation coefficient while in TMR 10 the dose rate is attenuated by two terms with different attenuation coefficients: in the first term the distance from the skull surface is multiplied with μ_0, which is the linear attenuation coefficient for the photon fluence along the beam and in the second term the distance from the focus point multiplied with the virtual attenuation coefficient for the particular beam. The new formulation gives an improved description of the dosimetry for shots placed far from the center of the head.

$$D_i = \dot{D}_i t$$

$$\dot{D}_i = \frac{\dot{D}_{center}\omega_{TMR10}^{\,c,r}\left(\frac{d_{TMR10,vsf}^{\,c,r}}{d_{TMR10,vsf}^{\,c,r}-dz}\right)^2 \exp(\mu_{TMR10}^{\,c,r}dz)\exp(\mu_0(80-d_{fei}))P_{TMR10}^{\,c,r}(d,\vartheta)}{\sum_{r=1}^{5} n_r \omega_{TMR10}^{\,c=16,r}}$$

Figure 1.8 Dose calculation TMR 10

$\dot{D}_i$	The doserate at the point (X_{ip}, Y_{ip}, Z_{ip}) from the source i
t	Irradiation time
$\dot{D}_{center}$	The dose rate is measured at the center of a 80 mm spherical water phantom with all the sectors having the 16 mm collimator. It includes the exponential attenuation in time due to the decay of the source.
$\omega_{TMR10}^{\,c,r}$	The output factor for the specific collimator size and ring. It is normalized to the 16 mm collimator in the second ring.
$d_{TMR10,vsf}^{\,c,r}$	The virtual source focus distance for the specific collimator size and ring.
dz	The distance along the beam axis from the point of focus to the intersection with the line that is perpendicular to the beam axis and connects to the point. Note that dz is positive in the direction towards the beam.
μ_0	The linear attenuation co-efficient for primary cobalt energies.
$\mu_{TMR10}^{\,c,r}$	The linear virtual attenuation co-efficient specific for each collimator size and ring.
d_{fei}	Distance of the focus point from the skull entry point of beam i
$d_{TMR10,scaling}^{\,c,r}$	Scaling distance (dose profile divergence distance)

$P_{TMR10}^{c,r}(d,\vartheta)$	Transverse dose profile: d is the distance from focus. ϑ is the angle between the direction of the line extending from the source to the point P and the axis perpendicular to the beam for which ϑ = 0. The dose profile is normalized, $\max P_{TMR10}^{c,r} = 1, \forall c, r$ d is related to the distance from the point P to the main through: $\frac{rd_{TMR10,scaling}^{c,r}}{d_{TMR10,scaling}^{c,r} - dz}$
n_r	Number of sources in the ring r

1.3.1.3 Convolution dose algorithm

Convolution is a commonly used algorithm for dose calculation in radiation therapy. For further information, see *A. Ahnesjö and M.M. Aspradakis, "Dose calculations for external photon beams in radiotherapy", Physics in medicine and biology, vol. 44, 1999, pp. R99-155*. The algorithm convolves a field describing the total amount of energy released by primary photons per unit mass (TERMA) with kernels describing how this energy is distributed by secondary particles.

The primary difference between the convolution algorithm and the TMR algorithm is that the convolution algorithm takes tissue heterogeneities in the patient into account and is able to model dose build-up effects close to tissue boundaries. This makes the algorithm more accurate at the expense of longer computational times compared to the TMR algorithm. The patients anatomy is defined by CT images from which relative electron densities are calculated. In order to calculate the dose correctly it is of great importance that the images does not contain severe artifacts and that the electron density calibration is correct.

The algorithm can compute the total dose received at any point within the three-dimensional stereotactic space defined by the frame coordinates. The convolution algorithm is separated into two parts:

- Calculation of dose due to scattering of the primary photons (primary dose)
- Calculation of dose from the higher order scattered photons (scatter dose)

Monte Carlo simulated data is extensively used to pre-calculate data for the convolution algorithm.

The TERMA, primary dose and scatter dose algorithms are discussed in separate sections in this manual.

TERMA calculation

The energy fluence, that is the flow of energy per area unit is calculated by scaling a reference fluence plane due to geometric factors and material heterogeneities. The reference fluence plane is calculated at the center of a water phantom with radius 80 mm using Monte Carlo simulations in a virtual model of the Leksell Gamma Knife®.

For the Leksell Gamma Knife® B, C, 4 and 4C, the energy fluence profiles are rotational symmetric around the beam axis. The profiles are therefore stored in 1D structures.

The energy fluence profiles for the Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™ 8 mm and 16 mm collimators lack rotational symmetry. Therefore the profiles are stored in polar coordinates along 40 directions around the beam axis. The 4 mm dose profiles are handled in the same way as the Leksell Gamma Knife® B, C, 4 and 4C profiles.

To calculate the TERMA from the fluence profiles the following is considered:

- The energy released per unit volume is the linear attenuation coefficient times the energy fluence. The linear attenuation coefficient is proportional to the electron density at the energy release point.
- Due to the divergent nature of the beams, the reference fluence is scaled with a geometrical factor depending on depth and the fluence is scaled with the inverse square law.
- The reference fluence is scaled by an exponential attenuation along the beam. The attenuation coefficient is scaled with the radiological path length of the beam. The path length is calculated by ray tracing a fan of rays for the beam and is stored in a table. The ray tracing samples the electron densities in steps of 1 mm and the spacing between the rays is 3 mm at the focus.
- To calculate the TERMA the expression for the energy released per volume unit is divided by the relative mass density to water.
- The TERMA is set to zero outside an off-axis threshold that depends on the collimator size.
- The TERMA is normalized such that the central value is 1 at the center of an 80 mm water phantom.

The relative (to water) electron densities are defined by a user defined calibration curve and a CT definition. The relative (to water) mass densities are calculated from the electron densities by a bi-linear model that is fitted to biological materials. For further information, see *M. Fippel, "Fast Monte Carlo dose calculation for photon beams based on the VMC electron algorithm", Medical physics, vol. 26, 1999, pp. 1466-75*.

Primary dose

The primary dose is calculated by convolution of an energy deposition kernel with the TERMA. The method is similar to the "CK-method" described in *W. Lu, M. Chen, T.R. Mackie, G.H. Olivera, and P.J. Reckwerdt, "Accurate convolution/superposition for multi-resolution dose calculation using cumulative tabulated kernels", Physics in Medicine and Biology, vol. 50, 2005, pp. 655-680*.

The kernel is pre-calculated by a Monte Carlo simulation forcing primary photons to interact at a point and tracing the scattered electron in a homogenous water material. The kernel describes the energy distribution from charged particles set in motion by primary photons interacting at a point. Alternatively it describes the amount of energy received at a point from photon interactions in the surroundings of that point. The latter is used in this algorithm.

The following assumptions are made:

- The electrons travel in straight lines between the interaction point and the dose deposition point.
- The radiological path lengths are assumed to be proportional to the average electron density between the interaction point and the dose deposition point. The radiological lengths are calculated with ray tracing where the electron densities are sampled in steps of 0.5 mm.
- The kernel is discretized in spherical coordinates in 8 polar angles around the beam axis and 7 azimuthal angles.
- The value of the linear attenuation for the TERMA at the dose calculation point is used for all the surrounding interaction points.
- The kernel is always directed along the central beam axis i.e. there is no kernel tilting due to divergent beams.

Scatter dose

The relative dose rate along the beam axis from scattered radiation is calculated by convolving the TERMA along the beam axis with a scatter kernel. The scatter kernel is found by least squares fitting of a double exponential to the kernels in an inverse convolution problem. The scatter kernel is pre-calculated and stored in tables used by the algorithm.

The convoluted relative scatter dose along the beam axis is used to scale pre-calculated scatter dose profiles perpendicular to the axis and normalized to 1 at the central point. The depth scatter dose curve and the scatter dose profile are both pre-calculated using Monte Carlo methods in an 80 mm water phantom.

The following approximations and considerations are made:

- One lateral profile and one kernel are used for each collimator size.
- The convolution is performed along the central axis of the beam.
- The size of the scatter dose profile is scaled with a geometric factor depending on the distance to the source.
- The kernel is not scaled due to tissue heterogeneities between the interaction points and the dose deposition point.
- The dose deposition at a point is scaled with the relative electron density to water and the inverse relative mass density to water at that point.

The relative mass and electron densities are defined in the same way as for the primary dose.

Other considerations

The calibration dose rate in a homogeneous water sphere is determined by a measurement of the largest collimator size (16 mm for the Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™, and 18 mm for the Leksell Gamma Knife® B, C, 4 and 4C). A calibration factor relates the measured calibration dose to the calculated dose. In addition to the calibration factor an output factors relates the dose for the largest collimator to the other collimators.

Convolution Dose calculation for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™

The dose contribution $D_{i,tot}$ at the point $\bar{r} = (X_{ip}, Y_{ip}, Z_{ip})$ from a source i to a single iso-center is determined as shown below:

Table 1.1 Convolution dose calculation

$$D_i(\bar{r}) = \dot{D}_{center} \frac{\omega^{c,r}}{\sum_{r=1}^{5} n^r \omega^{c=16,r}} (d_{i,pri}(\bar{r}) + d_{i,sca}(\bar{r}))t$$

, where

$$d_{i,pri}(\bar{r}) = \frac{\eta\ (\bar{r})}{\rho(\bar{r})} \iiint T^{c,r}(\bar{s})\rho(\bar{s})c^2 h_{pri}(c(\bar{r}-\bar{s}))d^3s$$

, with

$$T^{c,r}(\bar{s}) = \frac{\eta(\bar{s})}{\rho(\bar{s})} g_{dz}^2 \exp(\mu_0(80 - d_{rad}))\Psi^{c,r}(d,\vartheta)$$

and

$$d_{i,sca}(\bar{r}) = P_{sca}^c(d)\frac{\eta(\bar{r})}{\rho(\bar{r})} \int T^{c,r}(s)k_{sca}^c(s-z)\eta(s)ds$$

$D_i(\bar{r})$	The doserate at the point $\bar{r} = (X_{ip}, Y_{ip}, Z_{ip})$ from the source i.
t	Irradiation time
$\bar{s}$	Coordinates of the interaction points.

$d_{i,pri}(\bar{r})$	The contribution from the primary, i.e. un-scattered photons to the relative dose rate at the point $\bar{r}$ from the source i.
$d_{i,sca}(\bar{r})$	The contribution from the scattered photons to the relative dose rate at the point $\bar{r}$ from the source i.
$\dot{D}_{center}$	The dose rate is measured at the center of an 80 mm spherical water phantom with all the sectors having the 16 mm collimator. It includes the exponential attenuation in time due to the decay of the source. This factor relates the calculated dose rate with the measured dose rate.
$\omega^{c,r}$	The output factor for the specific collimator size c and ring r. It is normalized to the 16 mm collimator in the second ring.
n^r	The number of sources in the ring r.
μ_0	The linear attenuation coefficient for primary cobalt energies.
$\eta(\bar{r})$	The relative electron density to water at the point $\bar{r}$.
$\rho(\bar{r})$	The relative mass density to water at the point $\bar{r}$ calculated from the electron densities.
d_{rad}	The radiological distance from the source position $\bar{p}_s$ to the calculation point $\bar{r}$, that is $d_{rad} = \|\bar{r} - \bar{p}_s\| \int_0^1 \eta((1-t)\bar{p}_s + t\bar{r})dt$
c	The radiological length between the interaction point $\bar{s}$ and the deposition point $\bar{r}$. It is calculated in a similar way as for d_{rad}.
g_{dz}^2	The inverse square law that models the divergent photon field where $g_{dz} = \left(\frac{d_{sf}^{c,r}}{d_{sf}^{c,r} - dz} \right)$ $d_{sf}^{c,r}$ is the source to focus distance for the specific collimator size c and ring r. dz is the distance along the beam axis from the point of focus to the intersection with the line that is perpendicular to the beam axis and connects to the point, see figure below. Note that dz is positive in the direction towards the beam.
$\Psi^{c,r}(d,\vartheta)$	Transverse fluence profile for the collimator size c and ring r: d = $r_{axis}g_{dz}$ where r_{axis} is the shortest distance between the point $\bar{r}$ and the main axis and g_{dz} is the geometrical factor defined above, see figure below. The fluence profile is normalized, $\max(\Psi^{c,r}(d,\vartheta)) = 1, \forall c,r.$
$T^{c,r}(\bar{s})$	The energy per unit mass released at the point $\bar{s}$ for the collimator size c and ring r.
$T^{c,r}(s)$	The energy per unit mass released along the main axis of the beam at depth s for the collimator size c and ring r.
h_{pri}	The primary kernel. The kernel is generated using Monte Carlo methods and is parameterized in spherical coordinates.

k_{sca}^{c}	The scatter kernel for the collimator size c. The kernel is least squares fitted to a double exponential by solving an inverse convolution problem.
$P_{sca}^{c}(d)$	The scatter dose rate profile. One profile is used for each collimator size c. d = $r_{axis}g_{dz}$ as for the transverse fluence profile. r_{axis} is the shortest distance between the point $\bar{r}$ and the main axis and g_{dz} is the geometrical factor defined above, see figure below. The profiles are symmetric around the beam axis.

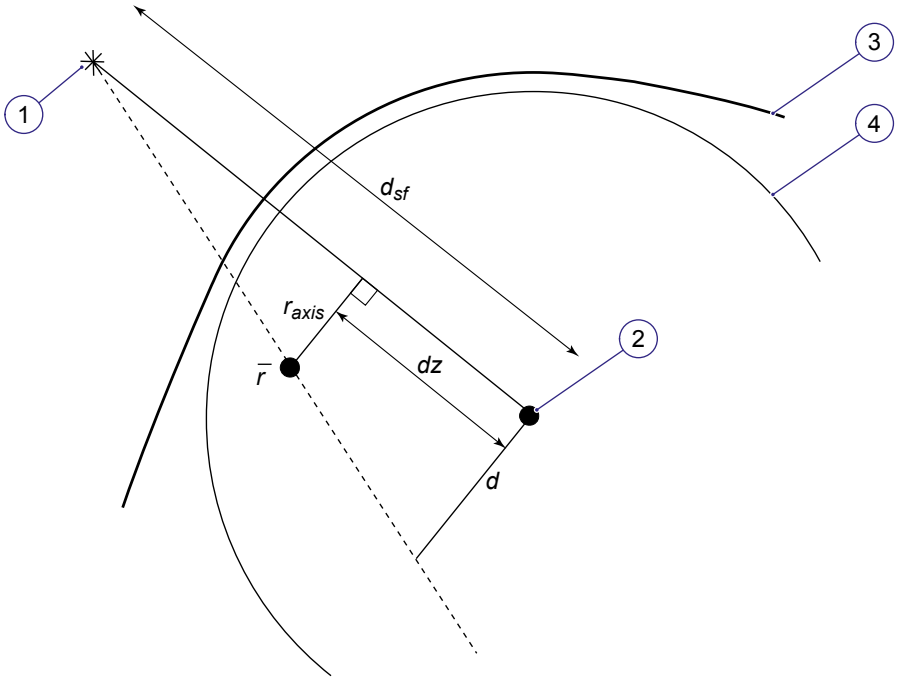


Figure 1.9 Geometry of beam in skull

(1) Source i
(2) Focus
(3) Skull boundary
(4) 80 mm spherical water phantom

Convolution Dose calculation for Leksell Gamma Knife® B, C, 4 and 4C

The dose contribution $D_{i,tot}$ at the point $\bar{r} = (X_{ip}, Y_{ip}, Z_{ip})$ from a source i to a single iso-center is determined as shown below:

Table 1.2 Convolution dose calculation

$$D_i(\bar{r}) = \frac{\dot{D}_{center}\omega^{c}(d_{i,pri}(\bar{r}) + d_{i,sca}(\bar{r}))t}{201}$$

, where

$$d_{i,pri}(\bar{r}) = \frac{\eta(\bar{r})}{\rho(\bar{r})}\iiint T^{c}(\bar{s})\rho(\bar{s})c^{2}h_{pri}(c(\bar{r}-\bar{s}))d^{3}s$$

, with

$$T^c(\bar{s}) = \frac{\eta(\bar{s})}{\rho(\bar{s})} g_{dz}^2 \exp(\mu_0(80 - d_{rad}))\Psi^c(d)$$

and

$$d_{i,sca}(\bar{r}) = P_{sca}^c(d)\frac{\eta(\bar{r})}{\rho(\bar{r})}\int T^c(s)k_{sca}^c(s-z)\eta(s)ds$$

$D_i(\bar{r})$	The doserate at the point $\bar{r} = (X_{ip}, Y_{ip}, Z_{ip})$ from the source i.
t	Irradiation time
$\bar{s}$	Coordinates of the interaction points.
$d_{i,pri}(\bar{r})$	The contribution from the primary, i.e. un-scattered photons to the relative dose rate at the point $\bar{r}$ from the source i.
$d_{i,sca}(\bar{r})$	The contribution from the scattered photons to the relative dose rate at the point $\bar{r}$ from the source i.
$\dot{D}_{center}$	The dose rate is measured at the center of an 80 mm spherical water phantom with the 18 mm collimator. It includes the exponential attenuation in time due to the decay of the source. This factor relates the calculated dose rate with the measured dose rate.
ω^c	The output factor for the specific collimator size c.
μ_0	The linear attenuation coefficient for primary cobalt energies.
$\eta(\bar{r})$	The relative electron density to water at the point $\bar{r}$.
$\rho(\bar{r})$	The relative mass density to water at the point $\bar{r}$ calculated from the electron densities.
d_{rad}	The radiological distance from the source position $\bar{p}_s$ to the calculation point $\bar{r}$, that is $d_{rad} = \|\bar{r} - \bar{p}_s\|\int_0^1 \eta((1-t)\bar{p}_s + t\bar{r})dt$
c	The radiological length between the interaction point $\bar{s}$ and the deposition point $\bar{r}$. It is calculated in a similar way as for d_{rad}.
g_{dz}^2	The inverse square law that models the divergent photon field where $g_{dz} = \left(\frac{d_{sf}^c}{d_{sf}^c - dz}\right)$ d_{sf}^c is the source to focus distance for the specific collimator size c. dz is the distance along the beam axis from the point of focus to the intersection with the line that is perpendicular to the beam axis and connects to the point, see figure below. Note that dz is positive in the direction towards the beam.
$\Psi^c(d)$	Transverse fluence profile for the collimator size c: $d = r_{axis}g_{dz}$ where r_{axis} is the shortest distance between the point $\bar{r}$ and the main axis and g_{dz} is the geometrical factor defined above, see figure below. The fluence profile is normalized, $\max(\Psi^{c,r}(d,\vartheta)) = 1, \forall c, r.$

$T^c(\bar{s})$	The energy per unit mass released at the point $\bar{s}$ for the collimator size c.
$T^c(s)$	The energy per unit mass released along the main axis of the beam at depth s for the collimator size c.
h_{pri}	The primary kernel. The kernel is generated using Monte Carlo methods and is parameterized in spherical coordinates.
k^c_{sca}	The scatter kernel for the collimator size c. The kernel is least squares fitted to a double exponential by solving an inverse convolution problem.
$P^c_{sca}(d)$	The scatter dose rate profile. One profile is used for each collimator size c. d = $r_{axis}g_{dz}$ as for the transverse fluence profile. r_{axis} is the shortest distance between the point $\bar{r}$ and the main axis and g_{dz} is the geometrical factor defined above, see figure below. The profiles are symmetric around the beam axis.

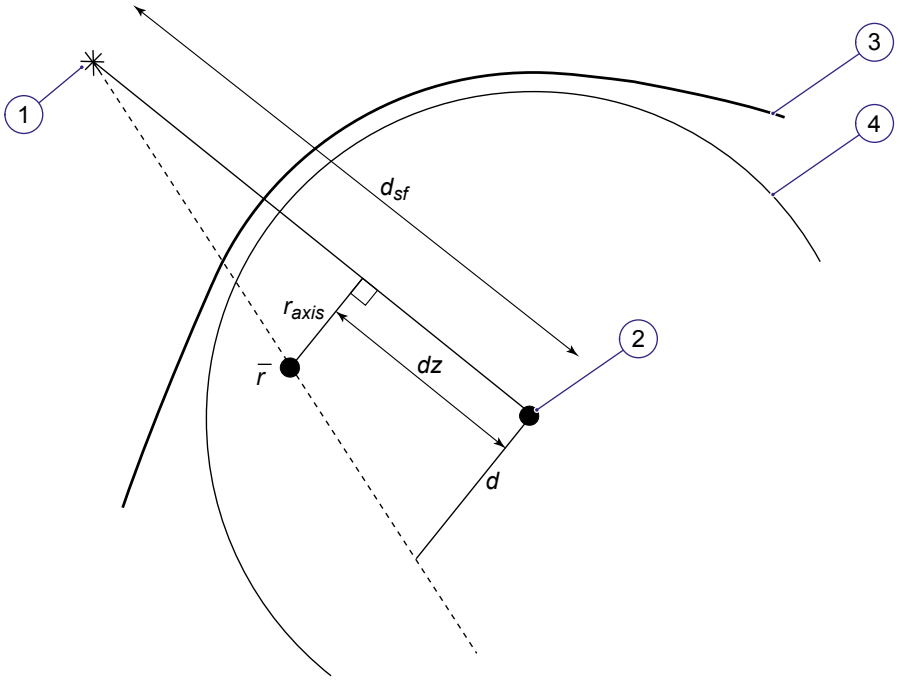


Figure 1.10 Geometry of beam in skull

(1) Source i
(2) Focus
(3) Skull boundary
(4) 80 mm spherical water phantom

1.3.2 Treatment plan dose grid

A single dose grid is used for the entire treatment plan. For performance reasons, the dose in this grid is reconstructed using a per source multi resolution calculation based on the point dose calculation formulas described in this manual. This multi resolution calculation is fine-tuned for the different dose algorithms to give neglible deviations compared to if a point dose calculation would be performed in each dose grid point.

All dose distribution and dose measurements displayed within the application is based on the calculated dose in the treatment plan dose grid with the following exceptions where an exact point dose calculation is always made:

- Point measurements in the measurement dialog
- The target reference point.

Related Links:

Point Dose calculation on page 310

1.3.2.1 Extent and alignment of the plan dose grid

The treatment plan dose grid is set up to cover as much of the skull as possible without containing grid points where dose cannot be reliably calculated with respect to the dose algorithm used.

For a given skull definition, the dose grid points will be the same regardless of the dose algorithm used, except for any grid points not included due to not being possible to be calculated reliably.

The grid is aligned according to the skull data. This means that upon transformation of the plan, e.g. when going from pre-plan to stereotactic definition, the dose grid will be fixed relative to the skull, i.e. the grid points will not move anatomically.

Extent for TMR dose algorithms

For the TMR dose algorithms, the treatment plan dose grid covers the entire skull.

Extent for Convolution dose algorithm

The anatomy is considered unknown inferior of the electron density since we know that there is anatomy there unlike in the other directions outside the electron density. Therefore the treatment plan dose grid is limited in the inferior direction to not include grid points for which the calculation of the primary dose depends on a primary photon interaction point that lies inferior of the electron density. In practice this removes all axial planes containing a grid point within the skull that is closer than 20 mm to the inferior border of the electron density.

1.3.2.2 Per source multi resolution calculation

For each source, the calculation of the dose contribution is divided into two parts with different resolutions, one with lower resolution and one with the chosen calculation resolution for the treatment plan. The lower resolution part consists of low dose with low gradient and is calculated in the entire low resolution grid. The plan resolution part consists of the rest of the contribution. Since a lot of the contribution from a single source within the entire treatment plan dose grid is low dose with low gradient, the remaining dose in the plan resolution part only needs to be calculated in a small subset of the grid points.

The total dose from a shot in the treatment plan dose grid is reconstructed by summing the low dose and low gradient contribution from each source to the low resolution grid which is then upsampled to the treatment plan dose grid using linear interpolation. The remaining dose is then calculated and added for each source (in the subset of points that is needed for that source) to give the total resulting dose. Note that the approximation in this compared to a point dose calculation lies only in the upsampling of the low resolution dose grid. Also note that the low resolution dose grid is aligned with the treatment plan dose grid. So for every low resolution dose grid point, the total dose in the coinciding treatment plan dose grid point will be the same as if a point dose calculation had been made.

Multi resolution calculation for TMR dose algorithms

For the TMR dose algorithms, the resolution of the low resolution dose grid is 4 mm.

The splitting of the TMR dose algorithm into the part with low dose and low gradient, and the other part with the rest of the dose, is done by splitting each dose profile into two parts. The original dose profile, which is expressed in a polar coordinate system, is split into two polar profiles, a base dose profile containing low intensity and low gradient and a dose profile with the

remaining intensity. Summing these two dose profiles gives exactly the original dose profile. The split is based on constraining the base polar profile to have a small maximum slope of 0.005 intensity units / mm (the intensity at the center of the dose profile is 1.0) when going towards the center point in the radial direction.

The base dose profile is used for the low resolution dose calculation, and the other dose profile containing the remaining intensity is used for the plan resolution dose calculation.

Multi resolution calculation for Convolution dose algorithm

For the Convolution dose algorithm, the resolution of the low resolution dose grid is 2 mm.

The Convolution dose algorithm already consists of two parts which gives a natural splitting. The scatter dose in the convolution formula is used for the low resolution dose calculation, and the primary dose is used for the plan resolution dose calculation.

1.3.2.3 Dose statistics calculation

Dose statistics calculations on volumetric objects are performed as follows. First, the bounding box aligned with the treatment plan dose grid is determined for the object. Then, the box is discretized into a measurement grid with a resolution that will give at least 1000000 grid points. This measurement grid is constrained so that all grid points in the treatment plan dose grid that lie within the bounding box will have a coinciding point in the measurement grid. The dose in the measurement grid is then calculated by linear interpolation from treatment plan dose grid, and the volume is voxelized according to the measurement grid.

Note that the above guarantees that all treatment plan dose grid points within the object will be part of the measurement calculation without interpolation.

1.3.2.4 Integral dose calculation

The integral dose is the volume integral of the dose deposited in the skull of the patient:

Integral dose = $V\rho\overline{D}\ [mJ]$

where $\overline{D}$ equals the mean dose to the volume of the skull *V*, assuming for simplicity that the entire volume is taken as water equivalent ρ=1 g/cm^3.

1.4 The accuracy and requirements of the TMR10 and Convolution dose algorithms

A radiosurgical beam being used to deliver a high dose to a target volume in a single fraction, requires a high degree of both geometrical and dosimetrical accuracy. There are several methods that can be used to compare dose distributions. The simplest is to compare two dose-distributions by looking at the difference in each voxel. The dose distributions from Leksell Gamma Knife® with steep gradients (up to 40%/mm in the penumbra) may result in that small spatial deviations translate into large deviation in dose, which may still be acceptable. Therefore, a method that considers deviations in both the dose and spatial domains is more appropriate. The IAEA-TRS430 discusses criteria of the acceptance of dose algorithms, the acceptable dose deviation and spatial deviation in various regions of a radiotherapy beam. Commonly used criteria vary from 2-5% dose deviation and a 2-5 mm distance to agreement (DTA)[2]. Requirements of a radiosurgical beam can also be defined in the same way but needs to be stricter in the spatial domain. However, for non-reference situations and complex geometries the

[1] "Technical Report Series 430", International Atomic Energy Agency, Vienna, 2004.
[2] "Technical Report Series 430", International Atomic Energy Agency, Vienna, 2004.

experimental uncertainties means that slightly higher tolerances in the dose requirements must be allowed[3,4].

Two interesting methods that apply requirements in both the dose and spatial domain are the γ-index method[5] and the Maximum Allowed dose difference method (MADD)[6]. The outcome of these methods is a binary Pass/Fail map of all the voxels in a volume based on a Normalized Dose Difference (NDD) Calculation, that combines the merits of both the MADD and the γ-index method. Here, the MADD method will be the choice of verifying the requirements imposed on the dose algorithms. In the calculation volume there will in general be a small fraction of the total number of voxels failing to adhere to the requirements, but as long as the failing volume is less than a few percent of the total volume the result is acceptable[7].

The following discussion is made to describe a method that can be used to determine the acceptance criteria and based on them derive requirements on the dose algorithms in Leksell GammaPlan®. The requirements imposed on an algorithm must reflect the design goals of the specific algorithm. Thus, for an algorithm designed to calculate dose in a homogeneous material such as water or tissue the requirement should reflect only this. If the algorithm is designed for dose calculations in heterogeneous materials the requirement must reflect this type of situations. In Leksell GammaPlan®, the "TMR Classic" and "TMR 10" algorithms are designed for dose calculation in homogeneous geometries, and the "Convolution" algorithm is designed for dose calculation in heterogeneous geometries. The set of requirements will also be balanced between the complexity in the geometry and the uncertainties in the calculations.

To be able to compare dose-distributions one test dose distribution and one reference dose distribution is needed. Each of the dose distributions are normalized to the reference dose value of the calibration geometry i.e.

$$D_T = \frac{d_{Test}}{d_{Test,Calibration}} \qquad D_R = \frac{d_{reference}}{d_{reference,Calibration}}$$

Method of comparison

The method that has been adopted in this report is the Maximum Allowed Dose Difference (MADD) and Normalized Dose Difference (NDD)[8] .

Denoting the Dose Difference map, $DD(r)=D_t(r)-D_r(r)$, where $D_t(r),D_r(r)$ is the test dose distribution and the reference dose distribution, respectively, at a given point *r*. If $|DD(r)| \leq MADD(r)$ (MADD is defined below) at a particular point *r*, by construction the test distribution intersects the acceptance region and the point (or rather the voxel) satisfy the dose requirement.

The acceptance region at *r* is defined by

$$S_\gamma = \left\{ (\Delta r = r' - r, \Delta D = D - D_r(r)) \middle| \sqrt{\left(\frac{\Delta r}{\delta r_0}\right)^2 + \left(\frac{\Delta D}{\delta D_0}\right)^2} \leq 1 \right\}$$

Figure 1.11 Equation 1

[3] "Technical Report Series 430", International Atomic Energy Agency, Vienna, 2004.

[4] "Tolerances for the accuracy of photon beam dose calculations of treatment planning systems", J. Venselaar,*, H. Welleweerd, B. Mijnheer, Radiotherapy and oncology. 60 (2001) 191-201. PMID: 11439214

[5] "A technique for the quantitative evaluation of dose distributions", Low DA, Harms WB, Mutic S, Purdy JA, Med Phys. 1998; 25(5):656-61. PMID: 9608475

[6] "On dose distribution comparison", S.B. Jiang, G.C. Sharp, T. Nelcu, R.I.Berbeco, et al, Phys. Med. Biol. 51 (2006) 759-776. PMID: 16467577

[7] "Technical Report Series 430", International Atomic Energy Agency, Vienna, 2004.

[8] "On dose distribution comparison", S.B. Jiang, G.C. Sharp, T. Nelcu, R.I.Berbeco, et al, Phys. Med. Biol. 51 (2006) 759-776. PMID: 16467577

where δr_0 is the maximum allowed uncertainty in position and δD_0 is the maximum allowed dose difference. S_γ is the same acceptance region used for the gamma-index method[9]. The normalized dose difference (NDD) may then be defined as

$$NDD(r) = \frac{|DD(r)|}{n(r)}$$

Figure 1.12 Equation 2

where

$$n(r) = \frac{MADD(r)}{\delta D_0}$$

Figure 1.13 Equation 3

In low dose regions where the gradient is small $n(r) \approx 1$ and there is no normalization; in high gradient regions $n(r) > 1$ and the dose difference is scaled down as expected. Introducing the following binary pass/fail map

$$I(r) = H(NDD(r) - \delta D_0)$$

Figure 1.14 Equation 4

where $H(r)$ is the Heavyside function. Thus every voxel scores either a 1 or a 0 depending on if the requirement fails or passes in the given voxel. The definition of MADD and thus NDD needs to be extended to allow the requirements $\delta r_0, \delta D_0$ to vary at different spatial points. This is important since the requirements on a dose calculation will be more or less stringent in different regions[10,11]. It shall also be pointed out that other acceptance regions may be defined by altering the definition of S_γ[12].

1.4.1 General requirements and special cases

1.4.1.1 General requirements

The requirements are based on the methodology used in[13,14] using strict requirements for simple geometries and slightly more relaxed requirements for complex geometries.

- For test cases in water, the acceptance criteria δr_0 is 1 mm and δD_0 is 2% or 3% for all dose algorithms, depending on whether the shot is at the center or off-center.
- For more complex test cases, which include dose calculations in the neighborhood of bony or air structures, requirements are only set for the convolution algorithm. The acceptance criteria δr_0 is 1 mm or 1.5 mm and δD_0 is 3% or 5%, depending on the complexity of the geometry.

9 "A technique for the quantitative evaluation of dose distributions", Low DA, Harms WB, Mutic S, Purdy JA, Med Phys. 1998; 25(5):656-61. PMID: 9608475

10 “Technical Report Series 430”, International Atomic Energy Agency, Vienna, 2004.

11 “On dose distribution comparison”, S.B. Jiang, G.C. Sharp, T. Nelcu, R.I.Berbeco, et al, Phys. Med. Biol. 51 (2006) 759-776. PMID: 16467577

12 “On dose distribution comparison”, S.B. Jiang, G.C. Sharp, T. Nelcu, R.I.Berbeco, et al, Phys. Med. Biol. 51 (2006) 759-776. PMID: 16467577

13 “Technical Report Series 430”, International Atomic Energy Agency, Vienna, 2004.

14 “Tolerances for the accuracy of photon beam dose calculations of treatment planning systems”, J. Venselaar,*, H. Welleweerd, B. Mijnheer, Radiotherapy and oncology. 60 (2001) 191-201. PMID: 11439214

1.4.1.2 Special cases

- No requirements are set for air volumes, i.e. air cavities inside and outside the defined geometry. If a calculation voxel has any overlap with an air voxel in the calculation geometry no requirement is set for this voxel. This is checked by investigating the nearest neighbors in the calculation geometry. Air is considered to be volumes with the relative electron density < 0.1.
- For doses 2% ≤ D_{ref} ≤ 10% the dose requirement δD_0 is set 30%. The 10% dose-level is defined from maximum dose-point (100%) in the local calculation matrix.
- For dose levels D_{ref} < 2% no dose requirement is set.
- The buildup region (5 mm) of the calculation is excluded for TMR dose algorithms. It is included for the convolution algorithm.

1.5 Quality assurance

Purpose

This section describes a procedure for how the precision of the dose delivery can be investigated and verified. Various factors may affect the dose distribution, such as, the strength of each radiation source, the exact alignment to the collimator system, and the tolerances to which the collimators are manufactured.

Method

In Leksell Gamma Knife®, with very steep dose gradients and complex geometry, it is recommended to use film dosimetry because of good spatial resolution and low energy dependence. Due to the designs with a large number of sources (201 sources for Leksell Gamma Knife® B, C, 4 and 4C, and 192 sources for Leksell Gamma Knife® Perfexion™ and Leksell Gamma Knife® Icon™), it is not possible to measure and investigate the beams from every single source. For Leksell Gamma Knife® B, C, 4 and 4C, the transmission through the collimator helmet would be too high and more than 50 beams are required to have an excessive transmission of less than 1%. For Leksell Gamma Knife® Perfexion™ andLeksell Gamma Knife® Icon™, it is not possible to use only one beam at all, because they are designed with sectors.

To investigate the precision in dose delivery, it is recommended to test the dose distributions from all beams in a standard geometry at the Leksell coordinate x,y,z = 100 mm for the various collimator sizes available on the treatment unit. The standard geometry is a spherical geometry with 8 cm diameter. It is recommended to use the spherical phantom (article number A0202-02) or the Elekta Dosimetry Phantom (article number 10022942).

For each collimator size to be investigated:

1 Prepare two films to the appropriate size for phantom (and collimator size).

2 In the selected phantom type, mount the film in the center plane of the phantom in the XY plane.

3 Prepare a test plan with the coordinates X,Y,Z = 100 mm, and select an appropriate dose for the film type used (e.g. 5 Gy, Gafchromic EBT type film recommended).

4 Expose the film to the selected dose.

5 Repeat steps **2** to **4** for the XZ plane.

6 Prepare eight films to the appropriate size for phantom (and collimator size).

7 Creation of a dose-intensity calibration curve: In the selected phantom type, mount the film in the center plane of the phantom in the XY plane.

8 Expose to various doses in the range (e.g. 0, 0.5, 1, 2, 3, 4, 6, 8 Gy for Gafchromic EBT type film).

9 Scan the films and measure the intensity profiles along the stereotactic main coordinate axes x,y,z direction through the dose distribution, convert the intensity profiles to dose, and compare with those calculated by Leksell GammaPlan®. The dose profiles in Leksell GammaPlan® are available on the reference data CD.

1.6 Computation of d_{fei} for a skull measured with Skull Scaling Instrument

The distance d_{fei} is calculated with reference to the patient's skull shape, see figure below.

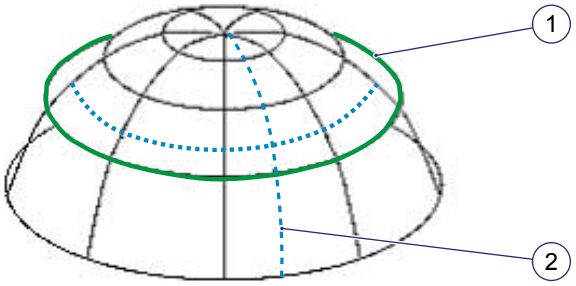


Figure 1.15 Skull geometry

(1) Measured values (2) Calculated values

In the above figure, solid line intersections (illustrated with green color (1)) represent measured values and dashed line intersections (illustrated with blue color (2)) represent calculated values.

The shape of the skull is determined by measuring the radial distance from the center of the stereotactic coordinate frame to the skull boundary. Measurements are taken in a number of directions. The measured directions are assembled in four latitudes of constant angle θ, each having between four and eight measured points that differ in angle γ.

The angles θ and γ are spherical, polar, angular coordinates in a rectangular coordinate system. The coordinate system is parallel to the coordinate frame system but originates at the coordinate frame center.

The radius of the skull can be considered as the distance from the coordinate frame center to the skull boundary. It can be determined in an arbitrary direction (θ, γ) by double cubic spline interpolation using the measured radii described above.

First the radii for the given value θ are ascertained for the two closest meridional planes on each side of the specified γ angle. These radii are then interpolated in angle γ to give the desired radius.

B Dose Optimization Algorithm

— Blank page —

1.1 Overall description

Inverse planning, in the context of radiosurgery and radiotherapy, is a mathematical method to create a treatment plan based on different objectives, for example achieving high target coverage and selectivity to a specified isodose, and, concurrently having a high gradient to ensure low dose to healthy tissue and organs at risk (OAR).

Preventing prolonged beam on time (BOT) is often regarded as an important objective. Usually, several of the objectives are in conflict with each other, leading to the need for making compromises.

Mathematically, the objectives are expressed as objective function terms in a so-called objective function; different compromises can be achieved by varying the weights multiplying the objective terms thereby giving different importance to the different objectives. The aim is to find the lowest value of the objective function given these weights.

In the following sections the details of the optimization method of the Fast Inverse Planning (FIP) are explained.

1.2 Convexity

An important property of FIP is that the optimization problem is convex, see **Figure 1.1**. Convexity is a highly desirable property that allows optimization problems to be solved reliably and efficiently. To ensure convexity the objective terms must be convex functions of dose and the dose must be a convex function of the degrees of freedom (DOF).

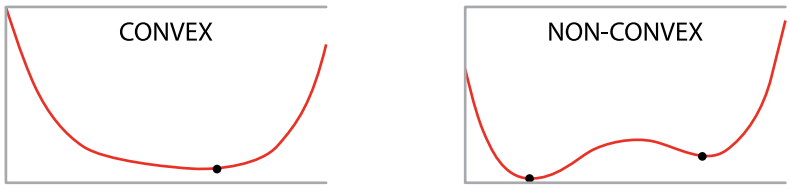


Figure 1.1 A convex problem has a single global minimum for which efficient algorithms exist

In manual planning the relative prescription dose and the absolute isodose level of each target is set and a plan is created by adjusting the following DOF:

- isocenter positions of each shot
- relative weight of each shot
- collimator configuration of each shot

However, basing an optimization on these DOF leads to a non-convex problem which is inherently difficult to solve. The difficulty arises because:

- The objectives are based on relative isodoses instead of absolute doses
- The dose distributions are not convex in shot position
- The collimator configurations are enumerated by integer numbers with no obvious metrics relating them
- The direct use of relative isodoses makes it difficult to simultaneously manage multiple targets and to enforce criteria such as the maximum dose to an OAR.

To achieve convexity, FIP is based on absolute dose and the isocenter positions are fixed during optimization.

1.3 Degrees of freedom

1.3.1 Irradiation times

To give full flexibility to the optimization, irradiation times of every collimator state in every sector in each isocenter position are treated as independent; optimization techniques based on these degrees of freedom (DOF) is referred to as sector-duration optimization[15] . The number of DOF (N_{dof}) is therefore:

$$N_{dof} = 24 * N_{iso}$$

Figure 1.2 Equation 1

where N_{iso} is the total number of isocenters for all the targets.

1.3.2 Isocenter positions

The quality of the optimized plan is dependent on having enough, well located isocenters in the target volumes. This is important since the isocenter positions are fixed in the optimization. In general, the solution to the optimization problem leads to that only a subset of the initial isocenters delivers dose. The setting of the objection function weights determines the particular subset being chosen and therefore, many well distributed isocenter positions are generated in each target to admit a wide range of plans with different objectives to be created.

An algorithm decides on isocenter positions according to two separate geometrical attributes of the target, namely the skeleton and the curvature. The algorithm will consider the bulk properties of the target and the surface curvature to fill the volume with isocenters with different sub-algorithms, see **Figure 1.3**. The sub-algorithms are:

- Center of mass algorithm: An isocenter is positioned at the center of mass of the target
- Skeleton core algorithm: The algorithm extracts the so-called target skeleton, which is a simplified representation of the target volume that preserves morphology. All the points on the skeleton are isocenter candidates and an iterative procedure is applied that covers the skeleton with spheres of a pre-defined radius and then selects the skeleton point within each sphere with the maximum distance to the surface as the isocenter point and discards the rest of the candidates.
- Skeleton bulk algorithm: The algorithm places isocenters in regions in between the skeleton and the target surface. The algorithm iteratively finds the point that is most distant to other isocenters and the target surface and assigns it as an isocenter; isocenters already generated by algorithm 1 and algorithm 2 are considered in this procedure. When there are no more points with a distance greater than a pre-determined constant, the algorithm stops.
- Curvature algorithm: Points on the surface with the highest curvature are iteratively selected as candidates: candidate positions within a certain radius of the selected candidate starting position are excluded from further selection. The isocenters are then placed in the target at distances proportional to the curvature at the chosen candidate points, inwards along the surface normal.

[15] “Automated treatment planning for a dedicated multi-source intracranial radiosurgery treatment unit using projected gradient and grassfire algorithms”, K. Ghobadi, H.R. Ghaffari, D.M. Aleman, D.A. Jaffray, M. Ruschin. Med Phys. 2012; 39:3134–3141.

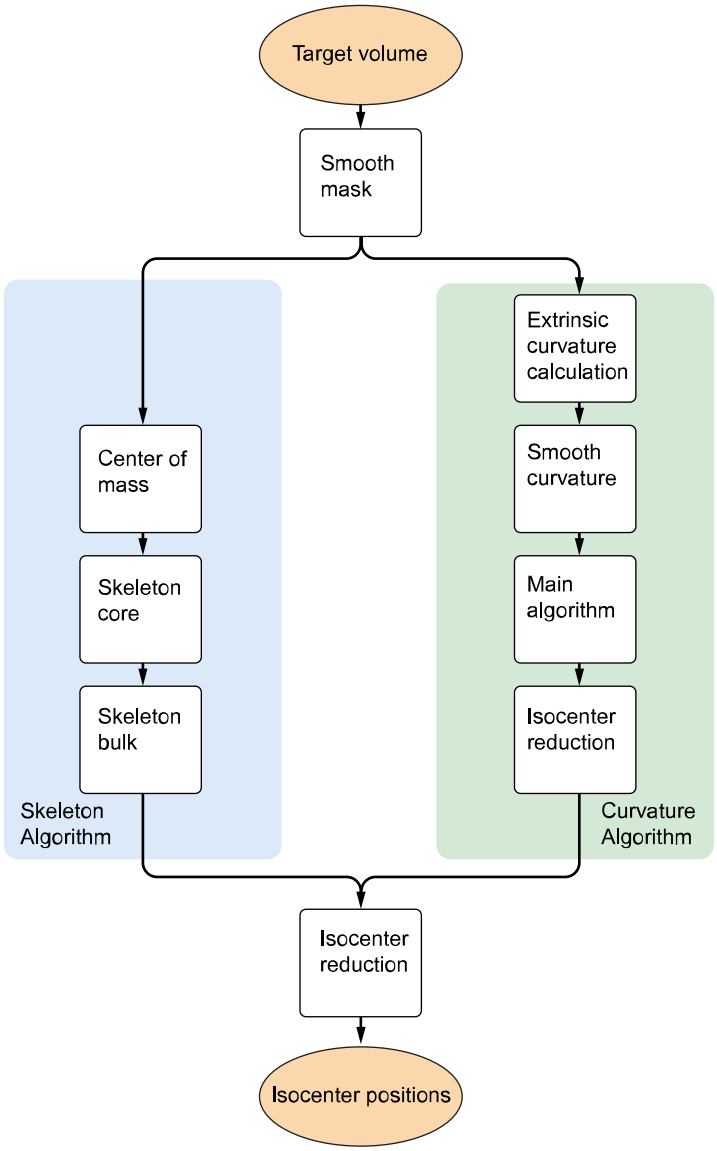


Figure 1.3 Flow chart to determine isocenter positions

The Curvature and Skeleton algorithms may position isocenters close to each other. Isocenters that are too close to any other isocenter will have limited individual influence and will be removed. The order of priority in keeping an isocenter is:

1 center of mass

2 skeleton core

3 skeleton bulk

4 curvature isocenters

See **Figure 1.4** for the different categories of isocenters for a Vestibular Schwannoma.

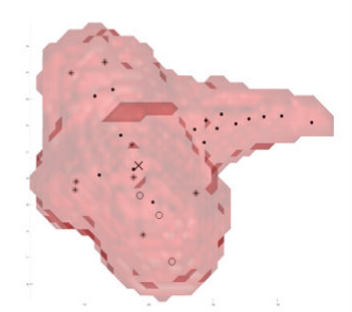


*Figure 1.4 Isocenters in a Vestibular Schwannoma: (a) center of mass, X, (b) skeleton core, (c) skeleton bulk (o), (d) curvature **

1.4 Problem formulation

The optimization problem to be solved is expressed in terms of objectives and constraints. Objectives express important clinical considerations as discussed in section *Overall description*.

The exact priority among these is provided by the user in terms of weights which quantifies the relative importance of the corresponding objectives in the cost function. Constraints are imposed to ensure that the dose is lower than a prescribed level in an OAR and targets.

A major difference between FIP and previous approaches based on sector-duration optimization is that it uses linear programming (LP). LP is a technique for the optimization of a linear objective function, subject to linear equality and linear inequality constraints. There are highly efficient, robust and well-established methods developed to find the global optimum for LP problems.

1.4.1 Geometrical structures

Before going into the details of the objective function and constraints, geometrical structures relevant to the problem need to be defined. In general, there is at least one target but there could be several. There could also be one or several outlined OARs, see **Figure 1.5**. To ensure good selectivity to the target(s), high dose gradients and a small volume of ambient low dose, extra geometrical structures are introduced. A ring, a region circumscribing each target, is defined to control the selectivity and the dose gradient. The ring is automatically constructed by expanding the target volume a predefined distance.

The low dose volume is single global volume surrounding all targets with the intention to suppress large volumes of low dose outside the target. The positioning and size of the low dose volume is automatically determined through a two-stage optimization procedure described below, see section *Finding the low dose volume*.

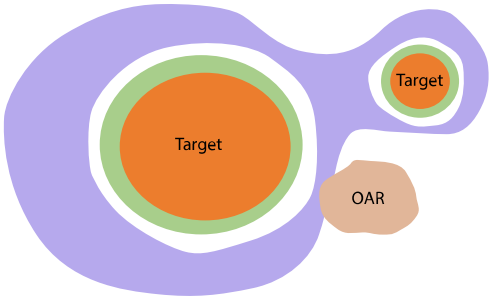


Figure 1.5 Example of a problem setup in the convex inverse planner, with two targets and one OAR . The green area outside each target is the ring volume, and the purple area is the global low dose volume.

1.4.2 Dose calculations

Denoting the irradiation times, t_{isc}, where i indicates the isocenter, s and c the sector and collimator state, respectively, the dose at an arbitrary position r in the head is:

$$d(r) = \sum_{isc} \Phi_{isc}(r, \xi_i)) * t_{isc}$$

Figure 1.6 Equation 2

Here Φ_{isc} (r,ξ_i) is the dose rate at position r from sector s in collimator state c at isocenter ξ_i. The dose can be written as a matrix multiplication of the dose rate kernel with the irradiation times vector and hence is convex in the degrees of freedom.

1.4.3 Objectives and constraints

The objective function to be minimized is a sum of terms that convex terms that promote high coverage, selectivity and gradient index, as well as low dose. Moreover, a BOT-penalization term to enable trade-offs between quality and BOT. The complete optimization model is:

$$\underset{t}{\text{minimize}} \quad f_{obj} = \frac{w_{\text{Ts}}}{S_{\text{tot}}} \sum_{k=1}^{N_{tg}} \left(\frac{S_k}{D_{k,\text{T}} N_{k,\text{Ts}}} \sum_{i=1}^{N_{k,\text{Ts}}} (D_{k,\text{T}} - (\Phi_{k,\text{Ts}} t)_i)_+ \right)$$

$$+ \frac{w_{\text{Ti}}}{V_{\text{tot}}} \sum_{k=1}^{N_{\text{tg}}} \left(\frac{V_k}{D_{k,\text{T}} N_{k,\text{Ti}}} \sum_{i=1}^{N_{k,\text{Ti}}} (D_{k,\text{T}} - (\Phi_{k,\text{Ti}} t)_i)_+ \right) + \frac{w_{\text{R}}}{N_{\text{target}}} \sum_{k=1}^{N_{\text{tg}}} \left(\frac{1}{D_{k,\text{T}} N_{k,\text{R}}} \sum_{i=1}^{N_{k,\text{R}}} ((\Phi_{k,\text{R}} t)_i - D_{k,\text{T}})_+ \right)$$

$$+ \quad w_{\text{LD}} \left(\frac{1}{D_{1,\text{LD}} N_{1,\text{LD}}} \sum_{i=1}^{N_{1,\text{LD}}} ((\Phi_{1,\text{LD}} t)_i - D_{1,\text{LD}})_+ + \frac{1}{D_{2,\text{LD}} N_{2,\text{LD}}} \sum_{i=1}^{N_{2,\text{LD}}} ((\Phi_{2,\text{LD}} t)_i - D_{2,\text{LD}})_+ \right)$$

$$+ \frac{w_{\text{BOT}}}{\sqrt{V_{tot}} * \frac{\sum_{k=1}^{N_{tg}} D_{k,\text{T}}}{N_{tg}}} \sum_{i=1}^{N_{\text{iso}}} \max_s \sum_{c=1}^{3} t_{isc}$$

Subject to

$$\Phi_{k,O} t \le D_{k,O}^{max}, \ \ for\ all\ OAR_k$$
$$\Phi_{k,T} t \le D_{k,T}^{max}, \ \ for\ all\ Targets_k$$
$$t \ge 0$$

Figure 1.7 Equation 4

Table 1.1 Notations

t(=t_{isc})	beam on time for each isocenter position, sector and collimator configuration
w_{Ts}, w_{Ti}, w_R, w_{LD},w_{BOT}	target surface, target interior, risk, low dose, and bot weight, respectively
S_k	surface area of target k
S_{tot}	total surface area of all targets
V_k	volume of target k

v_{tot}	total volume of all targets
N_{tg}	total number of targets
N_{iso}	total number of isocenters
$D_{k,T}$	prescription dose to the target k
$D^{max}_{k,T}$	max dose to the target k
$D^{max}_{k,O}$	max dose to organ at risk k
$D_{1,LD}$, $D_{2,LD}$	threshold dose for the two disjoint low dose regions
$\Phi_{k,Ts}$, $\Phi_{k,Ti}$, $\Phi_{k,R}$ $\Phi_{1,LD}$, $\Phi_{2,LD}$	dose rate contribution from each degree of freedom in the sampling points on the target surface, in the target volume, in the ring volume, and in the two low dose regions, respectively
$N_{k,Ts}$, $N_{k,Ti}$, $N_{k,R}$, $N_{1,LD}$, $N_{2,LD}$	the number of sampling points on the target surface, in the target volume, in the ring volume, and in the two low dose sections, respectively
$(a)_+$=max(a,0)	the maximum value of the variable a and zero

The first two terms contribute to the cost function only if the dose is less than the prescription dose in the surface voxels or in the volume voxels. The reason to separate the target voxels into two sets has to do with subsampling and will be explained more in section Sampling. For now, it is enough to say that more surface than interior voxels are needed to obtain high coverage of the prescription dose.

The third term aims at achieving high selectivity and high dose gradients by penalizing dose exceeding the prescription dose in voxels in the ring region close to the target. The fourth and fifth terms bring down the low dose volume by penalizing dose exceeding the threshold doses in the low dose region, see section *Finding the low dose volume*.

The last term penalizes irradiation times by picking the sector with the longest total beam on time at each isocenter. The effect of this term is to encourage the total beam on time of each sector to be equally long, which is advantageous since they can irradiate simultaneously.

Each of the objective terms include a normalization factor which makes each objective approximately of the same magnitude independently on number of targets, size of targets and rings and prescription dose and dose rate. The purpose is to let the setting of the weights determine the properties of the plan as much as possible: Ideally the same weights, independent of case, should give lead to similar trade-offs. The target weight, low dose weight and the BOT weight are customer adjustable parameters while the ring weight is fixed as is the ratio between the target surface weight and target interior weight.

The final part of the model is optionally adding hard constraint on the maximum dose to each of the organs at risk and targets. The above optimization model is referred to as the primal formulation.

1.4.4 Finding the low dose volume

The low dose volume is determined through a two-stage process. In the first step a model of dose fall-off as a function of the distance from each target is applied. Dose from all the targets is summed and two regions are created:

$$region\ 1 = \left\{r:\ \eta_1 * \min_k D_{k,T} \leq d(r) \leq \eta_2 * \min_k D_{k,T}\right\}$$
$$region\ 2 = \left\{r:\ \eta_2 * \min_k D_{k,T} \leq d(r) \leq \eta_3 * \min_k D_{k,T}\right\}$$
$$\eta_1 < \eta_2 < \eta_3$$

Figure 1.8 Equation 7

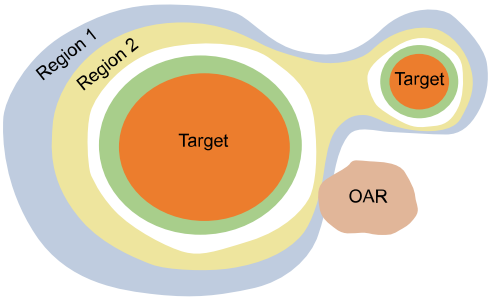


Figure 1.9 Low dose volume divided into two regions

The optimization problem, with approximate description of the low dose volume, is solved and a new dose distribution is derived. Based on this dose distribution the low dose regions are modified according to Equation 7.

1.5 Solving the problem

1.5.1 General considerations

The problem formulated in Equation 4 is a sum of piecewise linear convex functions in t_{isc}. To formulate it in a completely linear form, so called auxiliary variables need to be introduced. Consequently, the number of variables to optimize increases. How much will depend on the number of voxels there are to represent the geometrical structures and the number of isocenters. Moreover, there are many constraints introduced to recast the problem into LP, for details, see Appendix A[16] . The size of this constraint matrix could be of size (10^4,10^4) or larger. Solving the optimization problem could therefore be time-consuming at best but even impossible due to memory limitations. Thus, it is essential to reduce the size of the problem.

1.5.2 Representative subsampling

As a first step, the problem size is reduced by using an approximation referred to as representative subsampling. Representative subsampling is based on the observation that the dose tends to vary smoothly from one voxel to another. The positions are sampled randomly in all the structures. Since the dose gradients are largest close to the surface of the target the sampling is denser on the surface than in the interior. This justifies the introduction of two terms to penalize lack of coverage in Equation 3. For organs with maximum dose constraints only surface points are sampled since, by necessity, the max dose will be obtained on the surface.

The number of sampled voxels is based on the actual volume of the interior and actual area of the surface. A 2cc spherical target will have about the same number of interior sampling points and surface sampling points. For a target of the same volume but with a more complex geometry the number of surface points will be larger. To prevent small targets, for which the target

[16] ”A linear programming approach to inverse planning in Gamma Knife radiosurgery”, J. Sjölund, S. Riad, M. Hennix, and H. Nordström, Med. Phys. 46 (4), April 2019.

surface/volume ratio is high, to have too few sample points there is a fixed minimum number of sample points for them.

It has been found[17], that a subsampling fraction of 10% is enough to reproduce plan quality metrics with high precision for many investigated clinical cases with a standard deviation below 1%. Moreover, in the cases considered, a subsampling of 10% shortens the optimization time by a factor 8–22 compared to using all initial sampling points. Thus, this is a powerful technique to reduce calculation time at only a small expense in quality degradation.

1.5.3 Duality

As pointed out in General considerations, the introduction of auxiliary variables in the primal formulation increases the number of variables. The primal problem, Equation 4, can be written in terms of the auxiliary variables as[18]:

$$\begin{cases} \min_{\lambda} f_{obj} = \gamma^t v \\ A\lambda = \beta \\ \lambda \geq 0 \end{cases}$$

Figure 1.10 Equation 5

Here λ is the set containing the original degrees of freedom, t_{isc}, and the auxiliary variables. A is the constraint matrix, γ is the objective vector multiplying the variables and β is the constraint vector. The matrix A is highly structured; exploiting its structure makes it possible to reduce computation times drastically. This is done by introducing so-called Lagrangian multipliers as so-called dual variables and the problem can then be re-written as an equivalent linear dual problem; since strong duality holds for linear programming problems, the primal and dual problems are equivalent[19] .

The constraint matrix in the dual problem has considerably less elements than A. Many of the constraints in A are mapped into trivial lower and upper bounds restrictions in the dual formulation. The resulting size reduction leads to a drastic performance improvement compared to solving the original primal problem. Moreover, the computational gain due to dualization is entirely complementary to that of representative subsampling: depending on the features of case to be optimized, dualization reduces the computation time by a factor 5–20.

The irradiation times, meaning the solution to the primal problem, are the Lagrangian multipliers in the dual problem and are outputted by the solver together with the dual solution.

1.5.4 Solution algorithm

The optimization problem is solved by the simplex method. This is a solution method that was devised in 1947 by Georg Dantzig. The simplex method a highly efficient algorithms and it is still the standard method employed to solve optimization problems[20].

1.6 Post processing

After the main optimization two post processing are performed to derive the actual shots for the plan.

[17] ”A linear programming approach to inverse planning in Gamma Knife radiosurgery”, J. Sjölund, S. Riad, M. Hennix, and H. Nordström, Med. Phys. 46 (4), April 2019.
[18] ”A linear programming approach to inverse planning in Gamma Knife radiosurgery”, J. Sjölund, S. Riad, M. Hennix, and H. Nordström, Med. Phys. 46 (4), April 2019.
[19] ”Convex Optimization”, S. Boyd, L. Vandenberghe. Cambridge, UK: Cambridge University Press; 2004.
[20] “Origins of the simplex method”, Dantzig, George (May 1987). A History of Scientific Computing.

1.6.1 Shot sequencing

The result of the optimization is a set of irradiation times t_{isc}. To efficiently deliver dose, these sector and collimator state times are sequenced into deliverable shots. This means that t_{isc} is written as a sum of times for shots with different collimator configurations.

The total irradiation time for each isocenter position is determined by the sector that has the longest total irradiation time. In order to minimize the total treatment time, which also includes the time it takes to change collimator size, the smallest possible number of shots is preferred. The sequencing of t_{isc} into shots at a given isocenter i is performed by a so-called greedy algorithm. The algorithm is efficient both in terms of calculation time and finding the smallest number of shots[21] .

1.6.2 Reducing the number of shots

In general, the total number of shots after sequencing is quite large and especially there is a tail of short shots giving only a small contribution to the dose distribution but adds to the BOT. Moreover, shots that are shorter than the shutter time limit will be un-deliverable[22]. This risk is elevated in a fractionated scenario for which the impact of the discarded shots on the dose distribution can be substantial.

To mitigate this effect the following shot discarding strategy is employed:

1 Discard shots with the lowest weight until the accumulated weight removed reaches a specific limit proportional to the maximum weight of all shots

2 Discard shots with beam on time shorter than the shutter time limit

The relative weight is proportional to time but also depends on the size of the shot: a large shot has a larger relative weight than a small shot for equal shot times and thus influences the plan more. Shots are therefore sorted according to their weights and shots with the lowest weights are discarded. Removing shots will inevitably reduce the plan quality. To alleviate this effect, a final optimization is carried out with the remaining, N_s, shots. The same optimization problem as the original, Equation 4, will be solved with the following modifications:

1 The optimization degrees of freedom (DOF) are now the irradiation times t_s of the N_s shots.

2 The beam on time penalization objective, f_{BOT}^{RED}, will simply be a sum of the shot times, and is:

$$f_{BOT}^{RED} = \frac{w_{BOT}}{\sqrt{V_{tot}\frac{\sum_{k=1}^{N_{tg}} D_{k,T}}{N_{tg}}}} \sum_{s=1}^{N_s} t_s$$

Figure 1.11 Equation 9

The number of shots is in general much fewer than the DOF of the original problem which leads to short optimization times for this step. The final step after optimization is to discard shots with irradiation time shorter than the shutter time limit.

[21] It can be shown that the sequencing problem can be formulated as a mixed integer linear problem (MILP) with binary and continuous variables. For a large number of test cases the sequencing algorithm resulted in the same minimum number shots as the MILP for all the cases.

[22] The shutter dose time limit is about 0.1 min.

— Blank page —

C Co-registration algorithm

Section	Title	Page
1.1	**Image co-registration**	345

— Blank page —

1.1 Image co-registration

The image co-registration algorithm is used to find the best rigid transformation between anatomically corresponding positions in two images. The images can be of different modalities and can have different resolution and orientation.

The algorithm is intensity based and consists of two parts: a similarity measure and a numerical optimizer. The similarity measure scores how good a registration transformation is, producing larger values for better registrations. The numerical optimizer tests different transformations to find the one with the maximum similarity measure. The figure below shows a flowchart of the algorithm.

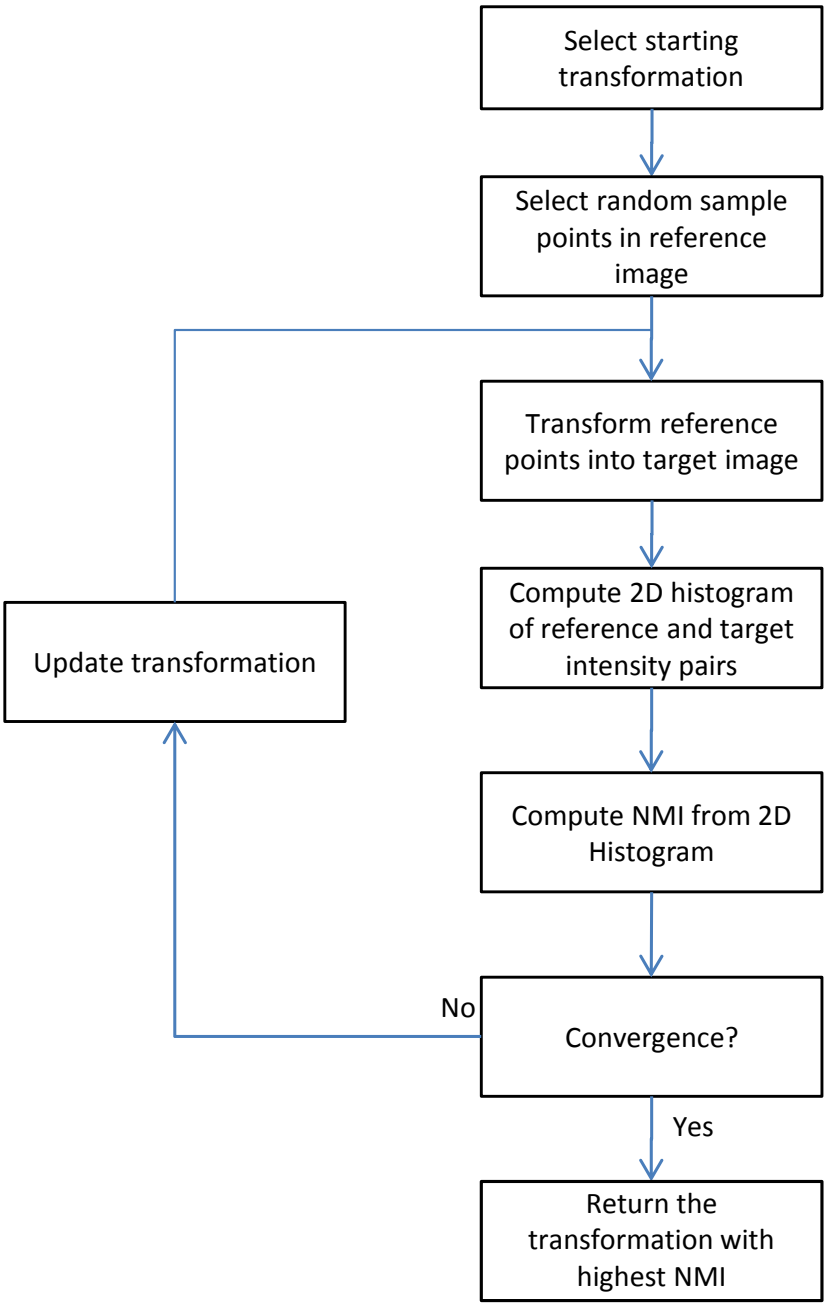


Figure 1.1 Flowchart of the co-registration algorithm

The algorithm is similar to the Mutual Information (MI) based method by Maes et al.[23], but uses an improved version of the similarity measure and a more robust and accurate optimizer, both described below. Maes et al. claim “subvoxel accuracy with respect to the stereotactic reference solution… which makes this method very well suited for clinical applications”. MI based registration methods quickly became the standard for multi-modal registration. A good survey regarding MI based registration of medical images is given by Pluim, Maintz and Viergever [24] .

The similarity measure used is Normalized Mutual Information (NMI), a version of Mutual Information that is less sensitive to the amount of overlap between the images[25] . The MI and NMI metrics work by constructing a 2D intensity histogram, which is similar to a regular histogram but is a function of two variables: the intensities in the reference and target images. For bad registrations, the relation between the intensities in the reference and target image is weak, resulting in a spread out histogram. A good transformation, however, results in a stronger relation between the intensities, producing a more concentrated histogram. MI and NMI is a measure of how strong this relation is and is computed from the histogram.

To construct the 2D histograms, random reference points are selected in the reference image. Randomly distributing the points reduces interpolation (described below) artifacts in the metric. The reference points are then transformed into the target image using the transformation for which the similarity measure should be computed. The intensities at the reference and target points are sampled using an interpolation algorithm called partial volume interpolation, which is similar to regular tri-linear interpolation but has the advantage of not disturbing the similarity measure by introducing new intensity values not present in the original images [26].

The numerical optimizer is a version of Simulated Annealing[27]. It is a global optimizer, meaning that it tries to avoid converging to local maxima. This extra robustness comes at the expense of execution time, since it needs more evaluations of the similarity measure.

The time required is proportional to the number of sample points, but more sample points improves accuracy. Therefore after the registration has converged, a second registration is performed using a much larger number of samples, starting from the registration found by the first registration. The second registration runs much slower per iteration, but because it starts close to the optimum, only a few iterations are needed.

A region of interest (ROI) can be used to limit the volume that influences the result and works by distributing the reference sample points within the ROI instead of within the complete image. The ROI can be used to avoid problematic areas of an image and also to concentrate the sample points to the actual anatomy by cropping large empty areas. Although ROIs can be helpful, small ROIs can have a negative effect by reducing the information that the algorithm has to work with. If no ROI is used, the smallest image study (by volume) is used internally as the reference volume. If the largest image was used as the reference, many samples would be wasted since they would end up outside of the other, smaller image.

Accuracy

As previously stated, the algorithm has been found to give subvoxel accuracy and is well suited for clinical applications[28] . The accuracy can be expected to be similar to framed based registration. As in frame based registration, the accuracy depends on the quality of the images.

[23] F. Maes et al., Multi-modality image registration by maximization of mutual information, IEEE Trans. Med. Imag., 16, 187-198, 1997.

[24] J.P.W. Pluim, J.B.A. Maintz, M.A. Viergever, Mutual-Information-Based Registration of Medical Images: A Survey, IEEE Trans. Med. Image., 22(8), 986-1004, Aug 2003.

[25] C. Studholme, D. L. G. Hill, and D. J. Hawkes, An overlap invariant entropy measure of 3D medical image alignment, Pattern Recognit., 32(1), 71–86, 1999.

[26] F. Maes et al., Multi-modality image registration by maximization of mutual information, IEEE Trans. Med. Imag., 16, 187-198, 1997.

[27] W. H. Press et al., Numerical Recipes in C: the Art of Scientific Computing, 2nd ed., Chapter 10.9, Cambridge University Press, New York, 1992.

[28] F. Maes et al., Multi-modality image registration by maximization of mutual information, IEEE Trans. Med. Imag., 16, 187-198, 1997.

Geometric distortions in MRI images can be significant and can dominate the error in the registration transformation. While the algorithm is very tolerant to intensity artifacts, geometric distortions cannot be compensated for with a rigid registration, and also add to the uncertainty in the registration result itself.

— Blank page —

D Tomographic image model

— Blank page —

1.1 Tomographic image validation visualization model

In the treatment planning application, the image study as a whole is compared to a visualization model, that is, a model of an image stack.

The visualization model is defined as having:

- Images of the same size
- Square pixels, all of the same size
- Equidistantly spaced images
- Images with the same orientation
- Images whose corners are aligned along a line perpendicular to the image plane.

The treatment planning application calculates a transformation between the image study and the visualization model that minimizes the deviations between the corners of the images (given by the image headers) and their corresponding positions in the visualization model.

Given the calculated transformation, the treatment planning application calculates the maximum deviation between the corners of the images and their corresponding positions in the visualization model. This measure is presented as “Deviation from visualization model”.

The treatment planning application also calculates and presents the gap and the overlap.

1.1.1 Definition of image characteristics

1.1.1.1 Slice distance difference (non-equidistance)

The deviation is defined as the difference between the maximum and minimum slice distance. The distance between two image slices is measured in their upper left corners.

1.1.1.2 Alignment offset

The alignment offset is defined as the maximum distance from the top-left corner of any image in the series to the line between the top-left corners of the first and last image in the series.

1.1.1.3 Orientation difference

The orientation difference is defined as the maximum difference in angle (degrees) between the orientation vectors in any two images in the series. The deviation is calculated for both the row and column orientation vectors for the images.

1.1.1.4 Gantry tilt

The vector between the top-left corners of the first and last image is calculated. The gantry tilt is defined as the angle between this vector and the normal vector of the first slice.

1.1.1.5 Gap

The gap is calculated as the distance between the upper left corner points of the images minus half the sum of the slice thicknesses of the images. Note that this calculation assumes that the images are aligned, parallel, and that there is no gantry tilt.

By design, in the treatment planning application pixel values from the image slices will be displayed in the gaps between the slices, that is, filling up the gap. Hence, it will appear that the image study does not have gaps.

Gaps in the images indicate that information may be missing in the image slices since they are not acquired from the entire volume. Small tumors or other regions of interest may not be visible in the image data.

1.1.1.6 Overlap

The overlap is calculated as half the sum of the slice thicknesses of the images minus the distance between the upper left corner points. Note that this calculation assumes that the images are aligned, parallel, and that there is no gantry tilt.

By design, in the treatment planning application the parts of the first and last image extending outside the visualization model boundary will not be visible.

Overlaps in images indicate that the exact position of structures in the direction perpendicular to the image plane can not be clearly defined. Structures may be blurred over several image slices.

1.1.1.7 Voxel size

The voxel size of a tomographic image stack is defined by the pixel size in the images and the slice distance in the calculated transformation.

1.1.2 Limits for rejections and warnings

The following limits are used:

Image characteristic	Warning at	Rejection at
Gap	0.1 mm	No rejection
Overlap	0.1 mm	No rejection
Geometrical error	0.1 mm	1 mm

1.2 Error, warning and notification messages at image import

The system issues an error message in the following cases:

Error	Description
AI Image not square error	The number of rows and columns in an angiographic image differs. An error message is displayed and the images are rejected.
Geometrical error	The maximum deviation from the visualization model exceeds a certain reject limit. An error message is displayed and the import is rejected. However, the Tomographic image study dialog is displayed to provide information about what geometrical aspects that were not fulfilled.
Inconsistent patient names error	The images in the series contain differing patient names.

Error	Description
Less than three images in tomographic study error	You tried to import a tomographic series containing less than three images.
Modality difference error	The modality differs within the image series.
Modality not supported error	The modality of the images is not supported by the treatment planning application.
Non-standard orientation error	The images have a non-standard orientation.
Orientation difference error	The image orientation (axial, coronal, sagittal) differs within the image series.
Pixels not square error	The serie contains images with pixels that are not square.
Same image position error	Several images in the study are at the same position.
Image size difference error	The tomographic image serie contains images with different sizes.
Pixel size difference error	The tomographic image serie contains images with different pixel sizes.
Study name not unique	There is already a study in the examination with the entered name. You are asked to enter a new name.

The system issues a warning message in the following cases:

Warning	Description
Gap warning	The images contain gaps exceeding a given limit. A warning message is displayed. You may choose to import the study anyway, or to cancel the import.
Geometrical warning	The maximum deviation from the visualization model exceeds a certain warning limit (lower that the Geometrical error limit above). A warning message is displayed. You may choose to import the study anyway, or cancel the import.
No patient orientation tag warning	You are trying to import an angiographic image without defined patient orientation. A warning message is displayed. You may choose to import the study anyway, or to cancel the import.
No slice thickness tag warning	The slice thickness tag is not defined in a tomographic image series. A warning message is displayed. You may choose to import the study anyway, or to cancel the import.
Overlap warning	The images contain overlaps exceeding a given limit.

Warning	Description
	A warning message is displayed. You may choose to import the study anyway, or to cancel the import.
Patient information warning	The patient name in the DICOM information does not contain both the first and last name of the patient currently open in the treatment planning application. A warning message is displayed. You may choose to import the study anyway, or to cancel the import. The same warning is presented if the patient id in the DICOM images differs from the patient id of the patient currently open in the treatment planning application.
Study date not comparable warning	The study date format is not the expected, and the study date cannot be compared to today's date. A warning message is displayed. You may choose to import the study anyway, or to cancel the import.
Study date not defined warning	The study date is not defined in the DICOM information of the images. A warning message is displayed. You may choose to import the study anyway, or to cancel the import.
Study date warning	The study date in the DICOM information differs from today's date. A warning message is displayed. You may choose to import the study anyway, or to cancel the import.
Unsupported Specific Character Set warning	The patient name etc may be erroneously displayed in the image import dialog. You may choose to import the study anyway, or to cancel the import.

The system issues a notification message in the following cases:

Notification	Description
Tomographic image not square notification	Tomographic image studies containing non square images cannot be used for fiducial based definition.

E Commonly used shortcuts

— Blank page —

1.1 Commonly used shortcuts

The following tables are quick references for some commonly used keyboard and mouse shortcuts in the treatment planning application and its environment. You can quickly accomplish tasks you perform frequently by using shortcut keys. For example, pressing <Ctrl>+<A> selects all shots in the Shot dialog.

Note: *The shortcut keys described below refer to the U.S. keyboard layout.*

Stop a hanging treatment planning application

<Ctrl>+<Alt>+<Esc>	The mouse pointer icon turns into a cross icon. Point the cross icon at the treatment planning application menu and press left mouse button.

Window management

<Alt>+<Tab>	Walk through windows
<Alt>+<Shift>+<Tab>	Walk through windows, reverse

Desktop management

Ctrl>+<F1>	Switch to desktop 1
<Ctrl>+<F2>	Switch to desktop 2 etc.
<Ctrl>+<Alt>+<L>	Lock session
<Ctrl>+<Alt>+<F1>	Go back to graphical desktop from console mode

Copy / Paste

<Ctrl>+<C>	Copy
<Ctrl>+<X>	Cut
<Ctrl>+<V>	Paste

Miscellaneous

<End>	End of line
<Home>	Beginning of line
<Tab>	Jump to next input field, button etc.
<Space>	Select current item in a list
Up/Down arrow	Move in a list
<CTRL>+<P>	Take snapshot

Regions and volumes

Middle mouse button	Undo last drawn point in a region

Image Exploration

Scroll wheel	Scroll in a poster view image stack, move exploration point in Coronal and Sagittal views
Right mouse button	Zoom in image
<Shift> + right mouse button	Zoom in selected view
<Ctrl> + right mouse button	Modify contrast setting
<Ctrl> + middle mouse button	Modify brightness setting

Target Edit/Create dialog

Scroll wheel	Adjust coordinates and grid size
<Ctrl> + Scroll wheel	Adjust coordinates and grid size

Target dialog

Double-click on target	View target

Shot dialog

<Ctrl>+<A>	Select all shots
Scroll wheel	Adjust X, Y and Z in steps of 0.1 mm
<Ctrl> + Scroll wheel	Adjust X, Y and Z in steps of 1 mm
Scroll wheel	Adjust shot weight in steps of 0.10
<Ctrl> + Scroll wheel	Adjust shot weight in steps of 0.01
<Ctrl>	On the fly selection of shot at mouse pointer position in views.

Open Patient

Double click examination	Open examination

F Protocols

— Blank page —

1.1 Skull and Leksell® Coordinate Frame G measurements protocol

Patient name:	
Patient id:	Date:

SKULL MEASUREMENTS (in millimeters)

Top radius:

	1	2	3	4	5	6	7	8
A		----------		----------		----------		----------
B	----------		----------		----------		----------	
C								
D			----------					

FRAME CAP FITS (applicable for Leksell Gamma Knife® Perfexion and Leksell Gamma Knife® Icon™ only)

☐ Yes

☐ No

FRONT PIECE

☐ Curved Downwards

☐ Curved Upwards

☐ Straight

☐ Slotted

FRAME CONFIGURATION (in millimeters, or hole number for curvated anterior posts)

	Code[1]	Superior	Inferior[2]	Srew	Offset[3]
Anterior Left					
Anterior Right					
Posterior Left					----------
Posterior Right					----------

[1] Use code listed in the Post Configuration Protocol; A=Anterior, P=Posterior, S=Squared, R=Rounded.

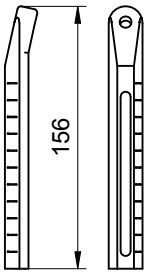
[2] For curved anterior posts, the inferior measurement is not needed.

[3] Offset measurements are only required for slotted front piece.

1.2 Fixation posts configuration protocol

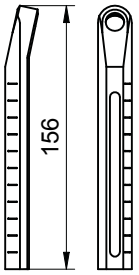
Patient name:	
Patient id:	Date:

ANTERIOR POSTS:



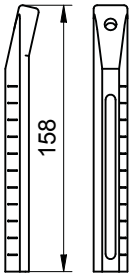
AR156
#717733
#1003830

☐ **Left** ☐ **Right**



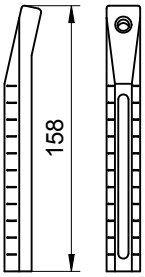
AR156 Insulated
#711466
#1002635

☐ **Left** ☐ **Right**



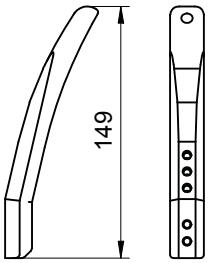
AS158
#13007110

☐ **Left** ☐ **Right**



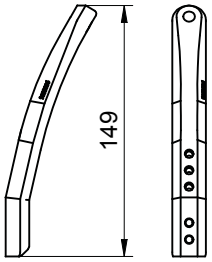
AS158 Carbon
#13004550

☐ **Left** ☐ **Right**



AS149 Curved
#707402

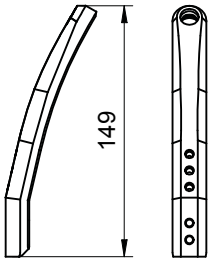
☐ **Left** ☐ **Right**



AR149 Curved

#1003836

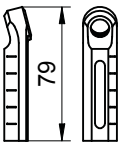
☐ **Left** ☐ **Right**



AR149 Curved Insulated
#711471
#1003826

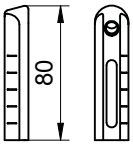
☐ **Left** ☐ **Right**

POSTERIOR POSTS:



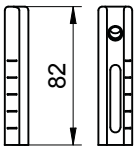
PR79 insulated
#711467
#1002636

☐ **Left** ☐ **Right**



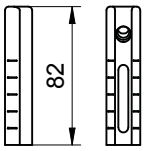
PR80
#717734
#1003831

☐ **Left** ☐ **Right**



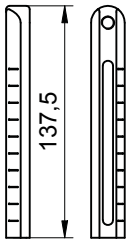
PS82
#13007120

☐ **Left** ☐ **Right**



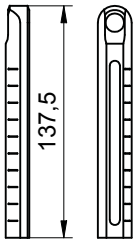
PS82 Carbon
#13004560

☐ **Left** ☐ **Right**



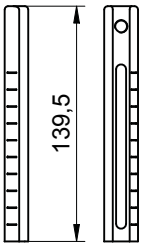
PR137,5
#717732
#1003832

☐ **Left** ☐ **Right**



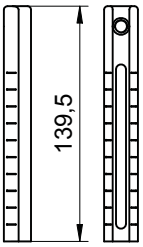
PR137,5 Insulated
#711468
#1002637

☐ **Left** ☐ **Right**



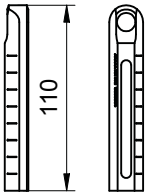
PS139,5
#13007100

☐ **Left** ☐ **Right**



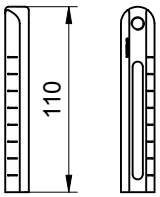
PS139,5 Carbon
#13004570

☐ **Left** ☐ **Right**



PR110 Insulated
#1000808

☐ **Left** ☐ **Right**



PR110
#1000940

☐ **Left** ☐ **Right**

— Blank page —

G Tomographic study definition

— Blank page —

This appendix provides a more detailed description of the method used for tomographic study definition. It also summarizes the recommendations for tomographic image acquisition, and explains how those recommendations have been obtained.

1.1 Algorithm description

The purpose of the algorithm for tomographic study definition is to calculate the coordinate transformation between the images and the Leksell® Coordinate System. The transformation consists of a rotation and a translation. The voxel size is calculated from the DICOM header, so it does not need to be estimated based on the fiducial positions.

The algorithm is based on the fact that each N-shaped rod on the indicator box gives rise to three fiducial points on an image slice. For axial images, a left and right plate must be used. A third (frontal) plate is recommended but optional. If the third plate is used, it is only used in the verification step, so it does not affect the definition results.

Step 1: Find and verify fiducial points in each slice

In the first step of the algorithm, the six (or nine) fiducial points are located in each image slice, either automatically or manually. Then a number of geometric consistency checks are applied to these points. For example, it is verified that the lines defined by the left and right fiducials are parallel to each other, and that their lengths are reasonable.

Step 2: Calculate the transformation to Leksell® coordinates for the whole study

Once the fiducial points have been located and verified, the transformation between study (image) coordinates and Leksell® coordinates is computed as follows:

1 Perform a least square fit with left and right fiducial N lines.

2 Calculate the four “corner” points for each of the left and right N shapes.

3 Estimate the transformation matrix by finding the rotation and translation that best maps the eight corner points onto their known locations in Leksell® space.

Step 3: Verify the registration and calculate the mean and maximum errors

The final step is to use the calculated transformation matrix to compare the predicted positions of the fiducial points with the actual positions in each image slice.

1 Compute the error defined as the Euclidean distance in mm between predicted and actual position for each fiducial.

2 Compute the mean and maximum error for each slice.

3 Compute the mean and maximum error for the entire image study.

If the third plate is used, these errors will be computed for all nine fiducial points. Otherwise only the six fiducial points from the left and right plates will be used.

1.2 Recommendations for tomographic image acquisition

A larger stack height and more slices used in the image study definition make the registration algorithm less sensitive to noise, thereby reducing the 3-D uncertainties in rotation and translation. This is especially important when the third plate is not used.

It is not possible to specify an exact value for the minimum stack height that will provide a “good enough” tomographic study definition, since this is a matter of definition and may depend on many factors such as image distortion etc.

However, one useful quality criterion is that the two-dimensional errors that the software can detect and report are on average at least as large as the three-dimensional uncertainty of the

transformation. Based on this quality criterion, we propose the following general recommendations for tomographic image acquisition:

- Use the third plate whenever applicable. This does not affect the definition results, but it makes it easier to detect three-dimensional uncertainties.
- If only two plates are used, use a stack height of at least 5 cm. (If the third plate is also used, this recommendation can be relaxed since 3-D uncertainties then typically give rise to noticeable 2-D errors even for small stacks.)
- Try to center the image stack at the center of the fiducial box.
- Avoid rotating the coordinate frame more than five degrees during scanning.

Note that these recommendations should be viewed as “rules of thumb” rather than absolute criteria. It may be possible to obtain excellent three-dimensional accuracy without observing these recommendations. Conversely, in the presence of non-uniform image distortion the accuracy can be inadequate even when the recommendations are followed. Distorted images should not be used for treatment planning.

Related Links:

Algorithm description on page 367

1.3 Test of the image acquisition recommendations by simulation

The image acquisition recommendations for two plates can be tested by applying the quality criterion mentioned above to a range of simulated conditions intended to represent normal use. In this section we present the results of such a simulation study.

Artificial images with known fiducial positions are used in order to have full control of the uncertainties in the model. Instead of trying to model the complex physical processes in the imaging device (MRI or CT), Gaussian noise is added to the fiducial positions. Note that this model does not take into account any non-uniform distortions in the images.

The parameters studied in the simulation are; noise in the images, number of images, slice thickness, rotation of the stack relative to the indicator box, translation of the stack normal to the image planes and position in the 3-D volume.

The parameters are varied around the following standard values:

- Slice thickness of 1.5 mm and 3.0 mm.
- No rotation of the stack relative the indicator box.
- The coordinate of the center of the stack is placed at the center of the indicator box.
- A test point with Leksell® coordinates X=100, Y=180 and Z in the middle of the stack, that is, a position inside but not at the center of an average head.

In the model the 2-D uncertainty is the standard deviation of the generated noise in the fiducial positions and the 3-D uncertainty is the distance between a point (X,Y,Z) in the 3D volume and the corresponding point in the images transformed back with the transformation estimated by the definition algorithm. In each simulation case we apply the quality criterion that the 2-D uncertainty should on average be at least as large as the 3-D uncertainty. As a result, we get the conclusions and recommendations for stack height and stack position and rotation, described in the following chapters.

Related Links:

Stack height on page 369

Stack position and rotation on page 369

1.3.1 Stack height

The minimum stack height is dependent on the slice thickness, but the dependency is not linear. It also depends on rotation and translation of the stack. Another observation is that the minimum stack height is independent of the magnitude of the noise in the images. For slice distances of 1.5 mm and 3 mm respectively, we obtain the following recommendations:

- For a slice distance of 1.5 mm an image stack height of at least 24 slices (or 36 mm) is recommended.
- For a slice distance of 3 mm an image stack height of at least 15 slices (or 43 mm) is recommended.

Note that the general “rule of thumb” to use a stack height of at least 5 cm covers these two cases, with some margin for other types of distortion not included in the simulation model.

1.3.2 Stack position and rotation

The uncertainties increase when the stack is translated from the center. The stack height recommendations are valid for all translations but it is recommended that the image stack is centered on the MR indicator panels and with rotation less than 5 degrees of the coordinate frame during scanning.

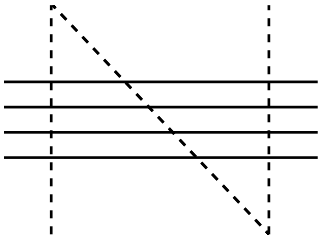


Figure 1.1 Axial image stack centered at the center of the fiducial box

— Blank page —

H Converted patient files

— Blank page —

This section describes the characteristics of patient files that have been converted from HP-UX versions of Leksell GammaPlan® for the purpose of follow up.

1.1 Working with converted patient files

When opening a converted examination you will be informed that the patient file has been converted from an HP-UX based version of Leksell GammaPlan®. If applicable, you will also be warned about critical limitations of the converted patient file. The same information and warnings will be displayed when importing a converted patient file into another examination.

Treatment plans that are part of a converted examination have the state **Converted** and can neither be modified nor approved for treatment. The treatment plans of converted patient files shall not be used for treatment.

1.2 Support for Leksell GammaPlan® U

In Leksell GammaPlan®, the support for Leksell GammaPlan® U is limited to viewing converted patient files for the purpose of follow up. Treatment planning for Leksell GammaPlan® U is similar to that for Leksell GammaPlan® B, with the important distinction that the layout of the radiation sources differs. For an in-depth description of dose planning for Leksell GammaPlan® U, refer to the original reference manual for Leksell GammaPlan® 5.34 (or prior).

1.2.1 Limitations of converted patient files

Not all data is preserved for patient files upon conversion. This section describe the differences of a converted patient file in comparison to the original patient file as displayed on Leksell GammaPlan® 4.x/5.x/4C.

- The Leksell GammaPlan® model and its configuration for a treatment plan are not preserved upon conversion. Converted treatment plan are assigned a Leksell GammaPlan® model that is consistent with the original treatment plan.
- For converted treatment plans the dose calibration date is set to the original examination date. The calibration dose rate is set to the dose rate for the original treatment plan at the examination date.
- Coordinate frame configuration and measurements are not preserved upon conversion, instead converted examinations will have “Simulate frame“ set. As a consequence, neither clearance estimates nor the ordering of shots in shot runs are preserved upon conversion.
- Plug patterns of type “Template“ and “Generated“ are not preserved upon conversion (although the effective plug pattern for each individual shot is preserved).
- Shots that are positioned outside the patient skull in the original treatment plan are deleted upon conversion. A warning will be displayed when opening the examination or importing the examination into another examination.
- Due to the risk for misinterpretation, the dose prescription is unset upon conversion for treatment plans where the global maximum dose is outside all targets in the original treatment plan. A warning will be displayed when opening the examination or importing the examination into another examination.
- Due to an automatic re-definition of angiographic image studies upon conversion of patient files from Leksell GammaPlan® 5.33 and prior, the Leksell® coordinates for angiographic image studies may differ compared to the original image study. A warning will be displayed when opening the examination or importing the examination into another examination.

- Due to changes of the Leksell® study definition introduced in Leksell GammaPlan® 5, volumes that are defined in the Leksell® study will be distorted upon conversion of patient files originating from Leksell GammaPlan® 4.x. A warning will be displayed when opening the examination or importing the examination into another examination.
- Due to changes of the algorithm for calculating intersection with the skull, the displayed dose distribution may differ for converted treatment plans for which “skull iteration failure“ was originally reported in Leksell GammaPlan® 4.x/5.x/4C. A warning will be displayed when opening the examination or importing the examination into another examination.
- The image number, displayed in the lower left of each image, may differ. In the HP-UX version of Leksell GammaPlan® the images where numbered according to image number of the imported images. In the current version of Leksell GammaPlan® the images are numbered according to their position in the Leksell® Coordinate System. The image number will be zero for the image with the lowest z-value (for axial images) or lowest y-value (for coronal images).

I AtlasSpace®Contours

Section	Title	Page

— Blank page —

1.1 Contour labels

The following label discrepancies between contour labels in AtlasSpace® and the Schaltenbrand-Wahren (SW) paper atlas exist:

SW Microseries	Slice	Name in AtlasSpace®	Name in SW paper atlas
Frontal	F.p 16,5	Ru.pc	Rt.pu
Frontal	F.p 5,0	Rt.c	Rt.im
Frontal	F.p 4,0	Z.im.i, Z.im.e	Z.im
Frontal	F.a 4,0	La.p.l	La.p.m
Horizontal	H.d +6,5	Ce	Ce.pc
Horizontal	H.d +0,5	B.co.i	B.co.s
Horizontal	H.v –1,0	A.aq	Aq
Horizontal	H.v –1,5	V.c.pc.i	V.c.i
Sagittal	S.l 20,0	D.im.i+Z.im	D.im+Z.im
Sagittal	S.l 20,0	Alv+Fx.p+La.m.sf	Alv+Fx.p+La.m.p
Sagittal	S.l 16,0	An.l+La.p.li+P	An.l+La.p.li+Pm
Sagittal	S.l 13,0	V.c.pc.i	V.c.pc
Sagittal	S.l 9,0	Rt.po	B.co.i
Sagittal	S.l 1,5	Ru.pc	Ru.pc+Ru.mc

1.2 Differences in contours

The following differences in shape between contours in AtlasSpace® and the Schaltenbrand-Wahren (SW) paper atlas, that were above 1 mm in the reference brain, exist:

SW Microseries	Slice	Contour
Sagittal	S.l 5,5	C.c
Sagittal	S.l 16,0	Ps.pd
Sagittal	S.l 20,0	Cd+Fu.st+Put

— Blank page —

J Diagnoses codes

— Blank page —

1.1 Reclassification of diagnosis codes

Since version 10.2 of Leksell GammaPlan®, medical diagnoses have a numerical diagnosis code, the number of available diagnoses is expanded, and diagnoses are divided into diagnosis groups.

When transferring patient data from Leksell GammaPlan® versions 10.1 and earlier, some of the diagnoses are automatically reclassified to the new diagnosis code as listed in the table below. Not all diagnoses can be reclassified due to that the earlier classification now corresponds to a group of diagnoses rather than to a specific diagnosis. See e.g. Epilepsy.

Diagnoses that are not automatically reclassified are by default set to the code R9999 and can easily be viewed in the Patient Management dialog.

Diagnoses not automatically reclassified can be reclassified manually by the user should the need arise.

Diagnosis codes in Leksell GammaPlan® (LGP)			
Diagnosis code	**Diagnosis name**	**Diagnosis name in LGP 10.1 and earlier**	
R10	**Behavioral Disorder**	N/A	
R1001	OCD		
R1002	Depression		
R1099	Other behavioral disorder		
R11	**Chordoma**	N/A	
R1101	Chordoma		
R12	**Chondrosarcoma**	N/A	
R1201	Chondrosarcoma		
R13	**Craniopharyngioma**		
R1301	Craniopharyngioma	Craniopharyngioma	Reclassified
R14	**Epilepsy**	Epilepsy	Not reclassified
R1401	Mesial temporal lobe epilepsy		
R1402	Hypothalamic hamartoma		
R1499	Other epilepsy		
R15	**Glioma**	Glial Tumor	Not reclassified
R1501	Juvenile pilocytic astrocytoma		
R1502	Diffuse astrocytoma, grade 2		
R1503	Anaplastic astrocytoma, grade 3		
R1504	Glioblastoma		
R1505	Oligodendroglioma, grade 2 or 3		
R1506	Ganglioglioma		
R1507	Medulloblastoma		
R1508	Ependymoma, grade 2 or 3		
R1599	Other glial neoplasm		

Diagnosis codes in Leksell GammaPlan® (LGP)			
R16	**Hemangioblastoma**	N/A	
R1601	Hemangioblastoma		
R17	**Meningioma**		
R1701	Meningioma, all grades	Meningioma	Reclassified
R18	**Metastasis**		
R1801	Metastasis - single	Metastasis Single	Reclassified
R1802	Metastases - multiple	Metastasis Multiple	Reclassified
R19	**Movement disorder**		
R1901	Parkinson's disease	Parkinsonism	Reclassified
R1902	Essential tremor		
R1999	Other movement disorder		
R20	**Ocular**		
R2001	Uveal melanoma	Uveal Melanoma	Reclassified
R2002	Glaucoma		
R2003	Macular degeneration		
R2099	Other ocular		
R21	**Pain and headache**		
R2101	Pain	Intractable Pain	Reclassified
R2102	Cluster headache		
R22	**Pineal region**	Pineal Region Tumor	Not reclassified
R2201	Pineocytoma		
R2202	Pineoblastoma		
R2203	Germinoma		
R2204	Non germinomatous germ cell tumor		
R2299	Other pineal region		
R23	**Pituitary adenoma**		
R2301	Pituitary adenoma	Pituitary Adenoma	Reclassified
R24	**Schwannoma**		
R2401	Vestibular schwannoma	Acoustic Schwannoma	Reclassified
R2402	Trigeminal schwannoma		
R2403	Jugular foramen schwannoma		
R2499	Other schwannoma		
R25	**Trigeminal neuralgia**		
R2501	Trigeminal neuralgia	Trigeminal Neuralgia	Reclassified
R26	**Vascular**		
R2601	Arteriovenous malformation	AVM	Reclassified
R2602	Cavernous malformation		

Diagnosis codes in Leksell GammaPlan® (LGP)			
R2603	Dural arteriovenous fistula		
R2699	Other vascular	Other vascular	Reclassified
R90	**Other benign tumor**	Other Benign Tumor	Not reclassified
R9001	Hemangioma		
R9002	Hemangioperycytoma, grade 2 or 3		
R9003	Neurocytoma		
R9004	Choroid plexus papilloma		
R9099	Other benign tumor		
R91	**Other malignant tumor**		
R9101	Nasopharyngeal carcinoma	NPH Carcinoma	Reclassified
R9102	Adenoid cystic carcinoma		
R9103	Squamous cell carcinoma		
R9199	Other malignant tumor	Other Malignant Tumor	Reclassified
N/A	**N/A**	Other functional	Not reclassified

Related Links:

Description of the Patient Management dialog on page 93

— Blank page —

List of Warnings and Cautions

— Blank page —

We are healthcare technology innovators, specializing in radiotherapy treatments for cancer and brain disorders.

We help clinicians to improve patients' lives through our forward-thinking treatment solutions and oncology informatics, creating focus where it matters to achieve better outcomes.

Elekta

Elekta Offices

Elekta AB
Kungstensgatan 18
Box 7593, SE-103 93 Stockholm
Sweden
T +46 8 587 254 00
F +46 8 587 255 00

Europe, Middle East, Africa
T +46 8 587 254 00
F +46 8 587 255 00

North America
T +1 770 300 9725
F +1 770 448 6338

Latin America, South America
T +55 11 5054 4550
F +55 11 5054 4568

Asia Pacific
T +852 2891 2208
F +852 2575 7133

Japan
T +81 3 6722 3800
F +81 3 6436 4231

China
T +86 10 5669 2800
F +86 10 5669 2900

elekta.com

/elekta

@elekta

/company/elekta