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Chapter 1 About This Guide

Information in this Guide

This guide contains reference information about the Eclipse treatment planning system, and instructions for tasks performed outside the daily treatment planning workflow. The information in this reference guide is complementary to the information in the corresponding instructions for use guide.

More information about the daily treatment planning tasks: Eclipse Photon and Electron Instructions for Use.

Who Should Read This Guide

The Eclipse Treatment Planning System (Eclipse TPS) is used to plan radiotherapy treatments for patients with malignant or benign diseases. Eclipse TPS is used to plan external beam irradiation with photon, electron and proton beams, as well as for internal irradiation (brachytherapy) treatments. In addition, the Eclipse Proton Eye algorithm is specifically indicated for planning proton treatment of neoplasms of the eye.

Eclipse should only be used by qualified medical professionals.

This guide is written mainly for medical physicists, radiation oncologists, dosimetrists, and radiation therapists, who may have specific tasks in the treatment planning process. These tasks may regard treatment planning or system configuration.

Visual Cues

This publication uses the following visual cues to help you find information:



WARNING: A warning describes actions or conditions that can result in serious injury or death.



CAUTION: A caution describes hazardous actions or conditions that can result in minor or moderate injury.



NOTICE: A notice describes actions or conditions that can result in damage to equipment or loss of data.



Note: A note describes information that may pertain to only some conditions, readers, or sites.



Tip: A tip describes useful but optional information such as a shortcut, reminder, or suggestion, to help get optimal performance from the equipment or software.

Related Publications

- *Eclipse Photon and Electron Instructions for Use*: Provides instructions and supporting information for using the Eclipse treatment planning system for daily treatment planning tasks.
- *Beam Configuration Reference Guide*: Provides reference information and instructions for beam data configuration required for performing dose calculation for external treatment plans in the Eclipse treatment planning system.
- *Eclipse Photon and Electron Algorithms Reference Guide*: Describes algorithms supported in the Eclipse treatment planning system.
- *RT Administration Reference Guide*: Provides reference information and instructions for configuring and managing radiation and imaging devices, system data and settings.
- *RT and Imaging Online Help*: Describes the functions available in Radiation Oncology applications and provides instructions for using them.

Contacting Varian Customer Support

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 - If you have an account, go to the next step.
4. Enter your user name and password.
5. Browse the information and then click the link that corresponds to what you want to do:
 - Fill out and submit a support request.
 - Find documents. Online documents in PDF format include customer technical bulletins (CTBs,) manuals, and customer release notes (CRNs).
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Chapter 2 Getting Familiar with Eclipse

What is New in Eclipse

Eclipse contains the following new and enhanced features:

- IMRT, VMAT and Siemens mARC plans can be optimized in the new Optimization dialog box. To use the new Optimization dialog box you need to select the new Photon Optimization (PO) algorithm to optimize the plans. If you use the PRO algorithm to optimize a VMAT plan, or the DVO algorithm to optimize an IMRT plan, plans are optimized in the IMRT and VMAT Optimization dialog boxes as in previous versions of Eclipse.
- RapidPlan: DVH estimates and optimization objectives can be generated from DVH estimation models. A DVH estimation model uses knowledge from existing treatment plans to generate DVH estimates and estimate-based optimization objectives in optimization. The data from the existing treatment plans is extracted and then used to train the DVH estimation models. DVH estimation models are configured, trained and managed in the DVH Estimation Model Configuration workspace. When you use a DVH estimation model to generate DVH estimates and objectives in a plan, you can use all the features in the Optimization dialog box in the same way as in optimization without a DVH estimation model.
- Changes and enhancements in optimization objectives that can be used with the PO algorithm include, for example, the following:
 - Generalized Equivalent Uniform Dose (gEUD) optimization objectives can be used in IMRT and VMAT plans
 - Mean dose objective can be used in IMRT plans.
 - The priority of new objectives is 0, and it must be modified for the objectives to have the intended effect on the optimization.
- Siemens mARC plans can now be optimized in Eclipse. Also conformal arc planning with Siemens MLC 160 is now possible in Eclipse.
- Structure codes have been added to identify the anatomical role of a structure, the treatment role of a structure (such as PTV or organ at risk), or both, with a single code. Structure codes are easier to use for reliably identifying structures than freely modifiable codes. Structure codes are used for automatic structure matching in DVH estimation models. The set of structure codes available in treatment planning is defined in RT Administration.
- It is now possible to save default CT values for different couch types. Saving CT values as defaults is a clinic-wide setting; it affects all workstations that are connected to the same database.
- The AAA dose calculation algorithm can now be used to calculate the dose distribution for Cobalt plans.

- Optimal fluences can now be converted into compensators in photon fields.
- Elekta MLC 160 is now supported in Eclipse.
- The Plan Conversion feature can be used to make changes in a photon source plan to best replicate the dose-volume histograms of the original plan when using another treatment unit. The changes are applied based on correspondence criteria for the new treatment unit by finding the best matches. After the plan conversion, you need to assign the intended new fraction number, and evaluate and approve the converted plan normally.
- Eclipse now uses the same user-defined Window/level presets as the SmartAdapt application.
- When using the multiple plane views in Plan Evaluation Application, you can now select between transversal, frontal and sagittal views.
- You can now create the DRR images for all fields simultaneously in a multi-field plan.
- When using the cross-hair tool to inspect the DVH, you can use the left and right arrow keys to move the cross-hair along the selected DVH curve.
- When exporting plans or dose planes, you can now set the selected export parameters as default for the export operations.

Getting Familiar with Eclipse

Eclipse is designed for 3D image viewing, definition of the tumor and other anatomical structures, field setup, virtual simulation, dose calculation and plan evaluation.

Eclipse is divided into different applications, each used for specific purposes at different phases of treatment planning: the Selection application is meant for importing and creating patient images, whereas External Beam Planning and Plan Evaluation applications provide tools for treatment planning and evaluation of the completed treatment plans.



Note: Ensure that individuals authorized to perform treatment planning functions are appropriately trained for the functions they perform.



Note: All treatment plan reports shall be approved by a qualified person before the information in them is used for radiotherapy treatment purposes.



NOTICE: Do not install any third party software, or updates to the operating system without instructions from Varian Medical Systems.



WARNING: It is the responsibility of the user to ensure the validity and integrity of the input data, and to understand that the quality of the output depends critically on the quality of the input. Any irregularities or uncertainties about input data, units, identification, or quality of any other nature shall be thoroughly investigated before the data are used.



WARNING: Always check the patient information displayed on screen, especially if multiple instances of the application are open, to make sure that you are working on the correct patient. The patient information is displayed in the title bar of the application main window, and in the Assistant menu bar.



NOTICE: Regional Settings in the Windows operating system using commas as the decimal separator are not recognized by Eclipse. For example, the entry “1,23” will not be recognized as “1.23”. The decimal point “.” should always be used regardless of the Regional Settings.

Contouring Application

Contouring and segmentation of the patient anatomy for treatment planning is available in the Contouring application. Some contouring tools are also available in External Beam Planning and Brachytherapy Planning. Preparing the patient image data and patient anatomy for treatment planning in the Contouring application involves the following:

- Importing and exporting therapeutic and diagnostic 2D image data (for instance, CT, MR, PET) in the Selection workspace.
- Constructing 3D image data and viewing the images in different 3D modes. While working with the images, you can also manipulate them for better viewing, and measure information on the images.
- Delineating treatment volumes and anatomical volumes by using diagnostic images to aid in the target definition. The patient volumes include the Body structure, relevant internal structures, and the location and size of the Target structure. You can use both CT or MR images for contouring and segmentation.

More information on the Contouring application: *Registration, SmartAdapt and Contouring Instructions for Use* or *Registration, SmartAdapt and Contouring Reference Guide*

Image Registration

Image registration is available in the Registration and SmartAdapt applications. Registration and SmartAdapt are used to spatially align image data sets, such as CT and MR images, to integrate information from different imaging modalities into treatment planning and contouring. Registering two image data sets can be done by using the automatic registration tool, manual translation and rotation and by using registration points.

External Beam Planning Application

External Beam Planning is used to construct treatment plans to irradiate the target volumes defined in the Contouring application. The purpose of the treatment plans is to achieve the prescribed dose with the required number of fields. Treatment planning in External Beam Planning involves

- Creating plans by setting up fields In External Beam Planning, you set up and visually optimize the position of fields in a two-dimensional or three-dimensional patient anatomy.
- Defining the relevant field accessories, such as MLCs, blocks and compensators, depending on the planned treatment modality.
- Creating DRRs as reference or field images for comparison with portal and simulator images.
- Sending plans to virtual simulation.

When the field setup is completed, you calculate the dose distribution for the plan.

Plan Evaluation Application

The Plan Evaluation application is used for analyzing and comparing alternative treatment plans to determine the most appropriate plan or combination of plans, which can then be approved for treatment.

You can visually evaluate the treatment plans in a number of ways:

- View the dose distribution two-dimensionally by using isodose lines and dose color wash.
- View the dose distribution three-dimensionally by using isodose surfaces and dose cloud mode.
- View the dose at reference points (available also in Brachytherapy Planning and External Beam Planning applications).
- Compare plans side-by-side

In addition to using the visual evaluation tools, you can:

- Display DVHs for multiple plans or structures.
- Normalize the dose (available also in External Beam Planning application)
- Weight fields (available also in the External Beam Planning application).
- Verify the absolute dose and the resulting MU (available also in the External Beam Planning application).
- Combine plans (both brachytherapy and external beam plans).

Navigating in the Applications

The applications each have:

- Assistant menu bar, which integrates the ARIA RTM Workflow Management components. The Assistant bar enables navigation between the components. More information: ARIA RTM Workflow Management documentation.
- Special image view layouts to provide an optimal environment for performing the selected procedure.
- Menus and toolbars that contain both a set of common, and a range of application-specific features and functions.
- Context window.
- Some of the applications are further divided into workspaces. Workspaces have the same main parts as applications.

The menus contain commands related to the application. The most commonly used menu commands are also available as toolbar buttons. The Context window displays the relevant objects belonging to the selected patient. The title bar of the application main window shows the information of the currently active patient.



WARNING: Always check the patient information displayed on screen, especially if multiple instances of the application are open, to make sure that you are working on the correct patient. The patient information is displayed in the title bar of the application main window, and in the Assistant menu bar.

Starting Applications

Each application is started from the Home screen. More information: ARIA RTM Workflow Management documentation.

You can also run multiple simultaneous application sessions. Using multiple application sessions allows you to

- Open data of multiple patients at the same time for viewing or editing.
- Work on one patient while the application is processing the other, for instance, performing optimization.

In workstations running a 64-bit operating system, you can use up to ten application sessions simultaneously. In 32-bit operating systems, the limit is four simultaneous sessions.



WARNING: Always check the patient information displayed on screen, especially if multiple instances of the application are open, to make sure that you are working on the correct patient. The patient information is displayed in the title bar of the application main window, and in the Assistant menu bar.



WARNING: The system uses a central database that allows running the application on different workstations simultaneously. If multiple simultaneous users work with the same data, this may lead to situations where another user has modified and saved the data that you are currently working with. Therefore, avoid situations with multiple users concurrently editing the same patient data. If you try to save your changes, the system will issue a warning message about another user already editing the same patient. Always carefully verify the synchronized data, because it may contain changes made by both you and the other user.

Start an Application Session

- In the Home screen, do one of the following:
 - On the Assistant menu bar, choose **Worklist** and then choose the desired task.
 - In the Task list, click a task.
 - Choose **Quicklinks** and then choose the desired application.
 - In the **Favorites** list, click the desired task.



Tip: You can start multiple application sessions from the Quicklinks menu of the Assistant menu bar. To do this, point at the application name in the menu and then click the right-pointing arrow shown next to the application name.

Switch to Another Application

You can easily switch to any other ARIA RTM Workflow Management component and start multiple simultaneous application sessions using the Quicklinks menu in the Assistant menu bar. To further ease accessing applications that you use frequently, you can add them to the Quicklinks Favorites list. More information: ARIA RTM Workflow Management documentation.

- To switch to an application included in your favorite applications list, in the Assistant bar, choose **Quicklinks** and then choose the name of the application. Alternatively, click the button of the application in the Favorites widget.

- To switch to any other application, in the Assistant bar, choose **Quicklinks**, then choose the application family name and the application name.
For instance, to switch to Selection, in the Assistant bar, choose **Quicklinks > Treatment Planning > Selection**.
- You can also switch between Selection, External Beam Planning, Brachytherapy Planning, Brachytherapy 2D Entry and Plan Evaluation by clicking the workspace in the **Workspace Bar**.

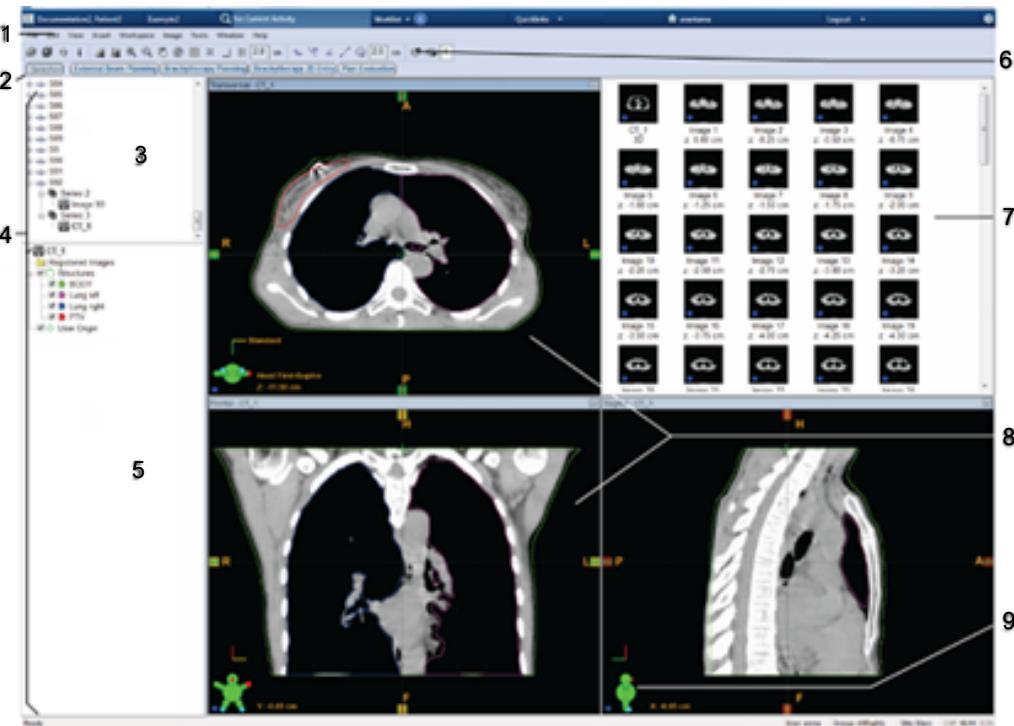
Tip: *To make the Workspace Bar visible, choose Window > Workspace Bar.*



Note: *You can start multiple application sessions from the Quicklinks menu of the Assistant menu bar. To do this, point at the application name in the menu and then click the right-pointing arrow shown next to the application name.*

Image Views in the Selection Application

In the Selection workspace, the Image Gallery displays thumbnails of the images in an image series. The images are also displayed in the tree structure in the Scope window. The 2D image views display images selected from the Image Gallery or the Scope window.



1. Assistant menu bar
2. Menu bar
3. Scope window
4. Context window
5. Focus window
6. Toolbar
7. Image Gallery
8. 2D image views
9. Patient orientation indicator

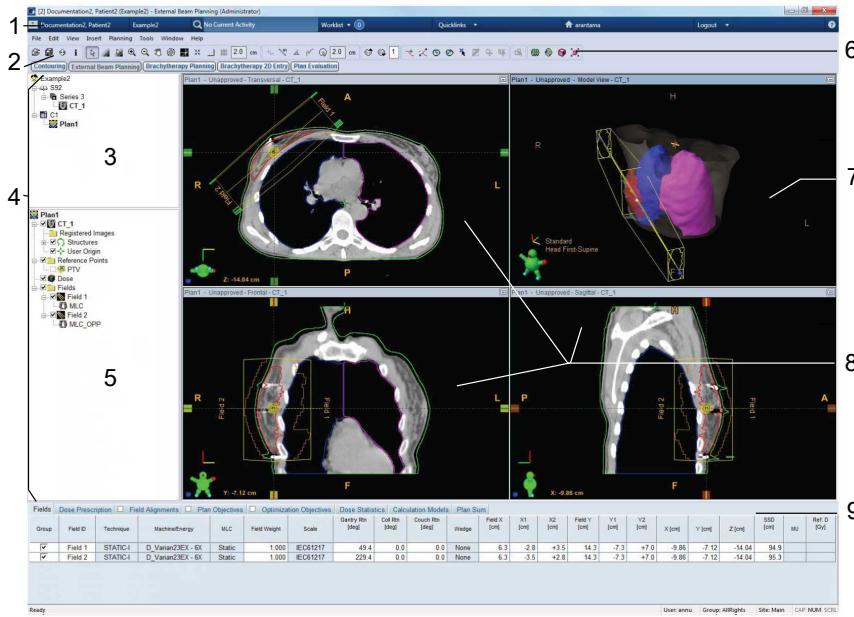
Figure 1 User Interface of Selection Application

Related Topics

[Patient Orientation Indicator](#) on page 51

Image Views in the External Beam Planning Application

The image view layout of the External Beam Planning application consists of three orthogonal views and a Model view.



1. Assistant menu bar
2. Menu bar
3. Scope window
4. Context window
5. Focus window

6. Toolbar
7. 3D image view
8. 2D image views
9. Info window

Figure 2 User Interface of External Beam Planning Application

Three of the image views display 2D images of the patient from three directions: transversal, sagittal and frontal. The order of the views depends on the patient's position when the original CT images were produced.

The fourth image view is the Model view that displays either a solid 3D or BEV image of the patient, or the DVH, if so selected.

The area below the Context window and the image views is called the Info view. It displays the field parameters for each field contained in the plan.

The Context window of External Beam Planning indicates the selected patient and image set attached to the plan as well as the selected plan and fields with field accessories contained in the plan.

Image Views in the Plan Evaluation Application

In the Plan Evaluation application, you can choose from the following image view layouts:

- Two orthogonal views—Two view sets consisting of three 2D views (transversal, frontal and sagittal).
- Two model/BEV views—Two view sets consisting of a 3D view.
- Multiple plane views (Transversal, Frontal or Sagittal)—One view set consisting of nine transversal, frontal or sagittal views displaying adjacent image planes.
- Orthoviews and BEV—One view set consisting of three 2D views (transversal, frontal and sagittal) and a 3D view.
- Multiple plans—Six transversal 2D views.

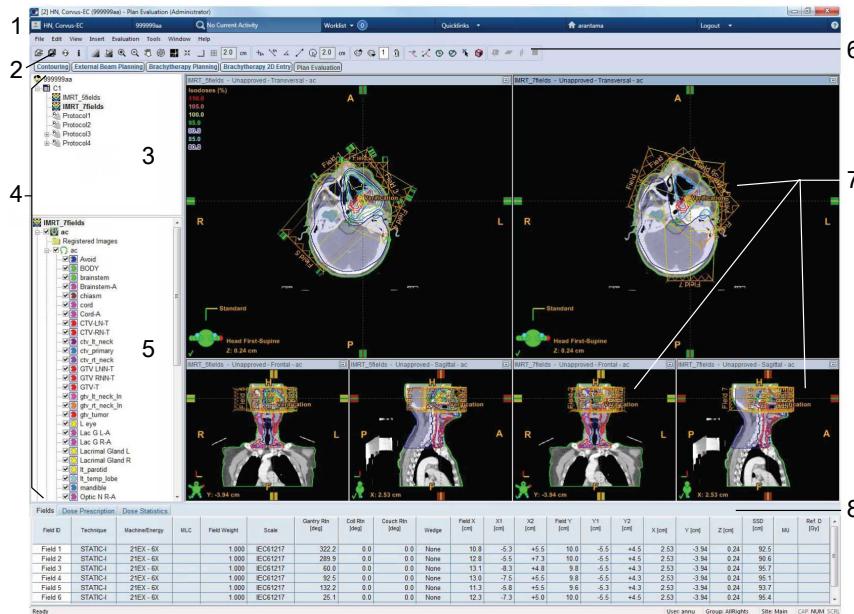
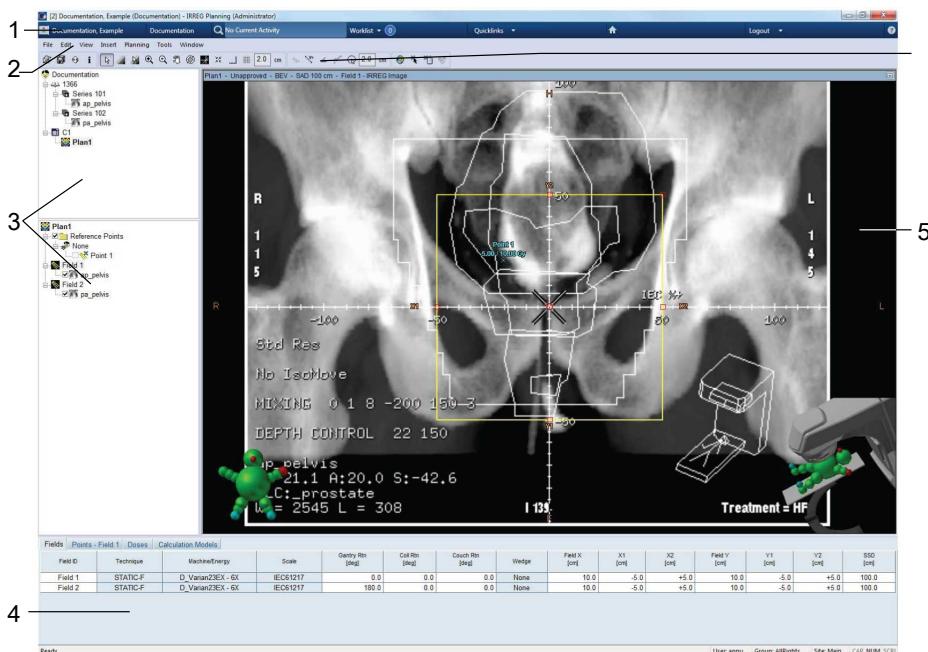


Figure 3 User Interface of Plan Evaluation Application

Image Views in the IRREG Planning Application

IRREG Planning consists of the same basic elements as other treatment planning applications.

The image view in IRREG Planning shows the 2D reference image aligned with the field selected in the Context window, the selected field in the Beam's Eye View mode or Model View mode, and reference points defined in the plan.



1. Assistant menu bar
2. Menu bar
3. Context window
4. Info window
5. Toolbar
6. Image view

Figure 4 User Interface of IRREG Planning Application (Beam's Eye View)

Select Image View Layout

1. Choose **Window > View Layouts**.
2. In the selected layout list, click the row of a layout to see its preview.
3. To select the layout, click **OK**.

Access the Application Workspaces

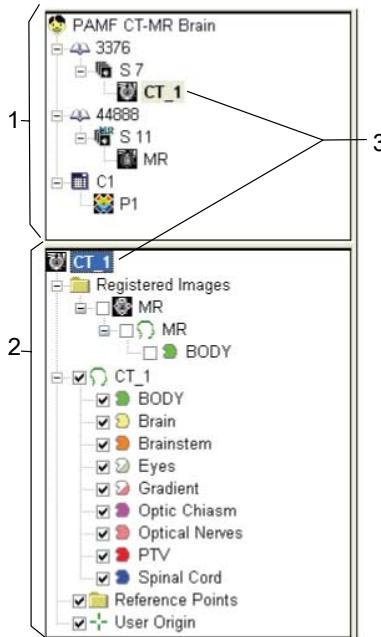
- Choose **Workspace** and select the workspace you wish to go to.
- Click the **Workspace Bar**.



Tip: *To make the Workspace Bar visible, choose Window > Workspace Bar.*

Context Window in Treatment Planning

The Context window is a means of viewing the patient, image and plan information. The information in the Context window is displayed as folders that are hierarchically organized in a tree structure. It is divided into two parts, the Scope window and the Focus window. The contents of the Focus window depend on the object selected in the Scope window.



1. Scope window displays the objects opened in the Object Explorer.
2. Focus window displays the contents of the object selected in the Scope window.
3. Selected object.

Figure 5 Context Window

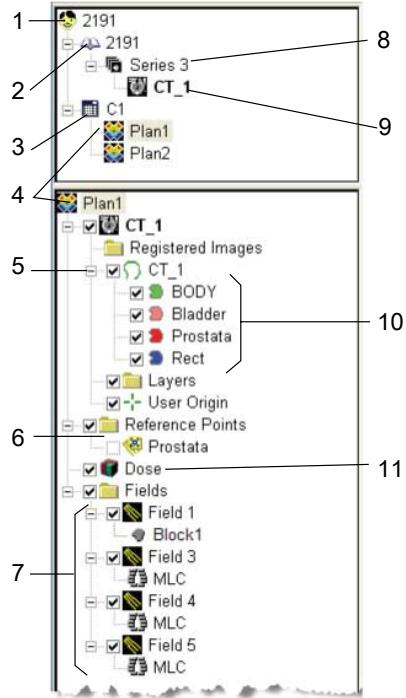
You can control the visibility of objects in the image views by selecting or clearing the visibility check boxes in the Focus window. The active (selected) object is always visible in the image views, regardless of the setting in the visibility check box.



Tip: Remember that you have to select an object in the Context window before you can modify it. For example, to contour a block you have to select the block object associated with the desired field in the Focus window.

Context Window in External Beam Planning

In External Beam Planning, the Context window shows objects relevant in treatment planning and evaluating completed treatment plans.

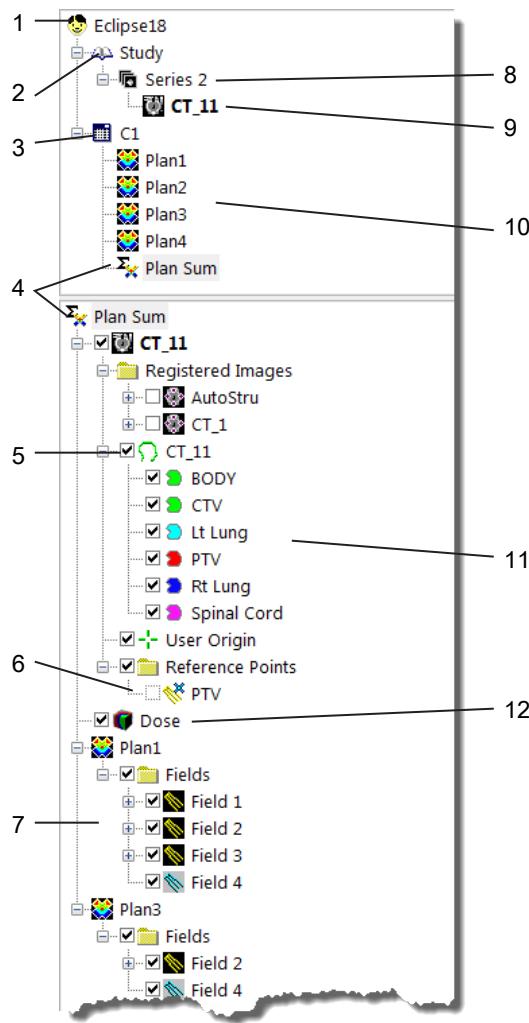


- 1. Patient
- 2. Study
- 3. Course containing two plans.
- 4. Selected plan
- 5. Structure set used in the plan
- 6. Reference points
- 7. Fields and field accessories defined in the plan
- 8. Image series
- 9. 3D image
- 10. Individual structures
- 11. Dose calculated for the plan

Figure 6 Context Window in External Beam Planning for Photons and Electrons

Context Window in Plan Evaluation

In Plan Evaluation, the Context window shows objects relevant in treatment planning and evaluating completed treatment plans.



1. Patient
2. Study
3. Course
4. Plan sum selected for viewing
5. Structure set used in the plan
6. Reference point
7. Fields and field accessories (collapsed in the view) in the plan
8. Image series
9. 3D image
10. Plans and a plan sum contained in the course
11. Structures contained in the structure set
12. Dose

Figure 7 Context Window in Plan Evaluation for Photon and Electron Plans

Managing Data in Treatment Planning

All data you work with is stored in the database, and you load the appropriate data to the memory of your computer to view and modify it. Changes you make to the data are not automatically saved to the database from your computer. To avoid losing important information, you need to save your work regularly.



NOTICE: Apart from saving your work regularly, create regular backups of your system to avoid losing important information. The regular backups should contain patient database including image directories, dosimetric data, and beam data.

Configure the short-date format for your Windows operating system to display the month and year in an unambiguous manner. This is defined using the Region and Language settings in Windows. Using a format like dd MMM yyyy for short dates in the Customize Format dialog box will produce unambiguous date displays for the English locale, for instance, “05 Sep 2013”.



WARNING: The system uses a central database that allows running the application on different workstations simultaneously. If multiple simultaneous users work with the same data, this may lead to situations where another user has modified and saved the data that you are currently working with. Therefore, avoid situations with multiple users concurrently editing the same patient data. If you try to save your changes, the system will issue a warning message about another user already editing the same patient. Always carefully verify the synchronized data, because it may contain changes made by both you and the other user.



CAUTION: Do not use the computer operating system to edit or delete any files used by the treatment planning application except when the use of the files is detailed and supported in the user documentation of the manufacturer of the treatment planning system.

Change Object Properties

Data and settings for all objects can be displayed and modified in the Properties dialog boxes. In this publication, details are described only for the parts of the property dialog boxes that are relevant to treatment planning.

- To display the Properties dialog box of a structure, for instance, select the structure in the Focus window and choose **Edit > Properties** .

Save Your Work to the Database

- Choose File > Save All.

Close an Item

Sometimes multiple objects opened in the Scope or Focus window are distracting. To clean up the view, and to avoid situations where you make changes to the wrong item, you can close extraneous items that you do not need to work with any longer. Closed items are just removed from the application windows; they are not removed from the database.

1. In the Focus or Scope window, select the item to be closed.
2. Choose File > Close.

If you have made changes to the item, you are prompted to save or discard the changes. If there are no changes, the item is closed without prompts.

Preventing Conflicting Edits of Patient Data

When you edit patient data, the treatment planning system retrieves several plans, plan sums and structure sets from the database to ensure the validity of various user operations. Normally these retrievals are invisible to the users, but if multiple users are concurrently editing the same patient's data, it is possible that these retrieved objects affect the planning outcome. For example, you may end up calculating the dose against a structure set which has changed in the database. The Advanced Plan Concurrency Check provides a mechanism that warns you about outdated data and prevents you from saving data dependent on it to the database. The check is performed in External Beam Planning, Brachytherapy Planning, IRREG Planning, Plan Parameters, Reference Points, Plan Evaluation and Contouring applications as well as within Acuity and Cone Planning.

The applications that are part of Eclipse and BrachyVision provide an active visual warning, while the other applications only show a warning during object activation. In both cases, saving the data is prevented in all applications with concurrent editing conflicts present.

The Advanced Plan Concurrency Check is performed on plans, structure sets, plan sums and RT prescriptions. A warning about concurrent editing is shown in the following cases:

- If you activate a plan which has changed in the database, or a plan with calculated dose whose structure set has changed in the database.
- If you activate a structure set which has changed in the database, or structure set with a referencing plan with calculated dose that has changed in the database.

- If you activate a plan sum which has changed in the database, or a plan sum with a member plan which has changed in the database.
- If you try to planning approve a plan linked to an RT prescription that has changed in the database.

In addition, the following is prevented:

- Dose calculation for a plan whose structure set has changed in the database.
- Selection of a plan or plan sum as the base dose plan for IMRT optimization if it has changed in the database.

When you activate a modified plan, structure set or plan sum (for example, by dragging and dropping it in the image views), a warning is shown, stating that the plan, structure set or plan sum has changed in the database, and suggesting for you to reload it. The details in the warning include the ID of the plan, structure set or plan sum that has changed, the User ID of the user who has made the changes, the application in which the changes were made, and the date and time when the changes were made.

When this kind of object is active, a warning icon may also appear in image views. This can happen, for example, when you have a plan open (displayed in the image views), and another user is simultaneously editing the structure set the plan is based on and then saves the changes, or if another user approves the structure set. Note that the warning icon is not available in all applications.

The Advanced Plan Concurrency Check is enabled in RT Administration. It is recommended to leave the Advanced Plan Concurrency Check on to prevent any issues related to concurrent editing.



Note: *If another user has deleted a structure set or a plan that you have had open, and you try to reload the structure set or plan, it will disappear from the context window and image views after the reloading is complete.*

Delete Information from the Database

All data you work with is stored in the database. Since the data modifications made are not automatically saved to the database from your computer, you need to communicate deletions to the database by saving the deletion. To avoid information losses, be careful when deleting information. For example, if you accidentally delete a course or a plan, you can reload the objects from the database to return to the previously saved state.



Note: Patients can be deleted from the database only in RT Administration with sufficient user rights.

1. Choose Edit > Delete.

The information is deleted from the memory of your computer.

2. Choose File > Save All.

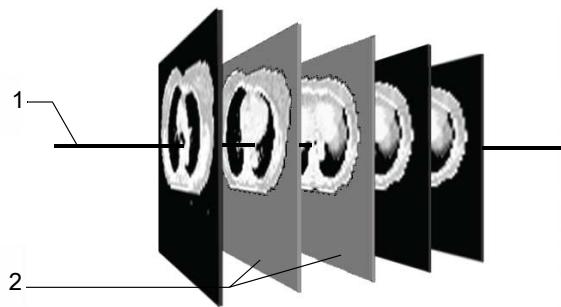
The information is deleted from the database.

Chapter 3 Visualization of Images

About 3D Modeling

Most image studies produced by medical imaging devices and used for radiation treatment planning are arranged as a series of 2D digital images. These images are imported from the imaging devices in digital format. The 2D digital image data is then used as a basis for generating a three-dimensional (3D) model of the patient.

The three-dimensional model, called the 3D image, is formed from a stack of imported 2D slices called the image set. Assuming that the slices in the image set are perfectly aligned and of exactly the same size, their outer limits would form the outer surface of the 3D model as in the following figure.



1. Normal
2. Interpolated planes

Figure 8 Stack of 2D Images

The gaps between the slices can vary considerably. In order to render the best 3D model possible, planes are interpolated into larger gaps between actual slices to make the image planes equidistant. If the 3D image contains interpolated image planes, a new image series is created in the database. This image series consists of the interpolated slices and copies of the actual image slices.

The slices used in constructing the 3D image must have parallel normals, and the image planes may not be rotated around the normal.

By using the treatment planning applications, you can overcome inconsistencies in the images, for instance, differences in coordinate axes or image sizes.

About 4D Modeling

Motion of the patient during CT imaging can create unwanted motion artifacts that can change the apparent geometrical shape and/or location of the organs or the target structure. Four-dimensional (4D) imaging introduces the additional dimension of time that accommodates movement during imaging. With 4D imaging, it is possible to view structure movement.

In 4D imaging, image data sets are typically obtained at various stages of the respiratory cycle. The obtained image data is binned; 3D images are organized according to the stages of the respiratory cycle using a third party external program. The image data can be either phase-binned (phase of a respiratory cycle) or amplitude-binned (such as breathing amplitude). These image data sets are then used for creating 4D images. A 4D image can be considered as an ordered set of 3D images.

A 3D image that is part of a 4D image study can be one of the following image types:

- Free Breathing image (FB)—A conventional CT scan where the patient is scanned without an attempt to control the patient's respiratory cycle or correct the CT scan data for respiration movement
- Phase image—An image taken during a particular phase of the respiratory cycle and labelled with a phase number (for example, 50%, 60%). Phase images can be displayed in a movie loop.
- Maximum Intensity Projection image (MIP)—An image containing the maximum intensity pixels derived from all phases. A MIP image is useful, for example, for showing bones, or a tumor that is of higher density than the surrounding area.
- Average image (Ave)—An image where the image data values for each pixel on each slice are averages of all the image values at the same pixel locations on the corresponding slices in each bin.
- Minimum intensity projection image (Min or MinIP)—An image containing low-intensity pixels derived from all phases.

A 3D image can belong to only one 4D image. A 4D image can contain only one 3D image of each type, except phase images, for which the phase numbers have to be unique.

You can view 3D images that are part of a 4D image in a movie loop or blended, and also display DRR images for them.

If you plan a treatment on the basis of a 4D image study and intend to apply heterogeneity corrections, do not use images with scaled HU values (MIP or MinIP images) for the primary 3D image. Instead, create a 3D image that is based on the average respiratory phase or on a particular respiratory phase itself.



Note: To find out more about the supported gated treatment techniques, refer to the documentation of the treatment unit to be used for the gated treatment.

Coordinate Systems

Three-dimensional modeling is based on a planning coordinate system that defines a static, clinic-wide coordinate axis system. The planning coordinate system defines how the (image) coordinate values entered in the system are interpreted. The planning coordinate system can be set to conform to the following room-based coordinate systems: the Standard coordinate system, IEC 61217 coordinate system, and a user-defined image coordinate system. In these cases the planning coordinate system is independent of any patient coordinate system. In addition, the planning coordinate system can be set to conform to the patient-based DICOM coordinate system.

The planning coordinate system is configured in RT Administration. The system should be configured to correspond to the coordinate system of the primary treatment unit.



Note: If you change the coordinate system, the directions of the coordinate axes described here are no longer valid.

More information on modifying the axis orientations: *RT and Imaging Online Help*.

Standard Coordinate System

By default, the planning coordinate system is set to conform to the Standard coordinate system, in which the Z-axis points towards the gantry, the X-axis points to the right when facing the gantry, and the Y-axis points towards the floor. In the figure, the DICOM patient orientation is Feet First Supine (FFS), but it has no effect on the Standard coordinate system.

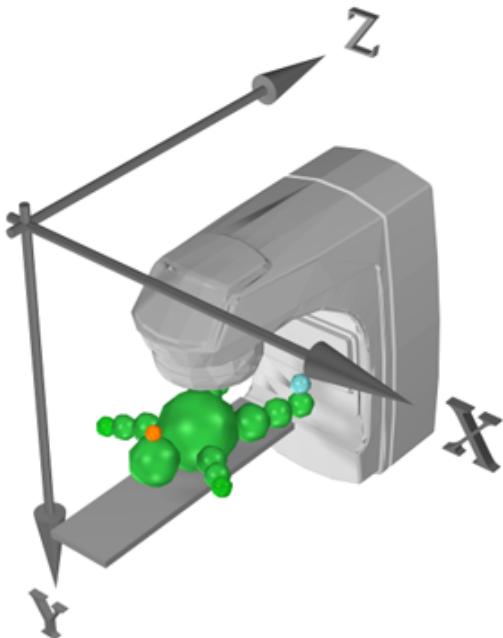


Figure 9 Standard Coordinate System

IEC 61217 Coordinate System

The planning coordinate system can also be set to conform to the IEC 61217 coordinate system. In this coordinate system, the Y-axis points towards the gantry, the X-axis points to the right when facing the gantry, and the Z-axis points towards the roof. In the figure, the DICOM patient orientation is Feet First Supine (FFS), but it has no effect on the IEC 61217 coordinate system.

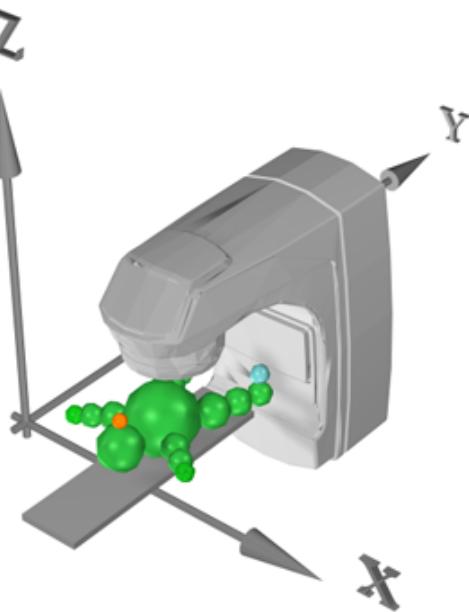


Figure 10 IEC 61217 Coordinate System

User-Defined Coordinate System

If neither the standard nor IEC 61217 coordinate system meets your clinical requirements, the system allows defining an arbitrary right-handed coordinate system. Use a descriptive name for the coordinate system.

DICOM Coordinate System

The DICOM coordinate system, used in imaging devices, can also be used as a patient-based planning coordinate system in treatment planning applications. The DICOM patient coordinate system is based on three axes (X, Y and Z).

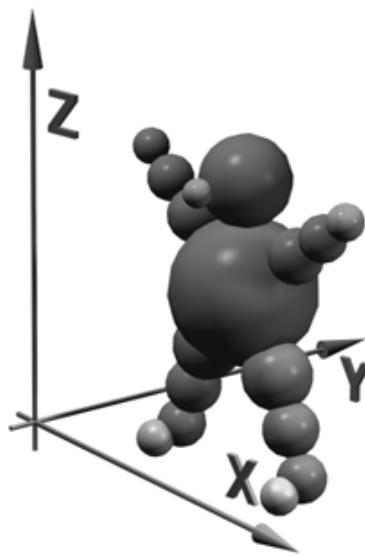


Figure 11 DICOM Coordinate System

In relation to the patient, the Z-axis is the feet–head axis. The Y-axis is the front–back axis, and the X-axis the shoulder–shoulder axis. The directions of the axes are always the same and do not depend on the position of the patient on the couch.

Image Views

The imported images which are included in the image set of the patient can be examined in two kinds of views: 2D views and 3D view.

The 2D image views display planes extracted from the 3D image. They can also display original individual 2D slices.

The 3D view is designed for examining the structure model of the patient.

For external beam plans, it is also possible to display live DRR images, field images (static DRRs, portal and simulation images), fields, orthogonal planes, and the dose distribution in the 3D view.

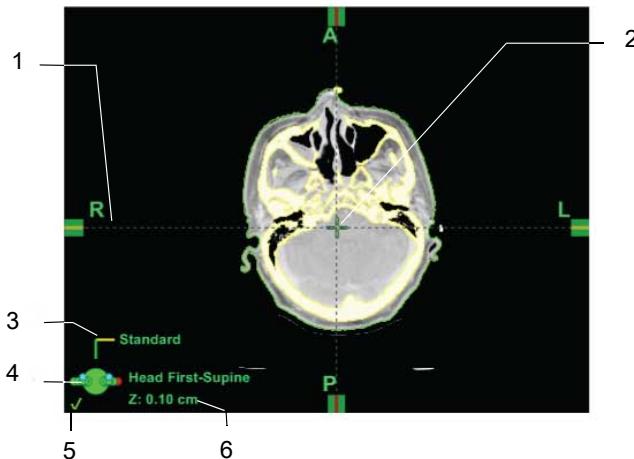
All objects are visualized both in the 2D and 3D views. This does not necessarily give a realistic visualization in all views, but an object can be shown realistically in a 2D view and as a symbol in a 3D view.

Related Topics

[3D View](#) on page 49

2D Views

The 2D views display two-dimensional planes, either those extracted from the 3D model or original slices. In everyday terms, you could think of these views as “flat”. The position, layout and size of the 2D views depend on the current application.



1. Plane sliders and patient orientation labels
2. Image origin
3. Axis orientation
4. Patient orientation
5. Approved image marker
6. Position of plane on Z-axis (shown only if selected in the View Options dialog box)

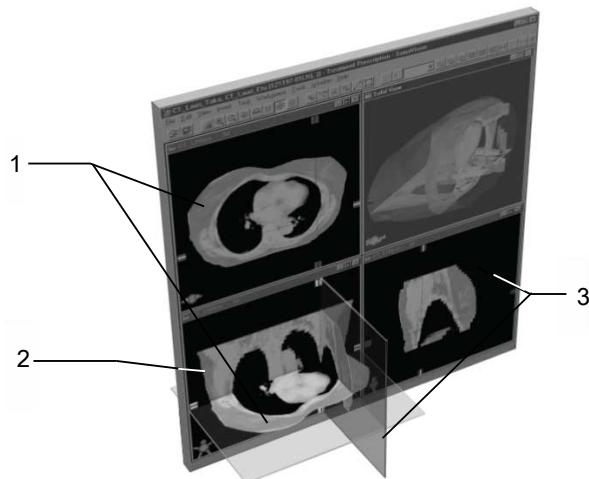
Figure 12 2D Image View



Note: The planes displayed in the 2D views are not necessarily the actual CT or MR images taken of the patient. When a 3D image is viewed, the 2D views display planes that are constructed from the 3D model.

Orthogonal Views

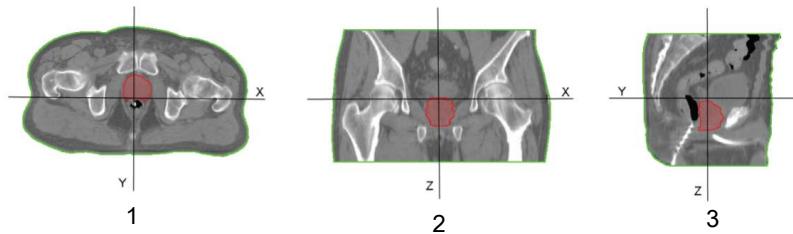
The 3D model displayed in the 3D view is divided into three orthogonal viewing planes, each displayed in their own view. By default, these viewing planes are transversal, frontal and sagittal.



1. Transversal plane
2. Frontal plane
3. Sagittal plane

Figure 13 Viewing Planes in Relation to 3D Model

By default, the 2D views, in which the viewing planes are displayed, are defined by three coordinate axes, namely the X-, Y- and Z-axis of the patient coordinate system.



1. Transversal
2. Frontal
3. Sagittal

Figure 14 Directions of the Orthogonal (2D) Views

In the transversal direction (1 in the figure), you are looking either up or down along the Z-axis at the XY-plane. The X-axis runs left and right, and the Y-axis up and down. The Z-axis is the primary axis in this direction.

In the frontal direction (2 in the figure), the X-axis runs left and right. The direction of the Z-axis is vertical, and you are looking at the image along the Y-axis. The Y-axis is the primary axis in this direction.

In the sagittal direction (3 in the figure), the Y-axis runs horizontally left and right. The Z-axis is vertical, and you are looking at the image along the X-axis. The X-axis is the primary axis in this direction.

Orthogonal planes can be freely rotated with the mouse. Once the orthogonal planes are rotated and zoomed as desired, it is possible to save the viewing plane setup as default.

On image planes along the primary axis (most often this is the transversal plane along the Z-axis), images are rendered using bilinear interpolation, and on oblique planes, images are rendered using trilinear interpolation.

3D View

The 3D view displays the three-dimensional (perspective) structure model of the patient. The 3D view is shown in the Model view. The location of the Model view on screen depends on the selected application.

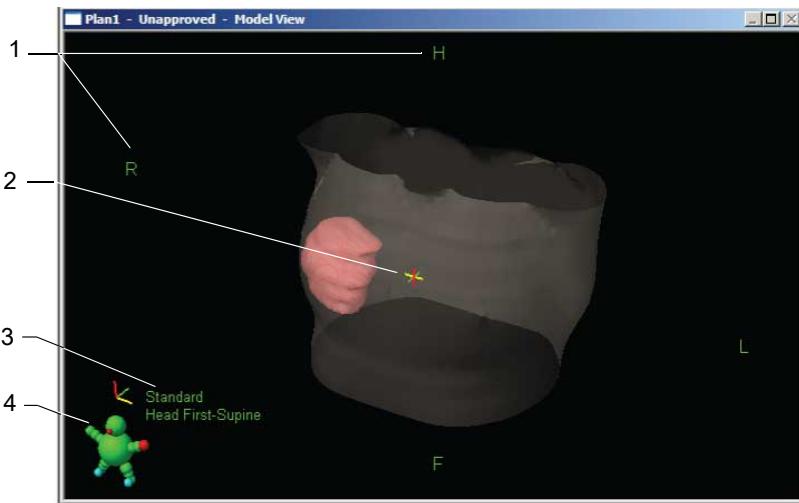
In External Beam Planning, a 3D image can also be viewed in the Beam's Eye View (BEV).



Note: Since the 3D view is a perspective view and the proportions in the image are not realistic, measurements done in it are not reliable.

Model View

The Model view displays the structure model of the patient from a freely selected viewing angle. By means of the viewing tools, you can change the viewing angle by rotating the structure model.



1. Patient orientation labels
2. Image origin
3. Clinic axis setting symbol and label
4. The patient orientation indicator shows the viewing angle to the patient

Figure 15 Model View

How the structures are displayed in the Model view depends on the color and style selected for the structures.

Related Topics

[Using Color and Style for Structures](#) on page 52

Patient Orientation Labels

You can show patient orientation labels next to the plane sliders in the image views to indicate the orientation of the patient. This option is defined in the View Options dialog box.

Table 1 Patient Orientation Labels

Indicator	Meaning
A	Anterior
F	Feet
H	Head

Indicator	Meaning
L	Left
P	Posterior
R	Right

Patient Orientation Indicator

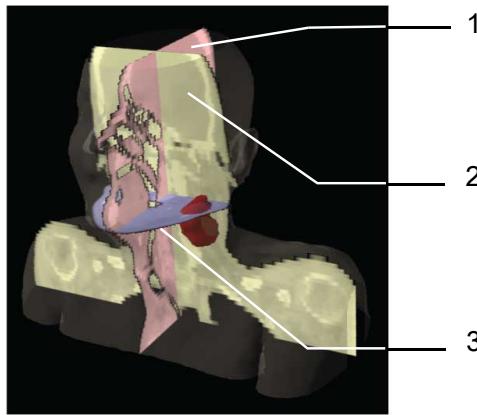
The patient orientation indicator, visible in the image views, shows the viewing angle to the patient. The red dot represents the patient's left hand. The following table lists some examples of the patient orientation indicator.

Table 2 Patient Orientation Indicators

Indicator	Meaning
	You are looking at the patient's face, along the Y-axis
	You are looking at the patient's back, along the Y-axis
	You are looking at the patient's head, along the Z-axis
	You are looking at the patient's feet, along the Z-axis
	You are looking at the patient's left side, along the X-axis
	You are looking at the patient's right side, along the X-axis

Orthogonal Viewing Planes and the Model View

The viewing planes extracted from the 3D image can be displayed in the Model view. The planes can perpendicularly intersect each other at any point.



1. Sagittal plane
2. Frontal plane
3. Transversal plane

Figure 16 Orthogonal Planes in Model View

Moving or rotating the planes in the orthogonal 2D views updates the Model view accordingly. You can also browse through the image planes in the Model View.

Using Color and Style for Structures

The selected display color and style defines how structures (for instance, Body, Bone or Target structure) are displayed in the 3D and 2D views.

The style options for structures are:

- Contour lines
- Solid surface
- Translucent surface
- Pre-defined renderings (for air channels, bone and skin)

All viewing colors and styles are available for all structures in all image views. However, structures displayed as translucent surfaces in the Model view are displayed as contours in the 2D image views. If you choose to display a structure as a solid surface in the Model view, it is rendered as a filled area in the 2D image views. Moreover, some styles can be displayed differently in 2D and 3D views. Configure color and style settings in RT Administration.

The 2D color defined for a structure is also visualized with an icon next to the structure ID in the Context Window. The icon also indicates whether the structure has been contoured or not:

-  —Indicates a structure that is not contoured.
-  —Indicates that at least one slice of the structure has been contoured.

When you change the color and style settings of a structure, the change is applied to all images under the patient.

The figure shows Body and Lung structures displayed using a different style in the Model view. The left picture uses Contour lines to represent the Body structure and Segment to represent the Lung structure. The right picture uses Translucent Body rendering and displays the Lung structure as a Translucent Segment.

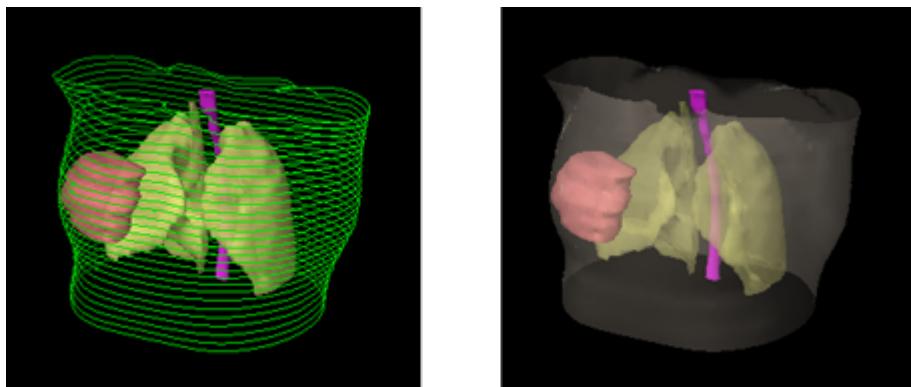


Figure 17 Body and Lung Structures with Different Styles

For surface models, different levels of transparency can be configured, which can be useful in viewing several overlapping structures in the Model view. You can display the innermost of these structures as a solid surface, and increase the level of transparency for the structures overlapping it.

**Note:** Selecting color and style is possible only for structures.

Select Color and Style for a Structure

1. If necessary, in the Focus window, display the structure set and the structures belonging in it.
2. Right-click the structure whose color and style you wish to change and choose **Color and Style**.

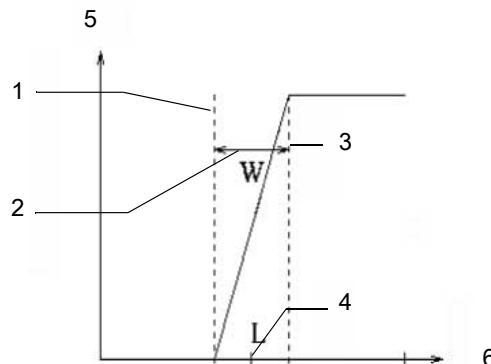
3. In the **Color and Style** drop-down list, select the desired appearance.
4. Click **OK**.

The change is applied to all images under the patient.

Changing Brightness and Contrast

You change the image brightness and contrast in the image views by modifying the window/level settings. Adjusting the window/level setting defines the contrast of pixels within the specified window range. The broader the range, the lower the contrast. The range is defined by two modifiable parameters:

- Window—Width of the range selected from the scale
- Level—Middle point on the selected range.

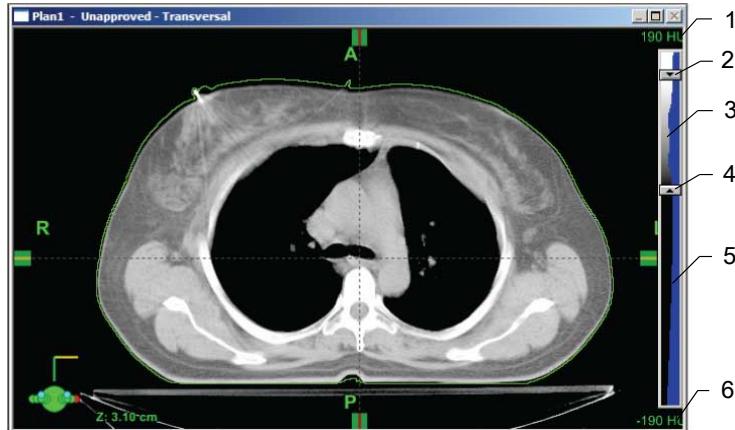


1. Lower window value
2. Window values
3. Upper window value
4. Level value
5. Screen gray-scale display values
6. Hounsfield units (HU)

Figure 18 Window/Level Parameters

Image Histogram

When you select the command to modify the window/level settings, the window/level slider with the image histogram appears to the right-hand side of the 2D image views.



1. Selected upper window value
2. Window/level slider
3. Level
4. Window/level slider
5. Grayscale histogram
6. Selected lower window value

Figure 19 Window/Level Slider and Image Histogram

The currently selected upper and lower window values are shown above and below the slider bar. You change the window/level settings by moving the sliders, and the level settings by moving the middle area between the sliders.

The image histogram is a graphical representation of the CT or grayscale values in the image. The range of the values appears on the vertical axis, and the horizontal axis indicates the portion of the image's values that match each point on the range.

When you adjust the window/level settings of an image that is part of a 4D image, the change affects all the images in the 4D imaging study.



Note: By default, the slider is displayed only in one 2D view. You can show the hidden slider in the other image views by maximizing the view.

Window/Level Presets

When working with CT images, you can use window/level presets to visualize different anatomical features better during contouring and planning. The window/level presets can also be used during automatic image registration using pixel data.

More information about automatic image registration: *Registration, SmartAdapt and Contouring Instructions for Use*.

Table 3 Default Values for Window/Level Presets

Preset name	Lower Level (HU)	Upper Level (HU)
Abdomen	-125	225
Bone	-400	800
Cerebellum	-20	100
Liver	-25	125
Lung	-1000	0
Pelvis	-160	240
Breast	-250	150
Acquisition W/L	Sets the window/level to the values used during image acquisition.	

You can open the menu containing the window/level presets by pressing the Ctrl key and right-clicking the window/level slider bar.



Note: Window/level presets can be modified in the SmartAdapt application.

More information: Registration, SmartAdapt and Contouring Reference Guide.

Adjust Window/Level Settings Automatically

- Choose View > Auto Window/Level.

The window level is set to an overview value.

Display the Slice Position

- Choose View > Options.
- Go to the General tab and select the **Display slice position** check box.
- Click OK.

The coordinates of the plane currently displayed in the 2D image views are shown in the lower left corner of the view.

Show Images with or without Interpolation

- Choose View > Options.
- To remove the tri-linear interpolation of the images, go to the General tab and clear the **Display images interpolated** check box.

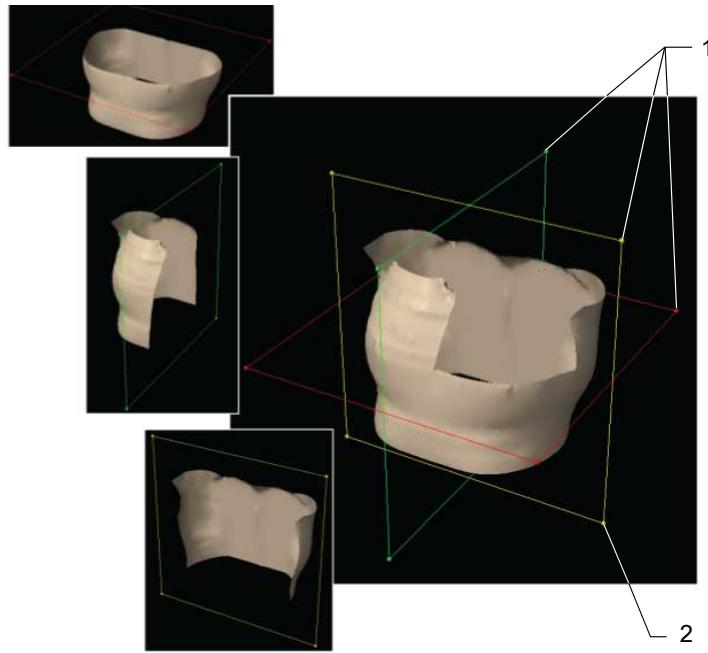
To show the images with interpolation, select the check box.

3. Click OK.

This option does not affect the BEV in Eclipse.

Clipping Structures

To better view structures under or behind another structure in the Model view, you can cut away part of the Body structure to see the target structures underneath.



1. Clipping planes
2. Moving handle

Figure 20 Clipping Structures

Clip a Structure

1. In the Focus window, select the structure to clip.
 2. Click the title bar of the Model view to activate it.
 3. On the Clipping Planes toolbar, click **Clipping Planes** .
 4. On the Clipping Planes toolbar, click the Clipping Planes buttons .
- The selected clipping planes appear in the Model view.

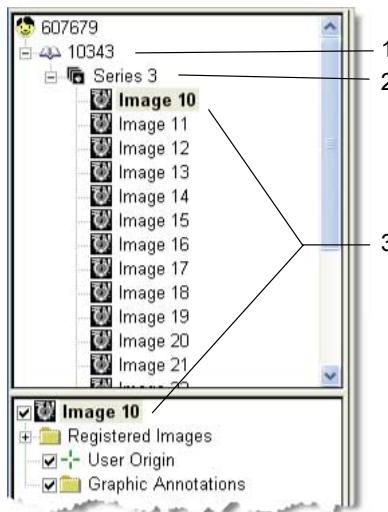
5. Do one of the following:

- To resize the clipped parts of the selected structure, move the planes with the mouse.
- To switch the part shown, press the Ctrl key and click the moving handle of the plane.
- To show the CT data on the planes, press the Ctrl and Shift keys and click a Body structure plane handle.

Chapter 4 Working with Images

Viewing Images in the Context Window

Below is an example of the Context window in the Selection workspace after an image series has been imported to a patient.



1. The Study the image series belongs to
2. Image series
3. The image selected in the Scope window is displayed in the Focus window

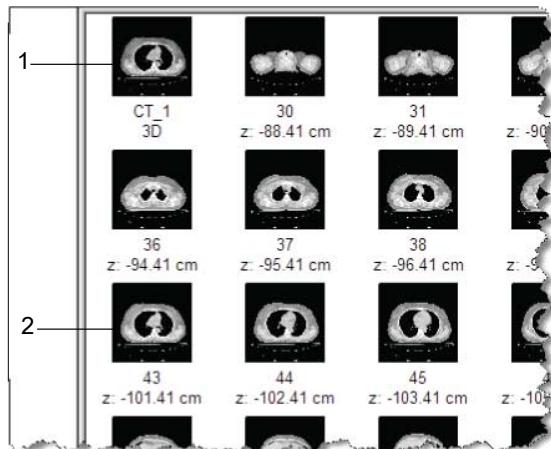
Figure 21 Images in Context Window

The image series and the study that the series belongs to are displayed under the patient in the Scope window. In the DICOM hierarchy an image series belongs to a study. In the example, the ID of the study is 10343.

The image series has a unique ID and the series contains images of the same modality. In the example, the ID of the image series is Series 3. Each image has a unique ID within an image series. You can have multiple images with the same ID (for example, CT_1), but they all must belong to different image series.

Viewing Images in the Image Gallery

After opening a patient with images to the Selection workspace, you can view the images in the Image Gallery.



1. 3D image
2. 2D image

Figure 22 Image Gallery

The images are arranged by their Z coordinates in descending order (usually from head to feet). The images can be 2D images or 3D images. 3D images are identified by the 3d string under the thumbnail. For 2D images, the direction of the image plane is indicated by their X, Y or Z coordinate values under the thumbnails. If a 2D image is not parallel to any of these three axes, the axis is replaced with d (distance between planes).

Select the Viewing Direction for Images

In orthogonal views, the orthogonal planes for 3D images are, by default, displayed in the directions of their primary axis. You can also force the 3D image to be displayed in the transversal direction.

1. Choose **View > Options**.
2. Select the Selection Workspace tab.
3. Clear the **Ortho Cube Adapts to Plane Normal** check box.

- Click OK to show the 3D image in the transversal direction.

Viewing 4D Images

After opening a patient with 4D images, the 4D image objects appear in the Scope window. When a 4D image object is dragged into the image view, the first 3D image in the 4D imaging study opens in the three different orthogonal image views and the detailed information about the 3D image is displayed in the Focus window.



NOTICE: Visually verify the display of 4D images in the application to confirm proper organization of the 3D images into a series of images that represent the breathing cycle.

The topmost item in the Focus window, the primary image, is the active 3D image dragged into the image view (if the 4D image object is dragged into the image view, then the primary image is the first 3D image in the 4D imaging study). You can show other 3D images of the 4D imaging study in the image views by selecting their visibility check boxes. When you segment structures in a visible 3D image, the segmentation is always saved to the primary image.

The Registered Images folder contains all the images registered with the primary image. These include the 3D images in the 4D imaging study, and can also include other 4D image objects. The IDs of the 3D images are created based on the information in the image series comments. The 3D image values, defined in the 4D Image Properties dialog box, are displayed in parentheses after 3D image IDs. You can modify both the IDs and values of the 3D images.

The structures shown under the structure set icon in the Focus window are a collection of structures from the 3D images belonging to the 4D image study. The structures contoured in the active image are shown with the contoured structure icon (red dot).

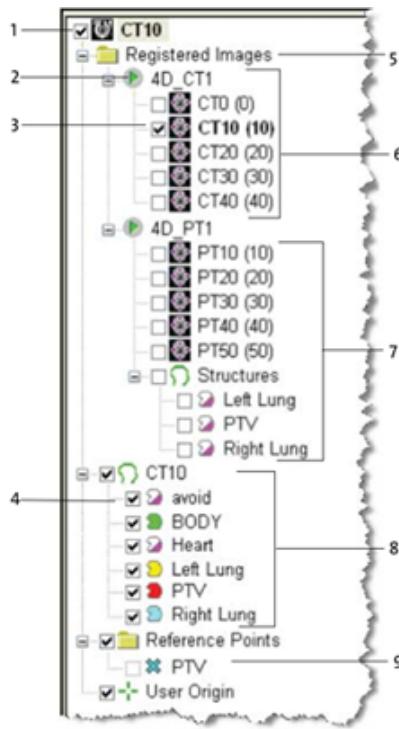
If a structure has no segmentation in the currently visible 3D image, it is indicated with an empty structure icon (see 4 in the figure). If structures have been contoured in the 3D images that belong to registered 4D image study, they are shown under the structure set icon of the registered image (see 5 in the figure).



Note: You can check which structures have been contoured in each registered 3D image by opening Object Explorer and viewing the structure sets in the All Structure Sets folder.

When you define structure visibility in a 3D image that is part of a 4D image, the visibility settings are applied to all 3D images in the 4D image. Similarly, if you modify the properties of a structure, the change is applied to all images under the patient.

The Reference Points folder contains all the reference points defined for the patient. When you are viewing a plan, the Reference Points folder displays the reference points belonging to the plan. If a reference point has no location in the currently visible 3D image, you cannot select its visibility check box.



1. Primary image
2. 4D image object
3. 3D image currently visible in the image views
4. Structure that has no segmentation in the currently visible 3D image
5. Folder containing all the images registered with the primary image
6. All the 3D images in the 4D imaging study
7. G. All the 3D images and the structure set of in the registered 4D imaging study
8. Structure set and structures defined for the patient
9. Reference points defined for the patient/plan

Figure 23 4D Image Visibility in the Focus Window

When a structure is selected in the Focus window, in addition to showing the contour or segment of the selected structure in the current 3D image, the image view shows and highlights the contour or segment of the selected structure in the primary image.

If you modify the window/level settings or resize the VOI for an image that is part of a 4D image, the change is applied to all images in the 4D imaging study. These changes are also saved to the database.

If you zoom in or out, pan or rotate an image view of an image that is part of a 4D image, the change is applied to all image views in the 4D imaging study.

View DRR Images in the Selection Application

1. In the Selection application, open the Object Explorer.
2. Select the **DICOM View** branch.
3. Select the study and series.
4. Click the DRR that you want to view.
5. Click **OK**.

The DRR image object appears in the Scope window, and the DRR image is displayed in the 2D image view.

In an external beam plan, also the field edges are displayed in the DRR image.



Tip: You can also drag DRR images from the Image Gallery to the 2D image view.

To print out the DRR image, print the image view where it is displayed, or use DICOM print.

Crop an Image

Sometimes an image may have areas that must be removed. When you crop an image, only the cropped area of the image will be saved.



Tip: Images can be cropped only before saving them to the database. Crop images before you create a 3D image and save them.

1. Drag the image you want to crop to the image view.
2. Click in the image view to make it active.
3. Choose **Image > Crop/Extract**.
4. Click in the image view.
5. In the Crop/Extract dialog box, click the **Crop** option button.

6. In the image view,
 - To resize the crop area, drag its handles.
 - To move the crop area, move the mouse pointer inside it and drag it to a new position.
7. Once you are satisfied with the crop area, click **OK**.
8. To save the changes, choose **File > Save All**.
9. To crop successive images, click in the center of the image to place the crop box in the same place as the last. The ability to define the crop area only happens the first time the Crop/Extract tool is used.

Extracting Images

Sometimes images are imported as scanned films consisting of a number of images. To be able to create 3D images of these scanned images, you need to extract the images from the films. The X and Y coordinates needed for the 3D image are defined as extraction parameters.

When extracting images, define two parameters in the Crop/Extract dialog box: the Position of the images and the Step between the images.

- Position—Position refers to the coordinates of the images on the film. View the film to find out the sequence of the images before beginning the extraction.
- Step—Step indicates the increment between the image coordinates on the film. Once you have defined the value, the position for the next image is calculated automatically. However, verify from the film that the increment is consistent throughout the film before using the automatic step calculation.

Extract an Image from a Film

1. Import the desired scanned film.



Note: Calibrate scanned films before doing the image extraction, if the film has not already been calibrated, to make sure that the planning based on the images is accurate.

2. Drag the film from which to extract the images from the Image Gallery to the image view.
3. If necessary, enlarge the image.
 - To magnify the film image, click **Zoom In**.
 - To enlarge the whole image view, click the **Maximize**  button in its upper right corner.
4. Choose **Image > Crop/Extract**.
5. Click in the image view displaying the film from which to extract the images.

6. In the Crop/Extract dialog box, click the **Extract** option button.
7. To have the selection tool maintain the shape of a square, select the **As square** check box.
8. In the image view,
 - To resize the extract area, drag its handles
 - To move the extract area, point inside it and drag it to a new position



Note: Ensure that the CT scale is also included in the area you select.

9. When the extract area is as desired, make sure that the extract tool appears exactly in the same place in the next image. Find a focal point in the image film that appears in exactly the same position in every image and right-click that point. This point will be used to align the images when creating the 3D data set. A cross appears where you right-clicked.
10. In the **Pos [mm]** text box, type the coordinate of the image. This information should be found on the scanned film.
11. In the **Step [mm]** text box, type the increment between the image coordinates on the film.



Note: Make sure that this information is correct, because it is used to generate the 3D data set and cannot be changed afterwards.

12. If the default settings are inappropriate, define the orientation of the patient in the image by clicking **Orientation**.
13. To select the orientation, click the appropriate button.
14. Click **OK** to return to the Crop/Extract dialog box.
15. To complete extracting the first image, click **OK**.
The extracted image opens in the Image Gallery with its ID and primary axis coordinate.
16. To move to the next image on the film, choose **View > Pan** .
17. Choose **Image > Crop/Extract**.
18. Place the mouse pointer on the focal point in the image and click the left mouse button.
The previously defined square appears in the image view. The image position data is automatically updated in the **Position** text box.
19. Make sure that the position and step values are still correct, and to complete extracting the second image, click **OK**.
The extracted image opens in the Image Gallery with its ID and coordinate.

20. Move to the next image in the film and repeat the necessary steps until you have extracted all the desired images from the film.
21. To save the changes, choose **File > Save All**.

Extending a Scanned Image Set

Selected image sets should be large enough to cover all of the areas of interest in the patient. This ensures that sufficient data is available for treatment planning, and helps to improve the handling of the image set when building a 3D image. In the 3D image, the patient surface is not automatically closed at the ends of the image, so the three-dimensional patient model resembles a hollow tube with open ends.

Because of the characteristics of the 3D image resembling a hollow tube, there are inaccuracies in dose calculation in External Beam Planning when using large or tangential fields entering the patient through the end of this hollow tube.

In External Beam Planning, to prevent inaccuracy in dose calculation due to the open ends of the 3D image, you can create artificial CT slices to be used for closing the 3D image. Artificial slices can be created in Eclipse after importing the scanned image set, or during patient imaging in the CT scanner. In Eclipse, the slice added to the slice set can be an artificial slice with a uniform density value or a copy of an existing slice.



Note: Always make sure that the images cover all necessary areas of interest in the patient.

Related Topics

[Field Types](#) on page 176

Extend an Image Series with Artificial Slices

1. Open the image series to be extended, for instance, a series where body pixel values can be found on the last slices or one with a limited number of slices.



Note: Be sure to open all slices in the scanned image set.

2. In the Image Gallery, select one of the image slices.
 - If you are going to add a copy of a slice, select the slice to be copied.
 - If you are going to add an empty slice, select any slice.
3. Choose **Image > Duplicate**.

4. In the **Position <z/y/z/d** box, type the coordinate of the position along the X, Y, Z or oblique axis to which to add the new slice. The axis shown depends on the primary axis of the selected slice.
 5. Do one of the following:
 - To add an empty slice, select the **Fill with** check box and type the desired density value to be used for all pixels in the slice. The units of this value depend on the image modality (HU for CT images; no unit for MR images).
 - To add a copy of the selected slice, clear the **Fill with** check box.
 6. Click **OK**.
- The new slice is added to the defined position on the primary axis.
7. Create a 3D image.

Parameters Used for Constructing 3D Images

3D image parameters are set in the Create 3D Image dialog box.



Note: Normally, the construction parameters that the application suggests are the most appropriate ones for the selected slice set.

First, give the 3D image you are constructing a name and ID and define the pixel size of the image. Generally it is not necessary to change the image size; the default size is correct.

If the slices are unevenly distributed, select the slices to use in the construction of the image, and the bind slice that must be represented as a plane in the 3D image. You can also define the current plane setup by defining the desired separation between the planes (in cm). The separation affects the number of interpolated and original planes in the image. Interpolated planes are automatically created estimates to make the 3D image as coherent as possible.



Note: If the 3D image contains interpolated planes, a new image series that contains the interpolated planes and copies of the original slices is created in the database. Also, if you create a 3D image by manually selecting slices from multiple image series with the same DICOM FOR (this may be necessary, for example, if the imaging device has created several image series during one imaging session), the slices will be copied into a new image series in the database.

By default, the user origin of the images is set to the DICOM origin. In many cases, it is more useful to set the origin so that it helps to identify locations and volumes needed in treatment. For example, the origin could be a clearly visible object, such as a bone structure, or a location easy to use in patient marking.

If the imaging device has had a reversed Z-axis (left-handed coordinate system), you can invert the image slice order before creating the 3D image.

Related Topics

[Inverting the 3D Image Slice Order](#) on page 73

Creating 4D Images

4D images are four-dimensional images created from multiple 3D images that have the same coordinate system (DICOM Frame of Reference) and modality. 4D images can be created either automatically (using all images in a 4D imaging study) or manually (using a range of manually selected 3D images in a 4D imaging study). To create a 4D image, you import the desired images, or if the image import is already done, open the 4D imaging study of the desired patient and continue by choosing the New 4D Image command.

You can also delete a 4D image. When deleting a 4D image, only the 4D image object is deleted from the Context window. All the 3D images that were part of the 4D image are still present and can be used in a new 4D image.

Create a 4D Image

1. Do one of the following:
 - Choose **Insert > New 4D Image**.
 - Select the 3D images from the Image Gallery by holding down CTRL and clicking the images. Then choose **Insert > New 4D Image**.
2. Type the appropriate identification information in the **ID** text box.
3. To set or change the image type in the 3D Images Included list box, click the **Type** cell of a 3D image and select an image type from the drop-down list that opens.



Note: Only phase images can be displayed in a movie loop.

4. To define the images displayed in the movie loop, select the check boxes of the 3D images.
5. To add 3D images to the 4D image, click **Add 3D Images**, select the desired images in the Add 3D Image dialog box that opens, and click **OK**.

To select several 3D images, hold down the Ctrl key while clicking the images.

You can only add 3D images that have the same coordinate system (DICOM Frame of Reference) and modality. If you select 3D images of a different modality or geometry, the **OK** button will be unavailable.

6. To remove 3D images from the 4D image, select the 3D images from the 3D Images Included list box and click **Remove 3D Image**.
7. Click **OK**.
The new 4D image object appears in the Scope window and the Movie Control tool appears in the image views.

Delete a 4D Image Object

1. In the Scope window, select the 4D image object to delete.
2. Choose **Edit > Delete**.
3. Click **Yes** in the confirmation dialog that opens.

The selected 4D image object is deleted. The 3D images it contained are still present and can be used for a new 4D image in the Selection workspace.

Create a Phantom Image Set

1. Choose **Insert > New Phantom Image Set**.
2. Do the following:
 - Type an ID for the phantom image.
 - Select the desired orientation in the **Patient Orientation** drop-down list.
 - Define the size of the image set in X- and Y-directions in pixels and in cm.
 - If you are creating a 3D phantom image set, define the number of planes in the image set, and the separation between the planes.
3. Click **OK**.
4. Continue by creating structures and structure outlines in the phantom image set.
5. To correctly calculate the dose using the phantom, assign CT values for the structures.

Using User Origin for Calculating Couch Shifts

The user origin can be used for automatically calculating the couch shifts required for the patient treatment. The user origin can be set to a reference setup point, such as the simulation isocenter. You can use the user origin to mark a reference setup point in the patient, such as the simulation isocenter (from the CT scanner or a conventional simulator). As an aid for setting the user origin, you can mark the reference setup points in the patient with fiducial markers during a treatment planning imaging session. When the images are imported to Eclipse, the reference setup points are visible in the images.

During treatment planning, you can calculate the required relative couch shifts in Eclipse from the user origin to the treatment isocenter(s). The calculated couch shifts, or the delta couch shifts, are shown in the treatment report of the plan, and in the Field Properties dialog box. You can also manually edit the calculated couch shifts using the Delta Couch Shift Editor.



WARNING: Verify and confirm the patient setup with an appropriate position verification method before treatment, especially when the delta couch shifts are used.

Sample plans may be generated using, for example, anthropomorphic phantoms and actual patient setup positions compared directly with couch shift values printed from Eclipse.



Note: The user origin must be placed to the reference setup point, such as the simulation isocenter for the results of the couch shift calculation to be usable and correct for the particular patient treatment.

Editing Image Parameters

Sometimes imaging sources do not transfer all the necessary information with the images. In this case, edit the image parameters separately.



Note: Be especially careful when changing image parameters. Changing the parameters has far-reaching effects, and making inappropriate changes may cause serious problems in the system.

Image parameters are managed in the Image Properties dialog box. In the tabs of the dialog box, the image properties can be quickly reviewed and changed if needed. The instructions provided here are only for parameters that can be modified.

In the General tab, define a name and status for the image. You can also change the horizontal and vertical labeling of the image.

In the Comments and Remarks tabs, type additional information about the images that you think is useful for yourself and other users. New comments overwrite the old ones. Remarks are written in the image properties and cannot be overwritten. Additional remarks can be made and appended.

Changing the Image Orientation

Sometimes an image produced by an imaging device can have an incorrect patient orientation indicator in the image view. For example, even though the slice image is a transversal image taken from the direction of the patient's feet, the patient orientation indicator may show that the image was taken from the direction of the patient's head.

When you change the image orientation, a new image series with the changed orientation is created in the database.

It is not recommended to change the image orientation for images used in a 4D image as it may cause unpredictable results in 4D image visualization.



Note: *The Pencil Beam Convolution, Generalized Gaussian Pencil Beam and Electron Monte Carlo calculation algorithms require that the image set is constructed from transversal slices and that the Z-axis of the 3D image runs from the feet to the head of the patient. All other image orientations result in an error message and abortion of the calculation.*

Change the Image Orientation

1. In the Image gallery or Scope view, select an image or an image series.
2. Choose **Image > Change Image Orientation**.
3. Select the orientation that matches the orientation of the image.
 - To change the orientation and close the dialog box, click **OK**.
 - To define the orientation angles in degrees, click **Advanced**.
4. Type the angles in the text boxes.
 - **Alpha** is the rotation angle around the X-axis.
 - **Beta** is the rotation angle around the Y-axis.
 - **Gamma** is the rotation angle around the Z-axis.
5. Click **OK**.

The angles are changed and the dialog box closes. If you changed the orientation of an image series, the new image series with the changed image orientation is shown in the scope window.



Tip: *To verify that the image has the correct orientation assigned to it, open it in an image view. The patient orientation indicator now reflects the new orientation of the image.*



Note: *Changing the orientation of PET images is not supported.*

Changing the Patient Imaging Position in Relation to the Couch

It can be necessary to change the patient imaging position in relation to the couch if the information is missing from the slices or the image series looks incorrect.

The options for the patient imaging position are the following:

- Head first—supine
- Head first—prone
- Head first—decubitus right
- Head first—decubitus left
- Feet first—supine
- Feet first—prone
- Feet first—decubitus right
- Feet first—decubitus left
- Face first—sitting

When you change the patient imaging position, a new image series is created in the database. The patient orientation indicator changes accordingly.

Related Topics

[2D Views](#) on page 47

Change the Patient Position



Note: *Changing the patient imaging position in PET images is not supported.*

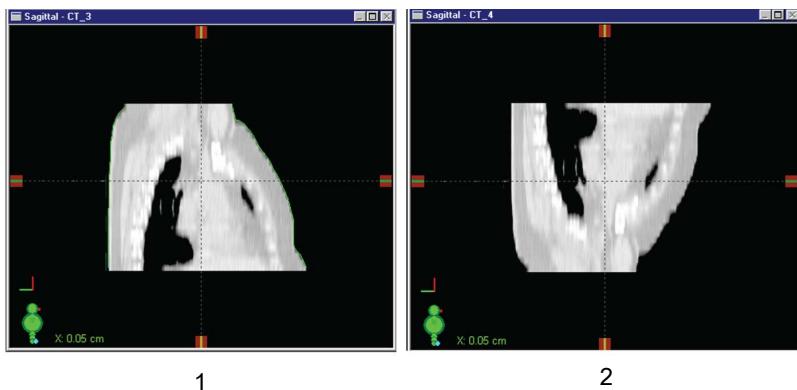


Tip: *In External Beam Planning you can change the treatment position of the patient in the Plan Properties dialog box.*

1. In the Scope or Focus window, select the image series.
2. Choose **Image > Change Patient Position**.
3. In the **New Patient Position** drop-down list, select the desired patient position.
4. Click **OK** to change the patient position.

Inverting the 3D Image Slice Order

The application arranges the slices in a 3D image in accordance with their primary axes. For instance, the Z-axis usually increases from feet to head in the DICOM system, and the 3D image created in the application is displayed in an upright position. Sometimes the original images may have had a reversed Z-axis, and the 3D image created from these images will appear upside down. Inverting the slice order corrects this problem by mirroring the 3D image along its primary axis. When you invert the slice order, a new image series with the inverted slice order is created in the database.



1. Original image slice order
2. Reversed image slice order

Figure 24 Inverting Slice Order

Note: Inverting the slice order of PET images is not supported.



Invert the 3D Image Slice Order

1. In the Scope window, select the image series.
2. Choose **Image > Invert Slice Order**.
3. To confirm the reversal and invert the slice order, click **Yes**.

A new image series with the inverted slice order is created.

Modify an Annotation

Annotations are created in the Contouring application.

1. Select the annotation in the Focus window.
2. Right-click and do one of the following:
 - To delete the annotation, choose **Delete**.
 - To modify the annotation, choose **Properties** and modify the comment as needed.
 - To move viewing planes to annotation in External Beam Planning, choose **Move Viewing Planes to Label**.

Assigning a New DICOM Frame of Reference

If there are multiple images that share the same DICOM Frame of Reference, you can use and view them in the same way as any other registered images. You can, for example, view these images using the Blend Control tool, and contour structures in them.

In some cases, images that have been taken during the same imaging session and share the DICOM Frame of Reference (FOR) need to be re-registered because of patient movement during the imaging session. To re-register the images, you need to assign a new DICOM FOR for one of the images. When you assign a new FOR for the images, the application creates a copy of the selected image series, and assigns the new FOR for the new image series.

Assign a New DICOM FOR

1. Open the image series for which you wish to create a new DICOM FOR.
2. Go to the Selection workspace.
3. Select the image series you opened in the Scope window.
4. Select **Image > Change Patient Position**.
5. Select the **Assign a new frame of reference** option.
6. Click **OK** to close the dialog box.

The new image series is shown in the Scope window.

To continue, create a new 3D image of the slices in this series. Then you can register the new 3D image with the other 3D image.

Markers

Markers placed inside the patient help locate the tumor during the course of treatment. A particular use of markers in treatment planning is in connection with Varian's OBI treatment unit. OBI is capable of detecting markers in patient images and saving them in a structure set. This structure set can then be imported into Eclipse or BrachyVision and used for verifying the patient positioning in images produced in further treatment sessions. You can also modify marker positions in Eclipse and BrachyVision between treatment sessions and then re-export the plan to the treatment machine. Approved markers cannot be modified.



Note: You can use a predefined parameter set for creating DRRs that display markers.

Markers defined to patient images are shown in the Focus window with a special icon (■) under the structure set icon. You can show or hide markers by selecting or clearing their visibility check boxes in the Focus window. Markers are displayed on all image planes.

The figure shows markers in a transversal image in a 2D view.



Figure 25 Markers in 2D Image View

Different visualizations are used to indicate the plane where each marker is located in relation to the active viewing plane:

- ■—Active marker located on the active viewing plane.
- ■—Inactive marker located on the active viewing plane.
- □—Active marker located in front of the active viewing plane.
- □—Inactive marker located in front of the active viewing plane.
- □—Active marker located behind the active viewing plane.
- □—Inactive marker located behind the active viewing plane.

Markers are also shown in the Model view. The following figure shows markers in the Model view.

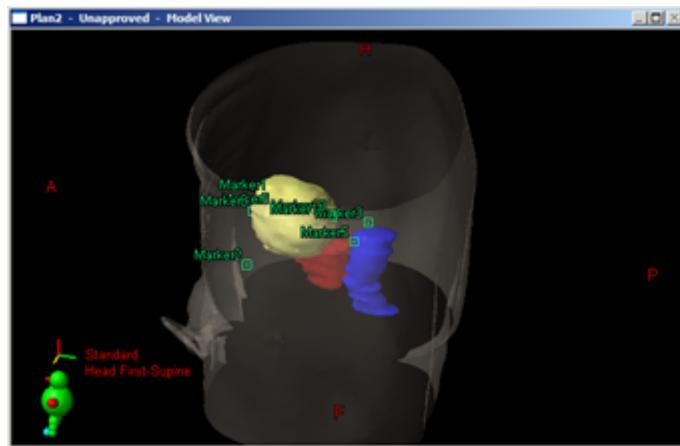


Figure 26 Markers in Model View

Markers may be seemingly invisible in the Model view. This is because they are positioned realistically in 3D space and, depending on the viewing angle, may be obstructed by a structure.

In External Beam Planning, markers are shown also in the BEV. They are always shown on top of all structures.

Related Topics

[Predefined Parameter Sets for DRR Calculation](#) on page 202

Add a Marker

You can add markers in External Beam Planning and Brachytherapy Planning.

1. Select **Insert > New Marker**.
2. Define the marker ID, name and location.
3. Click **OK**.
4. To adjust the location of the marker, click **Move Marker or Isocenter Marker** .
5. Drag the new marker to the desired location with the mouse.

Edit a Marker

You can modify and delete markers in External Beam Planning and Brachytherapy Planning.

1. From the Move Marker or Isocenter marker toolbar, click **Move Marker or Isocenter Marker** .
2. Click the marker that you wish to move to another location.
The image planes are moved to the location of the marker.
3. Drag the marker to the desired location with the mouse.
4. To delete the marker, right-click it and choose **Delete**.
5. Save your changes.

Isocenter Markers

Isocenter markers can be added to patient images to mark the location of the treatment isocenter to be used during external beam planning. If the patient images contain an isocenter marker, you can align a field to the isocenter marker in External Beam Planning.

Isocenter markers defined in patient images are shown in the Focus window with a special icon () under the structure set icon. You can show or hide the isocenter markers by selecting or clearing their visibility check boxes in the Focus window. Isocenter markers are displayed on all image planes.

The following figure shows an isocenter marker in a transversal image in 2D view.

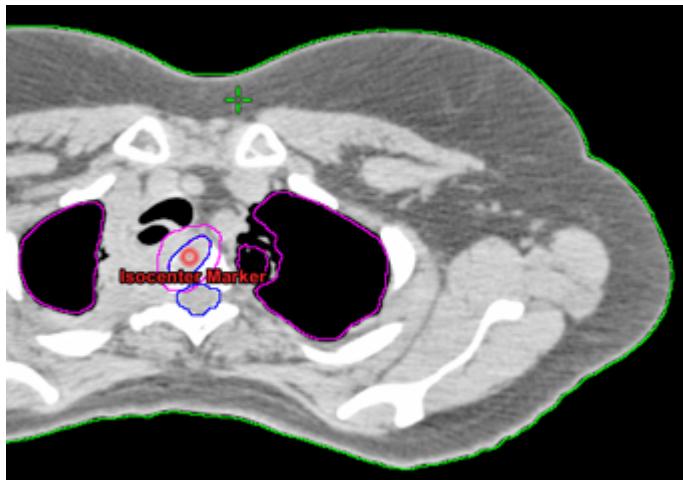


Figure 27 Isocenter Marker in 2D Image View

Different visualizations are used to indicate the plane where the isocenter marker is located in relation to the active viewing plane:

- ● — Active isocenter marker located on the active viewing plane.
- ● — Inactive isocenter marker located on the active viewing plane.
- ○ — Active isocenter marker located in front of the active viewing plane.
- ○ — Inactive isocenter marker located in front of the active viewing plane.
- ◎ — Active isocenter marker located behind the active viewing plane.
- ◎ — Inactive isocenter marker located behind the active viewing plane.

Isocenter markers are also shown in the BEV and the Model view. The following figure shows an isocenter marker in the Model view.

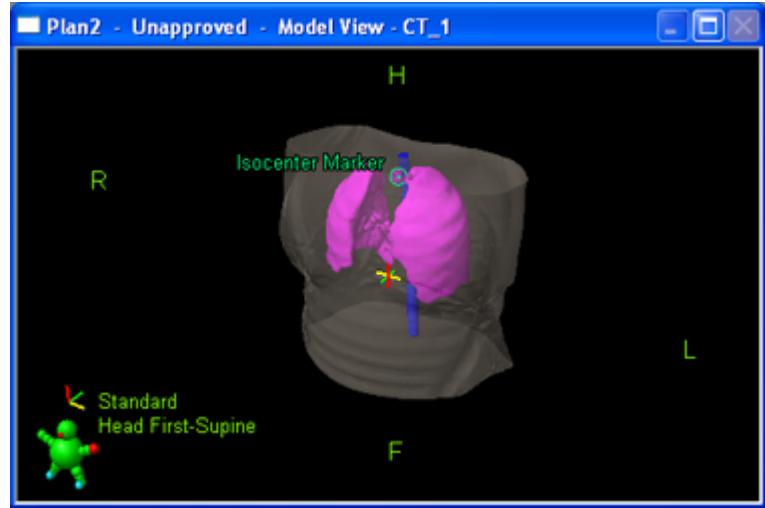


Figure 28 Isocenter Marker in Model View

An isocenter marker may be seemingly invisible in the Model view. This is because they are positioned realistically in 3D space and, depending on the viewing angle, may be obstructed by a structure. In the BEV, however, markers are always shown on top of all structures.

Add an Isocenter Marker

You can add Isocenter markers in External Beam Planning.

1. Select **Insert > New Isocenter Marker**.
2. Define the isocenter marker ID, name and location.
3. Click **OK**.
4. To adjust the location of the isocenter marker, click **Move Marker or Isocenter Marker** .
5. Drag the new isocenter marker to the desired location with the mouse.

Edit an Isocenter Marker

You can modify and delete Isocenter markers in External Beam Planning, with the exception of isocenter markers that have been approved.

1. Click **Move Marker or Isocenter Marker** .
2. Click the isocenter marker that you wish to move to another location.
The image planes are moved to the location of the isocenter marker.

3. Drag the isocenter marker to the desired location with the mouse.
4. Save your changes.

Rotate or Mirror an Image

Sometimes films may be accidentally scanned in an incorrect orientation and may need to be corrected by rotating or mirroring the image pixel data vertically and horizontally.

1. In the Selection workspace or in Brachytherapy 2D Entry, drag the image to an image view and activate the image by clicking the title bar of the image view.
2. Choose **Image > Rotate/Mirror**.
3. Select the appropriate options to rotate and/or mirror the image:
 - 90° clockwise
 - 90° counterclockwise
 - 180°
4. Do one of the following:
 - To apply the changes to the active image, select **Modify Original Image**.
 - To save the changes to a new image, select **Create New Image** and define a name for the new image in the **New ID** text box.
5. To finish, click **OK**.

Export Images

You can transfer image data to another system. The Export wizard guides you through the image export process.

1. Choose **File > Export > Wizard**.
2. Click the **Plan** or the **Image(s)** option button and click **Next**.
3. Do one of the following:
 - **Image(s)**: Select the source of the image(s) and select whether you wish to include the structure set with the images and click **Next**.
 - **Plan data**: Select what you wish to include in the plan and click **Next**.
4. Select the appropriate export filter and click **Next**.
5. In the list box, select the data to export.
6. If necessary, change the export directory for all data or for selected data:
 - To change the export directory for all data, click **Change for all Objects** and select the appropriate directory.
 - To change the export directory for selected data, click **Change for selected object(s)** and select the appropriate directory.

7. To remove data from the list, select them and click **Remove Selected Object(s)**.
8. To save the selected data to the defined export directory, click **Finish**.

Chapter 5 SRS Localization

Eclipse SRS Localization

The Eclipse SRS Localization application, or SRS Localization, is part of the Varian application suite for linear-accelerator-based stereotactic radiosurgery.

SRS Localization is designed for processing patient CT image series containing a head ring and a localizer box. The application precisely localizes the localizer box contained in the slices and creates a stereotactic volume (3D Image) for use in a treatment planning application, such as Eclipse Cone Planning or External Beam Planning. The input and output data of SRS Localization is loaded from and stored to the Varian System database. Frameless image data sets and CT series acquired with CT gantry tilt are not processed by SRS Localization.



WARNING: Incorrect mounting of the localizer box to the head ring leads to incorrect results, false planning and mistreatment. Eclipse SRS Localization cannot detect this error. After one person has attached the localizer box to the head ring, a qualified member of the personnel must verify the correct attachment of the frame to the head ring. If there is any doubt about the rotation and pitch angles of the transformation applied by Eclipse SRS Localization, check if the head ring is visible and parallel to the X-Y plane in the stereotactic volume. If the head ring is not visible, review the acquisition and process used to acquire the images. Always make sure that the localizer box is correctly mounted on the head ring. If possible, always include the head ring in your CT scanning range.



Note: The patient position (orientation) for the CT planning series must be "Head First Supine". Other Patient Positions or orientations will result in an incorrect stereotactic volume and, subsequently, in treatment planning errors. If not corrected, such errors may lead directly to patient mistreatment.

The stereotactic volume used for treatment planning must be aligned with the axes of the stereotactic coordinate system defined by the localizer box. SRS Localization calculates the translation and rotations required for aligning the stereotactic coordinate system with the coordinate system defined by the patient setup in the CT acquisition. The application is able to align images with rotations of up to 30 degrees (although rotations greater than 5 degrees are usually not observed). The required translation and rotations are determined by detecting the positions of the rods of the localizer box in the input slices.

Before approving and saving the stereotactic volume created by SRS Localization, carefully review its geometry, and, if necessary, repeat the calculation of the stereotactic volume after adjusting the detected rod positions and/or setting rod positions manually.

SRS Localization supports the following localizer models:

- VMS (Varian Medical Systems), containing six fiducials.
- BRW (Brown-Roberts-Wells), containing nine fiducials.

Concepts Used in SRS Localization

Head Ring	The head ring is a stereotactic device fixed to the patient's head during CT acquisition and treatment. During CT acquisition, the head ring is fixed to the localizer box, and it may also be attached to the CT couch. During treatment, the head ring is attached to the treatment couch or floorstand. In some contexts, the head ring or the combination of the head ring and the localizer box is referred to as the "head frame", but for accurate reference to localizer box and head ring these terms are used separately.
Localizer Box	The localizer box is a device attached to the top of the head ring during CT acquisition. The localizer box determines the stereotactic coordinate system in the CT image. The localizer box consists of rods that are easily detectable in a CT image, and other components for holding the rods and attaching the localizer box to the head ring. The localizer box rods are located in well-defined positions, which allows precisely determining the position and orientation of the CT slices that intersect with the localizer box. In some contexts, the localizer box or the combination of the localizer box and the head ring is referred to as the "head frame", but for accurate reference to localizer box and head ring these terms are used separately.
Rod	Rods, or localizer rods, are part of the localizer box. Usually rods are cylindrical objects of high density that can be easily detected in a CT image. Sometimes referred to as bar, fiducial rod, fiducial bar, or fiducial.
Localizer Model	The localizer model is a model, or geometric type, of the localizer box. SRS Localization supports two models, BRW (Brown-Roberts-Wells) and VMS (Varian Medical Systems).
Stereotactic Volume	A stereotactic volume is a 3D image created by SRS Localization as the output of the localization process. The stereotactic volume is positioned at the stereotactic origin and aligned with the axes of the stereotactic system defined by the localizer box. The stereotactic volume is used for treatment planning.

Workflow for Fully Automatic Stereotactic Localization in SRS Localization

Step	See
Start the SRS Localization application.	Starting the SRS Localization Application on page 85
Import the patient images. Application: External Beam Planning	<i>Eclipse Photon and Electron Instructions for Use</i>
Select the patient. Application: SRS Localization	Select an Image Series to be Localized on page 95
Select the image series to be localized. Application: SRS Localization (Series Explorer)	Select an Image Series to be Localized on page 95
Perform the localization. Application: SRS Localization (Detection View)	Fully Automatic SRS Localization on page 93
Review the stereotactic volume. Application: SRS Localization (Output View)	Reviewing a Stereotactic Volume on page 100
Approve and save the stereotactic volume. Application: SRS Localization (Output View)	Approving and Saving the Stereotactic Volume on page 106
(Optional) Erase localization box pixel data. Application: SRS Localization (Output View)	Erasing the Localizer Box Pixel Data in the Stereotactic Volume on page 107

Workflow for Step-by-Step and Manual Stereotactic Localization in SRS Localization

Step	See
Start the SRS Localization application.	Starting the SRS Localization Application on page 85
Import the patient images. Application: External Beam Planning	<i>Eclipse Photon and Electron Instructions for Use</i>
Select the patient. Application: SRS Localization	Select an Image Series to be Localized on page 95

Step	See
Select the image series to be localized. Application: SRS Localization (Series Explorer)	Select an Image Series to be Localized on page 95
Perform the localization. <ul style="list-style-type: none"><li>■ Perform step-by-step localization and create the stereotactic volume.<li>■ Perform manual rod detection and create the stereotactic volume.	Step-by-Step SRS Localization Using Automatic Rod Detection on page 94 Manual SRS Localization on page 97
Application: SRS Localization (Detection View)	
Review the stereotactic volume. Application: SRS Localization (Output View)	Reviewing a Stereotactic Volume on page 100
Approve and save the stereotactic volume. Application: SRS Localization (Output View)	Approving and Saving the Stereotactic Volume on page 106
(Optional) Erase localization box pixel data. Application: SRS Localization (Output View)	Erasing the Localizer Box Pixel Data in the Stereotactic Volume on page 107

Starting the SRS Localization Application

You can start the SRS Localization application from the Quicklinks menu of the Home Screen. You cannot open multiple simultaneous instances of SRS Localization.

Related Topics

- [Start an Application Session](#) on page 27
- [Switch to Another Application](#) on page 27

Navigating in the SRS Localization

The SRS Localization application has the following views:

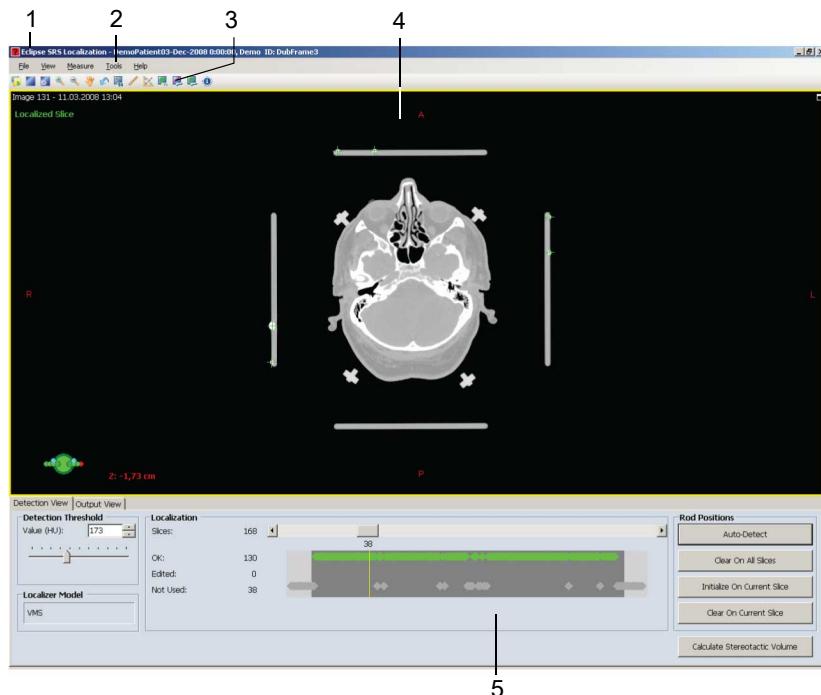
- Detection View—Used for automatic and manual rod detection.
- Output View—Used for reviewing, saving and approving the stereotactic volume. The Output View also contains the QA Mode, which is used for performing quality assurance (QA) procedures to verify the CT image quality and localizer box geometry.

You can switch between the views by selecting the tab of the view. The QA Mode is accessible with a menu command and can be entered only by authorized users.

Detection View in SRS Localization

The Detection View is used for automatic and manual rod detection. You can review single slices of the input series in the input slice 2D view.

The Detection View is shown if you open an input series without starting immediate processing, or if the fully automatic processing was interrupted due to a problem or uncertainty. The Detection View consists of the 2D Image View and the Detection Panel.

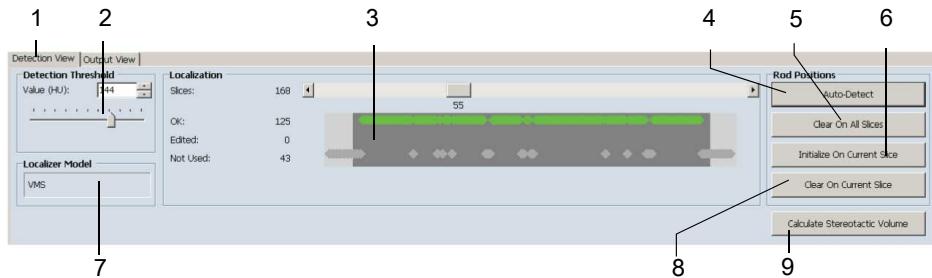


1. Title bar
2. Menu bar
3. Toolbar
4. 2D image view of input slices
5. Detection View panel

Figure 29 User Interface of the Detection View

The 2D Image view shows the slice image, the DICOM Z-coordinate (image position) of the CT scanner, and image number, acquisition date and time. The patient orientation labels and the patient orientation indicator mark the orientation of the patient.

The Detection View Panel below the 2D Image view is used for automatic and manual rod detection. You can start the calculation of a stereotactic volume from the Detection View Panel after the rod positions have been detected and accepted. To navigate to a particular slice, use the Slices slider in the Detection View Panel.



1. Tab for switching the view
2. Slider for defining the detection threshold
3. Slice localization plot
4. Starts automatic detection of the rod positions and the localization model
5. Clears the rod positions from all slices
6. Shows the localizer model
7. Adds initial rod positions to the current slice for manual detection
8. Clears the rod positions from the current slice
9. Creates a volume based on the detected rod positions

Figure 30 Detection View Panel

The detection threshold (number 2 in the previous figure) is the CT value used to identify the localizer rod pixels from their environment. The detection threshold is specified in Hounsfield units (HU). Once the threshold value has been defined, it is usually applicable for most cases, but it may be necessary to modify the value for some image series. The detection threshold value is stored each time you approve and save a stereotactic volume, and it is used as the starting value for the next localization.

Related Topics

- [Patient Orientation Labels](#) on page 50
- [Patient Orientation Indicator](#) on page 51

Localization Status Information in the Detection View

The upper left corner of the 2D image view indicates the localization status of the currently visible slice and the Slice Localization Plot shows the status of the rod detection for each slice.

Table 4 Status of Slice Localization

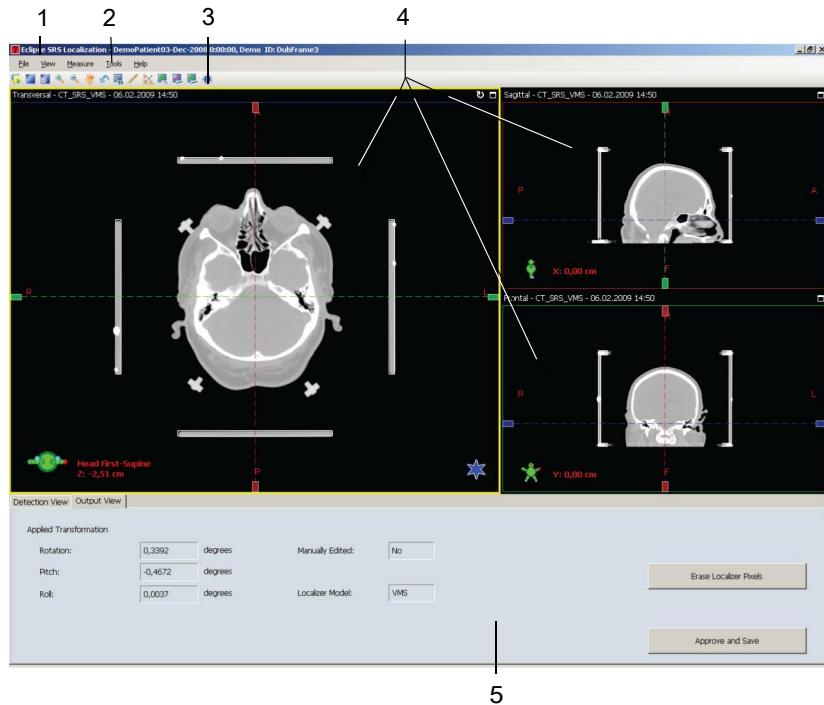
Label in 2D view	Localization Plot icon and label	Description
Localized Slice	— OK	All rod positions on this slice are defined and in use for calculation of the final transformation.
Edited	— Edited	Rod positions on this slice have been specified or modified manually.
No Slice Localization or Imprecise Localization	— Not Used	No rod positions are detected or specified, rod positions have been manually cleared or the detected or specified positions are not precise enough to be used for calculation of the final transformation.

The 2D image view also shows whether the detected rod positions in the slice are acceptable:

- — Illegal rod position. According to the selected detection threshold value, the image data at this position does not correspond to a localizer rod.
- — Rod position is accepted. According to the selected detection threshold value, the image data at this position may (but not necessarily does) correspond to a localizer rod. This mark only indicates that the current position is reasonable. You need to manually select and visually verify the exact position by, for instance, sufficiently zooming in to the image.

Output View in SRS Localization

The Output View is designed for reviewing, saving and approving the stereotactic volume. You can also make the localizer box pixels invisible to the planning system by erasing them. The Output View consists of the orthogonal image views and the Output View panel.



1. Title bar
2. Menu bar
3. Toolbar
4. Connected orthogonal views of the stereotactic volume
5. Output View Panel

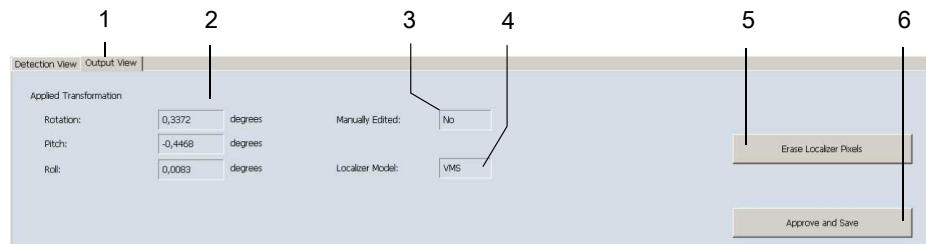
Figure 31 User Interface of Output View

The stereotactic volume can be reviewed using the orthogonal 2D views that show transversal, sagittal and frontal images. The patient orientation labels and the patient orientation indicator mark the orientation of the patient. The plane sliders mark the position of the viewing planes shown in the other views. You can move the plane sliders to show different reconstructed planes in the other 2D views.

The following symbols in the orthogonal views indicate the approval status of the image:

- —Unapproved image.
- —Approved image. No further modifications are possible after the approval.

The Output View Panel is used for erasing and restoring localizer box pixels, reviewing the transformation data, and for approving and saving the stereotactic volume. It shows the average transformation values applied to the active stereotactic volume, and contains information about manual modifications to the rod positions and the localizer model in use in the stereotactic volume.



1. Tab for switching the view
2. Shows the applied transformations (corrections) made in the stereotactic volume
3. Shows whether the rod positions have been manually modified
4. Shows the localizer model in use
5. Erases localizer pixels, removing HU information for dosimetry planning
6. Approves the stereotactic volume and saves it to the database

Figure 32 Output View Panel

Related Topics

[Patient Orientation Labels](#) on page 50
[Patient Orientation Indicator](#) on page 51

Spin, Tilt, Pitch, Rotation, and Roll in the Output View Panel

The Output View shows the Rotation, Pitch, and Roll angles used in the creation of the stereotactic volume from the input CT slices. The scanned orientation of the localizer box is described by either a Spin angle and a Tilt vector, or by the Rotation, Pitch and Roll angles.

For a localizer box which is perfectly aligned during CT scanning, the resulting SRS coordinate system matches the DICOM coordinate system. Otherwise, the Pitch, Rotation and Roll angles are used to describe the angles of rotation about the main axes in the DICOM coordinate system:

- Pitch—Angle of rotation about the DICOM X-axis
- Rotation—Angle of rotation of the localizer box about the DICOM Y-axis
- Roll—Angle of rotation about the DICOM Z-axis.

All angles are signed applying the right-hand screw rule stating that positive rotation of a right-hand wind screw pulls this screw into the direction of the rotation axis vector.

The Spin angle and Tilt vector are commonly used in radiosurgery:

- Spin angle is the same as roll, that is, the angle of rotation about the DICOM Z-axis.
- Tilt vector is used to describe a situation where the localizer box is scanned in a tilted orientation. In this case, its central, vertical axis does not coincide with the DICOM Z-axis, but points to a different direction, which is described by the Tilt vector. Sometimes Tilt angle is used to describe the degree of tilt with a single value. It is defined as the angle between the DICOM Z-axis and the Tilt vector (on the plane defined by the two vectors).

Seen by the patient, a positive Spin (or Roll) angle describes a rotation towards the left side, a positive Rotation angle describes a tilt of the head towards the patient's left shoulder, and a positive Pitch angle means a tilt of the head towards the patient's chest.

Related Topics

[DICOM Coordinate System](#) on page 45

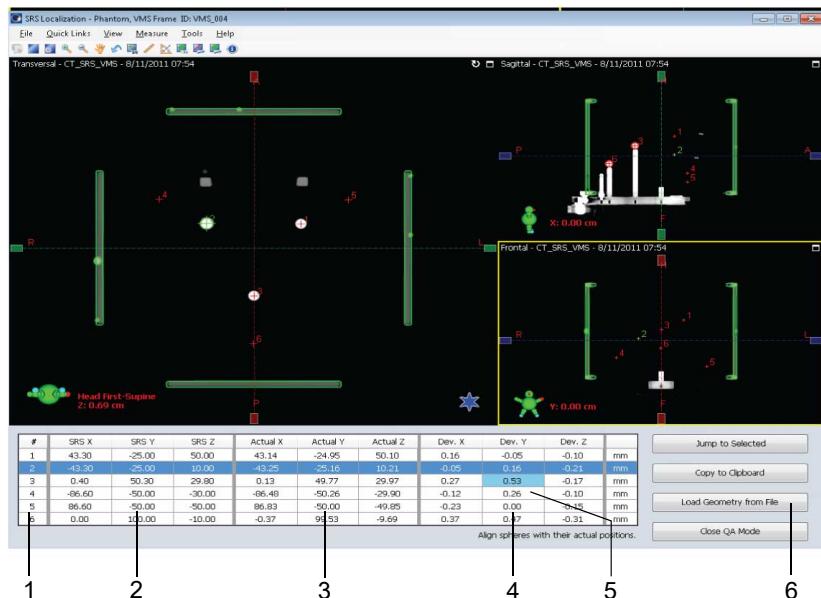
QA Mode of Output View in SRS Localization

You can use the QA mode of the Output View to perform the mandatory quality assurance (QA) procedure required to regularly verify the CT image quality and localizer box geometry. The QA procedure also helps in determining the CT scanner parameters suited for SRS localization and SRS planning. CT scans of an absolute phantom are required for this procedure.

The QA mode may be entered by authorized users only.



Note: A phantom specification file must be uploaded to the system before performing the QA procedure with a new or modified phantom or for the first time after installation. The phantom specifications file provides the exact, physically measured positions in SRS coordinates of the phantom currently in use. Phantom specification files can be uploaded by Varian service personnel only.



1. Sphere ID
2. Positions of spheres from the phantom specification
3. Measured positions of spheres on the image
4. Deviations between the specification and measured positions in millimeters
5. Indication of deviations exceeding the configured tolerance threshold value
6. QA functions

Figure 33 User Interface of Output View QA Mode

The QA Mode includes the following functions:

- Jump to Selected—Moves from the selected table entry to the corresponding actual sphere coordinates in the volume.
- Copy to Clipboard—Copies the table, including all values, date, time, user and ID, to the clipboard.
- For Varian service only: Load Geometry from File—Uploads a phantom geometry definition file to the system configuration.
- Close QA Mode—Exits the QA mode and returns to the Output View panel.

Performing Stereotactic Localization

Stereotactic localization can be performed in SRS Localization using the following methods:

- Fully automatic localization
- Step-by-step localization
- Manual localization.



WARNING: Always visually verify the result of the head frame detection carefully, and manually correct any visually incorrect results. Do not approve the detection if the results are incorrect to avoid forwarding incorrect results to treatment planning. It may not be possible to notice incorrect detection results after the head frame has been removed from the image, which may lead to incorrect treatment planning and mistreatment.

The result of each localization method is a stereotactic volume which is aligned with the localizer box and calculated based on the input slices. SRS Localization calculates the translation and rotations between the stereotactic coordinate system and the actual localizer position and orientation given by the currently defined rod positions.

Frameless image series and image series with an unsupported image orientation or a gantry tilt from the image acquisition cannot be used for SRS localization.

Fully Automatic SRS Localization

The easiest way to perform automatic localization, calculate and validate the stereotactic transformation, and create the stereotactic volume is to use fully automatic localization. Fully automatic localization is possible when:

- The image quality of the CT scan is adequate.
- The detection threshold value allows detecting the localizer rod positions automatically on a sufficient number of slices.
- The patient did not move during the image acquisition.

Fully automatic localization is selected in the Series Explorer when selecting the image series for localization.

Use Fully Automatic SRS Localization

1. Choose **File > Open Patient**.
2. In the Patient Explorer, select a patient.

If the patient you select is already open by another user in SRS Localization, a warning message is displayed. Always make sure that the other user is not performing stereotactic localization to the series you are about to select.

3. In the Series Explorer, select an image series to be localized.

Each patient can have several image series, but only one stereotactic volume can be approved and saved per input series. The Localized column in the Series Explorer indicates if a stereotactic volume already exists. If so, you are not able to open the series, and a notification is displayed.

If the series you selected has an unsupported image orientation or was acquired with gantry tilt, you are not able to open the series, and a notification is displayed.

4. Select the **Start Processing Immediately** check box.
5. Click **Open**.

All slices of the selected image series are loaded from the database. The rod positions are automatically detected, and the stereotactic transformation is calculated and validated. A stereotactic volume is created and displayed in the Output View.



Note: If any problems or uncertainties arise during fully automatic localization, continue localization using automatic rod detection or manual rod detection.

Related Topics

- [Manual SRS Localization](#) on page 97
[Review a Stereotactic Volume](#) on page 105

Step-by-Step SRS Localization Using Automatic Rod Detection

You can use step-by-step localization using automatic rod detection if you do not wish to perform fully automatic localization, or if it does not succeed. After selecting the image series for the step-by-step localization, you then manually initiate the automatic rod detection, which finds the rod positions and identifies the localizer model based on the positions. Any previously set rod positions are cleared.

Related Topics

[Perform Automatic Rod Detection](#) on page 96

[Manual SRS Localization](#) on page 97

Select an Image Series to be Localized

1. Choose File > Open Patient.
2. Select a patient in the Patient Explorer.

If the patient you select is already open by another user in SRS Localization, a warning message is displayed. Always make sure that the other user is not performing stereotactic localization to the series you are about to select.

3. In the Series Explorer, select an image series to be localized.
4. Clear the **Start Processing Immediately** check box.
5. Click **Open**.

All slices of the selected image series are loaded from the database.

6. Continue localization using automatic rod detection or manual rod detection.

Related Topics

[Manual SRS Localization](#) on page 97

[Perform Automatic Rod Detection](#) on page 96

Perform Automatic Rod Detection

1. To automatically detect the localizer rod positions and the localizer model, click **Auto-Detect**.

Auto-detection clears all previously set rod positions. After auto-detection is finished, the detected localizer model, an updated slice localization plot, and updated image annotations in the 2D view of the current input slice are visible.

2. If no warning messages are shown after auto-detection, and you are satisfied with the quality of rod detection, you can proceed to calculating stereotactic volume.

If any warnings or errors are shown, or you are not satisfied with the quality of rod detection, adjust the rod detection threshold. To find the appropriate detection threshold, do one of the following:

- If you know a threshold value that worked well in an earlier case with the same localizer model, type that value directly into the Detection Threshold text box. If your value is not accepted, you may adjust the limits by dragging the threshold slider to the respective end of the scale.
- Select a slice on which the rods are clearly visible. Drag the threshold slider while observing the changes in the 2D slice view. To change the threshold scale accordingly, drag the slider to the upper or lower end.
- Click the scroll arrows to raise or lower the threshold value. After adjusting the rod detection threshold, click **Auto-Detect**.



Note: If you have repeated this step several times without success, deficient image quality or a damaged localizer box may be the reason. Review or discuss any information available about the patient acquisition with other members of your team. Consider also checking the localizer box for damage. Proceed with manual localization.

If there is any doubt on whether the localizer box was firmly attached to the head ring, the current input series must be discarded and the patient must be rescanned using a correct attachment.

3. Click **Calculate Stereotactic Volume**.

The application verifies the rod positions and the slice localizations resulting from the rod positions. If any errors are detected, no stereotactic volume is created.

4. Review the stereotactic volume.

Related Topics

[Troubleshooting SRS Localization](#) on page 98
[Review a Stereotactic Volume](#) on page 105

Manual SRS Localization

Manual localization is usually performed if no successful result is produced by automatic localization or the step-by-step localization using automatic detection. Alternatively, you may choose to improve the localization by manually adjusting rod positions on individual slices, or manually clear rod positions on selected slices after automatic detection.

During manual adjustment, the detection threshold value is used to validate the rod positions you define. If you wish to start over with new rod positions, you may now chose a different threshold value. To start over, you may also try to get an initial set of positions by using the Auto-Detect command. However, notice that if the localizer model cannot be detected with the threshold value you choose, you will not get any rod positions.

When performing manual localization, it is not necessary to set the rod positions on all slices. For safety reasons, the minimal span of localized slices must be 70% of the vertical localizer rod length.

Related Topics

[Select an Image Series to be Localized](#) on page 95

[Step-by-Step SRS Localization Using Automatic Rod Detection](#) on page 94

Perform Manual Localization

1. Select a slice using the Slices slider in the Detection View panel.
2. Click **Initialize On Current Slice**.
3. Do one of the following:
 - If this is the first slice where the rod positions are initialized, select a localizer model (VMS or BRW).
 - If this is not the first slice, go to the next step.
4. As precisely as possible, drag the cross marks to the center of the localizer rods seen in the image slice. To see a rod more easily, zoom in to the rod.



Note: For the VMS localizer box, the centers of the rods are slightly below the plexiglass surfaces.

Red crosses placed at positions within the defined threshold value change to green. When all crosses are at legal positions, the slice status turns from "No Slice Localization or Imprecise Localization" to "Localized Slice". Edited slices are indicated by pink diamonds in the Slice Localization Plot.

To start again, do one of the following:

- To clear all previously set rod positions, click **Clear On Current Slice**.
- To remove the rod positions from all slices, click **Clear On All Slices**.

5. Repeat the previous steps as many times as necessary.

It is not necessary to set rod positions on all slices manually. To pass the SRS Localization safety checks, two slices must be localized. However, it is strongly recommended to localize more than two slices. The final stereotactic transformation is based on the average rotations found in individual slices. The final error is approximately the error of manual specification divided by the number of slices localized at that error.

6. To verify the modified positions and create a stereotactic volume, click **Calculate Stereotactic Volume**.



Note: *Slices with manually modified rod positions are always taken into account when calculating the final image transformation, unless their resulting localization error in the spin or tilt angle is greater than 2 degrees.*

7. Review the stereotactic volume.

Related Topics

[Review a Stereotactic Volume](#) on page 105

Troubleshooting SRS Localization

Troubleshooting Image Input

■ Inconsistent Image Orientation

If you attempt to open a series in which not all images have the same orientation, an error message is shown. Review the series in External Beam Planning and consider deleting the images with the wrong orientation, after having obtained approval by the physicist or physician in charge.

■ Unsupported Image Orientation

If an image orientation other than a standard axial orientation is detected in the input series, a notification is shown. Review the series in External Beam Planning and consider deleting the images with an unsupported image orientation, after having obtained approval by the physicist or physician in charge.

Series containing only images with an unsupported orientation cannot be used in SRS Localization.



Note: The patient position (orientation) for the CT planning series must be "Head First Supine". Other Patient Positions or orientations will result in an incorrect stereotactic volume and, subsequently, in treatment planning errors. If not corrected, such errors may lead directly to patient mistreatment.

- Undefined Patient Position in the Scan

If the patient position cannot be determined in the input series, you are prompted to confirm whether to continue. If you are sure that the series does have the patient position Head First Supine, confirm and continue. Otherwise, localization of this series is not possible.

Troubleshooting Automatic Rod Detection

- Localizer Model Could not be Detected

If no localizer box is present in the input images or the localizer box model cannot be detected, a warning message is shown. The automatic detection may fail also if an insufficient number of slices intersect the localizer box. If a localizer is visible, but not detected, adjust the threshold value and try again. If this fails, try step-by-step localization.

More information on how the localizer model is detected: *Eclipse Photon and Electron Algorithms Reference Guide*.

Troubleshooting the Creation of Stereotactic Volume

- Imprecise Slice Localization in Several Slices

If a significant number of slices (more than 10% of slices intersecting rods) have not been localized accurately, a warning is shown. The Slice Localization Plot indicates which slices have not been precisely localized.

- Rod Positions on Slices Ignored

SRS Localization automatically ignores all (manually or automatically defined) rod positions on slices for which

- The tilt or spin angle calculated from the rod positions differs by more than 2 degrees from the average found in all slices, or
- The stereotactic Z-position determined from the rod positions is outside the localizer box.

This indicates that the rod positions were incorrectly specified or detected. Such slices are automatically excluded from the calculation of the final transformation and a warning is shown. You can continue calculation without these slices, or interrupt and clear or correct the rod positions on these slices.

- Maximum Spin or Tilt Angle Exceeded

A stereotactic volume cannot be created if the maximum spin or tilt angle (30 degrees) is exceeded. In this situation, verify the rod positions in the Detection View. If the rod positions are correctly set and the large angles originate from the orientation of the patient in the input slices, the patient must be re-scanned.

- Large Calculated Spin or Tilt Angle

If you attempt to calculate a stereotactic volume that has a stereotactic transformation with rotations above 5 degrees, you are prompted to choose whether you wish to proceed. If you are sure that the stereotactic volume is correct despite these large rotations, continue by reviewing the stereotactic volume. If you wish to check the localization, use step-by-step localization.

- Possible Patient Motion during CT Acquisition

Very large average deviations in the detected spin and tilt angles between the slices indicate a potential patient motion during the CT acquisition. The limits for the average deviations are 1.0 degree for the spin and the tilt angle, and 2.0 mm for the tilt vector length. If the automatic slice detection notices deviations exceeding the limits, an error message is shown. In addition, if the spin or tilt angle exceeds the limit, a stereotactic volume is not created. Consider re-scanning the patient.

- Safety Check Fails

SRS Localization performs a safety check to ensure the quality of the localization, and prompts you to correct the situation. The safety check verifies that the range spanned by the localized slices is longer than 70% of the length of vertical localizer rod. If this is not the case, automatic localization is interrupted, a stereotactic volume is not created, and a notification is shown. Also notice that if your CT scan does not cover at least 70% of the height of localizer box, you may not create a stereotactic volume.

Related Topics

[Step-by-Step SRS Localization Using Automatic Rod Detection](#) on page 94

Reviewing a Stereotactic Volume

To make sure that the quality of the calculated stereotactic volume is sufficient for use in treatment planning, you can visually verify it in the Output View and use various tools for reviewing. Sufficient quality can be ensured by:

- Checking how the outline of the localizer box fits the image data.
- Verifying the transformations, such as the pitch or rotation angle (For instance, a large pitch or rotation angle (more than 2 degrees) may indicate incorrect attachment of the localizer box to the head ring.)
- Reviewing the Slice Localization Plot and the quality of the rod detection or manual rod positioning (in the Detection View).

Related Topics

[Troubleshooting SRS Localization](#) on page 98

Typical Errors Seen in the Output View

The following figure shows a situation where the compensation for the spin angle around the Z-axis is deficient. Red circles indicate examples of areas where the pixel data and the localizer box model are clearly not aligned.

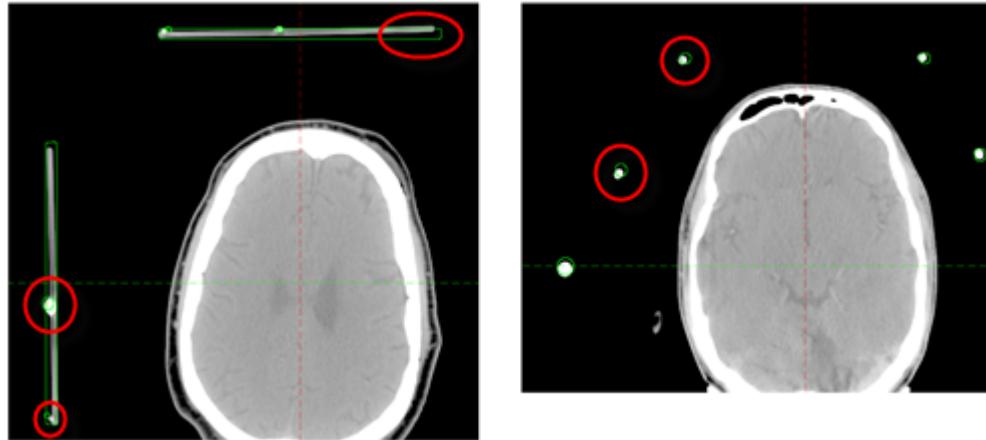


Figure 34 Deficient Spin Correction; VMS and BRW Localizer Box

In the figure, the detected localizer box is not perfectly aligned with the localizer box data seen in the patient image. An error message regarding maximum spin or tilt angle being exceeded is shown in this situation.

The following figure shows a situation where the compensation for the tilt angle around the X-axis or the Y-axis is deficient. Red circles indicate examples of areas where the pixel data and the localizer box model are clearly not aligned.

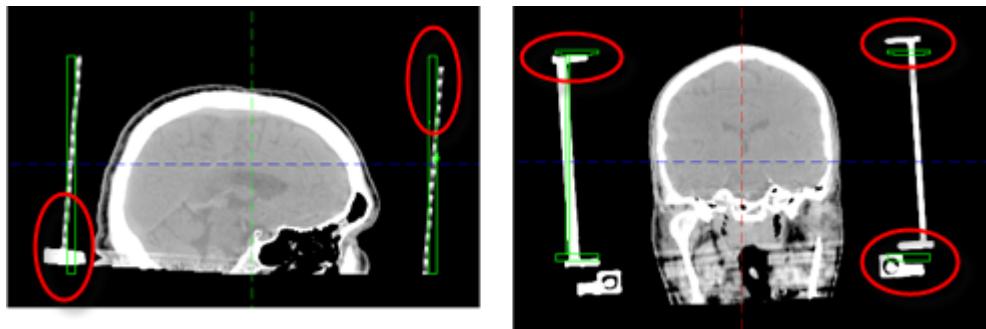


Figure 35 Deficient Tilt Correction; VMS and BRW Localizer Box

In the figure, the detected localizer box is not perfectly aligned with the localizer box data seen in the patient image. An error message regarding maximum spin or tilt angle being exceeded is shown in this situation.

The following two figures show a situation where the compensation for the Z-position is deficient. Red circles indicate examples of areas where the pixel data and the localizer box model are clearly not aligned.

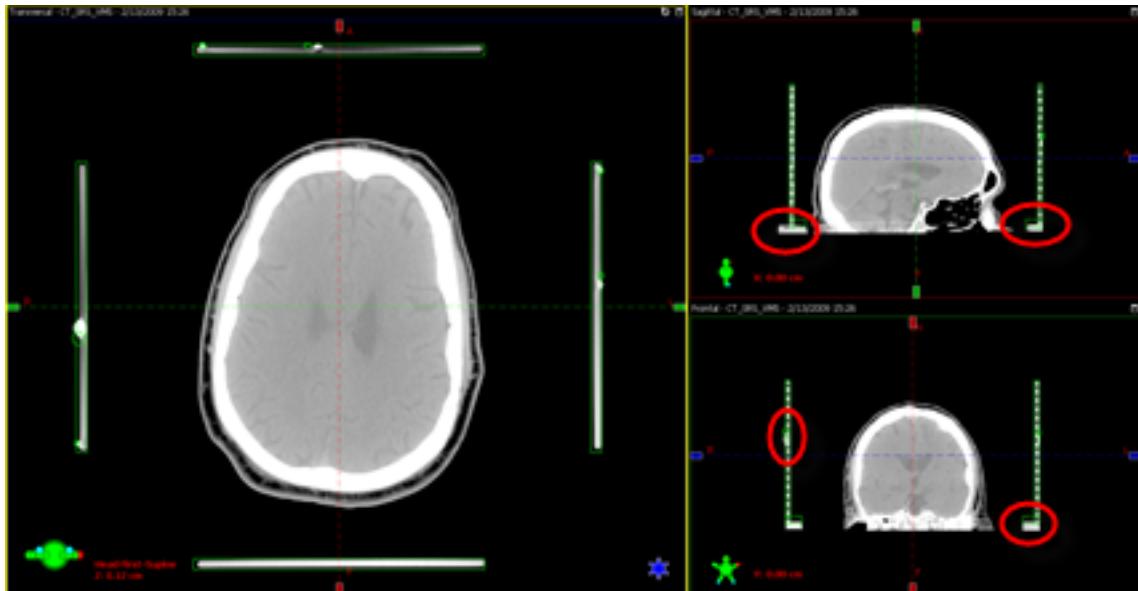


Figure 36 Deficient Z-Position; VMS Localizer Box

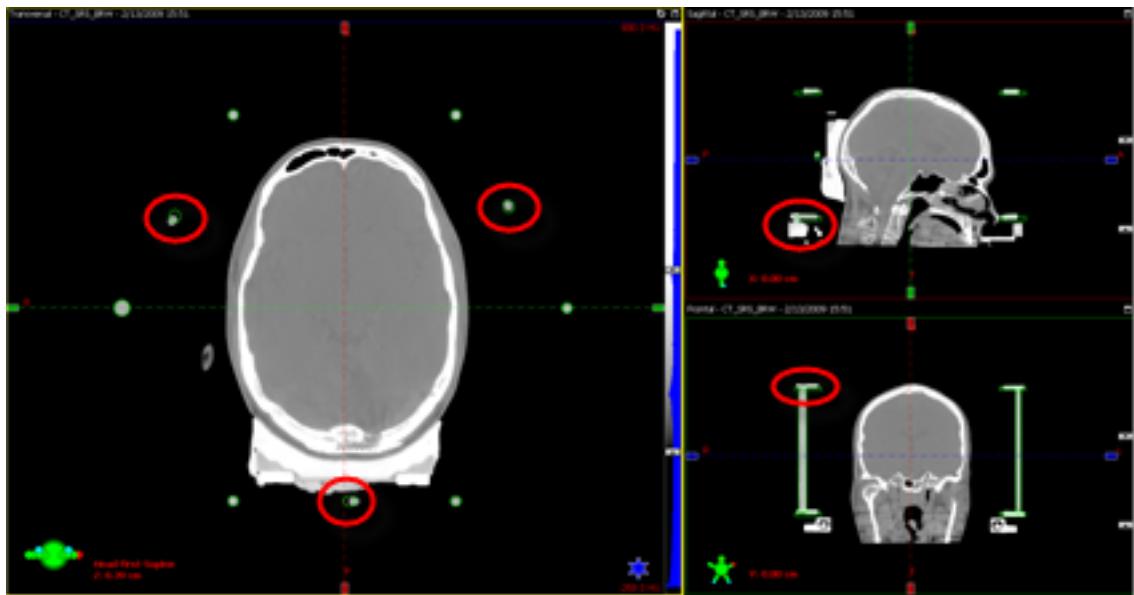


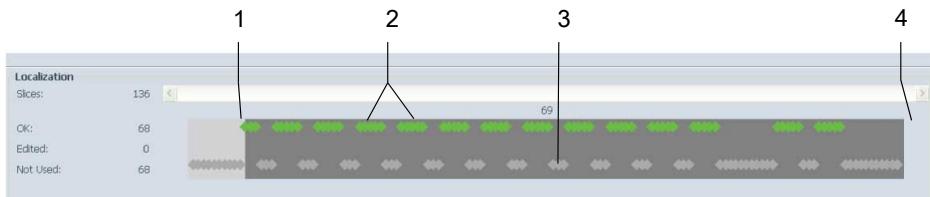
Figure 37 Deficient Z-Position; BRW Localizer Box

Related Topics

[Troubleshooting SRS Localization](#) on page 98

Typical Errors Seen in the Detection View

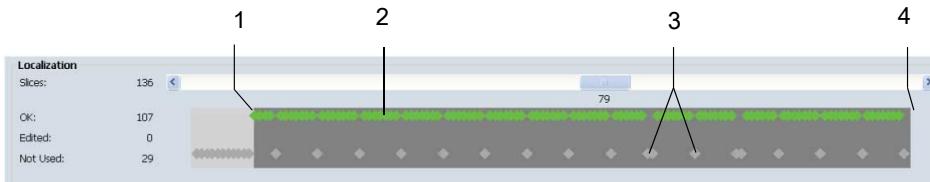
The following figure shows an example of the Slice Localization Plot after performing auto-detection with a non-optimal threshold value or with an image with inadequate image quality. In addition, the automatic rod detection shows a notification about imprecise slice localization. In this situation, consider re-defining the threshold value.



1. Start of the slice range
2. Localized slices
3. Non-localized slices
4. End of the slice range

Figure 38 Non-Optimal Threshold Value or Bad Image Quality

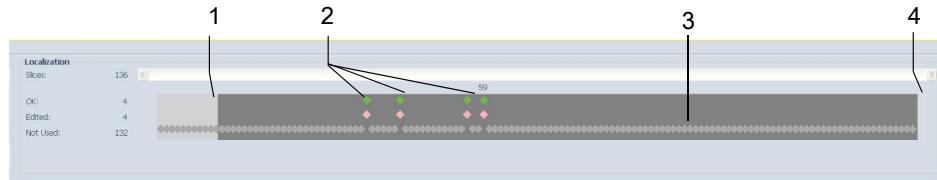
The following figure shows the Slice Localization Plot after the situation shown in the figure above has been corrected by using a more suitable threshold value. The calculation of a stereotactic volume may now be carried out, but a careful visual inspection of the output geometry is still required.



1. Start of the slice range
2. Localized slices
3. Non-localized slices
4. End of the slice range

Figure 39 Optimized Threshold

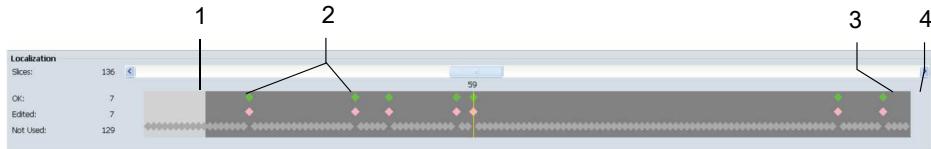
The following figure shows a situation where only a few slices have been localized, and all of them are located at one end of the CT series. The shaded area in the Slice Localization Plot displays where in the CT series localizer rods are found.



1. Start of the slice range
2. Localized slices: green = slice with successful rod positioning; red = edited slice
3. Non-localized slices
4. End of the slice range

Figure 40 Insufficient Range of Localized Slices

This situation can be corrected by localizing more slices and making sure that at least 70% of the span of the localization rods is covered. The figure below shows the Slice Localization Plot after the slices meet the range requirement. However, for precise transformation, more slices should be localized.



1. Start of the slice range
2. Localized slices: green = slice with successful rod positioning; red = edited slice
3. Last localized slice at the end of the range
4. End of the slice range

Figure 41 Insufficient Number of Localized Slices

Related Topics

[Troubleshooting SRS Localization](#) on page 98

Review a Stereotactic Volume

You can open the Output View only when a stereotactic volume exists.

1. Select the **Output View** tab.
2. Check that the outline of the localizer box drawn on top of the image fits the image data exactly.

3. Check the applied transformations reported in the Output View Panel.

If the reported values are not acceptable, review or discuss any information available about the patient acquisition with other members of your team. Also consider checking the localizer box for damage.



Note: A significant pitch or rotation angle (more than 2 degrees) may indicate incorrect attachment of the localizer box to the head ring. If there is any doubt on whether the localizer box was firmly attached to the head ring, the current input series must be discarded and the patient must be rescanned using a correct attachment.

4. Switch to the Detection View and check the quality of the rod detection or manual rod positioning, and inspect the slice localization plot.
5. If the quality of the stereotactic volume is sufficient, you can approve and save it.

Related Topics

[Typical Errors Seen in the Output View](#) on page 101

[Typical Errors Seen in the Detection View](#) on page 103

[Troubleshooting SRS Localization](#) on page 98

Approving and Saving the Stereotactic Volume

When the calculation of the stereotactic volume is completed and the result has been reviewed and found accurate, you can approve and save the stereotactic volume. A stereotactic volume must be approved before it can be saved.



WARNING: Always visually verify the result of the head frame detection carefully, and manually correct any visually incorrect results. Do not approve the detection if the results are incorrect to avoid forwarding incorrect results to treatment planning. It may not be possible to notice incorrect detection results after the head frame has been removed from the image, which may lead to incorrect treatment planning and mistreatment.

After you have approved a stereotactic volume, you can no longer open the QA mode, switch to the Detection View or make any changes to the volume.

Each input CT series can have only one stereotactic volume associated with it. If you wish to create another stereotactic volume for a series, you first need to erase the previously created volume in External Beam Planning. In a situation where you attempt to approve and save a stereotactic volume for a series that already has one, SRS Localization shows an error message.

Erasing the Localizer Box Pixel Data in the Stereotactic Volume

The localizer box is present (attached to the head ring) only during CT acquisition. Because of this, the localizer box pixels usually need to be erased from the stereotactic volume for treatment planning, because the localizer box pixels may affect the dose calculation and image registration.

The dose calculation algorithm in Cone Planning is not affected by localizer box pixels provided that the Body structure is delineated correctly (to exclude the localizer box). Other dose calculation algorithms used in External Beam Planning are generally affected.

Because of scatter effects present in CT acquisition, SRS Localization erases the localizer box pixels with a margin added. Consequently, part of the patient's anatomy in the immediate proximity of the localizer box components may also be affected. If this happens, first save the stereotactic volume with the localizer pixels included, and then, before using the stereotactic volume for treatment planning, adapt the localizer structures using the segmentation tools in External Beam Planning and assign CT value -1000 (air) to the structures.

Approve and Save a Stereotactic Volume

1. Create a stereotactic volume.
2. Review the stereotactic volume.
3. Click **Erase Localizer Pixels**.
4. Verify that no parts of the patient anatomy were erased.
This may happen in areas where the distance of the patient from the localizer box is shorter than 5 mm.
5. If necessary, click **Restore Localizer Pixels**.
6. Click **Approve and Save**.
7. In the Confirm dialog box, type in your user ID and password.



Tip: It is also possible for another qualified person with sufficient user rights, such as the physicist or physician in charge, to approve the stereotactic volume. Select Remember Password for 20 min, if more approvals have to be done in succession.

8. Click **Yes**.

The volume is saved and approved. An entry is created in the system log, including series UID, the localization method, the user ID, and the date and time of approval.

Related Topics

- [Fully Automatic SRS Localization](#) on page 93
- [Step-by-Step SRS Localization Using Automatic Rod Detection](#) on page 94
- [Manual SRS Localization](#) on page 97
- [Review a Stereotactic Volume](#) on page 105

Configuring SRS Localization

You can control the rod position tolerance, spin and tilt angle tolerances. These tolerance settings affect the result of the auto-detection process. The higher the tolerances, the more slices are used for calculating the final compensation transformations. For safety reasons, the default upper limits for the tolerance values are:

- Rod position tolerance: 2.00 pixels
- Spin angle tolerance: 2.00 degrees
- Tilt angle tolerance: 2.00 degrees

Tolerance Threshold

To control the accuracy of QA test, you can define the tolerance threshold setting. The configured value defines the threshold for the maximum allowable deviation between a sphere position entered by the user based on the localized stereotactic volume and the known geometry of the test phantom.

The smaller the required precision value, the stricter the QA test will be. For safety reasons, the default upper limit for this value is 0.5 mm. If your clinic requires higher precision, define a smaller value.

The specification of your clinic for the overall system tolerance will fluctuate based on the maximum tolerance configured for the QA mode test. If the QA test fails, it may not be possible to attain the precision required by your clinic. The overall system and QA precision must be discussed and approved by your clinic.

Configure SRS Localization



Note: Do not change the configuration if you are about to approve a verified stereotactic volume. Saving the configuration settings will clear all auto-detected rod positions in the active slices.

1. Choose **Tools > Task Configuration**.
2. To modify rod position tolerance, spin and tilt angle tolerances, select the Calculation tab and adjust the values.
3. To control the accuracy of QA test, select the QA tab and adjust the value of **Tolerance Threshold**.
4. Click **Save and Close**.

Using the QA Mode in SRS Localization

The QA mode of the Output View is used for performing the highly recommended quality assurance (QA) procedure required to regularly verify the CT image quality and localizer box geometry. The QA procedure also helps in determining the CT scanner parameters suited for SRS localization and SRS planning.



Note: *Damaged localizer boxes or head rings, incorrect phantom specifications or a carelessly conducted QA procedure may result in an incorrect stereotactic volume, incorrect treatment planning and mistreatment. The mandatory QA procedure ensures that image quality is sufficient and the localizer box is not damaged. CT localization with patient data must never be performed using a combination of CT scanner model, CT scanner settings, and localizer box that exceeds the tolerance threshold of the QA test. Always check the localizer box for deformations, verify that the correct phantom specification is used and conduct the QA process precisely for all the above combinations used for your SRS treatment planning.*

The QA procedure to be performed for the first time on your system after the installation or when using a new absolute phantom may only be done by Varian service. In this case, the phantom geometry specification file must be uploaded to the system configuration.

After the first one, it is also possible for a qualified person at the clinic to perform further QA procedures on a regular basis and after any change to the CT acquisition device or protocol or after any change or potential damage to the localizer box.

The QA procedure involves acquiring a CT scan of the absolute phantom with the localizer box attached, then creating a stereotactic volume of the scan in SRS Localization, and then verifying the positions of the phantom spheres in the QA mode. The results of the QA test are written to the system log.

After running the QA test, you can approve and save the stereotactic volume of the absolute phantom for reference purposes. This will also store the detection threshold value used in the QA test to the system configuration for further use with patient images. You can also easily copy the information in the sphere table (all values, date, time, user and ID) to the clipboard in textual format.

If the QA Test Fails

If the QA test exceeds the tolerance threshold, it is not possible to attain the precision required by the system or by the specification of your clinic. In this situation, discuss with other members of your team how to proceed. You can repeat the step-by-step localization and carefully consider any warnings that may indicate the root cause of the problem. Typical causes for failure of the QA test are the following:

- Insufficient image quality
- Improper attachment of the phantom to the localizer box

- Damaged phantom or localizer box
- Geometrical inaccuracies of the CT scanner.

For a root cause analysis of the QA test failure, check each listed item. To verify the geometrical and spatial correctness of the CT scanner data, perform image quality control or calibration procedures as recommended by the CT manufacturer. It is recommended to perform any testing of couch travel accuracy with a patient load present.

Related Topics

[Configuring SRS Localization on page 108](#)

Operate QA Mode

You must have the “Administer Radiation Oncology” user rights to access the QA mode.

1. Open a CT image series of the absolute phantom and try to fully automatically localize this series to create a stereotactic volume.
 - If fully automatic localization fails, try step-by-step localization.
 - If no stereotactic volume is created, the image quality is not sufficient or your localizer box is damaged. Do not try to continue the procedure using manual localization. Consider the QA test failed.
2. Verify the configuration to check whether the configured QA tolerance value is consistent with your institution’s specification.
3. In **Output View**, choose **Tools > Start QA mode**.
4. Varian service only: If the QA procedure is carried out for the first time on a system, you are prompted to load the phantom geometry data from a specifications file. Select the phantom geometry specification file corresponding to the phantom serial number and click **OK**.



Note: Only Varian service can perform this step.

5. Align all spheres to their actual positions:
 - a. Always zoom in to the spheres as much as possible.
 - b. To quickly find the spheres selected in the table, click **Jump to Selected**.
You can also double-click the ID of a sphere in the table listing the spheres.
 - c. To align the spheres approximately, use the mouse.

- d. To fine-tune the alignment, use the arrow keys.



Tip: To undo the last alignment, choose **Tools > Undo Sphere Move** or press **Ctrl + Z** several times.

To copy the information in the sphere table in textual format, click **Copy to Clipboard**.

6. Click **Close QA Mode** or choose **Tools > Close QA Mode**.

The results of the QA procedure are written to the system log.



Note: If the test exceeds the tolerance threshold, the precision required by the system or the specification of your clinic cannot be attained. Discuss with other members of your team how to proceed. Repeat the localization and carefully consider any warnings that may indicate the root cause of the problem.

7. If the tolerance threshold was met, you can approve and save the stereotactic volume of the absolute phantom for reference purposes.

This will also store the detection threshold value used in the QA test to the system configuration for further use with patient images.

Related Topics

[Configuring SRS Localization on page 108](#)

[Approving and Saving the Stereotactic Volume on page 106](#)

[Use Fully Automatic SRS Localization on page 94](#)

[Perform Automatic Rod Detection on page 96](#)

Chapter 6 Structures

About Structures

Structures are patient-wide objects that have image-specific geometric representations. Structures can be anatomical organs, treatment volumes used to define targets for treatment, or other regions of interest.

The properties of a structure are determined by the structure code, patient volume type, and patient volume code parameters:

- The structure code identifies the anatomical or treatment role of a structure.
- The patient volume code defines which anatomical structure of the patient the structure represents.
- The patient volume type defines the role of the structure in treatment.

Structures are formed by segments defined on 2D images or 3D images. In 2D image views, structures are graphically represented as contours or segments, while in 3D image views they can be rendered, for example, as translucent or solid surfaces.

New structures can be created one by one, or by using structure templates. All structures created for a patient belong to a structure set.

Structure Set

In DICOM, the structures that have been defined for a patient belong to a structure set. In other words, structure set is a container for the patient specific structures, including anatomical organs, treatment volumes and markers.

In External Beam Planning, the support structures defined for a patient also belong to the structure set.

In the Focus window all structures that have been defined for a patient are shown below the structure set icon (green circle with a white outline). If the patient has several 3D images with structures defined, each image has its own structure set that contains only the structures defined in that image.

You can create a new structure set simultaneously with the first structure, separately, or when you select an image series in the Object Explorer. Multiple image series taken during one imaging session can also be combined into one when creating a structure set.

You can open existing structure sets directly from Object Explorer. When you open a structure set, the referenced 3D image is also opened in the image views.

In DICOM hierarchy, plans reference a structure set and structure sets reference images.

If a structure set that has been created in Eclipse is going to be exported to other systems, you can check that the structure set is IHE-RO compliant.

Related Topics

[Exporting and Importing Plan and Image Data](#) on page 489

Selecting a Physical Materials Table for a Structure Set

You can select a physical material table for the structure set in the Structure Set Properties dialog box. Physical material tables are defined in RT Administration. The table is used by the Acuros XB dose calculation algorithm (photon planning) and the Segment High Density Artifacts tool. If no physical material table is defined, the Segment High Density Artifacts tool considers all densities higher than 3.0 g/cm³ as high densities. Otherwise, the tool reads the value (maximum density set for bone) from the selected physical material table. For more information on the Acuros XB dose calculation algorithm, refer to *Eclipse Photon and Electron Algorithms Reference Guide*.

Structure Codes

A structure code is assigned to a structure similarly to a volume code. A structure code identifies the anatomical or the treatment role of a structure. This is useful in identifying anatomical structures or treatment-related information of structures (such as PTV or organ at risk) for treatment planning in general. A structure code assigned to a structure is saved with the structure in templates.

In photon planning, structure codes are used for the automatic structure matching in DVH estimation models. On the basis of the defined structure codes (and structure identifiers), the plan structures can be automatically matched to corresponding model structures when you are adding a plan to a model, or when applying the model to a plan. To take full advantage of automatic structure matching, define a code for each structure, and use the codes consistently in your treatment plans.

Structure codes are managed in RT Administration. Availability of a structure code in treatment planning depends on the active structure code set defined in RT Administration. The available code schemes in RT Administration are: **FMA**, **RADLEX**, and **99VMS_Structcode**.

More information: *RT Administration Reference Guide*

Related Topics

[Structure Templates](#) on page 136

Patient Volumes

Each structure and reference point is linked to a patient volume. Patient volumes are abstract structures belonging to a patient, for instance, "Left Lung", and they represent the sites occupied by the structures in the patient. For instance, the "Left lung" patient volume may correspond to slightly differing structures in a CT and an MR image. The figure illustrates the relation between patient volume and structure. In the example, structure A belongs to patient volume A, and it has a different representation in the CT and MR image. Reference point A is marked in both the CT and MR image.

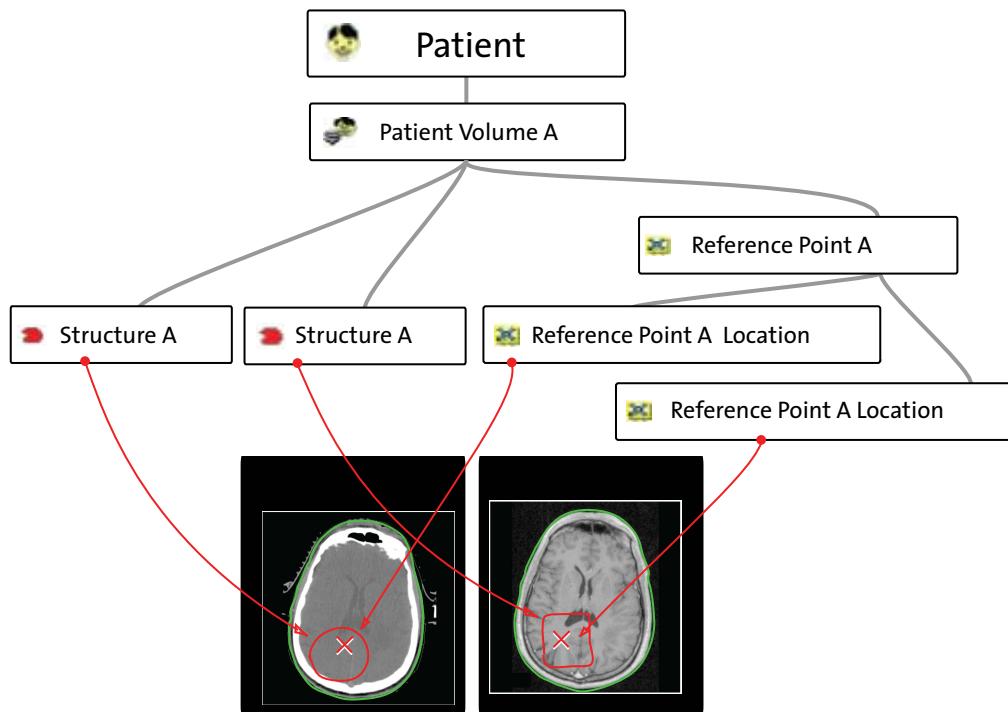


Figure 42 Patient Volume and Structure

When you insert new structures in a structure set that contains unused patient volumes, you can select a patient volume from a list or create a new patient volume.

Patient Volume Codes

The following volume coding systems are supported:

- ICD-O (International Classification of Diseases for Oncology, First Edition)
- ICD-O-2 (International Classification of Diseases for Oncology, Second Edition)
- ICD-9 (International Classification of Diseases, Ninth Revision)
- ICD-10 (International Classification of Diseases, Tenth Revision)

Using these codes provides suitable default values for the automatic tools for structure definition. The code can also be None, if you do not wish to use any of the ICD systems. The patient volume codes are configured in RT Administration.

Patient Volume Types

The following volume types have an interpretation in ARIA RTM applications:

- BODY—Body outline
- CTV—Clinical Target Volume
- GTV—Gross Target Volume
- PTV—Planning Target Volume
- Support — External patient support device (must be defined outside the BODY structure)

The following DICOM based volume types can be used for labeling:

- Avoidance—Volume to avoid in treatment
- Cavity — Anatomical cavity in patient
- Contrast Agent — Volume in which contrast agent is present
- Control — Dose optimization region (region of interest to be used as control volume in dose optimizations and calculation)
- Dose Region — Region of interest to be used as a dose reference
- Fixation — External patient fixation or immobilization device
- Irrad Volume —Irradiated volume
- None—Not defined
- Organ—Organ at risk
- Treated Volume —Treated volume

Body Structure

This information applies to External Beam Planning.

The Body structure must be defined in all planes, because the contours forming it are used to construct the 3D model of the patient.

Target Volumes

The target volume consists of the demonstrated tumors and any other tissue with presumed tumor. The following three target volume types are supported:

- GTV (Gross Tumor Volume)—According to ICRU 50, the GTV is defined first. This is a macroscopic volume where the tumor can be determined by means of clinical examination, radiographic, radioisotopic, ultrasonic and microscopic techniques.
- CTV (Clinical Target Volume)—Includes the microscopic spread of the tumor cells, and contains the tissues to irradiate.
- PTV (Planning Target Volume)— Includes, for instance, the movements of tissues during treatment and errors in patient positioning. In treatment planning, the PTV is the structure used to optimize the treatment.

Structures can be labelled both with the Volume Code and Volume Type if appropriate, for example when the GTV is also a part of an anatomical organ.

Organs at Risk

Defining crucial internal structures (spinal cord, lungs or liver) in treatment planning is necessary in order to expose them to as little radiation as possible. These structures are called organs at risk. Contouring organs as organs at risk is essential in determining the correct radiation dosage with the help of dose histograms.

Structure Properties

Structure properties are defined in the Structure Properties dialog box. You can modify the structure name and ID, structure code, volume code and type, color and style as well as the color and line style used for the structure in the DVH graph. The Structure Properties dialog box also shows data related to the structure generation algorithm, segmentation resolution, and structure approval status and history.



Note: When you modify the structure properties of a structure, the change is applied to all images under the patient.

General Structure Properties

The General tab in the Structure Properties dialog box enables you to define the following properties:

- ID—Structures must have a unique ID within each image. If you select a volume code for the structure, the code is used as the structure ID. You can edit the volume code based ID or define your own.

- Name—If you select a volume code for the structure, the name linked to the code is used as the structure name. You can edit the volume code based name or define your own. For instance, the name can be the name of an anatomical organ (for example, Lung, Kidney) or the name of the treatment volume (for example, Uterine Mass, Lung Tumor).
- Structure Code—Structures can have a structure code assigned to it to identify the anatomical role of a structure, the treatment role of a structure, or both. This is useful in identifying anatomical structures and treatment-related information of structures (such as PTV or organ at risk) for treatment planning in general.

In photon planning, structure codes are used for the automatic structure matching in DVH estimation models.

- Volume Type—Each structure must have a Volume Type defined. The Volume Type defines the role of the structure in treatment.
- Volume Code—Select a Volume Code for the structure or leave the structure without a Volume Code.

General Structure Properties (Continued)

The General (continued) tab in the Structure Properties dialog box enables you to define and review the following properties:

- Color and Style—The default color and style of the structure depends on the selected volume type. If the volume type is None, the default color and style depends on the selected volume code. The color selected for the structure is also shown in the icon in front of the structure name in the Focus window.
- DVH Visualization—You can select the line color, style and width to be used in DVH visualization.
- Generation Algorithm—Specify whether the structure was created by using manual tools, semiautomatically, or automatically. If the structure was generated automatically, the details of the algorithm are shown here.
- Referencing Plans—Shows the plans that use the structure set in which this structure is contained in, and how many DVH estimates are found for the structure.

Table 5 Information Shown in Referencing Plans

Item	Description
ID	ID of the plan that references the structure.

Item	Description
DVH Estimates	<p>Number of DVH estimates contained by the structure. Possible values are the following:</p> <ul style="list-style-type: none"> ■ 0: The structure does not have DVH estimates. ■ 1: The structure has one estimate, which is the dose level of the target. ■ 2: The structure has an estimate with an upper and lower limit.

Assign CT Value

If necessary, you can assign a CT value to a structure to make it a specified uniform density (no heterogeneity correction) in dose calculation. For example, a pelvic CT scan with the bladder full of contrast can alter the dose distribution unless the bladder is assigned a CT value. The structure is displayed with the assigned CT value in the image views.



NOTICE: In a case of determining the CT value where several structures with different CT values overlap, the highest CT value is used which is assigned to a non-body structure. A possible CT value assignment of a body structure is always overridden by other structures with assigned CT values.

In DICOM export, the assigned CT value of a structure is exported as electron density relative to water using the 'ROI Physical Property' attribute. Similarly, in DICOM import, the electron density relative to water is converted to a CT value and assigned automatically to the structure. If you do not want to use the automatically assigned CT value, clear the Assign CT Value selection for each structure.



WARNING: Be careful when assigning CT values to structures to be used in treatment planning. The CT value assignments directly affect the results of the dose distribution calculation in photon, electron and brachytherapy plans. In addition, the CT value assignments directly affect the determination of range and modulation for proton beams.

Assign Material

When you choose to assign a CT value to a structure, you can also assign a material for it. If a material is assigned, its CT value is automatically displayed in the CT value box.

However, you can change the default CT value if necessary. Information on the CT value ranges for different materials: *Eclipse Photon and Electron Algorithms Reference Guide* or *Acuros BV Algorithm Reference Guide*. Material densities are used by the Acuros XB and Acuros BV dose distribution calculation algorithms. More information on the algorithms: *Eclipse Photon and Electron Algorithms Reference Guide* or *Acuros BV Algorithm Reference Guide*.



NOTICE: In a case where two non-body structures with material assignment overlap, the material of the structure with the higher CT value is used. A possible material assignment of a body structure is always overridden by other structures with assigned materials.



WARNING: Be careful when assigning materials to structures to be used in treatment planning. The material assignments directly affect the results of the dose distribution calculation in photon and electron plans.

Modification Rules for Structures

Structures cannot be modified if one or several of the following are true:

- The structure is Approved.
- The structure ID would change, or the structure is assigned to a patient volume that cannot be modified.
- The structure belongs to an image that you do not have rights to modify.
- The structure is referenced by or used in a plan contained in a Completed or Archived course.
- The structure is a Body or Support structure and a calculated plan exists for the related structure set.
- The structure has assigned CT value and is not of type Bolus, and a calculated plan exists for the related structure set.
- The structure is a Bolus and you try to modify it in a non-treatment planning application.
- The structure is a brachytherapy structure and you try to modify it in a non-brachytherapy application.
- The CT value assignment of the structure would change and a calculated plan exists for the related structure set.
- The structure is used as a normalization target in a plan.
- The structure has a DVH estimate in a photon treatment plan.

Structures cannot be deleted from a structure set or patient volume if one of the following is true:

- Modification rules prevent the modification.

- The structure is referenced by fields or objectives and you try to modify it in a non-treatment planning application.
- The structure is referenced by an Approved plan.
- The structure is referenced by objectives in an Approved plan.

Create a New Structure Set

1. Choose **Insert > New Structure Set**.
2. Type the identification information for the structure set.
3. If appropriate, select the **Physical Material Table** for the structure set.
4. Click **OK**.

The structure set you created is shown in the Focus window.



Note: When you select an image series in the Object Explorer, you can create a structure set and a new 3D image using the images in the selected series by clicking **Create New Structure Set**.



Note: If you create a new structure set for an image that already has an existing structure set, the application creates a copy of the image.

Related Topics

[Structure Set](#) on page 112

[Selecting a Physical Materials Table for a Structure Set](#) on page 113

Combine Multiple Image Series into a Structure Set

Multiple image series taken during one imaging session can be combined into one when creating a structure set.

1. Select the image series you want to combine in Object Explorer.
2. Click **Create New Structure Set**.

Eclipse attempts to create a new 3D image and structure set using the images from all the selected series. The slices used in creating the new 3D image will be copied into a new series in the database.

Check which Structure Set an Image References

You can check which image a structure set references in Object Explorer.

- Right-click the structure set icon in Object Explorer and select **Properties**.

Duplicate a Structure Set

If a structure set has been used as a basis for a plan for which dose has already been calculated, the structures cannot be modified any longer. However, if you need to create a new plan for which you need to modify, for example, the body outline or some other structures, you can duplicate the structure set. You can then modify the structures in the new structure set and create a new plan based on them.

1. In External Beam Planning or Brachytherapy Planning, open the structure set you want to duplicate and the accompanying 3D image.
2. In the Focus window, right-click the structure set and choose **Duplicate Structure Set**.
3. In the **ID** and **Name** text boxes, type identification information for the structure set.
4. Click **OK**.

The application creates a copy of the image and the structure set.

Measure the Volume of a Structure

1. In the Focus window, select the structure.
2. Choose **View > Measure > Volume**.

The structure's volume and equivalent sphere diameter (diameter of a sphere with the same volume as the structure) are calculated and displayed in a message box.

3. To close the message box, click **OK**.

Moving a Structure

The Move Structure tool is available in External Beam Planning and Brachytherapy Planning.

To move an entire structure, use the Move Structure tool. The tool can be used in the transversal view to move a structure in X and Y directions only. The tool moves the active structure in all image planes simultaneously.

To move a segment of an active structure on the current image plane, use the Freehand tool.

To move all couch structures simultaneously, use the Move Support Structures tool.

Move a Structure

The Move Structure tool is available in External Beam Planning and Brachytherapy Planning.

1. In the Focus window, select the structure to move.
2. Click **Move Structure** .
3. Move the cursor on the structure and when the cursor changes to a four-headed arrow, do one of the following:
 - To move the structure freely, press the left mouse button down and drag the structure.
 - To move the structure in vertical and horizontal directions, press Shift, press the left mouse button down and drag the structure. The structure is moved to the direction dragged with the mouse.

The selected structure is moved in all image planes.

Clear a Structure

1. In the Focus window, select the structure to clear.
2. Do one of the following:
 - Display the plane on which to clear the structure and choose **Edit > Clear > from Current Plane of Primary Image** to clear all contours and segments of the selected structure from the current plane of the primary image.
 - Choose **Edit > Clear > from All Planes of Primary Image** to delete all contours and segments of the selected structure from all planes of the primary image.
 - Choose **Edit > Clear > from All 3D Images in 4D Image** to delete all contours and segments of the selected structure from all planes of the 3D images that are part of a 4D image.

Couch Modeling in Eclipse

Eclipse can model certain couches for photon treatment planning. A couch is modeled as a set of couch structures. The couch panel surface and interior, movable structural rails and grid (for Unipanel only) are each modeled as separate couch structures.

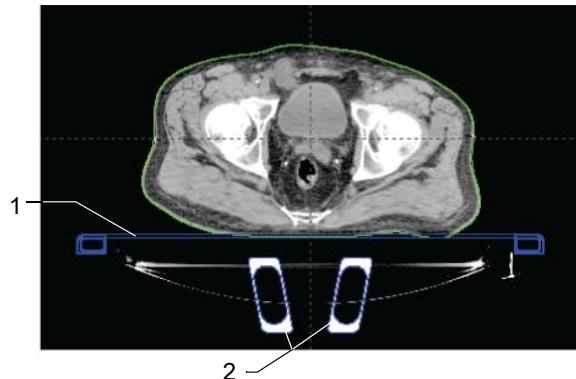
Eclipse models the following couches:

- Varian Exact couch: The flat panel, Unipanel (large window), and Unipanel (small windows).

- Exact IGRT couch: Thin, medium and thick panel.
- BrainLAB/iBeam couch: The main couch top and the H/N extension.
- Qfix Calypso kVue couch
- Siemens TT-A couch

The structure code of a couch structure is Support by default. You can change it to another structure code if necessary.

The volume type of a couch structure is always Support. Couch structures are modeled inside a 3D image. If the 3D image is too small, Eclipse can enlarge the image to fit the couch structures.



1. Couch panel (grid inside panel)
2. Movable structural rails

Figure 43 Couch Structures in 2D View

You can modify and move couch structures, and show and hide them in the image view. Couch structures are taken into account in dose calculation. If you already have calculated the dose distribution and want to remove couch structures from an image, you need to first invalidate the dose distribution.

For information on calculation algorithms that support couch modeling, see *Eclipse Photon and Electron Algorithms Reference Guide*.



Note: When working with couch structures, note that:

- Always verify the modeled and actual couch position as well as the position of movable rails, and make sure that the correct couch profile and couch accessories are selected before treating the patient.
- Couch structures do not automatically stay consistent with any changes in the treatment plan which affect the couch in the real world. For example, if the treatment orientation is changed, you need to change the couch structures accordingly.
- When using the Exact couch model with flat panel, small dips are present in the middle of the couch. These dips are designed to help measuring the rail distances from the center of the couch. The dips are designed to be so small that the effect in dose distribution is not significant. The visibility of the dips is dependent on the image resolution.

Chapter 7 Courses and Plans

Managing Courses

A course represents the course of treatment that a patient will be given. Every patient must have a course, and all plans always belong to a course. The course describes the intent and status of the treatment. One course may contain several plans, both approved and unapproved, including their fractionation schemes. This way courses can be used to gather up plans that represent different phases of treatment for a patient.



Note: When starting to create a plan for a patient, check whether the selected patient has any courses. If the patient has a course, check whether they can be used. For instance, if the same patient has been given a different diagnosis than before, you need to create a new course. Moreover, check which of the courses have already been approved for treatment, if any.

Create a New Course

1. Choose **Insert > New Course**.
2. Define the course properties:
 - Change the default ID, if necessary.
 - Select the intent of the course.
 - Define the date for starting the treatment.
3. Click **OK**.

Open a Course

1. Choose **File > Open**.
2. In the left list box, select the course.
3. Do one of the following:
 - To open the course and all plans under it, click **OK**.
 - To open the course and a particular plan, select the plan in the right-hand list box and click **OK**.

Modify a Course

1. In the Scope window, select the course.
2. Choose **Edit > Properties**.
3. Modify the general properties as necessary.
4. Attach or detach existing diagnoses on the Diagnoses tab as necessary.
5. Click **OK**.

Modify Fractionations in External Beam Plans

1. In the All Plans or Ref. Points tab of the Plan Organizer, click the row of the plan.
2. Do one of the following:
 - To add a fractionation, click **Add Fractionation to Plan**.
 - To delete a fractionation, click **Delete Plan: Fractionation**.

Copy and Paste an External Beam Plan between 3D Images

You can copy and paste plans to any 3D image imported to the database. This is useful, for example, for copying a plan between a set of 3D images representing the patient's respiratory cycle. You can copy and paste a plan regardless of whether the plan is already assigned to a structure set and 3D image or not. If the plan is linked to a 3D image, this original image and the other image must be registered with each other or have the same image size and resolution. Planned SSD is cleared if the 3D image the plan is pasted to refers to a different structure set than the original image.

1. Open the plan you are going to copy to another 3D image.
2. Open the 3D image that you are going to paste the plan to.
3. If the plan already is linked to a 3D image that is not registered with the new image or does not have the same image size and resolution, go to the Registration or the SmartAdapt application and register the images.
4. In the Scope window, select the plan.
5. Choose **Edit > Copy Plan**.
6. Do one of the following:
 - In the Scope window, select the 3D image to which you wish to paste the plan.
 - In the Focus window, expand the 4D image object, if necessary, and select the 3D image to which you wish to paste the plan.

7. Choose Edit > Paste Plan.

If images are registered, the isocenter is placed to the correct location in the new image, otherwise it is placed to the image origin.

RT Prescriptions

An RT prescription is a way of communicating dose prescription and treatment management information between ARIA RTM Workflow Management components and other applications. Using the RT prescription allows defining the dose prescription for the target before starting treatment planning. The prescription can be created, for instance, by the oncologist in the Prescribe Treatment workspace. The dose prescription can be defined for a volume, depth, isocenter or isodose percentage.

You can use RT prescriptions in your treatment plans by linking the appropriate RT prescription to the plan. The RT prescription must be found in the same course as the plan, and it must be in draft, reviewed, or approved status. It is also possible to base multiple plans on one single RT prescription. An RT prescription may also contain dose prescriptions for several targets, and you can create a separate plan for each of them.

In External Beam Planning and Brachytherapy Planning, RT prescriptions defined for a patient are displayed under the course they belong to in the Context window. Plans linked to an RT prescription are displayed under the RT prescription in question in the Context window. The statuses of the RT prescription are indicated by icons.

-  — Draft RT prescription
-  — Reviewed RT prescription
-  — Approved RT prescription
-  — An old revision of an RT prescription. This icon is shown only when a newer revision of the RT prescription exists, but there are plans that are still linked to the old revision.
-  — An RT prescription that has been errored out. This icon is shown only if there are plans that are still linked to the RT prescription.

Details of the RT prescription are shown in the RT Prescription tab of the Plan Properties dialog box, which also allows you to open the prescription in read-only mode in the Prescribe Treatment workspace. If the RT prescription contains prescription constraints that have been defined in the Prescribe Treatment workspace, they are shown on the Constraints tab in Prescription Properties.

If the course in which you are creating a plan contains an RT prescription, you can link the plan to the RT prescription during the plan creation. You can update the link from the plan to an RT prescription, exchange the link to another RT prescription or remove the link after creating the plan.

You can also create a photon plan by right-clicking the RT Prescription icon in the Context Window in External Beam Planning.

RT prescriptions are versioned in the Prescribe Treatment workspace. If an approved RT prescription is modified after it has been linked to a plan, the new revision is shown in the Plan Properties. The revision number is displayed after the name of the RT Prescription in the Context window and RT prescription properties. To copy the dose values from the new revision to the plan, you need to update the plan manually by clicking **Update Plan**. This also updates the link to point to the latest revision of the RT Prescription. If necessary, you can also view the original and the new revision of the prescription.

More information on RT prescriptions and the Prescribe Treatment workspace: ARIA RTM Workflow Management documentation.



Note: *If you have linked an RT prescription to a plan, and the RT prescription is changed in the Prescribe Treatment workspace, the dose values are not automatically copied to the plan. You need to update the plan manually.*

Create an External Beam Plan from an RT Prescription

If the patient file is not already open, use the Patient Explorer and the Object Explorer to open the desired patient and structure set. In addition, open the course the RT prescription is linked to in the Context window.

1. In External Beam Planning, right-click the RT prescription in the Context window, and do one of the following:
 - To create a plan for one target, select **Create plan for target**.
 - To create separate plans for all targets that have an RT prescription defined, select **Create One Plan Per Prescribed Target**.
2. In the Update Plan dialog, select the desired prescription target or targets and click **Create**.
3. Select a target volume for the plan. Click **Next**.
4. If prompted to do so, select a primary reference point for the plan.
5. Select the patient position and click **Finish**.
6. If you selected to create plans for multiple targets, complete the above steps for each prescribed target.



Note: All plan creation methods (for example, selecting a command in Insert menu or creating a plan from a clinical protocol) allow you to link a plan to an RT Prescription if the course you have selected contains one.

Update a Plan with a New Revision of an RT Prescription

When updating an RT prescription, you can select whether to update the dose prescription related data, or only data related to, for example, treatment management.

1. In the Scope or Focus window, right-click the plan and choose **Properties**.
2. Click the **RT Prescription** tab. If there is a new revision of the RT prescription, you can see an icon and a help text about the new RT prescription revision.
3. To view the new revision, click **Latest Revision Properties**. To view the current RT prescription, click **Linked Revision Properties**.



Tip: To view the details of the RT prescription in Prescribe Treatment workspace in read-only format, click **Open** in the Prescription Properties.

4. To update the current plan with dose prescription values from the new revision, click **Update Plan**.
5. In the Update Plan dialog box, you can compare the current dose prescription values in the plan and the new values from the new revision.
6. To apply the new values to the plan, select the corresponding check box and click **Update**. The plan is linked to the new revision of the RT prescription, and the new values are copied to the Dose tab.
7. In the Plan Properties dialog box, click **Apply** or **OK**. The new values are copied to the plan and are shown in the Dose Prescription tab of the Info window.

Change the RT Prescription Used in a Plan

1. In the Scope or Focus window, right-click the plan and choose **Properties**.
2. Click the **RT Prescription** tab.
3. Select the new prescription from the ID list.
4. In the Update Plan dialog box, you can compare the current values in the plan and the new values from the new RT prescription.
5. To apply the new values to the plan, select the corresponding check box and click **Update**. The plan is linked to the new prescription, and the new values are copied to the Dose tab.

- In the Plan Properties dialog box, click **Apply** or **OK**. The new values are copied to the plan and are shown in the Dose Prescription tab of the Info window.



Tip: You can view the details of the latest RT prescription revision by clicking **Latest Revision Properties**.

Creating Volumetric Plans from 2D Plans

In some treatment planning cases, you may want to continue plans originating from a 2D planning application (such as Treatment Preparation) by adding volumetric dose calculation in External Beam Planning. Volumetric dose calculation is possible in External Beam Planning only when the plan has a structure set and a 3D image attached. Normally, this is not the case in plans originating from a 2D planning application. To acquire volumetric dose to a 2D plan, you need to create a plan copy or a plan revision, and assign a 3D image to it in External Beam Planning by copying the plan to a 3D image or attaching a 3D image to the plan.

You can also open 2D plans in the IRREG Planning application.



Note: If the modifications do not require re-calculation of the volumetric dose, the plan can be modified outside External Beam Planning.

No isocenter may be present in plans originating from outside External Beam Planning. When you assign an image to a plan, External Beam Planning tries to find isocenters in the plan. If they are found, they remain in their correct locations. If isocenters are not found, the field isocenters are placed in the plan based on the couch position data found in the fields as follows:

- No couch position found in the plan—Isocenter positions of all fields are placed to the image origin in the plan.
- Couch position found in the plan—Isocenter position of the first field is placed to the image origin. If other fields have different isocenter positions, they are defined in relation to the isocenter of the first field.

If the plan contains live DRR images created in External Beam Planning, they are automatically re-calculated when the 3D image is changed. Imported DRR images remain as they were imported. MU values found in the plan are cleared. If no MU values are found, the primary reference point is created (without reference point location). All field weight values are set to 1, and the Calculated SSD is re-calculated for each field. Planned SSD is cleared when a new structure set is assigned to a plan.

Assign a Patient Image and a Structure Set to a Plan

1. Open the plan.
2. In the Scope or Focus window, right-click the plan and choose **Assign Structure Set**.
The Object Explorer opens, and you can select the appropriate structure set. If the patient has only one 3D image, it opens in the image views. The field isocenters are placed to the image origin depending on the couch position found in the plan.
3. Save the plan.

Dose Prescription Tab of the Info Window

For external beam plans, the Dose Prescription tab is used for viewing and setting the prescription information of a plan or plan sum. The Dose Prescription tab lists the dose-related parameter values of all the fractionations of the selected plan or plan sum.

Table 6 Information in Dose Prescription Tab

Column	Description
Plan ID	For a plan sum, ID of each plan in the sum.
Fractionation ID	For an individual plan, ID of each fractionation in the plan.
Dose/Fraction	Dose/fraction in Gy or cGy, for each fractionation.
Number of Fractions	Number of fractions in the plan.
Total Dose	Total dose in Gy or cGy, for each fractionation.
Primary Reference Point	Primary reference point in the plan, for each fractionation.
Total Dose at Primary	Total dose at the primary reference point in Gy or cGy, for each fractionation.
Relative Dose at Primary	Relative dose at the primary reference point in percentage, for each fractionation. Cannot be edited.
Prescribed Percentage	Treatment percentage prescribed for the plan, for each fractionation.
Plan Normalization Mode	Plan normalization used in the plan. Click to change the normalization mode.
Plan Normalization Value	Plan normalization value in percentage, for each fractionation. Cannot be edited.

The primary reference point and total dose at primary reference point can be edited in the Info window. Editing these values changes the normalization of the plan. The plan normalization value cannot be edited.



Note: In the case of an IMRT plan, it is advisable to run the Leaf Motion Calculator (LMC) after changes in the dose prescription.

Prescribe the Dose in the Plan Organizer



Note: The MU are not available for treatment if the primary reference point has not been defined.

1. Choose **Planning > Plan Organizer**.
2. To change the dose or fractionation settings, go to the All Plans tab, click the appropriate cell in the table and type the new value in the cell.
3. To include a plan in the total sum, go to the Ref. Points tab and select the corresponding check box.
4. Click **OK** to close the dialog box.



Tip: You can also define the dose in the Plan Properties dialog box where you can give prescribed dose/fraction, prescribed dose percentage and number of fractions for the plan.

Plan Organizer

The Plan Organizer is a tool for monitoring and managing the planning information for the plans in the active course. The Plan Organizer contains tabs for showing:

- All plans contained in the course
- Dose contribution of the plan for each reference point
- In External Beam Planning, dose data for each fractionation of each plan, including the MU values for each field and the dose at each reference point
- Timer setting for Cobalt treatment units for each field

The information in the tabs is shown in a table format. Cells containing unacceptable values are marked with a red frame.



Note: For external beam plans, use treatment applications to monitor the actual treatment process.

The Plan Organizer marks nominal field doses with the ~ character. Nominal field doses occur when the field dose matrices are unavailable for a reference point that has a location in the planned image. In this case, the field dose contributions are estimates based on the value in the plan dose matrix at the given reference point location. Nominal doses are also marked with the ~ character in the Reference Point Workspace.

When the Acuros XB dose calculation algorithm is used with the Plan Dose calculation option selected, all Gy values reported in the Plan Organizer are nominal (and marked with the ~ character). This means that the dose to reference points with locations cannot be used to independently verify MU calculation since the real calculated dose per field at the reference point is not known.



Note: Verify the plan information outside the Plan Organizer before approving it for treatment, because some of the information may be viewed in the Plan Organizer only by changing the column widths or by scrolling.

Related Topics

[Nominal Field Dose for Reference Point](#) on page 440

All Plans Tab (Plan Organizer)

The All Plans tab summarizes the plans that exist currently in the active course. Information about plans approved for treatment cannot be modified, and their rows are grayed out. You can monitor and define the following for the plans in the Plan Organizer:

- Change the name of the plan and fractionations.
- In External Beam Planning, add and delete fractionations.
- Check which fractionation belongs to each plan.
- Check and change the primary reference point that describes the prescribed dose for each plan in ARIA RTM applications.
- View the target volume of the plan.
- Change the prescribed dose defined for each plan.

Ref. Points Tab (Plan Organizer)

The Reference Point tab summarizes the information for the reference points contained in the plans in the active course. On the tab you can:

- View the plan data: the plan and fractionation ID and the number of fractions for each plan.
- Monitor the dose per fraction at the reference points.
- Sum up the total dose of the selected plans at the reference points.

- Change the total dose and the daily dose limits for the reference points.
- The cell of the primary reference point is marked with a yellow frame.



Note: *The patient may also have other reference points that are not listed in this tab, for example, reference points created in ARIA RTM applications. To have these reference points appear in the Plan Organizer, include the points in the plan by clicking the **Edit Reference Points** button.*

Tabs for Individual Fractionations in the Plans

In the Plan Organizer, the tab of each individual fractionation summarizes the dose data for the fractionation in the active course. Information in this tab cannot be modified.

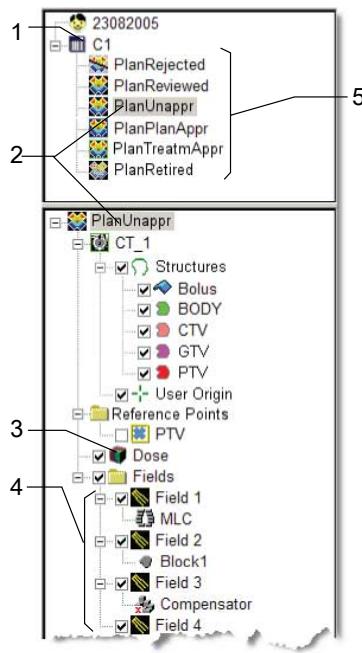
In External Beam Planning, you can monitor the following for individual fractionations:

- Fields included in the fractionation.
- Number of monitor units (MU) for each photon and electron field or timer setting for a Cobalt treatment unit.
- Coefficient MU/Gy indicating how many MU comprise one Gy at the primary reference point for the photon or electron field.
- Reference points included in the fractionation. The cell of the primary reference point is marked with a yellow frame.
- Field-specific dose data for the reference points: contribution of one field in one fraction at the point, dose per fraction in the fractionation and total dose.
- Reference dose (Gy) of the photon or electron field at the depth of dose maximum (d_{max}) on the field central axis.

If the total dose contributed by the plans included in the total dose exceeds the total dose of a reference point, the Planned Total Dose in the column of the reference point is marked with a red frame.

Treatment Planning Concepts in the Context Window

The division of treatment planning concepts is reflected in the Context window.



1. Course
2. Active plan
3. Dose matrix
4. Fields and field accessories contained in the active plan
5. Plans and plan statuses, top–bottom:
Rejected, Reviewed, Unapproved,
Planning Approved, Treatment Approved,
Retired

Figure 44 External Beam Plan Concepts in Context Window

Chapter 8 Templates and Clinical Protocols

Templates

Templates are collections of structures, objectives and plan properties that can be used to create new objects, such as new plans, that automatically possess the properties saved in the template. With templates you can simplify the treatment planning process by not having to define these properties separately for each created object. Templates that you create are available to other users of the system and provide default settings for the objects created based on the templates. You can create structure templates, objective templates and plan templates.

All users have rights to view templates. Depending on your user rights, you can also edit, approve and delete templates. In general, if you have, for example, rights to modify or approve plans, you have the same rights for all items under the plans. This document assumes that the user has full rights.

Structure Templates

A structure template stores structure information, such as the structure volume type and code, the color and style of the structure, the DVH line color, style and width used to describe the structure, and the searching options for the structure (upper and lower CT pixel values). A structure template group consists of individual structure templates.

Structure templates use existing structure codes and patient volumes. When creating structures using a structure template, the application checks whether structure codes already exist for the patient, and, if found, matches the existing structure codes with those used in the template. If structure codes are not found, the matching is done based on patient volumes.

A particular situation affected by this use of patient volumes is changing structure IDs in a setup where two different image sets and one structure template are used for a particular patient. In this situation, the structure IDs change for both image sets because they are linked to the internal patient volume IDs. This behavior also affects reference points, which are linked to patient volumes.

Templates are stored in a server directory in XML format.



Note: Since the templates are stored in a server directory, they are not included in database backups. To have your templates backed up, you can export them one by one or copy the directory to a desired location.

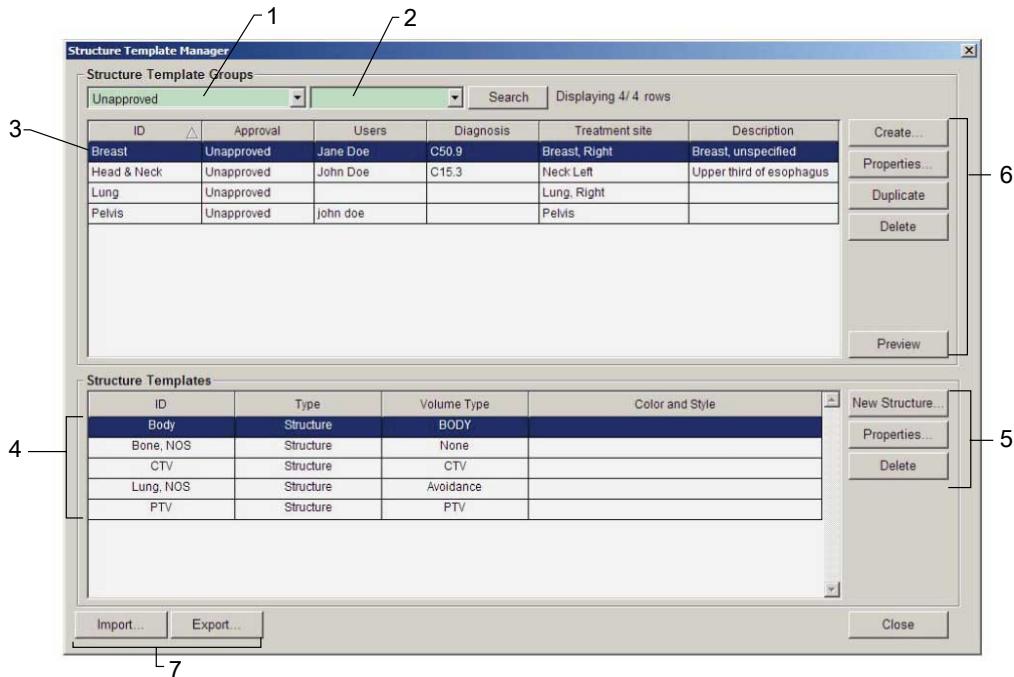
Related Topics

[Structure Codes](#) on page 113

Structure Template Manager

The Structure Template Manager displays structure template groups and the individual structure templates of the selected structure template group. For a structure template group, the manager displays the identification, approval status, the users assigned to the template group, the possible diagnosis, treatment site and description. For the individual structure templates, the manager displays the identification, structure type, volume type, and the color and style of the structure.

You can sort any column of the Structure Template Manager by clicking the column header. You can create, edit, duplicate, delete, preview, import and export structure template groups in the Structure Template Manager. You can also create new structures, and edit and delete individual structure templates of the selected structure template group.



1. The approval status of the displayed structure template groups.
2. Type the search words for filtering structure template groups.
3. The selected structure template group.
4. The individual structure templates of the selected structure template group.
5. Actions available for the selected individual structure template.
6. Actions available for the selected structure template group.
7. Actions available for the selected structure template group.

Figure 45 Structure Template Manager

Create a Structure Template Group Using Structure Template Manager

This information applies to External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Structure Template Manager**.
2. Click **Create**.
3. Fill in the necessary information and click **OK**.
4. To add a structure template to the new structure template group:

Click New Structure.

Fill in the required information and click **OK**.

5. To close the Structure Template Manager, click **Close**.

Create a Structure Template from Structure Set

This information applies to External Beam Planning and Brachytherapy Planning.

1. Create an image for the patient or open the desired patient image and create structures to the image.
2. Choose **Planning > Templates and Clinical Protocols > Create Structure Template from Structure Set**.
3. Fill in the necessary information and click **OK**.

Duplicate a Structure Template Group

This information applies to External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Structure Template Manager**.
2. To search for a structure template group in the **Structure Template Groups** group box, define the search criteria and click **Search**.
3. Select the structure template group to duplicate from the table.
4. Click **Duplicate**.

The name of the new structure template group is appended with the # character and a running number.

You can change the name to a more descriptive one by editing the new structure template group.

Edit a Structure Template Group and a Structure Template

This information applies to External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Structure Template Manager**.
2. To search for a structure template group in the **Structure Template Groups** group box, define the search criteria and click **Search**.
3. To edit a structure template group:
 - a. From the **Structure Template Groups** table, select the template group to edit and click **Properties**.
 - b. Edit the information as needed and click **OK**.
4. To edit a structure template in a structure template group:

- a. From the **Structure Template Groups** table, select the template group that contains the structure template to edit.
- b. From the **Structure Templates** table, select the structure template to edit and click **Properties**.
- c. Edit the information as needed and click **OK**.

If you want to edit an approved structure template group or structure template, you first need to change its status.

5. To close the Structure Template Manager, click **Close**.

Related Topics

[Changing the Approval Status of Templates, Clinical Protocols and Clinical Protocol References](#) on page 174

Delete a Structure Template Group and a Structure Template

To delete an approved template, you first need to change its status to Unapproved.

This information applies to External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Structure Template Manager**.
2. To search for a structure template group in the **Structure Template Groups** group box, define the search criteria and click **Search**.
3. To delete a structure template group, select the structure template group from the **Structure Template Groups** table and click **Delete**.
4. To delete a structure template from a structure template group, select the structure template from the **Structure Templates** table and click **Delete**.



Note: Deleting templates is a permanent operation, the deleted templates cannot be reloaded.

Plan Templates

A plan template stores standard plan characteristics in the database. When you use a plan template to create a plan, the new plan is based on the information stored in the template.

In External Beam Planning, plan templates include information on:

- field geometry
- treatment unit
- energy mode selection

- use of multileaf collimators, blocks and other add-ons
- live DRR images
- field alignment rules

For MLCs, blocks, compensators and bolus, only information about their presence and fitting parameters is included in the template.

Templates are stored in a server directory in XML format.

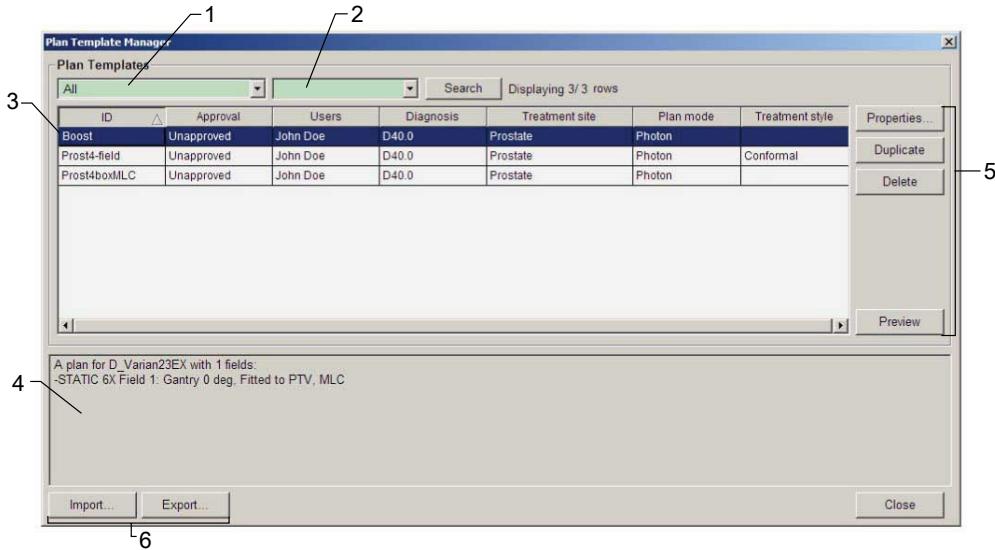


Note: Since the templates are stored in a server directory, they are not included in database backups. To have your templates backed up, you can export them one by one or copy the directory to a desired location.

Plan Template Manager

The Plan Template Manager displays plan templates. For a plan template, the manager displays the identification, approval status, the users assigned to the template, the possible diagnosis and treatment site, the energy mode of the plan, and the treatment style. A description of the selected plan template is shown on the bottom of the Plan Template Manager.

You can sort any column of the Plan Template Manager by clicking the column header. You can edit, duplicate, delete, preview, import and export plan templates in the Plan Template Manager.



1. The approval status of the displayed plan templates.
2. Type the search words for filtering plan templates.
3. The selected plan template.
4. Information on the selected plan template.
5. Actions available for the selected plan template.
6. Actions available for the selected plan template.

Figure 46 Plan Template Manager

Plan Geometry and Energy in Templates for External Beam Plans

In a new plan based on a plan template, the field geometry is based on the isocenter positioning, which you can define while creating a new plan from a template. You can place the isocenter:

- at field target mass center
- at image origin (user origin)
- at image center
- at viewing plane intersection
- relative to field target mass center
- relative to image origin (user origin)
- relative to image center
- relative to viewing plane intersection

When creating a plan template from a plan, the isocenter is placed based on the isocenter location in the original plan. You can change the placement of the isocenter as needed. The default isocenter positions in a plan template are:

- If the isocenter of a field in the original plan is at the 3D image origin, the isocenter is placed at the 3D image origin in the plan template.
- If a field in the original plan is fitted to a structure, the isocenter is placed relative to the field target mass center in the plan template.
- If neither of the above conditions is met and the original plan contains a 3D image, the isocenter is placed relative to the 3D image center in the plan template.
- If none of the above conditions are met, the isocenter placement is set to None.

If a connection between an aperture block and a structure has been saved in the template, these add-ons are fitted to the structure defined for the add-ons. You can also select the fit structure for each add-on separately or decide not to fit any of them.

In a photon plan, this applies also to MLCs.

Save an External Beam Plan as a Plan Template

You can create new plan templates in External Beam Planning.

1. Create a plan and save it.
2. Choose **Planning > Templates and Clinical Protocols > Create Plan Template from Plan**.
3. Fill in and modify the plan template information.

You can use the information in each of the above bullets for filtering plan templates in the Plan Template Manager.

Note that although you can change the information regarding the field geometry parameters in the text box, the actual fields in the template are not affected. For instance, the gantry angles of the fields are not changed even if you edit the angles in the text box.

4. Select the template items and, if desired, the prescription to include in the plan template.
5. To decide how fields and add-ons will be placed during plan creation, select an item in the Placement column, click the down-pointing arrowhead that appears in the end of the row, and select the desired option from the drop-down list.
6. Click **Finish**.
7. Save the new plan template.



Note: If the photon plan that the new plan template is based on contains field alignment rules or live DRR images, the information is also stored in the new plan template.

Related Topics

[Plan Geometry and Energy in Templates for External Beam Plans](#) on page 142

Duplicate a Plan Template

1. Choose **Planning > Templates and Clinical Protocols > Plan Template Manager**.
2. To search for a plan template in the **Plan Templates** group box, define the search criteria and click **Search**.
3. Select the template to duplicate from the table.
4. Click **Duplicate**.

The name of the new plan template is appended with the # character and a running number.

You can change the name to a more descriptive one by editing the new template.

5. Save the new plan template.

Edit a Plan Template

This information applies to External Beam Planning and Brachytherapy Planning.



Note: Fields in the plan template cannot be edited. If you need to edit the fields, create a new plan with modified field setup, save it as new plan template with a new name, delete the original plan template, and rename the modified plan template.

1. Choose **Planning > Templates and Clinical Protocols > Plan Template Manager**.
2. To search for a plan template in the **Plan Templates** group box, define the search criteria and click **Search**.
3. Select the template to edit from the table.

If you want to edit an approved plan template, you first need to change its status.

4. Click **Properties**.
5. Edit the information as needed and click **OK**.

Although you can change the information regarding the field geometry parameters in the Description text box in External Beam Planning, the actual fields in the template are not affected. For instance, the gantry angles of the fields are not changed even if you edit the angles in the Description text box.

6. To close the Plan Template Manager, click **Close**.
7. Save your changes.

Related Topics

Delete a Plan Template

To delete an approved template, you first need to change its status to Unapproved.

This information applies to External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Plan Template Manager**.
2. To search for a plan template in the **Plan Templates** group box, define the search criteria and click **Search**.
3. Select the template to delete from the table.
4. Click **Delete**.



Note: Deleting templates is a permanent operation, the deleted templates cannot be reloaded.

5. Save your changes.

Objective Templates

An objective template contains predefined dose-volume objectives to specify the optimization objectives of a plan. You define the optimization objectives by specifying the objective type (point or line), the structure to which the objective limits the dose, the dose limit (upper or lower), percentage of the structure volume to be receiving the dose, the intended dose, and the priority for the objective.

For RapidArc plans, the objective template also contains indication of the MU objective and the use of jaw tracking. These values can only be viewed using the Preview.

In External Beam Planning, if you have manually defined objectives for a plan and then decide to load an objective template to the plan, the objective values stored in the template override the manually defined objective values.



Note: In addition to optimization objectives that are used for an existing plan, there are plan objectives that are part of a clinical protocol.

Templates are stored in a server directory in XML format. Since the templates are stored in a server directory, they are not included in database backups. To have your templates backed up, you can export them one by one or copy the directory to a desired location.



Note: Dose objectives from a template cannot be used in the same plan as dose objectives from a DVH estimation model.

Related Topics

[Plan Objectives in Clinical Protocols](#) on page 155

Objective Template Manager

The Objective Template Manager displays the objective templates and the individual objectives of a selected objective template. For an objective template, the manager displays the identification, approval status, the users assigned to the template, the possible diagnosis, treatment site and description.

The objectives of the selected objective template are displayed both in numeric and graphic form. In addition to modifying the objectives in the numeric form, you can modify them in the graph with the mouse.

For the objectives, the manager displays:

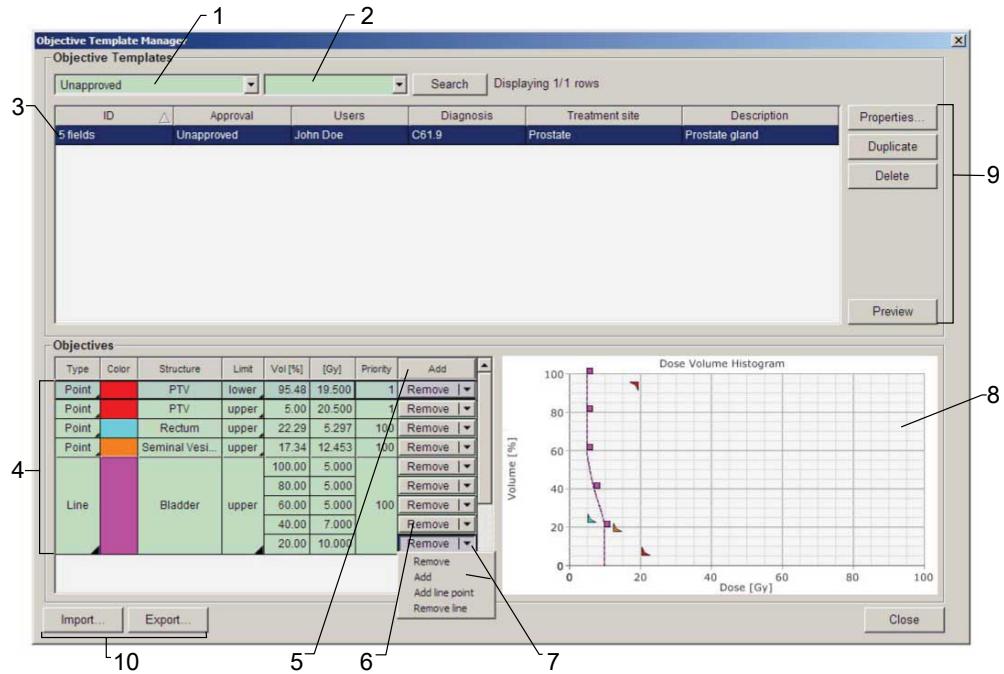
- the objective type (point or line) and color
- the structure to which the objective limits the dose
- the dose limit (upper or lower)
- the percentage of the structure volume to be receiving the dose
- the intended dose
- the priority for the objective.

In the graph, the line objectives are illustrated with small squares, and the point objectives are illustrated with small arrowheads. An objective has an arbitrary color in the objective template. When the objective is added to a plan, the objective color changes to the color of the structure to which the objective limits the dose.

You can sort any column by clicking the column header. You can edit, duplicate, delete, preview, import and export objective templates. You can also add and remove single objectives.

Even if you can see the objectives meant for Brachytherapy Planning, you cannot use them in External Beam Planning, and vice versa.

In addition to the Objective Template Manager, in External Beam Planning the objectives can also be accessed from the Optimizer dialog box.



1. The approval status of the displayed objective templates.
2. Type the search words for filtering objective templates.
3. The selected objective template.
4. The objectives of the selected objective template.
5. Click here to add a new objective.
6. Click here to remove the objective.
7. Click the down-pointing arrowhead to open the drop-down menu for selecting an action.
8. The graphic representation of the objectives in the selected objective template. You can modify the objectives with the mouse.
9. Actions available for the selected objective template.
10. Actions available for the selected objective template.

Figure 47 Objective Template Manager

Objective Template Group Properties

In External Beam Planning, the Objective Template Group Properties dialog box contains the following tabs: General, Normal Tissue Objective, GEOS and IMRT.

IMRT Tab (Objective Template Group Properties)

This information is only relevant for photon plans.

The IMRT tab contains the following information:

- The default smoothing values. A higher value smoothes more than a low value.
- The default dose minimization. A higher value minimizes the dose more than a low value.
- The default optimization type. The available types are Beamlet, Field weight and None.
- Information whether the fixed collimator jaws are used in the treatment or not.
- The maximum number of iterations at which point the optimization process is terminated.
- The maximum time limit in minutes after which the optimization is stopped even if the maximum number of iterations is not reached.
- Information on how the field fluence is displayed. The available options are Use colors and Interpolate.

Related Topics

[Optimization Parameters Specific to IMRT Optimization](#) on page 232

Normal Tissue Objective Tab (Objective Template Group Properties)

The Normal Tissue Objective tab contains the following information:

- Use Normal Tissue Objective—Defines if the objective is used or not
- Priority—Determines the relative importance of the Normal Tissue Objective in relation to other optimization objectives.
- Distance from target border—Determines the area where the Normal Tissue Objective value must be constant.
- Start dose—Determines the relative dose level in the Normal Tissue Objective in the area at the PTV border.
- End dose—Determines the relative dose level in the Normal Tissue Objective in the area furthest away from PTV border.
- Fall-off—Determines the steepness of the Normal Tissue Objective curve shape.

Related Topics

[Normal Tissue Objective in Photon Optimization](#) on page 230

GEOS Tab (Objective Template Group Properties)

This information is only relevant for photon plans.

The GEOS tab contains the following information:

- Initial field distribution—Defines whether the initial field distribution for the global optimization is coplanar or non-coplanar.

- Minimum number of fields—Defines the lowest number fields in the field geometry created by the global optimization.
- Maximum number of fields—Defines the highest number fields in the field geometry created by the global optimization.
- Maximum elevation angle for non-coplanar fields—Controls the maximum elevation from the coplanar plane in case a non-coplanar initial field distribution is being used.
- Maximum collimator variation—Controls how much the collimator angle values are allowed to vary from one field to the closest neighboring field in the initial field distribution.
- Local geometric optimization mode—Sets the mode for the local optimization.

Create an Objective Template from an External Beam Plan

1. Do one of the following:
 - Open an optimized plan containing the objectives you wish to save into an objective template and choose **Planning > Templates and Clinical Protocols > Create Objective Template from Plan**.
 - While optimizing a plan, in the optimization dialog box, click **Save Objectives to a Template** .
2. Fill in the necessary information in the **General** tab.
3. To set the Eclipse IMRT, select the **IMRT** tab and fill in the necessary information.
4. Click **OK**.

Related Topics

[Objective Template Group Properties](#) on page 147

Duplicate an Objective Template

1. Choose **Planning > Templates and Clinical Protocols > Objective Template Manager**.
2. To search for an objective template in the **Objective Templates** group box, define the search criteria and click **Search**.
3. Select the template to duplicate from the table.
4. Click **Duplicate**.

The name of the new objective template is appended with the # character and a running number.

You can change the name to a more descriptive one by editing the new template.

Edit Objective Template Properties

This information applies to External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Objective Template Manager**.



Tip: In External Beam Planning, you can also click **Manage Objective Templates**  in the optimization dialog box while optimizing a plan.

2. To search for an objective template in the **Objective Templates** group box, define the search criteria and click **Search**.
3. Select the template to edit from the table.

If you want to edit an approved objective template, you first need to change its status.

4. Click **Properties**.
5. Edit the information as needed and click **OK**.
6. To close the Objective Template Manager, click **Close**.

Related Topics

[Changing the Approval Status of Templates, Clinical Protocols and Clinical Protocol References](#) on page 174

Edit an Objective Template in the Numeric Form

This information applies to External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Objective Template Manager**.



Tip: In External Beam Planning, you can also click **Manage Objective Templates**  in the optimization dialog box while optimizing a plan.

2. To search for an objective template in the **Objective Templates** group box, define the search criteria and click **Search**.
3. Select the template to edit from the table.

If you want to edit an approved objective template, you first need to change its status.

4. To edit the objectives in the numeric form, in the **Objectives** group box:
 - Cells with small arrowhead: Click the cell and select an option from the drop-down list that opens.
 - Text boxes: Click the cell and type the new information.
 - To add an objective, click **Add**.
 - To remove an objective, click **Remove**.
5. To close the Objective Template Manager, click **Close**.

Related Topics

[Changing the Approval Status of Templates, Clinical Protocols and Clinical Protocol References](#) on page 174

Edit an Objective Template in the Graphic Form

This information applies to External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Objective Template Manager**.



Tip: In External Beam Planning, you can also click **Manage Objective Templates**  in the optimization dialog box while optimizing a plan.

2. To search for an objective template in the **Objective Templates** group box, define the search criteria and click **Search**.
3. Select the template to edit from the table.

If you want to edit an approved objective template, you first need to change its status.

4. To edit the objectives in the graph, do one of the following:
 - Drag the line type or point type objective with the mouse as desired.
 - Right-click in the graph and do one of the following:
 - Select **Add Upper objective**, click in the desired location in the graph and modify the new upper objective that appears in the numeric form.
 - Select **Add Lower Objective**, click in the desired location in the graph and modify the new lower objective that appears in the numeric form.
 - Select **Add Line Objective**, click in the desired location in the graph and modify the new line objective that appears in the numeric form.
 - Select **Move Objective** and drag the line type or point type objective with the mouse as desired.
 - Select **Zoom In**, click and hold down the left mouse button, move the mouse pointer to form a rectangular area, and release the mouse button when the rectangle covers the desired area. You can repeat zooming as many times as needed.
 - Select **Zoom Out**.
 - Select **Reset Geometry** to set the graph into its original scale.
 - Select **Pan** and drag the whole graph as desired.
5. To close the Objective Template Manager, click **Close**.

Related Topics

[Changing the Approval Status of Templates, Clinical Protocols and Clinical Protocol References](#) on page 174

Delete an Objective Template

To delete an approved template, you first need to change its status to Unapproved.

This information applies to External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Objective Template Manager**.



Tip: In External Beam Planning, you can also click **Manage Objective Templates**  in the optimization dialog box while optimizing a plan.

2. To search for an objective template in the **Objective Templates** group box, define the search criteria and click **Search**.
3. Select the template to delete from the table.

4. Click **Delete**.



Note: Deleting templates is a permanent operation, the deleted templates cannot be reloaded.

Import a Template

You can import all external beam templates in External Beam Planning and all brachytherapy templates in Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Objective Template Manager, Plan Template Manager or Structure Template Manager**.
2. Click **Import**.
3. Navigate to the directory from where to import the template and select the template to import.
4. Click **Open**.

If an identical template ID already exists, the template cannot be imported. If the control mechanism that was added to the template when it was exported notices that the template is changed outside the application, a warning is displayed.

Export a Template

You can export all external beam templates in External Beam Planning and all brachytherapy templates in Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Objective Template Manager, Plan Template Manager or Structure Template Manager**.
2. To search for a template in the template manager, define the search criteria and click **Search**.
3. Select the template to export from the table.
4. Click **Export**.
5. Navigate to the directory into which to save the template.
6. Define a name for the template.
7. Click **Save**.

The template is exported as an XML file to the defined location. A control mechanism (check sum) is added in the XML file. If the exported template is changed outside the application, the mechanism notices it and a warning is displayed when the template is imported back to the application.

Clinical Protocols

A clinical protocol contains a set of predefined values that guide the treatment planning process. Its purpose is to speed up treatment planning and to ease the clinicians work load in typical treatments.

A clinical protocol consists of:

- Predefined set of structures (structure template group)
- Predefined set of protocol plans defining the treatment phases (for example the original treatment and its boost):
 - Plan template—Contains the standard plan characteristics.
 - Plan objectives—Define the intended dose distribution for the target and critical organs realized by the plan. The overall prescription is a collection of plan objectives that limit the total dose distribution for the target and critical organs.
 - Optimization objectives—Contains predefined optimization objectives (dose-volume objectives).
- Review settings—Define structures included in the DVH.

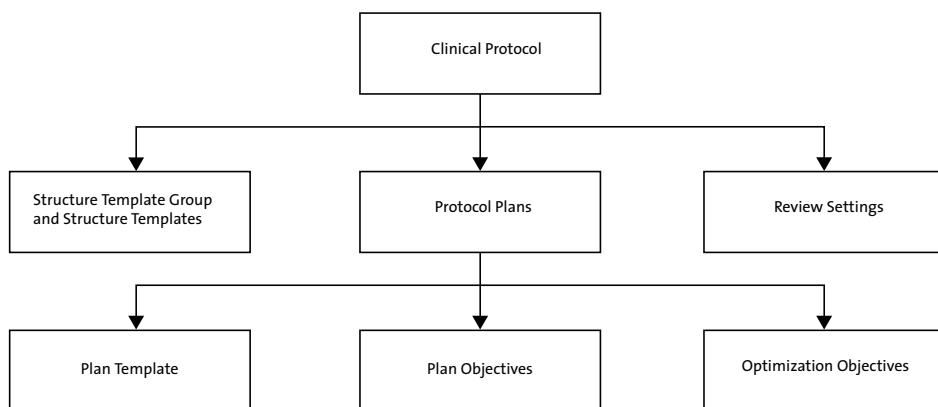


Figure 48 Clinical Protocol Structure

One clinical protocol can contain both external beam plans and brachytherapy plans. Clinical protocols can also be incomplete, as each element of the protocol is not required. It is possible that a clinical protocol contains only structures, but no protocol plan objectives.

All users have rights to view clinical protocols. Depending on your user rights, you can also edit, approve and delete clinical protocols.

Visibility of Clinical Protocol Information in Plans

When a clinical protocol is attached to a course, the clinical protocol reference icon () is shown under the course in the Scope window. Plans added from the clinical protocol are shown below the clinical protocol reference icon.

The plan objectives stored in the clinical protocol reference that is inserted to a course are shown in the Plan Objectives tab of the Info window. The dose prescription is determined by the primary plan objective. Treatment reports show the protocol ID, phase, prescription, and dosimetric quality information.

Related Topics

[Plan Objectives Tab of the Info Window](#) on page 160

Plan Objectives in Clinical Protocols

The plan objectives for a protocol plan define the intended dose distribution for the target and critical organs realized by the plan, plus the plan conformity objectives. In plan objectives, you can also define dosimetric quality parameters for the plan. The overall prescription is a collection of plan objectives that limit the total dose distribution for the target and critical organs realized by all the protocol plans in the clinical protocol.

The difference between plan objectives and optimization objectives is that plan objectives define the intended dose distribution, while optimization objectives try to meet them.

In External Beam Planning, optimization objectives also inform the optimization algorithm of the optimization constraints.

With certain limitations, plan objectives can be used as optimization objectives when creating a clinical protocol. One of the plan objectives is specified as the primary plan objective.

In External Beam Planning, the primary plan objective is used as the basis for the MU calculation and in fixing the absolute dosimetry for the plan. The application can calculate the plan and normalize as specified within the clinical protocol after the plan objectives have been specified. After the plan has been calculated, doses can be compared between the plan and doses specified in the objectives within both the Info window and Dose-Volume Histogram view.

Plan objectives can be divided into several types.

Objective for Structure Volume

This plan objective defines the limit for the percentage of the structure volume that receives the dose.

When the plan objective is set as the primary plan objective in a clinical protocol, plan normalization can be set according to this plan objective when creating the protocol plans.

Plan objective values are:

- At least <n> % receives more than <n> Gy/cGy
- At most <n> % receives more than <n> Gy/cGy
- Minimum dose is <n> Gy/cGy
- Maximum dose is <n> Gy/cGy

Conformity Index

The conformity index is defined as the volume closed by the prescription isodose surface divided by the target volume. Plan normalization mode cannot be set according to this plan objective. This plan objective cannot be used as optimization objective.

The plan objective values are:

- Conformity index is more than <value>
- Conformity index is less than <value>
- Conformity index is <value>

Gradient Measure

The gradient measure is defined as the difference between the equivalent sphere radius of the prescription and half-prescription isodoses. Plan normalization mode cannot be set according to this plan objective. This plan objective cannot be used as optimization objective.

The plan objective values are:

- Gradient measure is more than <value in cm>
- Gradient measure is less than <value in cm>
- Gradient measure is <value in cm>

Dosimetric Quality Parameter

Dosimetric quality parameters (DQPs) describe the desired dose-volume coverage for a structure. The target value of a DQP can be either absolute (in Gy or cm³) or relative volume/dose (in %). The unit of the target value is shown in square brackets after the DQP in the Plan Objectives tab of the Info Window.

DQP values are:

- D<n> is more than/is less than/is <value in % or Gy>

For example: D95.0 [% of dose] is more than 100 means that 95% of the structure volume receives at least 100% of the prescribed dose (as measured in cumulative DVH).

- D<n>cc is more than/is less than/is <value in % or Gy>

For example: D2.0cc [Gy] is less than 10 means that 2 cm³ of the structure volume receives at most 10 Gy (as measured in cumulative DVH).

- V<n> is more than/is less than/is <value in % or cm³>

For example: V100.0 [% of volume] is more than 98 means that the 100% isodose covers at least 98% of the structure volume.

- V<n>Gy is more than/is less than/is <value in % or cm³>

For example: V12.5Gy [% of volume] is <empty target value> shows the percentage of the structure volume receiving at least 12.5 Gy.

Objective for the Mean Dose

This plan objective defines the limit for the mean dose that the structure receives. If this type of plan objective is set as the primary plan objective in a clinical protocol, plan normalization mode can be set according to this plan objective when creating the protocol plans.

The plan objective values are:

- Mean dose is <n> Gy/cGy
- Mean dose is less than <n> Gy/cGy
- Mean dose is more than <n> Gy/cGy

Objective for Reference Point

This plan objective defines the limit for the dose that the reference point receives if the reference point has a location in the image. If this type of plan objective is set as the primary plan objective in a clinical protocol, plan normalization mode can be set according to this plan objective when creating the protocol plans.

Plan objective value is Reference point receives <n> Gy/cGy.

Objective for Isodose Line

This plan objective defines the limit for the dose that an isodose line receives. This plan objective cannot be used as optimization objective.

Plan objective value is Isodose <n> % line receives <n> Gy/cGy.

Objective for Depth

This plan objective defines the field-specific limit for the dose in a certain depth. Plan normalization mode cannot be set according to this plan objective. This plan objective cannot be used as optimization objective.

The plan objective values are:

- Depth at midpoint receives <n> Gy/cGy
- Depth at d_{max} receives <n> Gy/cGy
- Depth at <n> cm receives <n> Gy/cGy

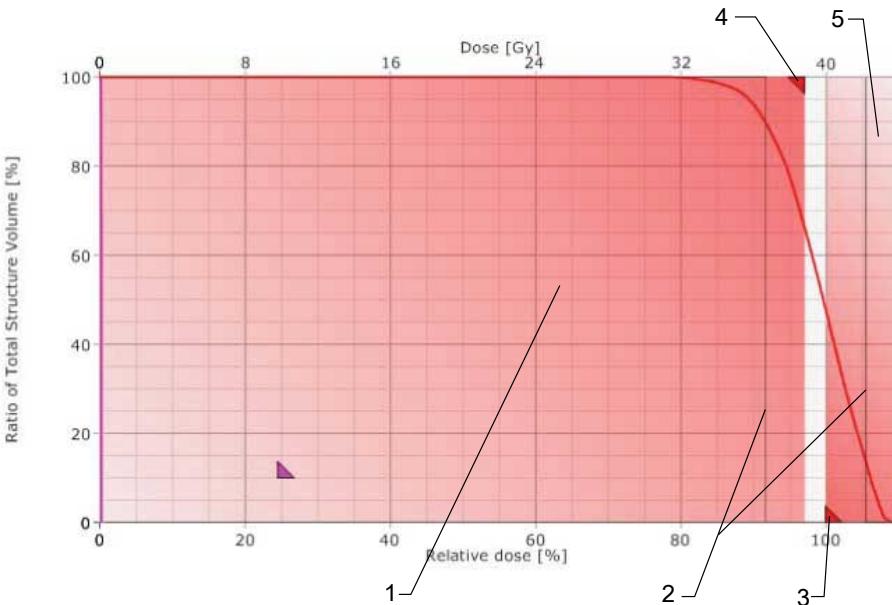
Related Topics

[Plan Objectives Tab of the Info Window](#) on page 160

View Plan Objectives in the Dose-Volume Histogram View

1. Open the plan whose plan objectives you want to view.
2. In the Info window, select the Plan Objectives tab.
3. To show the plan objective limits in the Dose-Volume Histogram view, select the check box next to the Plan Objectives tab name.
4. Do one of the following:
 - Select a structure in the Focus window.
 - Select a structure from the Plan Objectives tab of the Info window.

The area restricted by the plan objective is highlighted in the Dose-Volume Histogram view and the plan objective tolerance is displayed in the graph.



1. The area restricted by the plan objective is highlighted.
2. Tolerance limits for the plan objective.
3. Plan objective defining the maximum dose for the selected structure.
4. Plan objective defining the minimum dose for the selected structure.
5. The area restricted by the plan objective is highlighted.

Plan Objective Tolerance

You can define a tolerance limit for dose (Gy/cGy), or for volume (%) and dose (Gy/cGy). The tolerance limit has an effect on the plan objectives described below.

Objectives for the structure volume:

- At least <n> % receives more than <n> Gy/cGy
- At most <n> % receives more than <n> Gy/cGy
- Maximum dose is <n> Gy/cGy
- Minimum dose is <n> Gy/cGy

Objectives for the mean dose and reference point:

- Mean dose is <n> Gy/cGy
- Mean dose is more than <n> Gy/cGy
- Mean dose is less than <n> Gy/cGy
- Reference point receives <n> Gy/cGy

Examples

At least <n> % receives more than <n> Gy/cGy:

- Plan objective for PTV: At least 99% receives more than 10 Gy
- Dose tolerance limit: 3 Gy
- Volume tolerance limit: 10 %

When the tolerance limits are taken into account, the actual plan objective becomes "At least 89% receives more than 7 Gy".

Maximum dose is <n> Gy/cGy:

- Plan objective for PTV: Maximum dose is 20 Gy
- Dose tolerance limit: 13 Gy

When the tolerance limit is taken into account, the actual plan objective becomes "Maximum dose is 7-33 Gy".

Define Plan Objective Tolerance

1. Right-click the name of the Plan Objectives tab and choose **Change Plan Objective Tolerances**.
2. Type the plan objective tolerance limit in Gy or cGy, or in volume percentages.



Note: The volume tolerance limit affects only the "At least <n> % receives more than <n> Gy/cGy" and "At most <n> % receives more than <n> Gy/cGy" objectives.

3. Select the desired colors for the doses within and outside the tolerance limits. The colors are displayed in the Actual Total Dose column of the Plan Objectives tab of the Info window.



Note: This setting is clinic-wide; it affects all workstations that are connected to the same database.

4. To test the settings, click **Apply**.
5. To accept the settings, click **OK**.

Plan Objectives Tab of the Info Window

For external beam plans, the Plan Objectives tab of the Info window is visible in External Beam Planning.

The tab is used for viewing the plan objectives of the plan derived from a clinical protocol. You cannot modify the information displayed in the tab.

Table 7 Plan Objective Information in the Plan Objectives Tab

Item	Description
Primary	Defines the primary plan objective in the clinical protocol.
Prescription	Describes the prescription for the plan objective defined in the clinical protocol. Values in External Beam Planning: At least <n> % receives more than <n> Gy/cGy, At most <n> % receives more than <n> Gy/cGy, Maximum dose is <n> Gy/cGy, Minimum dose is <n> Gy/cGy, Mean dose is <n> Gy/cGy, Mean dose is less than <n> Gy/cGy, Mean dose is more than <n> Gy/cGy, Reference point receives <n> Gy/cGy.
Fraction Dose [Gy/ cGy]	The dose per fraction in Gy or cGy for the plan objective.
Total Dose [Gy/cGy]	The total dose in Gy or cGy for the plan objective.
Actual Total Dose [Gy/cGy]	The actual total dose corresponding the plan objectives received when the plan is calculated.

Table 8 Conformity Objectives in the Plan Objectives Tab

Item	Description
Structure	Structure for which the conformity objective is defined.
Index	Describes the prescription for the conformity objective defined in the clinical protocol. The values are: Conformity index is more than <value> Conformity index is less than <value> Conformity index is <value> Gradient measure is more than <value in cm> Gradient measure is less than <value in cm> Gradient measure is <value in cm>.
Target Value	Numerical value of the conformity objective.
Actual Value	Value obtained in dose calculation.

Table 9 Dosimetric Quality Parameters in the Plan Objectives Tab

Item	Description
Structure	Structure for which the DQP is defined.
Index	<p>Describes the prescription for the DQP defined in the clinical protocol.</p> <p>The values are:</p> <p>D<n> is more than/is less than/is <value in % or Gy></p> <p>D<n>cc is more than/is less than/is <value in % or Gy></p> <p>V<n> is more than/is less than/is <value in % or cm³></p> <p>V<n>Gy is more than/is less than/is <value in % or cm³></p>
Target Value	Relative (in %) or absolute (in Gy or cm ³) value of the DQP.
Actual Value	Value obtained in dose calculation.



1. To make the Info window float, point here and drag the window.
2. To display the plan objectives in the Dose-Volume Histogram view, select the check box.
3. Green color in the cells indicates that the actual total dose fulfills the plan objective.
4. Red color in the cell indicates that the actual total dose does not fulfill the plan objective.

Figure 49 Plan Objectives Tab in External Beam Planning

The color indicators shown in the Actual Total Dose cell are based on the plan objective and its tolerance limit. If the actual total dose does not meet the objective, but is within the tolerance limit, the value is shown in green. If the actual total dose does not meet the objective, and is also outside the tolerance limit, the value is shown in red. The used colors may be different depending on your selection in the Plan Objective Tolerances dialog box.

The Actual Total Dose cell is shown in green, for example, in the following case:

- Plan objective for PTV: At least 99% receives more than 10 Gy
- Dose tolerance limit: 3 Gy
- Volume tolerance limit: 10 %
- Actual total dose: 8 Gy

When the tolerance limits are taken into account, the actual plan objective becomes “At least 89% receives more than 7 Gy”. Therefore, if the actual total dose of the plan is 8 Gy, it is considered to meet the plan objective, and the value is shown in green on the Plan Objectives tab.

Related Topics

[Plan Objectives in Clinical Protocols](#) on page 155

Optimization Objectives Tab of the Info Window

For external beam plans, the Optimization Objectives tab is visible in External Beam Planning.

To display the optimization objectives in the Dose Volume Histogram view, select the check box in front of the tab title.

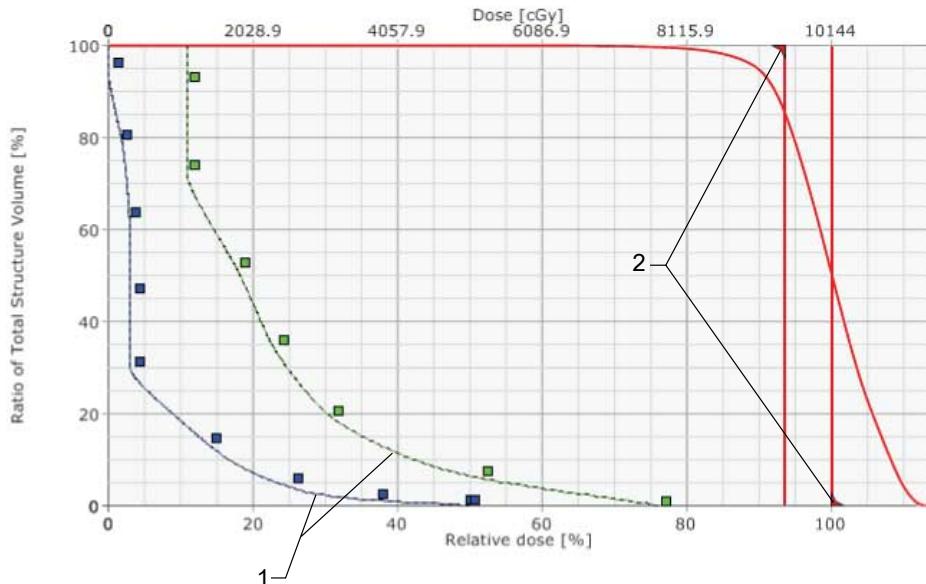
The Optimization Objectives tab is used for viewing the optimization objectives defined for the plan. If you use the Optimization dialog box for adding new optimization objectives for the plan, the new objectives are also displayed in the Optimization Objectives tab.

Table 10 Information in the Optimization Objectives Tab

Item	Description
Plan	Plan Sums only: Indicates plans that contain optimization objectives
Type	The objective type (point or line).
Color	The color of the structure.
Structure	The structure to which the objective limits the dose.
Limit	The dose limit (upper or lower)
Volume [%]	Percentage of the structure volume to receive the dose.
[Gy] or [cGy]	The intended dose in Gy or cGy.
Priority	The priority defined for the objective
gEUD a	Parameter a of Generalized Equivalent Uniform Dose (gEUD); the uniform dose that, if delivered over the same number of fractions as the non-uniform dose distribution of interest, yields the same radiobiological effect. Parameter a is a tissue-specific parameter that illustrates the effect of the volume on the dose.

View Optimization Objectives in the Dose-Volume Histogram View

1. Open the plan whose optimization objectives you want to view.
2. In the Info window, select the Optimization Objectives tab.
3. To show the optimization objectives in the Dose-Volume Histogram view, select the check box next to the Optimization Objectives tab name.



1. Line type optimization objectives.
2. Point type optimization objectives.



Tip: You can include the DVH estimates for structures that have them by selecting **Show DVHE** in the **Dose Statistics** tab of the **Info Window**.

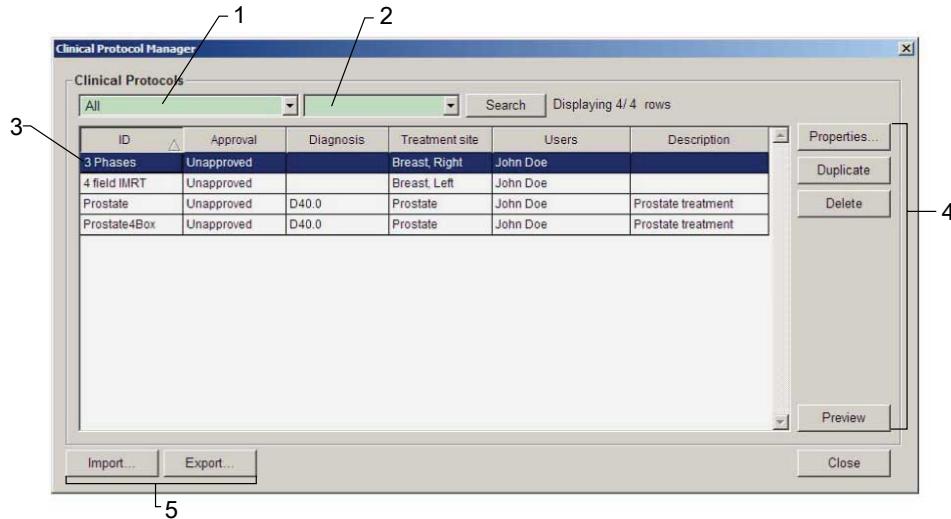
Clinical Protocol Manager

For a clinical protocol, the manager displays:

- identification
- approval status
- possible diagnosis and treatment site

- users assigned to the clinical protocol
- description

You can sort any column by clicking the column header. You can edit, duplicate, delete, preview and export clinical protocols in the Clinical Protocol Manager.



1. The approval status of the displayed clinical protocols.
2. Type the search words for filtering clinical protocols.
3. The selected clinical protocol.
4. Actions available for the selected clinical protocol.
5. Actions available for the selected clinical protocol.

Figure 50 Clinical Protocol Manager

Creating a Clinical Protocol from a Plan in External Beam Planning

When you create a clinical protocol from a plan, the information of the active plan is copied to the Protocol Properties dialog box, in which you can accept information or change it as needed. The clinical protocol properties taken from the active plan are:

- Structures defined in the planning image are set by default.
- Protocol plans are created automatically. If a plan is active, only one protocol plan is created. If a plan sum is active, a protocol plan for each plan in the plan sum is created. Protocol plan objectives and optimization objectives are mapped from the plan's dose prescription, Eclipse IMRT objectives, and normalization mode.

- The default values for treatment style, energy, technique, treatment unit, and field geometry are filled for each protocol plan according to the protocol plan or plan mapping.
- Review settings are filled from the DVH settings of the active plan.



Note: To create a clinical protocol that contains multiple protocol plans, first insert a plan sum containing the corresponding plans.

You need proper user rights for managing clinical protocols. Editing a clinical protocol in the Clinical Protocol Manager has no effect on the corresponding clinical protocol references that are already used in a patient plan.

You can also adapt the clinical protocol to better fit the requirements of each particular patient by editing the clinical protocol reference inserted to the patient. This does not affect the corresponding original clinical protocol.

Related Topics

[Adapt the Clinical Protocol Reference for an Individual Patient](#) on page 172

Define Protocol Information in the General Tab

1. Do one of the following:
 - New protocol: Choose **Planning > Templates and Clinical Protocols** and **Create Clinical Protocol from Plan**.
 - Existing protocol: Choose **Planning > Templates and Clinical Protocols > Clinical Protocol Manager**, and search the desired protocol.
2. In the Protocol Properties dialog box, select the **General** tab.
3. Define the desired information in the **Identification** group box.
4. Select the approval status of the clinical protocol.

Depending on the selected approval status and your user rights, you are prompted to give a password when you click **OK**. The **History** text box displays information on the approval status actions done earlier to the clinical protocol.

5. Click **OK** and save your changes, if you do not wish to make any modifications to the default information displayed in other tabs. Otherwise, proceed by modifying the information in other tabs.

Related Topics

[Changing the Approval Status of Templates, Clinical Protocols and Clinical Protocol References](#) on page 174

Modify Protocol Information in the Structures Tab

1. In the Protocol Properties dialog box, select the **Structures** tab.

The structures defined in the planning image are displayed in the table. You can sort any table column by clicking the column header.

2. To edit a structure:

- a. Select a structure from the table.
- b. Click **Properties** and modify the structure template properties as needed.
- c. Click **OK**.

3. To create a structure, click **New Structure**, define the required information and click **OK**.

4. To duplicate a structure, select a structure from the table and click **Duplicate**.

The name of the new structure is appended with a running number.

You can change the name to a more descriptive one by editing the new structure.

5. To delete a structure, select a structure from the table and click **Delete**.

When a structure is deleted, the plan objectives for the structure, the optimization objectives for the structure, and the review settings for the structure are also deleted.

MLCs and fields fitted to the structure are also deleted in External Beam Planning.

6. Click **OK** and save your changes, if you do not wish to make any modifications to the default information displayed in other tabs. Otherwise, proceed by modifying the information in other tabs.

Modify Protocol Information in the Plan Objectives Tab

1. In the Protocol Properties dialog box, select the **Plan Objectives** tab.
2. To remove a plan from the protocol, click **Remove** and answer **Yes** to the confirmation message informing that all the prescription items, field geometries and plan objectives of the plan will also be removed.
3. To modify the fraction information, click a cell and add or modify the information as desired.

4. In the **Plan Objectives** group box:
 - To add a new objective, click **Add** and modify the new objective as needed.
 - To remove an objective, click **Remove**.
 - To select a prescription item as the primary prescription, select the **Primary** check box.
 - To add a new conformity index or gradient measure, in the **Quality Indices** section, click **Add**, click the Index cell, choose the item to add and modify the new entry as needed.
 - To add a dosimetric quality parameter, in the **Quality Indices** section, click **Add**. Click the Index cell in the new entry, choose **Enter dosimetric quality parameter**, and define the DQP type in the dialog box that opens. Modify the new DQP as needed.
 - To edit a prescription item:
 - Cells with small arrowhead: Click the cell and select an option.
 - Text boxes: Click the cell and type the new information.
5. Click **OK** and save your changes, if you do not wish to make any modifications to the default information displayed in other tabs. Otherwise, proceed by modifying the information in other tabs.

Related Topics

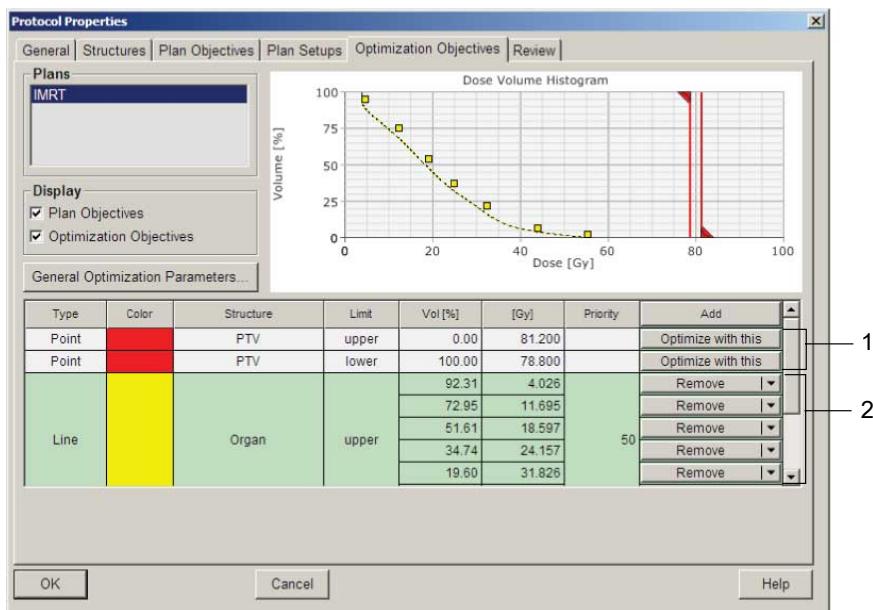
[Plan Objectives in Clinical Protocols](#) on page 155

Modify Protocol Information in the Plan Setups Tab

1. In the Protocol Properties dialog box, select the **Plan Setups** tab.
2. In the **Plans** group box:
 - Select the plan to view its fields, applicators or seeds.
 - To define the treatment technique, click the **Treatment Style** cell and select an option.
 - To define the default treatment unit, click the appropriate cell, click the down-pointing arrowhead, and select an option.
 - To specify the default treatment energy, type the value in the appropriate text box. (In External Beam Planning only.)
3. In the **Fields** group box, select a field or an applicator to view its information.
4. For a stereotactic plan, select the immobilization device and patient localization technique.
5. Click **OK** and save your changes, if you do not wish to make any modifications to the default information displayed in other tabs. Otherwise, proceed by modifying the information in other tabs.

Modify Protocol Information in the Optimization Objectives Tab

1. In the Protocol Properties dialog box, select the Optimization Objectives tab.



1. Plan objectives.
 2. Optimization objectives.
 2. Select a plan from the **Plans** list box.
 3. In the **Display** group box, select to show plan objectives and/or optimization objectives.
- The selected items are shown both graphically and in the table.
4. To define general optimization parameters for all fields or applicators:
 - a. Click **General Optimization parameters**.
 - b. Fill the Objective Template Group Properties dialog box as needed and click **OK**.

5. To edit an optimization objective:
 - Cells with small arrowhead: Click the cell and select an option.
 - Text boxes: Click the cell and type the new information.
 - Drag the line type or point type objective with the mouse.
 - To move an objective, right-click in the graph, select **Move Objective** and drag the line type or point type objective with the mouse.
 - To zoom in the graph, right-click in the graph, select **Zoom In**, click and hold down the left mouse button, move the mouse pointer to form a rectangular area, and release the mouse button when the rectangle covers the desired area. You can repeat zooming as many times as needed.
 - To zoom out the graph, right-click in the graph and select **Zoom Out**.
 - To set the graph into its original scale, right-click in the graph and select **Reset Geometry**.
 - To move the whole graph, right-click in the graph, select **Pan** and drag the graph.
6. To add an objective, do one of the following:
 - Click **Add** and modify the new objective that appears in the table.
 - Right-click in the graph and choose **Add Lower Objective**, **Add Upper Objective** or **Add Line Objective**, click in the desired location in the graph and modify the new objective that appears in the table.
7. To remove an objective, click **Remove**.
8. To use a plan objective in optimization, click **Optimize with this**. The plan objective is added as an optimization objective in the table.
9. Click **OK** and save your changes, if you do not wish to make any modifications to the default information displayed in other tabs. Otherwise, proceed by modifying the information in other tabs.

Related Topics

[Plan Objectives in Clinical Protocols](#) on page 155

Modify Protocol Information in the Review Tab

1. In the Protocol Properties dialog box, select the **Review** tab.
2. In the **DVH Structures and Expressions** group box:
 - Select the structures for which the DVH is calculated.
 - To add a virtual structure expression:
 - Click **Add expression**.
 - Create the structure in the Create expression dialog box, and click **OK**.
 - To remove a virtual structure expression, select the expression and click **Remove expression**.
 - To select all DVH structures and expressions, click **Select All**.
 - To clear all selections made for DVH structures and expressions, click **Select None**.
3. In the **DVH Statistics** group box, select the DVH statistics columns you want to display in the Dose Volume Histogram view.
4. Click **OK** and save your changes, if you do not wish to make any modifications to the default information displayed in other tabs. Otherwise, proceed by modifying the information in other tabs.

Delete a Clinical Protocol from the Clinical Protocol Manager

You can delete a clinical protocol from the Clinical Protocol Manager in External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Clinical Protocol Manager**.
2. To search for a clinical protocol in the **Clinical Protocols** group box, define the search criteria and click **Search**.
3. Select the clinical protocol to delete from the table.



Note: You cannot delete approved clinical protocols.

4. Click **Delete**.
5. Answer **Yes** to the confirmation message that opens.
6. Save your changes.

Related Topics

[Changing the Approval Status of Templates, Clinical Protocols and Clinical Protocol References](#) on page 174

Adapt the Clinical Protocol Reference for an Individual Patient

1. Select the clinical protocol reference.
2. Choose **Edit > Properties**.
3. Modify the properties of the selected clinical protocol reference in the same way as the properties of clinical protocols.

Remember that these modifications will not affect the original clinical protocol, but only the selected clinical protocol reference.

Related Topics

[Creating a Clinical Protocol from a Plan in External Beam Planning](#) on page 165

Import a Clinical Protocol

You can import clinical protocols in External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Clinical Protocol Manager**.
2. Click **Import**.
3. Navigate to the directory from where to import the clinical protocol and select the protocol to import.
4. Click **Open**.

The selected clinical protocol is imported and is visible in the Clinical Protocol Manager.

Export a Clinical Protocol

You can export clinical protocols in External Beam Planning.

1. Choose **Planning > Templates and Clinical Protocols > Clinical Protocol Manager**.
2. To search for a clinical protocol in the **Clinical Protocols** group box, define the search criteria and click **Search**.

3. Select the clinical protocol to export from the table.



Tip: You can click **Preview** to see how the clinical protocol looks.

4. Click **Export**.
5. Navigate to the directory in which to save the export file.
6. Define a name for the export file.
7. Click **Save** to save the clinical protocol to the defined export file.

The clinical protocol is exported as an XML file to the defined location. A control mechanism (check sum) is added in the XML file. If the exported clinical protocol is changed outside the application, the mechanism notices it and a warning is displayed when the clinical protocol is imported back to the application.

Previewing and Printing Templates and Clinical Protocols

You can preview and print templates and clinical protocols. The templates and clinical protocols are previewed in the HTML format in your default web browser.

Preview and Print a Template Group and a Template

This information applies to External Beam Planning and Brachytherapy Planning.

1. Choose **Planning > Templates and Clinical Protocols > Objective Template Manager, Plan Template Manager or Structure Template Manager**.
2. To search for a template group or template, define the search criteria and click **Search**.
3. Select the template group or template to preview or print from the table.
4. Click **Preview**.

Information of the selected template group or template is displayed in the HTML format in the default browser.

5. To print the template group information:
 - a. From the browser's menu, choose **File > Print**.
 - b. Select the printer and define the print settings as desired.
 - c. Click **Print**.

Preview and Print a Clinical Protocol from the Clinical Protocol Manager

This information applies to External Beam Planning and Brachytherapy Planning.

You can preview and print clinical protocols and clinical protocol references only after you have performed the Save All operation.

1. Choose **Planning > Templates and Clinical Protocols > Clinical Protocol Manager**.
2. To search for a clinical protocol in the **Clinical Protocols** group box, define the search criteria and click **Search**.
3. Select the clinical protocol to preview or print from the table.
4. Click **Preview**.
Information of the selected clinical protocol is displayed in the HTML format in your default web browser.
5. To print the clinical protocol information:
 - a. Choose **File > Print**.
 - b. Select the printer and define the print settings as desired.
 - c. Click **Print**.

Preview and Print a Clinical Protocol Reference Inserted to a Patient

You can preview and print clinical protocol references inserted to a patient in External Beam Planning and Brachytherapy Planning.

1. In the Scope window, right-click the clinical protocol reference item and select **Preview**.
Information of the selected clinical protocol reference is displayed in the HTML format in your default web browser.



Note: You cannot preview unsaved clinical protocol references.

2. To print the clinical protocol reference information:
 - a. Choose **File > Print**.
 - b. Select the printer and define the print settings as desired.
 - c. Click **Print**.

Changing the Approval Status of Templates, Clinical Protocols and Clinical Protocol References

You need proper user rights to change the approval status of templates, clinical protocols and clinical protocol references.

The approval statuses available for templates, clinical protocols and clinical protocol references are:

- Unapproved—The item is under construction and it cannot be used in treatment.
- Approved—The item is approved for treatment. You cannot change any information in an approved template or clinical protocol.
- Reviewed—The item is reviewed by a physician. The information in the template or clinical protocol can still be changed.
- Retired—The item is no longer used.

Change the Approval Status of a Template or Clinical Protocol

1. Do one of the following:
 - Choose **Planning > Templates and Clinical Protocols > Objective Template Manager , Plan Template Manager or Structure Template Manager.**
 - Choose **Planning > Templates and Clinical Protocols > Clinical Protocol Manager.**
2. To search for a template or clinical protocol, define the search criteria and click **Search**.
3. Select the template or clinical protocol to approve from the table.
4. Click **Properties**.
5. Select the desired approval status.

Depending on the selected approval status and your user rights, you are prompted to give a password when you click **OK**.
6. Click **OK**.
7. Click **Close**.
8. Save your changes.

Change the Approval Status of a Clinical Protocol Reference

1. Select the clinical protocol reference.
2. Choose **Edit > Properties**.
3. Select the desired approval status.

Depending on the selected approval status and your user rights, you are prompted to give a password when you click **OK**.
4. Click **OK**.

Chapter 9 Fields

Field Types

Depending on the treatment modality (photon, electron, or proton treatment), the fields in the treatment plan can be of different field type and use different field techniques.

The following field types are used in treatment planning:

- Fields —Fully modifiable fields that you work with in External Beam Planning. You can calculate the dose distribution and insert DRRs for fields. After the plan is approved for treatment, the fields can be scheduled in ARIA RTM applications.
- Setup fields —Fields that are used for moving the treatment unit to the correct treatment position.

In a photon plan, setup fields are also used for aligning the patient correctly for treatment.

Related Topics

[Creating Setup Fields](#) on page 210

Photon Field Techniques

Photon fields can be static fields or arc fields. One plan can combine both field techniques.

Static fields:

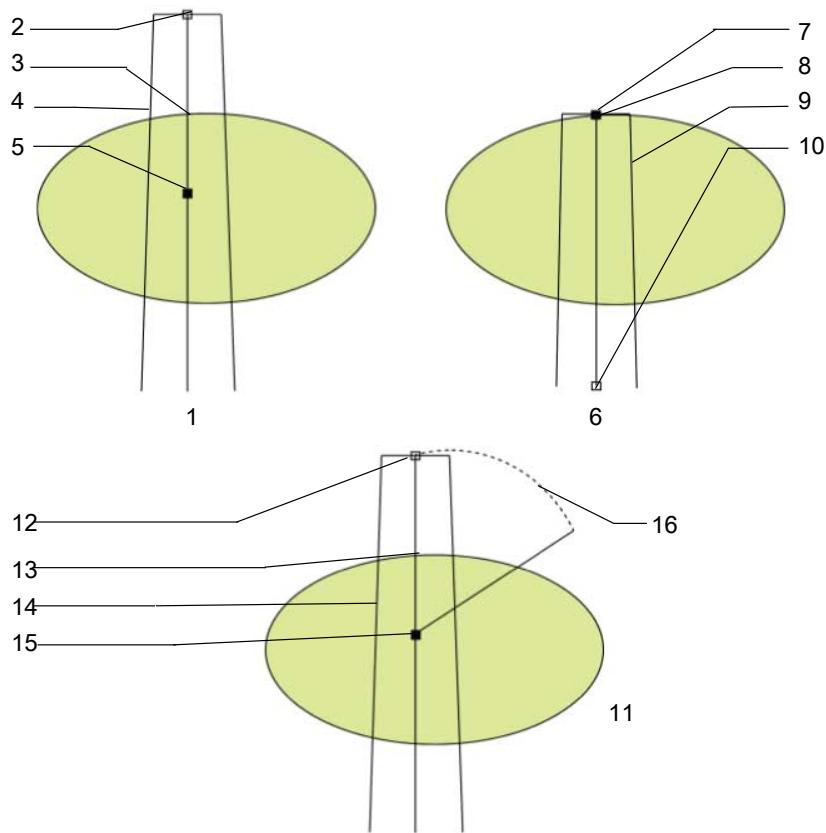
- Isocentric fields—The field position is defined by the isocenter. The isocenter is by default positioned in the center of the target volume of the plan.
- Fixed SSD fields—The field entry point defines the position of the field. The position of the field entry point on the body surface is determined based on the center of the target volume of the plan and the default gantry and couch rotations. You can define the Source-Field Entry Distance (SFED) if necessary.
- The SFED is used for defining fields that exceed the maximum field size of 40 x 40 cm.
 - Total body fields—Fixed SSD field for total body treatments

Arc fields: Rotational, isocentric fields

- Static arc field—Arc field with a static MLC

- Conformal arc field, VMAT field or Siemens mARC field—Arc field with dynamic MLC

After creating a new treatment unit in RT Administration, make sure that the unit has at least default technique set, otherwise the list of available energies might be empty when a new field is created using the new treatment unit. You can also define default energy and dose rates for the unit in RT Administration.



- | | |
|--------------------------|---------------------------|
| 1. Isocentric field | 9. Beam edge |
| 2. Field direction point | 10. Field direction point |
| 3. Field entry level | 11. Arc field |
| 4. Beam edge | 12. Field direction point |
| 5. Isocenter | 13. Field entry level |
| 6. Fixed SSD field | 14. Beam edge |
| 7. Field entry level | 15. Isocenter |
| 8. Field entry point | 16. Rotation span |

Figure 51 Photon Field Techniques

Electron Field Techniques

Electron fields are always static fields, and by default fixed SSD fields. Although the creation of isocentric electron fields is allowed in Eclipse, do not use them because of potential inconsistencies in the dose normalization.

In electron treatment, electron applicators are used to collimate the treatment area and to reduce scattering. In Eclipse, an electron applicator defines the field size instead of the collimator jaws. The electron applicator size is configured in RT Administration. In the image views, the position of the collimator jaws is not shown; instead the outline of the electron applicator aperture is shown. The applicator ID is shown next to the field outline defined by the applicator in the BEV.

Eclipse requires you to add an electron applicator to each electron field. The shape of an electron applicator can be rectangular or circular. To further specify the treatment area more precisely and to protect sensitive tissue, you can define electron cutouts for the electron field. The use of bolus is also supported in Eclipse.

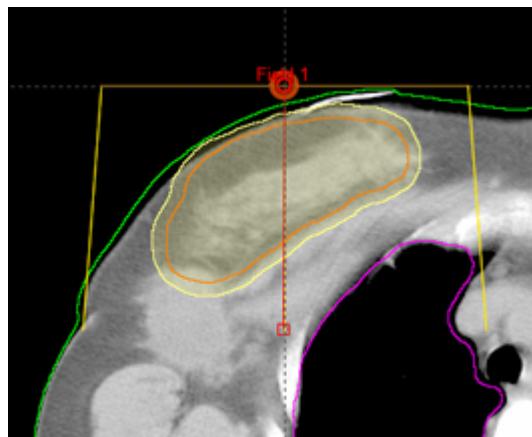


Figure 52 Electron Field



Note: When working with electron applicators, notice the following:

- The source-to-applicator head distance must be defined in RT Administration, otherwise the dose distribution calculation cannot be performed.
- Verify that the electron field size factors are correctly configured for each electron applicator size in Beam Configuration to ensure correct dose calculation.
- Changing the energy mode of a field to a mode not configured for the electron applicator in the field removes the applicator.

The Eclipse calculation algorithms do not support the use of electron arc fields, although it is possible to select the ARC field technique for an electron field.

3D planning or dose calculation for the HDTSE (High-Dose-Rate Total Skin Electron) technique is not supported in Eclipse.

Default Photon and Electron Field Parameters

The default field parameters for the first field added to a plan are:

- Field size: Depends on the selected treatment unit. For electron fields calculated with the eMC algorithm, the electron applicator defines the field size instead of the collimator jaws. Treatment units and the electron applicator size are configured in RT Administration.
- Gantry, Collimator and Couch rotation—Depend on the default values of the operating limits configured for the treatment unit in RT Administration.
- Isocenter position (for isocentric fields)—Center point of the plan target volume selected in the Plan Properties dialog box, if defined; otherwise the center point of the image, or the viewing plane intersection.
- Field entry point (for fixed SSD fields)— The position on the body surface is determined based on the center of the target volume of the plan and the default gantry and couch rotations.

Note: *The insertion of the first field is started automatically when you create a new plan.*



Table 11 Default Parameters for Fields Added after the First Field

Field Parameters	Isocentric Fields	Fixed SSD Fields
Treatment unit, field technique, field size, isocenter position, field symmetry/asymmetry, couch rotation	Copied from previous field	Copied from previous field
Gantry rotation, collimator rotation	Set to initial default value	Copied from previous field
Tolerance table	Added to the field	Added to the field

If any default value is outside the allowed limit, the value of the closest limit is used. You can modify the default values.

Calculated and Planned SSD Values

Each field has two SSD values shown in the Field Properties dialog box: Calculated SSD and Planned SSD:

- Calculated SSD value is calculated by Eclipse from the geometrical setup of the field. The value cannot be edited.
- Planned SSD value is user-defined and independent of the calculated SSD value. For new fields, the planned SSD value is empty; for fields coming in, for instance, from simulation, the planned SSD value shows the SSD value measured in simulation. The value can be edited after the plan has been planning approved. In

Plan Parameters you can also edit it for unapproved plans. For treatment approved plans the value is always read-only. Planned SSD is copied to verification plans that use the same structure set as the source plan, plans that result from splitting of large IMRT fields, plan revisions and plans without a structure set. Planned SSD is always used in DICOM import and export, regardless of the plan approval status.

Fields Tab of the Info Window

The Fields tab of the Info window is used in External Beam Planning and Plan Evaluation for viewing and editing the properties of the fields of the active plan, or plans contained in the active plan sum. For unapproved plans, you can edit the field weights on the Fields tab of the Info window in Plan Evaluation.

Table 12 Information for Photon and Electron Fields

Column	Description
Group	Check boxes used to select which fields are grouped together.
Plan ID	Plan identification. Shown for each field in a plan sum.
Field ID	Field identification.
Technique	Field technique: STATIC-I = static field, isocentric STATIC-F = static field, fixed SSD ARC-I = arc field, isocentric HDTSE-F = HDTSE field, fixed SSD TOTAL-I = total body field, isocentric
Machine/Energy	Name of the treatment unit and its energy mode.
MLC	MLC type: Static Arc Dynamic Dose Dynamic VMAT mARC
Field Weight	Field weight of the field.
Scale	Treatment unit scale.

Column	Description
Gantry Rtn [deg]	Gantry rotation in degrees.
	For arc fields, shows the gantry start angle in degrees, rotation direction (clockwise or counterclockwise), and the gantry stop angle in degrees. If the start angle or stop angle is in the extended area, "E" is shown after the degree. If any of the values is invalid, "Invalid" is shown in the table cell. This may happen if the values have been imported, or the treatment unit configuration has changed. You can edit the values directly for static fields. For arc fields, you need to do this in the Field Properties dialog box.
Coll Rtn [deg]	Collimator rotation in degrees.
Couch Rtn [deg]	Couch rotation in degrees.
Wedge	Wedge code if used. If not in use, "none".
Field X [cm] (default)	Dimension FX at the isocenter (isocentric fields) or field entry point (fixed SSD fields).
X1 [cm] (default)	The displacement from the field central axis to field edge X1 at the isocenter (isocentric fields) or field entry point (fixed SSD fields). Editable only for asymmetrical fields. Displayed in blue with tooltip if used in a field alignment rule.
X2 [cm] (default)	The displacement from the field central axis to field edge X2 at the isocenter (isocentric fields) or field entry point (fixed SSD fields). Editable only for asymmetrical fields. Displayed in blue with tooltip if used in a field alignment rule.
Field Y [cm] (default)	Dimension FY at the isocenter (isocentric fields) or field entry point (fixed SSD fields).
Y1 [cm] (default)	The displacement from the field central axis to field edge Y1 at the isocenter (isocentric fields) or field entry point (fixed SSD fields). Editable only for asymmetrical fields. Displayed in blue with tooltip if used in a field alignment rule.
Y2 [cm] (default)	The displacement from the field central axis to field edge Y2 at the isocenter (isocentric fields) or field entry point (fixed SSD fields). Editable only for asymmetrical fields. Displayed in blue with tooltip if used in a field alignment rule.
X [cm]	X-coordinate of the isocenter or the entry point.
Y [cm]	Y-coordinate of the isocenter or the entry point.
Z [cm]	Z-coordinate of the isocenter or the entry point.
Calculated SSD [cm]	Calculated source-to-skin distance in centimeters.

Column	Description
MU / Timer	<p>Monitor units.</p> <p>MUs are displayed only after the dose distribution has been calculated and the dose prescription defined. MUs are shown if there is only one fractionation. For an individual plan, you can define a preset MU value to be used in dose calculation.</p> <p>Timer for a Cobalt treatment. The time unit can be minutes or seconds depending on the setting defined in RT Administration. The timer setting is displayed only for Cobalt treatment units that are created in version 11.0 or later. For Cobalt treatment units created with earlier versions, MU are displayed.</p>
Ref. D [Gy]	<p>Reference dose in Gy (or cGy, depending on the configuration).</p> <p>Reference dose is displayed only after the dose distribution has been calculated and the dose prescription defined. Reference dose is shown if there is only one fractionation. Reference dose is not shown for IMRT fields or VMAT with DMLCs.</p>

The default labels of the field dimensions shown in the table can be configured in RT Administration.

For information on RT Administration, refer to the online help.



Note: When showing information of a plan containing fields that use different scales, or of a plan sum containing such fields, the column headers in the Info window show general labels for the field geometry instead of the ones configured in RT Administration. This is indicated with an additional label “[IEC1217]”. However, the actual field geometry values in the cells are shown using the particular machine scale of each field.

Tangential Fields and Dose Calculation

To enable correct dose calculation, fields should not intersect the first or last slice of the patient, because in this case CT data does not exist above or below the field. The patient surface is not automatically closed at the end of a 3D image, which can be seen in the Model view when using solid or translucent rendering for the Body structure: the patient model resembles a hollow tube with open ends. If a field passes through from the end of a 3D image like this, the calculation algorithm cannot find the intersection point of the fanline and the patient, and the dose distribution cannot be calculated correctly.

As a workaround, you can create an artificial CT slice to be used at the end of the 3D image to close it.



Note: No warning is issued in connection with field setup if a field intersects the last slice of the patient. However, after the dose calculation, a warning is shown in the Calculation Progress dialog box and on the Calculation tab of the Field Properties dialog box. Always make sure that you have enough slices to cover the entire treatment volume.

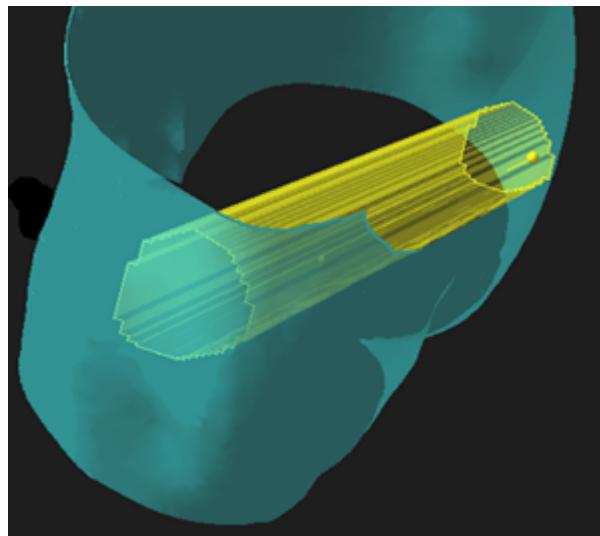


Figure 53 Field Direction to Avoid

Related Topics

[Extending a Scanned Image Set](#) on page 66

Adding Opposing Fields

Opposing fields are mirror images of existing fields. The following features of the original field with changes to the gantry, collimator and couch positions are copied to an opposing field:

- Field size (if asymmetric: mirrored in the opposing field).
- Field type (isocentric or fixed SSD, photon or electron).
- Isocenter coordinates.
- If the original field a fixed SSD field, the isocenter is not shared, but the opposing field is positioned on the patient's skin on the opposite side of the original field.
- Wedges for photon or electron fields (mirrored in the opposing field).
- Blocks (mirrored in the opposing field). If the block in the original field is fitted to a structure, the shape of the block is mirrored in the opposing field, but the block is not automatically fitted to the structure.

- Multileaf collimators (mirrored in the opposing field). If the MLC in the original field is fitted to a structure, the shape of the MLC is mirrored in the opposing field, but the MLC is not automatically fitted to the structure.
- Compensators. The compensator in the opposing field is not calculated. Compensators for photon or electron fields are mirrored in the opposing field.
- Live Digitally Reconstructed Radiograph (DRR) image. The live DRR is created for the opposing field using the DRR parameters of the original field.



NOTICE: When creating an opposing field, visually verify all field parameters and accessories of the opposed field prior to approval.



Note: When using opposing fields, note the following:

- If the properties of the original field, copied to the opposing field, are not allowed in the treatment unit, a warning is displayed and the field creation is cancelled.
- Field fluence is not copied to the opposing field.
- The maximum number of fields that should not be exceeded in any single treatment plan to ensure the integrity of calculated treatment plans is 25 fields.
- The maximum number of fields in arc verification plans is 99 fields.

As rotating the collimator mechanically takes a lot of time, the collimator rotation is minimized as much as possible when opposing fields are created. Eclipse tries to find the shortest possible rotation that is within the operating limits of the treatment machine. Verify, that the operating limits correspond to those of the treatment machine.

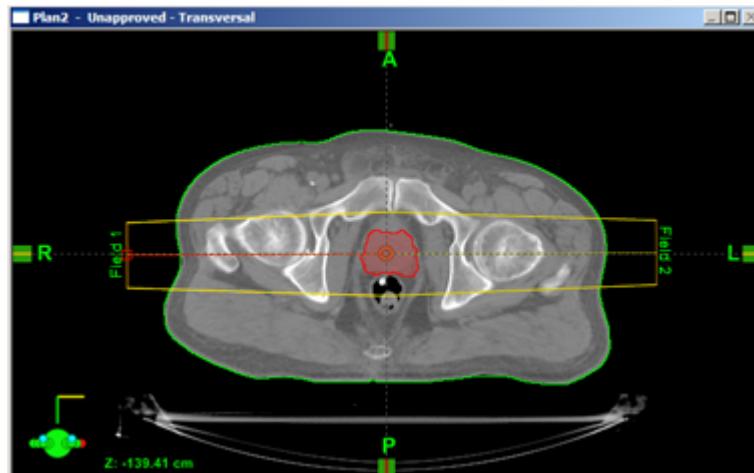


Figure 54 Opposing Fields

Wedges in Opposing Fields

By default, Eclipse tries to minimize the collimator rotation angle when creating opposing fields. With motorized wedges, only one collimator rotation angle is possible, as a motorized wedge can be applied from one direction only. For hard wedges, it is possible to use a clinic-wide setting that defines that the direction of the wedge is not changed when an opposing field is created.

The direction of the Dynamic Wedges or Enhanced Dynamic Wedges in fields is changed if minimizing the collimator rotation so requires.

Define the Hard Wedge Direction in the Opposing Field

1. Choose **Tools > Task Configuration**.
2. On the **Opposing Field** tab, do one of the following:
 - To define that the direction of a hard wedge is not changed when an opposing field is created, select the **Preserve hard wedge direction** check box. When this option is selected, the collimator is rotated instead. If the rotated collimator would violate the operating limits, the wedge direction is changed. In case that is not possible, the system creates an opposing field with a mirrored wedge and informs the user about this.
 - To define that the direction of a hard wedge can be changed when an opposing field is created, clear the **Preserve hard wedge direction** check box.



Note: This setting is clinic-wide; it affects all workstations that are connected to the same database.

Group Fields

You can group fields belonging to the same plan or plan sum to move their isocenter or entry points together. Isocentric fields are in a group by default.

When the fields in a photon plan are grouped, you can refit all MLCs and /or blocks and their collimator jaw positions at once.

Changes made to a field grouping are valid only for the active plan in the current session. Field groups cannot be saved.

1. In the Info window, select the **Fields** tab.
2. For each field to be included in the group, select the check box in the **Group** column.



Tip: To toggle the group selection for each field, click the Group title bar. To group all fields, press Shift and click the Group title bar.

Move Grouped Fields

1. In the Focus window, select the field.
2. Choose **Edit > Select**.
3. In an image view, select one of the grouped fields and drag it to a new position.

All the grouped fields are moved with the selected field.

Refit Grouped Fields

1. After grouping the fields, in the Focus window, right-click the plan containing the fields and choose **Refit grouped fields**.
2. Select the items to refit by clicking the corresponding buttons and click **Refit**.

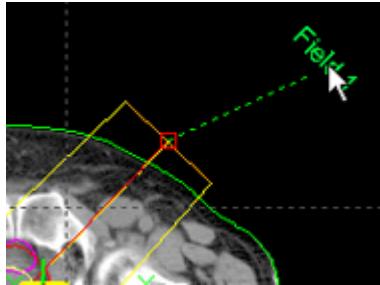
If more than one item is selected in a photon plan, collimator jaws are always fitted first, followed by MLCs and blocks, respectively.

Show the Field Labels

1. Choose **View > Options**.
2. On the **Plan Viewing** tab, select the **Field labels** check box.

Move a Field Label

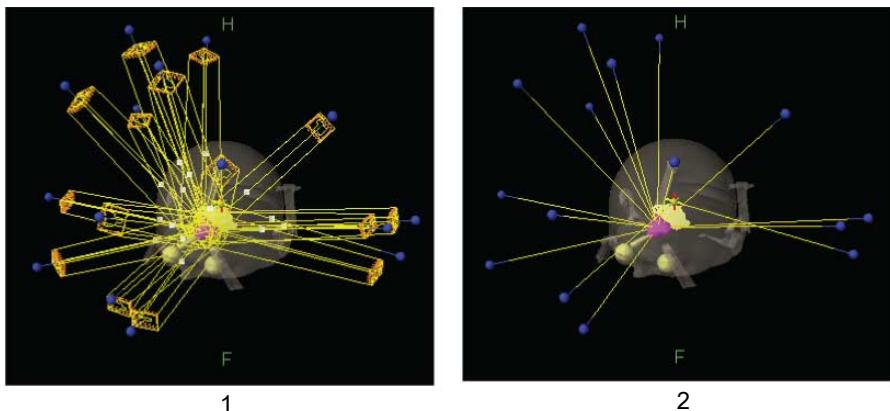
1. Point at the label in an image view and drag it to a new position.



2. To reset the field label positions, do one of the following:
 - To reset an individual field label, right-click on it.
 - To reset all field labels, click **Reset Geometry**

Showing Field Central Axis in the Model View

You can display only the central axis (CAX) of a field in the model view. This is useful, for example, if the plan contains multiple non-coplanar fields. This option hides field paths and all field accessories from the Model view.



1. Model View with field axes and field paths shown
2. Model View with Show CAX Only view

Figure 55 Show Central Axis only in Model View

The Show CAX only option can be used when displaying fields in cut mode or in projection mode, when field entry and exit shapes are displayed on the surface of the Body structure, and when dose color wash is displayed.

The Show Central Axis only option can also be used with arc fields.

Show the Field Central Axis Only

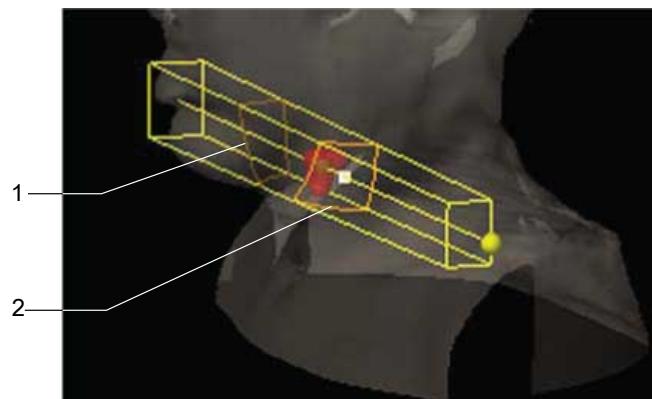
To display only the central axis for each field in the Model view,

- Right-click in the Model view and choose **Show CAX Only**.

Display the Field Shapes on the Body Surface

Use the Show Field Entry Shape on Body or Show Field Exit Shape on Body commands to display the field outlines on the surface of the Body structure in the Model view. This can be useful in positioning adjacent fields seamlessly next to each other.

1. Select the visibility check box of the Body structure in the Focus window, if not already selected.
2. In the Model view, right-click and choose **Show Field Entry Shape on Body** or **Show Field Exit Shape on Body**.

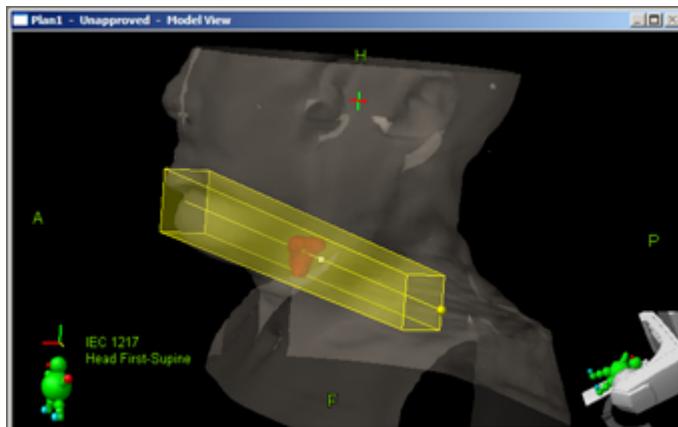


1. Field exit shape on body.
2. Field entry shape on body.

Show the Field Paths as Cones

To display the field outlines as a cone in the Model view,

- Right-click in the Model view and choose **Show Field Paths as Cones** to display the field paths as translucent surfaces.



Show the Transversal Plane in the BEV

- Choose View > Options.
- On the Plan Viewing tab, select the **Transversal slice in BEV** check box.

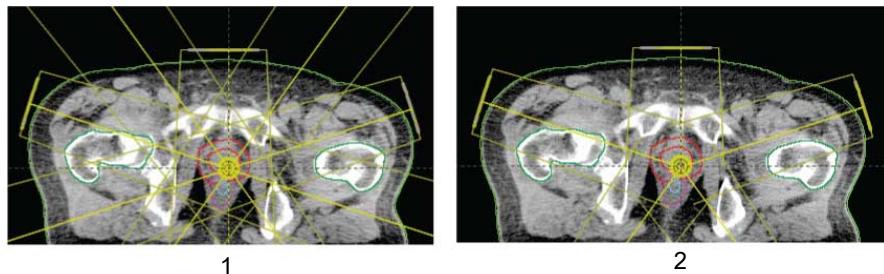
The intersection of the active transversal plane and the SAD plane of the active field is displayed in the BEV.

Change Between the Cut Mode and Projection Mode

- Choose View > Options.
- On the Plan Viewing tab, do one of the following:
 - To show the fields in the Cut mode, clear the **Field projections** check box.
 - To show the fields in the Projection mode, select the **Field projections** check box.

Cut the Fields at the Isocenter

1. Choose View > Options.
2. On the Plan Viewing tab, select the Cut field at isocenter check box.



1. Field projections are shown
2. Field projections are cut at the Isocenter

Aligning Fields

For reaching a uniform dose distribution over large volumes, for example in breast, and head and neck treatments, you can align open fields to form smooth junctions with other fields.

Each field contains 6 planes ($X1$, $X2$, $Y1$, $Y2$, XC , and YC) that can be aligned with another field's planes using field alignment rules. You can define that certain planes of two fields are always aligned with each other. If you move a field that is included in a field alignment rule, the gantry, collimator and couch rotations, field sizes, and even the isocenter of the other field are changed so that the planes stay aligned according to the defined field alignment rule. The figure shows the field alignment planes and their normal directions viewed from the BEV.

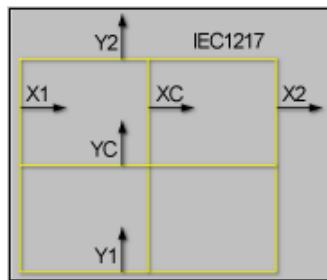


Figure 56 Field Alignment Planes

You can define a master field for a field alignment rule. The master field is not moved when field alignment rules are applied. All other fields are adjusted according to the master field. If the master field is not defined, the currently active field is considered as the master field and all other fields are adjusted accordingly. If there are several field alignment rules, the rules are applied in the order they are defined.

The following figure shows aligned fields in a breast treatment. The aligned planes are shown in yellow. If the Show Field Paths as Cones option is also selected, the aligned fields are visualized in lighter yellow.

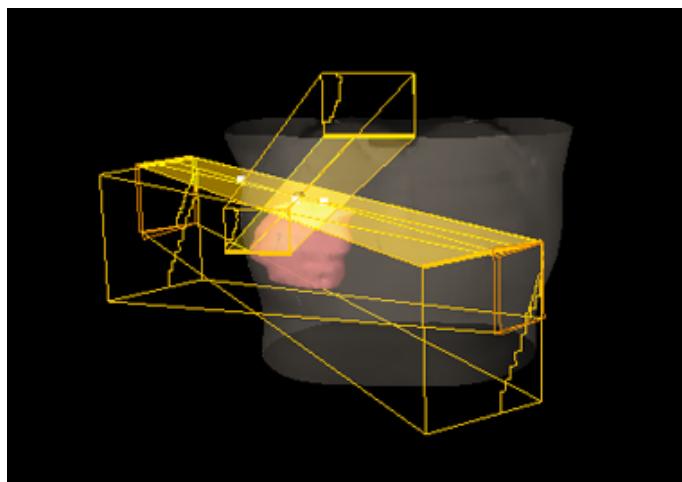


Figure 57 Aligned Fields

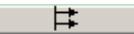
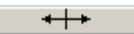
By default, when you start Eclipse the field alignment tool is off. It is possible to modify field alignment rules also when the tool is off. When the tool is switched on, it is active until you switch it off or until a new plan is opened and loaded into image views.

Field alignment rules can be applied to open fields only. They are not available for proton fields, plan sums or electron fields.

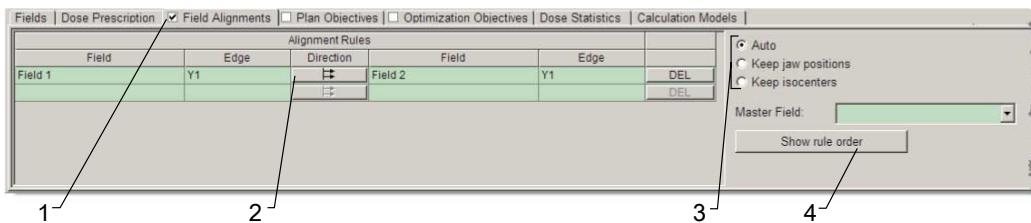
Field Alignments Tab of the Info Window

The Field Alignment tab of the Info window is used in External Beam Planning for viewing and editing field alignment rules.

Table 13 Information in the Field Alignments Tab

Item	Description
Field	<p>The field used in the alignment rule.</p> <p>Click the empty cell to display all fields in the current plan.</p> <p>A blue background in the rule indicates that the rule is not applied; the rule contains impossible field geometry, or it violates treatment unit limits.</p>
Edge	<p>The plane used in the alignment rule.</p> <p>Click the empty cell to display all six planes in the field (X1, X2, Y1, Y2, XC and YC).</p> <p>A blue background in the rule indicates that the rule is not applied; the rule contains impossible field geometry, or it violates treatment unit limits.</p>
Direction	<p>Toggle buttons showing whether the fields in the alignment rule are parallel or opposing.</p> <p> Fields in the alignment rule are parallel. Click the button to change parallel fields to opposing fields.</p> <p> Fields in the alignment rule are opposing. Click the button to change opposing fields to parallel fields.</p> <p> Deletes the field alignment rule.</p>
Auto	The application keeps either the jaw positions or isocenters during field alignment. If two fields have the same isocenter, the isocenters are kept. Otherwise, the jaw positions are kept.
Keep jaw positions	<p>Keeps field sizes during field alignment. When this option is selected, the isocenters are adjusted instead.</p> <p>The option is automatically selected for electron fields.</p>
Keep isocenters	<p>Keeps isocenters during field alignment. When this option is selected, the jaw positions are adjusted instead.</p> <p>If XC or YC is defined as an edge in the field alignment rule, this option cannot be used.</p>
Master Field	<p>The master field is not moved when field alignment rules are applied. All other fields are adjusted according to the master field.</p> <p>If the master field is not defined, the currently active field is considered as the master field and all other fields are adjusted accordingly.</p>
Show rule order	Displaying the order in which the field alignment rules are applied.

The picture in the right side of the Field Alignments tab shows the alignment planes X1, X2, Y1, Y2, XC and YC and their normal directions viewed from the BEV.



1. When the check box is selected, the field alignment rules are applied.
2. Toggle button showing whether the fields in the rule are parallel or opposing.
3. Options for handling isocenters during field alignment.
4. Displays the order in which the field alignment rules are applied.

Figure 58 Field Alignments Tab

Related Topics

[Fields Tab of the Info Window](#) on page 181

Define a Field Alignment Rule

1. In the Info window, select the **Field Alignments** tab.
2. To define the first alignment plane for the field alignment rule, click an empty cell in the first Field column.
3. Click the arrowhead and select the desired field.
4. Click an empty cell in the first Edge column and define a plane for the field alignment rule.

The selected plane is highlighted in the Model view.

5. Click the button to indicate whether the second field in the field alignment rule is parallel with or opposing to the first field you just defined.
6. To define the second alignment field for the field alignment rule, click the empty cell under the second Field column and select the field as before.
7. To define the second alignment plane for the field alignment rule, click the empty cell in the second Edge column and select the plane as before.
8. Repeat the above steps as many times as necessary to create all the needed field alignment rules.

9. Do one of the following:
 - To keep the field sizes unchanged during field alignment, select the **Keep jaw positions** option button. This option is automatically selected when electron fields are used.
 - To keep the field isocenters unchanged during field alignment, select the **Keep isocenters** option button.
 - To let the application decide how fields are handled during field alignment, select the **Auto** option button.
10. Select the master field. If the master field is not defined, the currently active field is considered as the master field.
11. To display the order in which the field alignment rules are applied, click **Show rule order**.
12. To activate the field alignment rules, select the check box in the upper left corner of the Field Alignments tab.

The planes used in field alignment rules are marked in blue on the Fields tab of the Info window. They also have a tool tip showing the field alignment rule.

Modify or Delete a Field Alignment Rule

1. On the Field Alignments tab of the Info window, click the field or plane to modify.
2. Click the arrowhead  and select the desired item.
3. To change parallel field to opposing and vice versa, click the toggle button located between the two alignment planes.
4. To delete a field alignment rule, click the  button next to the field alignment rule you want to delete.

Converting Asymmetrical Fields into Symmetrical Fields

Asymmetrical fields can be converted into symmetrical fields to support simulator workflows where the positions of the field edges are located first, and then the isocenter positioned automatically. The conversion can also be useful in cases where the images contain no contours. The target can then be defined as a rectangle limited by the collimator jaws, and the isocenter positioned in the middle of this rectangle.

The field size on the isocenter plane is not changed in the conversion.



Note: When converting asymmetrical fields into symmetrical fields, notice the following:

- Grouped fields that share the same isocenter: Only the selected field is made symmetrical by the conversion. The isocenters of the other fields contained in the group then follow to keep the isocenter of all the grouped fields the same. This may lead to unexpected results when using, for instance, opposing fields.
- Fixed SSD fields: The isocenter is automatically moved to the surface of the patient's skin.

Convert an Asymmetrical Field to a Symmetrical Field

1. Create a field and move the isocenter near the target area.
2. Adjust the collimator jaws so that the target area is covered.
3. In the Focus window, right-click the asymmetrical field that you wish to convert into a symmetrical field, and choose **Align Field to > Symmetric Jaws**. For grouped fields, choose **Align Grouped Fields to > Symmetric Jaws**.

The field properties are changed into those of a symmetrical one. The isocenter shifts to the field midpoint on the isocenter plane.

Measuring the Water-Equivalent Distance

To identify the water-equivalent distances in a patient image, use:

- WED for Field tool to measure the pathway length from the body outline to the selected point.

For arc fields, the WED tool displays the average value calculated from the values for each gantry angle.

The tool shows the ID of the active field and the water-equivalent distance (WED), expressed in centimeters with the accuracy of 0.001 cm. If the distance cannot be calculated, the tool shows a hyphen instead of a calculated value.

- WED and Distance tool to measure the water-equivalent distance and geometrical distance between two selected points. In addition to the water-equivalent distance, the tool also shows the geometrical distance between the points.

Both tools take bolus (photon and electron plans only) and the couch support structure, if any, into account. The values shown by the tools are updated when you move the point(s) in the 2D image view, or scroll or rotate the image viewing plane. The WED values are also included in the printout of the active view where the distance has been measured.

The calculation of the water-equivalent distance is based on the following:

- For photon and electron plans, the calculation uses the linear attenuation curves.

- The water-equivalent distance of a single point is calculated along that fanline of the treatment field that goes through the selected point, measured from the point where the fanline crosses the body outline or bolus to the selected point.

The water-equivalent distance between locations a and b is calculated as follows:

Equation 1

$$WED(a,b) = \int_a^b Conversion(HU(x))ds$$

where

		The integral is taken along the line from a to b.
HU (x)	=	The HU value of the image at x.
Conversion	=	The CT Scanner specific conversion curve (electron density curve for photon, electron and brachytherapy plans / proton stopping power curve for protons).

If the selected point of the point dose tool is inside two or more non-body structures that have material or HU value assigned, the material of the structure with the higher HU value is shown and taken into account in the calculation.

Measure the Water-Equivalent Length between Two Points

The WED tools are available in External Beam Planning and Plan Evaluation.

- Choose **View > Measure > WED and Distance** .

The mouse pointer changes to a line tool.

- To measure the water-equivalent distance between two points, click the start and end points in a 2D image view.

The physical distance and the water-equivalent distance between the selected points is calculated and the distance and WED values are shown in the image view.

- To change the distance, move the end points with the mouse.
- To deactivate the tool, choose **View > Measure > WED and Distance**  again.

Measure the Water-Equivalent Distance for a Single Point

The WED tools are available in External Beam Planning and Plan Evaluation.

1. In the Focus window, select the field for which you wish to measure the water-equivalent depth.
2. Choose **View > Measure > WED for Field** .

The mouse pointer changes to a point measurement tool.

3. To measure the water-equivalent distance for a point, click the point with the mouse.

The water-equivalent distance of the point for each field is calculated and the field ID of the active field and WED value are shown in the image view.

4. To change the location of the point, move it with the mouse.
5. To inactivate the tool, choose **View > Measure > WED for Field**  again.

Changing the Treatment Unit for Fields

You can change the treatment unit of fields, if necessary. When you change a treatment unit, the application compares the configuration of the suggested new treatment unit to the treatment unit currently used in the fields and looks for matching field parameter and add-on configurations. If exact matches are found, the change is done between the two treatment units with no changes to the fields or add-ons. Since treatment units often have differences in configurations, some modifications are often required in the fields and add-ons when changing the treatment unit.

If the system has a group or groups of dosimetrically equivalent machines configured, you can also change the treatment unit to one of the machines belonging to the group.

The table shows how the fields and add-ons are dealt with if no exact matches are found in the treatment unit configurations.

Table 14 Field Parameters and Add-ons in Treatment Unit Change

Field Parameter / Add-on	Action
Field technique	Treatment unit not changed if no match is found
Particle type	Treatment unit not changed if no match is found
MLC technique	Treatment unit not changed if no match is found
Field size limits	Treatment unit not changed if field size exceeds the limits

Field Parameter / Add-on	Action
Symmetry/asymmetry	Treatment unit not changed if no matching configuration is found
Collimator/Couch/ Gantry rotation limits	Treatment unit not changed if field rotations exceed the limits
Energy	Changed to the nearest corresponding energy
Dose rate	Changed to the nearest corresponding dose rate
Electron applicator size	Changed to the nearest larger electron applicator size
Wedge (fixed, Enhanced Dynamic, motorized)	Wedge angle and direction must match. Other parameters changed to the nearest corresponding wedge configuration.
Block	<p>Material changed to the material found. If no material is found, blocks remain in the fields but are left without material.</p> <p>Dose calculation is not possible for fields containing blocks with no block material.</p>
Compensator	<p>Material changed to the material found if the configured attenuation factor is the same. If no material is found, compensators remain in the fields but are left without material.</p> <p>Dose calculation is not possible for fields containing compensators with no compensator material.</p>
Static MLC	<p>You can select the MLC to be used if there are several possible MLCs.</p> <p>Supported only for Varian MLCs. Varian HD-MLC is not supported.</p>
DMLC	Treatment unit is changed if DMLC is supported in the new treatment unit. Fields containing a DMLC are converted if the same MLC model is found.
Fluence	<p>Actual fluences are always deleted.</p> <p>Optimal fluences remain in fields where a matching energy, machine model or MLC model is found.</p> <p>DMLCs are removed if optimal fluences exist.</p>

Change the Treatment Unit for Fields

1. In the Focus window, right-click a field or a plan and choose **Change Treatment Unit**.

If the dose has been calculated for the plan, and you have a group or groups of equivalent machines configured in the system, you are prompted to choose whether you wish to use one of the machines in the group(s). To do this, click **Yes**. To use some other treatment unit, click **No**.

2. Define whether to change the treatment unit for all fields in the active plan, or whether to change the treatment unit for fields using a particular treatment unit.
3. Select the treatment unit that you wish to use.

The change log displays the required modifications, and lists the fields for which the change is not possible. To save the change log text, copy it from the Change log box and paste it to a separate document.

4. To change the treatment unit, click **OK**.



Tip: You can change the treatment unit individually for each photon planning or setup field in the Field Properties dialog box.

Related Topics

[Changing the Treatment Unit to an Equivalent Machine](#) on page 483

Using Digitally Reconstructed Radiograph Images

A Digitally Reconstructed Radiograph (DRR) is an X-ray image, added to a field, and seen from the beam focus. The DRR can be a “static DRR” or a “live DRR”. The static DRR is imported to the database and added as a field image to the plan. The live DRR is created in Eclipse and is updated dynamically when the field geometry changes. The DRR layers define the transfer function from image pixel values to DRR pixel values. The DRR image is a weighted composition of the DRR pixel values projected to the DRR plane in a specific beam direction. There can be one to three layers in the DRR image. The DRR image is displayed in the BEV or the Model view. DRR images are field-specific and you can show or hide the DRR image individually for each field.

DRR images are always calculated from the 3D image shown in the image views, regardless of whether it is the primary 3D image or the registered 3D image. If you are viewing a registered MR image, the DRR is calculated from that MR image.

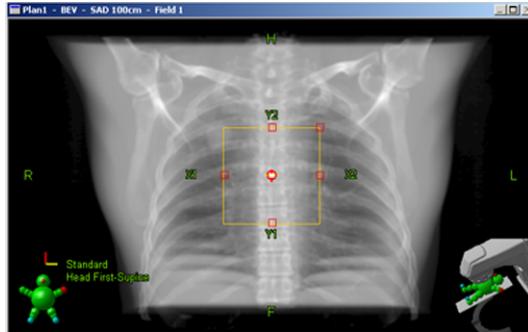


Figure 59 DRR Image in BEV

For a live DRR, you can change the field geometry, for example by changing the gantry angle, and the DRR image is recalculated and updated accordingly. The live DRR images are shown with a yellow DRR icon in the Focus window, and “Live” is shown in the DRR name. If the live DRR has been set as the reference image of the field, the icon is shown within a yellow rectangular .

Static DRRs are not recalculated or updated when you change the field geometry. They are shown with a gray DRR icon in the Focus window, and “Static” is shown in the DRR name. If the static DRR has been set as the reference image of the field, the icon is shown within a yellow rectangular .

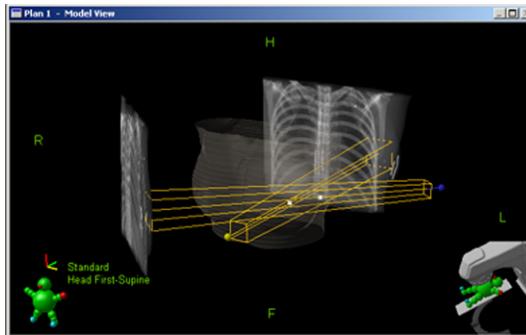


Figure 60 DRR Images for Two Fields in Model View

A DRR image is displayed when its visibility check box is selected in the Focus window. If you blend two 3D images that belong to 4D images, the DRR images are not visible in the image views even though their visibility check boxes are selected.

You can also generate live DRR images by using weighted CT values. The application provides the following calculation options for live DRR images:

- Calculating based on the whole or partial image volume

- Defining the CT value range to take into account
- Using predefined parameter sets and creating and saving new sets

Once you have added one live DRR image to a plan using a 3D image that is part of a 4D image, you can display temporary DRR images of all 3D images in that 4D image automatically by clicking the Play button of the Movie Control tool on the lower right corner of the image view. You can also select the visibility check boxes of the 3D images in a 4D image one by one to show the relevant temporary DRR image. The temporary DRR images displayed this way use the same parameters that were used in the original live DRR image. These temporary DRR images are calculated for temporary use and they are not saved in the database. The original live DRR image is saved in the database.

If you export a live DRR image, and import it back to Eclipse, it is changed to a static DRR.

Related Topics

[Associating Fields with Field Images](#) on page 206

Predefined Parameter Sets for DRR Calculation

The system features the predefined combinations of detailed calculation settings for the parameter sets.

Table 15 Predefined DRR Parameter Sets

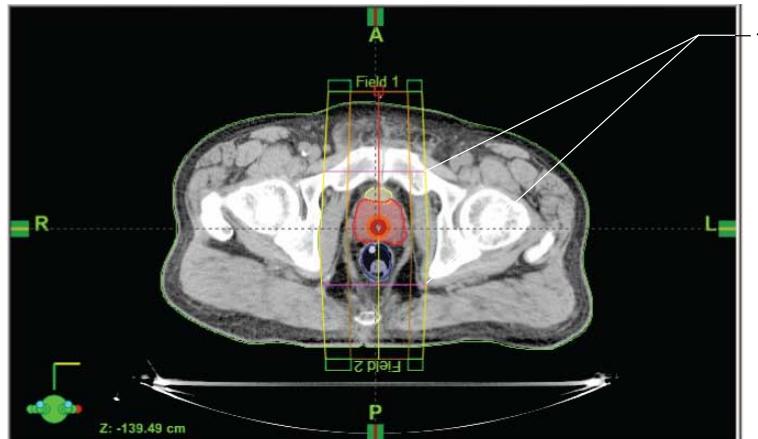
Parameter Set Name	Weight	HU Values		Description
		from	to	
Abdomen.dps	2.0	-16	126	Layer 1: (Soft tissue)
	10.0	100	1000	Layer 2 (Bones)
Airway.dps	1.0	-999	918	
Bones.dps	1.0	100	1000	
Breast.dps	5.0	100	1000	Layer 1 (Bones)
	0.2	-450	150	Layer 2 (Soft tissue)
	100.0	1600	3000	Layer 3 (Metal structures)
Chest.dps	0.6	-999	0	Layer 1 (Air/ lung tissue)
	0.1	-450	150	Layer 2 (Soft tissue)
	1.0	100	1000	Layer 3 (Bones)
Lungs.dps	1.0	-1000	-700	
OBI markers.dps	1.0	2000	3000	

Parameter Set Name	Weight	HU Values		Description
		from	to	
Pelvis Lateral.dps	10.0	300	1500	Layer 1 (Bones)
	0.2	-450	150	Layer 2 (Soft tissue)
	10.0	1600	3000	Layer 3 (Metal structures)
Soft Tissue	1.0	-450	150	

Use Detailed Calculation Parameters for a DRR Image

- To open the DRR Options dialog, right-click the DRR image in the Focus window or in the Image Gallery and choose **Edit DRR**.
- In the **Parameters** group box, select one to three layers to be used in generating the DRR image.
- Specify the DRR layer weight factor to use for the selected parameter. The weight factor determines how the images are composed together. Negative weight value subtracts the image from other DRR layer images.
- Define the range of CT window values in HU to use for visualizing the DRR image. CT window values are used in the gray levels varying from black to white.
 - The **From** value determines the darker end of the CT window. Anything below the set value is visualized as black.
 - The **To** value determines the lighter end of the CT window. Anything above the set value is visualized as white. Changing the **From** and **To** values inverts the gray values of the projected image.

5. To define the image volume of the DRR image, do one of the following:
 - To base the DRR calculation to full image volume, leave the **Clipping [cm]** option unselected. By default, the DRR is calculated to full image volume.
 - To base the DRR calculation to partial image volume, select the **Clipping [cm]** option and define the distance range from the isocenter with the **From** and **To** values.



1. Upper and lower limit of the distance range of a partial DRR.
6. In the **DRR size [cm]** box, define the resolution of the DRR image. The default value is 50 cm.
Decreasing the size of the DRR effectively increases the resolution of the DRR.
7. To calculate all live DRRs in a multi-field plan using the modified parameters, select **Apply to all fields**.
8. Click **Apply** to calculate the DRR image.

Manage DRR Parameter Sets

- To create a new parameter set, define the details and click **Save set**. Define a name for the parameter set.
- To specify a default parameter set that is automatically selected when the New DRR dialog is opened, select a parameter set and click **Set as default**.
- To modify a parameter set, define the details, click **Save set**, give the existing name for the set and allow to overwrite the old set.
- To remove a parameter set, select it and click **Delete**.

Related Topics

Printing DRR Images

In External Beam Planning, the simplest way to print out DRR images is to print the BEV.

You can print out DRR images by displaying them in an image view in the Selection application, and then printing the view where the DRR image is displayed.

Displaying DRR Images in the Transversal 2D Image View

This information applies to External Beam Planning and Plan Evaluation.

You can display DRR (Digitally Reconstructed Radiograph) images in the transversal 2D image view. For approved plans, the DRR will also show the selected structure outlines as layers. Structure outlines are shown as on the SAD plane. You can control the structure visibility in the Focus window by selecting or clearing the visibility check boxes. If you change the field geometry, the structure outlines are updated accordingly.

The field graticule is shown with a resolution of 1 cm.

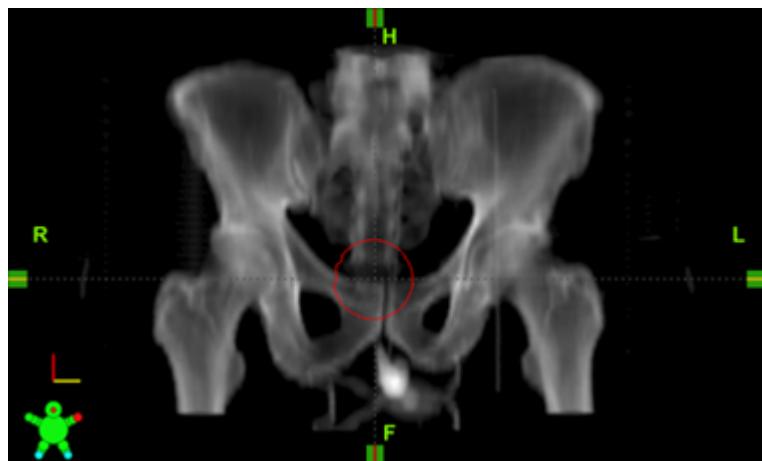


Figure 61 DRR of an Approved Photon Field in 2D Image View

Display a DRR Image in the Transversal 2D View

This information applies to External Beam Planning and Plan Evaluation.

1. In the Focus window, display the subbranches of the field whose DRR you wish to view.
2. Right-click the DRR image you wish to view and then select **Drop to view**. In Plan Evaluation, you may also be able to choose the 2D image view, depending on the view layout.

If you are viewing an approved plan, and structure outlines have been included in the DRR, the selected structure outlines are shown on the DRR image.

Associating Fields with Field Images

Field images are 2D images created in the simulator (including digitized film images), portal images created in connection with the patient treatment, or static DRRs. You can also create live DRRs in Eclipse, and use them as field images.

Each field can have multiple field images, for instance, one live DRR and one simulator image, of which one can be marked as the reference image. The reference image can be used later in the treatment process in, for instance, 4D Console and Offline Review for comparing portal images with the reference image.

There are some restrictions as to which images can be used as field images. The images must be RT images (projection images, such as simulation or portal images), and they must be scaled before adding them to fields.



Note: If you use the Vidar scanner to scan images digitally printed at a magnification factor of 1.0, define both the SAD and the SID values for the images to achieve correct scan results.

Add a Field Image

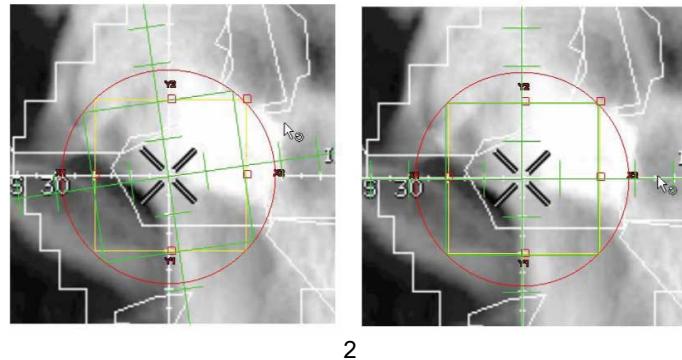
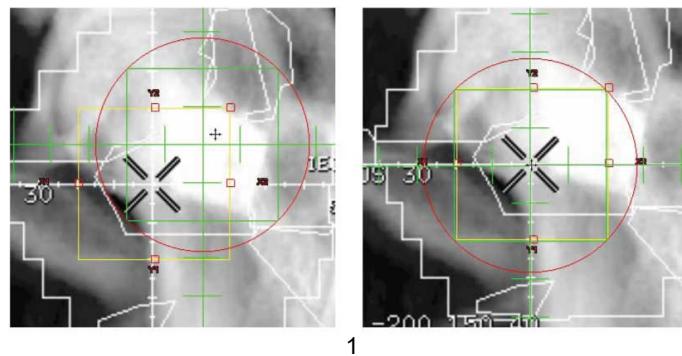
1. Open the plan.
2. In the Scope or Focus window, right-click the field to which you wish to add a field image and choose **Add Field Image**.
3. Select the image and click **OK**.

Align a Field Image in External Beam Planning

1. In the Focus window, select the field image to be aligned.
2. Choose **Edit > Align Image to Field CAX**.

The dialog box shows the current location of the field image. The field graticule is shown in the BEV. The mouse pointer changes to the alignment tool.

3. If the image SAD value is missing, enter the correct value.
4. Do one of the following:
 - To move the field, place the mouse inside the alignment circle and drag, or click inside the circle to move the field.
 - To rotate the field, place the mouse outside the alignment circle and drag.



1. To move the field, place the mouse inside the circle and drag.
2. To rotate the field, place the mouse outside the circle and drag.

- The position of the field image is updated in the dialog box.
5. When the field image is positioned as desired, click **OK**.

6. If there are more field images, repeat the steps for each image.

Show a Field Image in the 3D View

- In the Focus window, select the visibility check box of the field image to be shown.

The selected field image is shown in the Model view or the BEV, depending on which view is active.

Select the Reference Image of a Field in External Beam Planning

- In the Focus window, right-click the field image (DRR or RT image) that you wish to define as the reference image of the field and choose **Set Image as Reference Image**.

The Align Image to Field CAX dialog box shows the current location of the field image. The field graticule is shown in the BEV. The mouse pointer changes to the alignment tool.

- Verify the field alignment, and if necessary, drag the field graticule to the desired position.
- When the field image is positioned as desired, click **OK**.

The reference image is shown on the Reference Image tab of the Field Properties dialog box. In the Focus window, the image icon changes to indicate that the image is the reference image.

If you move the field after selecting and aligning the reference image, you need to re-align the image manually.

Displaying Field Images in the BEV or Model View

This information applies to External Beam Planning and Plan Evaluation.

You can display field images (DRR images, simulation images, and portal images) in the BEV and Model view. Displaying the field images requires that they have been correctly scaled and aligned.

You can show structures as outlines in field images, along with a field graticule, in the BEV. Structure outlines are shown as on the SAD plane. The visualization of the graticule is also available in IRREG Planning, but not the structure outlines. You can control the structure visibility in the Focus window by selecting or clearing the visibility check boxes. If you change the field geometry, the structure outlines are updated accordingly.

In the default BEV scale, the graticule is shown in a resolution of 1 cm. If you change the collimator angle, the SAD or some other parts of the field geometry that affect the BEV, or select another field, the graticule is updated accordingly. The graticule is not stored when the plan is saved.

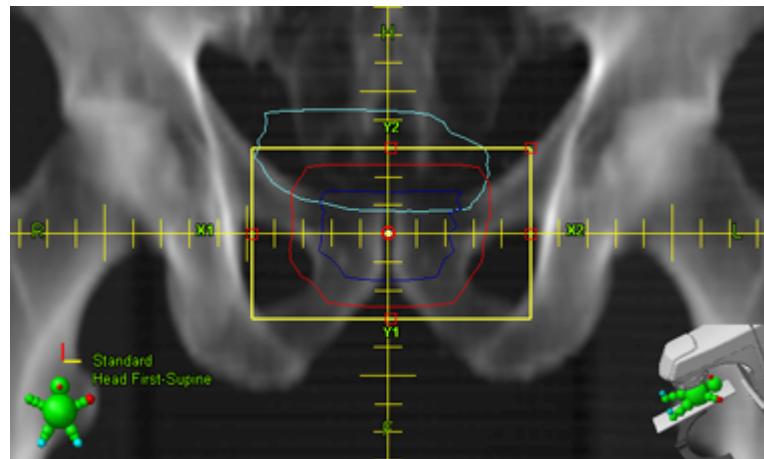


Figure 62 Structure Outlines and Field Graticule in BEV

Display a Field Image in the BEV or the Model View

1. In the Focus window, select the field for which you wish to view the field image.
2. In the Focus window, display the subbranches of the selected field.
3. Click the check box in front of the field image. The image is displayed in the BEV or the Model view.

Display Structure Outlines in a Field Image

1. In the BEV window, right-click and choose **Show Structure Outlines in BEV**.
2. To show or hide structures, click their visibility check boxes in the Focus window.

Display the Graticule in a Field Image

- In the BEV window, right-click and choose **Show Graticule in BEV**.

Creating Setup Fields

Setup fields are used for moving the treatment unit to the correct treatment position, or for aligning the patient correctly for treatment. The dose distribution is not calculated for setup fields, and they cannot be used for patient treatment.

You can generate a live DRR for each setup field if necessary and set the DRR as a reference image. Reference images can be used, for instance, in Ximatron Digital Imaging and Portal Imaging.

Setup field icons  are shown in the Fields folder in the Focus window in External Beam Planning and Plan Evaluation. The live DRR and field accessory icons are shown below the particular setup field.

Related Topics

[Default Photon and Electron Field Parameters](#) on page 180

[Using Digitally Reconstructed Radiograph Images](#) on page 200

Photon Setup Fields

Setup fields can be created from original treatment fields in External Beam Planning. The original field remains intact, while the created setup field is an exact copy of the original, including MLC but excluding the field dose, MU and other field accessories.

When you create new setup fields (not based on existing treatment fields), the location of the isocenter is copied from the previously added setup field. If no setup fields exist, the isocenter location is copied from the previously added treatment field. If no other fields exist, the isocenter will be in the geometrical center of the target volume, or in the image center (if no target volume exists).

When creating a setup field from an existing photon field, you can also create a new field aperture to the setup field. The created aperture is copied to the reference image of the setup field, and will not be updated if the original field or the setup field is modified.

If the original field contained a live DRR, the DRR is linked to the setup field as a reference image. For setup fields created from electron fields, the Energy setting is left empty.

You can also insert new setup fields in a plan using the default field settings.

All setup fields can be rotated as necessary. The original fields remain intact.

Chapter 10 Inverse Treatment Planning

Overview of Inverse Planning Features in Eclipse

The new Optimization dialog box enables you to optimize IMRT, VMAT (RapidArc and Elekta VMAT) and Siemens mARC plans. To use the new Optimization dialog box, you need to use the new Photon Optimization (PO) algorithm to optimize the plans. If you use the PRO algorithm to optimize a VMAT plan, or the DVO algorithm to optimize an IMRT plan, you optimize the plans in the IMRT and VMAT Optimization dialog boxes as in previous versions of Eclipse.

More information about optimizing IMRT plans with the DVO algorithm and VMAT plans with the PRO algorithm: *Eclipse Photon and Electron Reference Guide*.

In addition, you can generate DVH estimates and optimization objectives from DVH estimation models. When you use a DVH estimation model to generate DVH estimates and objectives in a plan, you can use all the features in the Optimization dialog box in the same way as in optimization without a DVH estimation model.

The new Optimization dialog box and the Photon Optimization algorithm support the following new features and introduce the following changes:

- The default priority of new objectives is 0, and it must be modified for the objectives to have the intended effect on the optimization.
- You can use mean dose objective in IMRT plans.
- You can add Generalized Equivalent Uniform Dose (gEUD) optimization objectives in IMRT and VMAT plans.
- You can select the optimization resolution in the Optimization dialog box (under the **Settings** expander).
- The 2D view in the Optimization dialog box shows an approximation of the dose distribution during optimization.
- The Photon Optimization (PO) algorithm uses a new voxel-based structure model where structures, DVH calculation and dose sampling are defined spatially by using one single matrix over the image.
- Before starting VMAT optimization, you need to open the Arc Geometry tool manually. It is not opened automatically by the system.
- You can optimize Siemens mARC plans in the new Optimization dialog box.
- Adding line objectives by drawing is not supported in this version. However, line objectives can be included in a DVH estimation model, and they can be loaded from optimization objective templates that have been created in the IMRT or VMAT Optimization dialog boxes. Line objectives cannot be edited in the new Optimization dialog box, but they can be deleted.

- Deleting objectives by selecting them with the mouse in the DVH view is not supported in this version. To delete an objective you need to Click the X on the row of the objective in the Structure list.

In the new Optimization dialog box, the settings and parameters are grouped under expanders, which are located below the structure and optimization objectives list. Some of the optimization parameters, for example *Smoothing x* and *Smoothing y* for IMRT plans and *Avoidance Sectors* and *Jaw Tracking* for VMAT plans, are located in the **Plan Information** drawer.

More information on the optimization and DVH estimation algorithms: *Eclipse Photon and Electron Algorithms Reference Guide*.

IMRT Optimization

Intensity-modulated radiotherapy (IMRT) planning in Eclipse creates highly conformal dose distributions by iteratively optimizing the beam intensity modulation to satisfy a set of user-defined dose volume objectives. IMRT plans enable you to deliver a relatively uniform dose distribution to a target volume while sparing surrounding healthy tissue. Eclipse IMRT planning combines intensity modulation and inverse planning to accomplish this goal.

IMRT plans are created following a particular workflow, which differs slightly from the workflow followed in conventional planning:

1. Contour patient structures, including targets and avoidance volumes. Since IMRT plans produce dose distributions that are highly conformed to the shapes of the targets, greater precision is typically required in defining structures for IMRT plans than in conventional planning.
2. Add fields to the IMRT plan. Use clinical protocols and plan templates, or add the fields manually.



Note: Eclipse IMRT does not automatically select field angles for plans. You can use Beam Angle Optimization before IMRT Optimization to optimize the field angles.

3. Optimize the IMRT plan. Define a set of dose-volume objectives for each target and critical structure of concern, and start the optimization. You can also define fluence smoothing parameters to achieve more deliverable DMLC sequences and fewer MU to treat the fields.
4. Calculate the dose and continue planning and plan evaluation as usual.

The following types of optimization objectives are used in IMRT optimization:

- Lower objectives, which ensure that a volume receives a minimum dose. Any structure with a lower dose-volume objective is considered to be a target.
- Upper objectives, which limit the dose to any structure and can be used to enhance dose uniformity in target volumes.

- Mean objectives, which are used to decrease the dose that a structure receives.
- gEUD objectives; Generalized Equivalent Uniform Dose (gEUD) is a uniform dose that, if delivered over the same number of fractions, yields the same radiobiological effect as the non-uniform dose distribution of interest. Structures with Lower gEUD and Target gEUD objectives are considered to be targets.



Note: If you use the DVO algorithm to optimize the plan, mean objectives and gEUD objectives are not available.

The optimization process is interactive: you can interrupt the iteration at any time during the optimization process and change the dose objectives according to the results of the optimization. The interactive optimization of the objectives achieves better dosimetric results in less time. You can also leave the optimization process to terminate on its own. The optimization stops when one of the following conditions are met:

- The objective function curve does not change anymore (in automatic optimization).
- The maximum time limit has been reached.
- The maximum number of iterations has been reached.

More information about the algorithms used in dose optimization: *Eclipse Photon and Electron Algorithms Reference Guide*.

Related Topics

[Define Dose Objectives in IMRT and VMAT Optimization](#) on page 237
[Objective Templates in Photon Optimization](#) on page 239

Intensity Modulation

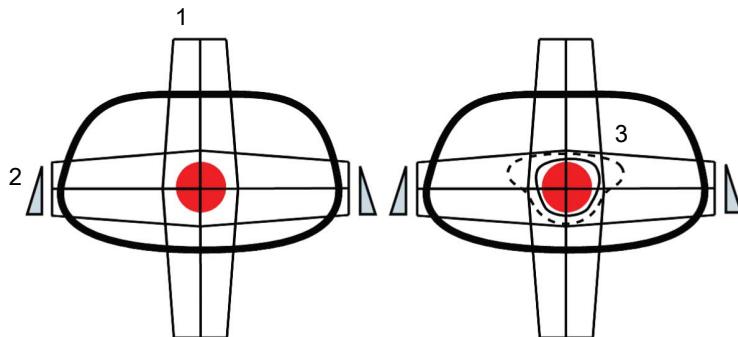
Intensity modulation is the act of varying the fluences of a field to shape the resulting dose distribution. Although the dose distribution of a single IMRT field is typically non-uniform, the combination of several IMRT fields can result in a very uniform target dose.

Eclipse produces the modulated field fluences based on user-defined dose-volume objectives. The field fluences computed by Eclipse are converted into DMLC motion patterns, and the modulated dose is delivered with a Dynamic MLC (DMLC) device.

Forward Planning vs. Inverse Planning

The difference between conventional forward planning and inverse planning is compared in the following figures.

Traditional forward planning is usually a trial and error process, where different field and field modifier setups are tried out to see whether they produce a dose that corresponds to the dose prescription.

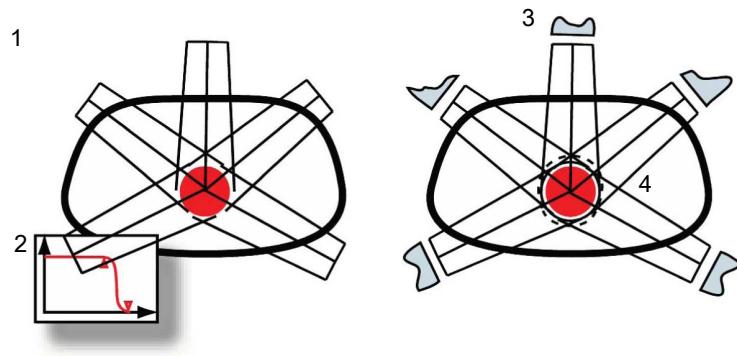


1. Setup of field geometry that conforms to the target structure.
2. Field modifiers to achieve desired shape of fields and dose distribution.
3. Resulting shape of dose distribution.

Figure 63 Forward Planning

Contrary to conventional treatment planning, inverse planning begins by specifying the desired dosimetric outcome of the treatment plan. The inverse planning engine works backwards from the desired outcome to generate a set of intensity-modulated fluence matrices. Eclipse optimizes the intensity modulation to produce dose distributions that conform to the planning target volume as closely as possible.

Inverse planning directly results in optimal beam profiles that are produced by the optimization program to correspond to the dose prescription (expressed for the optimization as dose objectives).



1. Setup of field geometry.
2. Definition of optimization objectives to achieve the desired dose.
3. Modulated fluence resulting from optimization.
4. Resulting shape of dose distribution.

Figure 64 Inverse Planning

Automated Optimization

You can automate the optimization to speed up IMRT planning. In the automated process, you first define the dose objectives, and then let the program optimize the plan, calculate an intermediate dose, continue the optimization and move to the leaf motion calculation and final dose calculation. To use the automatic optimization, configure a default LMC technique and delivery method, and select a calculation model for the volume dose. More information about configuration: *Eclipse Photon and Electron Algorithms Reference Guide*.

Related Topics

[Select the Calculation Model for External Beam Plans](#) on page 434

Intermediate Dose Calculation in IMRT Optimization

To improve optimization results, you can calculate an intermediate dose during the IMRT optimization. This is useful especially for heterogeneous targets, such as lungs. The intermediate dose is calculated from the current fluences in the plan, using the same dose calculation algorithm as in the final dose calculation. The calculated dose is compared with the internal, approximate dose generated during the optimization. The difference between these two doses is used for adjusting the optimal fluences during the rest of the optimization. As a result of adjusting the fluences, the DVHs produced during optimization and final dose calculation become more uniform.

You can set IMRT optimization to calculate the intermediate dose automatically during the optimization, or you can do it manually at any point during the optimization. In addition, when re-optimizing a plan that already has a dose distribution, you can use the existing dose as an intermediate dose during the optimization.

More information about the Photon Optimization algorithm and the Dose Volume Optimization algorithm versions that support intermediate dose calculation: *Eclipse Photon and Electron Algorithms Reference Guide*.

VMAT Optimization

VMAT optimization creates highly conformal dose distributions by iteratively modulating the MLC apertures and corresponding dose per degree until the prescribed dose objectives of the plan are optimally satisfied. The optimization process is interactive, allowing you to change the dose objectives according to the results of the optimization.

You can set the program to optimize a VMAT plan automatically. First, you have to define the dose objectives. After that, you can let the program optimize the plan, calculate an intermediate dose, continue the optimization and move to the final dose calculation. After the plan has been optimized and the dose calculated, the program saves the results automatically.

In VMAT optimization, the MLC leaf positions and dose per degree are calculated for a number of control points in an arc field. The resulting MLC leaf positions and dose per degree are stored in a number of control points in the field. The treatment machine control system determines how the dose rate and gantry speed need to be modulated in order to deliver the control point sequence in the plan. Finally, a volume dose is calculated for the plan with a version of the AAA or Acuros XB dose calculation algorithm that supports calculation of VMAT fields. After optimization, the MLC type in the Fields tab of the Info Window and in the MLC Properties dialog box is “VMAT”. VMAT plans can be exported/imported with DICOM.

The optimization process is iterative; it proceeds through several multi-resolution levels. During the optimization, you can set the optimization process to “hold” at a specific level for a continued period of time, in order to make changes to the objectives before the next resolution level is reached. It is recommended to make these changes in multi-resolution levels 1 and 2. You can also return to the previous level or jump to the next level if needed.

You can also continue the previous optimization of a plan containing fields that have either arc dynamic MLC or VMAT MLC. Previous optimizations are continued from the last multi-resolution level. Field geometry and jaw tracking are read from the previous optimization and cannot be changed. Avoidance sectors are also read from the previous optimization. However, if you need to adjust the avoidance sectors, it is recommended to start the optimization from the beginning.

After VMAT optimization, the final optimized plan can be saved as a template or as a clinical protocol. The MLC type (VMAT) is not saved in the template or clinical protocol; the field and optimization objectives are saved and the VMAT optimization process must be followed when the template or clinical protocol is used.

More information about the algorithms used in VMAT planning: *Eclipse Photon and Electron Algorithms Reference Guide*.

Target Coverage Visualization

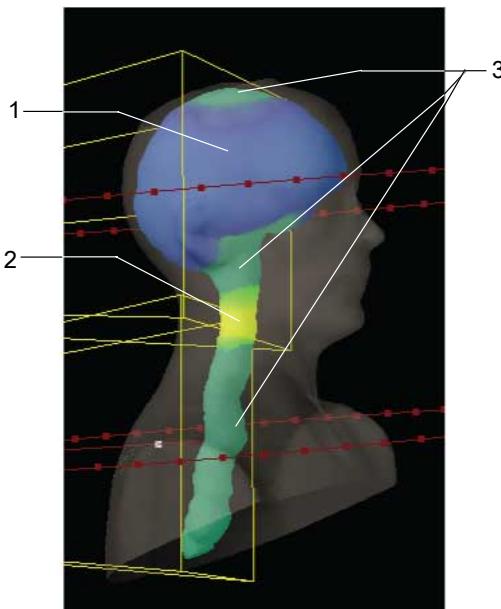
When the Arc Geometry Tool is active, the target coverage is visualized on the surface of the target in the model view and in the BEV. The target coverage on the target surface indicates how well the target is covered with the current plan geometry. You can rotate the collimator or adjust the size of the collimator opening in the BEV, and see how it affects the target coverage. The scale of the colors used to visualize the target coverage are shown in the Fine-tune Fields tab.



Note: The target coverage is not visualized for targets with the visualization style Contour.

The diagram showing scale of the colors on the Fine-tune Fields tab shows how the colors correspond to the number of degrees along the arc. Blue indicates that the modulation potential is reduced because the collimator opening is over 15 cm. Green indicates that the target can be modulated from 360 degrees. Yellow indicates the seam area between two fields (modulation from 720 degrees).

When you look at the colors in the BEV or Model view, you can see if part of the target is not covered at all, or in the case of a plan with multiple isocenters, the area of the target that is covered by fields targeted at different isocenters (the “seam area” between two fields; see the following figure). The meaning of the colors indicating the coverage is the same for single and multi-isocenter plans.



1. Blue indicates that the modulation potential is reduced because the collimator opening is over 15 cm.
2. Yellow indicates the seam area between two fields (modulation from 720 degrees).
3. Green indicates that the target can be modulated from 360 degrees.

Figure 65 Modulation Potential Visualization in Model View

About Approximated Minimum Distances and their Limitations

The Arc Geometry Tool shows approximated minimum distances from the treatment unit head model to the couch model and to the patient model. These distances are shown in the Fine-tune Fields tab. The approximated distances are based on the patient information in the CT image, and hence they are estimates only. There is no patient extension model included for the parts of the body superior or inferior to the CT images. The treatment unit head and couch dimensions are also approximated models (more information: *Eclipse Photon and Electron Algorithms Reference Guide*). None of the accessories or slot mounts that may be attached to the treatment machine or the couch are taken into account.

When estimating the distances, couch width is assumed to be 53 cm, and body center is assumed to be aligned with couch center. If the structure set contains couch structures, or patient support and fixation structures, all of them are taken into account (more information: *Eclipse Photon and Electron Algorithms Reference Guide*). If the distance from the treatment unit head model to the patient model or to the edge of the couch model is 7 cm or less, the tool displays a warning about the possibility of a collision in the lower left corner of the dialog box.

The distance to couch approximation is disabled if couch rotation exceeds 15 degrees.



Note: *The minimum distances the tool shows are approximations only. In addition, none of the accessories or slot mounts are taken into account. In consequence, it is possible that the tool does not detect all possible collisions. Therefore careful verification of the machine trajectory is necessary before starting the treatment.*

Fine-tuning the Initial Arc Geometry

You can fine-tune the field geometry by using the tools on the Fine-tune Fields tab of the Arc Geometry Tool.

For plans with multiple isocenters you can adjust the collimator fitting to the target isocenter by isocenter in order to avoid unnecessarily large openings. In other words, you can enlarge the area covered by one of the fields and make smaller the area covered by the adjoining field. This is useful in cases when fitting the whole target would lead to an unnecessarily large opening. These adjustments are done by using the VOI (Volume of Interest) tool.

You can display the VOI tool in the 2D views. If you are applying a setup with multiple isocenters, the isocenter of the field is set at the center of the VOI. You can adjust the size of the VOI and the location of the isocenter in the 2D views by dragging the moving handles of the VOI, and rotate it by dragging its rotation handle.

On the Fine-tune fields tab you can also specify a target margin for fitting the collimator, and let the Arc Geometry Tool adjust the isocenter position in X, Y and Z directions while fitting the collimator. You can also let the tool fit the collimator to the target without adjusting the isocenter position.

The approximated minimum distances from the treatment unit head model to the couch model and to the patient model are also displayed in the Fine-tune Fields tab.

Fine-tune the Arc Field Geometry Adjustment

1. In the **Planning > Arc Geometry Tool** dialog box, select the **Fine-tune Fields** tab.
2. For plans with multiple isocenters, you can use the VOI tool to specify how target is fitted in several parts:
 - Select the isocenters and fields you want to adjust in the **Show VOI in 2D views** text box.
 - In the image views, drag the moving handle of the VOI tool to adjust its size and location, or drag the rotation handle to rotate the VOI.
 - Adjust each VOI you are displaying in the same way.
3. Define the target margin (in cm) to be used for fitting the collimator.
4. To keep or modify the isocenter positions you adjusted with the VOI:
 - Select the **Adjust isocenter while fitting** in check box and then select the **X, Y or Z direction** check box to adjust the isocenter position in that direction.
 - If you do not want to change the isocenter position in a direction, clear the corresponding check box.
5. Click **Fit Collimator to Target**.
6. Verify the coverage displayed in the image views and in the Modulation Potential graph.



Note: The tool shows a warning text at the bottom of the dialog box if parts of the target are not irradiated at all, if parts of the target are irradiated with an open field (collimator X opening is larger than 30 cm), if the collimator X opening in a single field plan is larger than 20 cm, or if there is a risk of collision.

7. Click **Close** to close the tool.

You can now continue to VMAT optimization.

View the Progress of VMAT Optimization

During VMAT optimization, you can do the following in the Optimization dialog box:

- To show or hide structures in the DVH, click **Show or Hide Structures** and select **Show All Structures**, **Hide All Structures** or **Show All Structures with Objectives**.
- To view the relative cost of the objectives, go to the DVH view and move the mouse cursor on top of an objective. The relative cost is shown as a highlighted circle around the objective. The bigger the circle, the more cost the objective has in the optimization. The relative costs of the objectives are also shown as a objective function chart and bar chart below the 2D image view.

- To modify the objectives, type new values for each objective or change the values graphically.
- To move between the multiresolution levels, do the following:
 - To stay on the current level, click the  button. To continue the optimization, click the button again. The **Hold** text is displayed in the optimization progress pane when the button is down.
 - To return to the previous level, click the  button. The **Previous Level** text is displayed in the optimization progress pane until the resolution level changes.
 - To jump to the next level, click the  button. The **Next Level** text is displayed in the optimization progress pane until the resolution level changes.
 - To get the current optimization results and end the optimization process, click the  button until you reach the last level, and then click **OK**.

Intermediate Dose Calculation in VMAT Optimization

To improve optimization results, you can define that the program calculates an intermediate dose during the VMAT optimization. This is useful especially for heterogeneous targets, such as lungs. The intermediate dose is calculated by using the same dose calculation algorithm that is used in the final dose calculation.

You can start the optimization, let the program calculate an intermediate dose, and then use the calculated dose as guidance when continuing the optimization. The program adjusts the leaf sequences accordingly. As a result, the DVHs produced during optimization and final dose calculation become more uniform.

In addition, when you start re-optimizing a plan that already has a dose distribution, you can define that the program uses the existing dose as an intermediate dose during the optimization.

More information on the Photon Optimization algorithm and the Progressive Resolution Optimizer algorithm versions that support intermediate dose calculation: *Eclipse Photon and Electron Algorithms Reference Guide*.

Dose Calculation in VMAT Plans

Dose calculation is performed based on the MLC control points. For each control point, the fluence used in the dose calculation accounts for leaf motion based on the neighboring control points.

The dose calculation can also be started automatically at the end of the VMAT optimization, if desired. Field weights produced by VMAT optimization are used to achieve the wanted dose level in plan, and also to set the relative weight of each field of a multi-field plan. The calculation results can be saved automatically after the dose calculation has finished.

Configuring Operating Limits for VMAT Plans

To create optimal VMAT plans, it is important that you set the correct operating limits for the treatment unit in use. You can do this in RT Administration (Radiation and Imaging Devices > Operating Limits tab). The most essential operating limits are for gantry speed, leaf speed, and collimator speed. Violating the limits might cause the treatment time to double.

Table 16 Operating Limits for VMAT Plans

Treatment Unit	Operating Limit	Suggested Value
Varian C-Series Clinac	Gantry rotation	Motion mode: Dynamic Max Speed: 6 degrees/second
	Max MLC leaf speed ¹	2.5 cm/second
	Collimator X1	Max Speed: 2.5 cm/second
	Collimator X2	Max Speed: 2.5 cm/second
	Collimator Y1	Max Speed: 2.5 cm/second
	Collimator Y2	Max Speed: 2.5 cm/second
		Motion mode for all collimators: Dynamic
	Gantry rotation	Motion mode: Dynamic Max Speed: 6 degrees/second
	Max MLC leaf speed ¹	2.5 cm/second
	Collimator X1	Max Speed: 2.5 cm/second
	Collimator X2	Max Speed: 2.5 cm/second
	Collimator Y1	Max Speed: 2.5 cm/second
	Collimator Y2	Max Speed: 2.5 cm/second
		Motion mode for all collimators: Dynamic

Treatment Unit	Operating Limit	Suggested Value
Elekta SL20, Elekta Synergy (non-interdigiting MLCi or MLCi2)	Gantry rotation	Motion mode: Dynamic Max Speed: 6 degrees/second
	Max MLC leaf speed ¹	2.4 cm/second
	Collimator X1	Motion mode: Pseudo
	Collimator X2	Motion mode: Pseudo
	Collimator Y1	Motion mode: Dynamic. Max speed 1.6 cm/second.
	Collimator Y2	Motion mode: Dynamic. Max speed 1.6 cm/second.
Elekta Agility MLC 160 (interdigitizing)	Gantry rotation	Motion mode: Dynamic Max Speed: 6 degrees/second
	Max MLC leaf speed ¹	3.5 cm/second
	Collimator X1	Motion mode: Static
	Collimator X2	Motion mode: Static
	Collimator Y1	Motion mode: Dynamic. Max speed 9 cm/second.
	Collimator Y2	Motion mode: Dynamic. Max speed 9 cm/second.
Elekta BM	Gantry rotation	Motion mode: Dynamic Max Speed: 6 degrees/second
	Max MLC leaf speed ¹	2.4 cm/second
	Collimator X1	Motion mode: Static
	Collimator X2	Motion mode: Static
	Collimator Y1	Motion mode: Static
	Collimator Y2	Motion mode: Static

Treatment Unit	Operating Limit	Suggested Value
Siemens	Gantry rotation	Motion mode: Dynamic Max Speed: 6 degrees/second
	Max MLC leaf speed ¹	4.0 cm/second
	Collimator X1	Motion mode: Pseudo
	Collimator X2	Motion mode: Pseudo
	Collimator Y1	Motion mode: MultipleStaticPositions. Max Speed: 2.0 cm/second
	Collimator Y2	Motion mode: MultipleStaticPositions. Max Speed: 2.0 cm/second
		Motion mode for Field X must be set to Pseudo.

1. Maximum leaf speed for the MLC is defined in the MLC Configuration Properties dialog box in RT Administration.

The maximum gantry speed has an effect on how the application calculates the treatment time for a field, and how the control point specific information is shown in the Control Points tab of the Field Properties dialog box. In addition, parts of plan validation are based on this value.

If no gantry speed is defined in RT Administration, 4.8 degrees/second is used as default. For Varian TrueBeam treatment machines, this value will cause the treatment time to be overestimated, and it will also result in inaccuracies in both plan validation and in the displayed control point specific information.

Specifics of Arc Fields in VMAT Plans

VMAT optimization can optimize arc lengths between 30–359.8 degrees. The start and stop angles of an arc field must not be in the gantry rotation extended range. If the start or stop angles are in the extended range, they will automatically be changed to be within 0.1 degree from 180 degree IEC 61217. For example, if a counterclockwise (CCW) arc field is set with start angle of 181E degree and stop angle of 182 degree (IEC 61217), the start angle will be changed to 179.9 degree in order to move it out of the extended range. The stop angle remains as 182 degree because it is not in the extended area. You can also use non-zero couch rotation for VMAT fields.

To run VMAT optimization, it is recommended to keep the width of the field as small as possible, and not to exceed a leaf span of 14.5 cm. If you are using the PRO algorithm version 8.9 or earlier, and you are optimizing a plan that contains several arc fields, the maximum total arc length is 1500 degrees for the field size of 15 × 15 cm. For PRO algorithm version 10.0 or later there is no limit for maximum total arc length.

Defining the Angular Resolution in Arc Field Calculations

Some treatment units capable of Conformal Arc and VMAT treatments can support a very high number of control points defining these treatment fields. Typically, the dose calculation for such arc fields is performed individually for each of the machine control points. The results from the individual control points are then summed to generate the total dose distribution for the field. However, using a high number of control points can slow down the dose calculation process significantly.

To address this in the application, you can specify a fixed angular resolution to be used in all arc field calculations (standard arc, conformal arc, VMAT). The allowed range for the angular resolution that you can define is 1–5 degrees. The application integrates the existing machine control points into beams placed along the arc at the defined interval. When creating the beams, new control points are interpolated between machine control points to improve dose calculation accuracy. The machine control points are not modified in the process.

The angular resolution for all arc field calculations (standard arc, conformal arc, VMAT) is defined in Workstation Configuration (Settings for Distributed Calculation Framework tab). The global settings are clinic-wide, and they affect all workstations that are connected to the same database. They can be overridden by the local DCF settings. The angular resolution that was used in the calculation is shown in the calculation log, which is located in Field Properties (Calculation tab).

For more information on global and local DCF settings: *Beam Configuration Reference Guide*.

Define the Angular Resolution in Arc Field Calculations

1. Choose Tools > Workstation Configuration.
2. Select the **Settings for Distributed Calculation Framework** tab.
3. Do one of the following:
 - Select **Edit local DCF settings** if you want to override the global Angular resolution setting.
 - Select **Edit global DCF settings** to modify the global setting.

4. Select **Calculation** and do one of the following:
- Select the angular resolution to be used in the **Angular resolution in conformal arc and VMAT calculations** drop-down list. In addition to conformal arc and VMAT fields, this option applies also to standard arc fields.
 - Select **OFF**:
 - For conformal arc and VMAT fields, the beams are positioned at machine control points for calculating the dose.
 - For standard arc fields, the angular resolution is 5 degrees.



Note: For Siemens mARC fields, the angular resolution setting is ignored. Dose calculation uses one beam direction per arclet.



Note: The global settings are clinic-wide, they affect all workstations that are connected to the same database. They can be overridden by the local DCF settings.

5. Click **OK**.

Photon Optimization Parameters

For photon plans, you define the optimization objectives for each significant organ. For the target structures, you define upper and lower objectives. For other critical structures, you only define upper objectives. In addition, you can define a mean dose objective that should not be exceeded (If you optimize an IMRT plan with DVO algorithm, the mean dose objective is not supported). The mean objective is used to decrease the dose that a structure receives. You can also use the Normal Tissue Objective, and gEUD objectives (supported by the PO algorithm). More details on the parameters: *Eclipse Photon and Electron Algorithms Reference Guide*.

Structure Model in Optimization

This information applies to photon optimization using the PO algorithm in External Beam Planning.

The Photon Optimization (PO) algorithm uses a new structure model, where structures, DVH calculation and dose sampling are defined spatially by using one single matrix over the image. More information: *Eclipse Photon and Electron Algorithms Reference Guide*

Related Topics

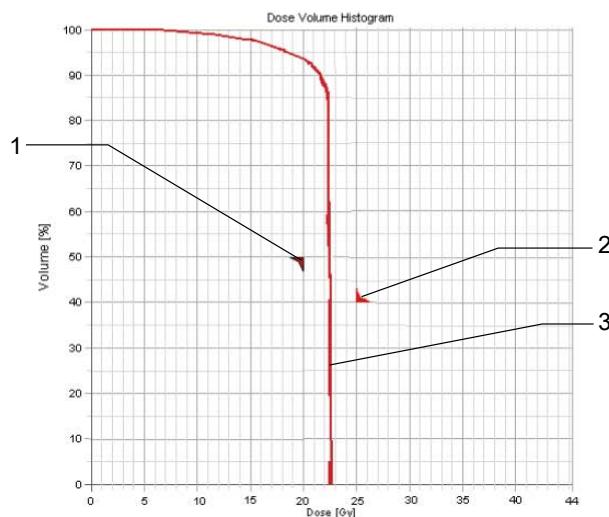
[Couch Modeling in Eclipse](#) on page 122

Upper and Lower Dose-Volume Objective in Optimization

This information applies to photon optimization using the PO, DVO and PRO algorithms in External Beam Planning.

- Upper objective—Is used to limit the dose in a given structure (for example, “no more than 20% of the structure may receive more than 25 Gy”).
- Lower objective—Is used to define desired dose levels in target structures (for example, “at least 70% of the structure must receive at least 20 Gy”).

The figure shows an example of an upper and a lower objective, plus a resulting DVH curve in an optimization dialog box.



1. At least 50% of the structure must receive at least 20 Gy.
2. No more than 40% of the structure may receive more than 25 Gy.
3. Possible DVH curve resulting from the objectives.

Figure 66 Upper and Lower Optimization Objectives

Generalized Equivalent Uniform Dose (gEUD)

This information applies to photon optimization using the PO algorithm in External Beam Planning.

The PO algorithm supports biological optimization objectives, which are based on generalized Equivalent Uniform Dose (gEUD). The gEUD is the uniform dose distribution that gives a biological effect equivalent to that of a given heterogeneous dose distribution. When using gEUD objectives, you need to define a value for a biological parameter a , which is a tissue-specific parameter that describes the volume effect of the gEUD. In other words, the a value defines on which part of the DVH curve the optimization focuses.

The parameter a value is negative for target structures and positive for OAR structures. The range is -40 to $+40$. If negative values are used, optimization focuses on the low-dose area, thus acting in a similar manner to a regular DVH-based lower objective. If positive values are used, optimization focuses on the high-dose area, trying to reduce the maximum dose of a structure. If parameter a value equals one, optimization aims at controlling the mean dose of a structure.

Optimization with gEUD objectives may steer the optimization to dose distribution that is potentially more directly related to the treatment outcome than dose distribution optimized with DVH-based objectives alone. Additionally, gEUD-based objectives may be less dependent on the variability of patient geometries, thus limiting the trial-and-error process necessary to plan complex cases with many structures. Because gEUD is based on observations of the biological response, the clinical relevance and validity of the gEUD directly corresponds to the quality of the referenced clinical data for parameter a .

Three types of gEUD objectives exist:

- **Upper gEUD**

Upper gEUD defines the maximum Equivalent Uniform Dose value that a structure (target structure or OAR) may receive.

- **Lower gEUD**

The lower gEUD objective defines the minimum Equivalent Uniform Dose value that a target structure must receive. The effect that a lower gEUD has on a structure is similar to a regular DVH-based lower objective.

- **Target gEUD**

Target gEUD defines the exact Equivalent Uniform Dose value that a target structure must receive. Target gEUD penalizes any deviations from the defined equivalent dose value.

Related Topics

[Tips for Using gEUD in Optimization](#) on page 229

Tips for Using gEUD in Optimization

This information applies to photon optimization using the PO algorithm in External Beam Planning.

Consider the following when using gEUD objectives in optimization:

- gEUD objectives are typically used for OARs, in conjunction with lower and upper DVH-based objectives for the target volumes.
- You can use gEUD for limiting the maximum dose for an OAR (instead of several DVH-based objectives with different priorities), but use a regular DVH-based objective for clinically relevant cut points.
- When using gEUD objectives for target volumes (typically target gEUD, lower gEUD, or both), make sure to control the heterogeneity of target dose. Consider using additional DVH-based objectives for the target volumes. Using only gEUD objectives on the target volumes may result in highly non-uniform dose distributions.
- If target structures overlap, use Lower gEUD instead of Target gEUD.

You might consider using the following initial values if you are new to gEUD-based objectives:

- Lower gEUD, $a \leq -10$: for target structures.
- Upper gEUD, $a = 1$: for parallel responding critical organs, such as parotid gland, liver, lung, and kidney.
- Upper gEUD, $a \geq 8$: for serial responding critical organs, such as rectum, spinal cord, brainstem, or optic nerves.

For more information on parallel and serial complications, refer to literature.¹

Always evaluate the plans based on established DVH-based criteria and the review of 3D dose distribution. For more information on gEUD and parameter a , refer to literature.²

Related Topics

[Generalized Equivalent Uniform Dose \(gEUD\)](#) on page 227

¹ "Use of Normal Tissue Complication Probability models in the clinic" Int. J. Radiation Oncology Biol. Phys., Vol. 76, No. 3, Supplement, pg. S10–S19, 2010.

² TG-166: "The use and QA of biologically related models for treatment planning: Short report of the TG-166 of the therapy physics committee of the AAPM" Med. Phys. 39 (3), pg. 1386-1409, March 2012. Chapter VI provides guidelines for using parameter a for OARs. Table VIII contains example values per structure used in the calculation of gEUD values (Gy) in sample plans.

Normal Tissue Objective in Photon Optimization

This information applies to photon optimization using the PO, DVO and PRO algorithms in External Beam Planning.

You can use the Normal Tissue Objective:

- to take into account the decrease in dose level as the distance from targets is increased
- to limit the dose level and prevent hot spots in healthy tissue
- for obtaining a sharp dose gradient around the targets

The Normal Tissue Objective is defined with the following parameters:

- Distance from target border—The distance from the target border where evaluation of the normal tissue dose begins, expressed in centimeters. For example, if the distance from the target border is defined as 0.3, the evaluation of the dose in normal tissue will begin at 3 mm from the target border.
- Start dose—The relative dose level in the Normal Tissue Objective at the target border, expressed in percentage of the upper objective for the target. If there are more than one upper objective defined for a target, the upper objective with the lowest dose value is used.
- End dose—The relative dose level in the Normal Tissue Objective away from the target border, expressed in percentage.
- Fall-off—The steepness of the Normal Tissue Objective fall-off.
- Priority—The relative importance of the Normal Tissue Objective in relation to other optimization objectives. The parameter is similar to that in the dose volume objectives. To apply the Normal Tissue Objective in the optimization, the parameter must have a non-zero value.

The shape of the Normal Tissue Objective is calculated as a function of the distance from the target border. The figure shows an example shape for the Normal Tissue Objective curve and the parameter values used for calculating the curve (distance from target border = 1 cm, start dose = 105%, end dose = 60%, and fall-off = 0.05). The X-axis shows the distance from target border, and the Y-axis shows the relative dose scale.

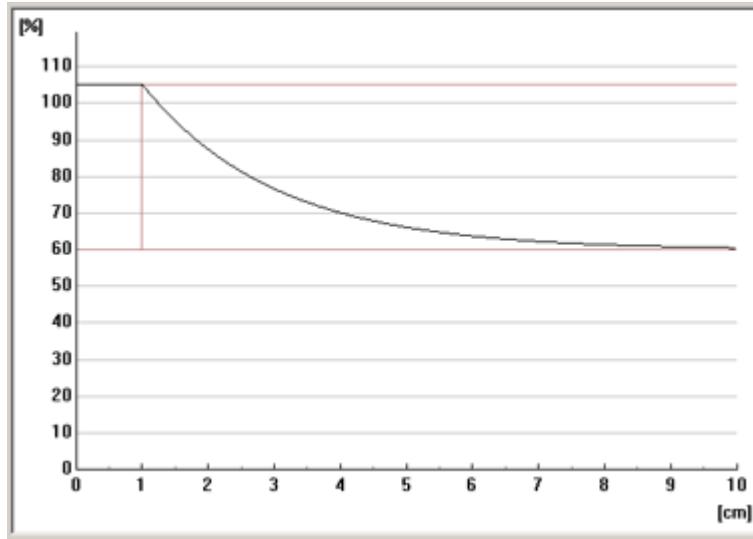


Figure 67 Example Shape of Normal Tissue Objective

The Normal Tissue Objective is normalized by taking level 1.0 (or 100%) to correspond to the lowest upper objective of the target. If the target has no upper objective, level 1.0 (or 100%) corresponds to a value 1.05 times the highest lower objective.

The Normal Tissue Objective values are calculated for all body points. If the plan contains several targets, the Normal Tissue Objective value for a specific point in the body is calculated from all targets, and the highest dose reported to that particular point is the value accepted by the NTO and used in optimization.

If you modify the priorities of the target, it is also important to increase the priority of the NTO appropriately.

Automatic NTO

Automatic Normal Tissue Objective is available in the following cases:

- VMAT optimization.
- IMRt optimization with the PO algorithm.

The automatic NTO has a separate, internal set of parameters that depend on the distance from the target. When it is used, the default normal tissue objective parameters, except the Priority parameter, are not used. The automatic NTO adapts to the patient anatomy and the optimization objectives, and automatically determines the dose fall-off criteria.

Optimization Parameters Specific to IMRT Optimization

This information applies to photon optimization using the PO and DVO algorithms in External Beam Planning.

For each optimization procedure, you define:

- **Maximum Optimization Time**, after which the optimization stops even if the maximum number of iterations is not reached.
- **Maximum Iterations**, at which point the optimization process is terminated. The optimization stops when it has computed the maximum number of iterations.

Optimization Parameters for the MLC Device

This information applies to photon optimization using the PO, DVO and PRO algorithms in External Beam Planning.

Table 17 Optimization Parameters for the MLC Device

MLC Parameter	Optimization Method	Optimization Algorithm	Description
MLC	IMRT	PO, DVO	Defines which of the MLC devices configured to the system is to be used in the treatment.
Optimization method	IMRT	DVO	Defines how the optimization should be performed.
X smooth and Y smooth	IMRT	PO, DVO	Reduces the degree of the beam intensity modulation.
Minimize dose	IMRT	DVO	Reduces hot spots in cases when a particular beam is delivering excessive dose.
Fixed jaws	IMRT	PO, DVO	Defines the use of fixed collimator jaws in the treatment.
Mean dose objective	IMRT, VMAT	PO, PRO	Defines the mean dose in Gy that should not be exceeded for a structure.
MU Objective	VMAT	PO, PRO	Increases MU values to add modulation in the optimization process, or keeps MU values as low as possible.
Jaw Tracking	VMAT	PO, PRO	Enables jaw tracking for VMAT optimization when using a treatment unit with jaw tracking available. Jaw tracking keeps the collimator jaws as close to the MLC aperture as possible to minimize leakage between the MLC leaves.

MLC Parameter	Optimization Method	Optimization Algorithm	Description
Avoidance Sectors	VMAT	PO, PRO	Avoidance sectors are ranges of gantry rotation where no MU are delivered. In the avoidance sectors the beam is turned off.

Optimization Method

The Optimization method parameter defines how the optimization should be performed. The values are the following:

- **Beamlet**—Produces optimal fluences for fields. Available for open photon fields only, no field accessories allowed.
- **Field weight**—Optimizes the field weights only, no fluences are created. Available for open fields and fields containing blocks or static MLCs.



Note: For the Field weight method, you must select PBC as the volume dose calculation algorithm before optimization. After optimization, you can calculate the volume dose using some other volume dose calculation algorithm, if needed.

- **None**—Ignores the field in the optimization. The possible dose contribution from these fields is not accounted for during the optimization. The given optimization dose prescription does not take these fields into account.

X Smooth and Y Smooth

The X Smooth and Y Smooth parameter reduces the degree of the beam intensity modulation.

It is not recommended to adjust the smoothing parameters without a good understanding of the effects of smoothing on the optimization results. The X smooth and Y smooth parameters control the fluence profiles by keeping them simple and easily treatable with the DMLC device. Remove drastic changes in adjacent fluence transmission values. A higher value smoothes more than a low value. Typically, the fluence should be smoother in the X-direction to ensure the minimal MU factor for the LMC. The X smooth and Y smooth are also priority values and related to the priority values of structures. For instance, when you increase the priority values but do not change the smoothing parameters, the resulting smoothing strengths will be lower. Smoothing in the Y-direction helps minimize tongue-and-groove effects. Smoothing in the X-direction has an effect on MU and the high frequency noise in the fluence.

You can define the default values in Beam Configuration by defining the calculation defaults for the optimizer algorithm.

More information: *Beam Configuration Reference Guide*.

Minimize Dose

The Minimize Dose parameter reduces hot spots in cases when a particular beam is delivering excessive dose. A high value minimizes the dose more than a low value. This is useful for reducing hot spots in normal tissue.

You can define the default values in Beam Configuration by defining the calculation defaults for the optimizer algorithm.

More information: *Beam Configuration Reference Guide*.

Fixed Jaws

By default, the optimization fits the collimator jaws to conform to all structures marked as targets. The Fixed Jaws parameter defines the use of fixed collimator jaws in the treatment. In this option, the collimator jaw positions of the field defined in the application are not changed during the optimization. Using fixed jaws may be useful in the case of:

- A multiple target plan, where one field is required to irradiate only one of the targets.
- Irradiating a large target with two smaller and separate fields instead of one large field divided to multiple carriage groups by the LMC. This allows effective positioning of the overlapping “sub-field” area.
- A match line defined along one collimator jaw (for example, in a breast case) which should be retained until the final treatment.

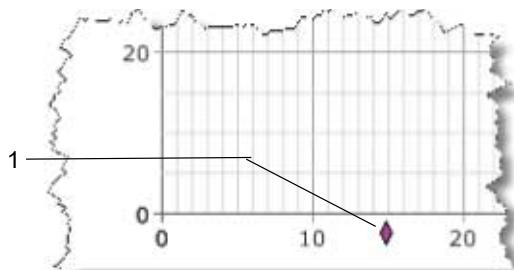
You can also define how you wish to view the field fluence in the Optimization dialog box during the optimization process. The fluence is updated after each iteration. The visualization of the fluence can be smoothed out, and it can be shown in colorwash or greyscale. The fluence pattern has a strong correlation with the BEV of each field.

Mean Dose Objective

The Mean Dose objective defines the mean dose that should not be exceeded for a structure. It defines the dose in Gy, but does not define the percentage of the structure. Mean dose objective is visualized in DVH during optimization, and it can be adjusted interactively during optimization.

Mean dose objective cannot be used to increase the dose to a structure.

- PRO: One mean dose objective per structure is possible
- PO: Multiple mean dose objectives per structure are possible



1. Mean Dose Indicator.

Figure 68 Mean Dose Objective

MU Objective

You can use the MU objective to increase MU, which tends to add modulation in the optimization process, or to ensure that the MU are kept as low as possible, if clinically required. In plans containing several arc fields, the MU objective refers to the total MU of all fields.

When using the MU objective, you need to define the strength, and the minimum and maximum MU values for the objective.

The strength value must be defined between 0–100. The value 50 is considered as medium strength. The strength value is not a priority, and it is not relative to the other priorities in the optimization. The strength value tells the system how quickly to converge to a solution and provide the MU value you have defined.

The range of minimum and maximum MU values for the MU objective are the following:

- PO: 0–4000
- PRO: 0–100 000

Jaw Tracking

The Jaw Tracking parameter enables jaw tracking for VMAT optimization when using a treatment unit with jaw tracking available. Jaw tracking keeps the collimator jaws as close to the MLC aperture as possible to minimize leakage between the MLC leaves. When jaw tracking is in use, algorithm uses the initial jaw settings as the maximum positions for the jaws.

More details on jaw tracking: *Eclipse Photon and Electron Algorithms Reference Guide*.

Jaw tracking is turned on as follows:

- PO: Optimization dialog box, **Plan Information** drawer.
- PRO: VMAT Optimization dialog box.

Even though a treatment unit supports VMAT, it may not support jaw tracking. You can turn on jaw tracking only if the treatment unit supports it, and jaw tracking has been enabled in RT Administration.

- PRO algorithm: Enable jaw tracking in **Radiation and Imaging Devices, Operating Limits** tab, **Field X (Motion Mode)** set as **Dynamic** and collimator speed defined in the **Max Speed** field).
- PO algorithm: Enable jaw tracking in RT Administration by defining the motion modes and speed limits for each collimator (IEC X1, X2, Y1, Y2). Collimator motion modes override the Field X setting used earlier for jaw tracking.

Avoidance Sectors

Avoidance sectors are ranges of gantry rotation where no MU are delivered. In the avoidance sectors the beam is turned off. You can define up to two avoidance sectors per arc field. The minimum length for an avoidance sector is 15 degrees. Similarly, the minimum length for the beam-on sector between two avoidance sectors, or between gantry start/stop angles and an avoidance sector is 15 degrees. You can use avoidance sectors, for example, to avoid dose delivery through any patient support device or prosthesis. You can also use avoidance sectors to exclude a body part from a plan. This may be necessary, for example, if the arm of a patient did not fit in the image.

Avoidance sectors are defined as follows:

- PO: Optimization dialog box, **Plan Information** drawer.
- PRO: VMAT Optimization dialog box.

It is not possible to add or modify an avoidance sector once the optimization process is started. The defined avoidance sectors are saved with the plan, and the existing avoidance sectors are used automatically when the optimization is restarted for the plan. However, the defined avoidance sectors are not exported with the plan.

Avoidance sectors are supported only for the following treatment units:

- Varian treatment units
- Siemens Artiste and Oncor treatment units equipped with Siemens MLC 160

More information on the PRO and PO algorithms: *Eclipse Photon and Electron Algorithms Reference Guide*.

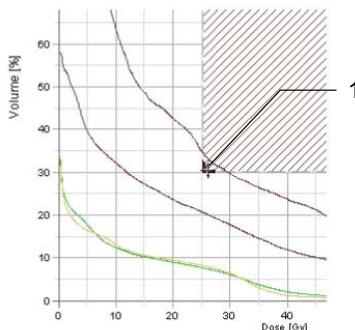
When using avoidance sectors, the optimization results may sometimes get worse as the optimization progresses. This may happen if the avoidance sectors occupy too large a portion of the arc, in which situation the gantry acceleration limits imposed during the optimization may prevent the optimizer from using sufficiently high MU/deg values to deliver the required dose. This may take place most commonly when using a single arc with two avoidance sectors and a large dose per fraction. If this happens, try separating the arc field into two separate arc fields so that it is not necessary to use two avoidance sectors in the same field.

Define Dose Objectives in IMRT and VMAT Optimization

This information applies to photon optimization using the PO, DVO and PRO algorithms. Dose objectives are defined in the Optimization dialog box.

1. To define the upper dose-volume objective, select a structure and click **Add Upper Objective**.

Type the value in the appropriate cell in the structure list or drag the arrow that appears in the DVH diagram.



1. Point at an objective and drag it to change the objective values.



Note: Indicate all desired dose objectives as unfractionated total doses.

2. If the selected structure is a target structure, click **Add Lower Objective** to define the lower dose-volume objective.

Type the value in the appropriate cell in the structure list or drag the arrow that appears in the DVH diagram. You can adjust the objectives during the optimization in the same way, either graphically or numerically.

3. **VMAT optimization only:** If you want to limit the mean dose that a structure gets, click **Add Mean Objective**.

Type the value in the appropriate cell in the structure list or drag the diamond that appears below the X-axis in the DVH diagram.

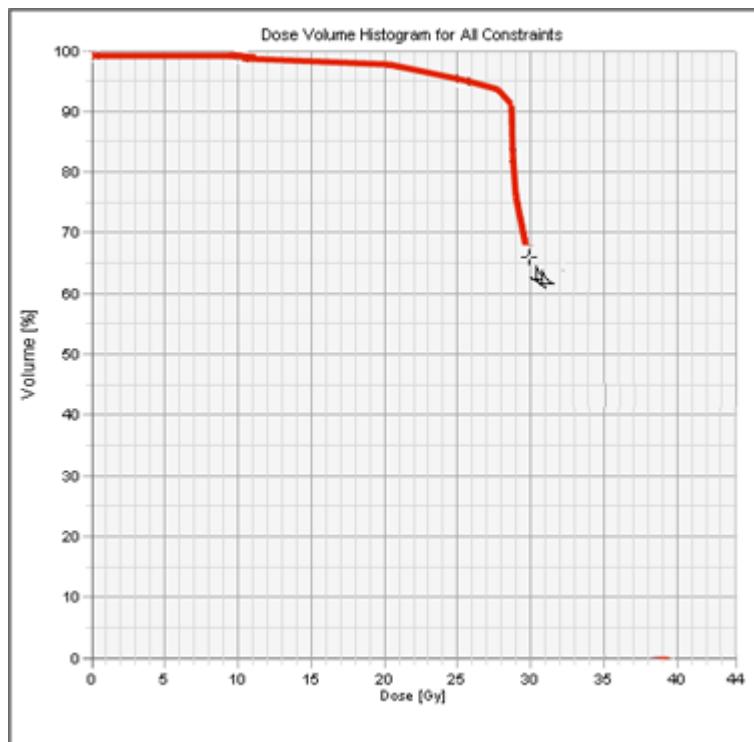


Note: Mean dose objective is also supported for IMRT plans if you optimize them with the PO algorithm.

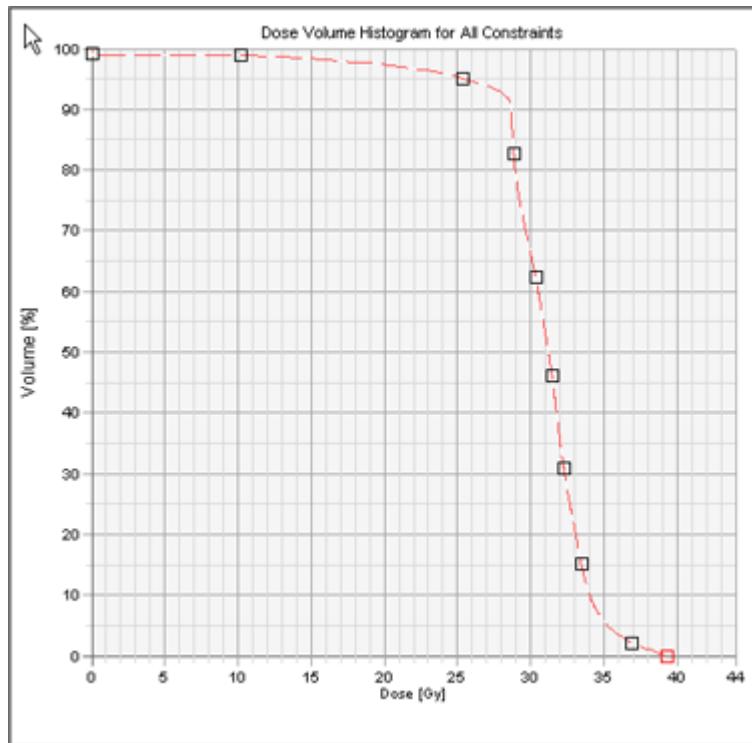
4. To draw a line to limit the dose, click **Draw Line** and draw the line in the DVH box.



Note: You cannot add line objectives by drawing them in the new Optimization dialog, but they can be included in and added from a DVH estimation model or from an objective template.



When using the DVO algorithm for optimization, the line objectives show small squares along the line. They are handles to change the line shape. The handles are not used in optimization with the PO algorithm. The objective values are shown in the Structures and Objectives list. Only the Priority value can be modified.



5. To delete objectives, do one of the following:

- *PO algorithm only:* Click the **x** button on the objective row in the objectives list.
- *DVO algorithm only:* To delete individual objectives, select the objective and click **Delete**; to delete multiple objectives, ensure that the **Select objectives** tool is active, draw a rectangle that covers the objectives to be deleted and click **Delete**.

Objective Templates in Photon Optimization

You can store customized objectives in templates to establish a starting point for optimization or to define a set of typical optimization solutions at your clinic, such as objective sets for prostate or nasopharynx cases.

You can create an objective template from dose-volume objective sets and gEUD objectives that have produced a satisfactory optimization result. The objective sets are saved in the template with user-defined names. Any set of objectives stored in an objective template can be re-used in subsequent inverse plans and included in clinical protocols.

If you use both optimization objectives from a template and manually added objectives in the same IMRT or VMAT plan, add the template objectives first, and then add the new manual objectives to avoid losing data.

Related Topics

[Objective Templates](#) on page 145

Base Dose for Optimization

In some cases, you need take into account a certain base dose for the optimization, for instance, in a boost treatment where the patient has already been treated up to a certain dose, and the treatment will be continued with some additional dosage. You can define the total dose and let the optimization create a plan that selectively increases the dose of the treated plan to the defined total dose.

The base dose plan can be any treatment plan, or a plan sum, with the following conditions:

- The plan or plan sum must have the same planning image as the current plan.
- The dose distribution must be calculated.
- The dose prescription must be defined.

If a plan sum is used as a base dose plan, the plan sum must meet the following additional conditions:

- The plan sum may not contain the plan that is currently under optimization.
- All the plan weights in the plan sum must be 1.0, and no minus operations are used in the sum.

Use a Base Dose in IMRT and VMAT Optimization

This procedure is an example of using base dose plans in optimization. The process is slightly different depending on whether you use the PO, DVO or PRO algorithm for optimization.

As a precondition, Plan 1 already exists, is calculated and its dose prescription is defined.

1. Create a new plan, Plan 2, to give additional dose to the dose prescription.
2. Choose **Planning > Optimization > Optimize**.
 - PO: Optimization dialog box opens.
 - DVO or PRO: IMRT Optimization or VMAT Optimization dialog box opens.
3. VMAT optimization with PRO algorithm: If prompted, select the MLC device to use and click **OK**.
4. Do one of the following:
 - PO: Open the **Base Dose Plan** expander and click **Select**.
 - PRO or DVO: Click **Select** next to the Base dose plan text box in the Optimization dialog box.
5. Select Plan 1 to be used as a base dose plan.
6. Define the final dose-volume objectives for the sum of the earlier plan, Plan 1 and the new Plan 2.
For example, if the dose prescription for Plan 1 is 50 Gy and for Plan 2 it is 20 Gy, optimization objectives for Plan 2 are for the total dose (70 Gy).
7. Click **OK**.
The optimization extracts the base dose from the total dose objectives when the dose objectives are evaluated, and returns the optimal fluence for Plan 2.
8. Calculate the dose distribution.

When you save Plan 2, Plan 1 will be saved as its base dose plan.

Evaluate the final dose distribution by summing up Plan 1 and Plan 2.



Tip: If you need to remove a base dose plan from Plan 2,

- PO: In the Base Dose Plan drawer, click **Clear Base Dose**.
- DVO: In the optimization dialog box, click **Select** next to the **Base dose plan** text box, and then click **Clear Base Dose Plan** in the Object Explorer.

Reconstructing a Partially Treated Plan

You can reconstruct partially treated IMRT or VMAT plans in Eclipse for assessing the dosimetric and clinical implications of partial treatments. In treatment reconstruction, you create a partial plan from a plan that contains dynamic MLCs. The partial plan contains the delivered portion of the original plan.

The partial plan is a verification plan. It is a copy of the original plan with the following exceptions:

- The actual fluences and existing dose distribution are removed

- The plan has only the delivered portion of control points
- The plan has only one fraction
- The dose will be calculated using the delivered number of MU

When creating a partial plan, you can choose to also create a second verification plan that has one fraction and full MU. This plan can be compared with the partial plan.

Partially treated Siemens mARC plans cannot be reconstructed.

Create a Partial Treatment Plan

1. Choose **Planning > Create Partial Treatment Plan**.
2. Modify the number of total MU, if necessary. By default, the MU value is the planned number of MU in the original plan.
3. For the new verification plan, do one of the following:
 - Define the start and end control points. For VMAT plans, the gantry start and end values change accordingly. For IMRT plans, the gantry start and end values are not displayed. The MU start and MU end values change accordingly.
 - Define the MU start and MU end values. By default, the MU end column displays the delivered MU value obtained from the treatment records. The CP start and CP end values, and the gantry start and end values change accordingly.
4. If desired, create a second verification plan with one fraction and full MU. This second verification plan can be used to compare the intended dose distribution to the partial treatment plan and assess the effect of the partial treatment.
5. Click **Finish**.

Continue by calculating the dose distributions and evaluating the created plans. Verification plans are automatically calculated using fixed MU.

Leaf Motion Calculation

The Leaf Motion Calculator (LMC) converts the optimal fluences into DMLC motion patterns. The LMC accounts for certain physical and mechanical characteristics of the DMLC device, such as leaf transmission value, leaf edge shape and motion limitations, which are not considered when producing the optimal fluences. The LMC program takes these limitations into account, and creates DMLC motions that reproduce the optimal fluence as closely as possible. The LMC supports the use of Varian, Elekta, and Siemens MLC devices.

Due to the characteristics of Varian's DMLC device controller, LMC divides large fields into multiple MLC carriage groups. Depending on the capacity of the treatment unit(s), the carriage groups in a field can be either saved to one field or divided each into a separate field.

The dose calculation algorithm uses the leaf motion patterns to calculate the actual field fluences. They may differ from the optimal fluences created by Eclipse IMRT, because the actual fluences accurately represent the fluence that will be delivered with the DMLC motions. The actual fluences are used in the dose calculation to ensure that the calculated and the delivered dose correspond to each other as closely as possible.

The calculated DMLC leaf motions can be exported to the treatment unit.

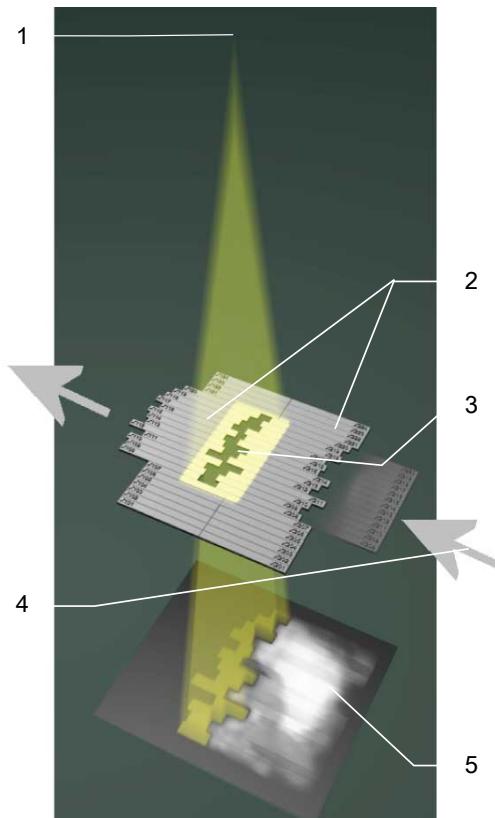
Supported Delivery Techniques in Leaf Motion Calculation

The field fluences are produced by varying the positions of the DMLC leaves during treatment. As a result, different portions of the field are exposed to a different amount of radiation. The total dose distribution is the integral of the dose distributions in all of the sub-fields or segments. Two different delivery techniques are supported: the sliding window technique and the multiple static segments (step-and-shoot) technique.

The default LMC technique to be used is configured in the Task Configuration dialog box. More information: *Eclipse Photon and Electron Algorithms Reference Guide*.

Sliding Window Technique

In the sliding window technique, the DMLC leaves move in the same direction across the beam during the beam-on. The size and shape of the aperture formed by the leaves change dynamically. As a result, different portions of the field are exposed to a different amount of radiation. The figure illustrates the sliding window technique of producing the field intensities.



1. Radiation source focus.
2. Moving DMLC leaves.
3. Changing aperture between the DMLC leaves.
4. The DMLC leaves move from right to left in this example.
5. Different field fluences produced by the DMLC.

Figure 69 Field Intensities Produced by DMLC with Sliding Window Technique

In this example, the DMLC leaves move in the direction indicated by the two arrows. The grayscale gradients in the field below the MLC leaves correspond to the amount of radiation received. The white areas are more exposed than the grey areas.

The sliding window technique is supported only for Varian MLC devices

Multiple Static Segments Technique

In the multiple static segments technique, often referred to as the “step-and-shoot” technique, the DMLC leaves do not move during beam-on. The delivery of each field is divided into segments. The beam is turned off and the leaf positions are changed between the delivery of each segment.

The multiple static segments technique is supported for both Varian and non-Varian MLC devices.

Fixed Jaws and Jaw Tracking

Eclipse IMRT will automatically resize the X and Y jaws to frame the completed irradiated area outline (CIAO) unless you choose to use fixed jaws, in which case the X and Y jaws are not changed by the LMC.

When planning a treatment to be performed on a machine with jaw tracking available, the X and Y jaws are set separately at each control point. In this case the Fixed Field Borders option acts as a bounding box. More information on the Fixed Field Borders option: *Eclipse Photon and Electron Algorithms Reference Guide*.

Converting Field Fluences to DMLC Leaf Motions

The optimal fluences calculated by IMRT optimization are converted into DMLC leaf motions. DMLCs are thin-leaf (vane) collimator systems used to shape fields and modulate field intensity in modern conformal radiation therapy. They are also used in electronic compensators.

The conversion of the optimal fluences into DMLC leaf motions is automatically started by running the Leaf Motion Calculator (LMC) when the IMRT optimization is completed. The program incorporates the physical characteristics of the DMLC device and the treatment method selected by the user. By using iterative calculation, the LMC determines realistic DMLC leaf motion patterns which best correspond to the optimal fluences.

You can also do the conversion separately, or later re-convert the fluences. This might be necessary if you make such changes to the IMRT plan that invalidate the dose and actual fluences (such as a change in the calculation model), which will require re-converting the fluences. These changes remove the MLCs and actual fluences from the plan, so you need to re-calculate the leaf motions and the dose.

The result of both the automatic and user-initiated conversion is saved to the database. DMLC leaf motion patterns can be viewed in the BEV.



Note: *The Varian DMLC system supports photon fields only.*



Note: DMLCs can also be used in place of conventional intensity modulation using physical compensating filters, such as wedges or compensators.



Note: If you use version 11.0 or later dose calculation algorithms, you must also use version 11.0 or later LMCs.



Note: If you change the prescription or normalization of an IMRT plan, it is advisable to run the Leaf Motion Calculator (LMC) again. This is because the original leaf motions with renormalized MUs may violate the operating limits of the treatment unit (maximum MLC leaf speed, and minimum MU limitation). Small changes in prescription or normalization (about 1-5 %) may not lead to the violation of the operating limits. However, if there are larger changes, always rerun the LMC and recalculate the dose. Before treatment, also verify the leaf sequences.

Convert Optimal Fluences into Leaf Motions (Varian and BrainLab MLCs)

This procedure applies to IMRT plans with Varian and BrainLab MLCs.

1. Do one of the following:
 - If you use automatic conversion, the leaf motion calculation starts automatically after you have optimized the field fluences in the **Optimization** dialog box.
 - If you want to do the conversion separately, choose **Planning > Dose Calculation > Calculate Leaf Motions**.
2. If prompted, select the LMC to use.

Note that the available LMCs depend on the dose calculation algorithm you are using.



Tip: You can modify the default LMC technique options for the plan by clicking **Edit Options** and then modifying the values in the Calculation Options dialog box. More information: Eclipse Photon and Electron Algorithms Reference Guide. The selected options are saved with the plan, and used each time you calculate leaf motions for this specific plan (instead of the Default LMC options defined in Task Configuration).

3. Select the beam delivery method for each field.

On the Delivery Method column, click on the row of each field, and do one of the following:

- To deliver the dose with a continuously moving DMLC aperture, select **Sliding Window**.
- To deliver the dose with multiple static DMLC segments, select **Multiple Static Segments**.
- To exclude a field from DMLC leaf motion calculation, select **None**. This option is useful, for example, if you need to re-calculate the leaf motions for a field after making some modifications, but you do not want to re-calculate the fields that have not been modified.



Tip: To select the same delivery type for all fields at the same time, click **Sliding Window** or **Multiple Static Segments**. To clear the selected delivery type from all fields, click **None**.

4. If you have Varian LMC, click the column on the All Fields row or on the row of each individual field, and do the following:

- In the **Intensity levels** column, define the number of intensity levels for the fields that have Multiple Static Segments as delivery method. The default value is determined in Task Configuration, or in the Calculation Options dialog (if you modified the values by clicking **Edit Options**). The intensity levels value is an indicatory value used in the leaf position calculation; the end result may not necessarily be exactly the same as the defined value.
- To keep the defined collimator jaw positions for a field, select the check box in the **Fixed Jaws** column.

5. If you have Smart LMC, click the column on the All Fields row or on the row of each individual field, and do the following:

- In the **Segments** column, define the number of static segments for the fields that have Multiple Static segments as delivery method, or the maximum number of control points for the fields that have Sliding Window as delivery method.
- To use fixed jaws for a field, select the check box in the **Fixed Field Borders** column for the field.
- To use jaw tracking on a treatment machine that supports the capability, select the check box in the **Jaw Tracking** column.

6. Click **OK**.

The LMC starts converting the field fluence into DMLC leaf motions. If the field is a large one, the LMC splits it into several carriage groups due to limitations of the MLC device.

Continue by verifying the DMLC motions.

Related Topics

[Verifying the DMLC Leaf Motions](#) on page 249

Convert Optimal Fluences into Leaf Motions (Siemens and Elekta MLCs)

This procedure applies to IMRT plans with Siemens and Elekta MLCs.

1. Do one of the following:
 - If you use automatic conversion, the leaf motion calculation starts automatically after you have optimized the field fluences in the **Optimization** dialog box.
 - If you want to do the conversion separately, choose **Planning > Calculate Leaf Motions**.
2. If prompted, select the LMC to use.

Note that the available LMCs depend on the dose calculation algorithm you are using.



Tip: You can modify the default LMC technique options for the plan by clicking **Edit Options** and then modifying the values in the Calculation Options dialog box. More information: *Eclipse Photon and Electron Algorithms Reference Guide*. The selected options are saved with the plan, and used each time you calculate leaf motions for this specific plan (instead of the Default LMC options defined in Task Configuration).

3. In the **Number of segments** column, define how many static field segments you wish to have created for each field if you do not want to use the default value.

The suggested value displayed in the Number of segments column is based on the default number of intensity levels value defined in the Default LMC tab (click **Edit**) in the Task Configuration dialog box (more information: *Eclipse Photon and Electron Algorithms Reference Guide*), or in the Calculation Options dialog box (if you modified the values by clicking **Edit Options**). The total number of intensity levels defined in Task Configuration is redistributed between fields based on their complexity: if there are multiple fields in a plan, the more complex fields get larger suggested values.

The Number of segments value is an indicatory value used in the leaf position calculation; the end result may not necessarily be exactly the same as the defined value.

4. Normally, you do not need to change the value in the **Number of iterations** text box, but you can change it if necessary. More information: *Eclipse Photon and Electron Algorithms Reference Guide*.

5. Click OK.

The LMC starts converting the field fluence into DMLC leaf motions. The progress indicator shows the objective function curve and numerical data of the calculation.

6. To stop the leaf motion calculation and to save the current calculation result as a sequence, click **Finish.**

Continue by verifying the DMLC motions.

Related Topics

[Verifying the DMLC Leaf Motions](#) on page 249

Verifying the DMLC Leaf Motions

You can verify the leaf motions of a fluence-based DMLC in the BEV.



CAUTION: Verify the maximum dose and its location inside the irradiated volume after the volumetric dose calculation.



WARNING: Always perform QA tests on a physics phantom to make sure that the plan is correctly transferred to the treatment machine. The delivered dose must correspond to the calculated dose.



Note: Verify the consistency of the DMLC and fluence using phantom or portal dosimetry testing to make sure that the DMLC will produce the actual fluence calculated by the dose calculation algorithm.



Note: Verify the plan with DVH analysis before transferring it to the treatment unit.



Note: Visually verify the shape of the initial DMLC before actual treatment.



Note: Evaluate the dose distribution visually.

View and Verify the DMLC Leaf Motions in the BEV

1. To show the desired field in the BEV, right-click in the BEV, choose **Set Beam's Eye View to** and then select the field.

The selected field is shown in the BEV. The Animate MLC Segments toolbar appears above the BEV.

2. To activate the DMLC leaves, go to the Focus window and select the MLC of the field shown in the BEV. (The MLC icon is shown below the fluence. If necessary, expand the tree structure by clicking the + sign next to the fluence icon.)

IMRT and VMAT Optimization Using DVO and PRO Algorithms

In some cases, you may want to use the DVO or PRO algorithms for optimization instead of PO.

To optimize an IMRT plan with the DVO algorithm, you must first select DVO in the Calculation Options. The IMRT Optimization dialog box is then used to define optimization settings instead of the new Optimization dialog box.

To optimize a VMAT plan with the PRO algorithm, you must first select PRO in the Calculation Options. The VMAT Optimization dialog box is then used to define optimization settings instead of the new Optimization dialog box.

Many of the optimization parameters and settings are the same as for the new PO algorithm. For more information on them, see the Related Topics list.



Note: *Different versions of the Progressive Resolution Optimizer algorithm have different capabilities. More information: Eclipse Photon and Electron Algorithms Reference Guide.*

Related Topics

[Photon Optimization Parameters](#) on page 226

[Base Dose for Optimization](#) on page 240

[Reconstructing a Partially Treated Plan](#) on page 241

Create an IMRT Plan (DVO Algorithm)

This information applies to IMRT plans optimized with the DVO algorithm.

1. Insert new plan.
2. Insert the fields in the plan one by one or use a template.

IMRT optimization is available for open (unwedged) photon fields only. The treatment unit used in the plan must be configured with a dose-enabled MLC. Fields that do not meet these requirements are disabled in the IMRT Optimization dialog box.

3. Choose **Planning > Optimization > Optimize**.

If the plan has been optimized earlier, you can choose to continue the previous optimization or start from the beginning. You can also select to use the calculated dose from the previous optimization as an intermediate dose.

4. To exclude structures from optimization, click **Exclude Structures** and select the structures to exclude.
5. Select structures for which to display the DVH and define the optimization objectives or load the objectives from an objective template.



Note: Indicate all desired doses as unfractionated total doses.

6. Modify the optimization object priority, if necessary. The priority determines the relative importance of the optimization object in relation to other optimization objects.
7. To minimize the dose received by organs outside the structures for which objectives have been defined, click **Define NTO Settings**, and define the Normal Tissue Objective parameters.
8. Define the calculation parameters:
 - **Max time (min):** Time after which Eclipse IMRT stops the iteration.
 - **Max iterations:** Number of iterations after which Eclipse IMRT stops the optimization process.
9. Select the MLC and smoothing parameters. Click the cells in the table and select a parameter in the list that appear at each cell. To avoid drastic changes in adjacent fluence transmission values, define the X Smooth or Y Smooth parameter.

For Field Weight optimization method, you must select PBC as the volume dose calculation algorithm before optimization. After optimization, you can calculate the volume dose using some other volume dose calculation algorithm, if needed.
10. Define how the field fluence is displayed.

11. Automate the optimization process, if so desired.

- To start leaf motion calculation and final dose calculation automatically after optimization, select the **Automatic optimization process** check box.
- To calculate an intermediate dose automatically during the optimization, select the **Automatic intermediate dose** check box. The program calculates an intermediate dose during the optimization, and uses it to improve the optimization results. If you want to return to manual intermediate dose calculation, clear the check box.



Note: If the automatic optimization process is on, intermediate dose calculation starts when there is no further change in the objective function. If the automatic optimization is off, intermediate dose calculation is initiated after the maximum time or maximum number of iterations is reached.

12. Click **Optimize**.

- You can change the dose objectives during the optimization.
- To manually calculate an intermediate dose, click **Calculate intermediate dose now**. You can do this several times during the optimization.
- To interrupt the optimization, click **Stop**.

13. When the calculation is finished:

- If you use automatic optimization, the program proceeds automatically to leaf motion calculation and final dose calculation.
- If you use manual optimization, click **OK**. You need to start the leaf motion calculation manually.

After optimization, evaluate the dose distribution visually. Verify the maximum dose and its location inside the irradiated target after dose calculation. Visually verify the shape of the initial DMLC before treating.

IMRT Optimization Dialog Box (DVO Algorithm)

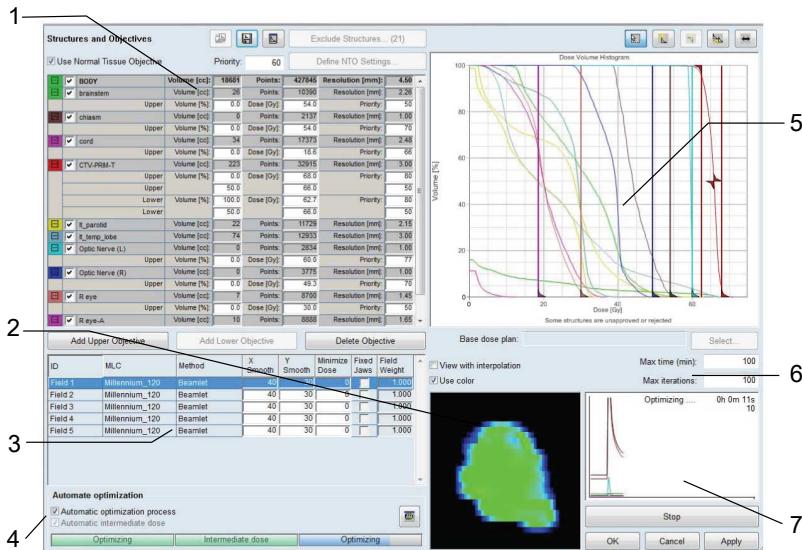
When using the DVO algorithm, plan optimization is controlled by the IMRT Optimization dialog box, where you define the objectives for the optimization. You can either define the optimization objectives for each plan separately, or use an objective template, which restores objectives defined earlier for other plans.

You can monitor the progress of the optimization process in the IMRT Optimization dialog box, which shows a DVH calculated for each structure after each iteration, the number of iterations and a fluence map for each field. Field weight values are shown for fields selected for field weight optimization. You can evaluate the effectiveness of the dose objectives and, if necessary, modify the objectives without stopping the optimization.

On the lower right corner of the IMRT Optimization dialog box, you can view the objective function as a line chart. It shows you the overall progress of the optimization, and how close to the target dose objectives the plan is.



Note: When the automatic optimization is on, the line chart not changing any more indicates that the optimization is about to end. If the automatic optimization is not turned on, the optimization continues until either the maximum time or maximum number of iterations limit is reached.



- Shows the structures contained in the plan, the volumes of the structures, the points and point resolution used for modeling the structures in the optimization, and the values of the defined objectives. Right-click to show or hide all structures, or only structures with objectives in the DVH.
- Shows the resulting field fluence.
- Shows the fields contained in the plan, the smoothing parameters and the optimization method for each field.
- Selection for automatic optimization and intermediate dose calculation, and an indicator of the overall progress of the IMRT optimization.
- Shows the optimization results in the form of a DVH. Allows graphical adjustment of dose-volume objectives.
- Shows the maximum time and iterations for the optimization process.
- Shows the objective function of the optimization as a line chart.

Figure 70 IMRT Optimization Dialog Box

The DVH is calculated and displayed in the DVH pane for each structure, and it shows how well the pre-calculated dose will conform to the set objectives. You can also modify the objectives in the DVH pane, as well as delete objectives. The DVH represents the dose for contoured volumes only. Always evaluate the dose distribution on each slice, noting hot and cold areas within the plan, especially in areas outside contoured structures.

Structure Model in Optimization (DVO and PRO Algorithms)

Structure Model in DVO and PRO

The Dose Volume Optimizer (DVO) and Progressive Resolution Optimizer (PRO) algorithms model structures in the optimization as three-dimensional point clouds. The respective optimization dialog box shows the number and resolution of the points in the point clouds. Initially, the number of points shown for each structure is only an estimate based on the structure volume and the point cloud resolution. After the point cloud generation, the number of points can differ significantly from the initial estimate. The point cloud generation algorithm places more points close to the structure's external surface to ensure proper representation of complex shapes. The resolution of the points is defined as the approximate distance between the points. The default values used for the resolution and number of points are chosen so that they provide adequate results without the need for changing the values:

- Structures greater than 5000 cm³ (typically the Body structure) have resolution of 4.5 mm.
- Structures 5000 cm³ or smaller have resolution between 1.0– 3.0 mm.
- The recommended minimum number of points in a structure is 2000.

If necessary, you can increase or decrease the number of points for each structure by changing the point resolution value. This affects the accuracy of the optimization, much like using different calculation grids in dose distribution calculation. However, too large a number of points in the point clouds slows down the optimization and may even prevent it completely because of higher memory consumption. If this happens, it is recommended to increase the point resolution value for structures of lesser importance in the optimization and start the optimization process again. It is also possible to exclude structures from optimization. Excluded structures are saved with the plan.



Note: Note the following:

- If you exclude structures in optimization, no point clouds are generated for the excluded structures.
- External patient support devices, such as the couch support structure, are not shown in the Structures and Objectives list in the optimization dialog box, and point clouds are not calculated for them. However, support structures are accounted for in the optimization.

Planning for Aperture Modulated Therapy (DVO Algorithm)

Aperture Modulated Radiation Therapy (AMAT) is a simple forward planning IMRT method in Eclipse where you first define the field apertures and then optimize the plan using the field weights, without the use of fluences or collimator jaw optimization. The method supports the use of multiple field apertures from the same direction. Field weights are simultaneously calculated for all fields. MLCs and blocks are allowed in the fields, but their shapes are not optimized.

Use Aperture Modulated Radiation Therapy (DVO Algorithm)

1. Start the optimization.
2. Define dose-volume objectives for the patient structures.
3. Click in the **Method** cells and in the drop-down list, select **Field Weight** for each field for which you wish to use the field weight optimization.
4. Click **Optimize**.
5. To finish, click **OK**.

Create a VMAT Plan (PRO Algorithm)

This information applies to VMAT plans optimized with the PRO algorithm.

VMAT plans are created using one static or arc field, or up to 10 arc fields as the input fields. If a static field is used, the system changes it to an arc field during the VMAT optimization process when the Arc Geometry Tool is opened. Any setup fields are ignored in VMAT optimization. The target structures must be defined before you start optimization. New targets cannot be added after the optimization has been started.

You can also continue the previous optimization of a plan containing fields that have either arc dynamic MLC or VMAT MLC. Previous optimizations are continued from the last multi-resolution level. Field geometry and jaw tracking are read from the previous optimization and cannot be changed. Avoidance sectors are also read from the previous optimization. However, if you need to adjust the avoidance sectors, it is recommended to start the optimization from the beginning.

1. Insert new plan.
2. Insert the fields one by one or use a template.

You can add one single static field or up to 10 arc fields as input fields in the plan. If you use a template to add fields, the fields may not contain any field accessories. The dose rate defined in the Field Properties dialog box will be the maximum dose rate used in the VMAT optimization. It is recommended to use the highest dose rate available on the treatment unit.

3. Use the Arc Geometry Tool to adjust field geometry before starting the optimization.



Note: The Progressive Resolution Optimizer algorithm does not modify the isocenter position, collimator rotation, or field size (unless jaw tracking is used). To modify them, you need to use the Arc Geometry Tool or adjust them manually

4. Choose **Planning > Optimization > Optimize**.

If the plan has been optimized earlier:

- You can choose to continue the previous optimization or to start from the beginning. If the earlier optimized plan contains avoidance sectors that you want to modify, it is recommended that you start the optimization from the beginning.
 - You can choose to use the calculated dose from the previous optimization as an intermediate dose.
5. To exclude structures from optimization, click **Exclude Structures** and select the structures to exclude.

Excluding structures from optimization will speed up the optimization process.

6. Define the optimization objectives or load the objectives from an objective template, and select structures for which to display the DVH. You need to add at least one lower objective for the target to be able to start the optimization process.



Note: Indicate all desired doses as unfractionated total doses.

7. To set an MU objective, select the **Use** check box and define the values for strength, minimum MU and maximum MU.
8. To define avoidance sectors in which dose is not delivered, click **Define Settings** and set the gantry angle ranges for the desired fields.



Note: You cannot add or modify avoidance sectors once the optimization process is started.

9. Define whether jaw tracking is used in the plan.

Even though a treatment unit supports VMAT, it may not support jaw tracking. You can turn on jaw tracking in a VMAT plan only if the selected treatment unit supports it, and jaw tracking has been enabled in RT Administration.

10. Automate the optimization process, if so desired.
 - To continue automatically to dose calculation after optimization, select the **Continue automatically to final dose calculation** check box.
 - To save the calculation result after optimization and dose calculation, select the **Save all after optimization and dose calculation** check box. You may wish to do this to make sure that the calculation results are saved even if, for example, there is a power outage.
 - To calculate an intermediate dose during optimization, select the **Automatic intermediate dose** check box.
11. Click **Optimize**.

During the optimization process, you can view the progress of the optimization, or move between or skip multiresolution levels.
12. After the first optimization round, the automatic intermediate dose calculation starts (if selected). To view calculation details, click **Expand**.
13. To cancel the optimization process:
 - To save the defined dose objectives before canceling, click **Apply**. Then click **Cancel**.
 - To cancel the optimization process and discard all optimization results, click **Cancel**.
14. When the VMAT optimization process is finished, do one of the following:
 - If you selected the option to proceed to final dose calculation automatically, you do not have to do anything. The dose calculation starts automatically.
 - Otherwise, click **OK** to accept the result of the optimization.

To check the changes done after the optimization:

- In the Info window, click the **Fields** tab. The MLC type is VMAT.
- Right-click the MLC, and select **Properties**.

The General tab shows that the plan type is VMAT.

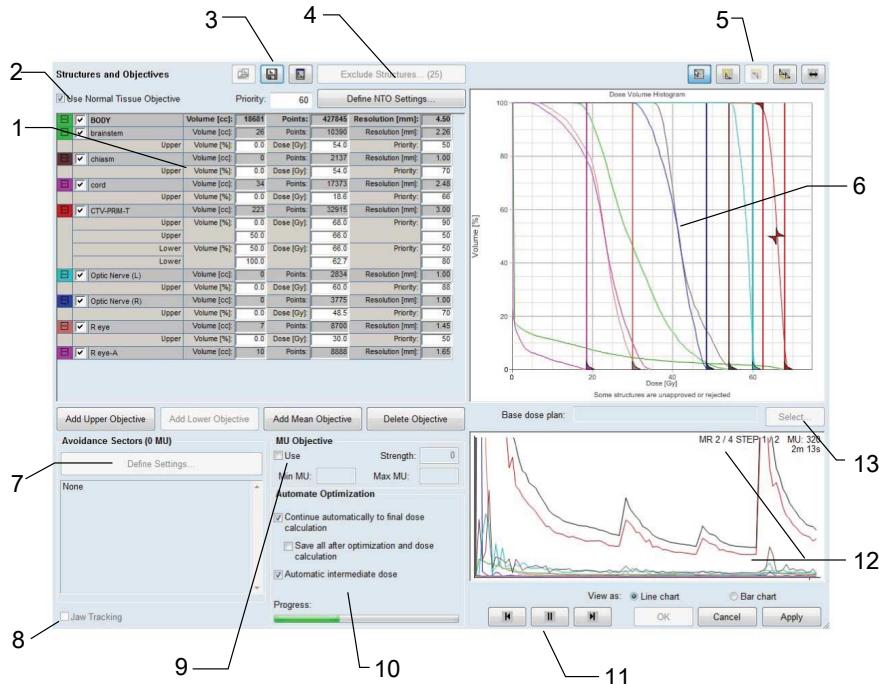
If the dose is calculated, the Control Points tab lists the meterset weight, jaw positions, gantry rotation, estimated dose rate, gantry speed, and estimated MU/degree. The control point information is also shown in the Field Properties dialog box.

When the optimized plan is saved, the following optimization parameters are also saved with the plan: MU objective, dose volume objectives, normal tissue objectives, avoidance sectors, base dose plan, excluded structures, and jaw tracking.

After optimization, evaluate the dose distribution visually, and visually verify the shape of the initial DMLC before treating. To verify the accuracy of VMAT plans, you can create verification plans using a phantom or using Portal Dose Prediction.

VMAT Optimization Dialog Box (PRO Algorithm)

When using the PRO algorithm, VMAT optimization is controlled by the VMAT Optimization dialog box, where you define the dose-volume objectives for the optimization. You can either define the optimization objectives for each plan separately, or use an objective template.



- Shows the structures contained in the plan (excluding couch structures), the volumes of the structures, the points and point resolution used for modeling the structures in the optimization, and the values of the defined objectives. Right-click to show or hide all structures, or only structures with objectives in the DVH.
- Selection for Normal Tissue Objective.
- Click to load objectives from an objective template, save objectives to a template, or manage objective templates.
- Click to exclude structures from optimization.
- Click to add or modify optimization objectives, or to scale the DVH.
- Shows the optimization results in the form of a DVH. You can also view the cost of each objective.
- Click to define avoidance sectors.
- Selection for using jaw tracking.
- Selection for MU objective.
- Selection for saving the optimization and dose calculation results automatically, and for using an automatic intermediate dose, and an indicator of the overall progress of the VMAT optimization process.
- Click resolution level buttons during optimization to move between optimization levels.
- Shows the progress of the optimization as a line chart or bar chart, and the phase and status of the optimization process.
- Click to add or remove a base dose plan.

Figure 71 VMAT Optimization Dialog Box (PRO Algorithm)



Note: Depending on the Progressive Resolution Optimizer algorithm version that you are using, all options in the Optimization dialog box may not be available. More information, see Eclipse Photon and Electron Algorithms Reference Guide.

In the VMAT Optimization dialog box, you can do the following:

- View the progress of the optimization. The progress of the optimization is shown from different aspects. You can view a DVH calculated for each structure and modify the objectives in the DVH pane, plus view an objective function curve and the current multiresolution level. You can move between the multiresolution levels forwards and backwards, pause and repeat multiresolution levels as necessary.
- Evaluate the effectiveness of the dose objectives based on the progress information.
- Modify the objectives without the need to stop the optimization process.
- Stop the optimization process by canceling it. Stopping the optimization will lose the results, apart from the objective settings.

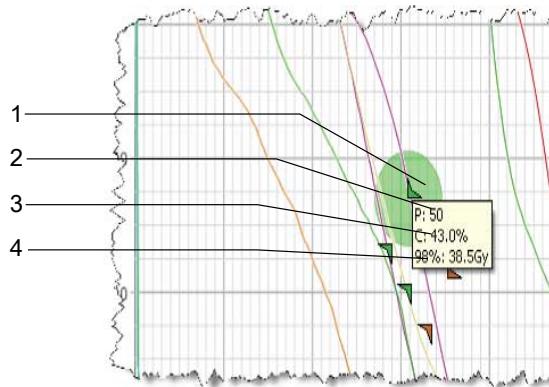


Tip: To finish the optimization quicker and keep the current optimization results, skip through the remaining optimization levels to the last level and then accept the optimization results.

The DVH is calculated and displayed in the DVH pane for each structure, and it shows how well the pre-calculated dose will conform to the set objectives. You can also modify the objectives in the DVH pane, as well as delete objectives. The DVH represents the dose for contoured volumes only. Always evaluate the dose distribution on each slice, noting hot and cold areas within the plan, especially in areas outside contoured structures.

Relative Cost of VMAT Objectives (PRO Algorithm)

You can also use the DVH pane to view the relative cost of each objective in the optimization. When you move the mouse cursor on top of an objective, it is highlighted with a colored circle showing the relative cost of the objective. The bigger the circle, the more cost the objective has in the optimization. In addition to the highlighted circle, the priority value and the percentual share of the objective in the optimization are shown. For PTV, CTV and GTV the dose that 98% of the structure receives is also shown, and for all other structures the mean dose is shown. The figure shows an example of viewing the relative costs of dose-volume objectives.



1. Move the mouse pointer on top of an objective to review its relative cost in the optimization.
2. Shows the priority of the structure in the optimization.
3. Shows the cost of the structure in the optimization in percentage.
4. Shows the dose that 98% of the structure receives (for PTV, CTV and GTV), or mean dose (for all other structures).

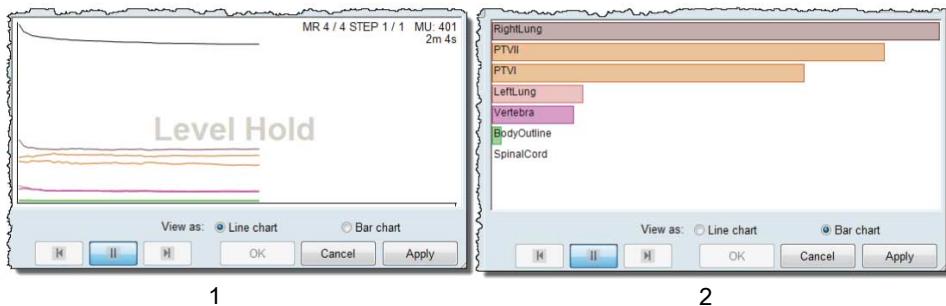
Figure 72 Relative Costs of Dose-Volume Objectives

Objective Function in VMAT Optimization (PRO Algorithm)

You can view the objective function, which illustrates the progress of the optimization towards improved results, as a line chart or a bar chart in the optimization progress pane of the VMAT Optimization dialog box:

- Line chart—Shows structure-specific curves. The line chart enables monitoring the quality and progress of the optimization, whereas the bars provide a visual overview of the importance of the structures in the optimization.
- Bar chart—Includes only structures that have objectives defined, are included in the DVH and have the most significant effect to the optimization result. The bar chart can also be used to view more details than are seen in the objective function line chart, especially if the line chart curves are very close to each other and difficult to read.

The figure shows an example of the objective function shown as a line chart and as a bar chart.



1. Objective function as a line chart
2. Objective function as a bar chart

Figure 73 Objective Function Viewed as a Line Chart and as a Bar Chart

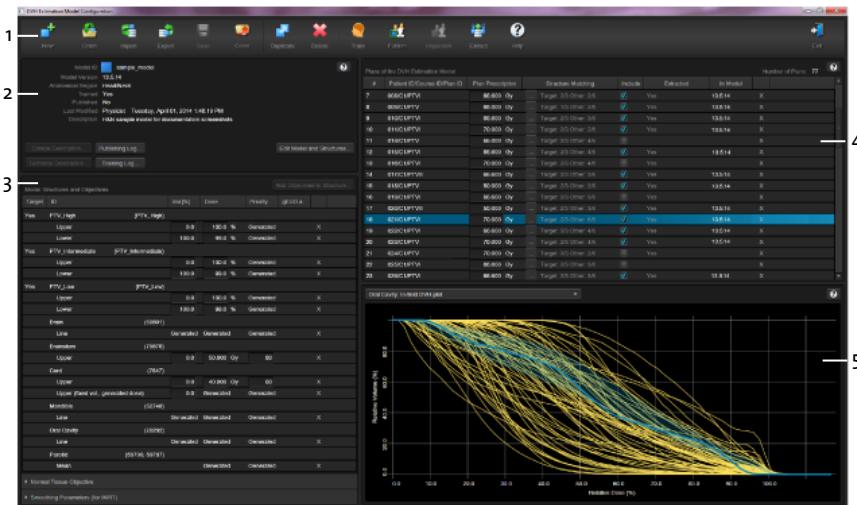
Chapter 11 Configuring DVH Estimation Models for RapidPlan

DVH Estimation Model Configuration

In DVH Estimation Model Configuration, you can create, train, and publish models to be used in treatment planning with RapidPlan. You can also modify or delete existing models, and import or export them.

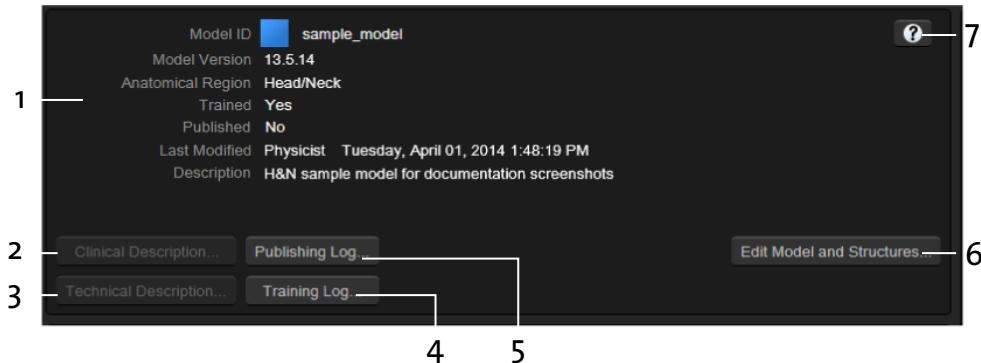
To open DVH Estimation Configuration, go to the Home screen. In the Assistant menu bar, choose **Quicklinks > Treatment Planning > Model Configuration**.

The following figures show an overview of DVH Estimation Model Configuration. It is divided into panels, which can be resized by dragging the edge of a panel to the desired size. The other panels are resized accordingly.



1. Toolbar for managing models (creating, importing, exporting, training, publishing, and so on).
2. Model properties panel.
3. Model structures and optimization objectives.
4. Plans of the DVH Estimation Model panel.
5. Statistical presentations panel.

Figure 74 DVH Estimation Model Configuration



1. Model properties. The blue square indicates that the model is unpublished. If the blue square has a green frame, the model is published.
2. Click to view the clinical description document of the model, if available.
3. Click to view the technical description document of the model, if available.
4. Click to view the training log.
5. Click to view the publishing log.
6. Click to modify model properties and structures.
7. Click to show a help topic.

Figure 75 DVH Estimation Model Configuration - Model Properties Panel

The model properties shown in DVH Estimation Model Configuration are the following:

- Model identifier.
- Version of the trained model (version of the DVH estimation algorithm).
- Anatomical region of the model.
- Training status of the model (Yes/No).
- Publishing status of the model: Yes (the name of the publisher, and the publishing date and time in server time) / No.
- User who has last modified the model, modification date and time (in server time).
- Short description of the model.

Model Structures and Objectives						Add Objectives to Structure
Target	ID	Vol [%]	Dose	Priority	gEUD a	
Yes	PTV_High (PTV_High)					
	Upper	0.0	100.0 %	Generated	x	
Yes	PTV_Intermediate (PTV_Intermediate)					
	Upper	0.0	100.0 %	Generated	x	
Yes	PTV_Low (PTV_Low)					
	Upper	0.0	100.0 %	Generated	x	
Brain	(50801)					
	Line	Generated	Generated	Generated	x	
Brainstem	(79876)					
	Upper	0.0	50.000 Gy	60	x	
Cord	(7647)					
	Upper	0.0	40.000 Gy	60	x	
Mandible	(52748)					
	Line	Generated	Generated	Generated	x	
Oral Cavity	(20292)					
	Line	Generated	Generated	Generated	x	
Parotid	(59798, 59797)					
	Mean	Generated	Generated	Generated	x	

- 2 → Normal Tissue Objective
 3 → Smoothing Parameters (for IMRT)

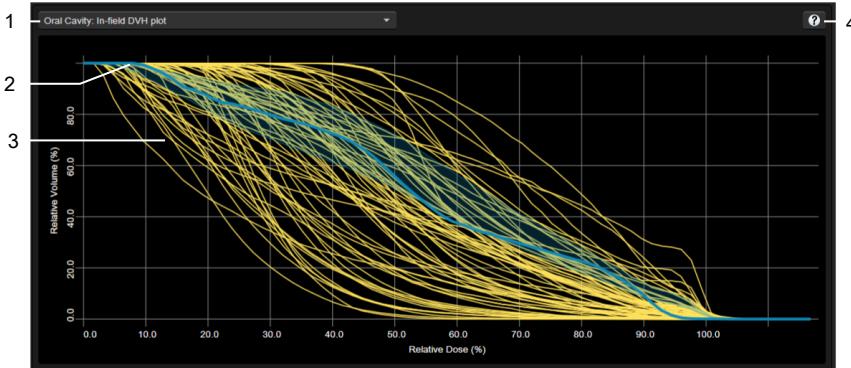
1. List of structures and optimization objectives used in the model.
2. Click to view and modify settings for Normal Tissue Objective.
3. Click to view and modify smoothing parameters for IMRT plans.
4. Click to add objectives to a structure.
5. Click to remove objectives from the structure.

Figure 76 DVH Estimation Model Configuration - Model Structures and Optimization Objectives

Plans of the DVH Estimation Model							Number of Plans
#	Patient ID/Course ID/Plan ID	Plan Prescription	Structure Matching	Include	Extracted	In Model	
008/C1/P/TVI	66.600 Gy	Target: 2/0 Other: 3/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	12
009/C1/P/TVI	66.600 Gy	Target: 1/0 Other: 3/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	11
010/C1/P/TVI	66.600 Gy	Target: 2/0 Other: 3/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	10
011/C1/P/TVI	70.000 Gy	Target: 2/3 Other: 3/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	9
014/C1/P/TVI	66.600 Gy	Target: 2/0 Other: 4/6	<input type="checkbox"/>				8
015/C1/P/TVI	66.600 Gy	Target: 2/0 Other: 4/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	7
016/C1/P/TVI	70.000 Gy	Target: 2/3 Other: 4/6	<input type="checkbox"/>				6
017/C1/P/TVI	66.600 Gy	Target: 2/0 Other: 4/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	5
018/C1/P/TVI	66.600 Gy	Target: 2/0 Other: 4/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	4
019/C1/P/TVI	58.000 Gy	Target: 2/0 Other: 3/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	3
021/C1/P/TVI	70.000 Gy	Target: 2/0 Other: 4/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	2
022/C1/P/TVI	66.600 Gy	Target: 2/3 Other: 4/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	1
023/C1/P/TVI	70.000 Gy	Target: 2/0 Other: 4/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	
024/C1/P/TVI	70.000 Gy	Target: 2/3 Other: 5/6	<input type="checkbox"/>				
025/C1/P/TVI	66.600 Gy	Target: 2/0 Other: 5/6	<input type="checkbox"/>				
026/C1/P/TVI	66.600 Gy	Target: 2/0 Other: 5/6	<input checked="" type="checkbox"/>	Yes	13.6.14	X	

1. Model plan set available for model training. For Varian-provided models, the list is empty.
2. Plan identification number. This number helps you identify this specific plan in the statistical presentations shown below this pane.
3. Plan identification information of the original treatment plan. Shows “N/A” for original treatment plans not linked to the model (for example, in imported models, or if the original plan has been deleted from the database).
4. Plan prescription (in a multi-target plan, the highest target dose level).
5. Number of matched target structures and organs at risk in the plan. Shows “Nothing” if no matches exist.
6. Click to verify or change the structure matching.
7. The check box is selected if the plan will be included in the next model training, cleared if it will not.
8. Shows whether the plan contains extracted plan data. The cell is empty if no extracted data exists, for example, if the model has been imported without plan data. The cell is cleared when changes made to the model require re-extracting the plan data.
9. Shows whether the plan has been used to train the model, and the algorithm version the plan was trained with.
10. Click to remove a plan from the model.
11. Number of plans in the model.
12. Click to open a help topic.

Figure 77 DVH Estimation Model Configuration - Plans of the DVH Estimation Model Panel



1. Click to select a statistical plot or table that you can use for verifying the quality of the model.
2. DVH band (blue curve and shaded area) of a structure contained in the plan highlighted in the Plans of the DVH Estimation Model panel.
3. DVH curves (yellow curves) of a structure contained in all plans in the Plans of the DVH Estimation Model panel.

Figure 78 DVH Estimation Model Configuration - Statistical Presentations for Model Verification Panel

Configuring a DVH Estimation Model

When you start creating a DVH estimation model, you need to consider for which anatomical region (for example, the pelvic area) you want to use the model. In addition, you need to decide whether to create a general model that suits a wide variety of patient cases, or a specific model that works best for specific patient cases. For example, you might want to create a prostate model that works for patient cases with different anatomical features, field setups, and dose prescriptions. Or you might want to create a prostate model for treating patient cases with specific anatomical features, field setup, and dose prescription.

After these initial considerations, you define the properties of the model in DVH Estimation Model Configuration and add those structures to the model, for which you want to generate DVH estimates. If you also want the model to generate optimization objectives, you need to add the desired optimization objectives to the model structures. When adding the optimization objectives, you can either define values for some of the parameters, or let the DVH estimation algorithm define them for you. It is also possible to add fixed optimization objectives, not based on DVH estimates, to be used for limiting the absolute maximum dose for critical organs. If you do not want to use DVH estimates or estimate-based optimization objectives, you can also create a model that contains only fixed optimization objectives. After adding the objectives, you may want to define the smoothing parameters (only for IMRT plans) and the Normal Tissue Objective (NTO) for the model. To help users in selecting an appropriate model in optimization, you can attach a model description document (.pdf) to each model.

Next, you can start adding plans to the model one by one in External Beam Planning. The plans must be clinically acceptable, and fulfill the intended treatment goal. In addition, they must be suitable for the type of model you are creating (general vs. specific). Keep in mind that the model can only produce results as good in the new plans as the results in the model plans. Therefore, you must review and if needed, fine-tune the plans carefully before adding them to the model. Existing models can be used as an aid in fine-tuning.

If you know for what kind of plans you are planning to use the model, add similar plans to the model plan set. If you are not quite sure yet, consider adding several types of plans to the model plan set, and only later, validate the model with a set of plans to see how it works for different types of plans. When you find out the plan types, in which the model works poorly, add more similar plans to the model plan set. When you add plans to a model, an initial automatic structure matching is performed between the model structures and plan structures. The matching is based on structure codes and identifiers used in the plans and in the model. You need to verify the results of the automatic matching and make the necessary corrections.

When a plan is added to the model, the system extracts the plan data needed for training the model. If the plan or model changes after this, you can re-extract the plan data later in DVH Estimation Model Configuration. After adding all the plans to the model, you have to train the model. During the training, the system analyzes the patient anatomy and DVHs in the plans, and creates the final mathematical DVH estimation model. You can verify the results of the model training in statistical presentations of the training set. They help you estimate the quality of the model and find potential outlier values that differ from the average in the training set. You have to process the outlier findings, and after that, re-extract the plan data if needed and retrain the model iteratively until the results are acceptable. You should carefully validate the model with a set of plans before taking the model into clinical use.

When the model is applied to a plan in the Optimization dialog box in External Beam Planning, the following happens:

- DVH estimates and estimate-based objectives are generated for those OAR structures in the plan that have been matched to trained OARs in the model.
- Target structures receive no DVH estimates or estimate-based objectives.
- Fixed objectives are generated for all matched structures, regardless of whether they have been trained.

The default NTO and smoothing parameters will also be applied. The optimization objectives, NTO, and smoothing parameters can be adjusted before or during optimization. After applying the model, it is important to verify the optimization results, since the model might not work optimally for all patient cases.



Note: *If multiple simultaneous users work with the same DVH estimation model, this may lead to situations where another user has modified and saved the model that you are currently working with. Therefore, avoid situations with multiple users concurrently working with the same model. If you try to save your changes, the system will issue a warning message about another user already editing the same model. Always carefully verify the synchronized model, because it may contain changes made by both you and the other user.*

Define the Model Properties and Add Structures

1. In the DVH Estimation Model Configuration workspace, click **New**.
2. In the DVH Estimation Model Properties dialog box, enter an identifier and description for the model.
The Model ID and Model Description will be shown in the Optimization dialog box.
3. To attach a clinical or technical model description document to the model, do the following:
 - a. Click **Browse for a PDF**.
 - b. Navigate to the location of the document (.pdf), select it, and click **Open**.
 - c. To view the document, click its hyperlink.
 - d. To remove the document from the model, click **Remove**.
The clinical description is available in the Optimization dialog box, in the Add a Plan to DVH Estimation Model dialog box, and in the DVH Estimation Model Configuration workspace. The technical description is available in the DVH Estimation Model Configuration workspace.
4. Select the anatomical region for the model.
If the anatomical region you are looking for is not on the list, select **Other**.

- To add structures to the model, click **Add Model Structure**.



Note: You must add at least one target structure and one non-target structure. Add 1-3 target structures to the model. The maximum number of target structures supported by the DVH estimation algorithm is 3. If you add more than 3 target structures, you are not able to add any plans to the model, extract plan data, or train the model.

- To add the model structures in the Structure Code Selection dialog box, do the following:

- To filter the structure codes, enter the structure label or part of it in the **Filter Structure Codes** search box. You can clear the filter by clicking the x button next to the search box.
- Select the structure code in the **Structure Dictionary** group box.
- Click **Add**.

The identifier of the selected structure appears in the Structure ID box. If necessary, you can modify the identifier, but make sure it remains unique within the model. The structure code is added to the structure code list.



Note: You must add at least one structure code to each structure.

- To assign another structure code to the same structure ID, select the structure code in the **Structure Dictionary** and click **Add**. For example, you might want to add the structure codes for both the right and left femoral head to the Femur structure.
 - Click **OK**.
- In the DVH Estimation Properties dialog box, check that all target structures have the check box selected in the **Target** column.
 - If you want to modify the structure identifier or structure codes, select the structure and click **Edit**. If you want to remove a model structure, click the X button next to the structure.
 - To add all required structures to the model, repeat the steps, and when done, click **OK**.

Next, you can add the desired optimization objectives for the structures, and define the NTO and smoothing parameters for the model. If you do not want to define any additional settings, you can start adding plans to the model.

Related Topics

[Creating a Model Description Document](#) on page 294

Adding Structures to a DVH Estimation Model

Keep the following in mind when adding structures to a DVH estimation model:

- Add those structures to the model for which you want to generate DVH estimates (OARs), estimate-based optimization objectives (OARs), or fixed optimization objectives (both target and OAR structures).
- At least one target structure and one OAR structure must be added to the model.
- The model can contain structures that are not included in the training set. If a structure is not included in the training set, you cannot generate DVH estimates or estimate-based objectives for it. However, you can add fixed optimization parameter values for the structure.
- The model does not need to contain all the structures that exist in training plans.
- Bilateral structures, such as femoral heads: Depending on the purpose of the model, create only one model structure for both, or a separate model structure for the right and left structure.
- Structure identifiers and codes are needed for generating DVH estimates and optimization objectives for structures, and for automatically matching model structures to plan structures when new plans are added to the model.
- At least one structure code is needed for each model structure. If the codes in your clinical plans vary, add all the used codes to the corresponding model structure.

Add Optimization Objectives, NTO, and Smoothing Parameters

After you have added structures to a DVH estimation model, you can define the optimization objectives, smoothing parameters (only for IMRT), and Normal Tissue Objective (NTO) for the model.

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. In the **Model Structures and Objectives** list, select a structure and click **Add Objectives to Structure**.
3. In the Objective Type list, select the type of optimization objective that you want to add to the structure.
Depending on the structure type (target or non-target), different objective types are available.
4. Enter the appropriate parameter values. Depending on the objective type, different parameters are available.

- a. In the **Dose** box, define the dose value for the objective. Select **Absolute** or **Relative** to show the dose values in Gy/cGy or %.
When a model is applied, the system considers the total prescribed dose as 100% dose. Other dose values are calculated based on that.
- b. In the **Volume** box, define the volume of the structure in percentage that the dose should or may cover.
- c. In the **Parameter A** box, define the a value for the gEUD objective.
- d. For **Priority**, to use a generated value, select the **Generate** check box, or to define your own priority value, type the value in the Priority box.

5. Click OK.

The objective and related parameter values appear in the Model Structures and Objectives list. The parameter values that will be generated by the DVH estimation algorithm are indicated by the “Generated” text string. To remove an objective from a structure, click the x button on the objective row.

6. To add more objectives to the structure, repeat the steps above.
7. To add the objectives for the rest of the structures, repeat the steps above.
8. To define the Normal Tissue Objective values for the model, click the **Normal Tissue Objective** expander and define your NTO parameters:

Option	Description
In Use	Select to apply the NTO values in the Optimization dialog box.
Priority	Define the priority for the NTO in this box. The relative importance of the Normal Tissue Objective in relation to other optimization objectives.
Automatic NTO	Takes automatic NTO into use.
Distance from Target Border (manual NTO)	Enter the distance from the target border where the evaluation of the normal tissue dose should begin.
Start Dose (manual NTO)	Enter the relative dose level in the NTO at the target border.
End Dose (manual NTO)	Enter the relative dose level in the NTO away from the target border.
Fall-off (manual NTO)	Enter the steepness of the objective fall-off.

9. To define the smoothing parameters for IMRT plans, click the **Smoothing Parameter** expander, and enter your value for reducing the beam intensity in the **X Smooth** and **Y Smooth** boxes.

You can also edit the optimization objectives, NTO, and smoothing parameters later, even after the model has been trained. You do not have to re-extract plan data or train the model again. Next, you can start adding plans to the model.

Related Topics

- [Photon Optimization Parameters](#) on page 226
- [Generalized Equivalent Uniform Dose \(gEUD\)](#) on page 227
- [Normal Tissue Objective in Photon Optimization](#) on page 230
- [X Smooth and Y Smooth](#) on page 233

Adding Optimization Objectives to a DVH Estimation Model

Keep the following in mind when adding optimization objectives to a DVH estimation model:

- Adding optimization objectives is optional. If you leave optimization objectives undefined, DVH estimates are still generated for trained OARs.
- Add those estimate-based or fixed optimization objectives that you want to be generated in optimization.
- All optimization objectives are supported for both VMAT and IMRT plans.
- Depending on the optimization objective type you are adding, different parameters are available: dose, dose percentage, volume percentage, parameter a (for Generalized Equivalent Uniform Dose, gEUD, objectives), and priority. Depending on the objective type, some parameter values will be automatically generated, and some you can manually define. By default, the priority of all the objectives is automatically set, but you can define your own priority value for each objective. In case of multiple model targets, the automatically generated priorities for the objectives of target structures work best with non-Boolean target structures.
- All the optimization objectives and their parameter values can be later changed in the Optimization dialog box (except you cannot modify the shape of line objectives).
- Define the NTO, and smoothing parameters (for IMRT plans) for the model, if necessary.

Optimization Objectives for Target Structures

The following types of optimization objectives are available for target structures in a DVH estimation model.



Note: If you use absolute dose for the optimization objectives of target structures, keep in mind that these optimization objectives work best for dose prescriptions that are similar to the ones used in the training set. If the dose prescription is very different, the estimate-based objectives may not be optimal.

Table 18 Optimization Objectives for Target Structures

Optimization Objective	Description	Model Parameters
Lower	This optimization objective defines the minimum dose value (Gy/cGy or %) that a target structure (%) must receive. For example, "at least 95% of the PTV volume must receive at least 95%".	Define the following parameters: <ul style="list-style-type: none">■ Absolute dose (Gy/cGy) or relative dose (%)■ Volume (%)■ Priority If the relative dose is selected, the optimization objective is based on the prescription of the plan, in which the model is applied. By default, the priority value is automatically generated by the DVH estimation algorithm. You can also manually enter the priority.
Lower gEUD	This optimization objective defines the minimum Equivalent Uniform Dose value (Gy/cGy or %) that a target structure must receive. For example, "PTV must receive at least 50 Gy".	Define the following parameters: <ul style="list-style-type: none">■ Absolute dose (Gy/cGy) or relative dose (%)■ Parameter a: The value can be from -40 to 1, but cannot equal 0. Example values:<ul style="list-style-type: none">$a < 0$: Lower doses are given high weight so that cold spots influence the gEUD to a large extent.$a < -10$: Often used for targets.■ Priority By default, the priority value is automatically generated by the DVH estimation algorithm. You can also manually enter the priority.

Optimization Objective	Description	Model Parameters
Target gEUD	<p>This optimization objective defines an exact Equivalent Uniform Dose value (Gy/cGy or %) that a target structure must receive. For example, "PTV must receive 99.0 %".</p>	<p>Define the following parameters:</p> <ul style="list-style-type: none"> ■ Absolute dose (Gy/cGy) or relative dose (%) ■ Parameter a: <p>The value can be from -40 to 1, but cannot equal 0.</p> <p>Example values:</p> <ul style="list-style-type: none"> $a < 0$: Lower doses are given high weight so that cold spots influence the gEUD to a large extent. $a < -10$: Often used for targets. $a = 1$: This corresponds to the mean dose. Cold and hot spots are given equal weight. ■ Priority <p>By default, the priority value is automatically generated by the DVH estimation algorithm. You can also manually enter the priority.</p>
Upper	<p>This optimization objective defines the maximum dose value (Gy/cGy or %) that a target structure (%) may receive. For example, "no more than 1% of the PTV volume may receive more than 60 Gy".</p>	<p>Define the following parameters:</p> <ul style="list-style-type: none"> ■ Absolute dose (Gy/cGy) or relative dose (%) ■ Volume (%) ■ Priority <p>If the relative dose is selected, the optimization objective is based on the prescription of the plan, in which the model is applied.</p> <p>By default, the priority value is automatically generated by the DVH estimation algorithm. You can also manually enter the priority.</p>

Optimization Objective	Description	Model Parameters
Upper gEUD	<p>This optimization objective defines the maximum Equivalent Uniform Dose value (Gy/cGy or %) that a structure may receive. For example, “Bladder may receive no more than 30 Gy”.</p>	<p>Define the following parameters:</p> <ul style="list-style-type: none"> ■ Absolute dose (Gy/cGy) or relative dose (%) ■ Parameter a: <p>The value can be greater than 0, but less than or equal to 40.</p> <p>Example values:</p> <p>$a > 1$: Higher doses are given higher weight so that hot spots influence the gEUD to a large extent.</p> <p>$a = 1$ for parallel responding critical organs, such as parotid gland, liver, lung, and kidney.</p> <p>$a \geq 8$ for serial responding critical organs, such as rectum, spinal cord, brainstem, or optic nerves.</p> <ul style="list-style-type: none"> ■ Priority <p>By default, the priority value is automatically generated by the DVH estimation algorithm. You can also manually enter the priority.</p>

More information on optimization objectives: *Eclipse Photon and Electron Algorithms Reference Guide*.

Related Topics

[Generalized Equivalent Uniform Dose \(gEUD\)](#) on page 227

[Photon Optimization Parameters](#) on page 226

[Tips for Using gEUD in Optimization](#) on page 229

Optimization Objectives for Organs at Risk

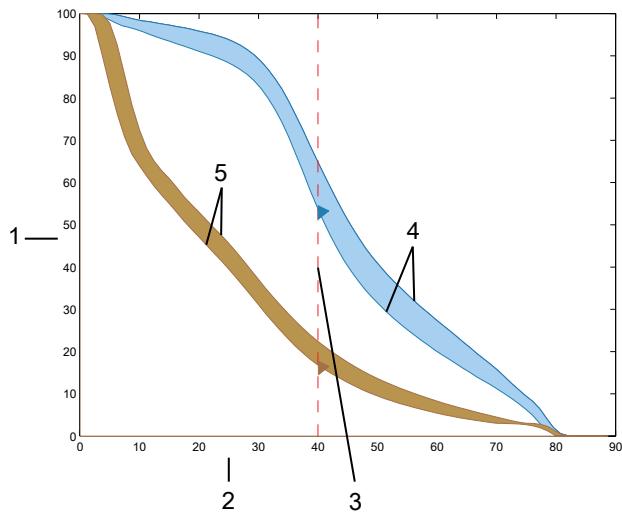
The following types of optimization objectives are available for organs at risk in a DVH estimation model.

Table 19 Optimization Objectives for Organs at Risk

Optimization Objective	Description	Model Parameters
Line	<p>This optimization objective is the DVH estimate-based line objective. It is located under the lower bound of the DVH estimate range.</p>	<p>The DVH estimation algorithm generates this optimization objective and priority according to the DVH estimate of the structure. You can also manually enter the priority.</p>
Mean	<p>This optimization objective defines the mean dose level (Gy/cGy or %) that should not be exceeded for a structure.</p>	<p>Define the following parameters:</p> <ul style="list-style-type: none"><li>■ Absolute dose (Gy/cGy) or relative dose (%) If you want the DVH estimation algorithm to generate the dose according to the DVH estimate of the structure, select the upper Generate check box.<li>■ Priority By default, the priority value is automatically generated by the DVH estimation algorithm. You can also manually enter the priority.
Upper	<p>This optimization objective defines the maximum dose value (Gy/cGy or %) that a structure (%) may receive. For example, "no more than 50% of the Bladder volume may receive more than 65 Gy".</p>	<p>Define the following parameters:</p> <ul style="list-style-type: none"><li>■ Absolute dose (Gy/cGy) or relative dose (%)<li>■ Volume (%)<li>■ Priority By default, the priority value is automatically generated by the DVH estimation algorithm. You can also manually enter the priority.

Optimization Objective	Description	Model Parameters
Upper (fixed dose, generated vol.)	<p>This optimization objective defines the maximum dose value (Gy/cGy or %) that a structure (%) may receive.</p>	<p>Define the following parameters:</p> <ul style="list-style-type: none"> ■ Absolute dose (Gy/cGy) or relative dose (%) ■ Priority <p>The DVH estimation algorithm generates the volume percentage and priority according to the DVH estimate of the structure. You can also manually enter the priority.</p>
Upper (fixed vol., generated dose)	<p>This optimization objective defines the maximum dose value (Gy/cGy or %) that a structure (%) may receive.</p>	<p>Define the following parameters:</p> <ul style="list-style-type: none"> ■ Volume (%) ■ Priority <p>The DVH estimation algorithm generates the dose and priority according to the DVH estimate of the structure. You can also manually enter the priority.</p>
Upper gEUD	<p>This optimization objective defines the maximum Equivalent Uniform Dose value (Gy/cGy or %) that a structure may receive. For example, "Bladder may receive no more than 30 Gy".</p>	<p>Define the following parameters:</p> <ul style="list-style-type: none"> ■ Absolute dose (Gy/cGy) or relative dose (%) ■ Parameter a: <p>The value can be greater than 0, but less than or equal to 40.</p> <p>$a > 1$: Higher doses are given higher weight so that hot spots influence the gEUD to a large extent.</p> <p>$a = 1$: This corresponds to the mean dose. Cold and hot spots are given equal weight.</p> <ul style="list-style-type: none"> ■ Priority <p>By default, the priority value is automatically generated by the DVH estimation algorithm. You can also manually enter the priority.</p>

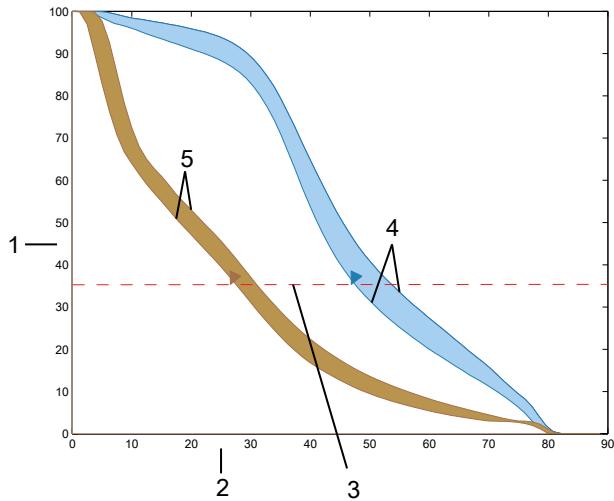
The following figure illustrates the Upper (fixed dose, generated vol.) objective:



1. Volume percentage
2. Dose
3. Manually defined dose level
4. Upper and lower DVH estimate for OAR1
5. Upper and lower DVH estimate for OAR2

Figure 79 Upper (fixed dose, generated vol.) Objective

The following figure illustrates the Upper (fixed vol., generated dose) objective:



1. Volume percentage
2. Dose
3. Manually defined volume percentage
4. Upper and lower DVH estimate for OAR1
5. Upper and lower DVH estimate for OAR2

Figure 8o Upper (fixed vol., generated dose) Objective

More information on optimization objectives: *Eclipse Photon and Electron Algorithms Reference Guide*

Related Topics

- [Generalized Equivalent Uniform Dose \(gEUD\) on page 227](#)
- [Photon Optimization Parameters on page 226](#)
- [Tips for Using gEUD in Optimization on page 229](#)

Creating a Model Plan Set

You need to consider for which kind of plans you are planning to use the DVH estimation model, and try to include similar plans in the model plan set. If you are creating a general model for a wide variety of patient cases, include a wide variety of plans into your plan set. If you are creating a more specific model for more specific patient cases, you can include a smaller variety of plans into your plan set.

You need to consider the general vs. specific aspect for each of the following plan features related to the anatomy of the patient:

- The size of the OARs (small, large, medium, or all; full, half full, empty, or all).
- The position of the OARs with respect to each other (overlapping, non-overlapping, or both).
- The size of the target (small, medium, large, or all).
- The relative position of the target with respect to OARs (far, close, or both; overlapping, non-overlapping, or both).

For example, if you want to use the model for patients with all types of bladder (full, half full, empty), include all bladder types in your model plan set. If you are planning to use the model only for specific patient cases, for example, for patients with full bladders, you can include a smaller variety of bladder types, in this case, full bladders, in your model.

In addition, you have to consider the general vs. specific aspect also for the following features related to field setup and dose prescription:

- Treatment technique (VMAT, IMRT, or both).
- The position of the fields (how much of the OARs are inside or outside the field).
- Non-coplanar vs. coplanar fields.
- The direction of the fields (entry angle).
- Different treatment orientations.
- Dose prescription (specific dose prescription, dose prescription range).
- Dose fractionation.
- Used dose calculation algorithm and version.

You need to consider the amount of variety you want to include into your model. Keep in mind that the more variation you want, the more treatment plans you need. If you add a wide variety of features into your model, but do not increase the number of treatment plans at the same time, the model will not work properly. The more variation your model will include, the more generic it will be and you are able to use it for a wider range of patient cases.

However, if you are creating a more specific model with a smaller variety of features, keep in mind that you do not narrow the features too much. For example, if most of the plan features are very similar in your training set, the model will not work properly despite the number of training plans you use for training the model. In this case, the model will work only for plans that are very similar to the training plans.

In addition, keep in mind the following aspects when selecting plans for your model:

- Use reviewed and clinically acceptable plans with optimal target coverage and organ-at-risk (OAR) sparing. The model can only produce results as good in new plans as the results in the training plans.
- Use plans that fulfill the treatment goal of the model.

- Use plans which have consistently high quality. The model is based on the mean values in the majority of the training set plans - not on the best plan in the training set. Therefore, only one or few good plans in the training set are not enough.



Tip: You can first improve the quality of a plan by optimizing it with an existing model. After that, you can add the plan to a model - either to the same model that you used for optimizing the plan, or to another one. In this way, the quality improvement becomes a continuous process - the model improves the quality of the training plans, which, in turn, improve the quality of the model.

Review a Model Plan

Review each plan, before adding it to the DVH estimation model. Make sure to check at least the following:

1. Structures in the plan:

- The structures to be included in the model are properly and consistently (if possible) contoured.
- The organs or volumes are fully visible in the CT slices and they are fully contoured.
- One Body structure exists with volume type defined as BODY in Structure Properties in External Beam Planning. The model identifies the Body structure on the basis of the volume type, not the structure identifier.
- If you import a plan from another treatment planning system, and the plan contains no Body structure, contour the Body structure before adding the plan to a DVH estimation model.
- No contour exists outside the Body structure. Any part of a structure that is outside the Body is ignored by the DVH estimation model.
- At least one target structure exists.
- Make sure that all structures contain correct structure identifiers.
- To take full advantage of automatic structure matching when adding plans to the model, check that each structure has a structure code, the code matches one of the codes defined for the corresponding model structure, and the structure identifier matches the one used in the model.
- The Body, target, and OAR structures to be included in the model are fully covered by the calculated dose.

2. Quality of the plan:

- The target coverage and organ-at-risk (OAR) sparing are optimal.
- The plan fulfills the treatment goal of the plan and the model.
- The dose calculation volume fully covers the structures which are to be included in the model.

3. Check that each structure that you want to include in the model has been optimized.

Number of Patients and Model Plans

When estimating the number of plans and patients you need for a model, keep in mind the following:

- Use enough plans from different patients to train the model. You need to add at least 20 plans to a model, before you can train it (click **Train**).
- You can start adding plans to the model one by one, but to evaluate the final number of plans you need for the model, you should validate the model very thoroughly.
- Consider how you intend to use the model for a certain anatomical region - for specific patient cases (similar structures, field setup, and dose prescriptions) or for all kinds of patient cases.

For example, if the model is intended for very specific patient cases, about 20-25 patients might be a good starting point. For a very generic model you might need a considerably greater number of patients, starting from 50-100 patients. Keep in mind that these figures are only examples and you should always validate the model carefully regardless of the number of plans in the model.

- Add only unique plans to the model. If you add several identical copies of a plan to the model, it is as if you added only one single plan. You may be able to train the model, but plan copies do not produce enough data variance for the model to work properly. This is true even if you used anonymized patient data, with no UIDs for series, image, or patient. This is because the models do not use UIDs for identifying plan data. They use patient anatomy and field setup information instead.
- The model plan set can include several plans of the same patient. If the field geometry and the structure matching of the plans are the same, it is equivalent to add a single plan whose dose is (approximately) the average dose of all the plans.
- The model plans can be with any plan approval status. However, if you use plans with Unapproved status, keep in mind that they are prone to modifications. These modifications may cause undesired effects in the model where the plans are used. This happens if you need to re-extract the data of all the plans in a model in DVH Estimation Model Configuration.
- If you later need to remove outlier plans from the model and the number of plans falls below 20, you should add new plans to the model.

Structures in Model Plans

Consider the following aspects regarding the structures in the model plans:

- The anatomical treatment region must be the same in all the plans (for example, prostate).
- To generate DVH estimates and estimate-based objectives for an OAR, you need at least 20 instances of the OAR in your plan set. This requirement does not apply to a structure (OAR or target), for which you are planning to add only fixed optimization objectives.
- Depending on the purpose of the model (general vs. specific), consider the form, size, and position of the structures in the plans. In a general model, these features can vary more than in a very specific model.
- Pay attention to the size of the structures in the plans. The generated DVH estimates for small structures may not be optimal. In addition, if your plan contains very small structures (all the voxels of the structure are only half a voxel or less in size), they may be skipped during the data extraction phase, and will not be used for training the model nor reported. It is also possible that the DVH estimation is not successful for very small structures.
- Not all plans need to contain all the structures included in the model.
- The plans can contain structures that are not included in the model. If you do not match the plan structures to model structures, they are not used for training the model.
- The plans must include one target, but can also contain multiple targets. The number of targets does not have to be the same as in the model. If multiple plan structures are matched to the same model target structure, the model structure is a union of the plan structures.
- The planning goals and prescription goals for structures should be consistent in the whole plan set to avoid different trade-offs in different plans. Keep in mind that the more planning and prescription goals a plan has for different structures, the more difficult it is to keep them consistent in the whole plan set.
- The structures in the whole plan set should be properly and consistently (if possible) contoured.

Field Setup in Model Plans

Consider the following aspects regarding the field setup in model plans:

- Depending on the purpose of the model (generic vs. specific), consider the field setup (number of fields and different entry angles), in your plans. If you are creating a generic model, include variable field setups in your plan set, where the number of used fields and their entry angles can be different. If you are creating a specific model, for example, for 5-field plans, where the beams for all plans enter the patient from the same 5 directions, the plan set does not have to include a wide variety of different field setups. The field setup is considered similar relative to the patient, which means that it is considered similar even though the gantry angles would be different. For example, in the following two cases, the field setup would be considered similar:
 - A beam enters a prostate patient from the right side. The patient orientation is head-first supine, and the gantry angle is 90 degrees.
 - A beam enters another prostate patient also from the right side, but the patient orientation is head-first prone. The gantry angle is 270 degrees.
- You can use any field direction, because the DVH estimation algorithm takes it automatically into consideration.
- Depending on the purpose of the model (specific vs. generic), compile model plan sets that have only VMAT plans, only IMRT plans, or that contain both.
- If you import a plan from another treatment planning system, and the plan contains setup fields, make sure that the setup fields are not converted to treatment fields in the import. If this is the case, remove these treatment fields before adding the plan to a DVH estimation model.

Dose Prescription in Model Plans

In a DVH estimation model, the dose prescription is only used to scale the dose matrices. Therefore, the training set does not necessarily need to cover the whole range of prescriptions to which you intend to apply the model. The reason for this is that usually, the dose prescription in a plan has no effect on the relative dose distribution, but is only used to scale the absolute dose.

However, sometimes the used dose prescription may affect the priorities in optimization. If this happens, different dose prescriptions in plans may also make the relative dose distributions different. For example, a certain OAR, such as spinal cord, might sustain a certain absolute dose that affects optimization, but only if the dose prescription is high enough. In this case, you should make sure that the training set represents the whole prescription range to which you intend to apply the model. In addition, it might be beneficial to add absolute objectives for this kind of model organ, for example, 45 Gy for spinal cord. This helps you avoid a situation where the dose maximum of spinal cord reaches critical values in a high-prescription plan.

Another option is to exclude certain OARs from the training set if the dose prescription level is low enough. The rational is that OARs that have not actually been optimized can be left out. This can happen, for example, if no optimization objectives have been used for spinal cord in low-prescription cases, or if all used optimization objectives are set so high that in practice, they do not contribute to the cost function. In such situations, the estimated DVH curves for the spinal cord might be somewhat more tight in case of low-prescription level (compared to corresponding validation cases). When making the decision about excluding OARs from the training set, keep in mind the purpose of the model (general vs. specific). A general model, trained with multiple prescriptions, can be applied to plans with different prescriptions, but the model produces less accurate DVH estimates. A more specific model produces more accurate DVH estimates, but works optimally only for the same prescription as has been used in model training.

It is, however, a good practice to include different dose prescriptions in the training set (and validation set), even if the dose prescription is not anticipated to affect the treatment planning. In addition, keep in mind the following:

- If you intend to use the model for plans with different dose prescriptions, for example, 60 Gy and 66 Gy, include plans with approximately the same dose prescriptions (60 Gy and 66 Gy) into your plan set. Remember to balance the number of each dose prescription in the plan set. For example, if your plan set includes 30 plans, include approximately 15 plans with a 60 Gy dose prescription, and 15 plans with a 66 Gy dose prescription. If you include only few, for example, 1-5 plans with a 60 Gy dose prescription, the model might not work properly for that dose prescription.
- If you intend to use the model for a certain prescription range, for example, 40-70 Gy, select plans that cover the whole dose prescription range.
- If you have used plans with either a 50 Gy or 70 Gy dose prescription in your model plan set, but you would like to use the model also for 60 Gy plans, you should carefully validate the model with 60 Gy plans. If validation fails, you could try adding 60 Gy plans into your training set. If that is not possible, you should not use the model for 60 Gy dose prescriptions.
- If you are creating a training set for a model in which the optimization objectives for target structures are defined as absolute dose values, pay special attention to the dose prescriptions in the training set. If the dose prescriptions in the training set differ considerably from the dose prescriptions used in the plans where you apply the model, the generated DVH estimates or estimate-based objectives may not be optimal.
- Dose prescriptions in the model are defined as the total dose for the primary target.
- Pay attention to the dose calculation algorithm and version that you are using in your plan set. If you intend to use the model for plans with a certain dose calculation algorithm and version, try to use the same algorithm and version in your training set. This is important especially for the lung models.

Add a Plan to a DVH Estimation Model

You can add new plans to a trained (unpublished or published) model in the same way as to an untrained model.

1. In External Beam Planning, open a calculated plan that you want to add to a DVH estimation model.
2. Right-click the plan in the Scope window and choose **Drop to view**.
3. Choose **Planning > Add Plan to a DVH Estimation Model**.
4. From the **DVH Estimation Model** list, select the model to which you want to add the plan.



Tip: To sort the models, select a sorting option from the **Sort Order** list. You can sort the models by the model identifier, anatomical region, or the date when the model was last modified.

5. Review the model information:
 - **Model Version:** Version of the algorithm used in training the model. If a model has never been trained, it does not show the algorithm version.
 - **Anatomical Region:** The anatomical region, for which the model has been created.
 - **Trained:** Yes / No.
 - **Published:** User name of who published the model; publication date and time.
 - **Modified:** User name of who last modified the model; modification date and time.
 - **Description:** Description of the model.

If a model description document is available, you can open it by clicking **Clinical Description**.

If the plan has already been added to the model, a message is shown below the **Clinical Description** button.



Note: If you add the same plan again, note that all modifications that have been made to the plan in External Beam Planning after the previous time the plan was added to the model will be applied to the model. In addition, the changes you make in structure matching or plan prescription in the Add Plan to a DVH Estimation Model dialog box are also applied to the model. The re-extracted plan data replaces the old plan data in DVH Estimation Model Configuration. If the plan has already been used for model training (model version is shown in the In Model column), the trained model, including the statistical plots, is removed. If the plan has not yet been used for model training, the trained model is not removed.

6. Check that the **Plan Prescription** value is correct.
 - By default, **Plan Prescription** shows the Total Dose of the plan (shown in External Beam Planning on the **Dose Prescription** tab).
 - If you have imported the plan, enter the dose prescription used at the treatment unit in Plan Prescription.
 - If the plan contains multiple targets, make sure that Plan Prescription shows the highest target dose level.

You can modify the value in DVH Estimation Model Configuration.

7. Check that the structures are matched correctly, and change the matched structures if needed.
 - To change the matched model structure, select another structure from the **Model Structure** column.
 - If a plan structure is not included in the model, the row in the **Model Structure** column is empty. To include a plan structure in the model, select a corresponding model structure from the drop-down list.
 - To exclude a plan structure from the model, select the empty row from the drop-down list.

You must match at least one model Target structure to the corresponding target structure in the plan.

8. Click **OK**.

The system starts to extract plan data.



Note: When you have opened a model in DVH Estimation Model Configuration, and you add plans to the model in External Beam Planning, the plans become visible in the **Plans of the DVH Estimation Model** list only after you either close the current model and open it again, or close the DVH Estimation Model Configuration workspace and open it again.

After adding plans to the model, select the plans that you want to use for model training (select the check boxes in the **Include** column) and train the model. If you added new plans to an existing trained (unpublished or published) model, note that the plans are not included in the trained model until the model is re-trained.

Related Topics

- [Guidelines for Structure Matching](#) on page 289
[Structure Matching Examples](#) on page 291

Automatic Structure Matching

When you are adding plans to a DVH estimation model, plan structures can be automatically matched to corresponding model structures. The matching is based on structure codes and structure identifiers defined for the model structures and plan structures.

A plan structure is automatically matched to a model structure in the **Add Plan to DVH Estimation Model** dialog box, if the plan structure code matches one of the structure codes defined for the model structure. If a plan structure has no code matching is based on the structure identifier. Structure matching is not case-sensitive. If neither a matching code nor a matching identifier exists, the structure is not matched automatically.

Target structures are matched automatically if both the model and the plan have only one target structure, and the target structure in the plan has been defined as the plan target (in **External Beam Planning > Plan Properties > General > Target Volume**).

If the model or the plan contain several target structures (Volume Type defined as PTV, CTV, or GTV in Structure Properties), the targets are not automatically matched.

To take full advantage of the automatic matching, structure codes and identifiers used in the plans should correspond to the ones used in the model. Even though the initial matching is done automatically, you should still check the matching, and change it if needed.

Related Topics

[Structure Codes](#) on page 113

Guidelines for Structure Matching

Structure matching is needed for associating model structures to corresponding plan structures. Correct structure matching ensures that the model uses appropriate structure data for generating the DVH estimates.

Follow these guidelines when matching model structures to plan structures:

- Make sure that you match the structure (organ) to the corresponding structure (organ), and not to any other organ. For example, match the bladder to bladder, not to rectum.
- Match only those plan structures that have been taken into account in optimization.
- Use consistent matching in the whole structure set.

- To train a model for a specific structure, you must match at least 20 instances of the structure to the corresponding structure in the model. For example, you must match at least 20 rectums in the training set to the rectum structure in the model. As a result of the training, you receive DVH estimates for this structure. In addition, estimate-based objectives are also available if you have added them for the model structure. If you do not match enough structure instances, you receive no DVH estimates or estimate-based objectives for this specific structure.
- If you only want to generate fixed optimization objectives for a structure in optimization, you do not have to match the model structure to any plan structures when creating the model.
- If you do not want to add information about a specific plan structure to the model, leave the structure unmatched. The plan will be included in the model, but the information of this specific plan structure will be ignored.
- Bilateral structures, such as femoral heads: If you are creating a model for patient cases, where the field setup is symmetrical for the bilateral structure, match both structures in a plan to the same model structure. For example, Left femoral head and Right femoral head in a plan to Femoral head in the model. If you are creating the model for plans, where the field setup is asymmetrical for the bilateral structure, and the differences are easily identifiable, you can have two separate structures for the right and left structure in the model. In this case, match Right femoral head in a plan to Right femoral head in the model, and Left femoral head in the plan to Left femoral head in the model.
- You must match at least one target structure in the model to the corresponding target structure in the plan.
- If a model plan has multiple targets, but the model only one, you can select which one of the plan targets is treated as the model target. Match the most relevant target (or targets) in the plan to the model target depending on the purpose of the model. For example, if the model has been created for treating the primary target, match the primary target to the model target. If the model has been made for boost treatments, match the model target to the boost target. If the model is a combination model for sequential boost treatments with only one model target, you can match the model target to the primary target in the first phase, and to the boost target in the second phase. You can also match several plan targets in a plan to the same model target if they have the same target dose level and the matching fits the purpose of the model. For example, if right lymph nodes and left lymph nodes are target 1 and target 2 in the plan and both are receiving the same dose, then both can be matched to the same target in the model with the corresponding dose level.
- If a plan has only one target, but the model has several, match the plan target to the model target with the highest dose level and leave the rest of the model targets unmatched. The same approach applies even if the dose level in the plan is for an intermediate dose level.
- If both a plan and the model have multiple targets with different dose levels, always match the targets correspondingly - high dose level to high dose level,

intermediate to intermediate, and low to low. For example, if a model contains three targets, but a plan has only two, match the plan target with the highest dose level to the model target with the highest dose level, and the other plan target to the intermediate model target.

- If you have contoured two different structures for the same anatomical organ - one structure for the PTV and one for an OAR structure, do not match the OAR structure to the model target. For example, if the right parotid is contoured both as the PTV and the right parotid OAR, do not match the OAR structure to the right parotid OAR in the model, but leave it unmatched instead.

Table 20 Example of Target Matching for a Simultaneous Integrated Boost Treatment Plan

Targets in Model	High Dose	Intermediate Dose	Low Dose
3 Targets in Plan	70 Gy target	63 Gy target	56 Gy target
3 Targets in Plan	66 Gy target	60 Gy target	54 Gy target
2 Targets in Plan	60 Gy target	54 Gy target	
2 Targets in Plan	50 Gy target	45 Gy target	
1 Target in Plan	60 Gy target		
1 Target in Plan	36 Gy target		
1 Target in Plan	50 Gy target		

Structure Matching Examples

The following table provides examples of structure matching for organs at risk.

Table 21 Structure Matching Examples for OARs

Matching Scenario	Structure Codes and IDs in Plan	Structure Codes and IDs in Model	Actions
The plan and the model contain a structure with the same structure code. The structure identifiers are different.	BladderA (15900)	Bladder (15900)	Because the codes are the same, the structures are automatically matched.
The plan structure has one code, but the model structure has several codes.	Rectum (14544)	Rectum (14544, 14626)	Because the plan structure code matches one of the model structure codes, the structures are automatically matched.

Matching Scenario	Structure Codes and IDs in Plan	Structure Codes and IDs in Model	Actions
The plan has more structures than the model.	Bladder (15900) Rectum (14544) Femurs (9611)	Bladder (15900) Rectum (14544)	Bladder and Rectum are automatically matched. Femurs structure is not matched to any plan structure, and the row in the Model Structure column remains empty.
No structure code has been defined for the plan structure.	Bladder	Bladder (15900)	Because the structure identifiers are the same, the structures are automatically matched, even though the plan structure contains no code.
The plan structure has one code, but the model contains several structures with the same code.	Rectum (14544)	Rectum (14544, 14626) Rectal Wall (14544, 14626)	Because two matching codes exist for Rectum, the structures are not automatically matched. You need to manually match Rectum.
The plan has fewer structures than the model, and no structure codes have been defined for the plan structures.	Bladder Rectum	Bladder (15900) Rectum (14544) Rectal Wall (14626)	Bladder and Rectum are automatically matched. If you want to change the matching for Rectum, you can match it to Rectal Wall in the model, and remove the matching from Rectum.
The plan contains bilateral structures that are matched to one model structure.	Femoral Head Left (55012) Femoral Head Right (55011)	Femoral Head (55011, 55012)	Femoral Head Left and Femoral Head Right are automatically matched to Femoral Head.

Train a DVH Estimation Model

1. In DVH Estimation Model Configuration, go to the **Plans of the DVH Estimation Model** list.
2. Select the plans that you want to use for model training.
To do this, select the check box in the **Include** column for each plan.
3. Check the prescription of each plan in the **Plan Prescription** column and change it if necessary.
4. To check the structure matching in each plan, go to the **Structure Matching** column and click the browse button on the plan row.

5. In the **Structure Matching** dialog box, check that all the plan structures that you want to include in the model are matched to a model structure. The unmatched model structures are shown right to the list.
6. If you want to make changes in the structure matching, do one or several of the following:
 - To include a new plan structure in the model, select the new model structure in the drop-down list.
 - To change the existing matching of a plan structure, select the new model structure in the drop-down list.
 - To exclude a plan structure from the model, select the empty row in the drop-down list.



Note: If you include a new plan structure in the model, exclude a plan structure from the model, change the structure matching, or modify the plan prescription, the earlier extracted data is removed and you must re-extract the plan data. Otherwise, the new plan data will not be used for the model training. If only one plan needs to be re-extracted, it is recommended to re-add the plan in External Beam Planning. The **Extract** command in DVH Estimation Model Configuration will re-extract the data for all of the plans in the model plan set.

7. Click **OK**.
8. Repeat the steps for each plan.
9. If you modified the plan prescription, or made changes in the structure matching, click **Extract**.
10. After the plan data has been extracted, the **Extract data succeeded** dialog box opens and shows the results of the data extraction.
The log shows how many plans were extracted. Also information about skipped structures or skipped plans is displayed (if there are no errors). If extraction fails, the log will contain errors.
11. To start processing the data from the plans, click **Train**.

After the model has been trained, the version number of the model is shown in the In Model column, and statistical plots of the features in the trained model appear under the model plan set.

Next, you need to verify the results of the training.

Training a DVH Estimation Model

For training a model, you need the extracted data from the model plan set. During model training, statistical techniques, such as Principal Component Analysis and regression analysis³, are applied to the extracted plan data. The training results are shown in statistical tables and plots that are available for you in DVH Estimation Model Configuration.

More information about model training: *Eclipse Photon and Electron Algorithms Reference Guide*.

The training status of the model is shown in model properties (Yes / No is shown after Trained).

If a plan is included in the trained model, the version of the model is shown in the **In Model** column. Some modifications you make in the model may remove the extracted plan data (**Extracted** column is empty), and /or the trained model. If the trained model is removed, the **In Model** column is empty and the statistical presentations are removed. In this case, you need to re-extract plan data (if necessary) and re-train the model.

If a trained model contains no plans that would be shown in the **Plans of the DVH Estimation Model** list (imported model with no plan data, or a Varian-provided model), the statistical presentations are still available for these plans. In addition, each value in the plot (a data point or DVH curve) still contains the identification information for the plan and structure in the tooltip.

If you retrain a model, the original trained model data is overwritten.

Related Topics

[Changes that Require Re-extraction or Re-training](#) on page 309

[Extracting Plan Data](#) on page 306

[Verifying the Results of Model Training](#) on page 310

Creating a Model Description Document

You can create model description documents for your DVH estimation model, save them as PDFs, and attach them to the model in DVH Estimation Model Configuration. You can attach two kinds of documents to your model:

- Clinical model description document:

Contains instructions for the clinical use of the model. This document is mainly aimed at treatment planners. The document is available in the Optimization dialog box, in the Add a Plan to DVH Estimation Model dialog box, and in DVH Estimation Model Configuration.

- Technical model description document:

³ Hastie T., Tibshirani R., Friedman J.: *The Elements of Statistical Learning: Data Mining, Inference, and Prediction*. Second edition. Springer. February 2009. Chapter 3 provides information about linear regression. Chapter 7 contains information about model assessment and selection (training set size, validation sets, and cross-validation). Chapter 14 explains PCA.

Contains information about the training and validation of the model. This document is mainly aimed at medical physicists who are creating models. The document is available in DVH Estimation Model Configuration.

Consider adding the following kind of information into the clinical document:

- The anatomical region for which the model was created.
- The field setup for which the model was created, for example, IMRT 7-9 fields, VMAT 1-2 full arcs, mixed IMRT and VMAT fields.
- Structures for which the model creates DVH estimates.
- Optimization objectives that the model creates.
- The number of target structures supported by the model.
- NTO settings that the model creates
- Smoothing parameters that the model creates (for IMRT plans).
- Used structure codes in the model.
- Contouring guidelines for plans where you intend to use the model.
- Treatment planning guidelines (treatment strategy, prescription, target coverage, OAR objectives).

Consider adding the following kind of information into the technical document:

- Contouring guidelines for training plans.
- Number and type of training plans used.
- Training details from the training log.
- Pictures of statistical plots.
- DVH graphs that illustrate the difference between the estimated DVHs and the original clinical DVHs.
- DVH graphs that illustrate the difference between the final DVHs achieved by using the model and the original clinical DVHs.
- Number and type of validation plans used.
- How the validation plans were obtained.
- How the validation was performed (both the validation of generated DVH estimates and optimization objectives).

For more information on the type of information you may want to include in these documents, see the model description documents attached to Varian-provided models. Varian-provided models contain only one document, which includes both the clinical and the technical information.

Modifying a DVH Estimation Model

By duplicating an existing model, you can create several model versions of the same model plan set. You can make modifications to the model duplicate, re-extract data (if needed), train the model, and save it. During the model verification and validation you can compare the new model to the original one and see which one of them produces better results. After comparison, you can consider whether you want to keep both of the models, or remove the one that produces worse results. When you duplicate a model, you lose the revision history of the original model (information about how many times it has been published).

You can modify the model, for example, to add new structures, or to modify the structure codes, identifiers, or optimization objectives of existing structures.

You can also modify the plan set of a model by adding new plans to it or by removing existing ones. You can study how the removal or addition of a single training plan affects the results of the model by including the plan in the model training, or by excluding it. You can also study, how the removal or addition of a single structure affects the results of the model by changing the structure matching of that structure.

If you have access to the original treatment plans, it is possible to modify them, for example, to re-contour or re-optimize, and re-extract their data to be used in the model. In this case, you have two options for re-extraction: you can extract the data of this specific plan by adding it to the model again, or you can re-extract the data of all plans by clicking **Extract** in DVH Estimation Model Configuration.

If the model has been published, most of the modifications are prevented, which means that you need to unpublish the model before you are able to modify it. In an imported model, you may not be able to make modifications that require re-extracting the data or re-training the model.

Some of the modifications remove the extracted plan data from the model. In this case, the text Yes in the **Extracted** column is cleared. If the model has been trained, the **In Model** column shows the version number of the model. Some of the changes you make in the model remove the trained model. In this case, the statistical presentations disappear from the lower part of the screen.

If your modifications remove the extracted data, you have to re-extract the plan data to make it available for model training. Re-extraction replaces the existing plan data with the new data for the whole model plan set, including the possible modifications made to the plan in External Beam Planning. To make sure that no unwanted modifications end up in your model, verify the changes that have been made to the original treatment plans in External Beam Planning before re-extracting the data. To apply the changes to the model, you need to retrain the model.

You cannot modify Varian-provided models. You can only duplicate them, which provides you the optimization objectives and structures of the original model. No other information about the original model or the model plan set is included.

When you export, import, or duplicate a model, the model description documents attached to the model are retained. If you duplicate a Varian-provided model, the documents are removed from the duplicate.



Tip: *If you have made changes to the model that you do not wish to keep, close the model without saving and open it again.*



Note: *When you are modifying a model, remember to save your changes frequently. If another user opens the same model, modifies it in the DVH Estimation Model Configuration application, and saves the changes, you may not be able to save your changes anymore. This may happen also if you are modifying a model, and another user adds plans to the same model at the same time in External Beam Planning.*

Related Topics

[Extracting Plan Data](#) on page 306

Modify the Model Properties

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. To unpublish an already published model, click **Unpublish**.
3. Click **Edit Model and Structures**.
4. You can do the following:
 - Modify the model identifier.
 - Modify the model description.
 - Change the anatomical region.
 - Change the model description documents attached to the model.
5. Click **OK**.
6. Click **Save**.

These changes do not remove the existing training results. The changed information is available for you when you optimize new plans by using this model, or when you add new plans to the model.

Add a Model Structure

You can add structures to DVH estimation models in DVH Estimation Model Configuration.

1. To open the model, click **Open**, select a model and click **OK**.
2. If the model has been published, click **Unpublish**.
3. Click **Edit Model and Structures**.
4. Click **Add Model Structure**.
5. In the **Structure Code Selection** dialog box, select the structure code, click **Add**, and repeat for any other model structures.
6. Click **OK**.
7. Add the optimization objectives for the new model structure.
 - a. In the **Model Structures and Objectives** list, select the structure and click **Add Objectives to Structure**.
 - b. Define the objective and click **OK**.
8. Click **Save**.
 - The new structure is available for structure matching when you add new plans to the model.
 - If the structure is a target structure, the trained model and the extracted data of the whole model plan set are removed. Match the new target structure to corresponding target structures in all relevant model plans. The new target structure needs to be matched to at least two target structures in the model plans.
 - If the structure is an organ at risk, the trained model remains, but the new model structure is not matched to any structure in existing training plans.
 - The new structure and optimization objectives are available when you optimize new plans by using this model.
9. To apply the change to existing model plans, match the model structure to the corresponding plan structures in the **Plans of the DVH Estimation Model** list.
10. To re-extract data from the model plans, click **Extract**.
11. To apply the change to the model, click **Train** and **Save**.

Remove a Model Structure

You can remove structures from DVH estimation models in DVH Estimation Model Configuration. If you remove a structure from a model and then add it back, you have to rematch all plan structures to the model structure in the model plan set.

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. If the model has been published, click **Unpublish**.
3. Click **Edit Model and Structures**.
4. Click the X button next to the structure.

In the model plan set, the matching is removed from those plan structures that were matched to this model structure.

5. Click **Save**.
 - The removed structure will no longer be available when you add new plans to the model, or use the model for optimizing new plans.
 - If the structure that you removed was a Target structure, the extracted data of the whole model plan set and the trained model are removed.
 - If the structure that you removed was an OAR, the extracted data of this specific OAR and the trained model are removed.
6. If the structure that you removed was a target structure, click **Extract**.
7. To apply the change to the model, click **Train** and **Save**.

Change the Target Structure in a Model

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. If the model has been published, click **Unpublish**.
3. Click **Edit Model and Structures**.
4. Clear the check box in the **Target** column for the existing target structure, and select the check box of the new target structure.

You can add up to 3 target structures to the model, but at least one target structure is required.

5. Click **OK**.
6. Click **Save**.
 - The trained model and the extracted data of the whole model plan set are removed. You must re-extract and re-train the model.
 - The new target structure and optimization objectives are available when you optimize new plans by using this model. The new target structure is also available when you add new plans to the model.

7. To make sure that the structure matching in existing model plans is still valid after the change, check the structure matching for each plan in the **Plans of the DVH Estimation Model** list.



Note: If you added a new target structure, match it to the corresponding target structures in all relevant model plans. The target structure needs to be matched to at least two target structures in the model plans. Every plan needs to have at least one structure matched to one of the model targets.

8. To re-extract data from the model plans, click **Extract**.
9. To apply the change to the model, click **Train** and **Save**.

Modify the Codes and Identifiers of Model Structures

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. To unpublish an already published model, click **Unpublish**.
3. Click **Edit Model and Structures**.
4. Select the structure and click **Edit**.
5. You can do the following:
 - Modify the identifier of the model structure. The structure identifier must be unique within the model.
 - Add a structure code to the model structure.
 - Remove a structure code from the model structure (if it has multiple codes).
6. Click **OK**.
7. Repeat the steps above for each structure that you want to modify.
8. Click **OK**.
9. Click **Save**.

The changed information is available for you when you optimize new plans by using this model, or when you add new plans to the model.

10. To re-extract data from model plans, click **Extract**.
You have to always re-extract the model plan data if you changed structure identifiers or structure matching.
11. To apply the change in the model, click **Train** and **Save**.

Modify Optimization Objectives, NTO, and Smoothing Parameters

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. To unpublish an already published model, click **Unpublish**.

3. You can do the following:
 - Add an optimization objective for a model structure: Select the structure in the **Model Structures and Objectives** list, and click **Add Objectives to Structure**.
 - Remove an optimization objective from the model structure: Select an objective in the **Model Structures and Objectives** list, and click the x button on the objective row.
 - Modify the parameters of an optimization objective. Edit the values in the **Vol [%]**, **Dose**, **Priority**, and **gEUD** a columns directly. If the values have been generated by the DVH estimation algorithm, the text **Generated** is shown. To modify a generated parameter value, you need to remove the whole objective, and add it again with desired values.
 - Modify the NTO settings under the **Normal Tissue** expander.
 - Modify the smoothing parameter settings for IMRT plans under the **Smoothing Parameter** expander.

4. Click **Save**.

The changed information is available for you when you optimize new plans by using this model.

Related Topics

[Optimization Objectives for Target Structures](#) on page 273

[Optimization Objectives for Organs at Risk](#) on page 276

[Normal Tissue Objective in Photon Optimization](#) on page 230

[X Smooth and Y Smooth](#) on page 233

Duplicate a DVH Estimation Model

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. Click **Duplicate**.

If the **Duplicate** button is not active, save the model first.

The new model ID is appended with a running number. The duplicated model contains all the information of the original model. If the original model was Published, the status of the duplicate changes to Unpublished.

3. Modify the duplicate model as desired.

If you duplicated a Varian-provided model, you should not make such changes that require re-training the model. If you duplicated an imported model that contains plan data, you should not make such changes that require re-extracting the plan data. If you duplicated an imported model that contains no plan data, you should not make such changes that require re-training the model.

4. If you made such changes that require re-extracting plan data, click **Extract**.
The data of all the plans in the **Plans of the DVH Estimation Model** list is re-extracted.
5. To train the model, click **Train**.
6. To save the model, click **Save**.

Modifying a Duplicate of a Varian-provided Model

If you duplicate a Varian-provided model, the duplicate contains the following information:

- Trained model (the **Trained** field in model properties contains the text **Yes** without statistical plots).
- Structures of the original model.
- Optimization objectives of the original model.

No other information about the original model or the model plan set is included.

You can modify only the following in the duplicate of a Varian-provided model:

- Modify the optimization objectives of existing structures: Add both fixed and algorithm-based objectives, remove objectives, or change any parameters. If a structure has not been used in model training, and you add algorithm-based objectives for it, they will not be available in optimization.
- Add new OAR structures and fixed optimization objectives for them. If you add algorithm-based objectives for the OARs, they will not be available in optimization.
- Modify NTO and smoothing parameters.



Note: You should not make such changes in a duplicate of a Varian-provided model that require re-training the model. For example, if you add new plans to the model, and re-train the model, the original training results are removed, and the statistical plots only show the training results of the new plans. To be able to use the original trained model, you have to duplicate the model again.

Delete a DVH Estimation Model



Note: You cannot delete Varian-provided models.

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. To unpublish an already published model, click **Unpublish**.
3. Click **Delete**.

The DVH estimation model and the related model plan set are removed. The original treatment plans in the database are not removed.

Remove a Plan from a Model

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. If the plan is in a published model, click **Unpublish**.
3. In the **Plans of the DVH Estimation Model** list, click the X button on the row of the plan that you want to remove.

The plan is removed from the list. The original treatment plan in the database is not affected. The trained model data is also removed. If you removed a plan that was not included in the previous training, the trained model data is not removed.

4. If the trained model data was removed, click **Train** to apply the change to the model.
5. Click **Save**.

Include or Exclude a Plan

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. In the **Plans of the DVH Estimation Model** list:
 - To include a plan in the next model training, select the check box in the **Include** column on the plan row.
 - To exclude a plan from the next model training, clear the check box in the **Include** column on the plan row.If the plan has already been used in model training (a model version number is shown in the **In Model** column), the plan is excluded from the next training, and from the statistical plots, except for the DVH plot and geometric plot.
3. To apply the change to the model:
 - a. If the model has already been published, you need to first unpublish it by clicking **Unpublish**.
 - b. Check the structure matching and plan prescriptions of the plans, and change them if needed.
 - c. If you made such changes in the model plans that require re-extracting data, click **Extract**.
 - d. To retrain the model, click **Train** and **Save**.

Change Structure Matching in a Model Plan

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. If you are going to change the structure matching in a plan that is in a published model, click **Unpublish**.
3. In the **Plans of the DVH Estimation Model** list, click the browse button on the row of the plan.
4. To change the structure matching of a plan structure:
 - To change the matched model structure, select another structure from the drop-down list in the **Model Structure ID** column.
 - If a plan structure is not matched to a model structure, the row in the **Model Structure ID** column is empty. To match a plan structure to a model structure, select a corresponding model structure from the drop-down list.
 - To exclude a plan structure from the model, select the empty row from the drop-down list.

You must match at least one model target structure to the corresponding target structure in the plan.

The extracted data of this specific plan and the trained model data are removed.

If you change the structure matching in a plan that has been trained at least once, but has been excluded from the previous training, the change does not remove the trained model. Note that the statistical presentations do not reflect the change in structure matching until you re-extract the plan data, include the plan in training again, and re-train the model.

5. Click **OK**.
6. To re-extract data from the model plans, click **Extract**.
7. If the trained model data was removed, click **Train** to apply the change to the model.
8. Click **Save**.

Related Topics

- [Guidelines for Structure Matching](#) on page 289
[Structure Matching Examples](#) on page 291

Change the Prescription of a Model Plan

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. To unpublish an already published model, click **Unpublish**.

3. In the **Plans of the DVH Estimation Model** list, enter a new prescription for the plan in the **Plan Prescription** column.



Note: If the plan contains multiple targets, enter the highest target dose level in this field.

The extracted data of this specific plan and the trained model data are removed.

If you change the prescription in a plan that has been trained at least once, but has been excluded from the previous training, the change does not remove the trained model. Note that the statistical presentations do not reflect the prescription change until you re-extract the plan data, include the plan in training again, and re-train the model.

4. Move the focus outside the **Plan Prescription** column (click outside the column).
5. To re-extract data from the model plans, click **Extract**.
6. If the trained model data was removed, click **Train** to apply the change to the model.
7. Click **Save**.

Modify a Plan in a Model

Sometimes you may have to modify a plan that has already been added to a DVH estimation model. This may happen, for example, if you need to modify the contours in the plan, or contour a new structure, and re-optimize the plan. To apply the changes to the model, you need to add the plan again to the model, and re-train the model. When re-adding the plan, note that the plan identification number changes.



Note: When you add a modified plan to the model in External Beam Planning, the plan will be included in the next model training by default. In other words, the check box in the **Include** column in DVH Estimation Model Configuration is selected. The check box is selected, even though it was cleared for the original model plan.

1. Open the plan in External Beam Planning.
2. Modify the plan as you wish.
3. Re-optimize the plan, and re-calculate the dose, if necessary.
4. Evaluate the dose distribution by using the standard plan evaluation tools.
5. When the plan is ready to be added to the model, right-click the plan in the Scope window and choose **Drop to view**.
6. Choose **Planning > Add Plan to a DVH Estimation Model**.
7. Select the model, in which the plan exists.
8. Verify the structure matching and plan prescription.
9. Click **OK**.

10. Go to DVH Estimation Model Configuration and click **Open** and select the model.
11. To include the modified plan to the next model training, make sure that the check box in the **Include** column for the plan is selected.
12. Click **Train and Save**.



Tip: If you make modifications to several plans in External Beam Planning, you can also choose to re-extract the plan data in DVH Estimation Model Configuration. In this case, the plan data is re-extracted for all the plans in the model plan set, which means that you do not have to add each plan separately to the model. After re-extraction, you need to train and save the model.

Re-extract Plan Data

If you have made such changes in a DVH estimation model or in the original treatment plans that require re-extraction of plan data, do the following:

1. In External Beam Planning, review all the plans of the model before re-extracting their data.

You need to review all the plans, and not only the modified ones, because the plan data is re-extracted from all the plans in the model plan set. Confirm that no such modifications were made to the plans that would make them unsuitable for the model.

2. In DVH Estimation Model Configuration, click **Extract**.

If you have already trained the model, the trained model and the statistical plots are removed.

3. Check the results of the data extraction.

You can copy-paste the contents of the dialog box and save it in a separate document. The log tells you if some plans or structures have been skipped, and their data has not been extracted. Excluded plans or structures will not be used in the model training.

4. Click **OK**.

After the plan data has been re-extracted, the **Extracted** column shows the text Yes. To apply the re-extracted data to the model, retrain the model.

Extracting Plan Data



Note: The time it takes to extract data for a model with a large plan set varies, but it may take several minutes. It is recommended to extract the data for models with large plan sets after normal working hours.

Extracted plan data is needed for training a DVH estimation model. The extraction is done automatically when you add a treatment plan to the model. Not all data stored in the original treatment plans is included. Only the following plan data is extracted and converted into model parameters:

Table 22 Plan Data Conversion to Model Parameters

Treatment Plan Data	Model Parameter
Field geometry, structure set, and dose matrix	Geometry-based Expected Dose (GED) histograms for each OAR. A GED measures how much dose a certain OAR voxel would receive if only the patient anatomy, the desired target dose level, and the field setup (position and orientation) would be taken into account. A GED histogram indicates how far away different voxels in a structure are from target surfaces. The relative target dose levels are calculated from the dose matrix, and they are scaled by using the defined Plan Prescription value. More information on GED: <i>Eclipse Photon and Electron Algorithms Reference Guide</i>
Dose matrix and structure set	DVH
Structure set	The volume of each OAR in cm ³ .
Field geometry and structure set	Overlap volume percentage of each OAR with the union of all the targets.
Field geometry and structure set	Out-of-field volume percentage of each OAR.
Structure set	Joint target volume (volume of all matched target structures) in cm ³ .

If a model plan contains extracted data, the text “Yes” is shown in the Extracted column. If you modify the original treatment plans (for example, the structure set) in External Beam Planning, you have to re-extract the plan data. You can do that by clicking **Extract** in DVH Estimation Model Configuration. You need to re-extract plan data also if you have made such changes in the model that have removed the extracted data. In this case, the **Extracted** column is empty.



Note: When you re-extract plan data, the data of all the original treatment plans (and not only the modified ones) is re-extracted. The new plan data overrides all existing plan data in DVH Estimation Model Configuration. This happens for both plans that are included in the trained model, and plans that are not.



Tip: If you need to modify only one (or a few) treatment plans in External Beam Planning, or change their plan prescriptions, or structure matchings, you can do that by adding the same plan again to the model. In this way, you re-extract only the data of this specific plan, and not the whole plan set. The new extracted plan data overwrites the old extracted plan data. No plans, structures, nor other plan data are added twice to the model. If you add such a plan to the model that has already been included in model training, the data of this specific plan is updated, but the trained model, including the statistical presentations, is removed.

If the plans in the training set contain no extracted data (the **Extracted** column is empty) and the plans have no link to existing treatment plans in the database (the **Patient ID/Course ID/Plan ID** column shows “N/A”), you should not try to re-extract the plan data. If you do, the current trained model is removed, and re-training is no longer possible. Even though a trained model does not contain any extracted data anymore, you can still use it for generating DVH estimates and optimization objectives.

If the plans in the training set contain extracted data, but have no link to existing treatment plans in the database, you can still modify the model, for example, add more plans to the model, and train the model. However, you should not try to re-extract the plan data, because re-extracting removes the existing data.

When you re-extract plan data in a model that has already been trained, the current trained model and the statistical presentations are removed. To apply the new extracted data to the model, you have to retrain the model.

Related Topics

[Changes that Require Re-extraction or Re-training](#) on page 309
[Training a DVH Estimation Model](#) on page 293

Data Extraction Log

The data extraction log contains the following information:

- Number of model plans, from which data has been extracted.
- Skipped plans, from which no data has been extracted. Plans may be skipped if they contain corrupted data, have no Body structure, have no dose, etc.
- Skipped structures, from which no data has been extracted. Structures may be skipped if the structure is too small (all the voxels of the structure are only half a voxel or less in size), or if an error occurred, for example, in retrieving the structure data or calculating the histograms, etc.

Changes that Require Re-extraction or Re-training

When you make such changes in a model that affect the extracted plan data or the trained model data, the current plan data and the trained model data are removed. In this case, you need to re-extract the data and retrain the model to apply the changes to the model. The following tables describe which changes remove the extracted plan data, trained model data, or both. In addition, the tables tell you which changes require you to re-extract plan data, re-train the model, or do both.

Table 23 Changes on the Model Level that Require Re-extraction or Re-training

Change	Removed Data	Action for Updating the Model
Modify the model properties (identifier, description, documents, anatomical region).	None	None
Add an OAR structure to the model and match the structure to plan structures.	Extracted data (of the plans where the structures are matched)	Re-extract and re-train
Add an OAR structure to a model with only fixed objectives.	None	None
Remove an OAR from the model. Applies also to models that contain only fixed objectives.	Trained model data	Re-train
Add, change, or remove a target structure. Applies also to models that contain only fixed objectives.	Extracted plan data and trained model data	Re-extract and re-train
Add, change, or remove structure codes of a structure (target or OAR). Applies also to models that contain only fixed objectives.	None	None
Modify a structure identifier (of a target or an OAR) in model properties. Applies also to models that contain only fixed objectives.	Extracted plan data and trained model data	Re-extract and re-train
Add, change, or remove optimization objectives, NTO settings, or smoothing settings.	None	None

Table 24 Changes on the Plan Level that Require Re-extraction or Re-training

Change	Removed Data	Action for Updating the Model
Modify structure matching (add, change, or remove) for a structure in a plan. Applies both to target and OAR structures.	Extracted data (of this specific plan) and trained model data	Re-extract and re-train
Modify the plan prescription in a plan.	Extracted data (of this specific plan) and trained model data	Re-extract and re-train
Remove a plan that has been included in the previous model training.	Trained model data	Re-train
Remove a plan that has not been used in the previous model training.	None	None
Select plans to be included to, or excluded from, the next model training.	None	Re-train
Add a plan to the model in External Beam Planning.	None	Re-train
Modify an original treatment plan of the model in External Beam Planning, and add the plan to the model again (overwrites the old data of this specific plan).	Trained model data	Re-train
Delete a plan in External Beam Planning.	None	None

Verifying the Results of Model Training

After the DVH estimation model has been trained, you need to verify the results. During the verification, you check the following:

- Model fit, in other words, how well the model is able to estimate plans that were included in the training set.
- The preliminary results of the estimation ability of the model, in other words, how well the model is able to estimate new patient cases. The final estimation ability of the model is checked in the model validation phase.

If the model fit is poor, it indicates that the model does not represent the training data, and has not been able to capture the relationship between anatomical features and DVHs. If the model fit proves to be good, it indicates that the model has been able to capture this relationship.

If the estimation ability of the model is good, it indicates that the model is likely to estimate new patient cases adequately. However, you should still make sure that this is the case by validating the model with a sufficient number of plans.

During the model verification, you need to pay attention to the following aspects:

- Make sure that the number of training plans and structures is sufficient for the model.
- Check the general quality of the model (initial model fit).
- Check that no overfitting of data occurs (good model fit, bad estimation ability). If this happens, consider adding more plans to the model.
- Check the consistency of the data in the training set - make sure that the data does not form multiple data groups. If this happens, consider adding more plans to the model, or dividing the model into separate models.
- Check that no gaps between data point groups exist. If this happens, consider adding more plans to the model that fulfill the gap.
- Identify influential data points that have a great effect on the model fit and the estimation ability of the model.
- Identify single training plans or structures that differ from the average in the training set (outliers).
- Verify the final model fit and estimation ability of the model.

You can use the statistical presentations (plots and tables) as an aid in model verification. If you want to make any changes to the model during verification, you can duplicate the model, make the changes, re-extract the plan data (if necessary), retrain the model, and compare the results to those of the original model. Because retraining may cause different outliers to appear, you have to start the verification process again from the beginning.

Outliers

Outliers are single training plans or structures with data values that do not seem to fit the data in the rest of the training set. An outlier differs considerably from the average in the training set. The difference can be in geometry, dosimetry, or both. An outlier may represent alone a certain plan feature in the training set, which means that the trained model may not produce optimal estimates for patient cases with this plan feature. For example, if you have one training plan with a full bladder, but all the other training plans have empty bladders, the model may not produce optimal results for patient cases with full bladders. You can view information about potential outliers in the statistical tables and plots.

Influential Data Points

Training plans may contain influential data points that have a great effect on the regression model. An influential data point is not necessarily an outlier, but it is a data point that has a significant influence on the outcome of the DVH estimation model (on the generated DVH estimates). Influential data points may also indicate dosimetric or geometric outliers.

You have the following tools for detecting influential data points in the model:

- Cook's distance (CD) values in the outlier statistics for structures.
- Regression plot for structures.
- Residual plot for structures.

Review training plans with influential data points with additional care in External Beam Planning to make sure that they will not have undesired effects on the model. To evaluate the actual influence of an influential data point, exclude the training plan from the model, and retrain the model.

After exclusion, check whether the slope of the regression plot changes and the distribution of the data points around it. Compare the DVH plot that the modified model produces to the original DVH plot. Evaluate whether the change in DVH estimates is dosimetrically significant. The change is significant if the shape or position of the DVH estimate is considerably different in relation to the original DVH estimate. For example, if the original DVH estimate was very close to the actual DVH curve, but after the exclusion the estimate is considerably below or above the actual DVH curve, the change is dosimetrically significant. The change is significant also if the shape of the DVH estimate does not follow the actual DVH curve anymore after exclusion. If the DVH estimate is almost similar in shape and in position when compared to the original DVH estimate, the change is likely to be dosimetrically insignificant.

If the change in estimates is dosimetrically insignificant, the training plan is not likely to be an outlier. You can consider keeping the training plan in the training set.

If the change in estimates is dosimetrically significant, verify that the training plan actually represents a typical dosimetric outcome for the geometry. If it does, consider keeping the training plan in the model, and adding more similar plans to the model. You may want to do this, especially if the influential data point is driving the regression model. If you cannot add more plans to the model, it is recommended that you remove the plan with the influential data point from the model. This might, however, reduce the scope of your model.

If the training plan does not represent the typical dosimetric outcome for the geometry, the training plan may be an outlier and you should consider removing it. If you remove the training plan, check whether the removal causes new influential data points to become visible.

You have the following options for processing the influential data points in the model:

- Remove the plans or structures with influential data points from the model.
Consider doing this if the plan or structure proves to be a real outlier.
- Leave the influential data point in the model, but add more similar plans to the model. Consider doing this if the plan or structure is not a real outlier.

Related Topics

- [Process Influential Data Points](#) on page 321
- [Outlier Statistics](#) on page 345
- [Regression Plot](#) on page 327
- [Residual Plot](#) on page 335

Geometric Outliers

A geometric outlier is a structure with different geometrical features than the same structure in the rest of the training plans. For example, if one of the bladder structures in the training set has been contoured when full, and the rest have been contoured when empty, the full bladder appears as a geometric outlier. Geometrical outliers can be caused, for example, by the following:

- The structures have been incorrectly matched.
- A different clinical protocol has been used for the training plan (for example, empty bladder vs. full bladder).
- The training plan represents a different clinical case. For example, only one prostatectomy case exists in the training set.

You have the following tools for identifying geometric outliers:

- Modified Z-score (mZ) values in the outlier statistics for structures.
- Geometric plots for structures.
- Regression plots for structures.

You have the following options for processing the outliers:

- Include more training plans with similar geometrical features in the training set.

In this case, the original outlier structure may no longer be an outlier. This option expands the use of the model to a wider range of patient cases. For example, if all but one training plans have been contoured with an empty bladder, and you remove the only plan with a full bladder, the model use will be limited to patient cases with an empty bladder. By adding more patients with a full bladder, the model use could be expanded. However, be aware that expanding the model is not always the best solution, because it may lead to compromises. For example, a specific model for an empty bladder may create better estimates for plans with an empty bladder than a general model that includes both empty and full bladders.

- Remove the outlier structure.

You can either exclude the whole training plan from the model, or remove the structure matching of this specific outlier structure. You may want to remove the outlier structure, if it has been caused by the use of a different clinical protocol, or if the training plan is a different clinical case than the rest of the training plans. However, by removing the outlier structure, you might limit the use of the model as described above.

- Leave the outlier structure in the model.

Verify the effect of this option very carefully, because a geometrical outlier is likely to have a significant effect on the estimation of any patient case. This is even more important if both the modified Z-score value and Cook's distance are over the threshold. Furthermore, make sure that the validation set contains plans with similar geometrical features.

Related Topics

[Process Geometric Outliers](#) on page 321

[Outlier Statistics](#) on page 345

[Geometric Plot](#) on page 326

[Regression Plot](#) on page 327

Dosimetric Outliers

A dosimetric outlier is a training plan with different dosimetric characteristics than what was estimated by the DVH estimation model. Dosimetric outliers can alter the DVH estimation model, especially if the outliers are influential. The dosimetric outliers can also increase the variance in the model, in other words, produce a wider estimated DVH range.

Dosimetric outliers can be caused, for example, by the following:

- The structures have been incorrectly matched.
- The training plan has been optimized more aggressively than the rest of the training plans, or vice versa.
- The training plan has different trade-offs between OARs or between the current OAR and target coverage.
- The training plan represents such variation in the plan or field geometry that has not been well taken account in the variation of the rest of the training set. This might happen, for example, if most of your training plans are 7-field IMRT plans, and this one specific plan is a VMAT plan. Or if most of your training plans are 9-field IMRT plans, and this one specific plan is a 5-field IMRT plan. Or if all training plans are 7-field IMRT plans, but in this specific plan, the field setup is completely different, for example, because of avoiding a prosthesis. Note that a different field geometry alone does not necessarily mean that you have to remove the training plan.

You have the following tools for identifying dosimetric outliers:

- Studentized residual (SR) and areal difference of estimate (dA) values in the outlier statistics for structures.
- Residual plots for structures.
- DVH plots for structures.
- In-field DVH plots for structures.

Dosimetric outliers may not be visible in the plots if the model is overfitting data. That is why it is important that you rule out overfitting (and process influential points and geometric outliers) before processing the dosimetric outliers.

You have the following options for processing the outliers:

- Remove the outlier structure.

You can either exclude the whole training plan from the model, or remove the structure matching of this specific outlier structure. Consider this option if you find no reason for the dosimetric outlier.

- Re-plan the original training plan in External Beam Planning.

Check if the dosimetric quality of the training plan can be improved by re-planning. You can use an existing model as an aid in re-planning. If the quality improves, add the modified plan to the model to replace the original one.

- Leave the training plan in the training set.

Consider this option if you find no apparent reason for the dosimetric outlier, and the training plan has no considerable effect on the model (Cook's distance is lower than 4). To verify the lack of effect, duplicate the model, exclude the training plan from the model, retrain the model, and compare the DVH plot of the modified model with the DVH plot of the original model. It is possible that what appears as a dosimetric outlier is indeed presenting a variation in the training set that has not been explained by the current geometric considerations.

Verify the affect of this option carefully, especially if the Cook's distance is also over the threshold. Make sure to validate the model with similar plans.

Related Topics

- [Process Dosimetric Outliers](#) on page 323
- [Outlier Statistics](#) on page 345
- [Residual Plot](#) on page 335
- [DVH Plot for Target Structures](#) on page 339
- [DVH Plot for Organs at Risk](#) on page 337
- [In-field DVH Plot](#) on page 341

Processing Outliers

During the model verification, you need to identify the potential outliers in the training set by using the statistical plots and tables as an aid. After identifying outliers in the training set, you need to decide what to do with them (remove, leave but add more plans, recontour, replan, etc.), re-extract the plan data, and retrain the model. Process the outlier data values iteratively. Try to identify first the influential data points. If you detect one, try removing the training plan from the model to confirm whether the plan was an outlier. Next, process the geometrical outliers (remove, leave but add more training plans, recontour, replan, etc.), and then re-extract the plan data (if necessary), and retrain the data. Only after this, process the dosimetric outliers. Remove the most significant outliers that seem to affect the regression line trend. Otherwise, the model may not produce optimal results. However, you do not necessarily have to remove all outliers.

If there is a gap between the outlier and the rest of the parameter values, and the trend between them remains unclear because of the missing values, you might want to add more plans to the model. After retraining, you can see how the trend has developed. If you cannot add more plan data, it is recommended to remove the outlier. After adding more plans, the following may happen:

- New outlier values may appear, and the plan proves to be a real outlier.
- New outlier values may appear, the plan proves not to be a real outlier.
- No new outliers appear, and the plan proves to be a real outlier.
- No new outliers appear, and the plan proves not to be a real outlier.

If new outlier values appear, you should investigate them further. If the plan proves to be an outlier, you should remove it from the model.

In many cases, the effects of outliers cannot be neutralized by merely adding more plans to the model. If you need to remove outlier plans from the model and the number of plans in the model falls below 20, you should add new plans to the model. In addition, if you leave outlier structures unmatched, and the number of matched structures per model structure falls below 20, you receive no estimates or estimate-based objectives for the structure. In this case, match more plan structures to that specific model structure.

Verify the Results of Model Training

The following provides you a general process for verifying the results of model training.

1. Check the initial results of model training by using the following tools:
 - Summary of training results.
 - Training log.
 - DVH plots for target structures.
2. Verify the *initial model fit* by using the following tools:
 - Coefficient of determination and chi square values in the summary of training results.
 - Notification in the summary of training results if the training set does not contain enough instances of a specific structure region, and therefore, the generated model type for this region has changed.
 - Regression (scatter) plots for structures.
 - Residual (scatter) plots for structures.
3. Identify and process influential data points in the model by using the following tools:
 - Cook's distance (CD) values in the outlier statistics for structures.
 - Regression plots for structures.
 - Residual plots for structures.
4. Identify and process geometric outlier values in the model by using the following tools:
 - Modified Z-score (mZ) values in the outlier statistics for structures.
 - Geometric plots for structures.
 - Regression plots for structures.
5. Identify and process dosimetric outlier values in the model:
 - Studentized residual (SR) and areal difference of estimate (dA) values in the outlier statistics for structures.
 - Residual plots for structures.
 - DVH plots for structures.
 - In-field DVH plots for structures.
6. Verify the *final model fit* by using the following tools:
 - DVH plots for structures.
 - In-field DVH plots for structures.

7. Verify the *estimation ability of the model* by using the following tools:

- DVH plots for structures.
- In-field DVH plots for structures.
- Goodness-of-estimation statistics in the training log.

Related Topics

[Tools for Model Verification](#) on page 325

Check the Initial Model Training Results

To start the model verification process, check the following:

1. In DVH Estimation Model Configuration, open the summary of training results for the model.
 - a. Check that enough plan target structures have been matched to each model target.
If not enough plan target structures have been matched, the training fails, and the reason for the failure is reported in the training log.
 - b. Check that all necessary OARs have been trained.
2. Open the training log by clicking **Training Log**, and check that no error messages have been generated.
3. Check the DVH plot for each target structure:
 - a. Check the shape of the DVH curves.
If the shapes are very different, check that the target structures have been matched correctly, and that the plans have a similar treatment goal.
 - b. Check that none of the DVH curves is apart from the rest.
If a DVH curve is apart, make sure that the plan prescription value is correct. If the value is correct, check that the target structure is correctly matched. If this is the case, open the plan in External Beam Planning for further investigation.

Related Topics

[Summary of Training Results](#) on page 343
[DVH Plot for Target Structures](#) on page 339

Verify the Initial Model Fit

1. In DVH Estimation Model Configuration, open the summary of training results for the model:

- a. Check the goodness-of-fit statistics (coefficient of determination and chi square) for each OAR to verify that the model is not overfitting data.

Sometimes it is possible to improve the statistics by adding more training plans and by making sure that the training plans do not contain highly influential data points or outliers. If the statistics of the model are poor and all of your plans are reported as outliers, make sure that all the plans you have added to the model are unique, and no identical copies exist. Even though the statistics would be good, you need to still identify and process the outliers, because they can worsen the quality of the model.
 - b. If the statistics are poor, check that enough plan structures have been matched to each model structure.
 - c. Check that enough structures with an in-field region have been matched to each model structure.

If this is not the case, check the suggested number of structures with an in-field region. Consider adding more structures to the training set.
 - d. Check that the number of structures has been sufficient for the region-specific models.

If the number of structures has not been enough, a highlighted “Yes” is shown in the **Trained** column. Hover your mouse over the cell to see a tooltip that shows which of the structure regions does not have enough instances, and which model type was created for this region instead of the standard one.
2. If you modified the model, re-extract plan data, retrain the model, and start the verification from the beginning.
 3. Check the regression plot for each structure:
 - a. Check that enough data points exist.
 - b. Check the influential data points.

An influential data point is usually far from the main group of data points, and tends to pull the regression line towards itself.

 - c. If an influential data point exists, consider the following options: add more plans to the model, remove the training plan or structure with the influential data point, or add more plans and leave the influential data point.
 - d. Check if the data points follow a joint trend or if the data points are divided into groups (that either follow the same trend, or follow different trends).
 - e. If the data points follow the same trend, but there is a gap between the upper end and lower end of the regression line, you may consider adding more training plans to cover the missing parts.
 4. Check the residual plots for each structure:

- a. Check whether the data points follow the identity line.
 - b. If the data points do not follow the identity line, the quality of the model is not good, and the training set may contain outliers or influential data points.
Analyze the outliers and influential data points.
 - c. Check the distribution of the data points, especially the width.
 - d. If the data points follow the identity line, but the distribution is very narrow (all data points are very close to or over the identity line), the model may be overfitting data.
In this case, add more plans to the model.
 - e. If the data points follow the identity line, but the distribution is wide, the variation in the training set may be too wide.
In this case, investigate the plan in External Beam planning (check for different trade-offs, clinical protocols, etc.).
5. If you modified the model, re-extract plan data, retrain the model, and start the verification from the beginning.

Related Topics

- [Summary of Training Results](#) on page 343
- [Regression Plot](#) on page 327
- [Residual Plot](#) on page 335

Check Outlier Statistics

- 1. In DVH Estimation Model Configuration, open the summary of training results for the model.
Check the number of potential outlier values for each OAR.
- 2. If an OAR has outlier values, open the summary of outlier statistics.
You can see the highest outlier statistics value for the OAR in each plan.
- 3. If any of the values for an OAR are highlighted, open the outlier statistics for the OAR.
You can see the outlier statistics values for the OAR in each plan. If any of the values is highlighted, the training plan and structure is considered a potential outlier.

Related Topics

- [Summary of Training Results](#) on page 343
- [Summary of Outlier Statistics](#) on page 344
- [Outlier Statistics](#) on page 345

Process Influential Data Points

1. In DVH Estimation Model Configuration, open the summary of the most important outliers for the model:
 - a. Check the Cook's distance value (CD) for each structure.
If the value for a structure is highlighted, investigate the case further.
2. View the regression plot for the structure.
Check if a data point is pulling the regression line towards itself, especially if a group of data points exists, and the regression line goes through a data point which is quite far from the data group. This indicates that the model may be overfitting data.
3. Check the residual plot for the structure.
Check those data points that are very close or over the identity line, and apart from other data points. Check if those data points also have a high Cook's distance value. If this is the case, the model may be overfitting data. Analyze the reason for the values, by opening the plan in External Beam Planning, and trying to find out how it differs from the rest of the plans. If the data point turns out to be an outlier, consider whether you want to remove the training plan or structure from the model, or add more plans to the model.
4. If you modified the model, re-extract plan data, retrain the model, and start the verification process from the beginning.

Related Topics

[Influential Data Points](#) on page 311

Process Geometric Outliers

1. In DVH Estimation Model Configuration, open the summary of the most important outliers for the model:
 - a. Check the modified Z-score value (mZ) for each structure.
If the value for a structure is highlighted, investigate the case further.
2. View the geometric plots for each structure.
Pay attention to the data points that are very high or very low in the plot and are apart from the other data points. They indicate a potential geometric outlier (if the modified Z-score is also highlighted).
3. If the geometric plot indicates an outlier, do the following:
 - a. Check that the structure is correctly matched.
 - b. Open the original treatment plan in External Beam Planning, and review the contours and field geometry of the plan.

4. You have the following options for processing the outlier:
 - Remove the outlier structure from the model.

To do this, exclude the whole training plan from the model, or remove the structure matching of the plan structure.
 - Add more training plans to the model with similar geometrical features as the outlier plan, and match the structures to the model structure.

Do this to fill in the gap between the outlier values and the rest of the data points in the geometric plot.
 - Leave the training plan in the training set.

Verify the effect of this option carefully, especially if the Cook's distance is over the threshold.
5. View the regression plot for each structure.

Pay attention to the data points that are far right or far left in the geometric x axis. Check if these points follow the behavior of the rest of the data points. Check how far they are from the rest of the data points in the x axis.
6. If the regression plot indicates an outlier, do the following:
 - a. Investigate the plan further in External Beam Planning.
 - b. Remove the training plan, or leave it, and optionally, add more similar training plans to the model.
7. If the regression plot suggest that there are multiple data groups instead of one, do the following:
 - a. Investigate the plans further in External Beam Planning, and try to find the plan feature that causes the multiple data groups.
 - b. If the data groups follow the same trend, but there is a clear gap between them, consider adding more plans to cover the missing parts.

For example, if the upper end of the regression line illustrates plans with big bladder sizes, and the lower end of the regression line illustrates plans with small bladder sizes, consider adding plans with medium sized bladders to fill in the gap in between.
 - c. If the data groups do not follow the same trend, consider whether or not you want to divide the different plan features into separate models.
8. If you modified the model, re-extract plan data, retrain the model, and start the verification process from the beginning.

Related Topics

[Geometric Outliers](#) on page 313

Process Dosimetric Outliers

1. In DVH Estimation Model Configuration, open the summary of the most important outliers for the model:
 - a. Check the studentized residual (SR) for each structure.
If the value for a structure is highlighted, investigate the case further.
 - b. Check the areal difference of estimate (dA) for each structure.
If the value for a structure is highlighted, investigate the case further.
2. Check the residual plots for each structure:
 - a. Check that the structures of the training plan have been correctly matched.
 - b. Review the difference between the actual and estimated DVH.
Verify that the data points follow a straight line trend. Data points that are far away from the identity line may indicate dosimetric outliers.
 - c. If you suspect a dosimetric outlier in a residual plot, check the residual plots also for other structures in the same plan.
This step verifies whether the quality of the plan is actually dosimetrically different, or if the outlier values are caused by different trade-offs used in the plan.
 - d. Open the plan in External Beam Planning for further investigation.
For example, check if the plan contains different trade-offs than the other training plans, or follows a different clinical protocol.
 - e. Process the outlier - remove the outlier plan or structure, or leave it in the model
3. Check the in-field DVH plot and DVH plot for each structure:
 - a. Check that the structures of the training plan have been correctly matched.
 - b. Check where the actual DVH curve lands in relation to the DVH range for each training plan.
 - c. Check if any of the DVH curves of training plans differs considerably from the rest.
 - d. Open the plan in External Beam Planning for further investigation.
Check whether the plan contains features that are not present in the rest of the training set. For example, check if the plan contains different trade-offs than the other training plans, or follows a different clinical protocol.
 - e. If you find differing features, consider how to process the outliers.
If you want to use the model for these types of plans, add more similar training plans and structures to the training set, and verify the modified model. You may also consider whether you need to create two separate models. If the outlier was accidental, consider excluding this plan feature from the model, and remove the outlier plan or structure.

4. If you modified the model, re-extract plan data, retrain the model, and start the verification process from the beginning.

Related Topics

[Dosimetric Outliers](#) on page 314

Verify the Final Model Fit

Check the in-field DVH plot and DVH plot for each structure in DVH Estimation Model Configuration. Do this only after you have processed influential data points and potential outliers in the model. Otherwise, the plots may not show reliable results.

1. Check where the actual DVH curve lands in relation to the DVH range for each training plan.
2. Check if any of the DVH curves of training plans differs considerably from the rest.
3. If the actual DVH curve does not land in the estimate range, or one of the curves is notably different:
 - Check that the structures of the training plan have been correctly matched.
 - Open the plan in External Beam Planning for further investigation.

Check whether the plan contains features that are not present in the rest of the training set. For example, check if the plan contains different trade-offs than the other training plans, or follows a different clinical protocol.

4. If you find differing features, consider how to process them.
If you want to use the model for these types of plans, add more similar training plans and structures to the training set, and verify the modified model. You may also consider whether you need to create two separate models. If the outlier was accidental, consider excluding this plan feature from the model, and remove the outlier plan or structure.
5. If you modified the model, re-extract plan data, retrain the model, and start the verification process from the beginning.

Related Topics

[DVH Plot for Organs at Risk](#) on page 337

[In-field DVH Plot](#) on page 341

Verify the Estimation Ability of the Model

1. In DVH Estimation Model Configuration, open the training log by clicking **Training Log**.
2. Check the goodness of estimation statistics in the training log.
3. Check the DVH plot and the infield DVH plot.

Related Topics

[DVH Plot for Organs at Risk](#) on page 337

[In-field DVH Plot](#) on page 341

[Goodness of Estimation Statistics](#) on page 348

Tools for Model Verification

You can use the following tools for verifying a DVH estimation model in DVH Estimation Model Configuration:

- Summary of training results that helps you evaluate how well the model represents the training data, whether the number of matched structures has been sufficient for the model, and the number of potential outliers for each structure.
- Summary of outlier statistics that provides you a list of highest outlier values per plan and per structure.
- Outlier statistics that provides you the outlier values from four different outlier statistics per plan and per structure.
- A geometric (box) plot that shows the distribution of geometric features, such as OAR-volumes, in the training set.
- Residual (scatter) plots that show the difference between the actual and estimated DVHs.
- Regression (scatter) plot that shows how well the dosimetric information in the plans (DVHs) can be estimated based on the geometric information in the plans.
- DVH plot that shows where the actual DVH curve lands in relation to the estimated DVH range.
- DVH in-field plot that shows where the actual in-field DVH curve lands in relation to the estimated DVH range.
- Training log that contains goodness-of-fit and goodness-of-estimation statistics.

Geometric Plot

The purpose of the geometric (box and whiskers) plot is to show the statistical distribution of the geometric model data. The geometric plot shows you whether the data is evenly distributed, or concentrated in some areas while spread in others. The geometric plot can be used for verifying geometric data in the model, and for identifying geometric outliers. The geometric plot is related to the modified Z-score statistics shown in the outlier statistics for OARs. The further away a data point is from the median, the bigger the modified Z-score value is. If you have values that are far away from the median, you can check the related modified Z-score values in the outlier statistics.

The geometric plot provides you information about the following regression model parameters or their combinations:

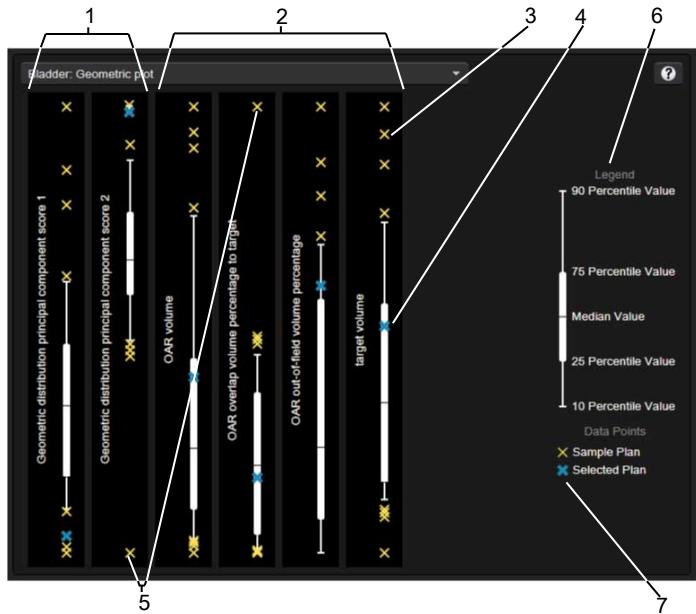
- Principal component scores of the geometric distribution.

The number of scores shown for a structure (typically between 1 and 3) varies depending on the actual trained regression model and can be different for different structures and training sets. Each plot for a principal component score shows data points only for those plans that were included in model training and for those structures that have an in-field region. If the number of in-field regions for a structure has not been sufficient for the regression model, the principal component scores are not available for this structure. More information about the structure regions used in a model: *Eclipse Photon and Electron Algorithms Reference Guide*.

- The following anatomical features of the patients' OARs:
 - The volume of the OAR.
 - The overlap volume percentage of the OAR with the target.
 - The out-of-field volume percentage of the OAR.
 - The volume of joint targets.

Each plot for an anatomical feature contains a data point also for those plans that have been excluded from model training, but contain extracted plan data, and for all structures regardless of the structure regions.

Each data point in the plot represents a structure in a plan. If several plan structures have been matched to the same model structure, they are shown separately in the plot. To view the corresponding plan and structure information, hover your mouse over the data point in the plot. To view the data points for a plan, select the plan in the **Plans of the DVH Estimation Model** list. The values are highlighted in the plot.



1. Principal component scores.
2. Anatomical features of the OAR.
3. Data point for a structure in a plan.
4. Data point for a structure in a plan that has been selected in the Plans of the DVH Estimation Model list.
5. Potential outlier values.
6. Legend that shows how the percentile and median values are visualized in the plots.
7. Colors for the data points in the plot. They indicate whether the plan has been selected in the Plans of the DVH Estimation Model list.

Figure 81 Geometric Plot

The length of the interval describes the concentration of the data. The longer the interval, the more spread the data is. The shorter the interval is, the more concentrated the data is. Data points that are located very high or very low in the plot may indicate outliers.

Regression Plot

In the regression (scatter) plot, you can check the correlation between the most important geometric regression parameter and the first DVH principal component score (or the main DVH parameter). The regression plot can be used for verifying geometric data in the model, and for identifying influential data points and geometric outliers in the training set.

The Y axis of the plot shows the first principal component score of the DVH.

The X axis shows the most important geometrical regression parameter, which can be a specific feature such as the first principal component score of the GED, or a composition of features, such as the first principal component score of the GED multiplied by the OAR volume. The X axis can show one of the following plan features or a composition of them:

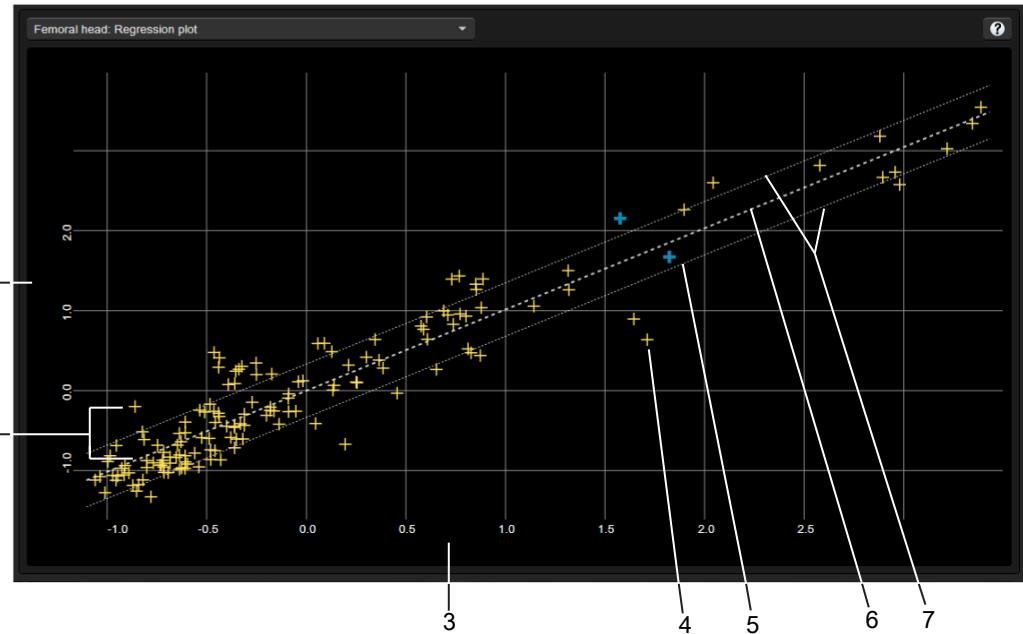
- A principal component score of the GED.
- The volume of the OAR.
- The overlap volume percentage of the OAR with the target.
- The out-of-field volume percentage of the OAR.
- The volume of joint targets.

Each data point in the plot represents a structure in a training plan. If several structures have been matched to the same model structure in a plan, the plot shows a separate data point for each structure. This plot shows data points only for those plans that were included in model training and for those structures that have an in-field region. If the number of in-field regions for a structure has not been sufficient for the regression model, the regression plot is not available for this structure. More information about the structure regions used in a model: *Eclipse Photon and Electron Algorithms Reference Guide*.

The plot shows the regression line and confidence interval for the data. The distance between the confidence interval line and the regression line is one standard deviation. The standard deviation is calculated from the fitting errors. The fitting error is the vertical distance between the data point and the regression line.

To view the corresponding training plan and structure information, hover over the data point in the plot. To view the data point for a training plan, select the training plan in the **Plans of the DVH Estimation Model** list. The value is highlighted in the regression plot.

The following figure exemplifies a regression plot for an OAR:

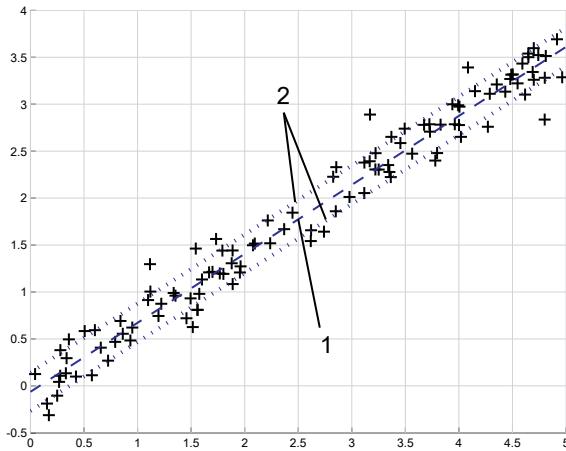


1. The first principal component score of the DVH.
2. Fitting error.
3. Geometric parameter (or a combination of parameters).
4. Data point for a structure in a training plan.
5. Data point for a structure in a training plan that has been selected in the Plans of the DVH Estimation Model list.
6. Regression line.
7. Confidence interval.

Figure 82 Regression Plot

Regression Plot Examples

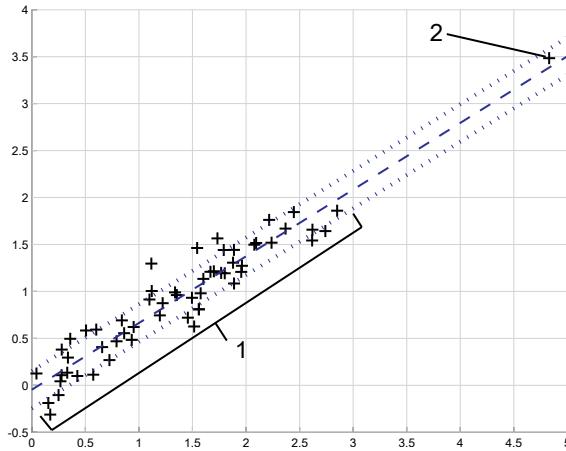
The following figure exemplifies a regression plot that does not seem to have any outlier values:



1. Regression line.
2. Confidence interval.

Figure 83 Regression Plot with No Potential Outliers

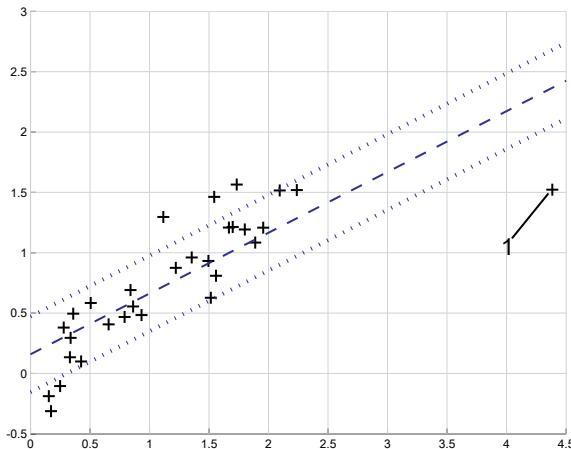
The following figure exemplifies a regression plot with a potential outlier value that may change your assumption about the trend of the data, but has no significant effect on the actual outcome of the model:



1. Main group of data points.
2. Potential outlier that may affect the assumption about the data trend.

Figure 84 Regression Plot with a Potential Outlier that May Affect the Assumption about the Data Trend

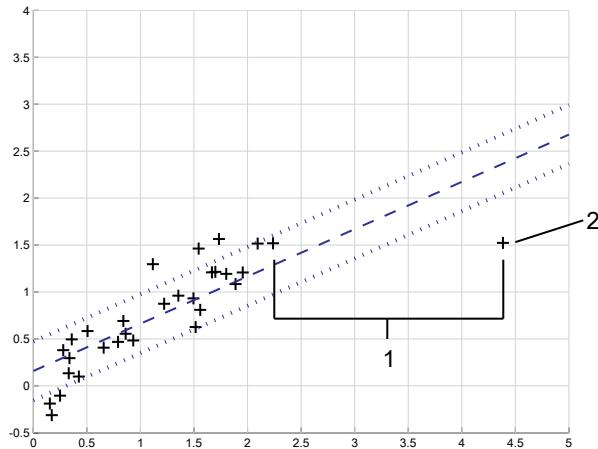
The following figure exemplifies a regression plot with a significant outlier value that may both change your assumption about the trend of the data and change the outcome of the model:



1. Potential significant outlier that may affect the outcome of the model.

Figure 85 Regression Plot with a Potential Outlier that May Affect the Outcome of the Model

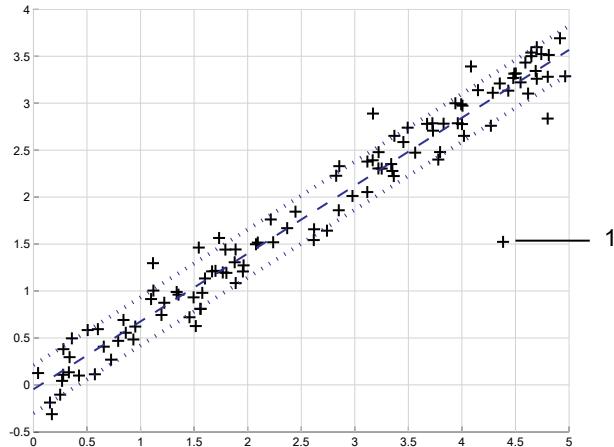
The following figure exemplifies a regression plot for a model with a gap in data points. The gap may or may not indicate an outlier. In the figure, you can view a data point that is located far away from the main group of data points. The data point is a potential outlier. Adding more data points to the model helps you find out whether the data point is a real outlier.



1. Gap in data.
2. Potential outlier.

Figure 86 Regression Plot with a Gap in Data

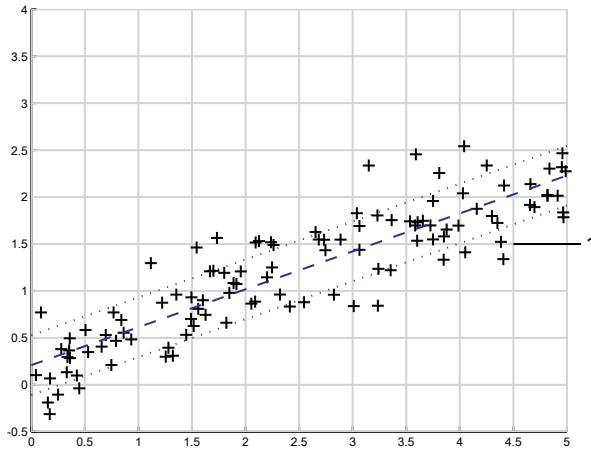
The following figure exemplifies the case when the data point turns out to be a real outlier after more data points have been added.



1. Data point that proves to be a real outlier.

Figure 87 Data Point that Proves to Be an Outlier

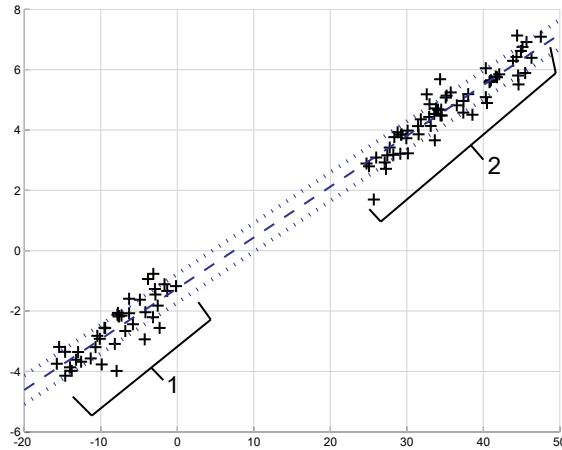
The following figure exemplifies the case when the data point proves to be no real outlier after more data points have been added.



1. Data point that proves to be no outlier.

Figure 88 Data Point that Proves to Be No Outlier

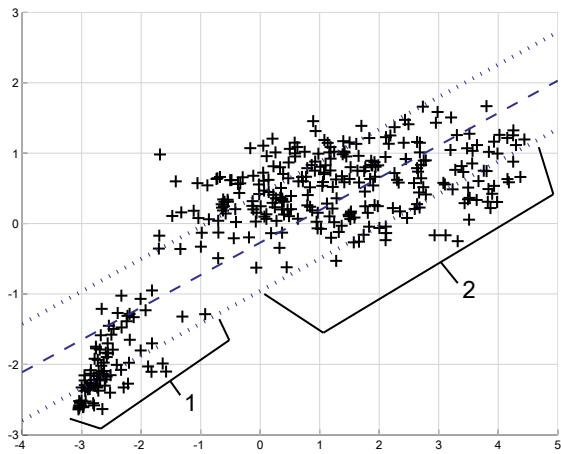
The following figure exemplifies a regression plot with training data that seems to form multiple data groups with the same trend:



1. The first potential data group.
2. The second potential data group.

Figure 89 Regression Plot with Multiple Data Groups and the Same Trend

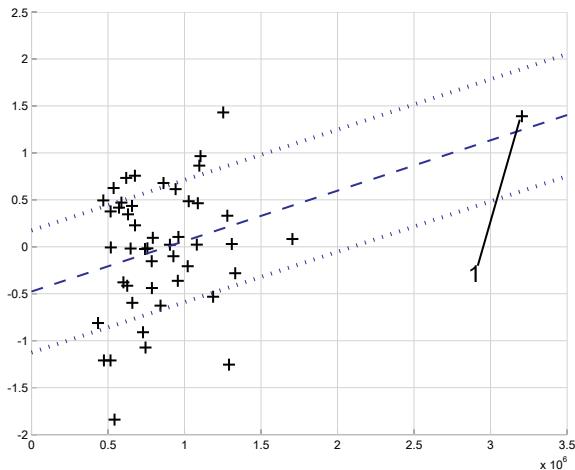
The following figure exemplifies a regression plot with training data that seems to form multiple data groups with different trend:



1. The first potential data group.
2. The second potential data group.

Figure 90 Regression Plot with Multiple Data Groups and Different Trend

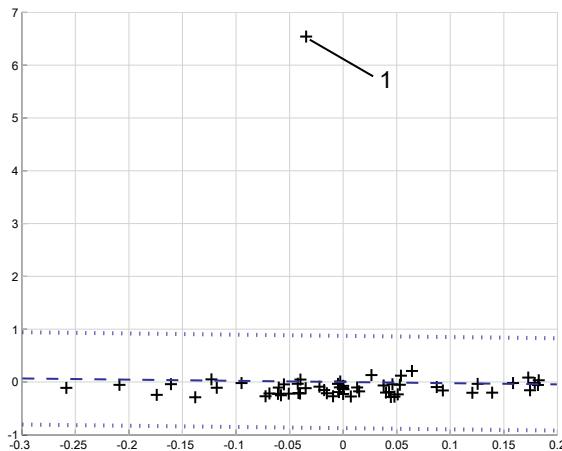
Towards the upper or lower end of the regression line, smaller deviations start to be significant, because these points tend to pull the regression line towards themselves. If this happens and Cook's distance is also elevated, the point is overfitting the data. The following figure exemplifies a regression plot which may be overfitting data:



1. A data point that may cause the overfitting of data.

Figure 91 Regression Plot with Overfitting Data

The following figure exemplifies a regression plot with a potential outlier value that may cause biased estimates (the coefficient of determination is bad):



1. A potential outlier that may cause biased DVH estimates.

Figure 92 Regression Plot with an Outlier that May Cause Biased DVH Estimates

Residual Plot

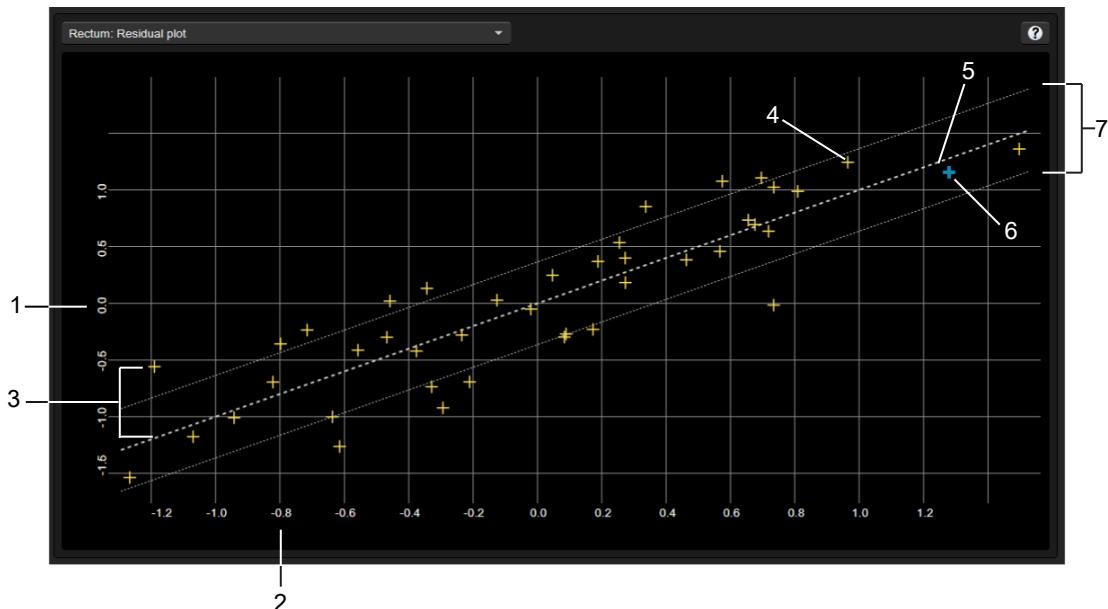
The purpose of the residual (scatter) plot is to illustrate how well the regression model represents the training data (model fit). It can also help you evaluate how the original DVH of a structure differs from the estimated DVH. The residual plot can be used for verifying dosimetric data in the model, and for identifying influential data points and dosimetric outliers in the training set. The residual plot is related to the goodness-of-fit statistics (chi square and coefficient of determination) available in the summary of training results for the model, and to the studentized residual statistics available in the outlier statistics for structures.

The X axis shows the first principal component score of the estimated DVH. The Y axis shows first principal component score of the actual DVH. Each data point in the plot represents a structure in a training plan. If several structures have been matched to the same model structure in a plan, the plot shows a separate data point for each structure. This plot shows data points only for those plans that were included in model training and for those structures that have an in-field region. If the number of in-field regions for a structure has not been sufficient for the regression model, the residual plot is not available for this structure. More information about the structure regions used in a model: *Eclipse Photon and Electron Algorithms Reference Guide*.

The plot shows the identity line and confidence interval for the data. The distance between the confidence interval line and the identity line is one standard deviation. The standard deviation is calculated from the residuals. The residual is the vertical distance between the data point and the identity line.

To view the corresponding training plan and structure information, hover your mouse over the data point in the plot. To view the data point for a training plan, select the training plan in the **Plans of the DVH Estimation Model** list. The data point is highlighted in the plot.

The following figure exemplifies a residual plot for an OAR:



1. The first principal component score of the actual DVH.
2. The first principal component score of the estimated DVH.
3. Residual.
4. Data point for a structure in a training plan.
5. Identity line.
6. Data point for a structure in a training plan that has been selected in the Plans of the DVH Estimation Model list.
7. Confidence interval.

Figure 93 Residual Plot

- If all the data points follow a thin straight line trend (the coefficient value is one), the model may overfit data.

- If a data point is close to or over the identity line (the residual is close to zero) and the Cook's distance is elevated, it may indicate that the data point is causing overfitting.
- If a data point is far away from the identity line, it may indicate an outlier.
- In the middle part of the identity line, the residual starts to be significant if it is 3 standard deviations away from the identity line
- If a data point is below the identity line and the residual is negative, the DVH of that OAR is better than expected.
- If the data point is above the identity line, (the residual is positive) the DVH of that OAR is worse than expected. The dose distribution of that OAR is possibly not fully optimized.

The following picture exemplifies a residual plot which may be overfitting data:

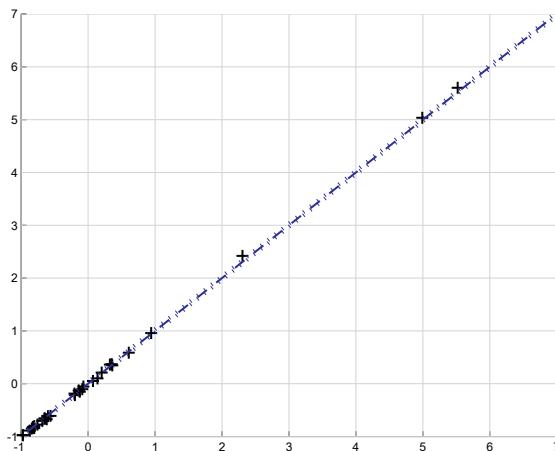


Figure 94 Residual Plot with Overfitting Data

DVH Plot for Organs at Risk

The purpose of the DVH plot for organs at risk (OARs) is to show:

- How the DVHs for an OAR are distributed in the whole model plan set.
- Where the original DVH of an OAR falls in the estimated DVH range.

The DVH plot represents the volumetric dose distribution of the whole structure (all the regions in the structure volume). More information about the structure regions used in a model: *Eclipse Photon and Electron Algorithms Reference Guide*. The estimated DVH range has been obtained by applying the last trained model version to all the plans in the Plans of the DVH Estimation Model list. The DVH plot shows DVH curves also for those plans that have been excluded from model training, but contain extracted plan data.

The DVH plots for the actual training plans can be used to evaluate the DVH fit, in other words whether the DVH estimates follow the original DVH adequately. If the original DVH is within the DVH estimate range in most of the plans, the DVH fit can be considered good. If the original DVH is mostly outside the DVH estimate range, the DVH fit can be considered poor.

The DVH plot for the rest of the model plans (excluded from model training) can be used for verifying the preliminary estimation results of the model. If the model plan set is small, the displayed results may differ from the results of the actual model. In this case, the DVH plot is related to the goodness-of-estimation statistics shown in the training log, and to the areal difference of estimate statistics shown in the outlier statistics for structures. Goodness-of-estimation is related to how well the original DVH curve falls into the estimation range.

The DVH plot can be used for verifying dosimetric data in the model, and for identifying dosimetric outliers in the training set.

Each curve represents an OAR in a model plan. If several OARs in a plan have been matched to the same model structure, they have different lines in the plot. The X axis shows the relative dose (%) of the OAR. The Y axis shows the relative volume (%) of the OAR.

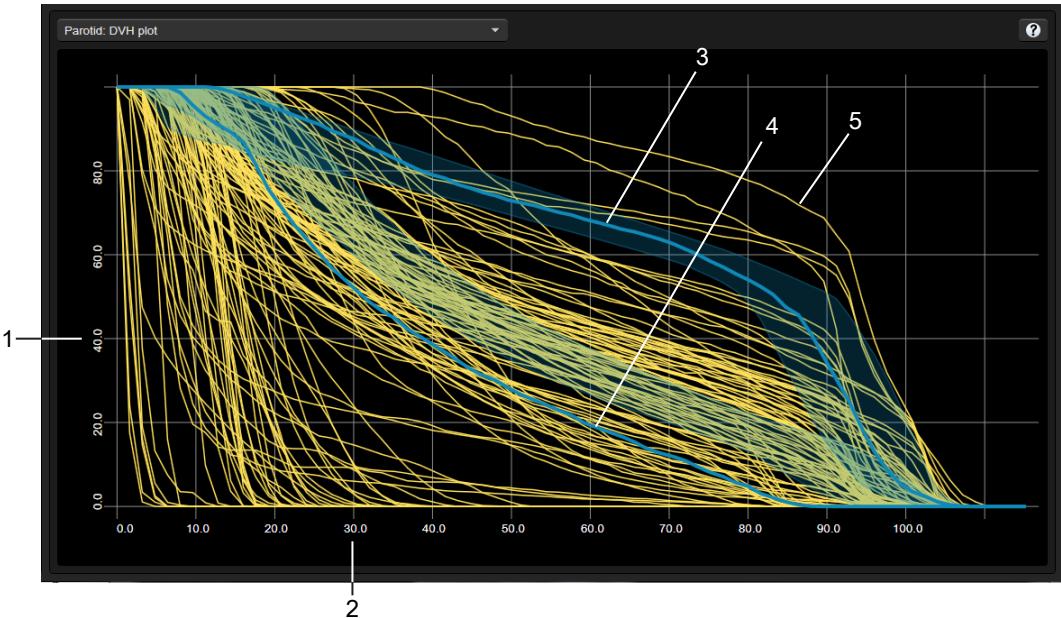
- To check, where the DVH curve of a specific OAR falls in the estimated range, select a model plan in the **Plans of the DVH Estimation Model** list. The DVH curve of the OAR is highlighted, and the estimated range is shown as a shaded area. To identify the OAR, hover over the highlighted line. You can see a tooltip which shows the structure identifier.



Note: Some structures may not show estimates since the algorithm was not able to calculate them. This is usually the case with small structures.

- You can also see the estimated DVH range by selecting a DVH curve in the plot. To identify the model plan, where this OAR is located, hover your mouse over the highlighted line. You can see a tooltip that shows the model plan number.
- To get an overview of the DVHs in the whole model plan set, select the first plan in the **Plans of the DVH Estimation Model** list, and use the arrow key to move down in the list.

The following figure exemplifies a DVH plot for an OAR:



1. The relative volume of the OAR structure.
2. The relative dose for the OAR structure.
3. DVH curve and estimated DVH range for a model plan.
4. A DVH curve that does not fall into the estimated range.
5. A DVH curve for a potential outlier.

Figure 95 DVH Plot for a OAR Structure

DVH Plot for Target Structures

The purpose of the DVH plot for target structures is to check the following:

- The plan prescriptions in the training plans are correct.
- The treatment goals in the training plans are correct.
- Structures have been correctly matched.

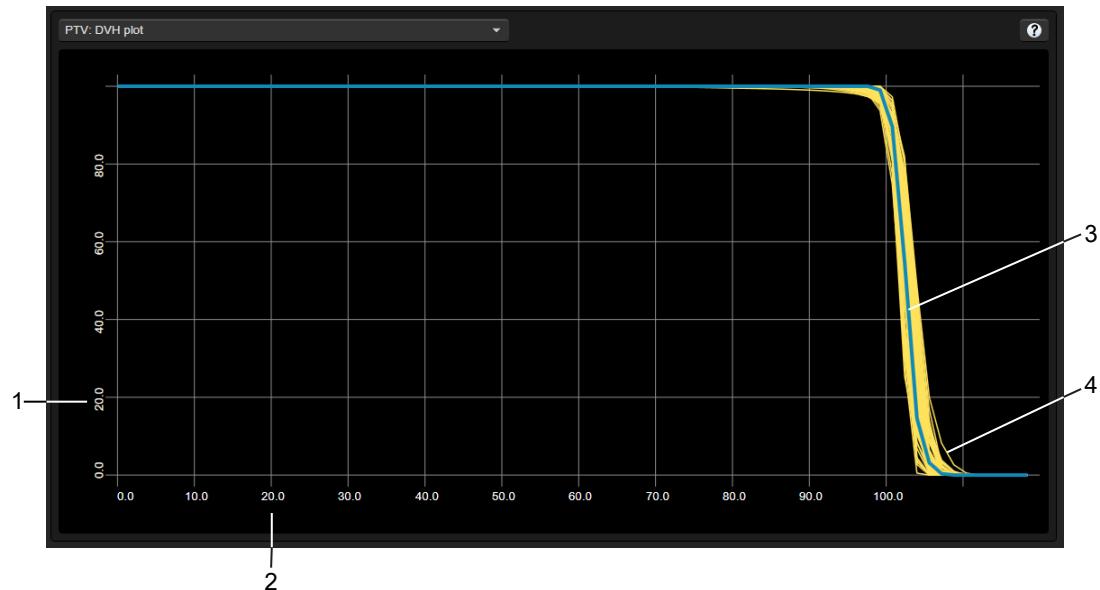
The DVH plot shows DVH curves also for those plans that were excluded from model training, but have extracted plan data. Each curve represents a target structure in a model plan. If several plan targets have been matched to the same model target, they are shown separately in the plot. The x axis shows the relative dose (%) of the target. The y axis shows the relative volume (%) of the target.

- To view the DVH curve of a specific target structure, select a model plan in the **Plans of the DVH Estimation Model** list. The DVH curve of the target is

highlighted. To identify the target, hover over the highlighted line. You can see a tooltip which shows the structure identifier.

- To see the plan to which a certain DVH curve belongs, hover your mouse over the curve. You can see a tooltip that shows the model plan number.

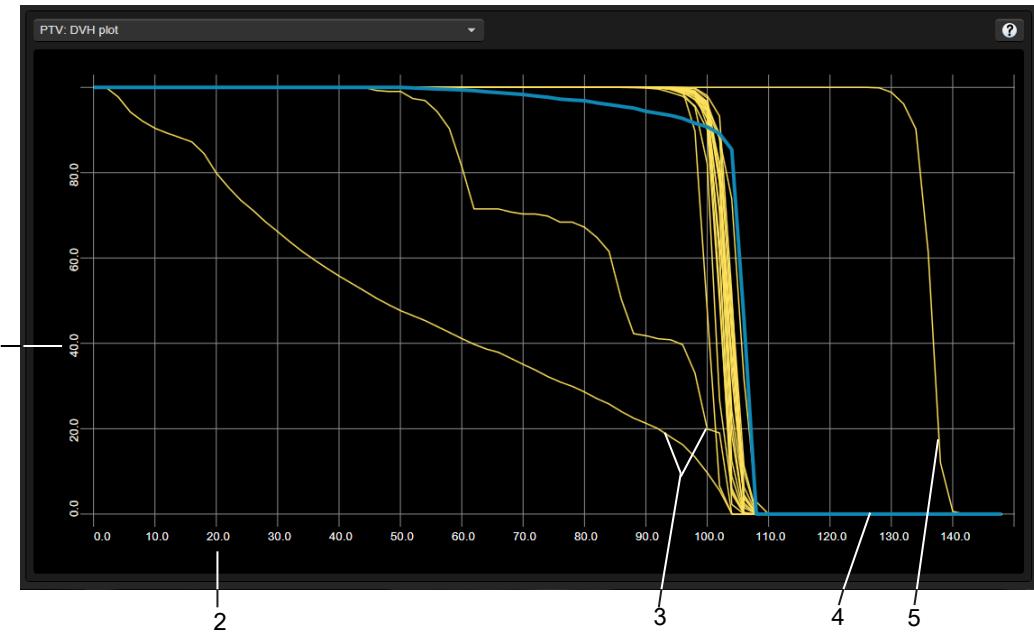
The following figure exemplifies a DVH plot for a target structure:



1. The relative volume of the PTV.
2. The relative dose for the PTV.
3. DVH curve for a PTV in a model plan that has been selected in the Plans of the DVH Estimation Model list.
4. DVH curve for a PTV in a model plan.

Figure 96 DVH Plot for a Target Structure

The following figure exemplifies a DVH plot for a target structure with potential outliers:



1. The relative volume of the PTV.
2. The relative dose for the PTV.
3. Outlier DVH curves indicating incorrect structure matching.
4. Outlier DVH curve indicating a deviant treatment goal in the plan.
5. Outlier DVH curve indicating an incorrect plan prescription.

Figure 97 Outliers in a DVH Plot for a Target Structure

If one of the DVH curves is far away from the rest, check the plan prescription in the **Plan Prescription** column. If the value shown differs from the prescription used in the plan, you can change it. The DVH curve is scaled accordingly.

In-field DVH Plot

The in-field DVH represents the volumetric dose distribution of the in-field region of the structure. The in-field region is the part of the structure that has overlap with target projection from the beam's eye view of at least one field. More information about the structure regions used in a model: *Eclipse Photon and Electron Algorithms Reference Guide*.

The purpose of the in-field DVH plot is to show:

- How the in-field DVHs of the structures are distributed in the whole training plan set.

- Where the original in-field DVH of a structure falls in the estimated DVH range.

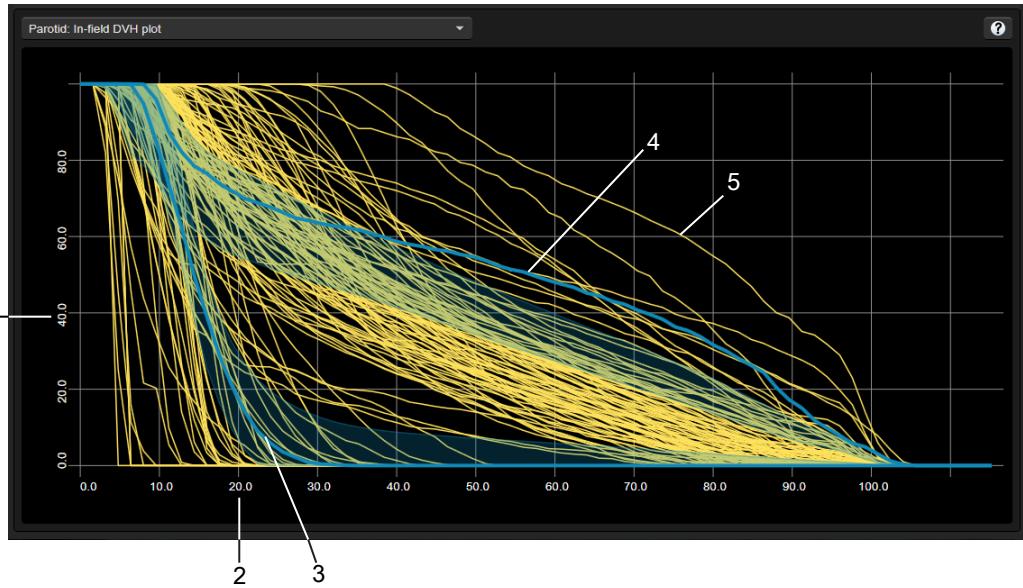
The in-field DVH plot is related to the goodness-of-fit statistics shown in the summary of training results and to the areal difference of estimate statistics shown in the outlier statistics for structures.

The in-field DVH plot can be used for verifying dosimetric data in the model, and for identifying dosimetric outliers in the training set.

Each curve represents a structure in a training plan. If several plan structures have been matched to the same model structure, they are shown separately in the plot. The DVH plot shows DVH curves also for those plans that were excluded from model training, but have extracted plan data. The x axis shows the relative dose (%) of the structure. The y axis shows the relative volume (%) of the structure.

- To check, where the DVH curve of a specific structure falls in the estimated range, select a training plan in the **Plans of the DVH Estimation Model** list. The DVH curve of the structure is highlighted, and the estimated range is shown as a shaded area. To identify the structure, hover over the highlighted line. You can see a tooltip which shows the structure identifier.
- You can also see the estimated DVH range by selecting a DVH curve in the plot. To identify the training plan, where this structure is located, hover your mouse over the highlighted line. You can see a tooltip that shows the training plan number.
- To get an overview of the DVHs in the whole training plan set, select the DVH curve in the far right, or far left, and use the arrow keys to move up or down.

The following figure exemplifies an in-field DVH plot:



1. The relative volume of the structure.
2. The relative dose for the structure.
3. DVH curve and estimated DVH range for a training plan.
4. A DVH curve that does not fall into the estimated range.
5. A DVH curve for a potential outlier.

Figure 98 In-field DVH Plot

Summary of Training Results



Note: This statistical table is not available for Varian-provided models.



Tip: Sort the values in the table by clicking the column headers. To copy the values to clipboard, right-click the table, and choose **Copy whole table to clipboard**.

- **Structure:**
Model structure, for which the statistics have been calculated.
- **Trained:**

Indicates, whether the model for this structure has been successfully trained (Yes/No). Shows “N/A” for target structures of the model. If the number of structures has not been enough for training a specific structure region, a highlighted “Yes” is shown in the **Trained** column. Hover your mouse over the cell to see a tooltip that shows which of the structure regions does not have enough instances, and which model type was created for this region instead of the standard one.

- Coefficient of determination (R^2):

Statistical parameter that measures the goodness-of-fit of the OAR model. The cell is empty for target structures, or for OARs that have not been successfully trained. The cell is empty also if the number of matched OAR instances with an in-field region has not been sufficient for training the regression model.

- Chi square (χ^2):

Statistical parameter that measures the goodness-of-fit of the OAR model. The cell is empty for target structures, or for OARs that have not been successfully trained. The cell is empty also if the number of matched OAR instances with an in-field region has not been sufficient for training the regression model.

- Matched:

Number of plan structures that have been matched to this specific model structure.

- In-field:

Number of plan structures that have been matched to this specific model structure, and have an in-field region. The cell is empty for target structures.

- Suggested:

Suggested number of plan structures with an in-field region for the regression model. If the cell is empty, the number of matched structures with an in-field region is sufficient for the regression model.

- Outliers:

Number of potential outlier values detected from all the outlier statistics. The cell is empty if the number of matched OAR instances with an in-field region has not been sufficient for training the regression model.

Related Topics

[Goodness of Fit Statistics](#) on page 347

Summary of Outlier Statistics



Note: This statistical table is not available for Varian-provided models.

The summary of outlier statistics lists the outlier values shown for each model OAR and for each plan.



Tip: Sort the values in the table by clicking the column headers. To copy the values to clipboard, right-click the table, and choose **Copy whole table to clipboard**.

- Plan #:

Identifier of the plan, for which the outlier statistics have been calculated.

- Model structure:

Shows the highest outlier statistics value of the model OAR. The value comes from one of the outlier statistics. The highest outlier statistics value is a potential outlier value, but only if the value is over the threshold value. If the cell is empty, the model OAR has not been matched to any OAR in this specific plan, or the model OAR has not been trained.

Outlier Statistics



Note: This statistical table is not available for Varian-provided models.

The outlier statistics contains the information listed below.



Tip: Sort the values in the table by clicking the column headers. To copy the values to clipboard, right-click the table, and choose **Copy whole table to clipboard**.

- Plan #: Identifier of the plan, for which the outlier statistics have been calculated.
- Structure: Plan structure identifier.
- Cook's distance (CD):

Cook's distance indicates influential data points in a regression model. A high value indicates that the structure has a significant effect on the regression line. Even if the structure does not fit well into the training set dosimetrically, the structure may not appear as a dosimetric outlier, because the model learns the particular behavior of this plan. A high Cook's distance value often co-occurs with geometric outliers. If the value is over the threshold, the regression and residual plots should also be checked. The Cook's distance is also shown in the training log. The log shows only those values that are over the threshold.

- Modified Z-score (mZ):⁴

The modified Z-score measures the difference of an individual geometric parameter from the median value in the training set. Values are normalized with the median absolute difference. The modified Z-score is calculated for each anatomical feature and geometrical principal component coefficient of a structure, but only the largest value is shown in the outlier statistics for OARs. Modified Z-score values identify geometric outliers. If the modified Z-score values are over the threshold, the geometric plots and regression plots should also be checked.

- Studentized residual (SR):

A residual measures the difference between the original data and the estimated data. A residual in a DVH estimation model indicates the difference between the original data and estimated data for each DVH principal component score (for example, between the first principal component score of the original DVH and the first principal component score of the estimated DVH). A studentized residual is the residual divided by the standard deviation of the residuals. Studentized residual takes only the in-field region of the regression model into account. Studentized residual reveals dosimetric outliers, but usually only after the influential data points and data points that cause the model overfitting have been processed. Studentized residual is a function of the absolute difference between the original and estimated data. In other words, studentized residual is influenced by the distance between the data and does not differentiate between cases where the estimated data is lower or higher than the original data. Highly influential data points may have small residuals since the influential data points tend to pull the regression fit towards them. If the studentized residual value is over the threshold, the residual plots, DVH plots, and in-field DVH plots should also be checked. The studentized residual values are also included in the model training log. The log shows only those values that are over the threshold.

- Areal difference of estimate (dA):

An areal difference of estimate indicates the difference between the estimated dose distribution and the actual one, in other words, how the estimated DVH curve for a structure differs from the actual DVH curve (what is the area that remains between them). The area is normalized with the standard deviation estimated by the model (half of the area between upper and lower estimates). The areal difference indicates dosimetric outliers. The areal difference of estimate is similar to studentized residual, but it is calculated also for those model plans that have been excluded from model training, but contain extracted plan data. If the value for areal difference of estimate is over the threshold, the residual plot, the DVH plot, and the in-field DVH plot should be also checked.

⁴ Boris Iglewicz and David Hoaglin (1993), "Volume 16: How to Detect and Handle Outliers", The ASQC Basic References in Quality Control: Statistical Techniques, Edward F. Mykytka, Ph.D., Editor.

The outlier statistics are shown for plans that have been included in model training and for structures that have an in-field region. The modified Z-score and areal difference of estimate are shown also for those plans that were included in model training, but do not have an in-field region, and for those plans that have been excluded from model training, but contain extracted plan data. The outlier statistics values that are over the threshold, are highlighted.

Goodness of Fit Statistics

The goodness of fit statistics helps you evaluate how well the DVH estimation model represents the plan data in the training set. The following goodness of fit statistics are available in the model training log.

Table 25 Goodness of Fit Statistics

Statistics	Description
The average fit of the principal components for DVH	Describes how well the model can reconstruct the original DVHs from the principal components that the model stores. This is performed by using Principal Component Analysis.
The average fit of the principal components for GED	Describes how well the model can reconstruct the original Geometry-based Expected Dose (GED) from the principal components that the model stores. Geometry-based Expected Dose (GED) is a metric that is used for evaluating how the geometrical position and distribution of different OARs (relative to the geometrical position and distribution of target structures) affects the achievable dose distributions under the current field geometry.
The coefficient of determination for the regression model parameters	Measures the fit of the training plan data over the regression line. The metric describes how well the regression model represents the training plan data, and how much of the variance is explained by the regression model. This metric together with the chi square value is used for finding out, whether the model is overfitting data. The scale is from 0.0 to 1.0. Larger value indicates a better model fit. High value can also indicate overfitting, in which case the estimation capability is reduced. This value is also available in the summary of training results.

Statistics	Description
The average chi square for the regression model parameters	<p>Measures the quality of the regression model. This value is related to Pearson's chi-squared test, and it is measured from the residuals (difference between the original data and the estimated data). The residuals should be independent and follow a Gaussian distribution approximately. This metric together with the coefficient of determination value is used for finding out, whether the model is overfitting data.</p> <p>The closer the value is to 1.0, the more certain it is that the quality of the regression model is good.</p> <p>This value is also available in the summary of training results.</p>
The fit of the whole estimation model	<p>Describes how well the whole estimation model represents the training plan data over the regression line.</p> <p>The scale is from 0.0 (bad) to 1.0 (good). If the value is close to 1.0, it is considered good. However, high value can also indicate overfitting, in which case the estimation capability is reduced. Take into account that the regression model is just a part of the estimation model.</p>
The average MSE of the whole estimation model	<p>Measures the Mean Squared Error (MSE) of the residuals. The MSE is an estimator of the variance of the error (the residuals).</p>

Goodness of Estimation Statistics

When the model is trained, an internal cross-validation is performed for the model. The training set is first divided into 10 parts. 10 models are trained, and each time a model is trained, a different tenth of the data points (plans) are left out, and used for validating the model. The average of the validation statistics generated during these 10 model training rounds is then shown in the training log. The results are shown in the goodness-of-estimation statistic, which helps you evaluate how well the model is able to estimate plans (that are not part of the training set). The goodness-of-estimation statistics are available in the model training log.

Table 26 Goodness of Estimation Statistics

Statistics	Description
Mean squared error between original and estimate	Describes how well the model is able to estimate the original DVH in a training plan. It measures the distance between the original DVH and the mean of the upper and lower bounds of the estimated DVH. The closer the value is to 0, the better the estimation capability of the model is.
Proportion of histogram bins outside boundaries	Defines how many bins of the original DVH were outside the upper and lower bounds of the estimated DVH. The value is in percentages.
Mean of absolute deviation of bins outside boundaries	Calculated for the bins outside the DVH estimate bounds. Shows if the original DVH is consistently above the upper bound or consistently below the lower bound. Values close to 0 indicate that the original DVH is as likely to be above the upper bound as below the lower bound, which indicates model consistency.
Mean squared error of bins outside boundaries	Calculated for the bins outside the DVH estimate bounds. Indicates the error of the distance from the original DVH to the estimate bounds.
Standard deviation of the error of bins outside boundaries	Indicates if the original DVH is consistently close to the estimate bounds, or if it is very far away in some parts, and very close in others. Indicates how well the original DVH follows the form of the estimate bounds. The closer the value is to 0, the more similar the forms are.
Mean of the error of bins outside boundaries	Calculated for the bins outside the boundaries. Indicates how far the original DVH is from the estimate bounds (distance). The closer the value is to 0, the better (original DVH is close to the estimate bounds).

Validating a DVH Estimation Model



Note: You should validate every DVH estimation model before using it clinically. This applies to all model types - the Varian-provided models, imported models shared by other clinics, and the models you create yourself.

The purpose of validation is to verify that the model can be used to estimate new patient cases with the required quality. During model validation, you should validate the following:

- DVH estimates produced by a model.
- The optimization results produced by using a model.
- The final dose distribution produced by using a model.

In validation, you compare existing clinical plans to plans that have been created by using a model. You can copy an existing clinical plan, and apply the model to the plan copy, and see how the results differ from the results in the original plan. You can apply unpublished models to plans in External Beam Planning for validation purposes if you have the appropriate user rights.

During the plan comparison, do the following for each plan:

1. Generate DVH estimates and optimization objectives for the plan copy. Check the DVH estimate range for each structure. A narrow range indicates a more accurate DVH estimate, and a wider range indicates a less accurate one. Check for each structure, whether the original DVH falls within the generated DVH estimate range. If you are validating a model that contains the plan data, you can also perform the initial validation of the DVH estimates by using the DVH plots in DVH Estimation Model Configuration. However, keep in mind that the DVH curves visible in the DVH plots are only approximations of the actual DVHs available in the DVH view in External Beam Planning.
2. Optimize the plan copy by using the model. Check whether the final DVH of each structure falls within the DVH estimate range.
3. Compare the DVHs in the plan copy to the DVHs in the original plan.

After comparing the plans, verify the final clinical quality of the validation plan.

If you are validating a Varian-provided model, see the model description document for further information about the preliminary validation of the model.

Avoid modifying the model during the model validation process. If you modify the model, start the validation process from the beginning.

Modifying a Published DVH Estimation Model

After a DVH estimation model has been published, you can modify the following:

- Add plans to the model plan set.
- Delete plans that have not been used for training the model.
- Select plans to be included in the next model training, or excluded from it. You cannot change the **Include** setting for plans that have been used for training the published model.
- Change the structure matching (add, modify, remove) for plans that have not been used for training the model. Applies both to OAR and target structures.
- Change the prescription for plans that have not been used for training the model.
- Duplicate the model.
- Modify the original treatment plans of the model in External Beam Planning.

The changes you make do not affect the actual published model until you unpublish the model, re-extract plan data, and re-train the model.

You cannot do the following for a published model:

- Retrain the model.
- Modify optimization objectives.
- Modify NTO and smoothing parameters settings.
- Modify model structures.
- Delete plans that have been used for training the model.
- Change the structure matching for plans that have been used for training the model.
- Change the prescription for plans that have been used for training the model.
- Add an existing plan to the same model in External Beam Planning.

Export a DVH Estimation Model



Note: When exporting a DVH estimation model:

- When you export a model to be shared with other clinics, make sure that you attach a model description document (both clinical and technical) to the model.
- A qualified person shall authorize the export of an unpublished model.
- You cannot export Varian-provided models.

1. In DVH Estimation Model Configuration, click **Open** and select a model.
2. Click **Export**.
3. Edit the name of the export file (.zip) if needed.

4. To select the location of the export file, click **Browse**, select a folder, and click **Save**.
5. Define whether or not you want to include extracted plan data in the export. If you choose to export the extracted plan data, only the extracted data and the training log is exported. No patient information is exported. However, the plan identification numbers that are shown in the # column of the plans list are retained when you export and import a model.
6. Click **Export**.

The model is exported as a password-protected .zip file that you cannot modify.

Import a DVH Estimation Model



Note: You should validate every DVH estimation model before using it clinically. This applies to all model types - the Varian-provided models, imported models shared by other clinics, and the models you create yourself.

1. In DVH Estimation Model Configuration, click **Import**.
2. Select the model file (.zip) you want to import and click **Open**.
The model data is imported. Depending on the setting selected during the export, the extracted plan data is also imported and is shown in the **Plans of the DVH Estimation Model** list. The status of the model is Unpublished.
3. Modify the imported model as desired.
 - If the plan data was included, make only such modifications that do not require re-extracting plan data, and click **Train**.
 - If no plan data was included, make only such changes that do not require retraining the model.
4. Click **Save**.

Modifying an Imported Model

An imported model may or may not contain the plan data that was used for training the model. This depends on the setting defined during the model export. If the imported model contains the plan data, the Plans of the DVH Estimation Model list shows the model plan set. If the imported model contains no plan data, the list is empty.

Even though the imported model would contain the plan data, the model contains no link to the original treatment plans that existed in the database at the time of model training. This is indicated in the Patient ID/Course ID/Plan ID column, which shows N/A. Because this link does not exist, it is not possible to re-extract the plan data anymore. When modifying an imported model, you should not make such modifications to the model that require re-extracting the plan data. If you do, the current plan data is removed and you have to re-import the model to be able to use it. You can re-import the model and use its plan data as long as the DVH estimation algorithm versions of the imported model is the same as the version of the current model. Even though you cannot make such changes that require re-extracting the plans you can still add more plans to the model and retrain the model.

You can modify the following in an imported model with plan data. These changes do not require re-extraction of data:

- Modify the model properties.
- Modify optimization objectives.
- Change the model description documents attached to the model.
- Add more plans to the model and retrain the model. The data of both the original plans and the newly added plans is used to train the model.



Note: *If you import a model that contains no plan data, you should not make such modifications to the model that require retraining the model. If you make such changes, the current trained model and statistical plots are removed and you have to re-import the model to be able to use it. This happens, for example, if you add more plans to the model and retrain the model. The training results from the added plans replace the training results of the imported model.*

You can modify the following in an imported model with no plan data. These changes do not require re-training the model:

- Modify the model properties.
- Modify optimization objectives.
- Change the model description documents attached to the model.

Chapter 12 Beam Angle Optimization

About Beam Angle Optimization

Beam Angle Optimization can be used in IMRT (intensity-modulated radiotherapy) treatment planning to assist in determining optimal beam angles for the fields in the plan:

- In conventional IMRT treatment planning, you start by selecting the suitable beam angles, and continue by optimizing the field intensities.
- When you use Beam Angle Optimization, the beam angles are selected automatically by optimizing the beam angles iteratively based on user-defined dose-volume objectives until the optimal positioning for treatment beams is achieved.

Using Beam Angle Optimization, the field setup becomes faster because it eliminates the need for trial-and-error work. The optimal result is a homogeneous dose delivered to the PTV in accordance with the dose prescription while minimizing the dose to the surrounding normal tissue, especially the organs at risk.

Beam Angle Optimization is based on the DVO algorithm, and it uses the same DVH-based objectives.

The optimization objectives are defined in the Beam Angle Optimization dialog box.



Note: *The optimality of the plan is defined with the optimization objectives—the Beam Angle Optimization does not automatically minimize the dose to the critical structures. It is helpful to define and place a priority on the normal tissue using the NTO. This way Beam Angle Optimization can evaluate and avoid larger peripheral doses.*



Note: *Although it is possible to use the Beam Angle Optimization without Dose Volume Optimization, the best results are achieved using it in conjunction with Dose Volume (IMRT) Optimization. You can use either the DVO or the PO algorithm as the algorithm for IMRT Optimization. If the Beam Angle Optimization is used in any other way, the optimality of the plan cannot be guaranteed.*

If you are re-optimizing a plan, remove all lower objectives from structures that are no longer needed in the optimization. If you only set the priority of lower optimization objectives as zero, the objectives still affect the optimization results.

Create a Plan Setup with Beam Angle Optimization

Beam Angle Optimization is available only for photon plans. Optimized field setups consist of static isocentric fields that share the same isocenter and contain no field accessories. Using Beam Angle Optimization for a plan that contains more than one field results in removing and replacing all but one of the original fields.



Note: Because the DVH-based constraints for the PTV and for organs at risk convey the optimization goal to the Beam Angle Optimization, these constraints should include all information needed for the evaluation of the final treatment plan. All objectives should be defined and complete before starting the Beam Angle Optimization. To achieve optimal results, it is not recommended to add or change objectives during Dose Volume Optimization.

1. Create a plan, add one field used as a “seed” to the plan, and define the dose prescription.
2. Choose **Planning > Beam Angle Optimization**.
3. If prompted, select the MLC to use.
The selected MLC is used in Beam Angle Optimization only. If you proceed to Dose Volume Optimization, you need to select the MLC again.
4. By default all structures are included in optimization.
To leave structures outside optimization, click **Exclude Structures**, select the structures to exclude, and click **OK**.
5. Select structures for which to display the DVH from the Structures and Objectives list and define the optimization objectives or load the objectives from an objective template.



Note: Indicate all desired doses as unfractionated total doses.

6. To change the field geometry calculation options, click **Edit** and then define the desired options.
More information on the calculation options: *Eclipse Photon and Electron Algorithms Reference Guide*.
 - You can rotate the graphical field geometry model during the optimization.
7. To continue automatically to Dose Volume Optimization after Beam Angle Optimization, select the appropriate check box.
8. To start the optimization, click **Optimize**.
You can follow the progress of the optimization in the Beam Angle Optimization dialog box.
9. To interrupt the optimization and close the dialog box, click **Cancel**.

- To view the graphical field geometry model from different angles, drag it with the mouse.
- When the optimization is completed, click **OK**.

Related Topics

[Photon Optimization Parameters](#) on page 226

[Calculation Options for External Beam Plans](#) on page 430

[Define Dose Objectives in IMRT and VMAT Optimization](#) on page 237

Calculation Options for Beam Angle Optimization

The calculation options are settings for the Beam Angle Optimization algorithm. The default calculation options are defined in Beam Configuration. The calculation options control the initial field distribution, optimization modes, iterations, and field reduction parameters.

Part of the calculation options for the Beam Angle Optimization algorithm are shown in the Beam Angle Optimization dialog box:

- Global optimization mode (coplanar or non-coplanar)
- Local optimization mode (Simplex or Powell)
- Minimum number of fields (lowest number fields in the field geometry created by the global optimization)
- Maximum number of fields (highest number fields in the field geometry created by the global optimization).

These and the rest of the calculation options can be accessed through the Beam Angle Optimization dialog box, Plan Properties dialog box or the Info window.

More details on the calculation options and their default values: *Eclipse Photon and Electron Algorithms Reference Guide*.

Related Topics

[Calculation Options for External Beam Plans](#) on page 430

Beam Angle Optimization Modes

To use Beam Angle Optimization, you need a plan with one field used as a “seed” for the optimization. The isocenter of the first field is taken to be the isocenter for all fields created by the Beam Angle Optimization. When you start the Beam Angle Optimization, it optimizes the beam angles in two stages:

- Global optimization
- Local optimization

Global Optimization Mode

Global beam angle optimization creates the new field geometry, which can be either coplanar or non-coplanar, depending on the selected optimization parameters. The optimization starts from a set of uniformly distributed fields, and then narrows the number of fields down to a set that best fulfils the optimization objectives defined for the patient structures.

The way new fields are created depends on the selected global optimization mode:

- Coplanar field geometry—Creates equally spaced fields by increasing the gantry values. The couch rotation is always zero.
- Non-coplanar geometry—Creates fields by uniformly positioning them in three-dimensional space. The angle of each field to its closest neighbor is approximately the same for all fields. Opposing fields are avoided.



Note: Fields that enter the patient through the end(s) of the CT stack are excluded by both the global and local optimization modes.

After creating the initial field geometry, the Beam Angle Optimization starts decreasing the number of fields by iteratively ranking the fields based on the relative importance of each field. Those with low importance are removed. The ranking is done using an objective function. You can control the number of fields to be excluded after each iteration with a parameter value (Field reduction rate parameter).

Local Optimization Mode

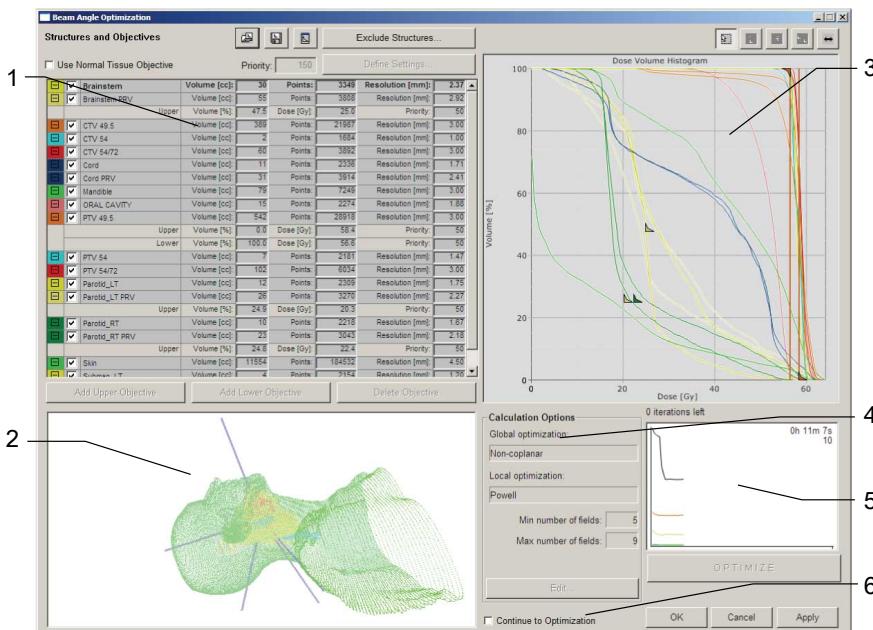
The local beam angle optimization continues from the result of the global optimization by fine-tuning the couch rotation (for non-coplanar field geometry) and gantry (for both coplanar and non-coplanar field geometries). The local optimization does not change the number of fields in the plan, but it can test any couch and gantry angle combinations to find the optimal geometry. The progress of the local optimization is shown with the objective function curve and the Number of iterations parameter.

The local optimization can be performed in two modes that are defined as a calculation option for optimization: the Downhill Simplex method and the Powell method. More information on these methods: *Eclipse Photon and Electron Algorithms Reference Guide*. In addition to the mode, the maximum number of local optimization iterations is controlled with a calculation option.

The local optimization can also be run alone without first running the global optimization. This might be useful for testing purposes. However, the best beam angle optimization results are achieved by running both global and local optimizations.

Beam Angle Optimization Dialog Box

You can monitor the progress of the optimization process in the Beam Angle Optimization dialog box, which shows a DVH calculated for each structure after each optimization, the number of fields left and a graphical model of the field geometry. You can evaluate the effectiveness of the dose objectives and see what the field geometry will look like.



- Shows the structures contained in the plan, the volumes of the structures, the points and point resolution used for modeling the structures in the optimization, and the values of the defined optimization objectives. Right-click to show or hide all structures, or only structures with objectives in the DVH.
- Show the 3D model of each field geometry setup calculated by the Beam Angle Optimization.
- Shows the optimization results in the form of DVH curves, one curve for each structure.
- Shows the selected calculation options for the optimization, allows modifying the options.
- Shows the objective function of the optimization.
- Once the Beam Angle Optimization is completed, automatically opens the Optimization dialog box for continuing to Dose Volume Optimization.

Figure 99 Beam Angle Optimization Dialog Box

The status of the fields being processed by the Beam Angle Optimization are marked with color coding in the 3D model of the field geometry:

- Red = Original field angles (resulting either from global optimization or manually added).
- Purple = Fields being processed.
- Green = The best field angles found.

Once the optimization is completed, all fields are momentarily shown in green.

Chapter 13 Multileaf Collimators

Multileaf Collimators (MLC)

Multileaf collimators (MLC) are thin-leaf collimator systems used to shape fields in conformal therapy.

MLC leaves are arranged around the target structure either with the fitting tools, or by changing the positions of individual MLC leaves.

All configurable MLC systems are supported, for example:

- Varian MLC systems
- Philips/Elekta MLC system
- Siemens MLC system
- BrainLab MLC system



Note: Eclipse does not accurately represent the collimator jaw structure of Siemens or Elekta (Agility and Beam Modulator) treatment units in dose calculation or the field visualization in External Beam Planning. Eclipse assumes that the field edges in both X and Y directions are limited by a collimator jaw block, whereas in Siemens and Elekta treatment units the MLC device replaces the collimator X jaws.

Prerequisites for Using MLCs

Before you can add an MLC to a field, the following settings must be configured in RT Administration for the MLC:

- MLC transmission factor and dosimetric leaf gap in photon fields.
- MLC leaf width.
- Maximum bank and leaf spans.
- MLC leaf overtravel distance.

MLC Types Available for Photon Fields

Generally, when used in photon fields, MLCs can be divided into static and dynamic. The distinction is that in static MLCs, the MLC leaves do not move during beam on, whereas in dynamic MLCs, the MLC leaves move during beam-on. There are a number of dynamic MLCs, depending on the plan type.

Table 27 MLC Types in Photon Fields

Field/Plan Type	MLC Type	Added by	Description
Static	Static	Manually as a field accessory	MLC shape is static for each field during beam-on.
Standard arc	Static	Manually as a field accessory	MLC shape is static during beam-on. Gantry angle changes between the start and the stop angle.
Conformal arc	Arc Dynamic	Manually as a field accessory	MLC aperture conforms dynamically with the outline of the target. MLC leaf positions change in each arc field segment during beam-on. Dose per degree is constant.
Siemens MLC 160 conformal arc	Arc Dynamic	Manually by fitting a Siemens MLC 160 to a target structure in an arc field	The MLC shape in each arclet conforms to the projection of target structure shape at central gantry angle of the arclet. The number of MU delivered in each arclet is constant.
IMRT	Dose Dynamic	IMRT optimization	Sliding window technique: MLC leaf positions change dynamically during beam-on. Gantry angle is static.
			Multiple static segments technique: MLC leaf positions change during beam-off. Gantry angle is static.
VMAT	VMAT	VMAT optimization, Arc Geometry tool	MLC leaf positions, gantry angle, and dose per degree change dynamically during beam-on.

Field/Plan Type	MLC Type	Added by	Description
Siemens mARC	mARC	Siemens mARC optimization, Arc Geometry tool	MLC leaf positions, gantry angle, and dose per degree change dynamically during beam-on.

Adjusting MLC Leaf Positions

After adding an MLC to a field, position the MLC leaves to limit the dosage to the desired areas only.



Note: Always carefully verify the MLC parameters before fitting the MLC, especially for opposed fields.



Note: If you change the photon treatment unit after adding an MLC to a field, the MLC type is converted to one that has been configured for the new unit. You are prompted to confirm the conversion. Verify the leaf positions. Varian HD-MLC is not supported in the conversion.

You can use automatic leaf editing tools to arrange the leaves around the target structure, or draw the MLC outline manually. After defining the initial leaf positions, it is possible to modify the positions of individual leaves with the mouse or by changing the leaf coordinates.

When moving MLC leaves, you can display the previously calculated dose distribution (persistent dose) and use the isodose lines as guides in making modifications.

Related Topics

[Showing the Persistent Dose in External Beam Planning](#) on page 441

Move MLC Leaves Manually with the Mouse

1. If the MLC tools are not visible in the toolbar, in the Focus window, right-click the MLC and choose **Edit**.

The 3D view changes to the BEV and the MLC tools are activated.



Tip: When arranging Dynamic MLC leaves, select first the segment with the next and previous buttons available in the animation toolbar.

2. On the MLC toolbar, click **Select MLC Leaves** .

3. Select the MLC leaves to move:
 - To select several individual MLC leaves, press **Ctrl** and click each leaf.
 - To select a range of MLC leaves, press **Shift** and click the first and last leaf in the range.
4. To move the selected leaves:
 - Point at them and move them with the mouse
 - Use the Shaping tool.
5. Fine-tune the leaf position coordinates in the MLC Properties dialog box if necessary.

Move MLC Leaves Manually with the Leaf Coordinates

1. In the Focus window, select the MLC.
2. Choose **Edit > Properties**.
3. Select the **Leaf Positions** tab.
4. In the **Bank A or Bank B** box, select the MLC leaves to modify.
 - To select individual MLC leaves, press **Ctrl** and click each leaf.
 - To select an MLC leaf range, press **Shift** and click the first and last leaf in the range.
5. In the **Edit Selected MLC Leaf Positions** dialog box, type the new values for the MLC position.
6. Click **OK** to display the changes in the BEV.
7. Click **OK**.

Lock the MLC Leaves

You can prevent accidental changes to MLC leaf positions by locking them.

1. If the MLC tools are not visible in the toolbar, in the Focus window, right-click the MLC and choose **Edit**.

The 3D view changes to the BEV and the MLC tools are activated.

2. On the MLC toolbar, click **Lock/Unlock**  to lock the MLC leaves.

Modify MLCs with the MLC Shape Tool

You can use the MLC Shape tool to define simple field shapes, with regular or variable margin between the target structure and the MLC outline. The tool is available for all manufacturers' MLC types, and only for static fields containing static MLCs.

1. In the Focus window, right-click the MLC and choose **MLC Shape Tool**.
2. To define the shape of the MLC aperture, select **Circular** or **Rectangular**.
3. To change the size of the aperture, define the new size in the **Diameter** (for circular aperture) or the **X size** and **Y size** boxes (for rectangular aperture).
4. To make a rectangular aperture asymmetrical, select the **Asymmetric** check box and then define the **X size** and **Y size**.
5. Select the following as necessary:

Option	Description
Leaf edge—contour meet point	Determine whether the MLC leaves are allowed to cross the MLC outline.
Closed leaf meeting position	Positions the MLC leakage area to a specific location.
 Note: If you use Elekta Beam Modulator, place the closed leaf meeting position either to Bank A or Bank B. This minimizes the leakage between the MLC leaves. If you do not do this, the application shows a warning message regarding the leakage when the dose calculation is started.	
Optimize collimator jaws (in a photon plan)	Adjusts the collimator jaws to best fit the MLC leaves to the structure.
Use recommended jaw positions (in a photon plan)	Adjusts the collimator jaw positions along the MLC aperture with an additional margin. The margin is defined by the Recommended Parallel Jaw Setback and Recommended Perpendicular Jaw Setback values in RT Administration.

6. Click **Apply** to arrange the MLC leaves.
7. Click **OK**.

Using the Fit and Shield Tool

Using the Fit and Shield tool, you can position MLC leaves around the target structure so that the aperture formed by the MLC leaves exposes the target, but, at the same time, the leaves cover critical organs. This is particularly useful in arc fields. When using the Fit and Shield tool, you need to:

- Select the target structure and the critical organs, and define their margins. Margins defined for critical organs always take precedence over those defined for the target.
- Create the necessary fields either manually or automatically. If you use the automatic option, the necessary fields and MLC leaf positions are automatically determined. The number of fields created depends on the number of critical organs. The field size is automatically positioned to conform to the target structure.
- Evaluate the MLC setup visually. You can set the BEV to show all MLC shapes that share the same isocenter, gantry and couch rotation, and SAD.



Note: *The Fit and Shield tool is primarily intended for arc fields. If you use this tool for static MLC fields, the proposed segments may not be satisfactory. Moreover, the Pencil Beam Convolution (PBC) algorithm does not calculate the small MLC outlines produced by the Fit and Shield tool with sufficient accuracy.*

Fit and Shield Tool in Conformal Arc Fields

You can use the Fit and Shield tool in conformal arc fields for modified hollow-out planning. The hollow-out technique is a conformal arc treatment technique in which critical organs are shielded while the target is exposed. Hollow-out treatments normally comprise multiple conformal arc fields. The Fit and Shield tool can automatically create the necessary number of conformal arc fields and determine the correct MLC leaf positions.

The following properties of the original conformal arc field are used in the created fields:

- Gantry, collimator and couch rotation
- Isocenter position
- Treatment unit and energy

The MLC segments in the original field are changed to segments with 2-degree intervals. The field size is automatically positioned to conform to the target structure.



Note: *The Fit and Shield tool cannot be used in conformal arc fields with Elekta and Siemens MLC devices.*

Specifics of Adjusting MLC Leaves in Photon Fields

You cannot modify the leaf positions in IMRT fields by using the leaf editing tools.

The collimator jaws must always be positioned in such a way that they protect the MLC carriage from radiation. If editing MLC leaves results in a situation where the MLC carriage is exposed, Eclipse moves the collimator jaws automatically to protect the MLC carriage from radiation. This can happen, for example, in the case of a Standard 80 MLC, if the Y-jaw opening exceeds 19.8cm, and the X-jaws are more than 8.12mm retracted beyond the most retracted MLC leaf. These limits depend on the MLC type. The jaw positions are verified when you finish editing the MLC shape and when the MLC is validated.

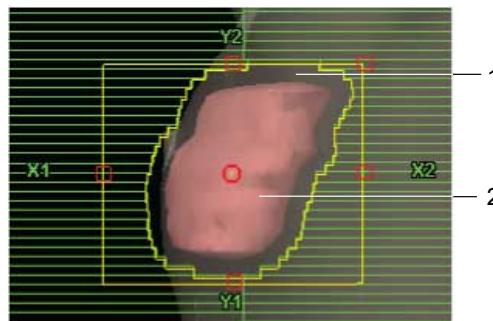
If you change the number of field segments in a conformal arc field, change the start or stop angles of the field, or rotate the field after arranging the MLC leaves, all leaves are closed. Refit the MLC leaves to re-arrange them.

MLC Margin Types

The MLC margin is the distance between the defined MLC outline and the target outline. Two types of automatic MLC margins are used: circular and elliptical. In addition, you can define the margin manually with the mouse.

Circular Margin

In a circular margin, the distance of the MLC outline from the target volume surface is always uniform. In the figure, a circular margin of 1 cm is used with the MLC.

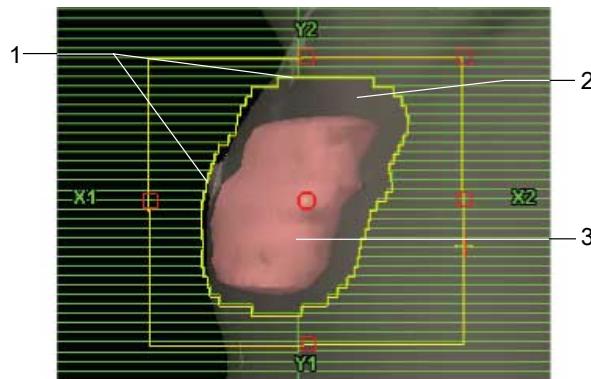


1. Circular margin between target and MLC leaves
2. Target

Figure 100 Circular Margin

Elliptical Margin

In an elliptical margin, the distance of the MLC outline from the target volume outline can be different in two orthogonal directions. In the figure, the margin is defined to be 0.5 cm along the X1 field edge, 1.5 cm along the X2 field edge, 1.0 along the Y1 field edge, and 2.0 along the Y2 field edge.

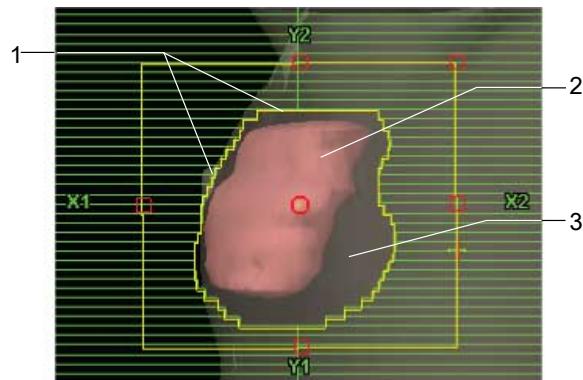


1. Field edges
2. Elliptical margin between target and MLC
3. Target

Figure 101 Elliptical Margin

Manually Delineated Margin

In a manually delineated margin, the distance of the MLC leaves from the target is defined with the mouse. The figure shows a freely varying manually delineated margin defined for an MLC.



1. Field edges
2. Target
3. Freely varying margin between the MLC leaves and the target

Figure 102 Manually Delineated Margin

MLC Coordinate Axis Types

For an elliptical margin, you also need to select axes to use for creating the margin. The axes are orthogonal coordinate axes, and they determine how the margin width varies along the axes. The axes can be determined either by the BEV coordinates or the collimator coordinates.

When the BEV coordinate axis option is used, the two coordinate axes are parallel to the sides of the BEV window. For an example of an elliptical margin using the BEV coordinate axis, see the figure. In this example, the elliptical margin is 0.5 cm along the X1 field edge, 1.5 cm along the X2 field edge, 1.0 cm along the Y1 field edge and 2.0 cm along the Y2 field edge.

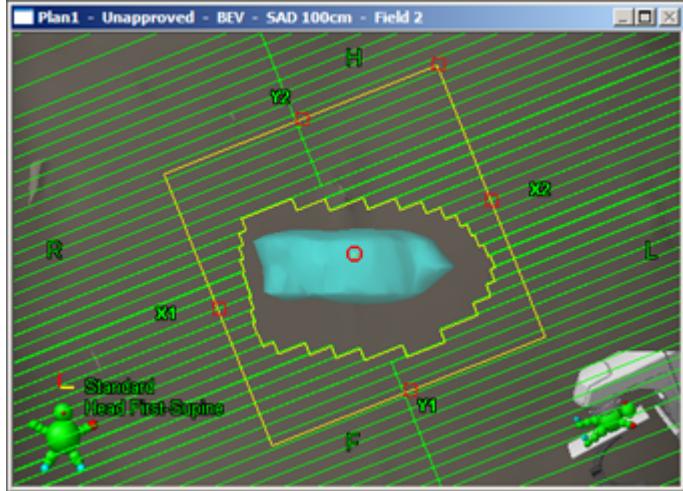


Figure 103 BEV Coordinate Axis

When the collimator coordinate axis option is used, the axes are parallel to the collimator. In the following figure, the elliptical margin is exactly the same as in the previous figure, but the coordinate axis is different.

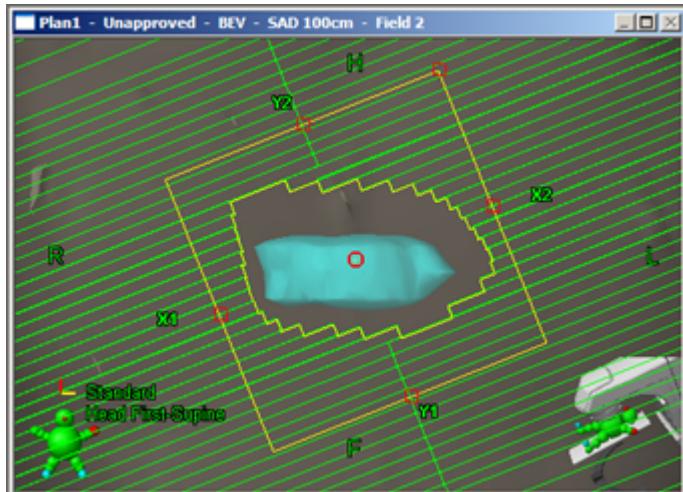


Figure 104 Collimator Coordinate Axis

MLC Leaf Fit

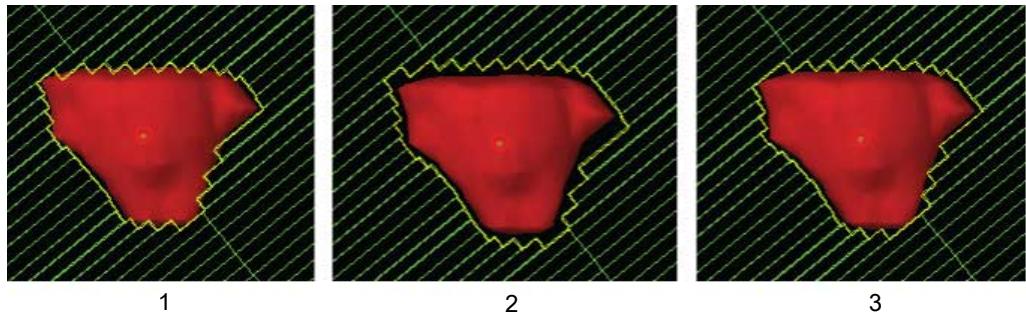
MLC leaves are arranged around the target structure by using the fitting tools, or manually, either by moving the leaves with the mouse or by defining the coordinate position of each leaf.

The Leaf Edge–Contour Meet Point option determines whether the MLC leaves are allowed to cross the structure projection outline or not.

Table 28 Leaf Edge–Contour Meet Point Options

Leaf Edge–Contour Meet Point Option	Description
Inside	MLC leaf edges are inside or on the structure projection outline. The final MLC aperture is slightly smaller than the defined structure projection outline.
Outside	MLC leaf edges are outside or on the structure projection outline. The final MLC aperture is slightly larger than the defined structure projection outline.
Middle	The MLC outline intersects the middle of the MLC leaves. The final MLC aperture is approximately the same size as the structure projection outline.

The figure shows an MLC with a different Leaf Edge–Contour Meet Point option. The other MLC parameters are the same.



1. Inside
2. Outside
3. Middle

Figure 105 Leaf Edge–Contour Meet Point Options

Related Topics

[Move MLC Leaves Manually with the Mouse](#) on page 362

MLC Leaf Bank

MLC leaf banks are the two MLC leaf storage areas on both sides of the collimator. The leaves are pushed towards the target structure from the leaf bank or pulled towards the leaf bank. The default names for MLC leaf banks are bank A and bank B. The configuration of your system can also contain other leaf bank names.

MLC Leaf and Leaf Bank Maximum Span

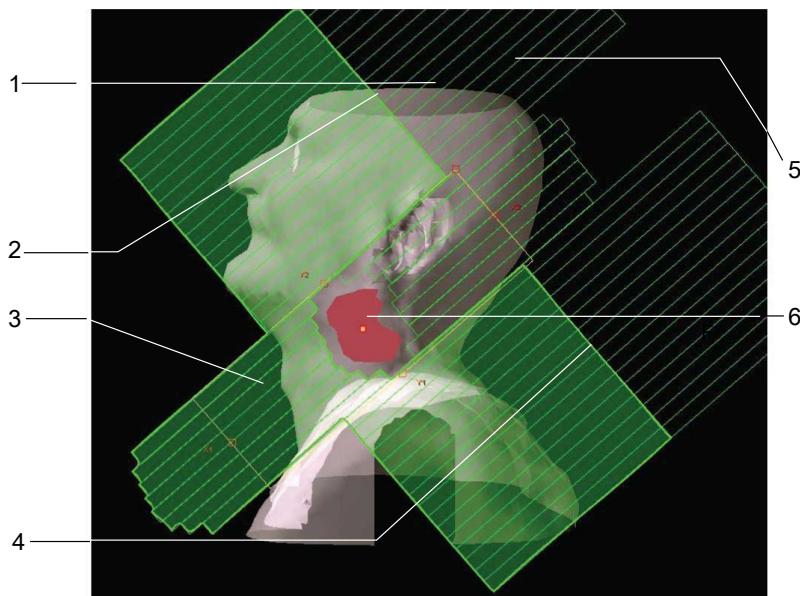
The movements of both the MLC banks and individual MLC leaves are restricted by their maximum spans—the MLC bank or MLC leaves cannot be moved over the maximum span limit. The maximum distance past the central axis of the MLC opening is called the leaf overtravel distance.

In some situations the maximum spans can be accidentally exceeded. If you first lock an MLC leaf or bank and then use the Fit to Structure command, the locked leaf or bank may end up under the fitted ones, and the maximum span is exceeded. In these situations, a warning is issued.

Closed Leaf Meeting Position

In areas closing the MLC aperture, two MLC leaves from facing leaf banks meet each other. To avoid any damage caused by the radiation leakage that always occurs in these areas, use the Closed Leaf Meeting Position options to position the MLC leakage area outside the patient's body outline, for example.

For example, the meeting position can be defined to be at the maximum overtravel distance of bank A or B. The figure illustrates a situation where the closed MLC leaves from bank B are pushed forward up to their overtravel distance.



1. MLC leaf bank A
2. Leakage area
3. MLC leaf bank B
4. Overtravel distance of bank B
5. Leaves moved to the side
6. Target structure

Figure 106 MLC Leaf Banks

The table describes the available Closed Leaf Meeting Position methods.

Table 29 Closed Leaf Meeting Positions

Closed Leaf Meeting Position	Description
Bank B	MLC leaves meet at the overtravel distance for the leaves of bank A
Center	MLC leaves meet at the aperture center
Bank A	MLC leaves meet at the overtravel distance for the leaves of bank B

The figure compares the Closed Leaf Meeting Position options with each other.

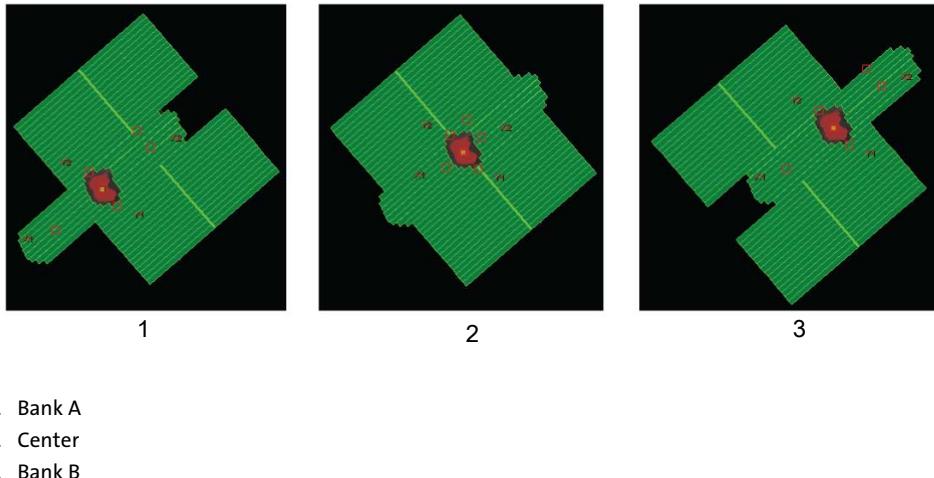


Figure 107 Closed Leaf Meeting Positions

Converting MLCs into Blocks

Sometimes it may be necessary to transfer a plan to a treatment unit that does not have an MLC device installed and configured. In these cases, you can replace the MLCs in the plan with blocks by using the MLC aperture outline for defining an aperture block.

Convert an MLC into an Aperture Block

1. In the Focus window, right-click the MLC to be converted into a block and choose **Copy to Block**.
2. Select whether you wish to optimize the collimator jaws or the collimator rotation to decrease the field size in a photon plan.
 - Optimize collimator jaws—the application moves the collimator jaws as close to the selected structure as possible.
 - Optimize collimator rotation—the application rotates the collimator jaws around the selected structure.
3. To check the block outline, click **Fit**.
4. Define the block properties and click **OK**.

The MLC is converted into a block.

5. Visually verify the created aperture block against the original MLC aperture in the BEV.
6. Do one of the following:
 - If you are happy with the result, click **Close**.
 - If you wish to change the block settings, repeat the steps above. You can repeat this as many times as is necessary. To finish, click **Close**.

If necessary, you can modify the block.

Related Topics

[Add a Standard Aperture Block](#) on page 381

Verifying MLC Leaf Positions

The MLC leaf positions of both static and dynamic MLCs can be verified against the physical limitations of the MLC device. The verification is also automatically done when the dose is calculated for a plan containing MLCs and when a plan is approved. The application automatically corrects the leaf positions by finding positions as close as possible to the initial position without violating the MLC device limitations.

The following limitations are verified:

- MLC leaf maximum extend and retract positions
- Maximum leaf span
- Minimum leaf gap (minimum gap to be maintained at all times between moving opposite DMLC leaves during the treatment)

- Leaf speed
- Interdigitation leaf gap (minimum gap for two diagonally adjacent leaves; verified for devices that do not allow interdigititation)
- Existence of completely closed leaf pairs inside the MLC aperture (not allowed in Elekta MLC devices)
- Closed leaf pair position for Elekta MLC devices

Show Multiple MLC Outlines in the BEV

1. Show the appropriate field in the BEV.
2. Right-click in the BEV and choose **Show All MLC Apertures in BEV**.



Tip: This option is intended to be used in arc plans containing several fields, each with an MLC attached. It shows deviations of MLC leave openings in different fields for the same control point. The compared fields must have the same isocenter and the same couch rotation. This option is particularly useful in displaying the combined aperture when the Fit and Shield tool is used.

Field-in-Field Technique

The field-in-field technique refers to a method of IMRT planning where the calculated dose is modified in certain areas of the dose distribution by adding new segments into the existing fields. The aim is often to smooth out or block hotter isodose lines in the plan. The field-in-field segments, or subfields, are added to one or several initial, or primary, fields containing an MLC. The isodose visualization is used as a reference when adding the field-in-field subfields to block the desired isodose line. You can show the primary field and the isodoses in the BEV and then manually draw the MLC outline of the subfield by tracing the desired isodose, or convert a selected isodose surface to a structure and then fit the MLC to that structure. The weights of all subfields and primary fields can be modified interactively during planning to correctly modulate the intensity of the radiation in each field. After defining the necessary number of subfields, they are merged into one conformal segmental MLC field.



CAUTION: Changes made to the original plan will not be conveyed to a new copy of the original plan or vice versa.



Note: Field intensity modulation with subfields is available only for plans consisting of photon fields containing static MLCs. The plan can contain bolus. However, blocks or wedges are not allowed.

Merging Subfields into Segmental MLC Fields

Each subfield in a primary field is transformed into a static segment and saved in a new IMRT plan. The subfields are merged in treatment order into segmental MLC fields (using the Multiple Static Segments technique) by following certain rules.

Merged subfields are subfields that have the same

- Geometry (gantry, collimator and couch rotation, jaw positions, isocenter)
- Treatment unit (energy, dose rate, treatment technique)
- MLC device

Subfields that cannot be merged are copied into new fields. As many subfields of a primary field are treated using the same carriage group as possible. Subfields that cannot use the same carriage group are further grouped, if possible, and saved into new IMRT fields using a different carriage group.

Fields and setup fields are included in the new plan. DRR images attached to the merged fields are not copied to the new plan; DRR images are copied only for fields that are not merged.



Note: In some cases the subfields cannot be merged because the collimator jaw position has been automatically moved to protect the MLC carriage from radiation, and in consequence, the subfields are not of the same size. If editing MLC leaves results in a situation where the MLC carriage is exposed, Eclipse moves the collimator jaws automatically to protect the MLC carriage from radiation. This can happen, for example, in the case of a Standard 80 MLC, if the Y-jaw opening exceeds 19.8cm, and the X-jaws are more than 8.12mm retracted beyond the most retracted MLC leaf. These limits depend on the MLC type. The jaw positions are verified when you finish editing the MLC shape and when the MLC is validated.



Note: Different collimator jaw positions are allowed for Elekta MLC devices.

The normalization mode of the new plan is automatically changed to the Plan Normalization Value option with the same normalization percentage as the original plan.

Create a Subfield (Field in Field)

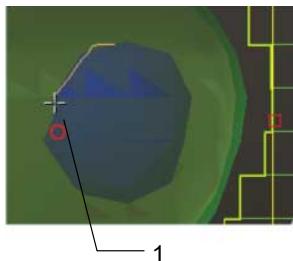
1. Create the primary field and add a static MLC to it.
2. Calculate the dose distribution.
3. In the Focus window, select the static MLC.

4. Choose Insert > New Field in Field.

A duplicate of the primary field appears in the Focus window. The new subfield has zero field weight and invalid MU value. For both fields, the MLC aperture and the dose distribution are shown in the BEV. The Shaping tool is activated. The MLC Fit Options dialog box and the Field Weights dialog box open.

The ID of new subfields is formed from the ID of the primary fields by adding an incremental digit to it, for example, subfields for primary field Field1 will be named Field1.0, Field1.2, Field1.3 and so forth.

5. Draw the MLC aperture in the BEV.



1. Draw the MLC aperture with the mouse. You can trace an isodose surface if necessary.
6. In the MLC Fit Options dialog box, select the following:
 - Leaf edge—contour meet point
 - Closed leaf meeting position The MLC leaves are fitted to the MLC aperture.
7. Re-calculate the dose.
8. In the Field Weights dialog box, set the weights and click **Close**.
9. Repeat the above steps if necessary.

Related Topics

[MLC Leaf Fit](#) on page 370

[MLC Leaf Bank](#) on page 371

[Using Field Weight Factors](#) on page 437

Merge Subfields into a New Plan

1. Create all the necessary primary fields and subfields, calculate the dose distribution, and define field weights.
2. In the Focus window, select the plan that contains the primary fields and the subfields.

3. Choose Planning > Merge Subfields.

A message box opens, showing the new plan and fields that will be created from the original plan, primary fields and subfields.

4. Click OK.

5. In the Setting MUs for IMRT Fields dialog box, check that the values are correct and click OK.

The new plan is created and saved into the active course. It contains the merged fields and copies of original fields that could not be merged. As a result of the merge, the merged fields will contain a DMLC that consists of static segments of the MLCs in the original fields. The status of the original plan changes to Rejected.

6. The dose calculation is started automatically.

Evaluate the plan, approve it and move it to treatment.

Related Topics

[Create a Subfield \(Field in Field\) on page 376](#)

Chapter 14 Blocks

About Blocks

Blocks are physical devices made of high-density material. They are used to prevent critical organs or other areas outside the target structure from being exposed to radiation. You can define the block shape either manually or automatically. You can mirror, rotate and move blocks. The block coordinate system is fixed to that of the treatment unit, in other words, rotating the collimator also rotates the blocks.

The block material parameters are defined in the treatment unit configuration, and cannot be changed during treatment planning.

If photon blocks are made by casting, a material with a low melting point is usually used. The block parameters for photon blocks include the block add-on material, block transmission factor, tray transmission factor, and the treatment units allowing the use of the block. They are configured in RT Administration.

More information on the add-on material configuration in RT Administration: *RT Administration Reference Guide*, refer to online help.

Block Types

The following types of blocks are used:

- Aperture blocks—Pieces of block material that leave the inside area of the block open, that is, the block has an aperture. The shape of the aperture is either regular (a circular or rectangular standard aperture block) or defined to surround the exposed area with a specified margin (a custom aperture block). There can be only one aperture block per field.
- Shielding blocks—Pieces of block material that shield the area within the block outline. One field can contain any number of shielding blocks.

Block Margin Types

The target outline and the block's inner outline are separated by a user-defined margin. The margin type can be circular or elliptical and tied to the collimator rotation or the BEV window.

In a circular margin, the distance of the block's inner outline from the target volume outline is uniform.



Figure 108 Aperture Block with a Circular Margin

In elliptical margins, the distance of the block's inner outline from the target volume outline differs in two orthogonal directions. In this example, the margin is defined to be 0.5 cm along the X1 field edge, 1.0 cm along the Y2 field edge, and 1.5 cm along the X2 field edge and 2.0 cm along the Y1 field edge.



Figure 109 Aperture Block with an Elliptical Margin

Block Coordinate Axis Types

For aperture blocks with elliptical margins, you also need to select the axis to use for creating the margin. The axes are orthogonal coordinate axes, and they determine how the margin width varies along the axes. The axis can be determined either by the BEV coordinates or the collimator coordinates.

When the BEV coordinate axis option is used, the margin axes are parallel to the sides of the BEV window.



Figure 110 Aperture Block, BEV Coordinate Axis

When the collimator coordinate axis option is used, the margin axes are parallel to the collimator jaws.



Figure 111 Aperture Block, Collimator Coordinate Axis

Add a Standard Aperture Block



Note: A field can contain only one standard aperture block. Adding a standard aperture block to a field clears the existing block aperture from the field.

1. Add a block object to the field.
2. In the Focus window, right-click the block structure and choose **Set Block Shape**.
3. Do one of the following:
 - To create a circular aperture, select **Circular** and define the diameter of the cut-out aperture in the **Diameter** box.
 - To create a rectangular aperture, select **Rectangular** and define the side lengths of the aperture in the **X size** and **Y size** boxes.

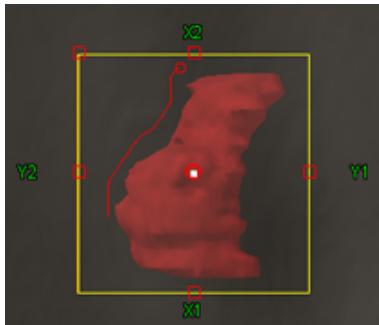
4. Click **OK**.

Delineate the Block Outlines Manually

1. In the Focus window, right-click the block and:
 - BEV not displayed: Choose **Edit**, and then on the Block Tools toolbar, click the **Freehand** tool 
 - BEV already displayed: Choose **Freehand**.
2. Using the selected tool, draw the block outline either as a continuous line or by clicking it point by point.

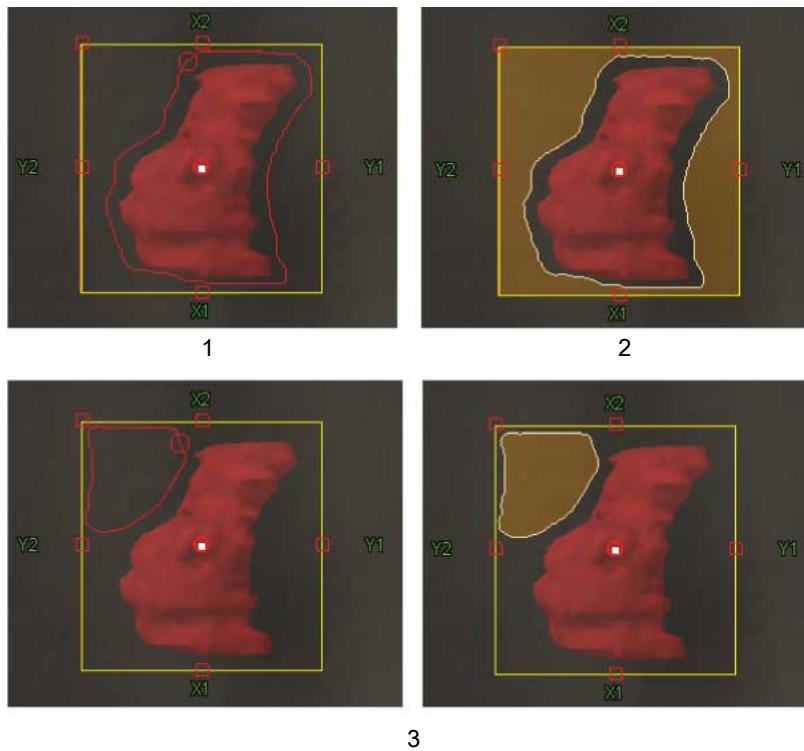


Tip: Use the Circle Cursor  tool as an aid to manually draw a margin of a determined width.



3. To close the outline, move the mouse pointer back to the same spot where you started drawing the line and release the mouse button when the connection point is highlighted.

The outline is closed. Depending on the selected block type, the area between the block outline and the field outlines or the area enclosed by the block outline is filled with block material.



1. Finish the outline.
2. Aperture block: The area between the block outline and the field outlines is filled with block material.
3. Shielding block: The area enclosed by the block outline is filled with block material.
4. To delineate another area which is part of the same block, repeat the above steps.

Related Topics

[Showing the Persistent Dose in External Beam Planning](#) on page 441

Digitize the Block Outline



NOTICE: Prior to digitizing radiographs, place reference marks on them as a means to verify the correct image orientation in the system.

1. Insert a block to a field.
2. In the Focus window, select the block to which you are about to import an outline.

3. Show the appropriate field in BEV.
4. If not selected, choose **Planning > Enable Digitizer**.
5. If necessary, calibrate the digitizer.
6. On the toolbar, click the **Digitize Block** tool 
7. To define the outline, click the points on the film with the first button of the digitizer mouse. The points are connected with straight lines.
To delete the entered points one by one, select the point and press Backspace on the keyboard or the second digitizer mouse button.
8. To close the line:
 - Press End on the keyboard.
 - Press the third digitizer mouse button.
9. To edit the outline, use the block editing tools.
10. When the block contour is ready, deselect the **Digitize Block** tool.
You can enter several outlines one after another. The calibration is valid as long as the selected field remains the same.
11. To disable the digitizer, choose **Planning > Enable Digitizer** again.

Edit a Standard Aperture Block

1. In the Focus window, right-click the block and choose **Set Block Shape**.
2. To change the shape of the aperture, select **Circular** or **Rectangular**.
3. To change the size of the aperture, define the new size in the **Diameter** (for circular aperture) or the **X size** and **Y size** boxes (for rectangular aperture).
4. Click **OK**.

Rotate a Block by Degrees

1. In the Focus window, right-click the block and choose **Rotate Block**.
2. Define the desired angle of the rotation. The default value is 90 degrees.
3. Define the direction of the rotation.
4. To rotate the block, click **Apply**.



Tip: To rotate the block by small increments, for instance, 5 degrees at a time, define the value of one increment in the rotation angle text box and then click **Apply** several times until you have reached the desired angle.

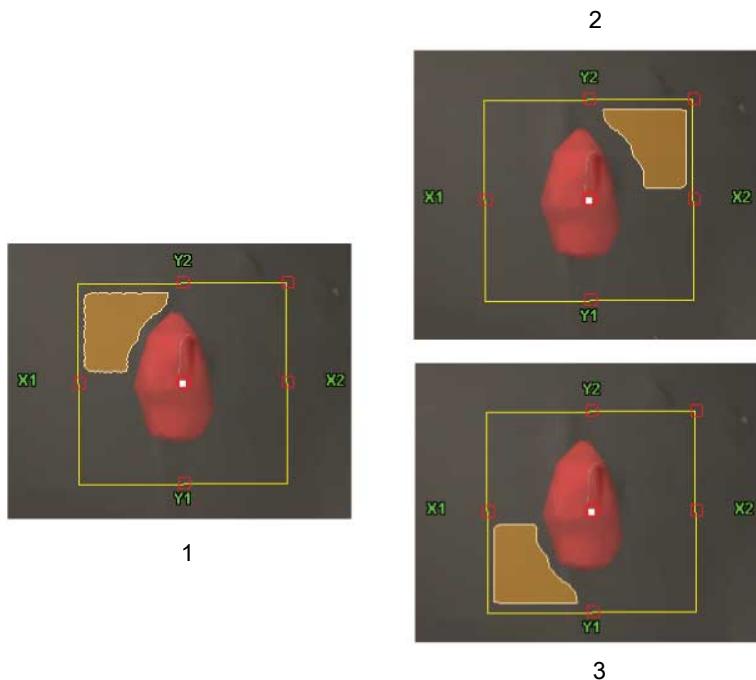
5. To close the Rotate Block dialog box, click **Close**.

Mirror a Block

1. Do one of the following:

- In the Focus window, right-click the block and choose **Edit** to open the BEV.
- Click **Mirror L/R**  or **Mirror U/D**  to mirror the block.

Patient orientation has an effect on how the blocks are mirrored.



1. Original block
2. Block mirrored left/right
3. Block mirrored up/down

Converting a Block into an MLC

Sometimes it may be necessary to transfer a plan from a treatment unit that does not have an MLC device installed and configured to a treatment unit that has one. In these cases, if blocks were used to modify the field shape, you can replace the blocks in the plan with MLCs by using the block aperture outline for positioning the MLC leaves around the target.

Convert an Aperture Block into an MLC

1. In the Focus window, right-click the block and choose **Copy to MLC**.
2. Define the MLC fitting options as desired:
 - Leaf edge—contour meet point.
 - Closed leaf meeting position.
 - Optimize collimator jaws—the application adjusts the collimator jaws to best fit the MLC leaves to the structure.
 - Use recommended jaw positions—the application adjusts the collimator jaw positions along the MLC aperture with an additional margin that is configured in RT Administration.
 - Optimize collimator rotation—the applicaton adjusts the collimator angle to best fit the MLC leaves to the structure.



Note: Remember to check that any other field modifier fits if you are using collimator rotation optimization.

3. Click **Fit** to arrange the MLC leaves in accordance with the selected options.
4. Visually verify the MLC aperture against the original block aperture in the BEV.
5. If necessary, change the MLC leaf fitting options and click **Fit**. You can repeat this as many times as necessary.
6. To keep the changes, click **Close**.

Verifying the Block Outline

If you want to verify the outline of a fabricated block against the block outline created in External Beam Planning, you can print the block outline shown in the BEV on a transparency. When specifying the printing options, you need to use the source-slot distance from the Block Properties.

Print the Block Outline

1. Right-click in the Model View, and select **Set Beam's Eye View to Field**.
2. Select **File > Print > View**.
3. In the **Plot distance from focus** group box, select **Other** and type in the source-slot distance for the block.
4. Click **OK**.

Chapter 15 Wedges

Wedge Types

You can add the following types of wedges in fields:

- Standard wedge—A standard wedge is a physical piece of material with an angle that is static during treatment.
- Dynamic wedge—Dynamic wedges are formed by a moving jaw of a standard collimator during irradiation.
- Enhanced Dynamic wedge—Enhanced dynamic wedges are similar to dynamic wedges, but they feature more wedge angles than simple dynamic wedges.
- Motorized wedge—Motorized wedges are standard wedges placed in the field for a user-defined fraction of the total treatment time.
- Elekta OmniWedge—Special type of wedge that combines an open field, motorized wedge and virtual wedge to create the desired wedge effect.

All wedge properties are configured in RT Administration. The wedge parameters specified in the configuration may set limits for the field size and wedge direction.



Note: When working with wedges, note the following:

- The wedge types available depend on the configuration of your database and the current treatment unit. If, for instance, Dynamic Wedges are not configured to your database, you cannot insert them in fields.
- For Varian treatment units, the minimum MU limit for Enhanced Dynamic Wedges is 20 MU. If a field has less MU, the field is not treatable. This limit is defined in RT Administration.

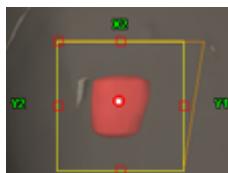
Related Topics

[Elekta OmniWedge](#) on page 389

Wedge Directions

Four different wedge directions are supported, as shown in the table. As the wedge direction is always defined in relation to a collimator angle of 0° (IEC), the list assumes that the collimator angle is 0° (IEC) and that the patient orientation indicator on screen is facing you. In the table, the wedge direction is expressed in relation to the patient, in accordance with IEC 61217.

Table 30 Wedge Directions in Relation to the Patient (Assuming Collimator Rotation α in IEC 61217 and Patient in the Head-First Supine Position)

Direction		Meaning	Illustration
IEC 61217	Eclipse		
0°	In	The sharp edge (toe) of the wedge points Superior. Default value.	
270°	Left	The sharp edge (toe) of the wedge points to the patient's left.	
180°	Out	The sharp edge (toe) of the wedge points Inferior.	
90°	Right	The sharp edge (toe) of the wedge points to the patient's right.	

Changing the collimator angle results in a change in the actual wedge direction, as the wedge is fixed to the collimator. However, in relation to the collimator, the wedge direction always remains the same.

Calculation of Motorized Wedges

The wedge weight factor is a parameter used for motorized wedges to indicate the dose percentage of the wedged and open part of a field containing a wedge. The weight factors range from 0 to 1.0, and the factor indicates the following:

- 0—fully open field

- 1—fully wedged field
- Other values—partly wedged field.

For example, a weight factor of 0.5 for a 60° motorized wedge is approximately equivalent to a field containing a 30° standard wedge.

The dose distribution of fields containing a motorized wedge is calculated on the basis of the weighted dose percentages for the wedged and open parts of the field. The Fields tab of the Info view displays the MU values and reference dose for both the open and wedged part of a field containing a motorized wedge.

In addition, the wedge dose displayed on the Field Properties tab is calculated as follows:

Equation 2

$$D = \frac{MU_{wedge}}{MU_{total}} = \frac{MU_{wedge}}{MU_{open} + MU_{wedge}}$$

View the Physical Wedge Properties



Note: *The wedge properties are configured in RT Administration. This function only allows you to view the properties.*

1. In the Focus window, select the wedge.
2. Choose **Edit > Properties**.

Elekta OmniWedge

A special type of wedge supported in Eclipse is the Elekta OmniWedge created by Elekta treatment machines. The Elekta Motorized wedge consists of the open field, the motorized wedge parts and the Elekta Virtual Wedge component, delivered by moving jaws. The wedge direction and angle is produced by the combination of these components. The AAA and Acuros XB are able to calculate Elekta OmniWedge fields. More information on Elekta OmniWedge and the dose calculation algorithms: *Eclipse Photon and Electron Algorithms Reference Guide*.

Add an Elekta OmniWedge

1. In the Focus window, select the field to add the wedge to.
2. Choose **Edit > Properties**.

3. Select the Accessories tab.
4. In the Wedge ID listbox, select the desired wedge.
5. Define the MU weights for the OmniWedge components:
 - Motor weight
 - Open weight
 - Virtual weight
 - To define which collimator jaw is moved to create the wedge effect in the virtual weight component, select the **Move jaw X2** or **Move jaw X1** option.

Adding an OmniWedge to a field automatically adds an MLC to the same field. The MLC is static, but it contains control points that indicate the movement of the X1 or X2 jaw (in the IEC scale).

6. If the selected treatment unit has multiple slots, select the accessory in the **Sslot** list boxes.
7. Click **OK**.

You can also modify the OmniWedge after adding it.

Modify the OmniWedge Settings

1. In the Context window, right-click OmniWedge and then choose **Adjust OmniWedge**.
2. To modify the OmniWedge angles, type the desired wedge angle and wedge orientation.

These values are modifiable only after the dose has been calculated.
3. To modify the OmniWedge component angles, type the desired motor wedge and virtual wedge angles.

Eclipse calculates the correct component weights from the defined angles.
4. To modify the component meterset weights, type the weight factor for motor weigh, open weight and virtual weight.
5. To define which collimator jaw is moved to create the wedge effect in the virtual weight component, select the **Move jaw X1** or the **Move jaw X2** option.



Note: *Changing this setting will invalidate the dose.*

6. Click **OK**.

If the plan has a calculated dose, it is updated in accordance with the changed OmniWedge settings.

Chapter 16 Compensators

Compensators in Photon Fields

Compensators are field modifiers placed between the radiation source and the patient's skin to achieve a desired dose distribution. Standard plane compensators allow dose compensation on a plane perpendicular to the field axis and at a given distance from the isocenter.

You have the following options to add a compensator:

- Create a standard compensator in Eclipse
- Import a compensator
- Convert an optimal fluence into a compensator



Note: Some calculation algorithms do not calculate MUs for fields that contain a compensator. To include the compensator transmission factor in the MUs for photon fields, calculate the effect manually and/or using measurements, because the compensator transmission factor is not automatically taken into account in the resulting MU values. More information on calculation algorithms: *Eclipse Photon and Electron Algorithms Reference Guide*.

Plane Compensators

When you create a standard plane compensator in Eclipse, you define the compensation plane on which the dose distribution should be uniform as well as the penumbra margin. The shape and thickness of the compensator piece are then calculated automatically according to your specifications.

The shape of the photon compensator is calculated using the PBC dose calculation algorithm version 11.0 or 10.0 (more information on the PBC algorithm: *Eclipse Photon and Electron Algorithms Reference Guide* for version 11.0 or version 10.0). The calculation produces the transmission matrix (or the field intensity matrix) of the compensator. The transmission matrix is converted into the compensator thickness map, using the linear attenuation factor.

The linear attenuation factor of a compensator, when the dose is calculated with the PBC dose calculation algorithm, depends on the combination of the compensator material and the photon energy. The compensator materials and the linear attenuation factor of each of them are configured in RT Administration.

More information on RT Administration: *RT Administration Reference Guide*.

Imported Compensators

You can also import a compensator in Eclipse. You might, for example, create an IMRT plan in Eclipse, export the plan, use a 3rd party software to create a compensator plan from the exported IMRT plan, import the compensator plan in Eclipse and calculate the dose distribution. When using the AAA or Acuros XB dose calculation algorithm, before importing a plan with compensator into Eclipse make sure that a slot with the source-to-slot distance matching to the imported compensator's source-to-compensator tray distance exists in RT Administration. More information on the AAA and Acuros XB dose calculation algorithms: *Eclipse Photon and Electron Algorithms Reference Guide*.

The linear attenuation factor of a compensator, when the dose is calculated with the AAA or Acuros XB dose calculation algorithm, is defined in Beam Configuration. Information on configuring compensators for AAA and Acuros XB: *Eclipse Photon and Electron Algorithms Reference Guide*.

Converted Compensators

If you want to use inverse planning methods but deliver the dose with a compensator, you can convert an optimal fluence into a compensator. You can also use the fluence of an irregular surface compensator. Unlike standard plane compensators, converted compensators do not have a compensation plane.

Related Topics

[Photon Compensator Properties](#) on page 393

Compensators and MU Calculation

You can calculate the dose for a photon field containing a compensator using either the PBC, AAA or Acuros XB dose calculation algorithm. More information on dose calculation algorithms: *Eclipse Photon and Electron Algorithms Reference Guide*.

PBC dose calculation algorithm versions 11.0 and 10.0 are supported in this version of Eclipse.

The PBC dose calculation algorithm is not reporting MU. To obtain the MU using PBC, calculate the MU manually and/or using measurements.

When the dose for a photon field containing a compensator is calculated using AAA or Acuros XB dose calculation algorithm version 11.0 or later, the compensator is taken into account in the MU calculation.

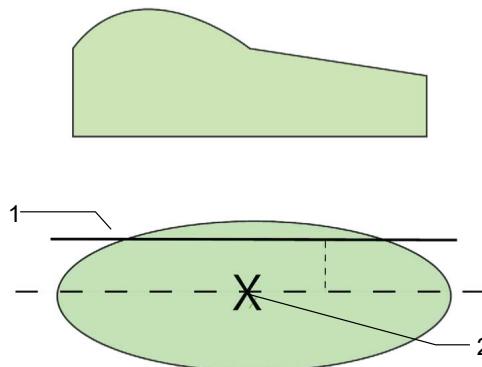
The way MU are shown for a photon field with a compensator was changed in Eclipse release 11.0. Changes are listed in the table.

Algorithm/Eclipse Version	MU Shown for the Field
PBC 11.0 or later/ Eclipse 11.0 or later	No MU shown
PBC 11.0 or later/ Eclipse 10.0 or earlier	No MU shown
PBC 10.0 or earlier/ Eclipse 11.0 or later	No MU shown
PBC 10.0 or earlier/ Eclipse 10.0 or earlier	MU are shown for open field, compensator MU not taken into account
AAA and Acuros XB 11.0 or later/ Eclipse 11.0 or later	MU shown, compensator MU taken into account
AAA and Acuros XB 11.0 or later/ Eclipse 10.0 or earlier	MU shown, compensator MU taken into account
AAA and Acuros XB 10.0 or earlier/ Eclipse 11.0 or later	No MU shown
AAA and Acuros XB 10.0 or earlier/ Eclipse 10.0 or earlier	No MU shown

Photon Compensator Properties

Compensation Plane

When adding a plane compensator to a field, you define the distance of the compensation plane from the isocenter. For imported compensators, the distance cannot be modified. The compensation plane location is perpendicular to the central axis of the selected field. The compensation plane is displayed in the image views.

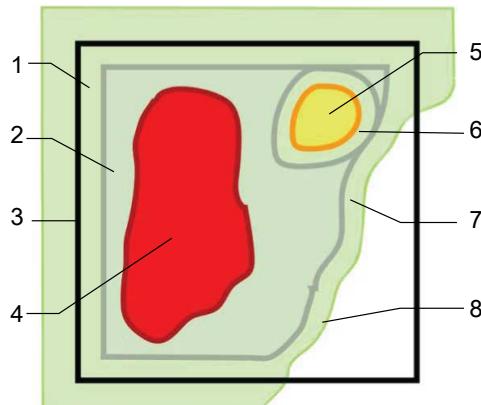


1. Compensation plane
2. Isocenter

Figure 112 Compensation Plane

Compensator Penumbra Margin

The figure shows how the compensator calculation area is defined on the basis of the penumbra margin value. When adding a new plane compensator or converting a compensator from fluence, you define the margin value. For imported compensators, the value cannot be modified.

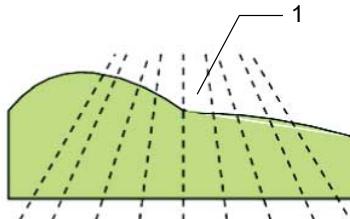


- | | |
|--|---|
| 1. Margin between the field edge and the compensation calculation area | 6. Margin between the block and the compensation calculation area |
| 2. Compensation calculation area | 7. Margin between the skin and the compensation calculation area |
| 3. Field edge | 8. Skin surface |
| 4. Target | |
| 5. Block | |

Figure 113 Compensator Penumbra Margin

Compensator Grid

The grid of a compensator determines the interval at which the compensator thickness is indicated for the compensator calculation. Photon dose calculation algorithms in Eclipse assume that the calculation grid is divergent.



1. Grid size

Figure 114 Compensator Grid

Compensator Thickness

The maximum and minimum compensator thickness is defined in RT Administration. If the maximum thickness is exceeded, the milling machine cuts the compensator in accordance with the selected slot.

Editing Compensators

Normally, the thickness and shape of the calculated compensator are acceptable. If necessary, you can do minor alterations on the shape of the compensator with the Compensator Editor tools.

Most likely, some alterations are needed if the calculated photon compensator could not be produced in a milling machine.

The Compensator Editor shows the calculated compensator matrix as a colored 2D surface in the BEV, in which you can modify the matrix point-by-point. The compensator surface is drawn on top of all other structures. You can adjust the color range and opacity. Isothicknesses and other isocurves are displayed on top of the texture.



Note: *The Compensator Editor allows editing the compensator matrix in the BEV only.*

To change how the compensator matrix is visualized, edit the compensator isolevels.

When editing a compensator, you can display the previously calculated dose distribution in persistent dose mode and use the isodose lines as guides in making modifications.

Related Topics

Edit the Compensator Matrix

1. In the Focus window, select the compensator you wish to edit.
2. Choose **Planning > Edit Compensator**.
3. For a photon compensator, select either **Transmission** or **Thickness**.

Only the transmission matrix is editable. More information about calculating compensator matrices: *Eclipse Photon and Electron Algorithms Reference Guide*.

4. Define a brush shape and size. The brush size range is 0.1–500 mm.
5. With photon compensator, define the transmission factor for the brush. The range is 0–1, 0 being equivalent to no compensator material.
6. Select the appropriate Compensator Editor tool.

In the BEV, the mouse pointer appears as the brush of the selected shape and size.

7. To measure the selected matrix value at a specific point, click the measurement button .

In the BEV, the mouse pointer appears as a cross-hair. When you click a point in the matrix, its value is displayed in the **Transmission factor** box for a photon compensator, and in the **Thickness** box for a proton compensator.

8. With the slider, adjust the opacity of the matrix shown in the BEV.
9. Define the visualization of the compensator matrix in the BEV.
 - Display the matrix in color, and define a color range in the Lower and Upper boxes.

Areas below the Lower value are displayed in blue; areas above the Upper value are displayed in purple.

- Display the matrix using shading.
- Display isothickness lines in the BEV window.

The isothicknesses are shown in accordance with the transmission factors in the compensator matrix (photon compensator) or compensator thickness (proton compensator).

To view isothickness lines only, move the Opacity slider to the left.

10. To finish, click **OK**.

Related Topics

[Fluence Editing Tools on page 397](#)

[Fluence Editing Brush Parameters on page 402](#)

Select the Compensator Isolevels

1. In the Focus window, select the compensator.
2. Choose **Planning > Compensator Isolevels**.
3. If necessary, edit the calculated thickness of an isolevel.
4. To change the isolevel color, click the cell and select a new color.
5. To change the isolevel line width, type a new width in the cell.
6. To add a new isolevel, click **Add level** and then fill in the cells as appropriate.
7. To delete an isolevel, select it by clicking the leftmost column, and then click **Delete level**.
8. To accept the changes, click **OK**.

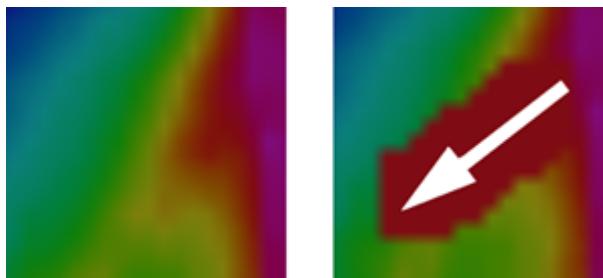


Note: The beam line settings are not automatically recalculated after modifications to a compensator.

Fluence Editing Tools

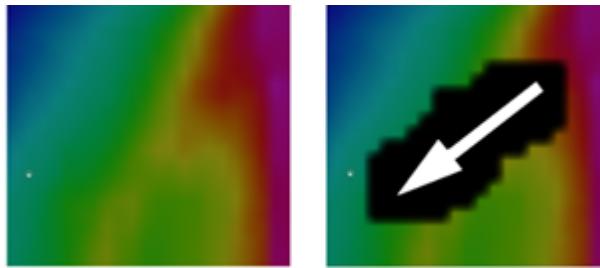
Set to Given Value Tool

The tool sets the matrix value in the painted area to the selected brush value. The arrow shows the stroke direction.



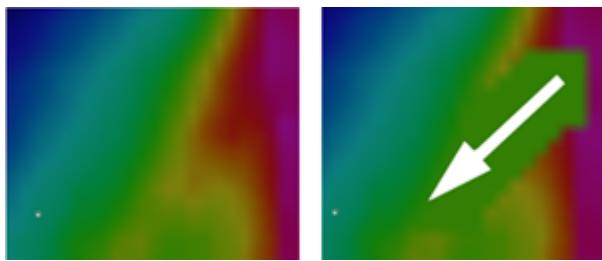
Set to Zero Tool

The tool sets the matrix value in the selected area to zero. The arrow shows the stroke direction.



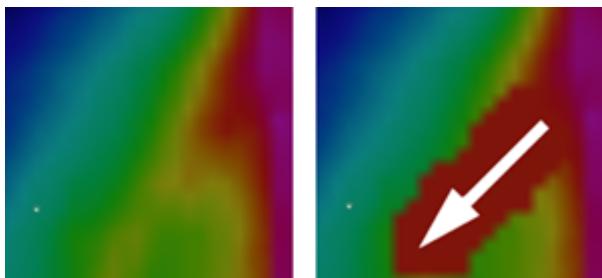
Change Values Above Given Value Tool

The tool sets the matrix values that are above the given level to the defined value. It adds only one layer on each brush stroke thus preventing unwanted results caused by false strokes. The arrow shows the stroke direction.



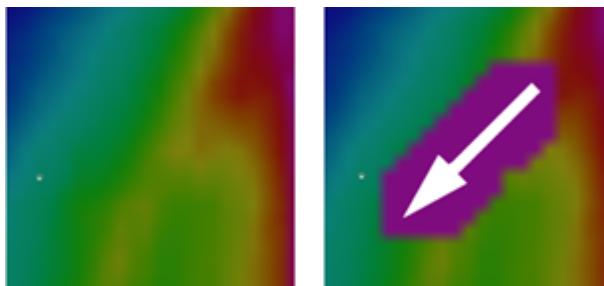
Change Values Below Given Value Tool

The tool sets the matrix values that are below the given level to the defined value. It subtracts only one layer on each brush stroke thus preventing unwanted results caused by false strokes. The arrow shows the stroke direction.



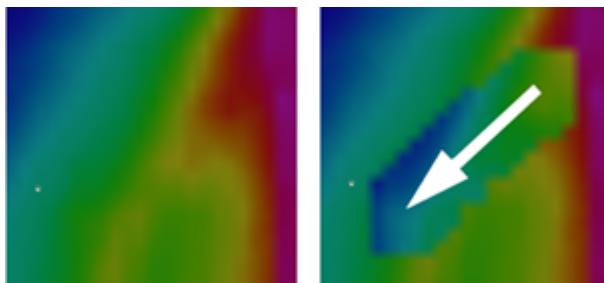
Increase by Defined Value Tool

The tool  increases the matrix values under the brush by the defined value. The arrow shows the stroke direction.



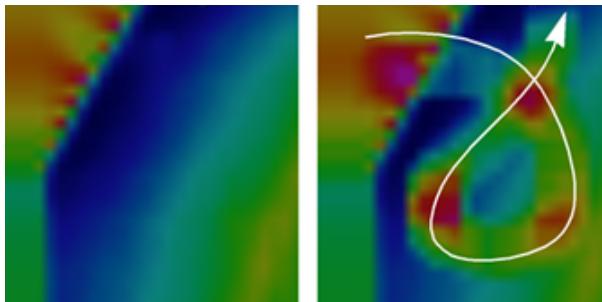
Decrease by Defined Value Tool

The tool  decreases the matrix values under the brush by the defined value. The arrow shows the stroke direction.



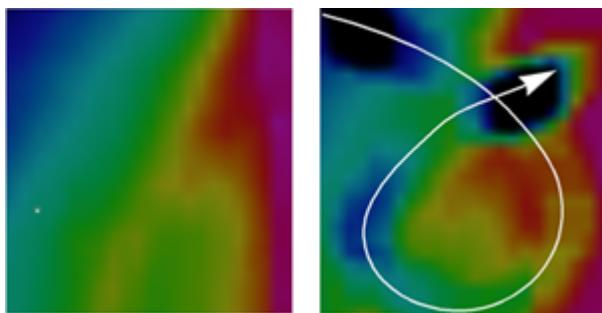
Build Up Tool

The tool  adds further layers with the same transmission value on top of each other by painting over the already painted areas. The arrow shows the stroke direction. Use small transmission values because each time you paint over the same area, another layer with the same transmission factor is added.



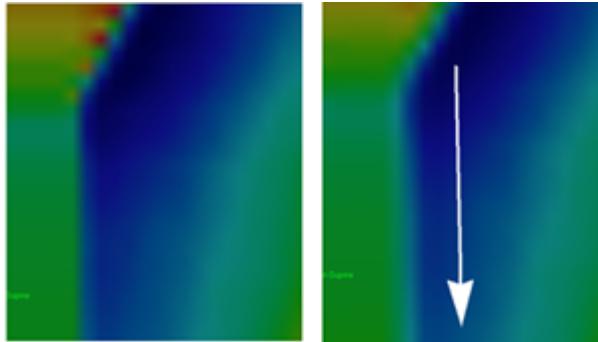
Erase Tool

The tool erases further layers with the same matrix value from the already subtracted areas. The arrow shows the stroke direction. Use small transmission values because each time you move the eraser over the same area, another layer with the same transmission factor is erased.



Smooth Tool

The tool smooths out sharp changes in matrix values and can be used to remove small irregularities. The arrow shows the stroke direction.



The Smooth tool takes into account the value of a pixel and its neighboring pixels when you smooth out sharp changes in the matrix values. The centers of the matrix pixels are defined as gridpoints.

When the circular or block-shaped brush is used, for each grid point that the brush touches, the gridpoint value is replaced with a weighted average of the neighboring grid points. This weighted average can be called the *smoothed value*. The weights are 1.5 for the center pixel, 1 for the immediate neighboring pixels and 0.6 for the corner pixels. For a pixel that has all these neighboring pixels, the sum of the weights is 7.9. The following figure shows an example of grid point values and weights.

<table border="1" style="margin-left: auto; margin-right: auto;"> <tbody> <tr><td>5</td><td>5</td><td>5</td></tr> <tr><td>1</td><td>1</td><td>1</td></tr> <tr><td>5</td><td>5</td><td>5</td></tr> </tbody> </table>	5	5	5	1	1	1	5	5	5	<table border="1" style="margin-left: auto; margin-right: auto;"> <tbody> <tr><td>0.6</td><td>1</td><td>0.6</td></tr> <tr><td>1</td><td>1.5</td><td>1</td></tr> <tr><td>0.6</td><td>1</td><td>0.6</td></tr> </tbody> </table>	0.6	1	0.6	1	1.5	1	0.6	1	0.6
5	5	5																	
1	1	1																	
5	5	5																	
0.6	1	0.6																	
1	1.5	1																	
0.6	1	0.6																	
1	2																		

1. Values
2. Weights

Figure 115 An Example of Grid Point Values and Weights

If the smoothing operation is now applied to the center pixel of the Values grid, the new value of that pixel will become $((1.5 \times 1) + (1 \times 5) + (1 \times 5) + (1 \times 1) + (1 \times 1) + (0.6 \times 5) + (0.6 \times 5) + (0.6 \times 5)) / 7.9 = 3.228$

When the conical or the Gaussian brush is used, the new value will be a weighted average of the original value and the smoothed value. This weight of this average depends on the distance from the grid point to the center of the brush. For the conical brush, the factor is a linear function that gets value 1 at the center of the brush and value 0 when the distance is 50% of the brush size (for distances greater than this, the value is always zero). For the Gaussian brush, the weighted average is the value of a Gaussian centered at the brush center with a standard deviation that depends on the brush radius.



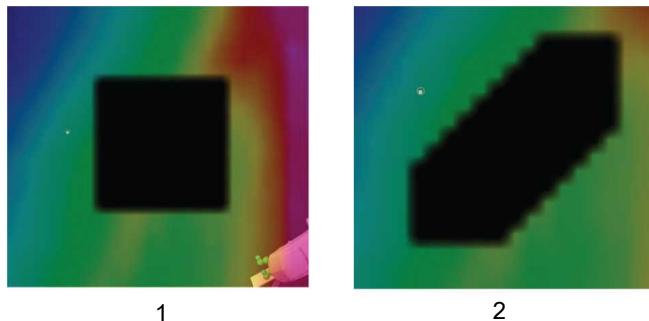
Note: The compensator smoothing algorithm does not take the row offset into account.

Fluence Editing Brush Parameters

There are four Brush head shapes available: square, circular, conical and gaussian.

Square Brush

Clicking in the fluence with the square Brush draws a square, dragging the Brush draws a line with a square-shaped end. The dimensions of the clicked area or line depend on the Brush size. The figure shows two examples of the square Brush.



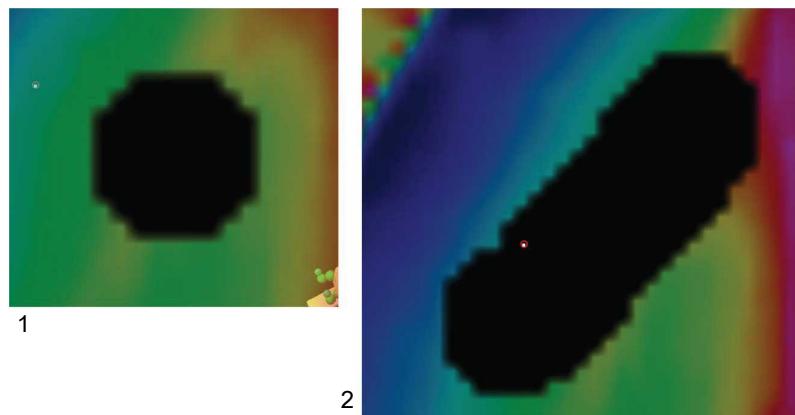
1. One click with the square Brush.
2. Line drawn with the square Brush.

Figure 116 Square Brush

Circular Brush

Clicking in the fluence with the circular Brush

 draws a circular area, dragging the Brush draws a line with a circular end. The dimensions of the clicked area or line depend on the Brush size. The figure shows two examples of the circular Brush.

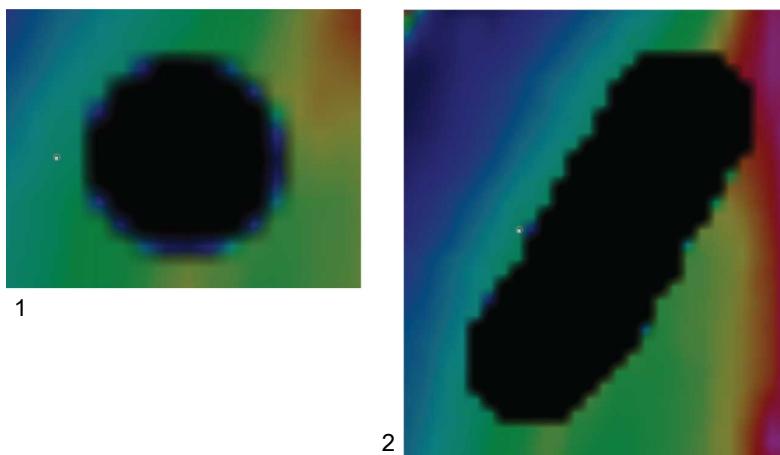


1. One click with the circular Brush.
2. Line drawn with the circular Brush.

Figure 117 Circular Brush

Conical Brush

Clicking in the fluence with the conical Brush  draws a circular area with linear color gradients from the center towards the edges of the Brush tip, dragging draws a line with a circular end and linear color gradients from the center of the line towards the edges of the line. The dimensions of the clicked area or line depend on the Brush size. The figure shows two examples of the conical Brush.

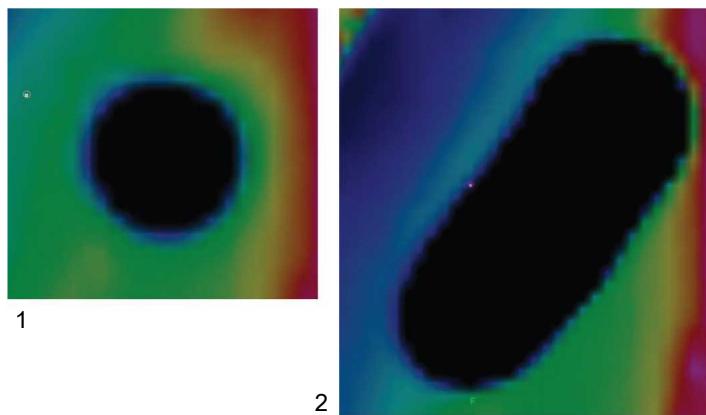


1. One click with the conical Brush.
2. Line drawn with the conical Brush.

Figure 118 Conical Brush

Gaussian Brush

Clicking in the fluence with the gaussian Brush draws a circular area with gaussian color gradients from the center towards the edges of the Brush tip, dragging draws a line with a circular end and gaussian color gradients from the center of the line towards the edges of the line. The dimensions of the clicked area or line depend on the Brush size. The figure shows two examples of the gaussian Brush.



1. One click with the gaussian Brush.
2. Line drawn with the gaussian Brush.

Figure 119 Gaussian Brush

Chapter 17 Electronic Compensators

About Electronic Compensators

An electronic compensator is a field modifier implemented by means of a Dynamic MLC (DMLC) that replaces a mechanical compensator. Electronic compensators can speed up the treatment, and also reduce skin dose, since they do not expose the patient to electron contamination from the compensator material or fixed wedge filters. Moreover, electronic compensation does not require the high overhead in production that is present in mechanical compensators, and multi-beam treatments are much faster because there is no need to install a different physical compensator before each treatment beam.

Electronic Compensator Calculation

You add an electronic compensator to a plan by first inserting a standard plane compensator in the plan and then converting it into an electronic compensator. The compensation method used is plane compensation.

The conversion of a standard plane compensator into an electronic compensator creates an optimal fluence, according to your calculation parameters. The calculation is done for each field by scanning all points within the field on the selected plane. The compensator calculation begins at the user-defined distance from the edge of the patient tangential border. The optimal fluences are converted into a pattern of DMLC leaf motions by the Leaf Motion Calculator (LMC). When the plan and the DMLC motions are completed, you can export the DMLC leaf motion file to the treatment unit.

The uniform dose distribution is computed using the dose back-projection method, in which the optimal fluences are defined. The dose back-projection is done in the diverging field coordinate system.

Related Topics

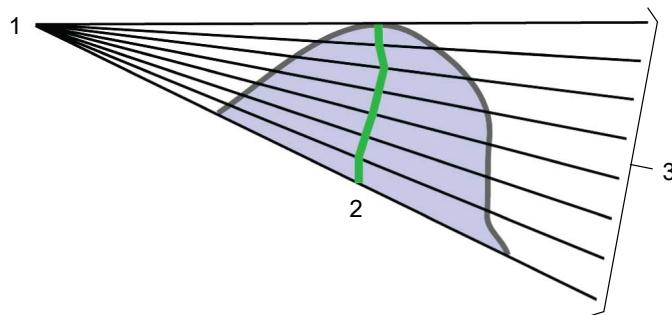
[Converting Field Fluences to DMLC Leaf Motions](#) on page 245

Irregular Surface Compensators

Irregular surface compensator is an electronic compensator designed for creating a curved compensation surface as opposed to a straight compensation plane in traditional physical compensators and normal electronic compensators.

Using a curved compensation surface provides better dose distributions in cases where the shape of the target volume is rounded, such as breast treatments. In breast cases, traditional compensators often create hot spots in the base of the breast near the skin, but this can be avoided with irregular surface compensation.

The shape of the irregular compensation surface is always specific to the shape of each patient's body outline. The position of the desired irregular compensation surface is defined by specifying the desired penetration depth. The penetration depth is the percentage of the penetration of the radiation along each fanline ray through the patient; calculated as path length = exit point - entry point. The penetration depth range is 0–100%, where 0% = entry point; 100% = exit point. A penetration depth of 50% creates a compensation surface that represents the mid-point of every ray. The figure shows schematically what the irregular compensation surface would look like for a curved structure, using penetration depth of 50%.



1. Radiation focus
2. Path of the irregular compensation surface, 50% penetration depth
3. Fanline rays

Figure 120 Penetration Depths, Medial 50% Penetration

The use of different penetration percentages affects the fluence. The larger the penetration depth percentage, the more fluence difference there will be between thin and thick parts of the patient. A value close to but smaller than 50% works well for breast cases.



Note: An irregular surface compensator does not apply any skin flash to the generated fluence. If necessary, you can apply additional skin flash to the fluence by using the Skin Flash tool.

The calculation of the irregular surface compensator is performed with the Dose Volume Optimizer algorithm using smoothing options. The result is an optimal fluence, which can be converted into an electronic compensator.

Irregular Surface Compensator Algorithm

The irregular surface compensation calculation is performed with the Dose Volume Optimizer algorithm, which uses the gradient method. The algorithm constructs an irregularly shaped surface corresponding to the penetration depths of the fanline rays traced through the patient. The algorithm modulates the intensity of each beamlet to achieve a uniform dose on the compensation surface. The irregular surface automatically includes the effects of beam divergence in both the X- and Y-directions. Patient geometry is considered in determining the compensation surface, but heterogeneity is accounted for in the field fluence calculation, not in determining the irregular surface. Smoothing options can be set for the algorithm.

More information about the Dose Volume Optimizer algorithm and the irregular surface compensation calculation: *Eclipse Photon and Electron Algorithms Reference Guide*.

Chapter 18 Working with Fluences

Fluence Editor

The Fluence Editor enables you to modify the transmission values and visualization of the optimal fluence. You can define the color range and opacity of the fluence matrix, and show the isodose lines on top of the matrix. The transmission values can be increased or decreased with special tools in the Fluence Editor.

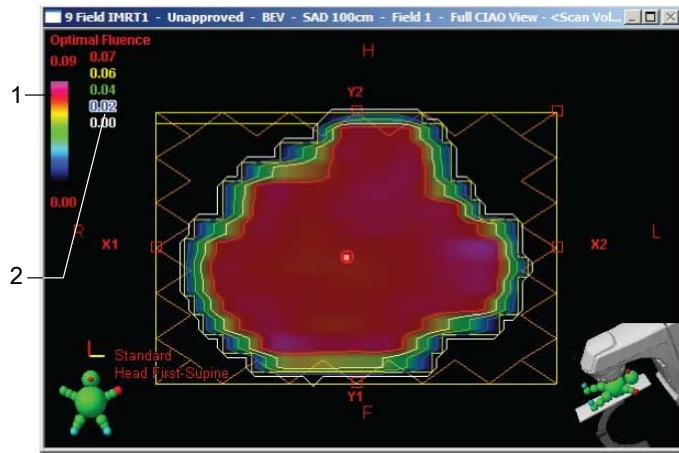


Note: The Fluence Editor allows editing the optimal fluence matrix only, and only works in the BEV.

Displaying and Modifying Optimal Fluences in the BEV

You can display the optimal fluence matrix as a fluence color wash, grey scale or an isofluence plot overlaid onto the BEV above all structures of the patient. The command used to display the fluence matrix also opens the Fluence Editor, a tool that allows you to modify the transmission values and visualization (color range, opacity, isolevels) of the fluence.

The figure shows a field and the optimal fluence map connected to the field plus the isolevels of the field in the BEV when the Fluence Editor is active. The Optimal Fluence legend shows the colors indicating different transmission factors in the optimal fluence map. If the isolevels are also displayed, the Isolevels legend is shown next to the Optimal Fluence legend to show the transmission factor indicated by the isolevel colors.



1. Optimal fluence legend
2. Isolevels legend

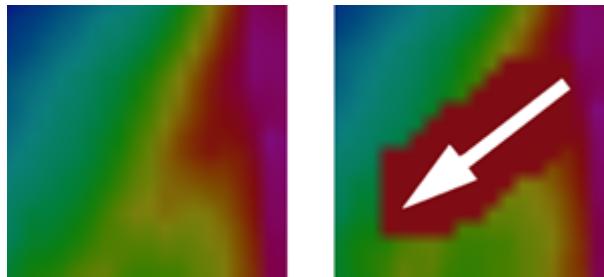
Figure 121 Isofluences and Fluence Map in BEV

After modifying the fluence, you can start the LMC to convert the modified optimal fluence into a deliverable DMLC leaf motion pattern.

Fluence Editing Tools

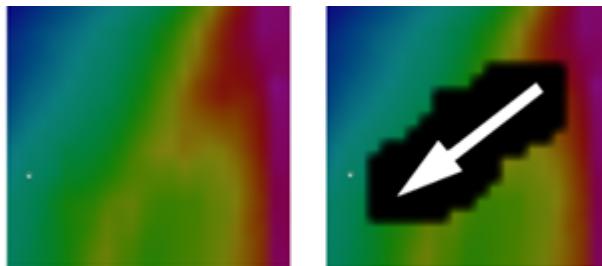
Set to Given Value Tool

The tool sets the matrix value in the painted area to the selected brush value. The arrow shows the stroke direction.



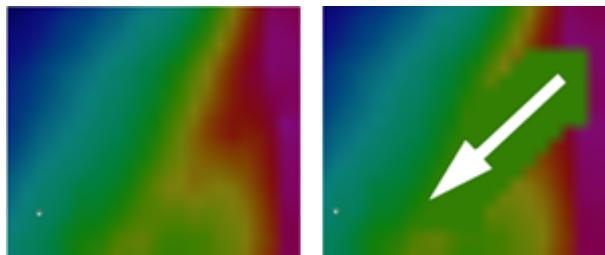
Set to Zero Tool

The tool  sets the matrix value in the selected area to zero. The arrow shows the stroke direction.



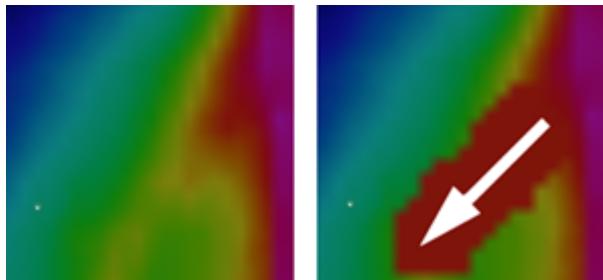
Change Values Above Given Value Tool

The tool  sets the matrix values that are above the given level to the defined value. It adds only one layer on each brush stroke thus preventing unwanted results caused by false strokes. The arrow shows the stroke direction.



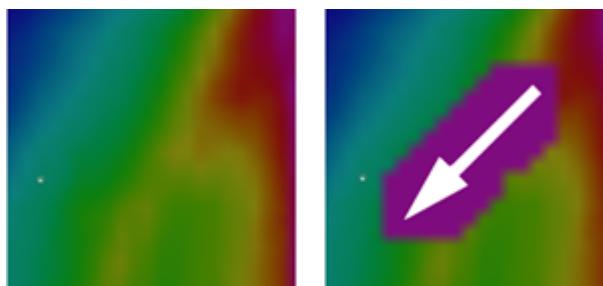
Change Values Below Given Value Tool

The tool  sets the matrix values that are below the given level to the defined value. It subtracts only one layer on each brush stroke thus preventing unwanted results caused by false strokes. The arrow shows the stroke direction.



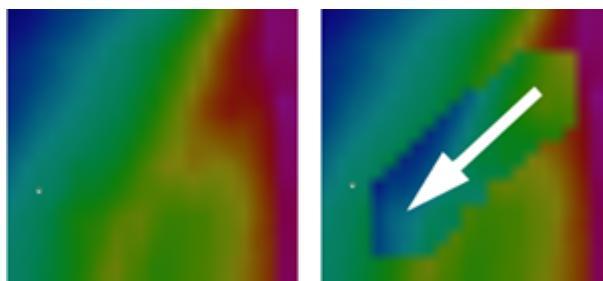
Increase by Defined Value Tool

The tool  increases the matrix values under the brush by the defined value. The arrow shows the stroke direction.



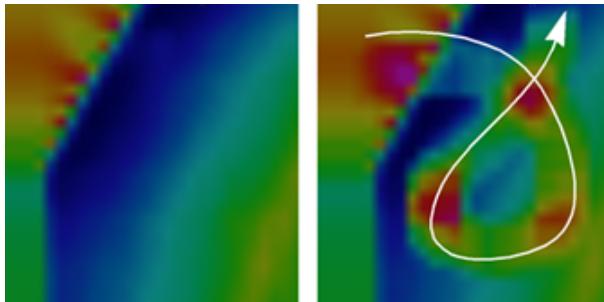
Decrease by Defined Value Tool

The tool  decreases the matrix values under the brush by the defined value. The arrow shows the stroke direction.



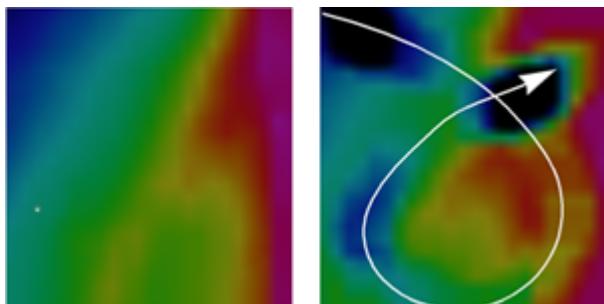
Build Up Tool

The tool  adds further layers with the same transmission value on top of each other by painting over the already painted areas. The arrow shows the stroke direction. Use small transmission values because each time you paint over the same area, another layer with the same transmission factor is added.



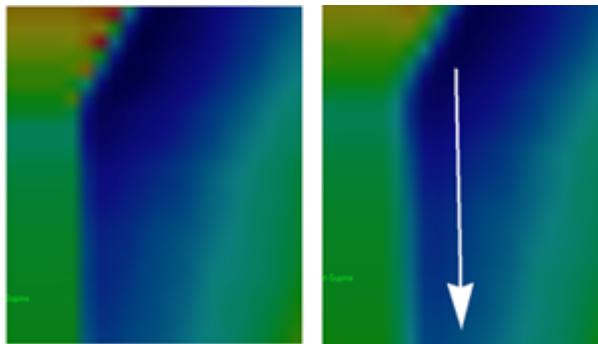
Erase Tool

The tool  erases further layers with the same matrix value from the already subtracted areas. The arrow shows the stroke direction. Use small transmission values because each time you move the eraser over the same area, another layer with the same transmission factor is erased.



Smooth Tool

The tool  smooths out sharp changes in matrix values and can be used to remove small irregularities. The arrow shows the stroke direction.



The Smooth tool takes into account the value of a pixel and its neighboring pixels when you smooth out sharp changes in the matrix values. The centers of the matrix pixels are defined as gridpoints.

When the circular or block-shaped brush is used, for each grid point that the brush touches, the gridpoint value is replaced with a weighted average of the neighboring grid points. This weighted average can be called the *smoothed value*. The weights are 1.5 for the center pixel, 1 for the immediate neighboring pixels and 0.6 for the corner pixels. For a pixel that has all these neighboring pixels, the sum of the weights is 7.9. The following figure shows an example of grid point values and weights.

<table border="1" style="margin-left: auto; margin-right: auto;"> <tbody> <tr><td>5</td><td>5</td><td>5</td></tr> <tr><td>1</td><td>1</td><td>1</td></tr> <tr><td>5</td><td>5</td><td>5</td></tr> </tbody> </table> 1	5	5	5	1	1	1	5	5	5	<table border="1" style="margin-left: auto; margin-right: auto;"> <tbody> <tr><td>0.6</td><td>1</td><td>0.6</td></tr> <tr><td>1</td><td>1.5</td><td>1</td></tr> <tr><td>0.6</td><td>1</td><td>0.6</td></tr> </tbody> </table> 2	0.6	1	0.6	1	1.5	1	0.6	1	0.6
5	5	5																	
1	1	1																	
5	5	5																	
0.6	1	0.6																	
1	1.5	1																	
0.6	1	0.6																	

1. Values
2. Weights

Figure 122 An Example of Grid Point Values and Weights

If the smoothing operation is now applied to the center pixel of the Values grid, the new value of that pixel will become $((1.5 \times 1) + (1 \times 5) + (1 \times 5) + (1 \times 1) + (1 \times 1) + (0.6 \times 5) + (0.6 \times 5) + (0.6 \times 5)) / 7.9 = 3.228$

When the conical or the Gaussian brush is used, the new value will be a weighted average of the original value and the smoothed value. This weight of this average depends on the distance from the grid point to the center of the brush. For the conical brush, the factor is a linear function that gets value 1 at the center of the brush and value 0 when the distance is 50% of the brush size (for distances greater than this, the value is always zero). For the Gaussian brush, the weighted average is the value of a Gaussian centered at the brush center with a standard deviation that depends on the brush radius.



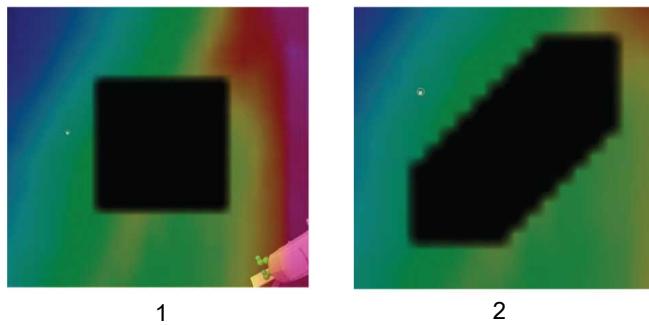
Note: The compensator smoothing algorithm does not take the row offset into account.

Fluence Editing Brush Parameters

There are four Brush head shapes available: square, circular, conical and gaussian.

Square Brush

Clicking in the fluence with the square Brush draws a square, dragging the Brush draws a line with a square-shaped end. The dimensions of the clicked area or line depend on the Brush size. The figure shows two examples of the square Brush.

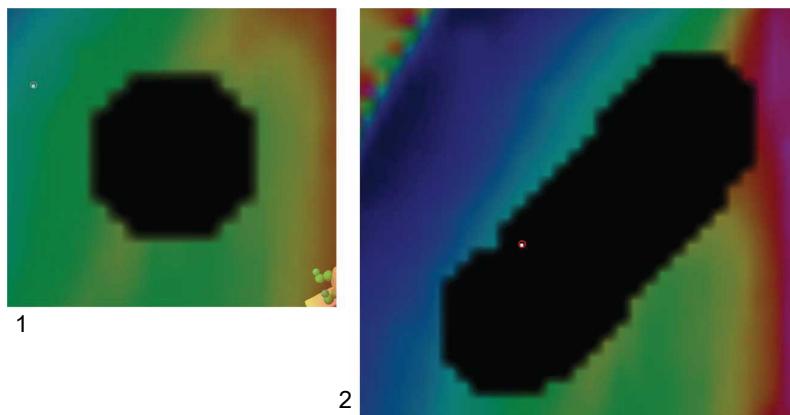


1. One click with the square Brush.
2. Line drawn with the square Brush.

Figure 123 Square Brush

Circular Brush

Clicking in the fluence with the circular Brush  draws a circular area, dragging the Brush draws a line with a circular end. The dimensions of the clicked area or line depend on the Brush size. The figure shows two examples of the circular Brush.

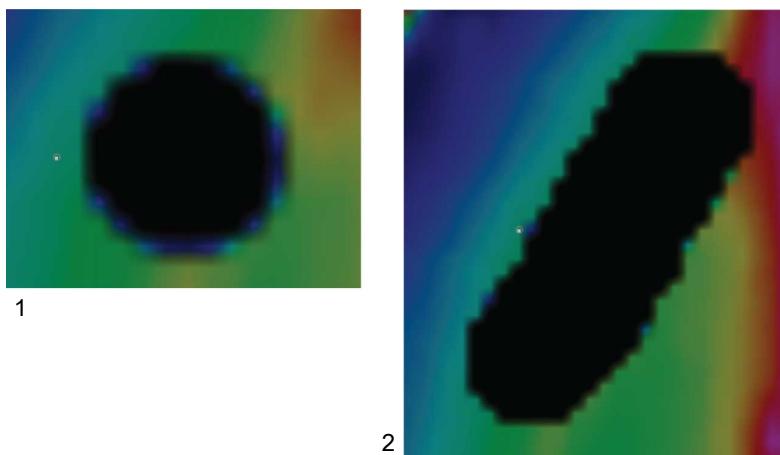


1. One click with the circular Brush.
2. Line drawn with the circular Brush.

Figure 124 Circular Brush

Conical Brush

Clicking in the fluence with the conical Brush draws a circular area with linear color gradients from the center towards the edges of the Brush tip, dragging draws a line with a circular end and linear color gradients from the center of the line towards the edges of the line. The dimensions of the clicked area or line depend on the Brush size. The figure shows two examples of the conical Brush.

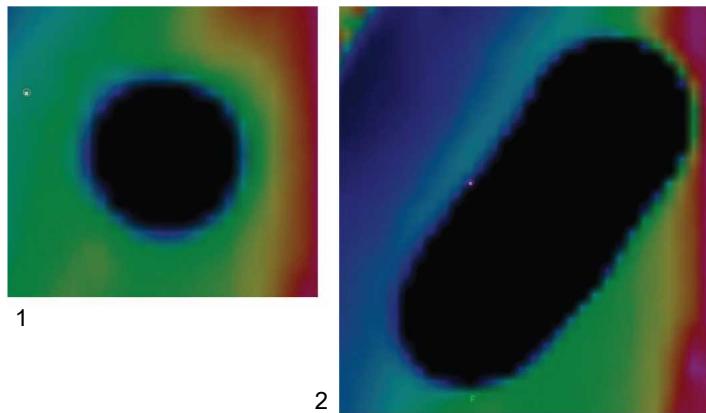


1. One click with the conical Brush.
2. Line drawn with the conical Brush.

Figure 125 Conical Brush

Gaussian Brush

Clicking in the fluence with the gaussian Brush draws a circular area with gaussian color gradients from the center towards the edges of the Brush tip, dragging draws a line with a circular end and gaussian color gradients from the center of the line towards the edges of the line. The dimensions of the clicked area or line depend on the Brush size. The figure shows two examples of the gaussian Brush.



1. One click with the gaussian Brush.
2. Line drawn with the gaussian Brush.

Figure 126 Gaussian Brush

View a Fluence

1. In the Focus window, right-click the fluence and choose **View fluence**. The fields that contain actual fluences have a slightly different DMLC icon
 2. Select the fluence type to view - optimal or actual. Note that you can view the actual fluence only after you have calculated the dose.
 3. To measure the selected matrix value at a specific point, click the measurement button
- The mouse pointer appears as a cross-hair in the BEV. When you click a point in the fluence matrix, its value is displayed in the Transmission Factor text box.
4. With the slider, adjust the opacity of the matrix shown in the BEV.
 5. Define how to view the fluence:
 - Use Color: Define the transmission value range for the color bar. Areas below the Lower value are displayed as transparent, very low values are displayed in blue, areas above the Upper value are displayed in purple.
 - Use Shading.
 - Isolevels: Displays isofluence lines in the BEV. The isofluences are shown in accordance with the transmission factors in the fluence.
 - Show actual fluence with resolution used in dose calculation. The fluence shown when this option is selected is an approximation of the fluence used in dose calculation.

6. To finish viewing, click OK.

Edit an Optimal Fluence

1. In the Focus window, right-click the fluence and choose **Edit fluence**.
2. Select **Optimal fluence**.
3. Use the measurement button  to determine the appropriate transmission factor. The value depends on the Fluence Editor tool that you are going to use. The range is 0–100 (0 = total blocking, 100 = open field).

4. Define a brush shape and size. The brush size range is 0.01–50 cm.

5. Select the Fluence Editor tool to use.

In the BEV window, the mouse pointer appears as the brush of the selected shape and size.

6. You can measure the selected matrix value at a specific point by clicking the measurement button .

The mouse pointer appears as a cross-hair in the BEV. When you click a point in the fluence matrix, its value is displayed in the **Transmission Factor** text box.

7. With the slider, adjust the opacity of the matrix shown in the BEV.

8. Define how to view the fluence:

- Use Color: Define the transmission value range for the color bar. Areas below the Lower value are displayed as transparent, very low values are displayed in blue, areas above the Upper value are displayed in purple.
- Use Shading.
- Isolevels: Displays isofluence lines in the BEV. The isofluences are shown in accordance with the transmission factors in the fluence.
- Show actual fluence with resolution used in dose calculation. The fluence shown when this option is selected is an approximation of the fluence used in dose calculation.

9. To finish, click OK.

Skin Flash Dialog Box and Parameters

The Skin Flash tool visualizes the fluence of the selected field as a colorwash area in the BEV. You extend the fluence by using the Brush  to paint the extension which is then filled with transmission values using the selected fill method and Brush parameters. You can also remove parts of the skin flash area with the Eraser  and measure the transmission factor of an area with the Measure tool .

The Skin Flash parameters are defined in the Skin Flash dialog box.

The following briefly describes the Skin Flash tool parameters and their effect on the extended fluence with some examples. However, the best way to learn more is to experiment with the fluence data available to you.

Brush Size

The Brush Size parameter defines the diameter of the Brush tool  and the Eraser tool  in millimeters.

Transmission Factor

The Measurement tool  measures and shows the transmission values in the fluence. The value is shown in the Transmission factor text box. The default transmission factor value is 1.

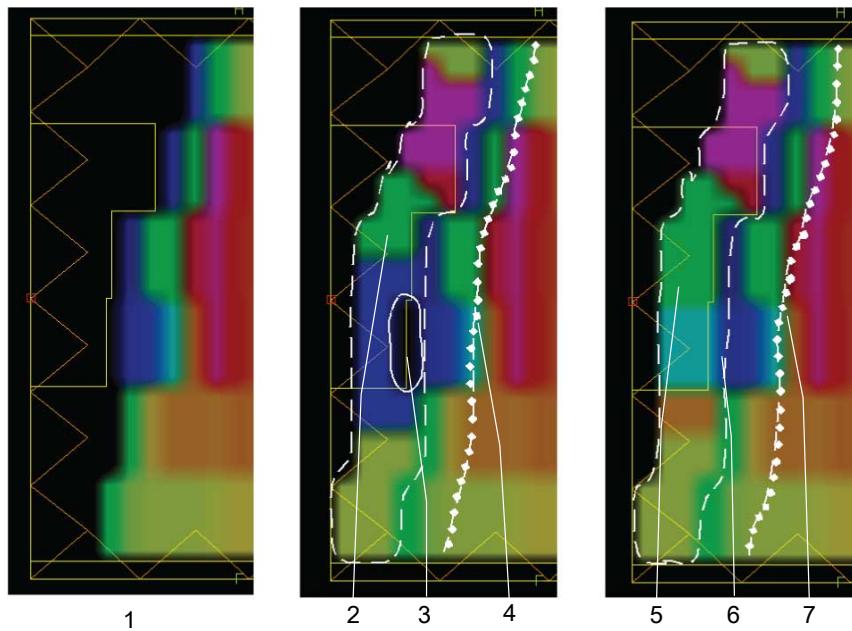
Fill Method

The Skin Flash tool supports two methods of filling the extension with transmission values:

- Nearest Cell method: Fills the extension with the transmission value of the nearest cell beyond the Cut Range limit.
- Erosion-Dilation method: Fills the extension with the transmission values defined by the Erosion and Dilation range.

Brush Ceiling

The Brush Ceiling parameter defines the area where you can paint the extension. The Brush Ceiling defines the upper threshold for the extension, that is, if the Brush Ceiling value is 0.1, you cannot paint on fluence areas with transmission values 0.1 or higher.



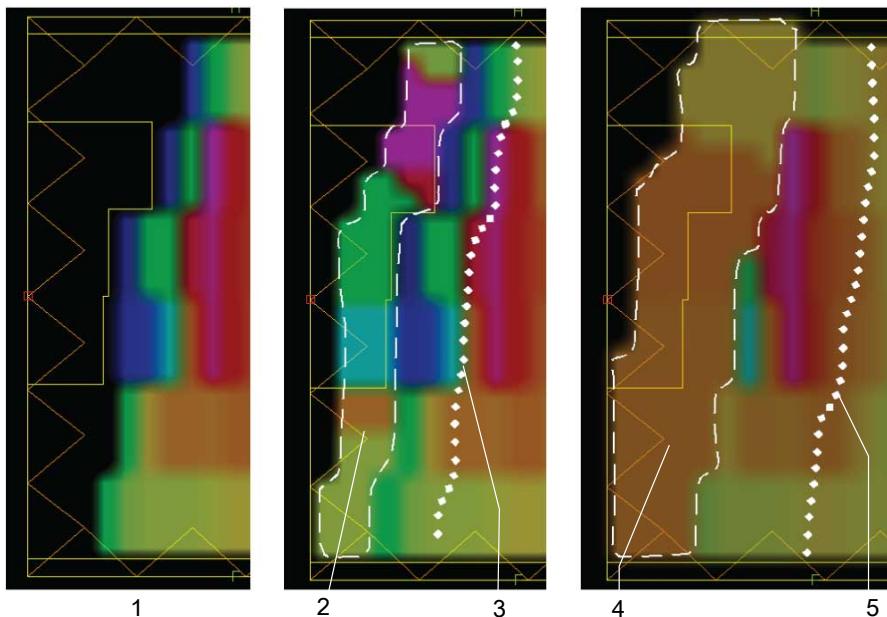
1. Starting point
2. Paint area with Brush Ceiling value 0.01
3. Hole in the paint area, caused by transmission values (0.017) above the defined Brush Ceiling.
4. Cut Range of 5 mm
5. Paint area with Brush Ceiling value 0.2
6. Hole disappears with new Brush Ceiling value
7. Cut Range value 5 mm

Figure 127 Examples of Brush Ceiling Values

In the example, an extension was first drawn using Brush Ceiling value of 0.01 with Cut Range of 5 mm. As a result, a hole appeared in the extension, because the transmission values inside the hole exceeded the Brush Ceiling value. This hole was filled by increasing the Brush Ceiling value slightly (in the example it was increased to 0.2). The diamond line marked with 4 and 7 shows the Cut Range limit (5 mm) at which the transmission values are taken.

Cut Range

The Cut Range parameter defines the range from which the transmission values for the extension are taken, measured from the edge of the Brush. The Skin Flash tool goes through all cells at the defined Cut Range, for instance, all cells at 10 mm from the edge of the Brush, and assigns the found transmission values to the cells in the painted extension. A low Cut Range value finds transmission values from cells near to the painted extension; a higher Cut Range value finds values further away from the painted extension.



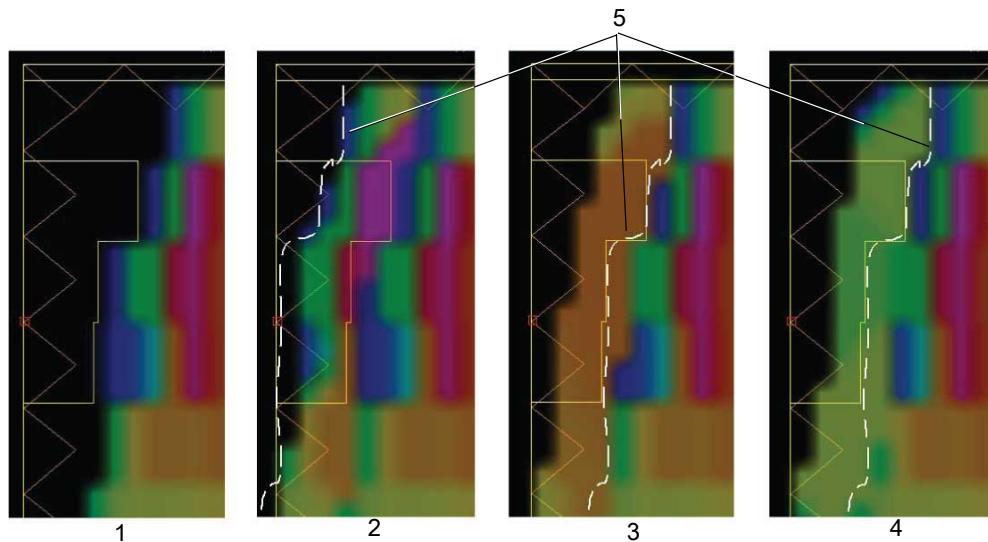
1. Starting point
2. Paint area with Cut Range value 5 mm and Brush Ceiling value 0.2
3. Outer limit of Cut Range
4. Paint area with Cut Range value 10 mm and Brush Ceiling value 0.2
5. Outer limit of Cut Range

Figure 128 Examples of Cut Range Values

In the example, a fluence extension was first painted using a Cut Range value of 5 mm with Brush Ceiling of 0.2 mm. The resulting extension was non-uniform because the values were picked up from an area in the fluence with a lot of fluctuations (the diamond line marked with 3 shows the outer Cut Range limit). Next, the Cut Range (5) value was increased to 10 mm to get the transmission values from a fluence area with less fluctuations. The Brush Ceiling was kept the same, but the fluence extension (4) was painted with more overlap with the existing fluence.

Erosion Range and Dilation Range

Both the Erosion Range and the Dilation Range parameters, which are used in the Erosion-Dilation method only, extend higher values in the extended fluence. The Erosion Range parameter defines the range in millimeters in which higher transmission values are removed from the fluence map. The Dilation Range parameter defines the range in which higher transmission values are extended in the fluence map.



1. Starting point
2. Erosion Range value 1, Dilation Range value 5, Brush Ceiling 0.2
3. Erosion Range value 5, Dilation Range value 10, Brush Ceiling 0.2
4. Erosion Range value 10, Dilation Range value 5, Brush Ceiling 0.2
5. Border of painted extension

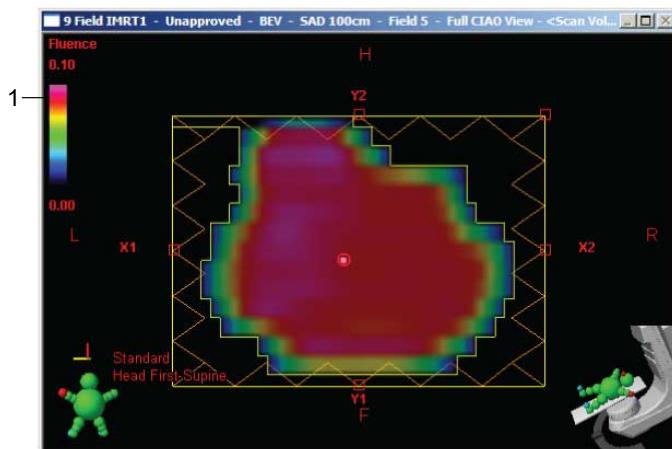
Figure 129 Examples of Erosion Range and Dilation Range Values

Extending Fluence with the Skin Flash Tool

You can use the Skin Flash tool to prevent sudden fluctuations, such as cold or hot spots, in the dose near the Body outline, by extending the optimal fluence.

Treatments using tangential IMRT fields (many breast, head or neck treatments) are prone to fluctuations in the Body outline area. Deviations may also arise from inaccuracies in patient positioning, patient movement, or as a result of respiration. The Skin Flash tool, which visualizes the fluence of the selected field in the BEV, allows you to graphically extend the fluence outside the Body surface with a brush, making the fluence smoother near the Body outline. The skin flash fluence is calculated automatically.

The figure shows a field and the optimal fluence map connected to the field in the BEV when the Skin Flash tool is active. The Fluence legend shows the colors indicating different transmission factors in the optimal fluence map.



1. Fluence legend

Figure 130 Isofluences and Fluence Map in BEV

Extend Fluence with the Skin Flash Tool

1. In the Focus window, right-click the fluence to be modified and choose **Skin Flash Tool**.
The fluence is shown in the BEV.
2. To define the diameter of the Brush, type the value in mm in the Brush size text box.
3. In the **Fill Method** drop-down list, select the desired method.
4. To define the skin flash parameters, click in the desired cell in the table and type in the new value.
 - Nearest cell method: Brush ceiling and Cut range
 - Erosion-dilation method: Brush ceiling, Erosion range and Dilation range
5. To activate the Brush, click **Brush** .
6. On the optimal fluence, paint the area to be modified by the skin flash tool.
While you paint the area, it is displayed in grey, but once you release the button, the painted area is displayed with the colors corresponding to the transmission factor.
7. To view the transmission factor of an area in the fluence, click **Measure**  and then click at the point in the fluence.
The transmission factor is shown in the Transmission factor box.
8. Modify the skin flash area, if necessary.
 - To remove parts of the skin flash area, click **Erase** .
 - To add to the skin flash area, click **Brush**.
9. Continue defining the area and previewing it until the skin flash fluence is acceptable.
10. Click **OK**.
11. Move on to another field and continue defining the modified fluence.



Tip: If you wish to work on multiple fields while keeping the Skin Flash tool dialog box open, click **Apply** before selecting another field to keep the changes made to the previous field. Moreover, to use multiple brush sizes or other parameters on the same fluence, click **Apply** before changing the parameters.

Continue by converting the field fluences to DMLC motions.

Chapter 19 Bolus

About Bolus

A bolus is a piece of tissue-equivalent material placed directly on the patient's skin to provide additional tissue and bring the maximum dose closer to the skin surface. Bolus structures are managed as image-specific structures, not as field-specific add-ons like blocks or compensators.

Consequently, when a field containing a bolus is copied from one photon plan to another, the bolus is not copied, but when an entire plan is copied, the bolus contained in a field or several fields is also copied.

Related Topics

[Using Color and Style for Structures](#) on page 52

Bolus with Arc Fields

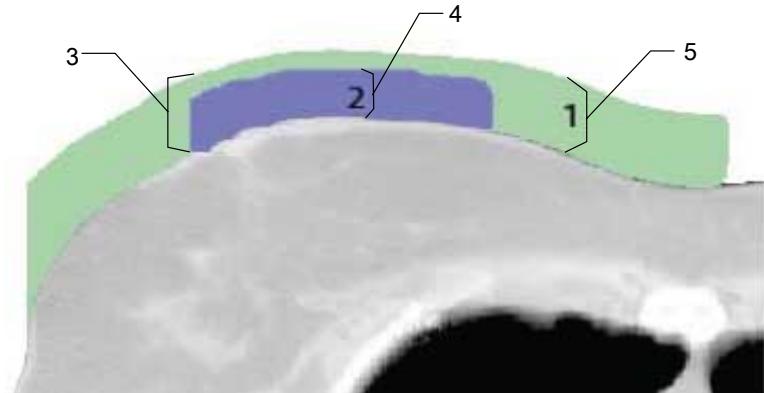
A number of bolus specific parameters are calculated and reported for bolus linked to fields: the Source Bolus Distance (SBD) is shown in the Field Properties dialog box, and the Source Bolus Distance (SBD) and CAX Path Length In Bolus are printed in treatment reports. The way these two parameters are calculated depends on the field technique:

- Static fields—SBD and CAX path length through the bolus are calculated along the field central axis (CAX).
- Arc fields—SBD is calculated along the field CAX at the gantry start angle. If the CAX at the start angle does not intersect with the bolus, the SBD is not reported at all. The CAX path length through bolus is the average water-equivalent bolus thickness calculated along the CAX path for the entire arc.

Adding Bolus

Bolus structure and material are added on the surface of the Body structure with a special tool. The bolus structure appears on the patient's skin in the 2D image views and the Model view.

You can add several bolus layers of different thicknesses on top of each other. However, notice that the thickness of overlapping layers is dealt with in a special way: The effective bolus thickness where layers overlap is measured from the skin surface to the upper surface of the top-most layer.



1. Bolus layer 1.
2. Bolus layer 2.
3. Effective thickness of overlapping layers.
4. Thickness of layer 2.
5. Thickness of layer 1.

Figure 131 **Bolus Layers**



Note: Dose calculation when using bolus can result to slight inaccuracy if there are multiple bolus geometrically on top of each other, or if the same bolus is linked to multiple photon fields. It is recommended to use only one bolus per field and to avoid overlapping boluses in a single field.



Note: In some rare cases, creating a bolus in Eclipse can result in a disconnected object: If the distance between the planes in the volume image is large and the Body outline changes are sharp under the bolus (that is, the Body outline deviates more than the thickness of the bolus between two planes), the resulting bolus has a hole between those two planes. In such situations, use a smaller plane distance when creating the volume image.

Chapter 20 Dose Calculation

Dose Distribution Calculation for External Beam Plans

The dose distribution can be calculated in External Beam Planning for both individual plans and plan sums containing a number of plans.



CAUTION: Make sure that the calculation volume covers the entire volume of interest.



CAUTION: Verify the maximum dose and its location inside the irradiated volume after the volumetric dose calculation.



CAUTION: Verify the dose calculation and dose display against independent verification methods, for example, manual calculations or measurements. This is to ensure that the following is correct:

- MU data is correctly interpolated and calibrated.
- MU calculation is correct.
- Configuration of the dosimetric data is correct.

The dose is displayed in External Beam Planning by interpolating it between the points of the calculated dose matrix. In the case of a coarse dose matrix, the interpolated dose might not accurately replicate the underlying dose in high dose gradient regions. If the Z resolution of the dose matrix exceeds 0.5 cm, Eclipse displays the following: "Dose matrix plane interval exceeds 0.5 cm".

When using the Acuros XB calculation algorithm for dose distribution calculation, information on the used radiation transport method (transport in medium) and whether the dose is reported to medium or water is displayed in the image views. When the inhomogeneity correction is on, radiation is always transported in medium.

The calculated dose is invalidated if you change the field geometry or field accessory settings.

All beam data used in dose calculation contain checksums. When calculating the dose, Eclipse re-calculates the checksum values and compares them with the original ones. If differences are found, you are prompted to go to Beam Configuration to verify and revalidate the beam data. This ensures that the correct beam data is used for dose calculations.

Accuracy of the Dose Distribution Calculation

The accuracy of the dose calculation depends on multiple things, the most notable of which are patient image resolution and accuracy, treatment plan geometry, the accuracy of beam data measurements and beam data configuration, and the calculation algorithm used. More information on calculation algorithms: *Eclipse Photon and Electron Algorithms Reference Guide* or *Proton Algorithm Reference Guide*.

The accuracy of the dose calculation for photon fields in a typical clinical setup is 2–3%. The accuracy of photon beam reconstruction model is $\pm 1\%$ for rectangular fields and $\pm 2\%$ for irregular fields, the oblique correction being within 1–2%. For electron fields in inhomogeneous material, the dose calculation accuracy is $\pm 5\%$ or $\pm 5\text{ mm}$.

Information in the Calculation Log

The details of the calculation and possible calculation errors or warnings are recorded in a calculation log shown on the Calculation tab of the Field Properties dialog box. If there was an error during calculation, only fields that were calculated correctly have dose and no plan dose is shown.

Dose Calculation and Cobalt Machines

Eclipse takes into account the radioactive decay of Cobalt, and displays the current required timer setting (at the time of calculation). The timer setting is expressed as minutes or seconds for Cobalt treatment units. To include the shutter error in the treatment time for Cobalt treatment units, add it manually to the reported timer setting.

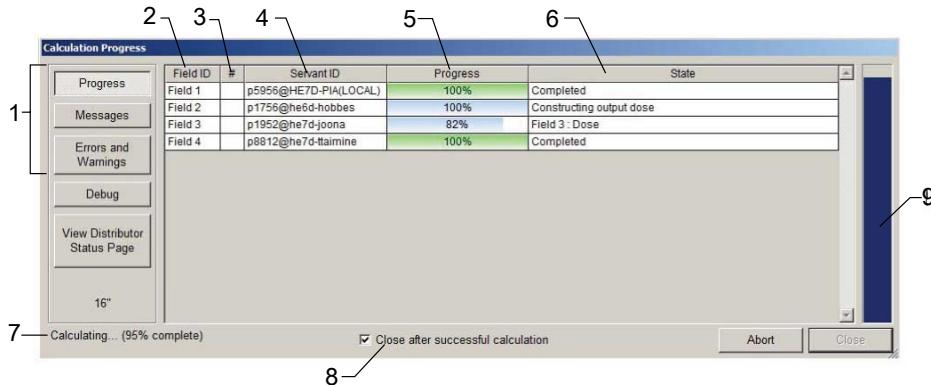


WARNING: Verify the dose calculation and dose display against manual calculations for Cobalt machines to ensure that the source decay used in the calculation corresponds to the actual source decay.

Calculation Progress Indicator in External Beam Planning

A calculation progress indicator is displayed during dose calculation. The progress indicator shows the field IDs of the fields to be calculated, calculation servants used for each field, color-indicated progress of the calculation of each field in percentages, and the state of the calculation. The colors in the Progress column indicate the following:

- Blue = processing data
- Green = completed
- Red = resulted in an error



1. Click the buttons to display calculation messages or errors and warnings, and to return to the progress indicator
2. Field IDs of the fields to be calculated
3. Shows a running number when calculation of one field is distributed to several calculation servants
4. Calculation servants performing dose calculation
5. Progress of the calculation of each field in percentages
6. State of calculation in different servants
7. State of the overall calculation
8. Select to define whether this dialog box is closed after successful calculation
9. Progress bar showing the overall progress of dose calculation

Figure 132 Calculation Progress Indicator

You can stop the calculation at any time by clicking **Abort**, or display calculation messages by clicking **Messages**. The **Messages** button is blinking if there is unread information in the messages pane. If there are errors or warnings in the dose calculation, the error and warning messages are displayed automatically after the dose calculation is done. When the dose calculation is performed in the Distributed Calculation Framework, you can view the status of the distributor by clicking **View Distributor Status Page**. If calculation servants are set to provide information during the calculation process, you can view it by clicking **Debug**.

More information on the Distributed Calculation Framework: *Beam Configuration Reference Guide*.

Calculation Options for External Beam Plans

For photon plans, you can select and change the calculation model and calculation options for the following:

- Compensator

- Volume dose
- Plan dose (This option is for Acuros XB only. Information on conditions for using the plan dose calculation in Acuros XB: *Eclipse Photon and Electron Algorithms Reference Guide*.)
- Beam angle optimization
- Irregular surface compensator
- Optimization
- Point dose
- Portal dose image prediction

For electron plans, you can select and change the options for calculating the field volume dose.

You can use a different calculation model for each of these items, for instance, use one calculation model for compensator calculation and another for field volume dose calculation. If you do not define any particular calculation options for a plan, the default settings defined for the Distributed Calculation Framework are used.

More information on the Distributed Calculation Framework: *Beam Configuration Reference Guide*.

External Beam Planning supports the use of a number of calculation algorithms, which can be configured in Beam Configuration.

Information on configuring the treatment planning system in Beam Configuration: *Beam Configuration Reference Guide*.

Description of the calculation algorithms supported: *Eclipse Photon and Electron Algorithms Reference Guide*.

Related Topics

[Select the Calculation Model for External Beam Plans](#) on page 434

Dose Calculation with Preset Values

With the Calculate Volume with Preset Values tool you can regenerate volumetric dose distribution based on specific MU values, timer setting (for Cobalt treatment units), or dose to a reference point. The tool remembers the original MU values or timer setting during the current application session.

This is useful in cases where the MU or timer setting has been entered manually and there is no volumetric dose distribution, or if a plan is first created or modified in Treatment Preparation, IRREG Planning or Simulation, and then opened in Eclipse for re-planning, volumetric dose calculation and DVH evaluation. This may be necessary in the case of an emergency treatment with no previous 3D planning, or mis-treatment (too many/not enough MU or treatment time for Cobalt treatment units) that needs to be compensated for by creating a new plan based on the treated MU or timer setting. Also, when dose distributions are calculated for verification plans, the calculation is automatically done using fixed MU or timer setting.

MU values or timer setting calculated for a plan are also cleared as a result of a number of actions, and it may be necessary to re-calculate the dose using the previous values.

Dose distribution calculation with preset values is not possible for a plan that contains a motorized wedge.

Eclipse calculates MU values and timer setting to greater precision than the treatment unit is able to produce. This may lead to minor discrepancies in calculated and delivered dose distributions. The Calculate Volume with Preset Values tool also allows re-calculating the dose using the precision of the treatment unit instead of the Eclipse internal precision. Notice that the Info window always displays the values in the precision of the treatment unit. To view the exact value calculated by Eclipse, place the mouse pointer over the cells in the MU/Timer setting column and view the value in a tooltip.

In addition to the Calculate Volume with Preset Values tool, you can use the Info window for defining preset MU values or timer settings for individual plans. However, if you have a plan that contains both treatment units showing MU and treatment units showing timer setting, the values cannot be modified in the Info window. In this case, calculation with preset values is also disabled.



Note: To be able to calculate the volumetric dose based on fixed MU values, the plan normalization mode must be set to No Normalization or Plan Normalization Value. Moreover, the plan may not contain more than one fractionation.

Calculate the Dose Distribution with Preset Values

1. Open the desired plan.
2. From the Scope window, drag the plan to an image view.
The original MU values or timer settings (for Cobalt treatment units) are saved temporarily.
3. If the plan has no image associated with it,

- a. Right-click the plan in the Focus window and choose **Assign Patient Image**.
For 2D plans, the image selection also sets field weights.
 - b. Adjust the isocenter locations.
The volumetric dose distribution (image views) and the MU values or timer setting for Cobalt treatment units (Info window) disappear.
4. If necessary, define the calculation volume.
 5. Choose **Planning > Dose Calculation > Calculate Volume with Preset Values**.
The original MU values or timer settings of the plan are shown.
 6. Do one of the following:
 - To use MU values, select the **MU** check box and define the desired MU values for each field in the **MU** column.
 - To use timer setting, select the **Timer setting** check box and define the desired timer setting for each field in the **Timer setting** column.
 7. To define the desired dose for a reference point, select the **Ref. Point** check box, select the reference point in the **ID** column, and define the desired dose.
 8. To show the values in the precision of the selected treatment unit, click **Round to machine precision**.
 9. To read the current values of the plan, click **Get current values**.
 10. In the Absolute Dosimetry group box, define the desired dose values.
 11. To calculate the dose, click **OK**.

The volumetric dose is calculated for all fields and the field weights are adjusted to retain the given MU or dose values.

Related Topics

[Edit the Calculation Volume](#) on page 435

Calculation Models Tab of the Info Window

In External Beam Planning, the Calculation Models Tab of the Info window lists the selected particles (photon, electron or proton), calculation types, calculation models and calculation algorithms for external beam plans. The information displayed in the tab depends on the global or local calculation settings. You can sort the displayed information by clicking any column header.

More detailed information on the calculation algorithms: *Eclipse Photon and Electron Algorithms Reference Guide* and *Proton Algorithm Reference Guide*.

Select the Calculation Model for External Beam Plans

1. In the Info Window, select the **Calculation Models** tab.
2. To change the calculation model, click the cell in the Calculation Model column and select a new calculation model.

You can select only one calculation model for each particle—calculation type combination. You can also change the calculation model in the Calculation Models tab of the Plan Properties dialog box.

Clear All Calculation Model Selections from an External Beam Plan

1. In the Scope window, select the plan for which to clear all calculation model selections.
2. In the Info Window, select the **Calculation Models** tab.
3. To clear all calculation model selections of the current calculation model, click **Clear all selections**.

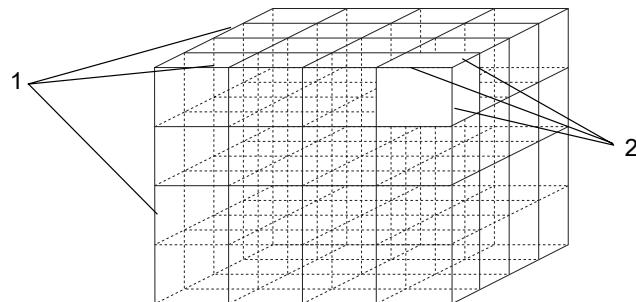
A confirmation message opens stating that if you proceed, all calculated dose distributions will be invalidated.

4. Click **Yes**.

All calculation model selections are cleared. You need to define a calculation model before you can calculate the dose distribution.

Dose Matrix

The dose distribution is calculated into a three-dimensional dose matrix. The dose matrix size is determined by the size of the rectangular calculation volume, which is defined by setting the lengths of the volume sides. The resolution of the dose matrix is determined by dividing it into smaller elements: The smaller the elements, the finer the resolution. The size of these elements is determined by defining their side lengths.



1. Dose matrix dimensions
2. Resolution

Figure 133 Dose matrix and resolution

The default size of the calculation volume depends on the contoured body volume.



CAUTION: Make sure that the calculation volume covers the entire volume of interest.

Edit the Calculation Volume



Note: If you edit the calculation volume, all calculated dose distributions for the plan are zeroed.

1. Click **Show/Edit calculation volume** .
2. Drag the corner points of the dimensions to resize the calculation volume.

The maximum size of the calculation volume depends on the algorithm selected for field volume dose calculation and the calculation grid size that has been defined for that algorithm in plan calculation options. The smaller the calculation grid size, the smaller the allowed maximum size of the calculation volume.

3. To inactivate the calculation volume, click the button again.

Reset the Calculation Volume



Note: If you reset the calculation volume, all calculated dose distributions for the plan are zeroed.

- In the Focus window, right-click the dose and choose **Reset calculation volume**



View the Dose Matrix Properties

1. In the Focus window, select the dose.
2. Choose **Edit > Properties**.
3. In the **General** tab:
 - **Position:** the coordinates of the center point of the volume.
 - **Size:** the width and the height of one dose plane.
 - **Resolution:** the width and the height of each dose pixel on a dose plane.
 - **Plane Separation:** the distance from one dose plane to the next.
 - **Number of Planes:** the number of dose planes in the volume.

Define the Default Plan Normalization Method for External Beam Plans

1. Choose **Tools > Task Configuration**.
2. Select the Default Plan Normalization Mode tab.
3. To select the normalization method, select the appropriate option button:
 - **100% at Body Maximum**
 - **100% at Target Maximum**
 - **100% at Target Mean**
 - **100% at Target Minimum**
 - **<n>% Covers <n>% of Target Volume** and then define the desired percentage of the dose and the target volume in the text boxes
 - **100% at Primary Reference Point**
 - **100% at Field Isocenter**
 - **Plan Normalization Value** and then define the value in the text box
 - **No Plan Normalization**

This setting is clinic-wide; it affects all workstations that are connected to the same database.

Plan Normalization Options for External Beam Plans

Both the default plan normalization method and the plan-specific plan normalization use the following normalization options.

Option	Description
100% at Body maximum	The maximum dose value in the body is normalized to 100%.
100% at Target maximum	The maximum dose value in the plan target volume is normalized to 100%.
100% at Target minimum	The minimum dose value in the plan target volume is normalized to 100%.
100% at Target mean	The mean dose value in the plan target volume is normalized to 100%.
<n>% covers <n>% of target volume	The dose in the user-defined amount of the plan target volume is normalized to the user-defined dose percentage.
100% at Primary reference point	The dose value at the reference point marked as the primary reference point is normalized to 100%.
100% at Field Isocenter	The dose value at the isocenter of the selected field is normalized to 100%.
Plan normalization value	The plan is normalized according to the user-defined normalization value, for instance, 200%
No normalization	The plan is normalized according to the normalization type defined for the calculation model in use.

In addition to these options, plans can also be normalized to 100% at the selected reference point. However, this option cannot be configured as the default normalization option.

Using Field Weight Factors

The total dose distribution of a plan is calculated by adding the individual field dose distributions. Before doing this, the dose distributions of each field are multiplied with the respective field weights, which indicate the relative weight of each field in a plan. How the field weights affect the dose distribution is determined by the selected field normalization method.

Eclipse enables you to change the field weights interactively to fine-tune dose distributions. A change made in the field weights automatically normalizes the dose (using the current default normalization method) and displays the new dose distribution on screen without the need for recalculation.

Information on field normalization: *Eclipse Photon and Electron Algorithms Reference Guide*.

Field weights of all fields included in the active plan or plan sum can be viewed and changed in the Field Weights dialog box. In this dialog box, you can change the

- Individual field weights (changes the total sum)
- Total sum of all weights (changes the individual weights)
- Dose percentage of each field, calculated from the total weight sum (modifies the individual field weight but does not affect the total sum)

The total sum is always the sum of the fields shown in the Field Weights dialog box, not necessarily the total sum of all fields in the active plan.

You can also lock the weights of the fields to keep them the same while changing the other weights. Locking a field weight also locks the total weight sum. However, the locking is valid only while the Field Weights dialog box is open. It is also possible to set the weights of all fields that have not been locked to the same value.



Note: When working with field weights, notice the following:

- You cannot change the weight factor of a field that belongs to an approved plan.
- Field weights can also be edited in the Field Properties dialog box and the Field Info view, but you can lock field weights only in the Field Weights dialog box. The locking is not valid outside the Field Weights dialog box.

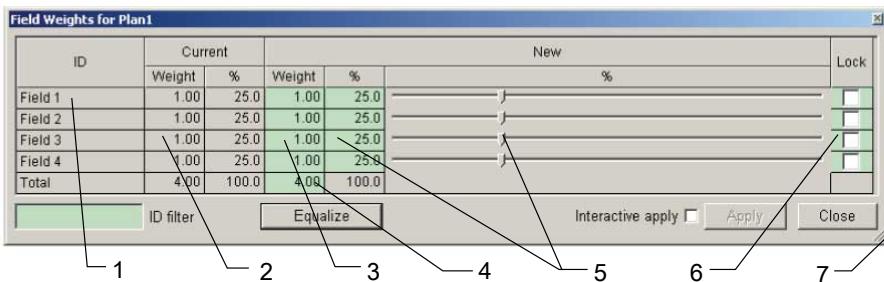
Related Topics

[Field-in-Field Technique](#) on page 375

Change the Field Weight Factors

1. Open the plan or plan sum.
2. Choose **Planning > Field Weight**.

If the dialog box obstructs your view to the plan, resize it by dragging the bottom right corner of the dialog box.



1. Field IDs (read by the ID filter).
 2. Current field weights.
 3. Type the new field weights here.
 4. Type the desired sum of the field weights here.
 5. Type the new field weight as a percentage of the sum of field weights here or use the sliders.
 6. Select these check boxes to lock the weights of individual fields and the sum of the field weights.
 7. To resize the dialog box, drag the corner of the dialog box.
3. To view only particular fields in the dialog box, type your filtering criteria in the **ID Filter** box and press ENTER. For instance, you can show only some specific fields from the active plan or in a specific plan in a plan sum. If you have three plans in the plan sum (Plan 1, Plan 2, and Plan 3) and only wish to see the fields in Plan 2, type "plan 2" as the criteria. The filtering is case-insensitive.
 4. To change the desired sum of the field weights, type in the new value in the **Total** row. This change affects only unlocked field weights.
 5. To change the weights of individual fields, do one of the following:
 - Type in the desired weight in the Weight column. The range is 0–100.
 - Type in the desired percentage in the % column. This is the percentage of the field weight of the total sum of the weights.
 - Move the slider handles with the mouse. This changes the field weight percentage.
 6. To lock the weight of a field or fields, select the check box of each field in the **Lock** column.
 - To lock/unlock all fields, click the **Lock** column title.
- The total sum of the field weights is always kept static unless you specifically change it by typing in a new value.
7. To set all the field weights that have not been locked to the same value, click **Equalize**.
 8. To keep previewing the effect of changing the field weights, select the **Interactive apply** check box.
 9. To preview the effect of changing the field weights, click **Apply**.

10. To close the dialog box, click **Close**.

Nominal Field Dose for Reference Point

When a reference point has a geometrical location in the planned image, but the field dose matrices are unavailable, the individual field dose contributions for the reference point are nominal. Nominal field dose contributions are estimates based on the value in the plan dose matrix at the given location. The sum of the nominal field dose contributions equals the calculated dose at the location of the reference point.

Nominal field doses are marked with the ~ character in the Plan Organizer and in the Reference Points Workspace.

For instance, the following functions can produce nominal reference point field doses:

- Acuros XB plan dose calculation
- Dose calculation in Cone Planning
- Splitting of large-field IMRT plan in Planning Approval.

Individual nominal field dose contributions cannot be used for independent MU calculation or verification in a phantom, because the exact calculated dose value is unavailable.

Copy Reference Points from One 3D Image to Another

1. In External Beam Planning or Brachytherapy Planning, open two or more 3D images.
To be able to copy reference point locations, the images must be registered.
2. If the images are not registered, go to the Registration application or the SmartAdapt application and register the images.
3. In the Scope window, select the 3D image that contains the reference point locations you wish to copy.
4. Choose **Edit > Copy > Reference Point Locations**.
5. To show the 3D image to which the points will be copied, drag it from the Scope window to the image views.
6. Choose **Edit > Paste Reference Point Locations**.

The reference point locations are pasted to the active 3D image. If a location with matching reference point already exists in the target image, the location is skipped.

Location of the Reference Points

Different visualizations are used to indicate the plane where each reference point is located in relation to the active viewing plane:

- —Active reference point located on the active viewing plane
- —Reference point located on the active viewing plane
- —Active reference point located in front of the active viewing plane
- —Active reference point located behind the active viewing plane or inactive reference point located in front of the active viewing plane

Showing the Persistent Dose in External Beam Planning

For external beam plans, you can define that the application shows the previously calculated, outdated dose distribution in all image views. This is useful, for example, if you need to modify blocks, MLCs, fluences or compensators after reviewing the calculated dose to improve the overall dose distribution. When the persistent dose is displayed, you can, for example, follow an isodose line to edit a block aperture.



CAUTION: Modifications to the treatment strategy should not be based on outdated or not fully visualized dose for any plans or plan sums, or dose for plan sums containing weighted plans.

When you select to show the persistent dose distribution, a warning message prompting to recalculate the dose is displayed in all image views if you change the plan information after the dose distribution for the plan is calculated.

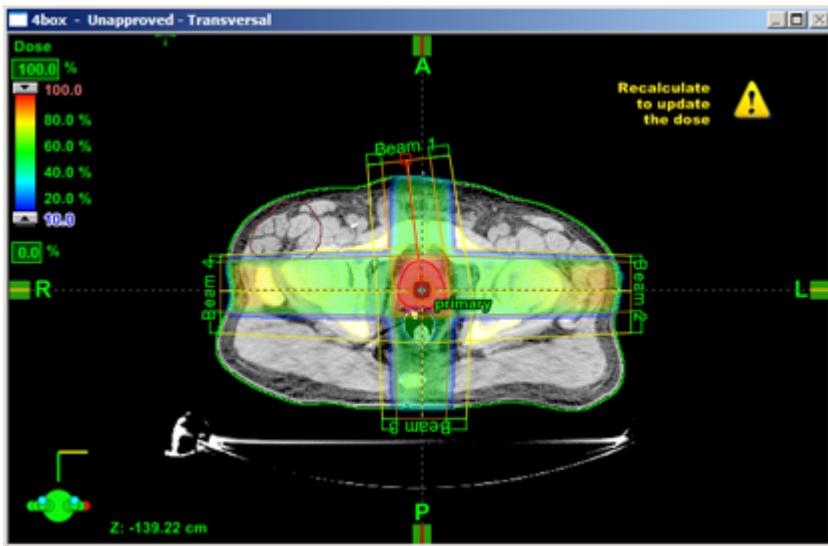


Figure 134 Visualization of Persistent Dose in External Beam Plans

When the persistent dose is displayed, the Point Dose and Dose Profile tools, reference points, and the Dose Volume Histogram view do not show any dose information. Modifying the field weight, dose prescription, fractionation, or adding or deleting fields has no effect on the persistent dose. You cannot change the dose mode from relative to absolute or vice versa when the persistent dose is displayed.

A message is displayed if you try to approve a plan, print or use DICOM print, approve a plan for treatment, normalize a plan, export a plan, or save a plan when the persistent dose is displayed. If you accept the message stating that the dose distribution is cleared, you can continue performing these operations. If you do not accept that the dose distribution is cleared, you are not allowed to perform the above operations.

If you copy a plan, the persistent dose distribution is cleared from the copied plan. The persistent dose is also cleared, if you change the size of the calculation volume.

The persistent dose setting is clinic-wide. It affects all workstations that are connected to the same database.

Show the Persistent Dose

1. Choose Tools > Task Configuration.
2. Select the Persistent Dose tab.

3. Do one of the following:

- To define that the persistent dose is visualized in the image views, select the **Use persistent dose** check box.
- To define that the persistent dose is not visualized in the image views, clear the check box.



Note: This setting is clinic-wide; it affects all workstations that are connected to the same database.

Chapter 21 Plan Evaluation

Show the Surface Dose in the Model View

- In the Focus window, right-click the desired structure and choose **Show Surface Dose**.

The surface dose is displayed and the slider appears in the upper left corner of the view.

Dose Maximum (Dmax) Point

You can show the location of the dose maximum (Dmax) in a plan. The 2D image views show the location of the Dmax on the active viewing plane; the Model view and the BEV (in External Beam Planning) show the location of the 3D dose maximum inside the three-dimensional calculation matrix.

The dose maximum point is shown as a red dot accompanied with the dose value at the point as in the figures.

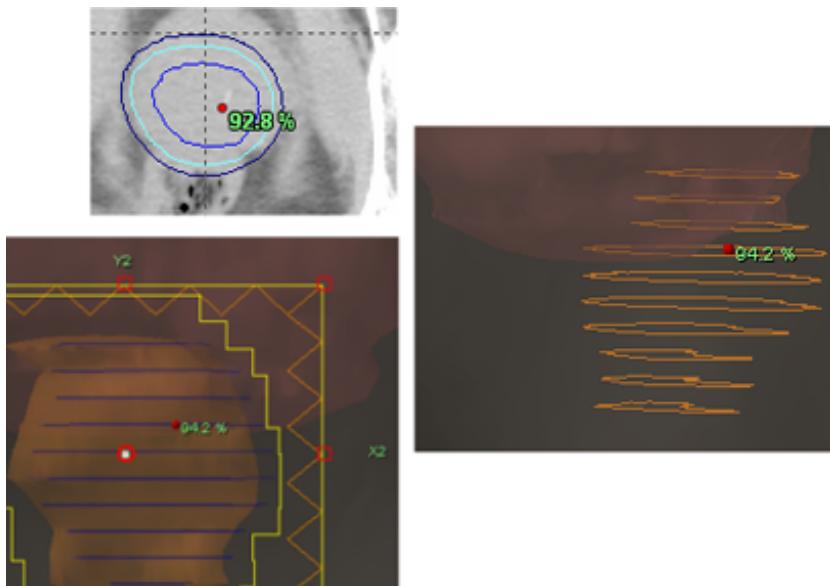


Figure 135 Dose Maximum Point in 2D Image View, Model View and BEV

The 3D dose maximum point may be seemingly invisible in the Model view. This is because it is positioned realistically in 3D space and, depending on the viewing angle, may be obstructed by a structure or an isodose visualization.

In the BEV, the 3D dose maximum point is always shown on top of all structures.

The Dmax point located at the intersection of the viewing planes is shown highlighted in the 2D image views in External Beam Planning and Plan Evaluation.

If a viewing plane shown in one of the 2D image views in External Beam Planning intersects with the location of the 3D dose maximum value point, the dose maximum point is highlighted on that viewing plane.

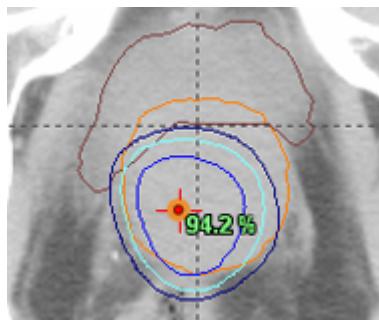


Figure 136 Highlighted Dose Maximum Point in 2D Image View

Statistical Dose Information

You can show the 2D dose statistics in every 2D view as a differential 2D dose-area histogram (DAH). The DAH is shown for the active structure. If no structure is active, the DAH is displayed for the target volume defined in the Plan Properties dialog box. The DAH shows the minimum, maximum and mean dose values for the structure. You can show or hide the DAH as is convenient. The DAH is available in External Beam Planning and Plan Evaluation.



Note: To have Eclipse work faster, hide the DAH whenever you do not need to view 2D statistical dose information.

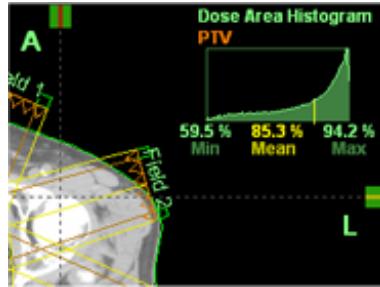


Figure 137 Dose Area Histogram in External Beam Planning

You can show the 3D dose statistics in the Model view. The statistics show the dose values inside the entire calculation volume. The information displayed includes the 3D dose maximum value, and maximum, mean and minimum dose in the plan target volume. You can show or hide the 3D dose statistics as is convenient. 3D dose statistics are available in External Beam Planning, Brachytherapy Planning and Plan Evaluation.



Note: In the case of a plan sum, the 3D dose statistics show statistical dose information for the target of the plans contained in the plan sum.

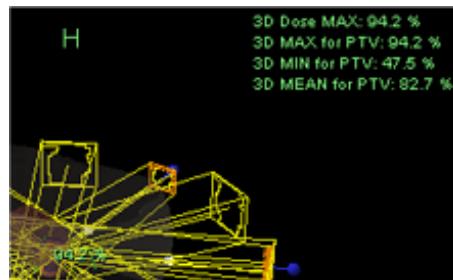


Figure 138 External Beam Plan Dose Statistics in the Model View

In a situation where a 2D view is maximized in External Beam Planning, and 3D dose statistics is selected in view options, the 3D dose statistics are shown in the 2D view side next to the dose statistics of the 2D image view.



Figure 139 3D Dose Statistics and DAH in a 2D Image View

Defining the Dose Levels Displayed in the Color Wash Mode

By default, the continuous color map contains all dose values in the defined dose range. You can either show the whole dose distribution from the minimum to the maximum dose or limit the visualization to view only the significant part of the dose distribution by:

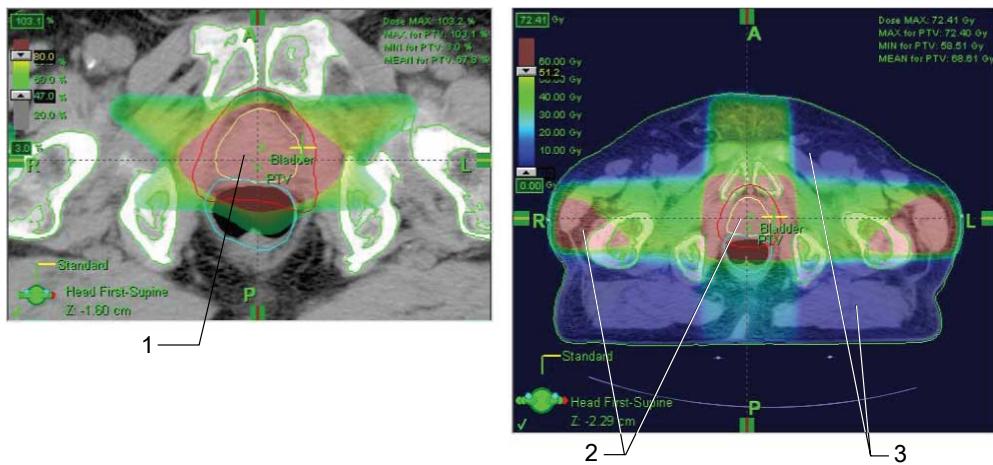
- Numerically defining upper and lower dose values to be shown.
- Defining the upper and lower dose values to be shown by moving the handles on the dose color wash slider with the mouse.
- Defining the lower dose value to the target minimum and the upper dose value to the target maximum.
- Using the lowest and highest isodose level in the selected isodose level set as the lower and upper dose value.

The whole spectrum of the continuous color map is stretched or compressed between the defined upper and lower dose value.

If you define the color wash dose levels for a plan that has the absolute dose display on, and then change any of the dose prescription values listed in the Dose Prescription tab of the Info Window, the dose levels will change accordingly. Plan normalization also changes the dose levels for both absolute and relative dose.

If some dose values fall outside the range when using the color wash slider to define the dose range, they are visualized in a particular way. In a single plan, dose values exceeding the range are shown with a special color, but dose values below the range are not visualized. In a summed plan (in Plan Evaluation), both dose values above and below the range are shown with special colors.

The figure shows how the dose above and below the defined dose range are displayed in External Beam Planning.



1. Dose values above the defined range in a single external beam plan.
2. Dose values above the defined range in a summed external beam plan.
3. Dose values below the defined range in a summed external beam plan.

Figure 140 Visualization of Dose outside Defined Range in External Beam Plans



Note: To view only significant isodose levels in the 2D image views in particular treatment cases, you can also use predefined isodose sets. The isodose levels included in each set as well as the default isodose level template are defined in RT Administration.

Modify the Isodose Levels in an Isodose Set

1. Choose **Planning > Isodose Levels**.
2. Do one of the following:
 - To change the isodose line width, click the cell in the Line width column and type the width in the cell. Use values from 1 (thinnest) to 5 (thickest). To use the same line width for all isodose levels, type the width on the All row.
 - To change an isodose level, click its cell in the Dose column and type the new isodose value in the cell.
 - To change the isodose color and style, click the cell in the Color and Style column, and select the desired setting in the list box.
 - To show the new isodose level in the 2D views, select the check box in the 2D column. To show all isodose levels in the 2D views, select the check box on the All row.
 - To show the new isodose level in the 3D model, select the check box in the 3D column. To show all isodose levels in the 3D model, select the check box on the All row.

The modified isodose level set is saved with the plan.

Add Isodose Levels to an Isodose Set

1. Choose **Planning > Isodose Levels**.
2. To add an isodose level, click **Add level**.
3. Edit the cells as necessary.
4. To show the new isodose level in the 2D views, select the check box in the 2D column.
5. To show the new isodose level in the 3D model, select the check box in the 3D column.

Delete Isodose Levels from an Isodose Set

1. Choose **Planning > Isodose Levels**.
2. To delete an isodose level, click one of the cells in the row.
3. Click **Delete level**.
4. To confirm the deletion, click **Yes**.

Converting an Isodose Level to a Structure

In External Beam Planning, to make, for example, the field-in-field planning less time consuming and more accurate, you can fit field apertures (MLCs and blocks) to a selected isodose level of the existing dose distribution. Before you can fit a field aperture to an isodose level, you must convert the isodose level to a structure.

Convert an Isodose Level to a Structure

1. If not already done, calculate the 3D dose distribution for the active plan.
2. In the Focus window, right-click Dose and choose **Convert Isodose Level to Structure**.
3. Type the isodose level in percentages or Gy to convert to a structure.
4. Click **OK**.
5. Fill in or modify the structure information as needed.

The default structure code of a structure created from an isodose level is always Dose. You can change it to another structure code if necessary.

Displaying the Point Dose

Point dose is the dose calculated for a point that you click on a plane displayed in an image view. You can use point dose, for example, to define the normalization value used for normalizing the dose distribution to a selected point, or to check the dose values at a critical point. You can display several point doses at the same time and drag the points to the desired locations.

In External Beam Planning, the point dose information includes:

- Absolute dose: The total dose in Gy or cGy to the selected point broken down into the absolute dose contribution from the individual fields
- Relative dose: The total dose as a percentage of the plan normalization value as well as the normalized and non-normalized relative dose contribution from each field
- Point coordinates: The (x, y, z) coordinates of the point expressed in centimeters. Point coordinates are displayed in respect to the user origin.



Note: If the point for which you are displaying the dose is located between dose matrix points, the displayed dose is trilinearly interpolated from the closest dose matrix points. The interpolation is dependent on the calculation grid points of the dose calculation algorithm. More information: Eclipse Photon and Electron Algorithms Reference Guide or Proton Algorithm Reference Guide).

Physical Property Tool

The Physical Property tool is available in External Beam Planning and Plan Evaluation.

You can use the Physical Property tool for checking important physical parameters associated with patient image data. The tool shows this information for a point that you click on a plane displayed in an image view. You can use the tool to verify the HU-to-physical-property conversion at any location of the image, and that the HU values have been assigned correctly. The tool checks this information from the CT calibration curve.

In addition, you can use the tool for checking, for example, how a support device, a mask or a screw affects the dose. The values that the tool displays are used for calculating the dose, so the tool can be used for evaluating this data.

You can access the Physical Property tool from the Point Dose tool dialog box. You can display several Physical Property tool dialog boxes at the same time, and drag the points to the desired locations. The data shown is updated automatically.

The following data shown by the Physical Property tool is read from the image:

- CT Value—The HU value of the point of interest.
- Assigned CT Value—The HU value assigned for a contoured structure. If no HU value is assigned for the structure, this field is empty.

The following data shown by the Physical Property tool is read from the CT calibration curve:

- Mass Density—The relative mass density at the point of interest.
- Relative Electron Density—The relative electron density that corresponds to the HU value of the point of interest.
- Relative Proton Stopping Power—The relative stopping power for protons at the point of interest.
- Physical Material Composition—The material composition of a structure at the point of interest based on the mass density, or assigned by the user in the Structure Properties dialog box. More information on the mass density to material conversion: *Eclipse Photon and Electron Algorithms Reference Guide*, or *Acuros BV Algorithm Reference Guide*.

If some of the curves is unavailable, the Physical Property tool shows “N/A” for that particular curve.

Display the Physical Properties of the Selected Point

1. Choose View > Measure > Point Dose .
2. In an image view, click a point of interest.
3. Select the **Physical Properties** tab to display information at the selected point.

Creating a Dose Profile

You can create a dose profile to derive additional information from the isodose plot of the dose distribution. The dose profile is useful to view the dose or dose gradients at critical locations in the plan. For the selected plot, the dose profile displays:

- Graph of the dose along an arbitrary line through the plan
- Graph of the dose contribution from each field
- Start and end points of the dose profile line
- Dose sampling steps and the step size
- Maximum dose along the line in percentage of the prescribed total dose or in absolute dose (Gy or cGy)

In Plan Evaluation, you can also compare the dose profiles of two alternative plans.

Export the Dose Profile

1. To save the dose profile as a text file, click **Export** in the Dose Line Profile dialog box.
2. Select the profiles to export and click **OK**.
3. Select the directory into which to save the export file, type a name for the profile and click **Save**.

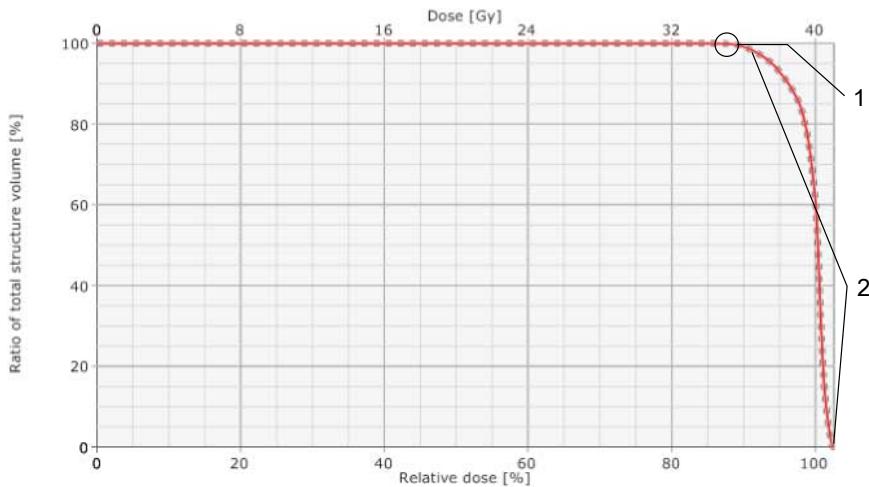
Available DVH Types

You can plot DVHs for multiple structures from a single plan on the same graph (single-plan DVH). Likewise, you can plot DVH curves for multiple structures from several different plans on the same graph (multi-plan DVH).

A dose-area histogram for any image plane can be calculated from within External Beam Planning.

Cumulative DVH

The cumulative DVH graph displays the percentage (relative) or volume (absolute) of structures that receive a dose equal to or greater than a defined dose. It is particularly useful for summarizing the dose delivered to a target structure.



1. For example, this point indicates that 100% of the structure receives at least 87% of the prescribed dose (or about 34 Gy).
2. The sharper the curve falls between the indicated points the more uniform is the dose distribution.

Figure 141 Cumulative DVH Graph in External Beam Planning

For structures that contain DVH estimates in photon plans, you can also include the estimates in the cumulative DVH graph.

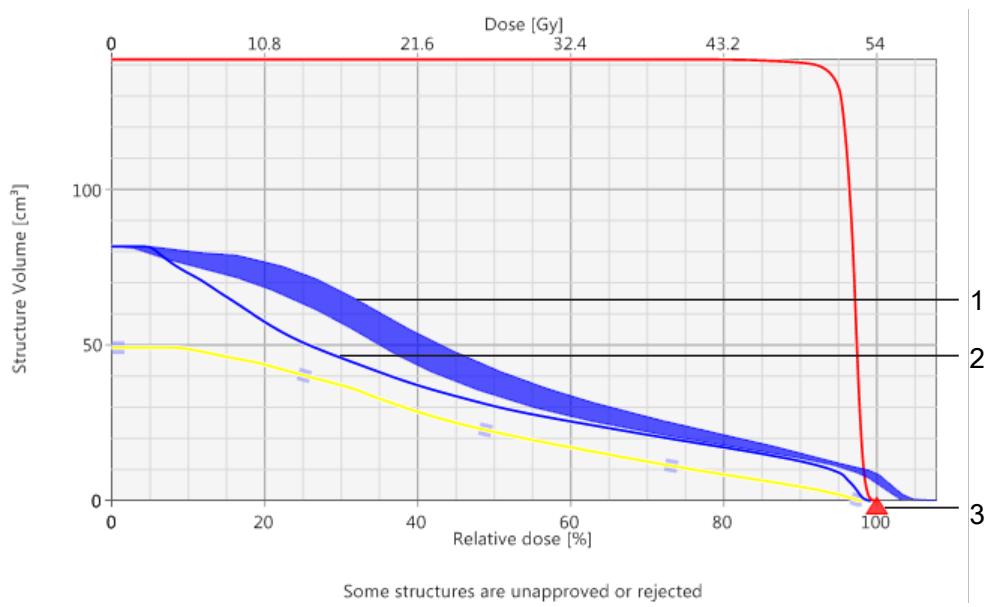


Figure 142 Cumulative DVH Graph with DVH Estimates in External Beam Planning

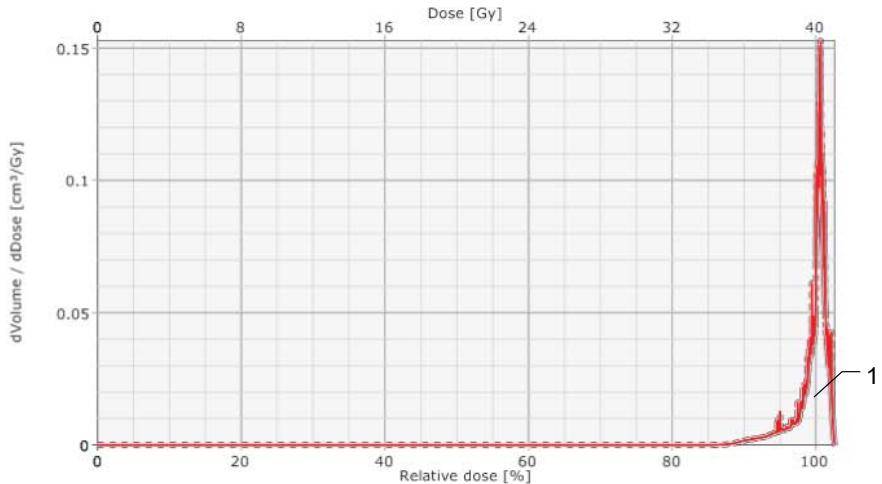
In the cumulative DVH graph, the Y-axis represents the proportion of the total volume of the structures receiving a particular dose. The proportion of the volume is indicated in percentage or cm³. The axes of the DVH signify the following:

- The upper X-axis represents the dose indicated in absolute dose.
- The lower X-axis represents the dose indicated either in percentages or in absolute dose between the dose range values defined in the Dose-Volume Histogram view.
- If both relative and absolute dose cannot be displayed, the lower X-axis represents the currently available dose mode.
- For plan sums, only the absolute dose can be displayed.
- If a plan has no prescription, only the relative dose is displayed.

Differential DVH

The differential DVH displays the share of the total volume in structures receiving a certain dose as a function of equivalent dose intervals. It is useful for summarizing the dose distribution to normal tissue.

DVH estimates cannot be shown in a differential DVH.



1. The wider the peak, the less uniform is the dose distribution.

Figure 143 Differential DVH Graph in External Beam Planning

In the differential DVH graph, the Y-axis represents the share of the total volume of the structures receiving the dose. The volume is indicated in cm^3/Gy , cGy or %. The axes of the graph signify the following:

- The upper X-axis represents the dose intervals in absolute dose.
- The lower X-axis represents the dose intervals with the dose indicated either in relative dose or in absolute dose
- If both relative and absolute dose cannot be displayed, the lower X-axis represents the currently available dose mode.
- For plan sums, only the absolute dose can be displayed.
- If a plan has no prescription, only the relative dose is displayed.

Natural DVH

The natural DVH type is designed for evaluating brachytherapy plans.

The natural DVH type displays the share of the total volume of structures receiving a certain dose against a set of non-equidistant dose intervals. More information on the natural DVH: *BrachyVision Reference Guide*.

Dose Statistics Tab of the Info Window

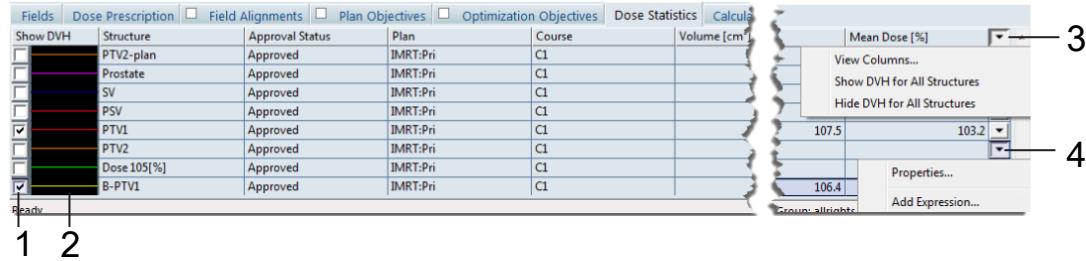
This information applies to External Beam Planning, Brachytherapy Planning and Plan Evaluation.

The Dose Statistics tab is used for viewing the selected dose statistics and editing the DVH graph. You can sort a column in the Dose Statistics tab by clicking the column header.

Table 31 Information in the Dose Statistics Tab

Item	Description
Show DVH	Selection of structures to be shown in the DVH graph, and the line style used for the structure in the DVH graph.
Show DVHE	Selection of structures with DVH estimates to be shown in the DVH graph, and the line style used for the structure in the DVH graph. The target structure used in the DVH estimation is marked with a triangle. The column is only shown if there are structures with DVH estimates in the active plan.
Structure	Structures from each image of the plan or plan sum that is displayed in the views.
Approval Status	The approval status of the structure.
Plan	The plan that produced the dose for the structure.
Course	The course that contains the plan that produced the dose for the structure.
Volume [cm ³]	The volume of the structure in cubic centimeters.
Dose Coverage [%]	The percentage of the structure volume covered by the dose matrix.
Sampling Coverage [%]	The percentage of the structure volume used for the DVH calculation.
Min Dose [%]	The minimum dose in percentages.
Max Dose [%]	The maximum dose in percentages.
Mean Dose [%]	The mean dose in percentages.
Modal	The modal dose in percentages.
Median	The median dose in percentages.
STD [%]	The standard deviation in percentages.
Equiv. Sphere Diam. [cm]	Equivalent sphere diameter of the structure, that is, diameter of a sphere with the same volume as the structure.
Conformity Index	Dose conformity index value (the volume closed by the prescription isodose surface divided by the target volume). Reported only for the plan target volume, and calculated only if the DVH coverage of the Body structure in the plan image is accurate enough.

Item	Description
Gradient Measure [cm]	Dose gradient value in centimeters (difference between the equivalent sphere radius of the prescription and half-presetation isodoses).
	Reported only for the plan target volume, and calculated only if the DVH coverage of the Body structure in the plan image is accurate enough.
▼	<p>View Columns: Opens the DVH Column Selection dialog box for defining the columns that are visible in the Dose Statistics tab.</p> <p>Show DVH for All Structures: Selects all structures to be calculated and shown in the DVH graph.</p> <p>Hide DVH for All Structures: Hides all structures in the DVH graph.</p> <p>Show DVH Estimates for All Structures: Shows the DVH estimates in the DVH graph for all structures that contain DVH estimates. Available only when DVH estimates exist.</p> <p>Hide DVH Estimates for All Structures: Hides the DVH estimates in the DVH graph for all structures that contain DVH estimates. Available only when DVH estimates exist.</p> <p>Properties: Opens the Structure Properties dialog box of the structure in question.</p> <p>Add Expression: Opens the Expression Properties dialog box for adding virtual structures to the DVH graph.</p>



1. The selected structures are included in the DVH calculation.
2. The line style used for the structure in the DVH graph.
3. Opens the dialog box for defining the columns visible in the Dose Statistics tab, and contains commands for showing and hiding the DVH for structures.
4. Opens the dialog box for editing structure properties of the structure in question, or adding virtual structures in the DVH graph.

Figure 144 Example of the Dose Statistics Tab of the Info Window

Modify the Style of a DVH Line

1. In the Dose Statistics tab of the Info window, click the down-pointing arrowhead in the end of the row of the structure whose DVH line you want to modify and choose **Properties**.
2. In the **DVH Visualization** group box, select the desired line color, style or width.
3. Click **OK**.

Exporting DVHs

You can export the DVH, or save it as a text file which can be opened, for example, in a spreadsheet program for further analysis.



Note: Notice the following about DVH export:

- Only the values within the dose range set in the DVH graph are exported.
- DVH can also be exported in the DICOM format with the dose data using the Export/Import wizard.

The export function saves the DVH to an ASCII file. The export file of both a single-plan and multi-plan DVH contains:

- Name and ID of the patient
- Comment stating whether the export file is for a single-plan or multi-plan DVH
- Export date and time
- Name of the person who exported the file
- DVH type (cumulative, differential or natural) and description
- ID of the plan(s)
- Plan status
- ID of the course
- ID of the selected structure(s)
- Approval status of the selected structure(s)
- Structure information in numerical format (percentage of volume calculated, volume of the structure)
- Dose information in numerical format (prescribed dose, treatment percentage, dose minimum and maximum, dose mean, median and modal, standard deviation, equivalent sphere diameter, conformity index, gradient measure)
- DVH graph information in numerical format, depending on the type of the DVH (cumulative, differential or natural)

The structure information is written for each structure included in the DVH.

Export a DVH

1. Display the DVH graph in the Dose Volume Histogram view.
2. Set the DVH graph to display the dose range you want to save in the export file.
3. To change the interval at which the dose values are printed to the export file, define the desired value in the **Step size** text box of the DVH Options dialog box. (To open the dialog box, right-click in the Dose Volume Histogram view and choose **DVH Options**.)
4. To export the DVH, do one of the following:
 - Right-click in the Dose Volume Histogram view and choose **Export DVH in Tabular Format**.
 - Choose **File > Export > Export DVH in Tabular Format**.
5. Select the directory into which to save the export file and define a name for the file.
6. Click **Save** to save the DVH to the defined export file.

DVH Export File Format

The export function saves the DVH to an ASCII file. The export file of both a single-plan and multi-plan DVH contains the following information:

- Name and ID of the patient
- Export date and time; name of user who did the export
- DVH type (cumulative, differential or natural)
- ID of the course
- ID of the plan(s)
- ID of the selected structure(s)
- Approval status of the selected structure(s)
- Structure information in numerical format (percentage of volume calculated, volume of the structure)
- Dose information in numerical format (prescribed dose, treatment percentage, dose minimum and maximum, dose mean, median and modal, standard deviation, equivalent sphere diameter, conformity index, gradient measure)
- DVH graph information in numerical format, depending on the type of the DVH (cumulative, differential or natural)

The DVH information for a single-plan DVH is saved in the export file in the following format:

Table 32 DVH Export File Format

Export File Entry	Value
Patient Name:	Name of the patient
Patient ID:	Identification of the patient
Comment:	User-defined comment
Date:	Date and time as defined in the Windows operating system
Exported by:	User name of the user who exported the DVH
Type:	Cumulative/Differential/Natural Dose Volume Histogram
Description:	Description of the DVH type exported
Plan:	Plan ID
Uncertainty plan:	Plan ID (variation of plan: <Plan ID>)
Course:	Course ID
Plan Status:	Approved/Reviewed/Unapproved/Rejected
Prescribed dose [Gy]:	Prescribed dose in Gray
% for dose (%):	Treatment percentage
Structure:	ID of the structure
Approval status:	Approved/Reviewed/Unapproved/Rejected
Plan:	ID of the plan
Course:	ID of the course
Plan Status:	Approved/Reviewed/Unapproved/Rejected
Volume [cm ³]:	Volume
Dose Cover. [%]:	Percentage of the dose coverage
Sampling Cover. [%]:	Percentage of the structure volume used in DVH calculation
Min Dose [%]:	Dose minimum
Max Dose [%]:	Dose maximum
Mean Dose [%]:	Dose mean
Modal Dose [%]:	Dose modal
Median Dose [%]:	Dose median
STD [%]:	Standard deviation

Export File Entry	Value
Equiv. Sphere Diam. [cm] :	Equivalent sphere diameter value
Conformity Index:	Conformity index value
Gradient Measure [cm] :	Gradient measure value
Dose [Gy]	Dose in Gray
Relative Dose [%]	Dose in percentage
Ratio of Total Structure Volume (%)	Percentage

The structure information is written for each structure included in the DVH.

The DVH information for a multi-plan DVH is saved in the export file in same following format. The plan information is written for each plan included in the DVH. The structure information is written for each structure included in the DVH.

DVH Print-Outs

You can print both single-plan and multi-plan DVHs. In both cases, the DVH print contains the DVH graph, and the following information, depending on the type of the DVH:

- Name and ID of the patient
- DVH type (cumulative, differential or natural)
- DVH line type(s) and ID(s) of the selected structure(s)
- DVH estimates, if selected to be shown for a structure, and the target structure markers. DVH estimates are only included in single-plan DVH prints.
- ID(s) of the selected plan(s)
- Plan approval status(es)
- ID(s) of the course(s)
- Approval status of the selected structure(s)
- Structure information in numerical format (coverage, volume)
- Dose information in numerical format (min., max., mean, modal, median, standard deviation)
- User defined comment, if any
- Print date and time

DVHs are printed using the DVH.xml template file.

The DVH graph in a DVH print-out is similar to that displayed in the Dose-Volume Histogram view.

Related Topics

Plan Uncertainty Parameters

The Plan Uncertainty Parameters dialog box contains the information shown in the table below.

Item	Description
ID	Identification of the plan uncertainty dose that is calculated using the parameters on the row. The ID is created automatically.
Patient Setup Error	<p>Change in isocenter position in X/Y/Z direction [cm], specified in the same planning coordinate system as the isocenter of the field. The planning coordinate system is selected in RT Administration.</p> <p>Estimates how a change in patient setup may affect the dose distribution.</p>
Target Shift	<p>Change in isocenter position in X/Y/Z direction [cm], specified in the same planning coordinate system as the isocenter of the field. The planning coordinate system is selected in RT Administration.</p> <p>Estimates the effect on the dose distribution if the target moves in relation to other structures.</p>
Curve Error [%]	<p>Variations in the calibration curve for HU to electron density or HU to mass density.</p> <p>If the value specified is positive, the radiation attenuation increases and the range becomes shorter compared to the range of the nominal plan, thus moving closer to the source.</p> <p>If the value is negative, the radiation attenuation value decreases and the range moves further from the source.</p> <p>The correction is relative to the electron density or mass density value in the calibration curve: if the electron density or mass density value on the curve is 0, the correction is 0, but as the values on the curve increase, also the correction gets bigger.</p>
Calculation Status	Shows whether the plan uncertainty dose has been calculated.

Displaying Plan Uncertainty Doses in Image Views

You can display plan uncertainty doses using the Plan Uncertainty View, in which you can view the nominal plan and any of the plan uncertainty doses side by side. The nominal plan is always displayed in the image views on the left and the plan uncertainty dose in the image views on the right. Plan uncertainty doses are visualized using the same isodose levels that are selected for the dose in the nominal plan.

When you are displaying a plan uncertainty dose in the 2D views, a warning text is shown stating the displayed dose is a plan uncertainty dose. The title bar of the image views shows the parameters that were used to create the plan uncertainty dose (isocenter shift in X/Y/Z direction, calibration curve error).



1. Nominal plan.
2. Plan uncertainty doses.
3. Warning text indicating that the dose is a plan uncertainty dose.
4. The parameters that were used for generating the plan uncertainty dose are shown in the title bar.

Figure 145 Photon Plan Uncertainty Dose in Plan Uncertainty View

You can use the following tools to evaluate individual plan uncertainty doses when they are displayed in the 2D views:

- Point dose tool—Can be used to check the dose value at a point in a plan uncertainty dose.
- Dose line profile—Can be used to evaluate the dose or dose gradients at critical locations in a plan uncertainty dose.
- Show field dose—Can be used to show the dose for one field at a time in the 2D views.

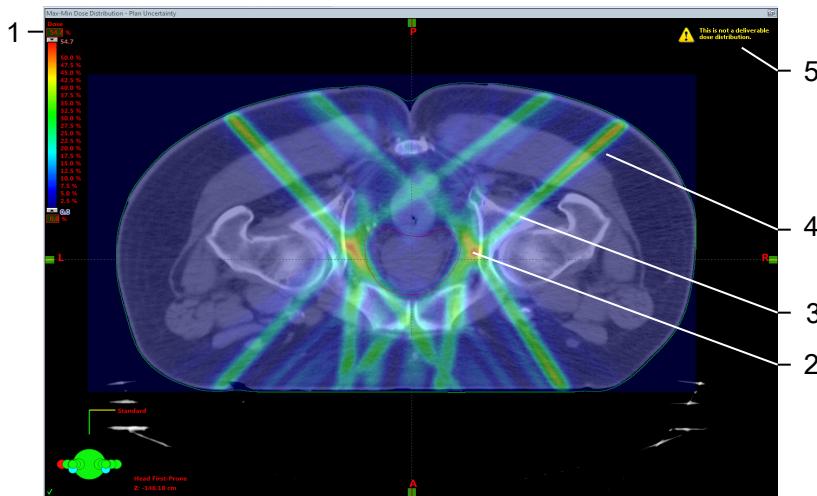


Note: The above mentioned tools are not available for the Max-Min dose.

Displaying the Max-Min Dose

In addition to individual plan uncertainty doses, you can display a Max-Min dose that shows where the biggest differences in dose may occur, if all plan uncertainty doses are taken into account. It is a derived dose difference calculated based on the dose from the original plan (nominal dose) and all plan uncertainty doses. The Max-Min dose is displayed using the Plan Uncertainty View with a warning text stating that the dose distribution is not a deliverable dose distribution.

The Max-Min dose is always visualized in color wash. Red color indicates the biggest differences in dose, and blue indicates a very small difference, or no difference. The percentages the colors correspond to depend on the plans and the amount of variance generated by the plan uncertainty parameters used.



1. Shows the scale of the dose difference.
2. Red indicates location where the difference between the highest and lowest dose is the biggest among all calculated plan uncertainty doses.
3. Green indicates areas where the difference between the doses is considerable.
4. Blue indicates areas where the difference in dose among all plan uncertainty doses is small.
5. Warning text about max-min dose being displayed.

Figure 146 Max-Min Uncertainty Dose in a Photon Plan

The Max-Min dose is the pointwise difference between the maximum of the calculated doses and the minimum of the doses:

Equation 3

$$D_{\text{Max-Min}}(x) = D_{\text{Max}}(x) - D_{\text{Min}}(x)$$

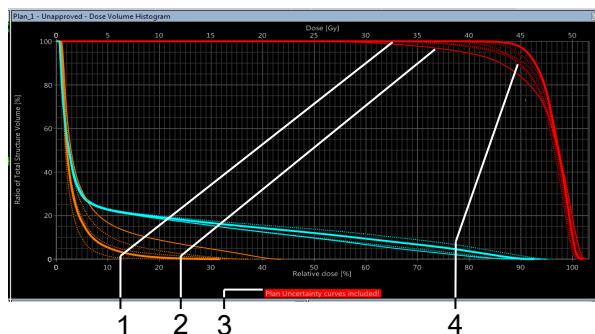
where

$D_{\text{Max}}(x)$	=	Maximum of all of the calculated dose distributions (nominal dose included) at point x.
$D_{\text{Min}}(x)$	=	Minimum of all of the calculated dose distributions (nominal dose included) at point x.

Showing Plan Uncertainty Doses in the DVH

You can also evaluate plan robustness using the DVH. The DVH can be used to view the dose volume histograms from all calculated plan uncertainty doses.

The DVH curves showing the dose for a structure in the nominal plan is plotted with a thick curve. The plan uncertainty dose to the same structure is plotted with the same color but with a dotted or dashed curve. A dashed curve is used if the structure in the nominal plan is plotted with a dotted curve. For each structure selected in the Dose Statistics tab of the Info Window, there is one curve plotted per calculated plan uncertainty dose.



1. DVH curve from the nominal plan is plotted with a thick line.
2. DVH curve from the plan uncertainty dose that is currently selected in Focus window is plotted with a thin line.
3. Warning about plan uncertainty curves being shown.
4. DVH curves from plan uncertainty doses are plotted with dotted lines.

Figure 147 Photon Plan Uncertainty Doses in DVH

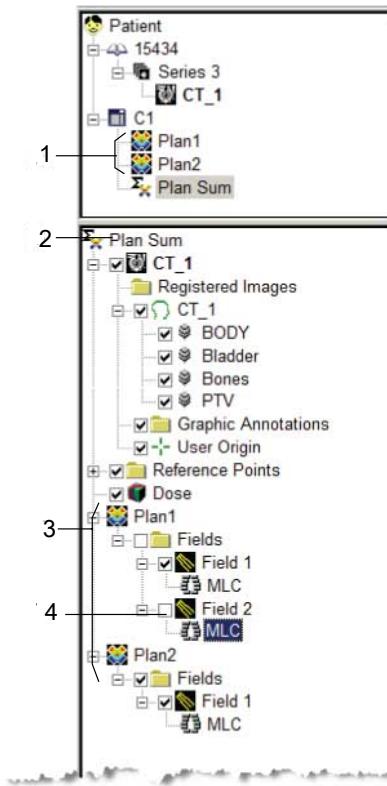
If there are large variations in the DVH curves of a structure (for example, the target structure or an organ at risk), this indicates that declared position and plan uncertainty causes a large error in dose.

When you are displaying DVH of plan uncertainty doses, the cross-hair tool displays the ID of the plan uncertainty dose the curve is from. If one of the plan uncertainty doses is selected in the Focus window, the DVH curves from it are highlighted (plotted with a thin line, as in the previous figure).

Plan Sum in the Context Window

This information applies to External Beam Planning and Plan Evaluation.

Plan sums are shown in the Focus window with a special icon  . The Focus window shows the plans included in plan sum.



1. Individual plans used to form the plan sum.
2. Plan sum.
3. Plans and fields included in the plan sum.
4. A hidden field not visible in the image views. If the field accessory of the hidden field is selected in the Focus window, the accessory is displayed in the image views.

Figure 148 Plan Sum in Focus Window in External Beam Planning

Dose Matrices in Summed Plans

The calculation volume for the dose in the plan sum encompasses the total irradiated volume of all fields in the plan sum. This way the dose contributions from all fields are taken into account for all regions covered by the plan sum. If the original dose matrices have different resolutions, a warning message is displayed when you calculate the dose for the plan sum.

If the original dose matrices are of different size, the application displays a warning message when you calculate the dose for a plan sum and, if you so choose, resets the dose matrices to the largest possible size to cover all the volumes in the sum. This warning is also displayed when you planning approve a plan sum containing dose matrices of different size.

For the summed plan, the DVH is calculated only for those areas of the original plan matrices that are shared by all the plans. Similarly, the dose distribution displayed in the image views is shown only for those areas of the original plan matrices that are shared by all the plans.

Registered Images and Plan Sum Calculation

When creating a plan sum from plans using different 3D images, the images must first be registered. The plan sum is calculated using the image registration. The image registration can be a spatial rigid registration, or a DICOM coordinate based registration (the images share a single frame of reference, FOR). In the case of spatial rigid registrations, the plan sum cannot be calculated if there are multiple registrations. DICOM coordinate based registration is always used if all the images in the plan sum share a single frame of reference.

Plan sums are calculated by summing the point doses in each plan using tri-linear interpolation. The interpolation of the doses can lead to inaccuracy in the plan sum. When the images in the plans being summed share a single frame of reference, the resulting plan sum is an intersection of the dose matrices; otherwise the result is the union of the dose matrices. (In a union of the dose matrices, part of the voxels within the calculation volume may be uncalculated or only calculated in part of the plans included in the plan sum.) The resolution of the dose matrix of a plan sum is determined from the dose matrix resolutions of the individual summed plans: on each dose matrix axis, the resolution is the highest resolution among the summed plans.



Note: Prior to creating a plan sum, make sure that the images used in the plan sum are compatible with each other to the degree acceptable for the purpose of the plan sum.

The accuracy of the plan sum depends on the following:

- Accuracy of the registration of the patient anatomy between the plan images.
- Interpolation of the doses in the plan sum calculation.

Plan Sum Tab of the Info Window

This information applies to External Beam Planning and Plan Evaluation.

In the Plan Sum tab, you can view and edit the properties of the plan sum. When you edit the properties of the plan sum, the plan sum is updated accordingly in the image views. This tab shows the type of summing (adding/subtracting), the dose prescribed for the plans, and lists the parameters related to the summation procedure.

Table 33 Information in Plan Sum Tab

Column	Description
In Total	Select the check boxes to visualize the dose distribution of a plan in the image views.
Plan ID	Identification of each plan included in the sum.
Course ID	Identification of the course to which each plan in the sum belongs. Cannot be edited.
Operation	Indicates whether the plan is summed with ("+" or subtracted from ("-") the other plans in the sum.
Plan Weight	Weight of each plan included in the sum.
Target	Target volume of each plan included in the sum. Target volumes of external beam plans can be edited only in External Beam Planning.
Prescribed Percentage	Prescribed dose percentage of each plan included in the sum.
Dose / Fraction	Dose per fraction in Gy/cGy of each plan included in the sum.
Number of Fractions	Number of fractions of each plan included in the sum.
Total Prescribed Dose	Total dose in Gy/cGy of each plan included in the sum.
Plan Normalization Mode	Plan normalization mode used for each plan in the sum.
Field ID	External beam planning: Identification of each field in the plans included in the sum.

Column	Description
MU/ Timer setting/ Multiple units	<p>External beam planning: Monitor units or timer setting (for Cobalt treatment units) of each plan included in the sum. Cannot be edited.</p> <p>If the calculated MU are outside of the operating limits of the treatment machine, the MU are shown in red.</p> <p>If the plan sum contains different units (MU, timer setting) or treatment units using different scales, the column heading changes to Multiple units.</p>
Field Weight	External beam planning: Field weight of each field in the plans included in the sum.

Reference Points in External Beam Plan Sums

You can add new reference points in a plan that is included in a plan sum when the plan sum is displayed in the image views. You can add reference points directly to individual plans in the plan sum, or to the plan sum image and then assign them to the desired plan using the Reference Point Organizer.

You can also move all the reference points included in the plan sum. If a plan in the plan sum is normalized to a reference point and the dose distribution is calculated, the reference point can be moved only in External Beam Planning. If the same reference point is used in plan normalization outside plan sum, you cannot move the reference point.

Insert a Reference Point in an External Beam Plan Sum

1. Show the plan sum in the image views.
2. Do one of the following:
 - To add a reference point directly to a plan in the plan sum, right-click the plan and choose **New Reference Point and Location**.
 - To add a reference point to a plan sum image:
 - Right-click the Reference Points folder and choose **New Reference Point and Location**.
 - Then right-click the desired plan in the plan sum, choose **Reference Point Organizer** and assign the reference point to the plan.

Evaluating and Editing Plan Sums

You can evaluate the summed dose distribution with viewing tools and dose measurement tools. You can also use the Plan Sum tab of the Info Window for defining how plan sums are visualized in the image views, and for editing plan sums. You can specify, for example, which dose distributions of individual plans are visualized in the image views, and change plan weights and dose prescriptions. If you have a plan sum that contains both external beam plans and brachytherapy plans, you cannot use the Plan Sum tab to edit brachytherapy plans in External Beam Planning and vice versa.

In External Beam Planning, you can also edit a plan sum by adding or removing fields from plans included in the plan sum, by adding new plans to the plan sum, and by removing plans from the plan sum.



CAUTION: If a plan included in an existing plan sum is edited, the changes to the edited plan may affect the combined dose of the plan sum. The dose of all plan sums must be reviewed if any of the component plans forming the plan sum will be used for treatment.

Related Topics

[Plan Sum Tab of the Info Window](#) on page 469

Copying and Pasting Plan Sums

When you copy a plan sum, all the individual plans are copied in the new plan sum. The copied plans are renamed to avoid confusion with the original plans.

In External Beam Planning, all fields and field accessories are also copied. In addition, you can copy fields and plans inside plan sums.

When a plan sum is the active object and any plan is copied and then pasted, the plan is added to the plan sum. If you want to copy and paste the plan without adding it to the plan sum, drag this plan to an image view to activate it, then copy and paste the plan to any course.

Copy and Paste a Plan Sum

1. Open the patient and the course that contains the plan sum to copy.
2. In the Scope window, select the plan sum to copy.
3. Choose **Edit > Copy Plan Sum**.

4. In the Scope window, select the course into which to paste the copied plan sum and choose **Edit > Paste Plan Sum**.

If the plan sum is pasted into the same course with the original plan sum, the new plan sum and the individual plans forming the plan sum are renamed.

Chapter 22 Preparing Plans for Treatment

Verification with Phantom

When using the phantom verification method, you can connect the verification plan to a verification structure set and image, (normally an artificial or a scanned phantom image). The selected structure set and image are copied to the active patient if they do not already belong to the active patient. Reference point locations are transferred to the verification plan. Reference points (named Verification <number>) are added during the creation of the verification plan and connected to a patient volume named "Phantom" with the type "None". The "Phantom" patient volume can be shared between the plans if several verification plans have been created for the patient.

Photon verification plans are automatically calculated using fixed MU. The resulting number of MU for a plan that contains a motorized wedge may be different than the number of MU in the original plan.

Isocenter Placement in Verification with Phantom

The first field isocenter is positioned to the center of the image that the verification structure set refers to. If the selected image has a user origin defined, the first field isocenter is positioned to the user origin. Other isocenters are positioned in relation to the first isocenter. If the verification structure set is the same that was used for planning, the isocenter locations are copied from the treatment plan.

Related Topics

[Dose Calculation with Preset Values](#) on page 431

Verify the Leaf Motions Using Test Fluences

1. Create a plan for a phantom, for example, a water phantom.
2. Import the desired arbitrary test fluence into the plan.
3. Calculate the leaf motions with the LMC.
4. Calculate the dose distribution.
5. Move the plan to treatment, schedule and treat it using the phantom.
6. Compare the measured dose against the calculated doses.

7. Evaluate the LMC conversion.
 - Compare the optimal fluence with BEV printouts containing the actual fluence in Eclipse
 - Compare BEV printouts containing the optimal fluence with field images on film
 - Compare the optimal fluences with the actual fluences in the ASCII format

Verify the Leaf Motions Using a Re-Generated DMLC

1. Create an optimized plan.
2. Export the actual fluence.
3. Import the actual fluence as optimal fluence.
4. Start the LMC to re-generate the DMLC motion patterns.
5. Compare the DMLC motion patterns with those created by the original optimization.

Verification with Portal Dose Prediction

Verification plans using portal dose prediction are not connected to any verification structure set. After you create the verification plan, the portal doses for each field are calculated automatically. The portal doses are copied to the generated fields, and the correct portal imaging device distance is marked to the fields to enable the use of the verification plan in Portal Imaging. You can create verification plans using portal dose prediction for IMRT, RapidArc and conformal arc fields.

You can also view the predicted portal dose images in the transversal view in Eclipse. They are shown with an icon (■) under the corresponding field in the Focus window.

Due to the characteristics of Varian's DMLC device controller, large fields containing Dynamic MLCs are split into smaller, deliverable subfields when the plans are moved to treatment. Likewise, large DMLC fields are split to subfields when creating a verification plan. All fields, including subfields, are saved into the same verification plan.



CAUTION: Changes made to the original plan will not be conveyed to a new copy of the original plan or vice versa.

Portal dose prediction is possible only for fields with a DMLC. The FFF energy mode is allowed only if the 43 × 43 cm imager is configured for the machine.

When using Acuros XB, there may be differences of up to 5% in low dose regions far from the isocenter between RapidArc plans and verification plans if subarcs are used in the verification plan. Subarcs may utilize a different primary volume of interest (PVOI) for the calculation than the full RapidArc field. To minimize differences when subarcs are used for the verification plans, use 2.5 mm dose calculation resolution or less (1 mm is optimal). More information on the PVOI: *Eclipse Photon and Electron Algorithms Reference Guide*.



Note: Portal dose prediction can be used only for comparing the predicted portal dose images with the measured portal dose images. Portal dose prediction is supported only for Varian treatment units.

Portal Dose Prediction Calculation

Portal dose prediction in Eclipse enables you to predict the portal dose of a treatment plan for pre-treatment verification without using patient data, which is especially useful in the case of IMRT and VMAT plans. The patient or the couch are not modeled in the prediction. You can calculate portal dose prediction in connection with creating a verification plan.

A portal dose image is a 2D dose distribution measured by the detection plane of an electronic portal imaging device. The imaging device is used to acquire a portal dose image during the irradiation for the measurement of the dose. The measured and calculated portal dose images can then be compared in Portal Dosimetry. The comparison is done using the absolute mode.

Portal dose prediction in Eclipse supports DMLCs.

The algorithm used for the portal dose prediction calculation is selected in the Calculation Models tab of the Info window. The configuration of the algorithm is done in Beam Configuration.

More information about the algorithm: *Eclipse Photon and Electron Algorithms Reference Guide*. Information on using Beam Configuration: *Beam Configuration Reference Guide*.

Splitting Arc Fields in Sub-Fields During Verification Plan Creation

You can split arc fields into smaller arcs during verification plan creation, and define the desired size for the arcs in degrees. If necessary, new control points are added to the fields for splitting. However, the last arc that is created may be smaller than defined. The following rules are designed to minimize the creation of very small arcs:

- If an arc field is split into two arcs only, then the arcs that are created should be of equal size.

- If an arc field is split into more than two arcs, the last arc can be smaller than the other arcs. If the size of the last arc will be smaller than 2.0° or if it is smaller than 50% of the other arcs, then the last arc is added to the second last arc. If the control point distance is larger than 2.0° , then the control point distance determines the smallest arc size allowed. If this causes the arc count to be two, then the arcs are split into equal sized arcs.

Avoidance sectors are always attached to an adjoining split arc field in the verification plan. This prevents the creation of split arc fields that consist entirely of an avoidance sector, and have no dose. In addition, if the number of monitor units in a split arc field is smaller than the configured minimum MU, the split arc is attached to an adjoining split arc.

If a small arc does not contain any gantry speed or dose rate variation, a warning is shown in the plan approval phase about MLC type mismatch. You can ignore this warning. These fields will not be recognized by 4DITC as VMAT fields, but they will be recognized as arc dynamic fields.

Siemens mARC fields are not split into smaller arcs during verification plan creation. Instead, static fields are created for each optimization point. Static fields are also created for each MLC aperture where multiple MLC apertures share a single optimization point.

Determining the Couch Shifts for Patient Treatment

To facilitate correct patient setup during treatment, you can use Eclipse to communicate the couch shifts required in the treatment room. You can use Eclipse to calculate the required couch shifts automatically from the DICOM origin or the user origin defined in the image referenced by the plan. If the field isocenters do not coincide with the user origin, Eclipse can calculate the relative couch shifts, or the delta couch shifts, from the user origin to the treatment isocenter(s).

The calculated and manually determined couch shifts are shown and can be edited in the Delta Couch Shift Editor. You can also modify and clear the automatically calculated couch shift values in the editor.

You can open the Delta Couch Shift Editor separately to determine the shifts, or use the editor in connection with planning approval (you need to have the Show Delta Couch Editor upon Plan Approval setting selected in RT Administration). In the approval wizard, you can only calculate and clear delta couch values; you cannot edit the values.

More information on RT Administration: *RT Administration Reference Guide*

The delta couch shift values are included in:

- DICOM import
- DICOM export of planning approved plans

- DICOM export of treatment approved plans

Delta couch shift values are not included in:

- DICOM export of unapproved plans
- DICOM export of planning approved plans when shifts are inconsistent

The couch shift values defined in the Delta Couch Shift Editor and the directions of the shifts are printed on treatment reports, and will be shown in Treatment Preparation and 4D Console (this requires 4D console version 10.0 or higher). The values are also shown in the Field Properties dialog box.

Delta Couch Shift values are retained for copy/pasted plans. But if they become inconsistent due to a change in the isocenter of a field, a message will be printed on treatment reports and shown in the approval wizard (when the Show Delta Couch Editor upon Plan Approval setting has been selected in RT Administration). The message is also shown when exporting approved plans with DICOM. If you get this message, make sure that your couch shift values are correct.

Related Topics

[Using User Origin for Calculating Couch Shifts](#) on page 69

Delta Couch Shifts in Treatment Reports

The calculated couch shift values and directions are printed on treatment reports per each isocenter in the plan. If the couch shift values are not defined, they do not appear in the treatment report. The shifts are printed in numerical values (for instance, Shift [cm] 9.20). The directions are shown verbally together with a graphical representation:

Table 34 Delta Couch Shifts on Treatment Reports

Report Text	Graphic	Description of the Direction
Right		Graphic printed out if the couch is to be moved to the right.
Up		Graphic printed out if the couch is to be moved up.
Left		Graphic printed out if the couch is to be moved to the left.
Down		Graphic printed out if the couch is to be moved down.

Report Text	Graphic	Description of the Direction
In		Graphic printed out if the couch is to be moved towards the gantry.
Out		Graphic printed out if the couch is to be moved away from the gantry.

If you enter couch shift values different from the calculated values in the Delta Couch Shift Editor, a related message is printed in treatment plan reports.

Planning Approval Wizard

Planning approvals for external beam plans are given using the Planning Approval wizard. The wizard first validates the plan and notifies about inconsistencies that might prevent the delivery of the plan on the treatment unit. If the plan contains multiple fractionations, all fractionations are included in the planning approval. In addition to granting the plan the Planning Approval status, you can perform the following actions in the Planning Approval wizard:

- Review the dose prescription and 3D dose statistics for the plan target volume.
- Review, calculate and clear the delta couch shift values.
- Create live DRR images
 - A live DRR image is created for each field that does not yet have one. The DRRs are automatically aligned correctly. The DRR is used as a reference image for the field, if no reference image has been defined for it before.
- Include the outlines of the selected structures in the live DRR images. The structure outlines will be visible as layers in ARIA RTM applications.
- Define the planned SSD for the fields in photon plans.
- Calculate the treatment time for the fields in photon plans.
- Split large IMRT fields containing multiple carriage groups into smaller fields or retain them as single fields, depending on the treatment unit.



CAUTION: Changes made to the original plan will not be conveyed to a new copy of the original plan or vice versa.

Related Topics

[Calculation of the Treatment Time](#) on page 481

Plan Approval Statuses

Depending on their approval statuses, plans are dealt with in different ways.

Unapproved Status

The Unapproved status of a plan refers to a plan used for planning the treatment of a patient. Unapproved plans are unlocked in the database, which means that they are fully modifiable.

Rejected Status

The Rejected status of a plan refers to a plan that has been created as a potential candidate but rejected for actual use in treatment. Similarly to Unapproved plans, Rejected plans are unlocked in the database, which means that they are fully modifiable.

Reviewed Status

The Reviewed status of a plan refers to a plan that has typically been initially verified, but still requires further approvals. Similarly to Planning Approved plans, Reviewed plans are locked in the database, which means that they cannot be changed without first changing the plan status to Unapproved or making a copy and editing the copy.

Planning Approved Status

The Planning Approved status of a plan refers to a plan approved by a qualified specialist that is intended to be used for the treatment of a patient.

External beam plans must further be scheduled and given the Treatment Approval status to use it for the actual patient treatment.

Planning Approved plans are locked in the database, which means that they cannot be changed without first changing the plan status to Unapproved or making a copy and editing the copy. None of the dose-relevant properties can be modified once the status has been changed to Planning Approved. However, properties that do not affect the dose can be modified.

Each photon field has two SSD values: planned SSD and calculated SSD. When giving a plan the Planning Approved status, these values are treated in a particular way: the calculated SSD values are either copied to the planned SSD values and you can accept them or type in new values, or for fields that have a planned SSD, you are prompted to confirm whether it should be kept.

Treatment Approved Status

The Treatment Approved status of a plan refers to a plan approved by a qualified specialist that is intended to be used for the treatment of a patient.

Limited changes are allowed to Treatment Approved plans in treatment planning (changes to imager and couch related parameters). To make treatment planning related changes to the plan, you first need either to unapprove the plan, or make a copy of the plan and edit the copy, or create a plan revision of the original plan and edit the revision.

Limited changes are also allowed to external beam plans outside External Beam Planning.

3rd Party Approval

The 3rd Party Approval status refers to a plan with approval status in its DICOM data, imported into the system. The status of a 3rd Party Approved plan can be changed to Unapproved or Planning Approved. They are also locked in the database, and managed in the same way as Planning Approved plans. 3rd Party Approved plans must be Planning Approved (in ARIA RTM or Eclipse) before they can be Treatment Approved.

Related Topics

- [Post-Approval Changes to Plans in External Beam Planning](#) on page 486
- [Plan Revisions of External Beam Plans](#) on page 487
- [Default Photon and Electron Field Parameters](#) on page 180

Plan Approval Status Icons in Treatment Planning

Each plan approval status is marked with an icon in the Context window.

Table 35 Plan Approval Status Icons

Approval Status	Modality	Icon
Unapproved	Brachytherapy Plan	
Unapproved	External Beam Plan	
Planning Approved	Brachytherapy Planning	
Planning Approved	External Beam Planning	
Treatment Approved	Brachytherapy Planning	
Treatment Approved	External Beam Planning	
3rd Party Approval	External Beam Planning	

Large DMLC Fields and Approving Plans for Treatment

Due to the characteristics of Varian's DMLC device controller, the LMC divides large DMLC fields into multiple MLC carriage groups. Depending on the capacity of the treatment unit(s) used in a plan, the carriage groups in fields are dealt with as follows:

- Treatment unit can handle fields with multiple carriage groups—You can choose to retain carriage groups as one field or split them into smaller fields (default setting for this option is defined in Task Configuration). The collimator X-jaws and MLC banks move only during beam hold, otherwise they remain stationary. Photon plans are supported.
- Treatment unit cannot handle fields with multiple carriage groups—Carriage groups are split into individual fields and saved to a new copy of the original plan. The new copy will have the Planning Approved status. The status of the original plan changes to Rejected. If you are approving a plan sum, the original plans are removed from the plan sum, and the new plans are added to the plan sum. Photon plans are supported.

Define the Default Field Split Option for Large IMRT Fields

1. Choose Tools > Task Configuration.
2. Select the **Large Field IMRT** tab.
3. To split large IMRT fields (containing multiple carriage groups) into smaller fields when the plan is approved for treatment, select the **Split large IMRT fields in Eclipse** check box. To retain large IMRT fields, clear the check box.



Note: This setting is clinic-wide; it affects all workstations that are connected to the same database.

4. To finish, click OK.

Calculation of the Treatment Time

This information applies to photon plans.

The treatment time of a plan is calculated from the MU and the dose rate of the plan, using a treatment time factor:

$$\text{Treatment time} = \text{Treatment time factor} \times \frac{\text{MU}}{\text{Dose rate}}$$

For VMAT treatments the treatment time is calculated as the sum of treatment time in each segment. For each segment (the section between two successive machine control points) it is calculated whether delivering the monitor units or rotating the gantry takes longer:

Equation 4

$$\sum_{i=0}^n \max\left(\frac{MU_i}{MaxDoseRate}, \frac{Angle_i}{MaxGantrySpeed}\right)$$

where

i	=	runs through all the segments
MU	=	the monitor units in segment i
MaxDoseRate	=	the maximum dose rate of the field
Angle	=	the gantry rotation in the segment
MaxGantrySpeed	=	the maximum gantry speed of the machine



Note: This equation applies only to Varian treatment units.

Changing the Treatment Unit in a Plan

Sometimes it is necessary to change the treatment unit in a plan for different reasons. The treatment unit to be used in the actual patient treatment may not be known when the planning process is started. The change may also be called for if the original treatment unit is unavailable for scheduled treatments and treatment unit becomes suddenly unavailable for patient treatment (for reasons such as treatment unit break-down, treatment unit or system upgrades, or installing new parts). In these cases, the plans scheduled for that machine need to be re-planned with another machine to enable rescheduling and continuing the treatment.

Related Topics

[Changing the Treatment Unit for Fields](#) on page 198

Changing the Treatment Unit to an Equivalent Machine

ARIA RTM allows changing the treatment unit for an equivalent machine in the course of a treatment without recalculation. Equivalent machines are treatment units having the same, or equivalent, configuration with each other. You can freely transfer a treatment from one equivalent machine to another without changing the original plan. This is possible in External Beam Planning, Treatment Preparation, and Plan Parameters. You can define which treatment units are interchangeable in treatment by creating Equivalent Machine Groups in RT Administration.

Changing the treatment unit to an equivalent machine is possible for plans with a calculated dose, or plans in reviewed or approved state.

Changing the treatment unit to an equivalent machine creates a new plan revision of the original plan. The revision is an exact copy of the original plan, and it will retain the original dose and approval status. Any scheduled treatment sessions are also retained. The original plan is set to Retired status, and its entire approval history is retained.

The following preconditions apply for the plan and are checked by Eclipse when you change the treatment unit to an equivalent machine:

- The plan is calculated or in reviewed or approved state.
- For photon plans that are unapproved and do not have a calculated dose, the Change Treatment Units function is used.
- The treatment unit for all fields is the same.
- In photon plans the fields can use multiple energies within the same treatment unit.
- The original treatment unit and the equivalent machine belong to the same group of equivalent machines and use the same beam data. The equivalent machine must be in Active state.
- The equivalent machine contains dosimetric equivalents for all accessories, and the accessories are in Active state.
- The dose rate in the equivalent machine supports the primary fluence and energy mode combinations used in the plan.

Related Topics

[Changing the Treatment Unit for Fields on page 198](#)

Change the Treatment Unit to an Equivalent Machine

Changing the treatment unit to an equivalent machine is possible for plans with a calculated dose, or plans in a reviewed or approved state.

1. In the Scope window, select the plan and choose **Planning > Change Treatment Units**.



Note: If the plan is unapproved and does not have a calculated dose, the dialog box opens to change the treatment unit to any user-selected treatment unit. This will require re-calculating the dose.

2. From the list of equivalent machines, select the one you want to use and click **Convert**.

You can view remarks, errors and warnings regarding the checks performed in the Message log box.

3. To confirm the creation of a new plan revision from the original plan, click **OK**.

Converting the Plan for Another Treatment Unit

The Plan Conversion feature makes changes in the source plan to best replicate the calculated dose when using another treatment unit. You can also convert a plan between treatment techniques (for example, convert a VMAT plan to an IMRT plan). The tool is trying to reproduce the DVH of the original plan using the selected treatment unit. After the plan conversion, you need to evaluate and approve the plan normally.

The plan conversion creates a new plan revision of the source plan and sets it to the Unapproved state. The dose distribution is calculated automatically using fixed MU, and the normalization mode is set to No Normalization. Any setup fields or scheduled treatment sessions are deleted. The revision will retain the dose per fraction information. The comment field of the converted plan contains a reference to the source plan. The converted plan is deleted if there is an error in the dose calculation, or if you abort the dose calculation.

The original plan is not touched; it will retain the original plan information.

The following preconditions apply for the plan and are checked by Eclipse when you convert a plan for another treatment unit:

- The plan contains a calculated dose.
- Dose/fraction is defined.
- The plan approval status is one of the following: Planning Approved, 3rd Party Approved , or Treatment Approved.
- All fields in the plan are photon fields.

- All fields in the plan use the same treatment unit.

Plan sums, cone plans and workflow supported plans cannot be converted for another treatment unit.

The treatment unit used in plan conversion must meet the following requirements:

- The treatment unit has one active MLC configured.
- MLC and the collimator jaws have symmetric operating limits.
- The MLC leaves move in the X direction as in the IEC61217.
- Any non-fixed collimator jaws support asymmetric collimator jaw positions.
- IMRT is supported.

Convert a Plan for Another Treatment Unit

1. In the Scope window, select the plan to be converted and choose **Planning > DVH Based Plan Converter**.
2. In the Treatment Unit list, select the treatment unit for which the plan should be converted.
3. If you are converting a VMAT plan to an IMRT plan, enter the number of fields in the **IMRT fields** box.
4. Enter the number of planned fractions.

The value can be between 1 and the number of non-treated fractions in the original plan.

5. Select dose relevant structures used in the conversion. The plan will be optimized for the new treatment unit to meet the DVH of the selected structures as close as possible.

Ensure that the volume types of the structures are correctly defined. Check if the source plan uses the same couch structure as the couch on the treatment unit of the converted plan. If not, it is possible to copy the structure set after the plan conversion and replace the existing couch structure with the correct one.

6. To view the conversion log, click **Show conversion log**.
7. Click **OK** to convert the plan.

The plan is converted, dose distribution is calculated and the converted plan is saved. The name of the converted plan is appended with a running number.

8. Evaluate the plan for approval.

Review the plan to verify that the conversion is correct. Pay attention to the target, critical structures, and collision prevention.

9. The original plan including the plan scheduling will remain untouched. Once you have verified the converted plan, make sure that you retire the original plan and that you schedule the correct number of fractions for the converted plan.

Chapter 23 Re-Planning

Post-Approval Changes to Plans in External Beam Planning

In some treatment planning cases, it may become necessary to edit existing plans to reflect changes during the patient treatment. These cases include the following:

- Approved plans originating from External Beam Planning: If the modifications required for the plan affect the dosimetry, the volumetric dose must be re-calculated and the plan re-evaluated in External Beam Planning. These can include plans based on 4D image data that represent different time phases in patient motion, such as respiration motions.
- Approved plans originating from a 2D planning application (such as Treatment Preparation): Planning is continued in External Beam Planning to acquire volumetric dose.

To make changes to an approved plan (with Planning Approved or Treatment Approved status) in External Beam Planning, you need to make a new copy of the approved plan and edit the copy, or create a new plan revision. Using plan copies is also a good way of distinguishing dosimetric changes from patient setup changes.



Note: *If the plan has been Treatment Approved but the actual patient treatment has not yet been started, you can also make modifications to the plan in External Beam Planning by opening the plan and changing the status of the plan to Unapproved.*

Related Topics

[Plan Revisions of External Beam Plans](#) on page 487

Post-Approval Changes to Plans outside External Beam Planning

If the modifications do not require re-calculation of the volumetric dose, the plan can be modified outside External Beam Planning. The changes allowed are limited to the following:

- Couch parameters
- Field setup notes
- Plan and image scheduling of the plan
- The treatment unit used in the plan for a dosimetrically equivalent machine

If treatment has already been started, it is only possible to exchange the treatment unit for a dosimetrically equivalent machine. To make changes to couch parameters, field setup notes or plan and image scheduling, you need to change the Treatment Approval status to Planning Approval.

In addition, for Planning Approved plans for which treatment has already been started, it is possible to make changes to setup fields.

Related Topics

[Plan Approval Statuses](#) on page 478

[Creating Setup Fields](#) on page 210

Post-Approval Changes to Setup Fields

Limited changes are possible to setup fields in Planning Approved plans for which treatment has already been started. These changes to setup fields will not invalidate the dosimetric data of the plan, and no plan revision is created after these changes. The following changes are allowed:

- Adding new setup fields (insert new setup fields or create setup fields from treatment fields).
- Editing setup fields (which have not been used for imaging).
- Deleting setup fields (which have not been used for imaging).

No changes are allowed to setup fields that have been used for imaging. This means that any setup fields that have some other images than reference images attached to them cannot be changed.

Plan Revisions of External Beam Plans

You can create new revisions of treatment approved plans in the database. New plan revisions are exact copies of the original plans, and they automatically have the Unapproved status. The original plan is set to the Retired state when a revision is created. No changes are possible to Retired plans. You can open and use the plan revisions in exactly the same way as any other plans.



Note: A plan revision of a photon plan has the same planned SSD value as the original plan. When you approve the plan revision after it has been modified, you can select whether to keep the calculated SSD or the original planned SSD.



Note: When you create a new plan revision, always verify the field weights and plan normalization mode.

Plan revisions are identified by their plan ID, which consists of two parts separated by a colon, for instance, Prostate:1, in which Prostate is the plan ID of the original plan, :1 marks the revision. You can freely modify the IDs of plan revisions, but it is recommended to use a colon in the ID to indicate that it is a plan revision. If the purpose is to create a completely new plan from the revision, it should also be completely re-named to avoid confusion.



Note: If you create a new plan revision of a treated plan in Eclipse, ARIA RTM applications, ARIA RTM Workflow Management components or 4D Treatment Console, the status of the original plan is automatically set to Retired. Eclipse displays the originally planned number of fractions as the number of fractions for Retired plans. Treatment Preparation displays the delivered number of fractions as the number of fractions for Retired plans. If a Retired plan is used as a base dose plan for IMRT optimization or in a plan sum, its contribution will be the originally total planned dose, not the delivered dose.

Create a Plan Revision

1. In the Scope window, right-click the treatment approved plan from which you wish to create a new revision.
2. Choose **Create Plan Revision**.

The original plan is set to Retired state, and it is no longer possible to make changes to it.

Chapter 24 Exporting and Importing Plans

Exporting and Importing Plan and Image Data

To be able to import or export data to another system, configure export filters for all data formats you need to use, for instance, DICOM.

When using the Vidar, Matrox or Bitmap filters to transfer data, choose **Quicklinks > DICOM > Import Export**.

More information on using the DICOM Import Export: *DICOM Import and Export Reference Guide*.

With other filters, use the Export/Import wizard to import or export data, such as images, structure sets, plans, plan sums, and dose data.



NOTICE: When importing structures or structure sets , the structures that are not compatible with the Eclipse or BrachyVision internal data model are discarded, which can cause missing structures (for instance, structures defined on non-equidistant slices or outside the image area, or minuscule structures). It is recommended to use equidistant slices in imaging, and always visually verify any imported structures.

In DICOM import, the electron density relative to water is converted to a CT value and assigned automatically to the structure. If you do not want to use the automatically assigned CT value, clear the Assign CT Value selection for each structure.

When importing an IHE-RO geometric plan, it is possible that the treatment unit data for some fields is missing. In this case, a virtual treatment unit is used for that field in Eclipse. For this purpose, one treatment unit can be marked as a virtual treatment unit in RT Administration. Note that a plan with a virtual treatment unit cannot be approved.



WARNING: Before transferring a plan to treatment, make sure that all necessary approvals have been obtained for the plan and that a qualified medical professional has reviewed the intended treatment plan and plan parameters in their entirety.



NOTICE: When working with stereotactic plans, it is advisable to give plans Treatment Approval before exporting them to the OGP system. The Treatment Approval locks the plan in the database, which will prevent making changes to the plan after the export to OGP. Changes made in plans after the export in Cone Planning are not automatically reflected in the plans in OGP. Such changes include, for example, changes in the treatment order of fields.



Note: Before exporting data, check the following:

- Verify all data before exporting it.
- You can check that the structure set is IHE-RO compliant (Integrating the Healthcare Enterprise – Radiation Oncology). To check the IHE-RO compliance of a structure set, select the structure set and choose **Planning > IHE-RO Compliance > IHE-RO Structure Set**.
- You can check that an external beam plan is a compliant IHE-RO geometric plan. To check the IHE-RO compliance of a plan, choose **Planning > IHE-RO Compliance > IHE-RO Geometric Plan**.
- You can check that an external beam plan is compliant with IHE-RO advanced RT objects interoperability. To check the compliance, choose **Planning > IHE-RO Compliance > IHE-RO Advanced RT Objects Interoperability**.

Related Topics

[Configuring Import and Export Filters](#) on page 536

Export Options

Export as IHE-RO Geometric Plan

Eclipse fulfills the requirements for IHE-RO Geometric Planner, and you can export external beam plans as IHE-RO Geometric Plans. This option is available only if the plan you are exporting is IHE-RO compliant. If the plan is non-compliant or if the plan type is not supported, this option is grayed out.

Include Structure Set

You can select whether to include the structure set in the exported plan.

Include Reference Images in Export

For external beam plans, you can include reference images (such as DRRs) linked to fields in the exported plan data. You can also choose to include structure outlines, generated during the export, with the reference image.

Dose Export

You can export the total plan (volumetric) dose separately or with other plan data. The dose is exported either as absolute or relative dose, and in accordance with the DICOM standard.

In External Beam Planning and Plan Evaluation, you can also export the dose distribution on the active plane separately with the **Export Dose Plane** command.

Planar Dose Details in Export

You can export the dose on the viewing plane currently shown in the active image view either in the absolute or relative mode. The export is done in accordance with the DICOM standard.

You can determine the resolution of the dose by defining the lengths of the sides of the dose matrix in X and Y directions and the number of pixels inside the dose matrix.

For external beam plans, you select the field with which the dose matrix is aligned. If the field central axis (CAX) is not parallel to the active image view, the center of the matrix is placed to the intersection of the field CAX and the image view. If the image view and the field CAX are parallel, the center of the matrix is positioned to the projection of the field isocenter.

You can also mark the corners of the image with high dose pixels for correct alignment of the dose image and set the selected export parameters as default for exported plans.

DVH Export Details

A DVH is exported in accordance with the DICOM standard, along with the volumetric dose and the plan. The options for DVH export are:

- DVH Structures: Structures to have the DVH calculated and exported. You can also include or omit structures for which the DVH has been partially calculated. By default, the DVH is calculated for all structures, and all structures are included in the DVH export.
- Dose bin width: Resolution of the DVH, expressed in Gy for absolute dose and in percentage for relative dose. The range for this value is 0–10 exclusive.
- DVH type
- Dose unit
- Volume unit: Unit of measurement in which the volume of the structures included in the DVH are expressed.

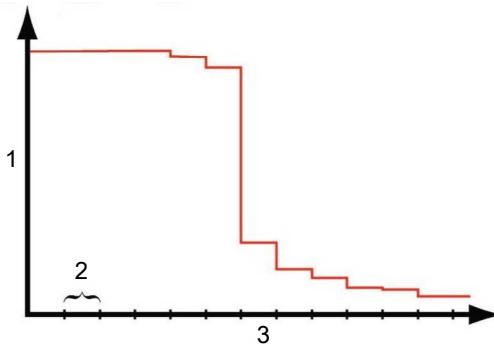


Note: The DVH can be exported only with the volumetric dose.

DVH Dose Bin Width Parameter

The dose bin parameter defined in the export expresses the resolution of the DVH calculated during the export. The parameter is defined in Gy or percentage, depending on the dose mode.

For external beam plans, the dose bin interval is equidistant for the entire DVH curve as shown in the figure.



1. Volume axis
2. Dose bin width
3. Dose axis

Figure 149 Dose Bin Width Parameter for External Beam Plans

Export the Dose Plane

1. In an image view, display the desired viewing plane.
2. In the Focus window, right-click the dose and choose **Export Dose Plane**.
3. Define the dose export options and click **Next**.



Tip: To set the selected export parameters as default for exported plans, click **Set as Default**.

4. Select the appropriate export filter and click **Next**.
5. Check the items to be exported.
6. To save the dose plane data to the defined export directory, click **Finish**.

Perform film dosimetry. You can align the dose image with the film using the corner marks.

Exporting IHE-RO Compliant Plans

IHE-RO (Integrating the Healthcare Enterprise – Radiation Oncology) is an initiative that promotes the integration of healthcare systems.

Eclipse fulfils the requirements for the following IHE-RO actors: contourer, geometric planner, dosimetric planner and dosimetric displayer. Eclipse also fulfils the Advanced RT Objects interoperability IHE-RO profiles. Before you export structure sets and plans, you can check that they are IHE-RO compliant.

When you check the IHE-RO compliance of a structure set, the application verifies that:

- The structure set is defined in an image that does not have interpolated image planes. If the image has interpolated planes, a new structure set and image with no interpolated planes are created.
- The structure set is defined on CT slices.
- All the structures have RT ROI interpreted types set.
- All the structures have their generation algorithm set. If the algorithm is missing from a structure, it is set to Manual.
- None of the structures is empty.
- None of the structures has more than 100 contours per plane. If necessary, the number of contours is reduced to 100.

When you check the IHE-RO compliance of a geometric plan, Eclipse verifies that:

- The plan is not a brachytherapy or proton plan.
- The plan has a structure set assigned.
- No electron energies are used.
- None of the fields have MUs or reference point doses defined.
- No wedges, compensators or boluses are used.
- None of the fields is an arc field or has more than two control points.
- All the blocks are divergent and the outlines have been defined.
- None of the fields has more than one aperture block outline.
- All fields have setup technique defined.

When you check the IHE-RO compliance of advanced RT objects interoperability, Eclipse verifies that:

- The plan is not a brachytherapy or proton plan.
- The plan has a valid structure set assigned.
- Plan intent is defined.
- The primary reference point of the plan has a location.
- All fields have a valid dose to the primary reference point, setup technique, isocenter location, energy mode, dose rate, collimator, couch and gantry rotation angles, SAD, SSD (if the setup technique is fixed SSD), monitor units (if there is either a motorized wedge or an Omnidrive in the field), and contain no more than 8 blocks (in DICOM each block contour is counted as a separate block).
- All compensators have a valid tray, slot, source to tray distance, material, transmission matrix, and thickness matrix.
- All blocks have a valid tray, slot, source to tray distance, material, and material thickness.

More information on Eclipse or BrachyVision IHE-RO support: IHE-RO Integration Statement document available on www.varian.com.

Related Topics

[Exporting and Importing Plan and Image Data](#) on page 489

Exporting Data with DICOM

The application uses the methodology defined in the DICOM (Digital Imaging and Communications in Medicine) standard to transfer image, structure, plan, dose and DVH data to another system. The purpose of the standard is to standardize the communication of therapeutic information, such as radiotherapy images and therapy plans, between devices that produce different image formats.

How the application conforms to the standard is defined in Varian System Server DICOM Conformance Statement (go to http://www.varian.com/us/oncology/services_and_support/resources/dicom_statements.html).

The transferred data includes the following, depending on the plan:

- Field data:
 - Isocenter positions
 - Field accessories
 - Gantry, collimator and couch rotation
 - Vertical, longitudinal or lateral position of the couch
 - Field fluences
 - Treatment unit ID
- Dose data:
 - Relative or absolute field doses, or relative or absolute plan dose
 - DVH data for selected structures
- Structure set data:
 - Structure set includes physical structures, markers, the isocenter marker, and registration points. In export, the assigned CT value of a structure is converted to an electron density relative to water.
- Image data.

The imported DICOM images can be linked to different types of fields in an external treatment plan as follows:

- Portal images—To session fields or fields
- DRR images—To fields



Note: With DICOM, note that to achieve a reliable result in the transfer, the treatment unit configuration must be exactly the same in both the source and destination system.

In DICOM export, the electron density curve of the connected scanner is used to convert the assigned HU value to an electron density. If the image of the structure set is not connected to a scanner, the electron density curve of the default scanner is used instead. If the electron density curve of the default scanner is not available, the HU assignment is not exported and a warning is written to the export log. Also, if the HU value is outside of the calibration curve, the assignment is not exported and a warning is written to the export log.

In DICOM import, the electron density curve of the connected scanner is used to convert the electron density to an HU value. If the image of the structure set is not connected to a scanner, the electron density curve of the default scanner is used instead. If the electron density curve of the default scanner is not available, the HU assignment is not imported and a warning is written to the import log. Also, if the electron density is outside of the calibration curve, the assignment is not imported and a warning is written to the import log.

Transform a DICOM File to an ASCII File

Files exported from Eclipse for photon plans in the DICOM format can be converted into the ASCII format using the Dcm2Ascii.exe application, which saves the converted files to the defined folder, over the network or locally. The input file must be in the Implicit VR Little Endian Uncompressed format, which is the format used in Eclipse. The Dcm2Ascii.exe application cannot be used to read data that uses the Explicit VR Little Endian Uncompressed format.

1. To start the ASCII converter, navigate to the directory that contains the Dcm2Ascii.exe file.
2. Double-click the file.
3. Select the input file, output options and output directory.
4. Click **Apply**.

Exporting Plan Data for Clinical Trials

The ATC (Advanced Technology Consortium), a multi-institutional cooperative organization for cancer research, collects treatment histories to be used as the basis of analyses and reports from the members.

You can export RT data (image and plan data) from the application to participate in the ATC studies. To be able to complete the export, you need the ITC DICOMPiler application (3rd party software). The export is done in the DICOM format, and the data is then modified for the ATC in DICOMPiler, which creates the DICOM file set required. To transfer the DICOM file set, the data must be copied to a transfer medium (CD or FTP server). You also need to configure the DICOM Storage Service SCU filter.

For more information on the ITC DICOMpiler application, refer to Varian Installation Instructions, ITC DICOMpiler Software Installation Guide and ITC DICOMpiler Quick Start Guide. The ITC DICOMpiler documentation is available at the ITC website (<http://itc.wustl.edu>). For an FTP account, contact the ITC at ict@castor.wustl.edu or go to the ATC website or the ITC website.

The ATC sets the following restrictions for plans and images exported for ATC studies:

- Image orientation must be HFS (head-first-supine).
- Contours must be closed. Point contours or open-ended line contours are not supported.
- Plans must contain a primary reference point with a location, the volumetric dose must be calculated, at least one valid dose prescription and valid plan treatment percentage must be found in the plans.

If these restrictions are not fulfilled in the plan and images to be exported, the Export wizard shows warnings concerning the unacceptable parts.



Note: *Ultrasound images or Boolean structures cannot be exported for the ATC.*

Export Planning Data for Clinical Trials in DICOM Format

Make sure that you have the DICOMpiler program installed and that it is running. If DICOMpiler is not running, start it by double-clicking ITC_DICOMpiler.exe. In the ITC DICOMpiler window, start the Receiver by clicking **Run DICOM Receiver**.

1. Choose **File > Export > Wizard with ATC DICOM Checks**.
2. Select whether to export the plan or the images and click **Next**.
3. Define the export options and click **Next**.
4. Check any remarks about the export and click **Next**.
5. In the Configured Export Filters list box, select the appropriate filter for the export and click **Next**.
6. Check the items to be exported.
7. To remove data from the list, select them and click **Remove Selected Object(s)**.
8. To save the selected data to the defined location, click **Finish**.
9. Transfer your files to the ATC via an internet-based transfer, such as FTP.

Import Plan Information

This information does not apply to Vidar, Matrox or Bitmap filters. To transfer data using Vidar, Matrox or Bitmap filters, choose **Quicklinks > DICOM > ImportExport**.

More information on using the DICOM Import Export: *DICOM Import and Export Reference Guide*.

1. Choose **File > Import > Wizard**.
2. Select the appropriate import filter and click **Next**.
3. If the data is located in separate subdirectories, select the **Scan subdirectories** check box.
4. Select the data to be imported from the appropriate directory.
5. Click **Next**.
6. Select the target patient to whom to import the data or create a new patient.
7. You can connect the images to the object hierarchy under the selected patient either automatically or by hand. To let the wizard automatically import the data to the selected patient, select the **Try automatic import** check box.
8. Click **Next**.

Automatic import: The wizard closes after the automatic import is completed.

Import by hand: The wizard proceeds to the next step.

9. Do one of the following:
 - If the data has gray indicators in the tree structures in the Import Data and ARIA Data panes, you need to connect the data to the object hierarchy under the selected patient. To do this, drag the data from the Import Data pane to an appropriate place under the patient in the ARIA Data pane. Click **Finish** to close the wizard.
 - If the data has green indicators in the tree structure, click **Finish**.

Exporting and Importing Fluences in DICOM Files

You can export fluences in the DICOM format along with other data exported through the DICOM export, using the Export wizard. All data in the fluence export is stored as distinct DICOM files, one main file containing references to the other files. You can convert the export files into the ASCII format using the RT2ASCII converter for word processing or spreadsheet applications. You can import the separate ASCII file containing the fluence back into Eclipse.

You can also import optimal fluences into the active DMLC field in ASCII format. If the active field contains an optimal fluence, it is replaced by the imported fluence. The MLC plan—including actual fluences—in the active field is removed, and the dose is invalidated for the active field.



Note: When transferring DMLC plans to treatment:

- Always make sure that a qualified person verifies the prescriptions on the MLC viewing station, or do phantom testing before starting the treatment.
- Verify the plan with DVH analysis before transferring it to the treatment unit.
- Always make sure that you use the same treatment unit for treating a patient as you used for creating the plan.

DICOM Fluence Export File

For all fields included in the exported plan, the following information is included in the DICOM export file:

- Optimal fluences
- Actual fluence
- DMLC parameters (both DMLC and conformal arc treatments), collimator jaw settings, collimator rotation, and gantry rotation
- Portal dose prediction
- Dynamic tolerance information



Note: When exporting fluences, note that:

- Plan-specific volume optimization objectives are not included in the DICOM export file.
- The fluence data is exported using the DICOM Compensator definition with an extension to the Compensator Type attribute.
- Carriage group information is not included in the export file.

DICOM Fluence Import File (ASCII)

The import format for the optimal fluence is the following.

Table 36 Fluence Import File

Header	Meaning
SizeX	Number of fluence elements in field X-direction
SizeY	Number of fluence elements in field Y-direction
SpacingX	Resolution of the fluence elements in field X-direction, in mm
SpacingY	Resolution of the fluence elements in field Y-direction, in mm
OriginX	Location of the first fluence element center in X-direction in relation to the field central axis, in mm. X-position coordinates increase towards X2 jaw.
OriginY	Location of the first fluence element center in Y-direction in relation to the field central axis, in mm. Y-position coordinates increase towards Y2 jaw.

Header	Meaning
Data	<p>Fluence values for each element. Values are separated by spaces, tabs or new line characters. Fluence values are listed for increasing X and secondly for increasing Y positions. Position of the nth fluence element center point in relation to the field central axis expressed in millimeters is:</p> $\text{PosX} = \text{OriginX} + \text{SpacingX} * [(n-1) \bmod \text{SizeX}]$ $\text{PosY} = \text{OriginY} - \text{SpacingY} * [(n-1) \bmod \text{SizeY}]$

Below is an example of the ASCII-format fluence import file defining $1.0 \times 1.0 \text{ cm}^2$ unity fluence on field center.

Table 37 Example of Optimal Fluence Import File

```
#Central 16 fluence elements
#
OptimalFluence
SizeX 10
SizeY 10
SpacingX 2.50
SpacingY 2.50
OriginX -11.25
OriginY 11.25
Values
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
0.0 0.0
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
0.0 0.0
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
0.0 0.0
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
0.0 0.0
0.0 0.0 0.0 1.0 1.0 1.0 1.0 0.0
0.0 0.0
0.0 0.0 0.0 1.0 1.0 1.0 1.0 0.0
0.0 0.0
0.0 0.0 0.0 1.0 1.0 1.0 1.0 0.0
0.0 0.0
0.0 0.0 0.0 1.0 1.0 1.0 1.0 0.0
0.0 0.0
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
0.0 0.0
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
0.0 0.0
0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
0.0 0.0
```

Export Fluences with DICOM

Click **Next** to proceed after each step in the Export wizard.

1. Choose **File > Export > Wizard**.
2. Select the **Plan** option.
3. Select the **Include fluences** check box.
4. Select the DICOM Media File Export filter.
5. Click **Finish** to complete the export.

Importing Fluences in ASCII Files

You can import a fluence file that has been created earlier for a patient to the selected field. You can use imported fluence files to verify the dosimetry of individual DMLC fields in a phantom.



Note: When importing fluences, note that:

- The plan contains one fractionation.
- The optimal fluence file format is comma-delimited ASCII.
- The optimal fluence does not contain information about MLC type used to generate it.

The fluences and DMLCs in other fields in the plan are unaffected.

Import Fluences in ASCII Files

Click **Next** to proceed after each step in the Import wizard.

1. In the Focus window, right-click the field to which to import the fluence and choose **Import Optimal Fluence**.
2. Navigate to the location of the ASCII file containing the optimal fluence and click **Open**.

Exporting and Importing MLC/DMLC Plans

The MLC or DMLC data to be imported must exist in the Varian MLC file format (refer to MLC File Format Description for the Multileaf Collimator). The supported file format is H and above.



Note: Actual fluences are removed from the imported DMLC data. The icon in the Focus window under each relevant IMRT field indicates that the actual fluence is not calculated. Actual fluences are calculated during the dose calculation.



Note: When approving DMLC plans for treatment:

- Always make sure that a qualified person verifies the prescriptions on the MLC viewing station, or perform phantom testing before starting the treatment.
- Verify the plan with DVH analysis before transferring it to the treatment unit.
- Always make sure that you use the same treatment unit for treating a patient as you used for creating the plan.

The MLC Plan export stores the MLC or DMLC leaf data in an ASCII export file which you can then transfer to Varian MLC workstations. Each export file can contain one DMLC carriage group.



Note: When exporting MLC or DMLC data, note that:

- Structures are not exported with the MLC.
- Always verify the MLC before exporting it.
- DMLCs can currently be exported only to Varian MLC systems. DMLC export for non-Varian MLCs is not supported.

Export an MLC or DMLC File

1. In the Focus window, select the MLC or DMLC to export.
2. Choose **File > Export > Export MLC Plan**.
3. Define the location for saving the MLC/DMLC export file.
4. Type a new name for the MLC file if necessary.
5. Click **OK**.

Import an MLC or DMLC File

1. In the Focus window, select the field to import the MLC or DMLC into.
2. Choose **File > Import > MLC Plan in varian MLC Format**.
3. Select the appropriate MLC type and click **OK**.
4. Locate the import file.
5. Select the MLC file to be imported.
6. Click **Import** to add the MLC to the plan.

Processing of Data in the Export to Virtual Simulation

The Export to Virtual Simulation function generates the coordinates of the isocenter, field aperture and MLC aperture of the selected field(s) in the active plan and saves the coordinates to an export file or files, which are transferred to the laser alignment system and used to mark the field coordinates on the patient's skin.

The coordinate systems used in the export to virtual simulation depend on the laser alignment system as follows:

- 3 adjustable laser axes: All points are relative to the origin of the laser alignment system. No CT coordinate system corrections are done for the Y and Z (IEC 61217) axes.
Points other than the isocenter can be marked only in LAP CT-1-4 and A2J.
- 2 adjustable laser axes: The selected isocenter points are exported. The Y coordinates (IEC 61217) of the isocenter positions are exported in the coordinate system of the CT scanner; the X and Z coordinates (IEC 61217) are relative to the origin of the laser alignment system.
- 1 adjustable laser axis: The selected isocenter points are exported. The Y and Z coordinates (IEC 61217) of the isocenter positions are exported in the coordinate system of the CT scanner; the X coordinates (IEC 61217) are relative to the origin of the laser alignment system.

Virtual Simulation with Gammex

When using a Gammex laser alignment system, notice the following:

- The device does not have 3D capability.
- The device cannot show points on the patient's back (in supine orientation). Because of this, the field coordinates to be marked must be frontal.
- The CT scanner couch position is always set manually by moving the CT couch to the correct position in relation to all field coordinate points.
- In Gammex 5.0 file format, the coordinates are expressed in millimeters instead of centimeters.

Gammex Laser Alignment System Parameters

Dialog box for configuring the virtual simulation interface when using Gammex laser alignment systems.

Table 38 Configuration Parameters for Gammex

Parameter	Description
Default Export Directory	Defines the path of the directory where the exported field coordinates are saved. If you select the Start lasers automatically check box, the file name is fixed to be AUTORUN.CTS, otherwise the file name is prompted for during the export process.
Browse	Navigates to the location of the directory where the exported field coordinates are saved.

Parameter	Description
Markup	Defines the interval at which the lasers are moved to show each exported point. Value 0 indicates that laser positions are changed manually.
Markup delay <n> seconds (0=manual)	
Start lasers automatically	Turns the lasers on automatically after the field coordinate export.
Data Interface	Selects the interface to the Gammex system.

Virtual Simulation with LAP

When using a LAP CT4 laser alignment system, notice the following:

- The device cannot show points on the patient's back (in supine orientation). Because of this, the field coordinates to be marked must be frontal.
- The transversal lasers can only move 60 cm, and the device cannot show points located further than 60 cm from the first scanned image. Using fields exceeding this distance may result in a warning message.
- The CT couch must be manually moved to the position indicated by the field coordinates on the first slice. For subsequent points, the CT couch moves automatically.
- Eclipse calculates all virtual simulation coordinates using the reference plane position, which is taken to be the first CT image regardless of where the first CT image is located in the imaged CT set. This means that it is no longer necessary to manually move the CT couch to the first image slice position to define the reference plane for LAP CT-1-4. Note that since the movement span of the transversal lasers is 60 cm in LAP CT-1-4, the device cannot show points located outside this span. Using fields exceeding this span may result in a warning message.

LAP Laser Alignment System Parameters

LAP devices allow transfer of data either via FTP, shared directories or a serial port. The shared directories method is recommended. However, if FTP data transfer is selected, the Eclipse workstation must be configured as an FTP server. The FTP service must be enabled when Eclipse is running.

Table 39 Configuration Parameters for LAP

Parameter	Description
Serial Port	Defines a serial port as the method of data transfer from Eclipse to LAP. Selection activates a drop-down list for selecting or typing in the name of the serial port. The serial port can be one of the predefined selections COM1–COM4 or any other port.

Parameter	Description
File	Defines a file as the method of data transfer from Eclipse to LAP. Selection activates a text box for defining the directory path and file name and the Browse command button for navigating to the location of the file. The default file name is LAPDATA.LAP.
Data Interface	Selects the interface to the LAP system.

Virtual Simulation with A2J

When using a A2J laser system, notice that Eclipse does not convey whether the points are located on the left or right side of the patient. When marking skin points, always check the green ceiling laser to make sure which side of the patient the points are.

A2J Laser Alignment System Parameters

Dialog box for configuring the virtual simulation interface when using A2J laser alignment systems.

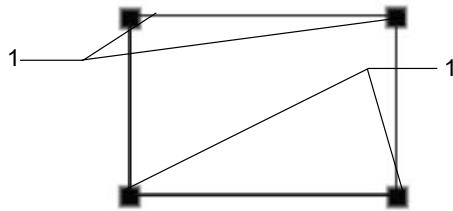
Table 40 Configuration Parameters for A2J

Parameter	Description
File	Defines a file as the method of data transfer from Eclipse to A2J. Selection activates a text box for defining the directory path and file name and the Browse command button for navigating to the location of the file. The default file name is a2jdata.txt.
Data Interface	Selects the interface to the A2J system.

Marking the Field Coordinates in the Virtual Simulation Export

The coordinates of the field isocenter, field aperture, and field central axis on the patient's skin are marked with points by using a laser alignment system as follows:

- The isocenter is shown for markup first using all lasers. After that, the lasers show the subsequent points, either one at a time or all at the same time, depending on the laser alignment system.
- Static fields: Each corner formed by the field aperture is marked with a point, altogether four points (see the figure), and the field central axis on the patient's skin is marked with one point. You can choose to use none or all of these points to mark the field.
- Arc fields: The field apertures at arc angles defined in the export are marked (at, for instance, 10, 20, 30 and 40 degrees).



1. Points used to mark static field.

Figure 150 Field Coordinate Points for Static Fields



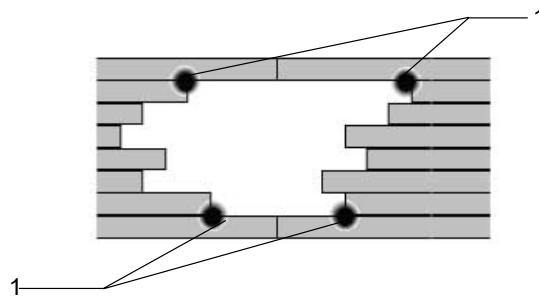
Note: *The use of the Gammex system is recommended only for marking the isocenter on the patient's skin, because it does not accept laser control information. However, if you wish to use the Gammex system for displaying skin points, manually turn off all lasers except the green one while viewing the Review display.*

Some laser alignment systems sort the field coordinates in the export file and do the markup in a particular way, depending on the virtual simulation interface. The field coordinates are sorted according to the isocenters and saved either in one single export file or multiple export files. In laser alignment systems that save the isocenter coordinates in separate files, the fields are sorted according to the isocenters so that fields with the same isocenter are consecutive. Interfaces that require moving the CT table manually in the Y-axis direction further sort the points in each field by the Y-axis direction.

Marking the MLC Aperture in the Virtual Simulation Export

MLC apertures are marked with four points that mark the intersection points of the beam and the patient's skin at the corners of the MLC aperture as follows:

- Static fields: For the first and last open leaf pair (see the figure).
- Static arc fields (static MLC): At arc angles defined in the export (at, for instance, 10, 20, 30 and 40 degrees).
- Conformal arc fields (Dynamic MLC): For each segment of the conformal arc field. The number of segments is defined in the MLC Properties dialog box.



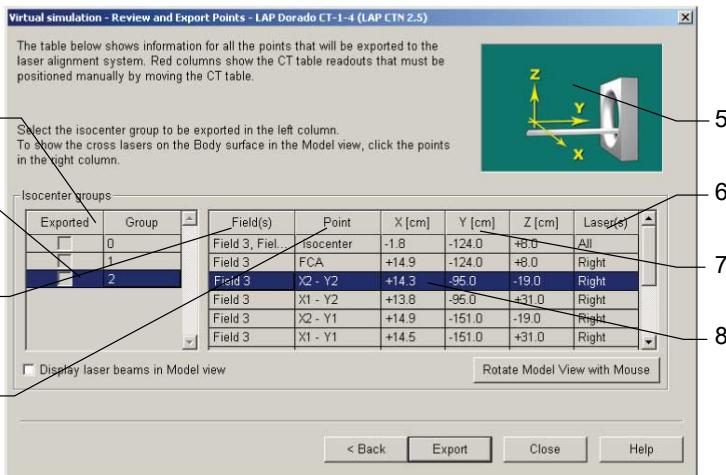
1. Points used to mark an MLC.

Figure 151 MLC Points in Field Coordinate Export

Reviewing the Laser Markings in the Virtual Simulation Export

You can review the laser beams as simulated projections and the cross lasers marking each point on the patient model in the Model view before starting the export to virtual simulation. The laser beams are shown in the Model view using special color-coding.

In the Virtual Simulation wizard, you can also review all transferred points together with the field and aperture data, the active lasers used to display the skin points, and the coordinates of the transferred points. The figure shows the page of the Virtual Simulation wizard where you can review the laser markings before the export.



1. Isocenter groups to be exported
2. Select the row of a group to view its information in the table
3. Field(s) from which the points in the selected group originate
4. Characterization of the points (isocenter, FCA = field central axis on skin, field aperture corner)
5. Diagram showing the directions of the coordinate axes on the current CT device
6. Laser(s) to be activated to show each point
7. Coordinates of the points on the X-, Y- and Z-axis
8. Select the row of a point to view the field and the cross lasers for the point in the Model view

Figure 152 Virtual Simulation Wizard Point Review Page

Isocenter grouping is only shown for laser alignment systems that sort field information per isocenter in the export file. The information in the columns of the axes along which the couch must be moved manually is shown in red.

You can also review and simulate the lasers after the export is complete.

The figures show the laser projections in the Model view.

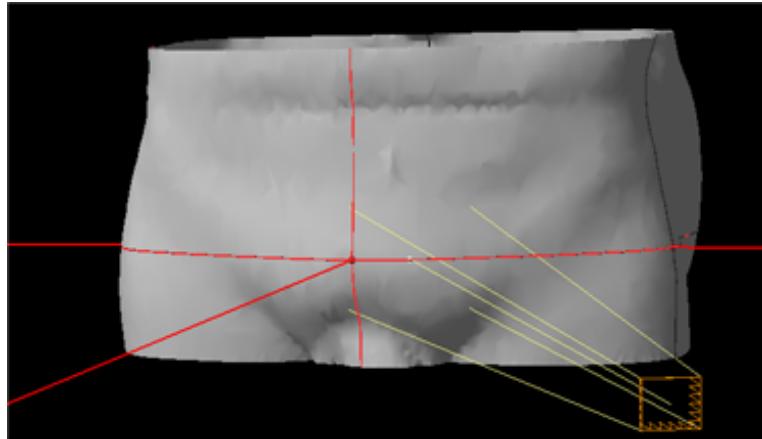


Figure 153 Isocenter Cross Laser and Laser Beam Review in Model View

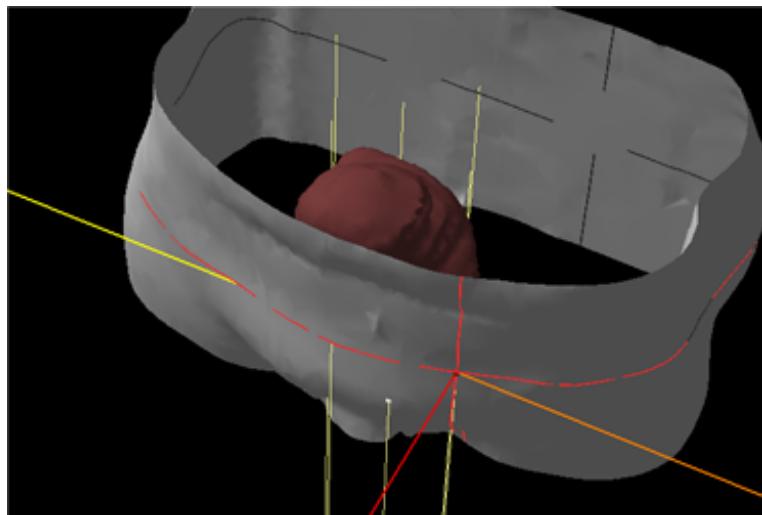


Figure 154 Field Aperture Cross Laser and Laser Beam Review in Model View

The following color coding is used in the Model View:

- Red: Active lasers

At the laser alignment system, only one of the lasers is activated for marking the skin points, but all lasers are activated for marking the isocenters (or entry points for fixed SSD fields).

- Yellow: Inactive lasers that intersect the patient's skin in an unacceptable position in relation to the point being displayed

- Orange: Lasers made inactive because they intersect the patient's skin at an excessively narrow angle (under 45°)

Configure the Laser Alignment System and CT Scanner

1. Choose Tools > Workstation Configuration.
2. Select the **Virtual Simulation** tab.
3. Select the laser alignment system to be configured.
4. To define the parameters for the selected laser alignment system, in the Virtual Simulation Hardware group box, click **Configure**.
5. Define the desired laser alignment system parameters and click **OK**.
6. To define the parameters for the CT scanner device, in the CT Scanner group box, click **Configure**.
7. Define the desired CT scanner parameters and click **OK**.

These settings apply to the workstation you are using.

Related Topics

[Gammex Laser Alignment System Parameters](#) on page 502
[LAP Laser Alignment System Parameters](#) on page 503

CT Scanner Parameters

Dialog box for configuring the CT scanner properties for virtual simulation.



Note: *In certain imaging protocols, the center of the CT image does not match the center of the CT scanner isocenter. This could happen, for example, if zooming is used in CT imaging. Always carefully check that the laser alignment system points to the correct position.*



Note: *In the virtual simulation process, the Eclipse Laser System is aligned either to the Dicom Origin or to the CT Center Pixel. Alignment to CT Center Pixel means that the CT scanner isocenter is in the center of the CT image which is then aligned to the Laser System. However, the CT Scanner protocol may shift the CT image in a way that the center pixel of the image is no longer the CT isocenter. This may occur for example if the scan region is defined arbitrarily from a scout image. Ensure with sufficient testing that patient markings are accurate for a variety of reconstructed field views, scan regions, or other CT scanner protocol selections which may affect the co-location of the CT Center Pixel and the CT scanner isocenter.*

Table 41 Configuration Parameters for CT scanner

Parameter	Description
CT Isocenter	Defines how the CT isocenter X-Z projection (IEC 61217) is determined. The CT isocenter can be projected to the image slice midpoint (Defined by pixel data center option) or to DICOM position (0,0) (Defined by DICOM origin option).
CT Table	Defines the CT couch settings.
Table in/out direction increases towards gantry / Table up/down direction increases up	Defines the in/out readout of the CT couch to increase when the couch is moved towards the gantry of the CT scanner, or the up/down readout of the CT couch to increase when the couch is moved upwards.
Table in/out direction can be zeroed / Table up/down direction can be zeroed	Specifies whether the CT device supports zeroing the in/out or the up/down readout of the CT couch.
Unit of table position display	Selects the unit of CT couch position readouts on the display panel(s). Possible values are mm or cm.
Patient Reference Plane	Reference plane is the transversal zero plane check box for specifying that the Y-coordinates of the image slice at the reference plane is zero.

Chapter 25 Printing Plan Information

Using Print Templates

You can save your print settings as a template after which these settings will be available for all workstations. You can also modify existing print templates, delete them from the server, and define a default template for your workstation.



Note: When using print templates note that:

- At least one printer must be defined for your workstation.
- Print templates are not available for plan sums.

The print settings of each template include both item-specific print settings as well as printer-specific options.

It is possible that print templates created before version 8.6 do not work with version 8.6 or later. This is affected by changes in printer drivers and operating system upgrades. It is recommended to verify all existing print templates after upgrading to a newer version of the product, or updating printer drivers and the operating system. To use older shared print templates, open the template in version 8.6 or later, refresh the print settings and save the template again.

Related Topics

[Print Settings for Active Image Views](#) on page 515

Print Setup Dialog Box

This information applies to DVH, Treatment Report, BEV, Model View, 2D View, Arc Plane View and Brachy QA Prints.

In the Print Setup dialog box you can select the printer to use and define some printer-specific settings, for example the paper size and orientation. You access the dialog box by clicking the Print Setup button in the Print Using Templates dialog box.

You can define more advanced settings for the printer by clicking the **Properties** button. The settings vary depending on the selected printer. You can, for example, define the number of copies to print, the paper size, and color or monochrome printing. Note that the selected printer and printer driver determines where these settings are changed. For more information and instructions for using your particular printer(s), refer to the printer's user documentation.



Note: The final appearance of the print-out is determined by combination of printer options you select both from the Print Setup dialog box (for example, scaling) and from the printer-specific settings (for example, pages per sheet or scaling). For example, if you select 50% scaling in the Print Setup dialog box and then 50% scaling in the printer-specific settings, the image size on the final print-out will be one fourth (1/4) of the original.



Note: When printing treatment reports, the paper size is defined by the treatment report template. In other words, the paper size definitions you make in printer settings will be ignored by the application (excluding, for example, the situations where the printer cannot support the A3 paper size). If you, for example, want to print a treatment report using the Full.tml or BrachyFull.tml layout and you set A3 as the paper size in printer settings, the application will print the report in the A4 size since this has been defined as the paper size to be used in the treatment report template.

DICOM Prints

When you select the DICOM print item in the Print Using Templates dialog box and click the Print Setup button, the dialog box that is dedicated to DICOM prints only opens. In the dialog box, you can set margins for your print-outs and define the number of copies to be printed. Print-outs are printed to a specific printer supported by the DICOM protocol. The printers shown in the Name box must have been configured beforehand (**Tools > DICOM Print Configuration**).

Create a New Print Template

1. Choose **File > Print > Using Templates**.
2. If there already are templates in the Print templates list, select a template that suits your needs and modify its settings. If the template list is empty, go directly to the Print items list.
3. In the **Print Items** list, define the print item(s) and the related settings for the new template.

Example: If you want to create a template that produces a DVH print-out and uses a local printer, select the DVH check box in the print items list and click **Print Setup**. In the Print Setup dialog box that opens, select the desired printer and click **OK**. Check that other print item settings also suit your needs.

4. To save these settings as a template, click **Save as**.
5. Give a name for the template and enter a description into the **Comment** box (for example, indicate which local printer you selected for this template).

The Location and Modified from boxes indicate where this information will be saved and from which workstation the changes were made.

6. Click **OK**.

7. The template you created appears in the Print templates list.

Other users are now able to use this template, to modify and override its settings or to create a new template based on these settings.



Note: If you created a new template based on an existing one, it now seems in the Print Using Templates dialog box as if the settings of the original template were changed, too. This is, however, not the case. When you click **Cancel** to close the dialog box and open it again, you can see that the settings of the original template remained unchanged and the new template now contains the settings you saved.

Related Topics

[Print Settings for Active Image Views](#) on page 515

Modify a Print Template

1. Choose **File > Print > Using Templates**.
2. Select the template that you want to modify.
3. Select or clear the check box of the print item and modify the settings as needed. After that do one of the following:
 - To print without saving the changes, click **Print**. The application will not store the changed settings.
 - To override the current settings and to save the changes prior to printing, click **Save**. Then print the image(s) with the newly defined settings.
 - To create a new template based on the changes you made, click **Save as**. Then print the defined information.

Saving the new template with an existing file name will override the existing template.

Related Topics

[Create a New Print Template](#) on page 512

Set a Default Print Template

1. Choose **File > Print > Using Templates**.
2. To define a template as the default template for your workstation, select a print template from the Print templates list and click **Set as Default**.

The default template is now indicated with (Default) next to its name in the Print templates list.

After this, when the print template dialog box is opened on this workstation, this template will be selected by default.

Delete a Print Template



Note: The template is deleted from the server, not only from your workstation. Carefully consider deleting templates, since other users may still be using them.

1. Choose File > Print > Using Templates.
2. To delete a template, select it from the print templates list and click Delete.
The application does not warn you about deleting the template.

Updating Customized Treatment Report Templates for Unicode

To ensure that your customized treatment report templates and brachytherapy brief report templates support Unicode correctly, you need to convert all of them for Unicode. In a multisite system, you need to convert all templates in all locations where the templates are located.



Note: Print reports are disabled in the application until the templates have been converted. The conversion must be performed only once. If you have no customized templates, no conversion is needed.

The conversion of templates to support Unicode is done using the ConvertTml tool, which converts multi-byte TML files (such as Japanese or Chinese) into Unicode. The ConvertTml tool is located in ..\Program Files (x86)\Varian\Vision\13.0\Bin64\ConvertTml.exe. The tool reads the character set from the OSP setting System Code Page. If the result is not correct, you can define the character set in question by using switches in the conversion command.

Table 42 Switches in ConvertTml

Switch	Use of Switch
/chinese	Multi-byte TML or DAT files
/japanese	Multi-byte TML or DAT files
/latin	Single-byte TML or DAT files with non-ASCII characters (for instance, Swedish)

The ConvertTml tool creates a backup of the original file(s): <file name>.tml.backup, or <file name>.dat.backup. However, it is recommended to create a backup all print templates prior to the conversion.

Update Customized Treatment Report Templates for Unicode

1. Open Command Prompt.
2. Move to the folder where your customized treatment report templates are stored, for instance, to the following locations:
 - External beam and proton plans: ..\va_data\$\ProgramData\Vision\VD\
 - Brachytherapy plans: ..\va_data\$\ProgramData\Vision\BT\In a multisite system, templates may be stored in a number of locations.
3. Type in convertttml and name of the .tml file. If necessary, add the appropriate explicit switch. You can also use wildcards (ConvertTml *.tml).
If you type convertttml custom.tml, the custom.tml file will be converted to Unicode.
If you type convertttml /chinese *.tml, all .tml files in the current folder will be converted from Chinese to Unicode.



Tip: To check which switches are available, type in convertttml.

4. If you have a multisite system, repeat the above steps to run the convert utility against all templates in all locations where the templates are stored.

Print Settings for Active Image Views

Print templates are only available in External Beam Planning.

When printing images from the system (either with or without print templates), you can define various settings for each print item. These settings are available for each print item both with and without a template. With print templates, printer-specific settings like the number of copies etc., are defined in a specific print setup dialog box.

- DVH settings
- BEV settings
- Arc Plane view settings
- Model view settings
- 2D view settings
- DICOM settings

DVH Settings for Printing

Table 43 DVH Settings

Item	Option	Description
Layout	Printing with a template: Various options.	Printing with a template: Check that a suitable report template is selected. Printing without a template: The selection is always disabled.
Description		This box is always disabled.
Print comment		A description shown in the upper part of the print-out (below patient information).

BEV Settings for Printing

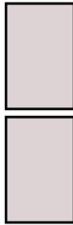
Table 44 BEV Settings

Item	Option	Description
Fields(only available with print templates)	Selected field	Prints the BEV image of the selected field only.
	All fields	Prints the BEV image of all fields.
Plot distance from focus	Source to Skin Distance (SSD)	Prints the image to 1:1 scale at the SSD.
	Source to Axis Distance (SAD)	Prints the image to 1:1 scale at the SAD.
	Source to block distance (SBD)	Only available with print templates: Prints the image in 1:1 scale at the SBD.
	Other (cm)	Prints the image in 1:1 scale at the distance defined in the text box.

Item	Option	Description
Page layout	Use X x X pages	<p>Define the number of pages used horizontally and vertically. For example:</p> <ul style="list-style-type: none"> ■ Entering 1 x 2 produces a separate header page and two image pages as follows: 
		<ul style="list-style-type: none"> ■ Entering 2 x 1 produces a separate header page and two image pages as follows: 
	Automatically arrange on multiple pages	The print-out is arranged on multiple pages (produces a separate header page and divides the image on several pages).
Include in print	Draw lines as black	Prints lines black, for example, field lines.
	Separate page for header	Prints the textual information and the image on separate pages.
	Print comment	A description shown in the upper part of the print-out (below patient information).

Arc Plane View Settings for Printing

Table 45 Arc Plane View Settings

Item	Option	Description
Fields (only available with print templates)	Selected field (only available if the active field is an arc field)	Prints the Arc Plane view of the selected field only.
	All arc fields	Prints the Arc Plane view of all fields.
Scale	Fit to page	The application zooms the image on the selected number of pages.
	Scale (%)	Define the zoom ratio (%).
Page layout	Use X x X pages	Define the number of pages used horizontally and vertically. For example:
		<ul style="list-style-type: none"> ■ Entering 1 x 2 produces a separate header page and two image pages as follows: 
		<ul style="list-style-type: none"> ■ Entering 2 x 1 produces a separate header page and two image pages as follows: 
	Automatically arrange on multiple pages	The print-out is arranged on multiple pages (produces a separate header page and divides the image on several pages).

Item	Option	Description
Include in print	Field summary	Prints field information above the image.
	3D image	Prints a CT image in the active view.
	Use white background	Prints the image on a white background.
	Draw lines as black	Prints lines in black, for example, field lines.
	Separate page for header	Prints the textual information and the image on separate pages.
	Print comment	A description shown in the upper part of the print-out (below patient information).

Model View Settings for Printing

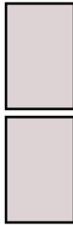
Table 46 Model View Settings

Item	Option	Description
Scale	Fit to page	The application zooms the image on the selected number of pages.
	Scale (%)	Define the zoom ratio (%).

Item	Option	Description
Page layout	Use X x X pages	<p>Define the number of pages used horizontally and vertically. For example:</p> <ul style="list-style-type: none"> ■ Entering 1 x 2 produces a separate header page and two image pages as follows: 
		<ul style="list-style-type: none"> ■ Entering 2 x 1 produces a separate header page and two image pages as follows: 
	Automatically arrange on multiple pages	The print-out is arranged on multiple pages (produces a separate header page and divides the image on several pages).
Include in print	Field summary	Prints field information above the image in External Beam Planning.
	Draw lines as black	Prints lines, for example field lines or reference lines, in black.
	Separate page for header	Prints the textual information and the image on separate pages.
	Print comment	A description shown in the upper part of the print-out (below patient information).

2D View Settings for Printing

Table 47 2D View Settings

Item	Option	Description
Views (only available with print templates)	Selected view	Prints a 2D image of the selected view only.
	All displayed views	Prints a 2D image of all displayed views separately.
Scale	Fit to page	The application zooms the image on the selected number of pages.
	Scale (%)	Define the zoom ratio (%).
Page layout	Use X x X pages	Define the number of pages used horizontally and vertically. For example:
		<ul style="list-style-type: none"> ■ Entering 1 x 2 produces a separate header page and two image pages as follows: 
		<ul style="list-style-type: none"> ■ Entering 2 x 1 produces a separate header page and two image pages as follows: 
	Automatically arrange on multiple pages	Let the application decide the number of pages used (produces a separate header page and divides the image on several pages).

Item	Option	Description
Include in print	Field summary	Prints field information above the image in External Beam Planning.
	Draw lines as black	Prints lines, for example field lines or reference lines, in black.
	Separate page for header	Prints the textual information and the image on separate pages.
	3D image	Prints a CT image in the active view.
	Use white background	Prints the image on a white background.
	Print comment	A description shown in the upper part of the print-out (below patient information).

Related Topics

[Print Setup Dialog Box](#) on page 511

Information in Print-Outs of Active Views

The print-outs of active views contain textual and graphical information about the items visible in the view at the moment of producing the print-out.

In addition, print-outs done in External Beam Planning or Plan Evaluation also contain field information. If the active view contains hidden fields, a caution is included in the print-out stating that the hidden field and field accessory outlines are not included in the print-out. You can display the field accessory of a hidden field by selecting the accessory in the Focus window.

Textual Information in Print-Outs of Active Views

The textual information in the print-out of an active view depends on the application from which it is produced.

Table 48 Textual Information in Header

Information printed	Module
Patient's name and identification codes 1 and 2	All
Hospital	All
Last modification date and time of the plan and the name of the modifier	All

Information printed	Module
Image comment: Text typed in the Comment tab of the Image Properties dialog box.	All
Comment: Text typed in the Print View dialog box	All
Plan Comment: Text typed in the Comment tab of the Plan Properties dialog box	External Beam Planning Plan Evaluation Brachytherapy Planning
	Note: Hidden field and field accessory outlines not included in the printout!
Course identification code	External Beam Planning Plan Evaluation Brachytherapy Planning
Plan identification code	External Beam Planning Plan Evaluation Brachytherapy Planning
Image series name	Contouring More information on Contouring: <i>Registration, SmartAdapt and Contouring Instructions for Use or Registration, SmartAdapt and Contouring Reference Guide</i>
Image identification code	All
Visible image identification code	External Beam Planning Contouring Plan Evaluation Brachytherapy Planning
Plan normalization value	External Beam Planning Plan Evaluation
Calculation grid	External Beam Planning Plan Evaluation Brachytherapy Planning

Information printed	Module
Maximum dose in the plan (if calculated)	External Beam Planning
	Plan Evaluation
	Brachytherapy Planning
Maximum and minimum dose in PTV (if calculated)	External Beam Planning
	Plan Evaluation
	Brachytherapy Planning
Mean dose in PTV (if calculated)	External Beam Planning
	Plan Evaluation
	Brachytherapy Planning

Table 49 Textual Information in Footer

Information printed	Module
Patient's name and identification code	All
Course identification code	External Beam Planning
	Plan Evaluation
	Brachytherapy Planning
Plan name and identification code	External Beam Planning
	Plan Evaluation
	Brachytherapy Planning
Image series name	Contouring
	More information on Contouring: <i>Registration, SmartAdapt and Contouring Instructions for Use or Registration, SmartAdapt and Contouring Reference Guide</i>
Image identification code	Contouring
Printed image plane (not shown in Model view or BEV prints)	All
Plotting distance (shown only in BEV prints)	External Beam Planning
Arc viewing angle	External Beam Planning
	Plan Evaluation
Scaling factor	All
Patient treatment orientation	All

Information printed	Module
Offset of the image user origin from the DICOM origin and user origin comment, if defined	All
Application name and version	All
Date and time	All
Page number	All
Grid size (if grid is on)	All

Graphical Information in Print-Outs of Active Views

Print-outs produced of an active view contain the same graphical information as on screen. Items not visible on screen are not included in the print-outs.

Table 50 Graphical Information in Image View Print-Outs

Graphical Information	Module
Patient orientation indicator	All
Coordinate axes indicator	All
Image scale indicator	All
Orientation labels	All
Grid (if grid is on)	All
Structure outlines	All
Image origin	All
Reference points	All
Markers	All
Field outlines	External Beam Planning Plan Evaluation
Field isocenter (coplanar fields) or field central axis – viewing plane intersection (non-coplanar fields)	External Beam Planning Plan Evaluation
Arc angle indicator	External Beam Planning Plan Evaluation
Wedge indicator	External Beam Planning Plan Evaluation
Bolus, block, and MLC projections	External Beam Planning Plan Evaluation

Graphical Information	Module
Compensator	External Beam Planning
	Plan Evaluation
Isodose curves or color wash	External Beam Planning
	Plan Evaluation
	Brachytherapy Planning
Dose maximum point	External Beam Planning
	Plan Evaluation
Structure 3D models	External Beam Planning
	Plan Evaluation

Field Information in Print-Outs of Active Views

If the **Field summary** check box is selected in the Print View dialog box, the field information lines are printed between the header and the image. Also the field information of the hidden fields is included in the print-out when the active view contains hidden fields.

Table 51 Textual Information in Field Information Lines, External Beam Planning

Print-Out Text	Description
Field ID	Field identification code
Technique	Field technique
Machine	Treatment unit name
Scale	Treatment unit scale
Energy	Treatment unit energy mode
Wedge ID	Wedge identification code
Weight	Field weight
X1 [cm] X2 [cm]	Field size in X direction; if symmetric, only one number is shown
Y1 [cm] Y2 [cm]	Field size in Y direction; if symmetric, only one number is shown
Gantry Rtn [deg]	Gantry rotation in degrees. For arc fields, shows the gantry start angle and stop angle in degrees, and the rotation direction (clockwise or counterclockwise). If the start angle or stop angle is in the extended area, "E" is shown after the degree.
Coll Rtn [deg]	Collimator rotation angle
Couch Rtn [deg]	Table rotation angle

Print-Out Text	Description
X [cm]	Isocentric: Isocenter X-coordinate Fixed SSD: Field entry point
Y [cm]	Isocenter Y-coordinate Fixed SSD: Field entry point
Z [cm]	Isocenter Z-coordinate Fixed SSD: Field entry point
SSD [cm]	Source-to-Skin Distance
MU/Timer setting	Monitor Units or timer setting (for Cobalt treatment units); if there are two or more fractionations, the field is empty.

Print a DVH

1. Display the DVH graph in the Dose Volume Histogram view.
2. Right-click in the Dose Volume Histogram view and choose **Print DVH Report**.
3. Select the printer to use.
4. Select the number of copies to print.
5. Type a print comment for the DVH, if desired.
6. To preview the graph before printing, click **Preview**.
7. To print the DVH graph, click **OK**.

Use DICOM Print

1. Choose **File > Print > DICOM Print**.
2. Define the print settings as necessary.
3. Click **OK**.

Related Topics

[DICOM Settings for Printing](#) on page 528

DICOM Print

DICOM prints are available for fields and setup fields in External Beam Planning and Plan Evaluation. DICOM prints are scalable to allow film comparison on the light box (comparison of DRR image with simulation or verification image).

The following information is printed in textual or numerical format:

- Patient name and ID
- Course ID
- Plan ID
- Field ID
- Print date
- Collimator, gantry and couch settings

The following information is printed in graphical format as overlays, if selected to be printed:

- Collimator jaws
- Field accessories
- Structure outlines
- Field graticule
- Layers in the reference image (DRR), if any

The DICOM printer can be configured as necessary. More information: RT and Imaging Online Help.



Note: When using DICOM print the printer needs to be carefully configured in order to print images in correct scale. Check the printer configuration by printing a test image with an object of known dimensions in X and Y directions.

Related Topics

[Information in Print-Outs of Active Views](#) on page 522

[Using Print Templates](#) on page 511

DICOM Settings for Printing

When using a print template, settings like the name, the number of copies and margin definitions can be found in the Print Setup dialog box.



Note: When using DICOM print the printer needs to be carefully configured in order to print images in correct scale. Check the printer configuration by printing a test image with an object of known dimensions in X and Y directions.

Table 52 DICOM Settings

Item	Option	Description
Fields	Selected field	Prints a DICOM image of the selected field only.
	All fields	Prints a DICOM image of all displayed fields separately.
Scale	Fit to page	Let the application zoom the image on the selected number of pages.
	Scale (%)	Define the zoom ratio (%).
Page layout	Various options	Define how the image will be divided on pages.
Include in print	Field summary	Prints field-specific information.
	Jaws and wedges	Shows the position of jaws and draws the outline of possible wedges.
	Graticule	Draws the graticule in the image.
	Plan info	Prints plan-specific information, for example, plan ID, field ID, field name.
	Aperture (MLC, blocks)	Shows the aperture of MLC and the outline of possible blocks.
	Structure outlines	Prints the outline of the defined structures.
	Print comment (only available with print templates)	A description shown in the upper part of the print-out (below patient information).

Related Topics

[Print Setup Dialog Box](#) on page 511

Chapter 26 IRREG Planning

IRREG Field Images

Field images are 2D images created in the simulator (including digitized film images), DRR images created in Eclipse or portal images created in connection with the patient treatment. Each field can have multiple field images, for instance, one DRR and one simulator image, of which one can be marked as the reference image. The reference image can be used later in the treatment process in, for instance, 4D Console and Off-line Review for comparing portal images with the reference image.

Field images can be added to fields from among images imported to the Varian system database. After adding a field image, the image must be aligned with the particular field, using a special field image alignment tool.

There are some restrictions as to which images can be used as field images. The images must be RT images (simulation or portal images), and they must contain data about the image detection unit position, image resolution, image SAD, and beam collimator rotation.

Calculating the Dose for IRREG Plans

In IRREG, the Anisotropic Analytical Algorithm (AAA) dose calculation algorithm calculates dose at a given point based on SSD and depth information. The result corresponds to a water phantom measurement at that point with the field perpendicular to the phantom surface which is assumed to be flat. In the case of several fields, the contribution of each field to a given point is calculated independently and added to the total dose at that point. Dose calculation for flattening filter free beams is not supported in IRREG.

For cobalt units, either Anisotropic Analytical Algorithm (AAA) version 13.6, or Pencil Beam Convolution (PBC) dose calculation algorithm version 11.0 or 10.0 must be used.

Information on the distributed calculation framework and instructions for defining global or local dose calculation settings: *Beam Configuration Reference Guide*.

IRREG Reference Point Properties

The following parameters must be defined for reference points to enable dose calculation:

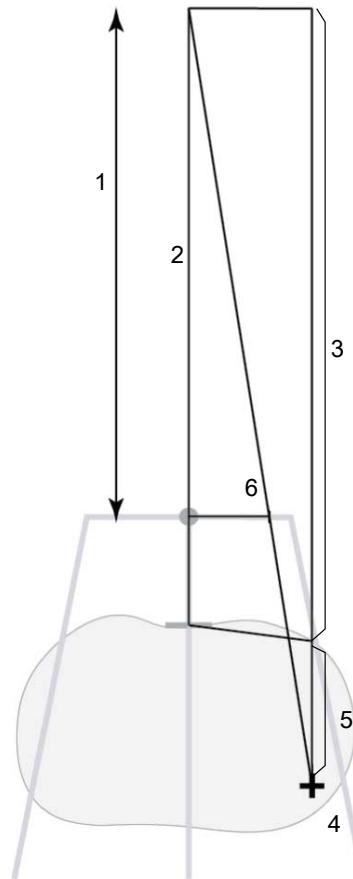
- Location in relation to the field—X and Y coordinate (field central axis is the origin). The locations of the reference points are unique for each field in the plan. Whenever a point is shared by several fields, its X-Y location, depth and SSD values are different in each of the fields.



Note: IRREG Planning uses an internal beam coordinate system in which the X and Y coordinates (projected to the isocenter plane) are the same as those of the IEC 61217 beam limiting system coordinate system, except that the sign of the Y coordinate is inverted.

- Perpendicular Source-to-Skin Distance (PSSD)—Distance from the source to a point on the patient skin. The distance is measured in a geometry where the source is directly above the reference point, and the reference point is thus located on the field central axis.
- Depth from the skin surface.
- Dominant field—Field in which each reference point was originally defined. You can change the X-Y location and the depth of a reference point only in relation to its dominant field. To change the location and depth in relation to other fields, define the PSSD value for the point. The depth and location are calculated from the PSSD value.

The calculation geometry used in IRREG Planning is shown in the figure.



1. Source-to-Axis Distance (SAD)
2. Source-to-Skin Distance at field central axis (SSD)
3. Perpendicular Source-to-Skin Distance (PSSD)
4. Reference point
5. Depth from the skin surface
6. Location (X, Y) of the reference point in relation to the field

Figure 155 IRREG Geometry

Insert IRREG Reference Points with the Digitizer

1. Choose Planning > Enable Digitizer.
2. If necessary, calibrate the digitizer.

3. On the Digitizer toolbar, click the **Digitize Reference Point** tool .
4. Click the reference point on the film with the digitizer mouse.
5. Click each reference point as necessary.

Modify IRREG Reference Points in the Reference Point Properties Dialog Box

1. In the Focus window, select the reference point.
2. Choose **Edit > Properties**.
3. In the General tab, edit the ID and name of the reference point.
4. In the Location tab, define the location in field coordinates.
5. Click **Apply** to view the changes in X-Y location.
6. To accept the changes, click **OK**.



Tip: You can also define the primary reference point, and edit the X-Y location, depth and SSD of the reference points for the active field in the Info Window. For reference points of fields other than the active one, you can only change the SSD value.

Printing IRREG Plans

In IRREG Planning, you can print

- The active view
- Treatment reports

Instructions on printing: *Eclipse Photon and Electron Reference Guide*.

The application contains a few ready-made treatment report templates, determining the layout of and the information included in a treatment report. You can define the layout of the treatment report according to your needs, and include only the information relevant in your environment.

Info Window in IRREG Planning

Fields Tab of the Info Window (IRREG Planning)

The Fields tab of the Info Window is used for viewing and editing the properties of the fields of the active plan.

Table 53 Information in Fields tab

Column	Description
Field ID	Field identification code.
Technique	Field technique (STATIC-F).
Machine/Energy	Name of the treatment unit and its energy mode.
Scale	Scale of the treatment unit.
Gantry Rtn [deg]	Gantry rotation in degrees. If the start angle is in the extended area, "E" is shown after the degree.
Coll Rtn [deg]	Collimator rotation in degrees.
Couch Rtn [deg]	Couch rotation in degrees.
Wedge	Wedge code if used. If not in use, "None"
Field X [cm]	Field dimension in FX direction at the field entry point.
X1 [cm]	The displacement from the field central axis to field edge X1 at the field entry point. Editable only for asymmetrical fields.
X2 [cm]	The displacement from the field central axis to field edge X2 at the field entry point. Editable only for asymmetrical fields.
Field Y [cm]	Field dimension in FY direction at the field entry point.
Y1 [cm]	The displacement from the field central axis to field edge Y1 at the field entry point. Editable only for asymmetrical fields.
Y2 [cm]	The displacement from the field central axis to field edge Y2 at the field entry point. Editable only for asymmetrical fields.
SSD [cm]	Source-to-Skin Distance

Points Tab of the Info Window (IRREG Planning)

The Points tab of the Info Window is used for viewing and editing the properties of the reference points in the active plan, and for defining the primary reference point.

Table 54 Information in Points tab

Column	Description
Ref. Point ID	Reference point identification code.
X [cm]	X-coordinate of the point.
Y [cm]	Y-coordinate of the point.
Depth [cm]	Depth from the skin surface.
PSSD [cm]	Perpendicular Source-to-Skin Distance.
Primary Point	If selected, the dose is prescribed for this point.

Doses Tab of the Info Window (IRREG Planning)

The Doses tab of the Info Window is used for viewing the dose for the reference points in the active plan, and for defining the desired dose for the primary reference point.

Table 55 Information in Doses tab and Individual Fractionation tabs

Column	Description
Field ID	Field identification code.
MU/Timer setting	Total Monitor Units. Timer setting for Cobalt units.
MU/Gy or s/Gy	Monitor Units/Gray. Seconds/Gray for Cobalt units.
Point <n>	Identification code for reference point <n>

Appendix A Import and Export Filters

Configuring Import and Export Filters

This information applies to DICOM filters.

Information on Vidar, Matrox or Bitmap filters: *DICOM Import and Export Reference Guide*.

Import and export filters are needed for transferring information with different file formats from various sources and to a number of destinations. Generally, the filters are configured during system configuration. For detailed instructions, refer to the online help.



Note: You need sufficient user rights to configure Import and Export filters.

Add a New Import/Export Filter

The procedures for adding an import or export filter are identical. In the following, an import filter is added to the system.

1. Choose **Tools > Import/Export Configuration**.
2. Click **Add**.
3. Define whether to make the filter available for the entire site.
Modifications made to such filter in one workstation changes the filter parameters in all the workstations using the filter.
4. Select the appropriate filter and click **Add**.
5. If necessary, type a new identifier.
6. Define the parameters of the filter.
7. Click **OK** to add the filter.



Note: There can be various configurations for a particular import filter. For example you can make two different configurations for a DICOM Media File Filter with different import directories by defining a different name and parameters for the two filters. Name the filters with easily recognizable, descriptive names.

Modify the Import/Export Filter Configuration

In this example, the filter modified is the Dicom Media file filter.

1. Choose **Tools > Import/Export Configuration**.
2. Select an installed filter.
3. Click **Configure**.
4. Define the necessary modifications for the selected filter.
5. Click **OK**.
6. Continue to configure more filters or quit by clicking **Exit**.



Note: There can be various configurations for a particular import filter. For example you can make two different configurations for a DICOM Media File Filter with different import directories by defining a different name and parameters for the two filters. Name the filters with easily recognizable, descriptive names.

Delete an Import/Export Filter

The procedures for removing an Import or Export filter are identical. In the following step list an Import filter is removed from the registry.

1. Choose **Tools > Import/Export Configuration**.
2. Select the filter and click **Remove**.
You are prompted to confirm the deletion.
3. Click **OK**.

Appendix B Keyboard Shortcuts

Application Keyboard Shortcuts

The following tables list keyboard shortcuts for Selection, External Beam Planning, Brachytherapy Planning, Brachytherapy 2D Entry and Plan Evaluation applications.

Table 56 Keyboard shortcuts common to all applications

Shortcut	Action
Alt+Enter	Opens the Properties dialog box of the active object
Ctrl+C	Copies the active object
Ctrl+N	Creates a new patient
Ctrl+O	Opens the Object Explorer. When there is no active patient, opens the Patient Explorer.
Ctrl+P	Prints the active window
Ctrl+Shift+P	Activates printing using templates
Ctrl+S	Saves all data to the database
Ctrl+V	Pastes the copied object (if it can be pasted to the selected place)
Ctrl+W	Automatically adjusts the Window/Level settings
Ctrl+Y	Activates the structure-specific redo operation
Ctrl+Z	Activates the structure-specific undo operation
Del	Deletes the active object
F1	Opens the online help
F4	Starts planning approval
Page Down	Shows the previous imaging plane
Page Up	Shows the next imaging plane

Table 57 Keyboard shortcuts specific to External Beam Planning

Shortcut	Action
Ctrl+Shift+1	Switches to Orthogonal Views and BEV
Ctrl+Shift+2	Switches to Plan Uncertainty View
F3	Opens the Field Weight dialog box
F5	Calculates the dose distribution within the calculation volume

Shortcut	Action
Shift+F5	Calculates the dose distribution with preset values
F6	Calculates the dose distribution on the active plane
Shift+F6	Calculates portal dose
F7	Opens the IMRT Optimization dialog box
Ctrl+F7	Opens the VMAT Optimization dialog box
Shift+F7	Opens the Beam Angle Optimization dialog box
F8	Creates a new plan
F9	Creates a new field
F10	Creates a new opposing field
F11	Calculates the MLC leaf motions

Table 58 Keyboard shortcuts specific to Brachytherapy Planning

Shortcut	Action
Ctrl+Shift+1	Switches to Ortho layout
F5	Calculates the dose distribution within the calculation volume
Ctrl+F5	Calculates the inhomogeneity corrected dose

Table 59 Keyboard shortcuts specific to Brachytherapy 2D Entry

Shortcut	Action
Ctrl+Shift+1	Switches to Entry layout (2 views)
Ctrl+Shift+2	Switches to Entry layout (3 views)

Table 60 Keyboard shortcuts specific to Plan Evaluation

Shortcut	Action
Ctrl+Shift+1	Switches to Two Orthogonal Views
Ctrl+Shift+2	Switches to Two Model/BEV Views
Ctrl+Shift+3	Switches to Multiple Plane Views
Ctrl+Shift+4	Switches to Orthogonal Views and BEV
Ctrl+Shift+5	Switches to showing multiple plans

Appendix C Editing Report Templates

Editing Report Templates

Reports are printed on predefined layouts that are called templates. The templates are .tml files stored to a Report Templates Directory. You can check the location of the Report Templates Directory by choosing **Help** and then choosing to see information about the application. Select **System Info** from the dialog box that opens, and the location of the templates is displayed on Report Templates Directory row.

In External Beam Planning the available templates are Full.tml, DVH.tml, ShortSummary.tml and ShortSummaryTabular.tml. In Brachytherapy Planning, the available templates are BrachyFull.tml, DVH.tml and QAExport.tml.

You can customize the template files or create new templates in a text editor. If you edit the DVH.tml template file, you must save it using the original file name. The Full.tml and BrachyFull.tml templates can be used as examples and they contain the basic instructions on how to edit the templates. In addition, AllVariables.tml and BrachyAllVariables.tml templates are provided for reference. These templates list all variables that can be used in treatment report templates.



Note: *To avoid loss of data, always make a backup copy of the template files before editing them.*



Note: *The template files contain symbols for variables. Each of these variables begin with the symbol \$. The software only recognizes the variables listed in the AllVariables.tml or BrachyAllVariables.tml templates. Moreover, do not mix variables designed for External Beam Planning (Full.tml) and Brachytherapy Planning (BrachyFull.tml, QAExport.tml). If an unknown variable is used in the template, the text “undefined variable name” is printed in the report.*

Report Template File Structure

Each template file contains three main sections: Header, Footer, and Form (the report body).

- In the Header section, you define the space reserved for the header. Next, you define the font, place and content of each text line printed in the header of each report page.

- In the Footer section, you first define the space reserved for the footer and then the font, place and content of each text line printed in the footer of each report page.
- In the Form section, you define the font, place and content of each text line printed in the report.

The template files consist of lines. Each line comprises a command followed by an “equals” (=) sign and parameter value(s).

All dimensions, including font sizes, are given in 1/10 millimeters. For example, 2000 stands for 200 mm or 20 cm. Font weights, in turn, can have values ranging 1 to 999.



Note: You can also include comment lines in the template file by inserting a pound (#) sign at the beginning of the comment line.

Report Template Commands



Note: Avoid long print text lines. The print-outs will include only text that fits on one line when using the selected paper size and font.

Section=Header|Footer|Form

Defines the template section (Header, Footer, or Form) to which the formatting commands apply.

Height=Y

Defines the height of the section. The command is only valid for the Header and Footer sections. The height is defined in 1/10 millimeters. For example, Height=400 defines a header height of 4 centimeters.

LineSpacing=X.x

Defines the multiplier for line spacing between the printed lines. The line space equals to LineSpacing times the height of the current font. For example, LineSpacing=1.5 defines a line space of one half of the height of character M in the current font.

Description=string

A text line describing the template file. This is shown in the Print Report dialog box to assist in selecting a correct template file for printing out reports.



Note: When editing report templates, notice the following:

- Type the description on one line. The length of a description line is not limited.
- Successive Description commands override previous ones.

For example:

```
Description=This report will print out all blocks in all files
```

#string

The # character at the beginning of a line defines the line as a comment line. Comment lines do not appear in the printed report. For example:

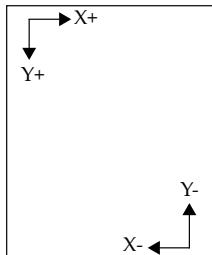
```
Font=40;400;Arial  
Text>Hello  
#Text=Good Bye
```

prints out as



Move=X[;Y]

Moves the starting location of the next text string X units right and Y units down measured from the left and top edges of the form, respectively. Negative X and Y values are measured from the right and bottom edges, respectively. Y is optional. One unit is 1/10 millimeters.



For example:

```
Move=100;100      To location (100, 100)
```

Move= 200	To location (200, 100)
Move=-200	To location (1800, 100)
Move= 100;-200	To location (100, 2700)

RelativeMove=X[;Y]

Moves the starting location of the next text string X units right and Y units down measured from the current position. Y is optional. One unit is 1/10 millimeters. For example:

Move=100;100	To location (100, 100)
RelativeMove=100;200	To location (200, 300)
RelativeMove=-200	To location (0, 300)
RelativeMove= 100;-200	To location (100, 100)

MoveText= X[;Y]

Moves the starting location of the next text string X units right and Y units down measured from the left and top edges of the form, respectively. Negative X and Y values are measured from the right and bottom edges, respectively. Y is optional. One unit in the horizontal direction is the width of the letter M using the current font. In the vertical direction, one unit is the height of one line. For example:

Font=100;400;Arial	
LineSpacing=1.5	
MoveText=1;2	To the second line of the first column
MoveText=-2	To the second last column, first line
MoveText=3;-2	To the third column, second last line

RelativeMoveText= X[;Y]

Moves the starting location of the next text string X units right and Y units down measured from the current position. Y is optional. One unit in the horizontal direction is the width of the letter M using the current font. In the vertical direction, one unit is the height of one line.

Text=string

Prints the given string starting from the current location and ending at a line break. After the command, the cursor moves one line down and returns back to the X-location where it was before executing the Text command.

The text string can include variables that are replaced with the correct values when printing the report. All variables are named as \$<name>.



Note: To print a space after a variable value, type two spaces in the command line.

For example:

```
Font=100;400;Arial  
Text=This is a text line  
Move=100  
Text=This line is indented  
Text=This one also  
Move=0  
Text=This is not anymore  
Text=Patient: $PatientFirstName $PatientLastName  
Text=Patient: $PatientFirstName $PatientLastName
```

prints out as

```
This is a text line  
    This line is indented  
        This one also  
    This is not anymore  
    Patient: Test Patient  
    Patient: Test Patient
```

LineText=string

Prints the given string starting from the current location. After executing the LineText command, the cursor remains at the end of the string. For example:

```
Font=100;400;Arial  
Text=This is a text line  
Move=100  
Text=This line is indented  
LineText=One  
LineText=Two  
Text=Three  
Text=This is even more indented  
Move=0  
Text=This is not anymore  
LineText=Patient:  
LineText= $PatientFirstName  
Text= $PatientLastName
```

prints out as

```
This is a text line
    This line is indented
        OneTwoThree
            This is even more indented
This is not anymore
Patient: Test Patient
```

TextRight=string and TextLineRight=string

Print the given string as Text=string and LineText=string commands but ending the string on the current cursor position. Allows adjusting text to right on any column. For example:

```
Font=100;400;Arial
Move=0
Text=This is written to the left edge of the page.
Move=-1
TextFromRight=This is written to the right edge of the page.
Move=1000
Text=This starts from the middle.
Move=1000
TextFromRight=This ends in the middle.
```

prints out as

```
This is written to the left edge of the page.
    This is written to the right edge of the page.
        This starts from the middle.
This ends in the middle.
```

TextCenter=string and LineTextCenter=string

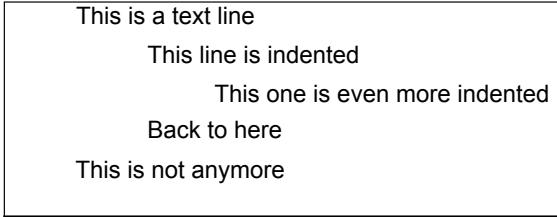
Print the given string as Text=string and LineText=string commands but the middle point of the string is at the current cursor position. Allows centered text on any column.

Margin=X

Sets the left margin to a given position X. All horizontal movement from here on is done in relation to the margin.

```
Font=100;400;Arial  
Margin=0  
Text=This is a text line  
Margin=100  
Text=This line is indented  
Move=100  
Text=This one is even more indented  
Move=0  
Text=Back to here  
Margin=0  
Text=This is not anymore
```

prints out



```
This is a text line  
    This line is indented  
        This one is even more indented  
    Back to here  
This is not anymore
```

Font=size;stroke;name

Defines the font to be used from this point on until the next Font command. The size of the font is given in 1/10 millimeters. The stroke is a value ranging between 1 and 999. The following lists some common stroke values with corresponding numeric values:

- 100—Thin
- 300—Light
- 400—Normal
- 700—Bold
- 900—Heavy

The name of the font is a string. The default font is 3 mm high normal Times New Roman, for example:

```
Font=100;400;Arial  
Text=This is 1cm high Arial  
Font=60;700;Times New Roman  
Text=This is 6mm high bold Times New Roman
```

prints out

```
This is 1 cm high Arial  
This is 6 mm high bold Times New Roman
```

HorizontalLine=X1;X2

Draws a thin horizontal line from position X1 to position X2.

PageBreak=X.x

Inserts a page break into a report. A value can be given to make the page break optional depending on how much page space has been used. The given value can range from 0.0 to 1.0. For example, if the value is set to 0.8 it means that when a page is 80% full, a page break is inserted. Value 0.0 forces the page break always while 1.0 does so only if the page is completely full. This command does not affect automatic paging; an automatic page break is inserted always when a page is full. Valid only in the Form section.

PaperOrientation=<keyword>

Defines the paper orientation used for the report. Available keywords are portrait and landscape. The default keyword is portrait.

PaperSize=<keyword>

Defines the paper size used for the report. Available keywords are A4, A3, legal, letter and tabloid. The default keyword is A4.

Report Template Syntax

Loop=<keyword>

EndLoop

In the External Beam Planning, one plan can contain several fields, fractionations, reference points etc. Furthermore, one field can contain several blocks or wedges etc. In the Brachytherapy Planning, one plan can contain several applicators, reference points etc.

To print out these kind of multiple item lists you need to specify a loop into the report template. All the commands between Loop and EndLoop are repeated as many times as there are objects defined by the keyword in the plan. For example, if an external beam plan contains three fields, the Fields loop is repeated three times, and if a brachytherapy plan contains three applicators, the Applicators loop is repeated three times.

Available loop keywords are listed below.

Table 61 Loop Keywords

	Brachytherapy Planning	External Beam Planning	
		Photon	Proton
Catheters (lists applicator data)	X	N/A	N/A
SeedCollections (lists seed collection data)	X	N/A	N/A
SourcePositions (lists source position data including zero source positions)	X	N/A	N/A
SourcePositionsNoZero (lists source position data excluding zero source positions)	X	N/A	N/A
Fields (lists field data)	N/A	X	X
Fractionations (lists general fractionation data)	X	X	X
Structures (lists structure data)	X	X	X
RefPoints (lists reference point data)	X	X	X
RefLines (lists reference line data)	X	N/A	N/A
RefLinePoints (lists reference line point data)	X	N/A	N/A
PhotonAlgOptions (lists photon dose calculation algorithm options)	N/A	X	X
ProtonAlgOptions (lists proton dose calculation algorithm options)	N/A	N/A	X
ElectronAlgOptions (lists electron dose calculation algorithm options)	N/A	X	X

Some of the loops can be used inside each other to list different variables. RefPoints loop can be used inside Fractionations loop (or vice versa) to list reference point-dependent fractionation data.

In External Beam Planning, also Fields loops can be used:

- RefPoints loop inside Fields loop
 - Lists field-dependent reference point data
- Fractionations loop inside Fields loop (or vice versa)
 - Lists fractionation-dependent field data

For example, AlgOptionName and AlgOptionValue loops inside a PhotonAlgOptions loop can be used to print out the properties of the photon calculation algorithm selected for the plan:

```
Loop=PhotonAlgOptions
Move=100
LineText=$AlgOptionName
Move=600
Text=$AlgOptionValue
EndLoop
```

Prints out the names and values of all the options in the calculation algorithm selected for the plan.

The following loops can be used only inside Fields loop:

- Blocks
- Wedges (only photon)
- Bolus
- CalculationWarnings
 - Lists warnings from dose calculations for this field
- CalculationErrors
 - Lists errors from dose calculations for this field
- CalculationInfos
 - Lists information messages from dose calculations for this field
- CalculationNotes
 - Lists notes from dose calculations for this field

If=[\${<variable>}]

Else

EndIf

The commands between If and Else (or If and EndIf, if no Else branch is used) are processed only if the variable has a defined non-empty and non-zero value. The Else branch is processed if the value is not defined, empty or zero. For example:

```
If=$ImageApprovalDate
LineText=Image Approval:
Text=$ImageApprovalDate by
$ImageApprover
Else
Text=IMAGE NOT APPROVED
EndIf
```

If the image is approved, prints out the approval date and approver.

Image Approval: Wednesday, October 31, 2007 1:57:20 PM by Mr Smith

otherwise prints out:

IMAGE NOT APPROVED

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