PHILIPS

Pinnacle^3

TumorLOC

Instructions for Use

Release 16.4 (English)

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Medical Device Directive
Pinnacle^3 Radiation Therapy Planning
System is CE Marked to the Medical
Device Directive 93/42/EEC.

CE 2797

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Device Description

The Pinnacle^3® Radiation Therapy Planning (RTP) software is composed of several modules including the core Pinnacle^3 functionality, Syntegra™, P^{3}IMRT®, and AcQSim^3™. The Pinnacle^3 RTP software runs on a Solaris UNIX (or UNIX compliant) computer, which allows qualified medical personnel to enter patient data into the system, use that data to construct a plan for radiation therapy, and evaluate the plan. Optionally, the qualified medical personnel may output the plan in an electronic or printed form for use by other systems in the delivery of treatment to a patient.

Pinnacle^3 includes networking capabilities to provide connectivity to other Pinnacle^3, Syntegra, AcQSim^3, or P^{3}IMRT workstations, input devices and output devices, as well as access to the Pinnacle^3 database from any Pinnacle^3 workstation available on the network. The system can be run from a single workstation but has network capability to other Pinnacle^3 workstations and to both input and output devices via local area network (LAN) or wide area network (WAN). The Pinnacle^3 RTP System also has an enterprise configuration for larger sites requiring a centralized data center environment. This system consists of one or multiple rack mountable servers on which Pinnacle^3 sessions run which enables display on any network accessible computer. The expected service lifetime of the software is five (5) years.

To enable use of the software, a license key must be issued by the installer after software installation has been completed. If you have any software issues, please contact your service representative: Customer Support (1-800-722-9377 for US and Canada), your local Philips Customer Service provider, or your local Distributor. Beginning with Pinnacle^3 16.4, you will need to provide your service representative with the equipment ID assigned to your software kit. Your equipment ID can be found in the **About** window and is used to direct your call to the appropriate service personnel.

Intended Use

Pinnacle^3 Radiation Therapy Planning System is a software package intended to provide planning support for the treatment of disease processes, utilizing photon, proton, electron and brachytherapy techniques.

Indications for Use

Pinnacle^3 Radiation Therapy Planning System is a software package intended to provide planning support for the treatment of disease processes. Pinnacle^3 Radiation Therapy Planning System incorporates a number of fully integrated subsystems, including Pinnacle^3 Proton, which supports proton therapy planning. The full Pinnacle^3 Radiation Therapy Planning System software package provides planning support for the treatment of disease processes, utilizing photon, proton, electron and brachytherapy techniques.

Pinnacle^3 Radiation Therapy Planning System assists the clinician in formulating a treatment plan that maximizes the dose to the treatment volume while minimizing the dose to the surrounding normal tissues. The system is capable of operating in both the forward planning and inverse planning modes. Plans generated using this system are used in the determination of the course of a patient's radiation treatment. They are to be evaluated, modified and implemented by qualified medical personnel.

Contraindications

There are no known contraindications regarding the use of the Pinnacle^3 RTP system.

Intended Audience

This manual is written for qualified medical personnel trained as users of Pinnacle^3 RTP systems. You should make sure that you have thoroughly read and completely understand the manuals and release notes that are delivered with the software. Keep this manual and all other manuals delivered with the software near your Pinnacle^3 system and review them periodically. The initial installation procedure will be performed by a Field Service Engineer. If you suspect that your system has an error, discontinue its use and contact Customer Support or your local distributor.

Minimum Requirements

This section provides the minimum requirements concerning hardware and software related to running the current product release as intended.

Professional

- Solaris 11 version 11.3 or later with Oracle X6-2
  (Note for existing sites: 11.2 or later with Oracle X5-2)
- 64GB RAM (based on number of concurrent users)
  - Additional RAM requires upgrade
  - Upgradeable to 384GB RAM
- Rack Management: 1U each server

Network

- 10,000/1,000/100 Mbps Base-T Ethernet
- 1,000/100 Mbps Base-T Ethernet for remote management (ILOM)
- 4/8/16GBs HBA ports supported for communication between Smart Enterprise Cluster servers and the SAN

Third-Party Software

- OVDC(VCC) is used to access Pinnacle[3]
- Third-party software installations are not supported on any Pinnacle[3] system server without proper validation.

Smart Enterprise (Cluster Server Nodes)

- Solaris 11 version 11.3 or later with Oracle X6-2
  (Note for existing sites: 11.2 or later with Oracle X5-2)
- Solaris Cluster required on cluster nodes
- 64GB RAM (based on number of concurrent users)
  - Additional RAM requires upgrade
  - Upgradeable to 384GB RAM
- Rack Management: 1U each cluster server

Smart Enterprise (Application Servers)

- Solaris 11 version 11.3 or later with Oracle X6-2
  (Note for existing sites: 11.2 or later with Oracle X5-2)
- 64GB RAM (based on number of concurrent users)
  - Additional RAM requires upgrade
  - Upgradeable to 384GB RAM
- Rack Management: 1U each application server

Notes

Equipment specifications are subject to alteration without notice. All changes will be in compliance with regulations governing manufacture of medical equipment.

Pinnacle^3 and P^{3}IMRT are registered trademarks, and AcQSim^3 and Syntegra are trademarks of Philips. Other brand or product names are trademarks or registered trademarks of their respective holders.

Use of Symbols in Labeling

Philips Healthcare complies with International Standards and FDA requirements for the use of symbols in labeling. An online glossary of symbols used by Philips Healthcare is available at http://www.symbols.philips.com.

General Device Warnings

Do not load non-system software onto the computer used by this system without the direct authorization of Philips Medical Systems. Feature performance and safety may be compromised.

To assure proper treatment, it is critical that a qualified medical person review and verify all system treatment plan parameters using an independent verification method prior to treating patients using the plan.

Report the occurrence of a serious incident in relation to this device to Philips Customer Support and the competent authority of the Member State in which the user and/or patient is established.

We recommend that you review TG40, TG53, and other pertinent radiation therapy treatment standards and incorporate those methods into your clinical practice to ensure that your use of the system results in the most accurate treatment plans. TG40, TG53, and other reports are available publicly at the American Association of Physicists in Medicine (AAPM) website.

- **Comprehensive QA for radiation oncology: Report of AAPM Radiation Therapy Committee Task Group 40. *Medical Physics* 21(4), 1994.**
- **American Association of Physicists in Medicine Radiation Therapy Committee Task Group 53: Quality assurance for clinical radiotherapy treatment planning. *Medical Physics* 25(10), 1998.**

The following clinical practices are recommended to verify the accuracy of each treatment plan:

- **An independent calculation of the monitor units for each beam of a plan and treatment time for each brachytherapy plan.**
- **Acquisition and review of portal images or review of multi-leaf collimator (MLC) leaf positions after import to the treatment system.**
- **A chart check prior to the plan being delivered or during the first week of treatment.**
- **Independent review of the treatment plan prior to the delivery.**
- **Cross-functional review of the plan in a weekly chart round.**
- **Manual verification of record and verify settings after transfer to the treatment machine.**
- **Verification of the SSD and field shape during patient setup.**

These reviews should be performed for a new plan or when a change is made to any component of a plan.

U.S.A. law: CAUTION: Federal law restricts this device to sale by or on the order of a physician.

This software product is a Medical Device.

Only qualified medical personnel should operate the system. New personnel should receive training prior to unsupervised operation of the system. For more information, contact Customer Support or your local distributor.

Serious injury to patients can result due to the misapplication of this product. Make sure that you thoroughly understand all the user instructions prior to using this device.

Pinnacle^3 treatment plans may include the statement NOT FOR CLINICAL USE. Based on the machine or isotope data and the treatment plan, the software determined that the plan cannot be delivered clinically. Do not treat patients with plans that are not for clinical use.

Pinnacle^3 includes sample data. This information is for reference purposes only. Do not treat patients with plans based on sample machines or other sample data.

1 Getting Started

The Tumor Localization (TumorLOC) software provides the tools that you use to perform isocenter localization and simple CT simulation at the time of scan acquisition. In addition to standard, non-gated studies, you can also use these tools for gated pulmonary studies (including all phase information).

> **NOTE**
> The TumorLOC system should not be used within the space where surfaces may come into contact with the patient or with an attendant who can touch the patient. This space is defined as 1.83 meters (6 feet) outside the perimeter of the intended location of the treatment table and 2.29 meters (7.5 feet) above the floor.

Start the Software

To start the TumorLOC software from the CT console, click **Simulation** on the console.

If you use remote access to connect to the TumorLOC software, log on to the server and choose one of the following:

- **If you are logged in as a TumorLOC user**—click the **TumorLOC** icon in the front panel at the bottom of the Solaris desktop.
- **If you are logged in as a Pinnacle^3 user**—in the **Launch Pad** menu, click the arrow below the **Planning** icon to open the **Planning** flyout tool, and click the **TumorLOC** icon.

TumorLOC User Interface

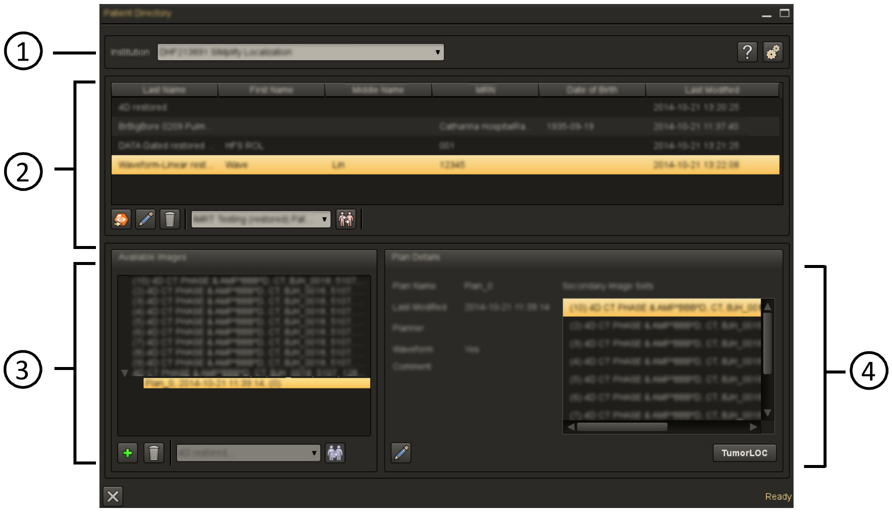
There are two main windows in the TumorLOC software: the **TumorLOC Patient Directory** and the **Simulation** window. The **Launch Pad** menu also contains tools that you will use to manage databases and access the physics tools.

TumorLOC Patient Directory

The **TumorLOC Patient Directory** is the first window that opens when you start the TumorLOC software. In this window you can do the following tasks:

- Access the physics, backup, restore, and system administration tools
- Import image data sets
- Add, edit, and delete plans

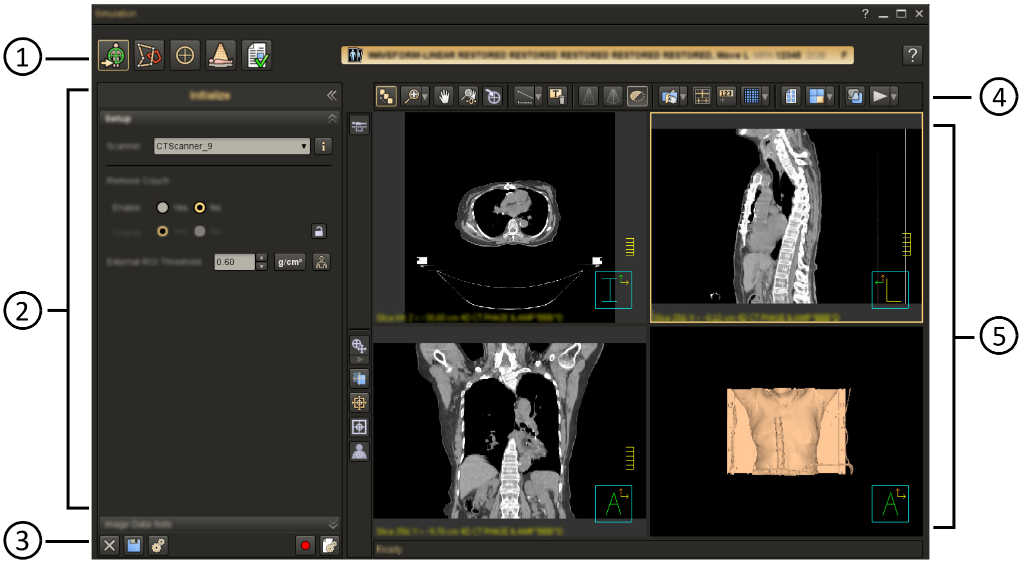
- Manage your patient information



1	The **Institution** list, from which you select the current institution
2	The list of patients in the current institution, and the tools necessary to import images, edit patient information, delete patients, and transfer patients from one institution to another
3	The list of image data sets and plans for the selected patient, and the tools necessary to add a plan, delete an image data set, delete a plan, and transfer image data sets from one patient to another
4	Information about the selected image data set or plan, the list of secondary image data sets associated with the plan, and the tool necessary to edit plan information

Simulation Window

The **Simulation** window is the main window of the TumorLOC software. You will use the tools in this window to create your simulation plan.



1	The simulation worksteps
2	The workstep panel, which contains tools necessary to complete each workstep
3	The Common toolbar
4	The Visualization toolbar
5	The viewing windows

The workstep icons across the top of the window let you move between the worksteps as you create your plan.

Workstep Icon	Description
	Initialize workstep. See *Initialize*.
	Segment workstep. See *Segmentation*.
⊕	**Point** workstep. See *Points of Interest*.
	Beam workstep. See *Beams*.

Workstep Icon	Description
	Finalize workstep. See *Finalize*.

Launch Pad Menu

The **Launch Pad** menu provides access to the physics tools and the database operations for the current institution. To access the **Launch Pad** menu, click **Settings** in the **TumorLOC Patient Directory**.

Icon	Description
	Add, select, or delete institutions. See *Institutions*.
	Access the physics tools. See *Physics*.
⚙	Access system administration functions. See *System Administration*.
	Archive patient and physics data. See *Backup*.
	Restore archived patient and physics data. See *Restore*.
⇦	Exit the **Launch Pad** menu and return to the **TumorLOC Patient Directory**. Note: If you use remote access to connect to the TumorLOC software and you are logged in as a Pinnacle^3 user, click the **TumorLOC** icon in the **Planning** flyout tool to return to the **TumorLOC Patient Directory**.

Close the TumorLOC Patient Directory

For system maintenance purposes, we recommend that you close the **TumorLOC Patient Directory** once a day so that the system can complete file maintenance procedures and terminate processes to free up memory. The end of the workday is a good time to close the directory.

Click **Exit** in the **TumorLOC Patient Directory**. The directory closes, and the window is black. After several seconds, the directory reopens.

NOTE
If you use remote access to connect to the TumorLOC software and you are logged in as a Pinnacle^3 user, click the **Exit** button in the **Launch Pad** menu, and click **Yes** to exit the software. Then restart the Pinnacle^3 software and the TumorLOC software.

DICOM Conformance

DICOM (Digital Imaging and Communications in Medicine) is a standard for the electronic transfer of digital images and associated information, developed by the American College of Radiology and the National Electrical Manufacturers Association. The Pinnacle^3 software operates within DICOM standards and within the standards of the manufacturer's Conformance Statement for DICOM. The DICOM conformance statement is available on the Philips Healthcare website (www.healthcare.philips.com).

2 Institutions

All treatment machine and patient information is associated with an institution. If you provide simulation services to more than one institution, or if your facility has more than one simulation suite, you can set up multiple institutions and organize the patients and treatment machines under their respective institutions.

NOTE
You must create at least one institution before you import image data sets.

All of the functions that you need to manage your institutions are located in the **Select Institution** window.

1. In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. Click **Institutions**. The **Select Institution** window opens.

See the following sections to create and manage your institutions.

Add an Institution

1. Click **Add** in the **Select Institution** window. The **Add Institution** window opens.
2. Click **Add Institution**. The **Edit Institution** window opens.
3. Enter information about the institution.
4. Click **Close** to save the information and return to the **Select Institution** window. The new institution's name and address appear in the **Select Institution** window.
5. Click **Close** to return to the **Launch Pad** menu.
6. Click **Return to TumorLOC Patient Directory**.

NOTE
If you use remote access to connect to the TumorLOC software and you are logged in as a Pinnacle^3 user, click the **TumorLOC** icon in the **Planning** flyout tool to return to the **TumorLOC Patient Directory**.

Set a Default Institution

1. Select the institution that should be the default institution from the **Default Institution** list in the **Select Institution** window.
2. Click **Close** to return to the **Launch Pad** menu.
3. Click **Return to TumorLOC Patient Directory**.

NOTE
If you use remote access to connect to the TumorLOC software and you are logged in as a Pinnacle^3 user, click the **TumorLOC** icon in the **Planning** flyout tool to return to the **TumorLOC Patient Directory**.

Edit an Institution

1. In the **Select Institution** window, highlight the name of the institution to be edited.
2. Click **Edit**. The **Edit Institution** window opens.
3. Change the information as necessary.
4. Click **Close** to save the information and return to the **Select Institution** window.
5. Click **Close** to return to the **Launch Pad** menu.
6. Click **Return to TumorLOC Patient Directory**.

NOTE
If you use remote access to connect to the TumorLOC software and you are logged in as a Pinnacle^3 user, click the **TumorLOC** icon in the **Planning** flyout tool to return to the **TumorLOC Patient Directory**.

Delete an Institution

NOTE
Deleting an institution will permanently remove it from the system.

If an institution includes patients, you cannot delete it.

1. Click **Delete** in the **Select Institution** window. The **Delete Institution Confirm** window opens.
2. Select the institution to be deleted.
3. Click **Delete Selected Institution**.
4. Click **Close** to return to the **Launch Pad** menu.
5. Click **Return to TumorLOC Patient Directory**.

NOTE
If you use remote access to connect to the TumorLOC software and you are logged in as a Pinnacle^3 user, click the **TumorLOC** icon in the **Planning** flyout tool to return to the **TumorLOC Patient Directory**.

3 Physics

Before you can begin using the TumorLOC software, you must define your CT scanners and commission your photon machines in the physics tools.

NOTE
If you are using TumorLOC with an existing Pinnacle^3 database, you can use the CT scanners and machines that you have already commissioned for Pinnacle^3 treatment planning with the TumorLOC software. If you want to define CT scanners and commission machines only for use with the TumorLOC software, then follow the instructions in this manual. If you want to define CT scanners and commission machines for use in both TumorLOC and the Pinnacle^3 treatment planning software, then follow the instructions in the *Pinnacle^3 Physics Instructions for Use*.

Access the Physics Tools

1. In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. Click **Physics**.
3. At the next prompt, enter the physics tool password and click **OK**. The **Physics Tools** window opens.

NOTE
The default password is “physics”. To change the password, see *Change the Physics Tool Password*.

4. Choose one of the following:
   - To define a CT scanner, see *CT Scanner Configuration*.
   - To define a photon machine, see *Working with Machines and the Machine Database*.

Change the Physics Tool Password

To prevent physics data from being changed inadvertently, the physics tools are password protected. The default password is “physics”, but you can change it from the **Physics Tools** window.

1. Click **Change Password** in the **Physics Tools** window.
2. In the **Change Physics Tool Password** window, type the old password and click **Continue**.
3. At the next prompt, type the new password and click **Continue**.

NOTE
The password is case-sensitive. If you capitalize letters when specifying the password, you must capitalize them when accessing the physics tools.

4. When prompted, retype the password to confirm it, and then click **Continue**.

CT Scanner Configuration

To configure a CT scanner, click **Scanner Configuration** in the **Physics Tools** window. The **CT Scanner Configuration** window opens. In this window, you can define CT to density tables and laser configuration tables, and configure CT scanners.

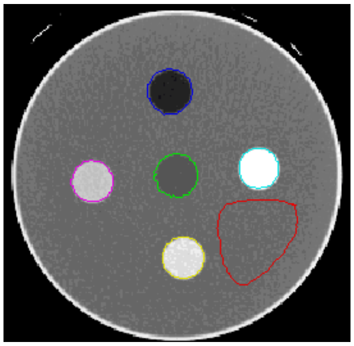
> **NOTE**
> When you click **Save** in the **CT Scanner Configuration** window, the information in all of the tabs is saved.

Obtain the CT Mapping Information

Before you define a CT to density table, you can obtain the CT numbers for materials of known densities by scanning a CT calibration phantom. You can then read the image set into the software to determine the CT numbers to enter in a CT to density table.

We suggest that you create a CT to density table for each scanner kVp that you use to generate patient images for simulation and treatment planning, because the data in each table varies depending on the scanner kVp setting.

When you have created a plan using the CT calibration phantom images, create a region of interest (ROI) for each material and use the ROI contouring or autocontouring tools to draw a contour for each ROI. We recommend that you contour multiple slices for each ROI.



Next, contract the ROIs to ensure that they are completely within the material boundaries and calculate statistics on them to determine the average CT number for each material type. You can then enter this value with the corresponding physical density value in the **CT to Density Tables** physics tool. See *Segmentation* for information about ROIs.

CT to Density Tables

The density information inherent in the patient CT images is used to account for tissue inhomogeneities in Pinnacle^3 photon and electron dose calculations. For every CT scanner used to obtain patient images for treatment planning, you must scan a CT calibration phantom with known physical densities, determine the CT numbers associated with those densities, and enter a table that maps the CT numbers to the appropriate densities.

During planning, the software reads in the CT numbers and then determines the density for each voxel of the patient using the selected CT to density table. The density is used to look up mass attenuation coefficients and is used for density scaling during superposition.

The software uses mass attenuation coefficient tables stored for several material types in determining the TERMA distribution in heterogeneous media. Each material-specific table is stored with its physical density. The mass attenuation coefficient for each density in the CT volume is then determined through linear interpolation between the materials closest in physical density. This allows the software to account for the different material types that may be present in the treatment volume.

The physical density is also used to scale the dose deposition kernel during the superposition to account for the effects of heterogeneities on scattered radiation. This is accomplished by tracing a ray line between a TERMA interaction site and the dose computation point, and accumulating the radiological distance along the ray.

⚠ **WARNING**
The density information entered in this table is critical to correct dose calculations. Failure to specify the CT to density table for a CT scanner used to obtain treatment planning images may result in erroneous dose calculations.

To help you learn the software while you obtain the required physics data, the software includes a default CT to density table with a set of simplified mappings. For more information, see *Default CT to Density Table*.

Default CT to Density Table

If you start the software with no CT to density tables defined, the software automatically creates a default, linear table called Linear DRR Table. The table is only valid for generating DRRs, not for dose computation.

In physics mode, the software creates a CT to density table called Physics Table. This table is always assigned to the plan when in physics and is used for all DRR generation. The table is valid for dose computation and has the same values as the Linear DRR Table:

CT Number	Density (g/cm^3)
0	0.000
1000	1.000
21410	21.410

To ensure that the Linear DRR Table and the Physics Table are not edited, saved, or deleted, they do not appear in the **CT to Density Tables** list.

Add or Edit a CT to Density Table

⚠ **CAUTION**
If you edit or rename an existing CT to density table, the software invalidates dose in all plans that used that CT to density table. If a CT to density table is used by several plans, do not edit the table. Instead, create a new table and assign it to the appropriate scanner.

> **NOTE**
> The software prevents you from closing the **CT Scanner Configuration** window if you have not finished defining the CT to density tables. To be complete, each CT to density table must contain at least three data points, and the data points must increase monotonically.

When you enter CT to density table information, you must enter the physical density (g/cm^3) for the phantom materials with their corresponding CT numbers.

1 Select the **CT to Density Tables** tab in the **CT Scanner Configuration** window.

2 Do you want to add a new table or edit an existing table?
   - Add a new table—Click **Add Table**. A new table appears in the **CT to Density Tables** list.
   - Edit an existing table—Select the table that you want to edit from the **CT to Density Tables** list.

3 In the **Name** field, type a name for the CT to density table.

4 Select whether the table will be used for DRRs only or for both DRRs and dose computation.

5 For the **In (toward the gantry)** direction, select the **+Y** or **-Y** coordinate for laser export.

> **NOTE**
> Pinnacle^3 uses IEC +Y as the **In (toward the gantry)** direction. However, this direction may be reversed (-Y) for some scanners. Make sure you select the correct coordinate that indicates movement toward the gantry (+ Y or -Y) for your scanner.

6 Select the X coordinates for laser export.

X coordinates (Right/Left) for TumorLOC laser export can be reversed from other CT simulation systems. In TumorLOC, +X is to the right as you are standing at the foot of the table facing the gantry, while in other CT simulation systems +X is to the left. As a result, you must choose +X or -X as the right (toward gantry) direction for laser export so that the X coordinates in TumorLOC will match the X coordinates of other CT simulation systems.

> **NOTE**
> The X coordinate for Gammex lasers must be positive to the right as you are standing at the foot of the table facing the gantry. As a result, when you export laser localization coordinates for Gammex lasers, the software always exports +X for the X coordinate regardless of the selection that you make for the X coordinate when you commission the CT to density table.

7 Set the default for isocenter shift display by selecting **Laser**, **Table**, or **Patient** from the **Display Isocenter Shift As** list.

> **NOTE**
> In the TumorLOC software, the Left/Right isocenter shift is always displayed from the laser regardless of the setting you select here. This setting is important if you plan to use this CT scanner for planning as well as for simulation.

8 If you are adding a new table, click **Insert After** to add the first row to the table. Then click **Insert Before** or **Insert After** to insert new rows before or after the currently selected row.

9 Enter the CT numbers and their corresponding density values (in g/cm^3). Enter the CT numbers and densities in ascending order, and make sure that all CT values are positive.

To enter CT numbers and density values, click the field you want to edit, and then type the value in the field that appears above the table. Click the green check mark next to the field or press **Enter** to accept the value. Click the red **x** to cancel the change. After you enter the second value, the graph appears to the right of the table.

10 Click **Save**.

Delete a CT to Density Table

1 In the **CT to Density Tables** tab, click **Delete Table**. The **CT to Density Table Delete** window opens.

2 Select the CT to density table that you want to delete.

3 Click **Delete Selected CT to Density Table** to delete the table.

If the CT to density table is used by a CT scanner configuration, you cannot delete the table unless you first delete the CT scanner that relies on the table. If necessary, click **Examine objects** to view the CT scanners that rely on the selected table.

Laser Calibration Tables

In the **Laser Settings** tab of the **CT Scanner Configuration** window, you can set up laser calibration tables. Laser calibration tables allow you to set the difference between the center of the field of view and the horizontal and vertical position of the lasers.

For Philips image data sets that are sent to the Pinnacle^3 system via DICOM, you can select the calibration table for the laser system you used and the software recalculates the coordinates to account for the offset. Laser calibration tables are unique to each institution and each CT scanner. Therefore, if you have multiple institutions or multiple scanners, you must set up tables for each one.

Add or Edit a Laser Calibration Table

1 Select the **Laser Settings** tab from the **CT Scanner Configuration** window.

2 Do you want to add a new laser or edit an existing laser?

- Add a new laser—Click **Add Laser**. A new laser appears in the **Laser Calibration Tables** list.
- Edit an existing laser—Select the laser that you want to edit.

3 In the **Name** field, type a name for the laser calibration table. The name of the table should be related to the specific laser or scanner.

4 Enter the horizontal and vertical offsets of the laser system.

5 Click **Save**.

Delete a Laser Calibration Table

1 In the **Laser Settings** tab, click **Delete Laser**. The **Laser Delete** window opens.

2 Select the laser that you want to delete.

3 Click **Delete Selected Laser Calibration** to delete the laser.

If the laser is used by a CT scanner configuration, you cannot delete the laser unless you first delete the CT scanner that relies on the laser. If necessary, click **Examine objects** to view the CT scanners that rely on the selected laser.

Define the Export Settings

Before you can export information to the laser system, you must define the export settings that you want to use for this laser system.

1 In the **Transmission Method** field, select the method you want to use for export.

- **Text File**—Can be used to export either absolute or relative marking coordinates. Continue to step 2.
- **DICOM**—Can only be used to export absolute marking coordinates. Continue to step 4.

2 In the **Export Directory** field, type the directory path that you want to use, or click **Browse** and select the necessary directory path. This directory is where your exported files will be saved.

3 In the **Output File Name** field, type the name for the export file.

NOTE
For Gammex A3000 and Gammex A4000 laser alignment systems, the output file name can be a maximum of 8 characters in length and must use an extension of ".CTS" ("CTS" must be in all capital letters).

4 In the **Destination AE Title** field, select the destination to which you want to export the absolute marking coordinates.

5 In the **Images to Send** field, select the number of images that should be exported. The following are the laser systems supported by the software and the number of images we recommend that you send for each system.

Laser Controller	Number of Images
Gammex	1
LAP CARINAiso	10
LAP CARINAsim	10 or All
LAP IsoMark	1
LAP CARINAnav	1

The performance of your system can be affected by the number of images that you choose to send. Sending more images will increase the time needed to export the images and import them into the laser system. However, sending fewer images can limit the anatomy that is visible after import. Be aware of these issues as you define your DICOM export settings.

CT Scanners

In the **CT Scanners** tab, you can add, edit, or delete a CT scanner configuration. A CT scanner configuration associates a scanner with a CT to density table, laser calibration table, and a laser alignment system.

Add or Edit a CT Scanner

To perform this procedure, you need the manufacturer name and model name of the CT scanner exactly as it appears in the DICOM file for any image data set that is created using the scanner. You also need the kVp at which the scanner operates, especially if the scanner operates at more than one kVp. If a DICOM station name has been defined for the scanner, you will need that information as well. If necessary, you can access this information on the CT scanner prior to completing this procedure. Be sure to write the values down exactly as they appear, including capitalization and symbols.

> **NOTE**
> The kVp and DICOM station name information are not required as part of CT scanner configuration; however, we recommend that you define the kVp for the scanner.
>
> If a CT scanner operates at more than one kVp, you should configure a separate CT scanner for each kVp value at which the scanner can operate. Each scanner must have a unique name, but the manufacturer name and model name should be the same for each kVp configuration. The CT to density table should be different for each kVp configuration.

1. Select the **CT Scanners** tab from the **CT Scanner Configuration** window.
2. Do you want to add a new scanner or edit an existing scanner?
    - Add a new scanner—Click **Add Scanner**. A new scanner appears in the **CT Scanners** list.
    - Edit an existing scanner—Select the scanner that you want to edit in the **CT Scanners** list.
3. In the **Scanner Name** field, type a name for the scanner. The name of the CT scanner should be related to the specific configuration or scanner. This name is used to define the scanner used for image acquisition.
4. Select the CT to density table that you want to associate with the selected CT scanner.
5. Select the laser calibration table that you want to associate with the selected CT scanner.
6. Select the laser alignment system that you want to associate with the selected CT scanner.
7. Information that you enter in the remaining fields on the **CT Scanners** tab is used by the software to identify the scanner configuration when you import an image data set. It is not mandatory that you define this information, but any information that you do define will be used by the software to assign a CT scanner to a plan when the scanner information matches the data in the primary image data set that is used in the plan.

    Type the manufacturer name and model name of the CT scanner.
8. If you want to define the station name, select **Use Station Name** and type the station name in the field.

9 If the CT scanner operates at more than one kVp, select **Use kVp** and type the kVp value in the field.

If the CT scanner only operates at one kVp, you do not need to enter the kVp value.

10 Click **Save**.

Delete a CT Scanner

1 In the **CT Scanners** tab, click **Delete Scanner**. The **Delete CT Scanner Confirm** window opens.
2 Select the scanner that you want to delete.
3 Click **Delete Selected CT Scanner** to delete the scanner.

Working with Machines and the Machine Database

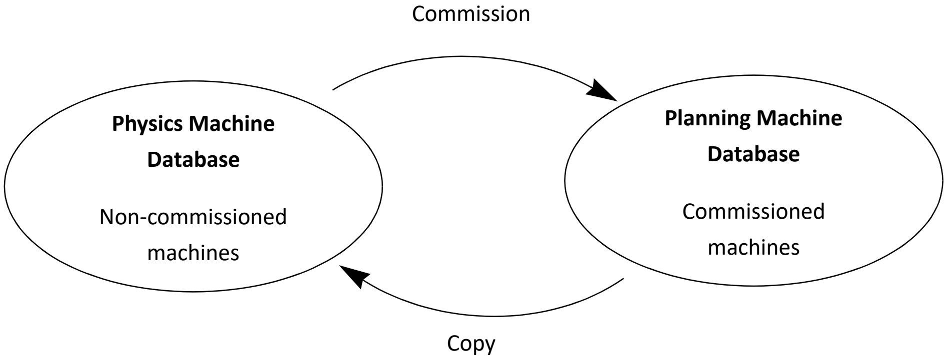
In Pinnacle^3, the physics information for all external beam treatment modalities is organized in a machine database you create using the physics tools. The database consists of all the linear accelerators that are available for an institution. The information stored for a machine includes its physical characteristics, treatment modalities, and energies.

This chapter describes how the machine database is organized and how to create, delete, and commission machines for use in simulation.

The Pinnacle^3 Machine Databases

Pinnacle^3 maintains two machine databases:

- The physics machine database. This is a “workshop” database; the machines stored in it are in the process of being built using the physics tools and are not available for planning.
- The planning machine database. Once a machine is built and ready to be used for simulation, it is removed from the physics machine database and added to the planning machine database, a process called commissioning.



When a machine is commissioned, it is “stamped” with the date and time of commissioning. This stamp identifies the version of the machine. All plans include information about the version of the machine used to create them.

To make changes to a machine after it has been commissioned, you must copy it back into the physics machine database, make the changes using the physics tools, and recommission the machine. The new version of the machine is then available in the planning machine database.

When plans created with an old version of the machine are read into the simulation software, you are given the option of using the old version or updating to the new version of the machine.

Machine Data Organization

Use the Photon physics tool to create machines and enter physics information for each machine.

First, you must enter the machine’s physical characteristics (couch, gantry, and collimator angle limits, the source to axis distance (SAD), the maximum MU setting, etc.). Since these characteristics are specific to the machine but not to treatment modality, a single characteristics file is created and used for all treatment modalities on the machine. The characteristics are used to limit the machine angles and settings in the simulation software and to translate your machine settings to the internal Pinnacle^3 coordinate system. Then, after entering the machine characteristics, define energies for each machine.

Machine Data and New Versions of Pinnacle^3 Software

When you install a new version of Pinnacle^3 software, be sure to review the release notes and determine the impact of the new software on existing physics machines. If the new software requires you to recommission or remodel machines, you should create a new institution in which you can remodel and recommission machines without affecting an institution that is currently in use for clinical work. We recommend that you create the new institution by backing up the physics data for an existing institution and then restoring the data to a new institution.

Be sure to use the new version of the physics tool when you recommission or remodel machines in the new institution. Follow the procedure below to select the new version of the physics tool.

1. From the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. In the **Launch Pad** menu, click **Institutions**.
3. Select the new institution from the list of available Institutions.
4. Click **Dismiss**.
5. In the **Launch Pad** menu, click **Configure**.
6. In the **Configuration Options** window, click **Default Tool**. The **Tool and Version** window opens.
7. Select the new version of Pinnacle^3 software from the **Default** list.
8. Click **Dismiss** to close the **Tool and Version** window, and click **Dismiss** to close the **Configuration Options** window.
9. In the **Launch Pad** menu, click **Physics** to open the physics tool.

   When you have completed this physics session, open the **Tool and Version** window again and select the version of Pinnacle^3 software that you are using clinically from the **Default** list. You will avoid accidentally creating plans with the new version of the Pinnacle^3 software before you are ready to use the new software clinically if you change the default tool back to the version that you are currently using clinically.

   NOTE
   Physics machines are not backward-compatible with physics tool versions. This means that if you launch a newer version of the physics tool on an institution that contains older versions of non-commissioned machines, and you save the machines, these non-commissioned machines will no longer be accessible through the older version of the physics tool.

   NOTE
   The simulation software will only recognize machines that were commissioned in the same or previous version of the physics tool. Therefore, plans combining machines that were commissioned in different Pinnacle^3 versions must be opened using the latest version of the machines needed for the plan.

10 When you are ready to use the new version of the software clinically, select the new version of the software from the **Default** list in the **Tool and Version** window so that the new version is the default planning and physics software.

Add Machines to the Physics Database

1 If necessary, open the **Physics Tools** window. See *Access the Physics Tools* for information.

2 Click **Photon Physics Tool** in the **Physics Tools** window. The **Photon Physics Tool** window opens.

The machines shown in the **Machine List** are not commissioned for use in the software. Some machines in this list may be copies of machines that have already been commissioned.

3 Click **Add** beneath the **Machine List**. The **Add New Machine** window opens.

You can add a new machine or copy an existing one to the **Machine List** from the **Available Machines** list, which contains non-commissioned, commissioned, and sample machines on the system. In addition to non-commissioned and current commissioned machines, you can copy and modify the following types of machines:

- **Old Commissioned Machines** are old versions of current machines.
- **Deleted Commissioned Machines** are commissioned machines that have been deleted from the planning machine database. However, they are not deleted completely from the system. If necessary, you can reproduce dose distributions from calculations using a deleted machine.
- **Sample Machines** can be used to experiment with the physics tools when you first receive your system and to perform quality assurance tests.
- **Commissioned Brachytherapy Simulators** are versions of simulators that have been commissioned for brachytherapy. You can disregard the **Commissioned Brachytherapy Simulators** option because it is not applicable for the TumorLOC software.

4 To copy an existing machine for modification in the physics tool, first select the class of machine to copy by clicking the appropriate button (for example, **Non-Commissioned Machines**).

5 From the updated list of machines, select the one you want to copy and click **Copy Selected**. The machine is copied into the **Machine List** in the **Photon Physics Tool** window for modification.

6 If you cannot find the machine you want to copy, click **Locate** in the **Add New Machine** window. The **Machine Locator** window opens.

Go to either the ReadOnlyMachineDB or the ReadWriteMachineDB in the *usr/local/adacnew/Patients/Institution_xx/Physics* directory. The machines in the selected directory are listed by their machine ID (for example, Machine.12). To see the name of the machine in the **Machine** field, click the machine ID.

Select the machine and click **Copy Located** to add a copy to the physics machine database.

After confirming that you are copying the correct machine, you are asked if you want to copy it to the commissioned list or the non-commissioned list. This option is available only when a commissioned machine is copied, and is useful when a patient is planned in one institution and then transferred to a different institution for later treatment. The commissioned machine that was used to plan the patient can be imported to the institution where the patient will be treated.

7 To add a new machine that is not based on an existing machine, click **Create Default** in the **Add New Machine** window. A new machine with a default name such as “Machine_1” is added to the **Machine List** in the **Photon Physics Tool** window.

For each machine, you must enter the physical description and physics information, as described in the following sections, and then commission the machine for use in simulation.

Enter the Physical Machine Characteristics

After adding a machine, you need to enter information for the machine's physical characteristics. You can use the worksheets in *Physics Data Worksheets* to record the machine description information.

Required Physical Description Information

You must enter the following physical description parameters for your machine:

- Collimator jaw attributes, including whether the jaws can be independent and the minimum, maximum, and default jaw position settings.
- Source to axis distance, source to jaw distances, and monitor unit limits.
- Couch attributes, gantry attributes, and collimator attributes, including the minimum, maximum, and default angles and the calibration angle and direction of positive rotation.
- Multi-leaf collimator (MLC) attributes, including the source to MLC distance, the leaf pair geometry, minimum and maximum leaf positions, rounded leaf ends, and travel speed.
- The proper jaw and MLC orientations and labels.

Enter all angles and settings using your machine's coordinate system.

1 Select the machine for which you want to enter information from the **Machine List** in the **Photon Physics Tool** window.

2 Click **Edit** beneath the **Machine List**. The **Machine Editor** window opens.

The tabs located near the top of the window let you display information about the jaw, couch, collimator, and gantry angles and other general machine parameters. The photon, electron, and stereo energy lists at the bottom of the window show the energies that are available for each modality on the machine.

NOTE
The electron and stereo energy lists that are shown in the **Machine Editor** window are not applicable for machines being commissioned for use with TumorLOC software.

3 Enter the machine name and select a machine type.

- **Machine name**—This name is used in the simulation software to identify the machine. If you plan to use DICOM RT to export plans, limit the machine name to 16 characters or less.
- **ID = n**—The ID number is used by the software internally to identify the machine.
- **Machine type**—Select the machine type from the list of machines.

NOTE
If the type of machine that you are defining does not appear in the **Machine type** list, select the machine that most closely matches the machine that you are defining.

4 Enter the other machine parameters as described in the following sections.

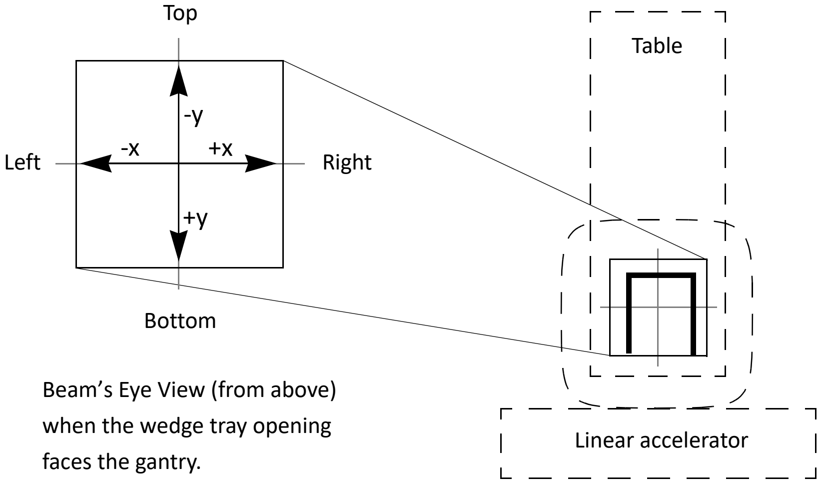
⚠ **WARNING**
If you enter information incorrectly in the Machine Editor window, the software may report incorrect output during simulation.

5 To save your changes, click **Dismiss** to close the window and click **Save Current Machine** in the **Photon Physics Tool** window.

Enter Jaw Information

CAUTION
The coordinate system used for the jaw definitions is also used to identify X profile and Y profile directions for measured scan data. These are oriented in reference to the tray opening and NOT to the labels used for the jaw names. We recommend that you define the collimator angles and jaw names correctly prior to importing machine scan data.

The software refers to the **Left**, **Right**, **Top**, and **Bottom** jaws when the collimator angle is such that the tray opening faces the gantry, as indicated in the following illustration. These labels are used in the **Machine Editor** window for all collimator jaw parameters. If your institution uses different terminology, you can set your labels in the jaw name and jaw pair name fields.



Beam's Eye View (from above) when the wedge tray opening faces the gantry.

Click the **Jaws** tab in the **Machine Editor** window. The jaw information appears in the window.

1 Specify the following jaw information.
   - **Machine has a fixed jaw**—This option lets you specify that the machine has a fixed jaw.

     NOTE
     If you set **Machine has a fixed jaw** to **Yes**, the **Can be asymmetric** and **Jaw Min and Max Position** fields do not appear in the window.

   - **Left, right, top, and bottom jaw names**—The names you enter in these fields are used as labels for the collimator jaws in the simulation software.
   - **Jaw pair names**—The names you enter in these fields are used as labels for the collimator jaw pairs in the simulation software.
   - **Jaw pair thickness**—These values are the thicknesses (in centimeters) of the specified jaw pairs.
   - **Can be asymmetric?**—These options let you specify whether the specified collimator jaws can move independently.

- **Jaw Min and Max Positions**—These values are the minimum and maximum jaw positions (in centimeters) projected at isocenter as measured from the central axis. If the jaws move past the central axis, enter negative values for the jaw limits.
- **Jaw positions**—These positions specify the jaw positions used when a beam is added in the simulation software.

  NOTE
  For fixed jaw machines, the jaw positions entered here are the jaw positions used in the simulation software and cannot be edited from the simulation software. For machines that do not have fixed jaws, the jaw positions are default positions.

- **Decimal places**—These values are the number of decimal places allowed for collimator jaw settings. For example, a setting of one decimal place allows you to specify 5.5, but not 5.25. If independent jaws will be used, you should specify two decimal places.

2 In the **Photon Physics Tool** window, click **Save Current Machine**.

Enter Couch Information

1 Click the **Couch** tab in the **Machine Editor** window. The couch information appears in the window.

2 Specify the following couch information.

- **Minimum angle**—This value is the minimum couch angle that is allowed by the machine. Enter the angle in the field or rotate the couch in the graphic.
- **Maximum angle**—This value is the maximum couch angle that is allowed by the machine. Enter the angle in the field or rotate the angle in the graphic.

NOTE
Depending on the origin and direction of rotation, the minimum angle can be greater than the maximum.

- **Default angle**—This value is the couch angle used when a beam is added using this machine.
- **Decimal places**—This value is the number of decimal places that are allowed on this machine when setting the couch angle.

3 Enter the couch angle when the foot of the couch points away from the gantry. This field is located below the graphic on the **Couch** tab. This information is used to translate the couch angles to the coordinate system used in the Pinnacle^3 planning software.

4 Specify the direction of positive rotation when viewing the couch from above by selecting **Yes** or **No** next to **When viewed from above, is positive rotation clockwise?**. This information is used to translate the couch angles to the coordinate system used in the Pinnacle^3 planning software.

NOTE
Positive rotation means that the angle is increasing when rotating (for example, 0 degrees to 90 degrees).

5 Enter the minimum, maximum, and default values (in centimeters) for the vertical, lateral, and longitudinal positions of the couch in the **Couch position in cm** section. These values are used to limit the couch position settings in the Pinnacle^3 planning software and to translate the couch position to the coordinate system used in the software. If necessary, refer to the manufacturer's information to determine the values.

6 In the **Photon Physics Tool** window, click **Save Current Machine**.

Enter Collimator Information

1 Click the **Collimator** tab in the **Machine Editor** window. The collimator information appears in the window.

2 Specify the following collimator information.

- **Minimum angle**—This value is the minimum collimator angle that is allowed by the machine. Enter the angle in the field or rotate the collimator in the graphic.
- **Maximum angle**—This value is the maximum collimator angle that is allowed by the machine. Enter the angle in the field or rotate the collimator in the graphic.

  NOTE
  Depending on the origin and direction of rotation, the minimum angle can be greater than the maximum.

- **Default angle**—This value is the collimator angle used when a beam is added using this machine.
- **Decimal places**—This value is the number of decimal places that are allowed on this machine when setting the collimator angle.

3 Enter the collimator angle when the tray opening faces the gantry. This field is located below the graphic on the **Collimator** tab. This information is used to translate the collimator angles to the coordinate system used in the software.

> **NOTE**
> If the collimator on your machine cannot be rotated to this position, enter the angle that would be used if you could rotate the tray opening to face the gantry.

4 Specify the direction of positive rotation when viewing the collimator from above by selecting **Yes** or **No** next to **When viewed from above, is positive rotation counterclockwise?**. This information is used to translate the collimator angles to the coordinate system used in the software.

5 In the **Photon Physics Tool** window, click **Save Current Machine**.

Enter Gantry Information

1 Click the **Gantry** tab in the **Machine Editor** window. The gantry information appears in the window.

2 Specify the following gantry information.

- **Minimum angle**—This value is the minimum gantry angle that can be achieved by the machine. Enter the angle in the field or rotate the gantry in the graphic.
- **Maximum angle**—This value is the maximum gantry angle that can be achieved by the machine. Enter the angle in the field or rotate the gantry in the graphic.
- **Default angle**—This value is the gantry angle used when a beam is added using this machine.
- **Decimal places**—This value is the number of decimal places that can be used on this machine when setting the gantry angle.
- **Arc allowed?**—Specify whether the gantry can be rotated to generate arcs. You must set this option to **Yes** if you want to use photon arcs.
- **Arc rotation direction**—Specify whether the gantry rotates in the clockwise direction only (CW), counterclockwise only (CCW), or in either direction.

3 Enter the gantry angle when the beam is aimed straight down at the floor. This field is located above the graphic on the **Gantry** tab. This information is used to translate the gantry angles to the coordinate system used in the software.

4 Specify the direction of positive rotation when facing the gantry from the foot of the couch by selecting **Yes** or **No** next to **When facing gantry, is positive rotation counterclockwise?**. This information is used to translate the gantry angles to the coordinate system used in the software.

5 Does your machine have a C-Arm?

- Yes—Select **Yes** next to **Machine has C-Arm?**. Go to step 6.
- No—Select **No** next to **Machine has C-Arm?**. Go to step 7.

NOTE
C-Arm is available for photon beams and can be used with static, step-and-shoot, arc, and conformal arc beam types. C-Arm is only available if you are licensed for C-Arm.

6 Enter the maximum rotation angle (0 - 60 degrees) for the C-Arm.

NOTE
You cannot change the C-Arm decimal places field. Also, the couch angle is set to 0 degrees for machines that are commissioned with a C-Arm, and you cannot change the couch angle.

7 In the **Photon Physics Tool** window, click **Save Current Machine**.

Enter Delivery Information

1 Click the **Delivery** tab in the **Machine Editor** window. The delivery information appears in the window.

2 In the **Maximum gantry rotation speed** field, enter the maximum speed that the machine's gantry can rotate.

3 In the **Maximum jaw speed** field, enter the maximum speed that the machine's jaws can move.

4 In the **Maximum MLC leaf speed** field, enter the maximum speed that the machine's MLC leaves can move.

5 Do you want to enable conformal arc beams?

- Yes—Select **Yes** next to **Conformal Arc**.
- No—Select **No** next to **Conformal Arc**.

6 Do you want to enable dynamic arc beams?

- Yes—Select **Yes** next to **Dynamic Arc**. Additional options appear for dynamic arc beams. Continue to step 7.
- No—Select **No** next to **Dynamic Arc**. Continue to step 12.

> **NOTE**
> To enable conformal arc beams or dynamic arc beams, the machine must have a multi-leaf collimator and be capable of arc delivery.

7 Select the method of dose delivery that the machine uses for dynamic arc beams:

- Constant dose rate—Select **Yes** next to **Dose rate constant?**. The software finds the optimal dose rate to deliver to all control points during a VMAT optimization.
- Continuously variable dose rate—Select **No** next to **Dose rate constant?**, then select the **Continuously variable** option that appears. The software uses the smallest and largest dose rate values that you enter in the **Allowable Dose Rates** table in the **Machine Photon Energy Editor** window to determine the dose rate range during a VMAT optimization.
- Binned dose rate—Select **No** next to **Dose rate constant?**, then select the **Binned** option that appears. The software uses only the dose rate values that you enter in the **Allowable Dose Rates** table in the **Machine Photon Energy Editor** window during a VMAT optimization.

> **NOTE**
> The dose rate delivery behavior that you choose applies only to dynamic arc beams. To specify the allowable dose rates for other beam types, you must enter the dose rate values in the **Machine Photon Energy Editor** window. See *Add Photon Energies for a Machine*.

8 In the **Maximum gantry MU delivery** field, enter the maximum number of MUs that the machine can deliver during a single degree of gantry rotation.

9 In the **Minimum gantry MU delivery** field, enter the minimum number of MUs that the machine can deliver during a single degree of gantry rotation.

10 In the **Minimum MLC leaf MU delivery** field, enter the minimum number of MUs that the machine can deliver during one centimeter of MLC leaf motion.

11 Does the machine limit the gantry acceleration?

   - Yes—Select **Yes** next to **Limit gantry acceleration?**, then enter the maximum acceleration value in the **Maximum gantry rate change** field that appears. During a VMAT optimization, the software does not allow the gantry speed to increase or decrease by greater than this value when moving between two neighboring control points.
   - No—Select **No** next to **Limit gantry acceleration?**.

12 In the **Photon Physics Tool** window, click **Save Current Machine**.

Enter Other General Machine Parameters

1 Click the **Misc** tab in the **Machine Editor** window. The general machine parameters appear in the window.

2 Specify the following information.

- **Primary collimation angle**—This value is the half angle (in radians) of the primary collimator. This parameter is used only for systems that have conical primary collimation. If the accelerator uses non-circular primary collimation, you do not need to adjust this parameter. The default value (0.8 radians) is large enough to ensure that the incident fluence for even the largest fields is not truncated.

  If the hardware specifications are unavailable for the accelerator, then you can determine this parameter by measuring the dose in a water phantom along a scan diagonal to the jaw-collimated field for the largest field size possible. The measurement can be taken at a distance of SAD from the source, and a depth of 10 cm (i.e., SSD = SAD - 10 cm). From the scan, identify the distance from the beam central axis to where the dose is 50% of the central axis value. This distance divided by the machine SAD is almost equal to the tangent of the primary collimator angle.
- **Source to axis**—This value is the source to gantry axis distance (in centimeters).
- **Source to (bottom of) flattening filter**—This value is the distance (in centimeters) from the source to the bottom of the flattening filter. This information should be available from the accelerator manufacturer.
- **Source to (bottom of) top/bottom jaw**—This value is the distance (in centimeters) from the source to the bottom of the collimators for the Top/Bottom jaw pair.

  NOTE
  For fixed jaw machines, there is only one source to (bottom of) jaw distance field. The source to jaw distances are used to determine the most limiting collimating device when computing the scatter field. For the Elekta Beam Modulator machine, the millstone will generally be the most limiting collimating device (with the MLC). Therefore, use the distance to the bottom of the millstone for the Elekta Beam Modulator machine.
- **Source to (bottom of) left/right jaw**—This value is the distance (in centimeters) from the source to the bottom of the collimators for the Left/Right jaw pair.
- **Source to (top of) block tray**—This value is the distance (in centimeters) from the source to the top of the block tray.
- **Source to image receptor**—This value is the distance (in centimeters) from the source to the image receptor.
- **Simulation only (without dose profiles)**—Specify whether the machine will be commissioned as a simulation-only machine. If you set this option to **Yes**, you will not be able to compute dose with this machine. Set this option to **Yes** to commission machines for use with TumorLOC.

NOTE
If you set this option to **Yes**, you do not have to import or compute profiles, automodel, or compute output factors when you commission the machine. You only have to enter the machine parameters as described in this chapter.

If, in the future, you want to use this machine to compute dose, set the **Simulation only (without dose profiles)** option to **No**, and then complete the commissioning process as described in the *Pinnacle^3 Physics Instruction for Use*.

- **Monitor Unit decimal places**—The software uses the values in the **Beams** field and the **Control points** field to round the monitor units for beams and control points, respectively. The software rounds the monitor units after you calculate dose in Planning or IMRT.

  If you set the monitor units decimal places to 0 for beams or control points, the software rounds the number of monitor units to a whole number, which may result in differences between the monitor units in Pinnacle^3 and hand-computed monitor units.
- **Maximum MU setting**—This value is the maximum allowable monitor unit setting per beam for a machine.
- **When MU limit exceeded, warn and**—Specify the behavior of the system when the maximum monitor unit setting is exceeded.

  If you select the **Limit beam MU to maximum setting** option, the actual monitor units required for a prescription are not displayed. Instead, the maximum monitor unit setting is displayed. The dose that is displayed is proportional to the limited MUs.

  If you select the **Allow beam MU to exceed maximum** option, the software will allow the beam to exceed the maximum MU setting you defined so that the MU displayed will be the actual MU required for the prescription.
- **Default block/field edge overlap (cm)**—This value is the margin of overlap that should exist between a block and the edge of the field. This sets the default value that appears in the **Export** window of the planning software.
- **Delivery time multiplier**—This is the default value that is used to calculate the maximum delivery time for each beam in a treatment plan. We recommend that you enter a default value based on the type of plan you deliver most often. As needed, you may change the default value for a beam during treatment planning.

3 In the **Photon Physics Tool** window, click **Save Current Machine**.

Enter Multi-Leaf Collimator Information

If the machine is equipped with a multi-leaf collimator (MLC), you must enter information about the leaf geometry and leaf position limits.

1 In the **Machine Editor** window, click **MLC**. The **MLC Editor** window opens.

2 Select **Yes** next to **Machine has Multi-leaf Collimator (MLC)** to specify that the machine has an MLC.

> **NOTE**
> For fixed jaw machines, **Machine has Multi-leaf Collimator (MLC)** is set to **Yes** and cannot be changed.

3 Continue to the sections that follow and enter the MLC configuration for the machine.

Set General Parameters

1 In the **MLC Editor** window, click the **General** tab.

2 Specify the MLC vendor.

3 Define the direction of movement for the MLC leaves by specifying whether the leaf motion is parallel to the **Left/Right** or **Top/Bottom** jaw pair motion. Refer to the drawing in *Enter Jaw Information* to verify the correct jaw pairs and positions.

⚠ **CAUTION**
If you specify that the MLC leaves should replace one pair of jaws, Pinnacle^3 will assume that pair of jaws does not exist when calculating dose only if the Use MLC? option is set to Yes. The jaws will appear in the software and on plan reports, but Pinnacle^3 will not include them in any calculations.

4 Specify whether the MLC replaces the jaws on the machine. If the MLC does not replace the jaws, specify the distance from the source to the bottom of the MLC leaves, in centimeters.

> **NOTE**
> If you change this setting after you have computed profiles, the software will invalidate the profiles.

> **NOTE**
> If the machine is an Elekta machine, for proper commissioning you must set this setting to **No**.

> **NOTE**
> For fixed jaw machines, **MLC replaces jaw?** is set to **No** and cannot be changed.

5 If the MLC always tracks the jaws, select an option from the **MLC tracks jaws?** list. The specified behavior is applied during dose computation, even for beams that do not have the MLC turned on.

> **NOTE**
> The **MLC tracks jaws?** list does not appear for fixed jaw machines.

NOTE
The jaws listed in the **MLC tracks jaws?** list are relative to the Pinnacle^3 MLC orientation, so the X jaw option always corresponds to the jaw to which the MLC is parallel. For example, if leaf motion is parallel to the **Top/Bottom Jaw** and you select the **MLC tracks X jaws for open fields** option, the MLC will always track the top/bottom set of jaws.

NOTE
For machines in which the MLC replaces jaws, setting the MLC to not track the jaws is equivalent to setting the MLC to track the X jaw because the MLC is the X jaw in Pinnacle^3.

6 Specify the thickness (in centimeters) of the MLC leaves. The thickness of the leaves is the thickness along the rayline of the beam.

7 Specify the number of decimal places for MLC leaf positions. The leaf positions created in the simulation software are reported using the number of decimal places you enter.

8 Specify names for the banks of leaves. By default, names correspond to the left and right banks of leaves. If you aligned the leaves with the **Top/Bottom Jaw**, specify names for the top and bottom banks.

9 Specify whether the top jaw is positioned at **+Y** or **-Y**.

The **-Y** selection is the default. If you aligned the leaves with the **Top/Bottom Jaw**, you specify whether **+X** or **-X** corresponds to the left jaw.

10 Select **Yes** for **MLC has rounded leaves?** if your MLC leaves have rounded leaf ends. The **Rounded leaf end specs** button appears on the tab, and the **Rounded Leaf End Specification** window opens. See *Set Up Rounded Leaf Ends* to create the rounded leaf end table.

11 Select **Yes** for **MLC has carriage?** if your MLC travels with the carriage. This setting applies to Varian machines only.

If you select **Yes**, the **Maximum tip position from the jaw (cm)** field appears. Enter the maximum distance a leaf is allowed to extend out from the jaw.

12 In the **Photon Physics Tool** window, click **Save Current Machine**.

Set Up Rounded Leaf Ends

You can set up a table that describes the offset of the MLC to accommodate the difference between the actual leaf position and the Pinnacle^3 leaf position (the leaf position on the accelerator readout). See the *Pinnacle^3 Physics Reference Guide* for more information about leaf position.

NOTE
We strongly recommend that you confirm that the leaf offset tables you are using are accurate for all vendors and MLC devices. Contact your linear accelerator vendors for this information.

For Varian, the leaf offset data can be found in the MLCTABLE.TXT file on the MLC controller. The data are also available in the Varian sample machine provided with the Pinnacle^3 software. The offset values in the Pinnacle^3 **Leaf Offset Calibration** table can be derived from the MLCTABLE.TXT file by taking the values in the second column of the table in the MLCTABLE.TXT file and subtracting the values in the first column. The leaf positions in the **Leaf Offset Calibration** table should be the values in the second column of the table in the MLCTABLE.TXT file.

For Elekta, the leaf offset data are available in the Elekta sample machines provided with the Pinnacle^3 software. See *Add Machines to the Physics Database* for information about adding a sample machine to the database.

1. On the **General** tab, click **Rounded Leaf End Specs**. The **Rounded Leaf End Specification** window opens.
2. Enter the radius of curvature for the rounded leaf end in the **Rounded Leaf Tip Radius** field. For detailed information about the radius of curvature, see the *Physical Machine Characteristics* chapter in the *Pinnacle^3 Physics Reference Guide*.
3. To have the software enter default values for the table, click **Create Default Table**.
4. To edit the values in the table, click the cell that you need to edit and enter a value in the field above the table.

   NOTE
   The limits for offset values are -1 cm to +1 cm.

5. To add a leaf position, click **Ins Before** or **Ins After**.

   To delete a leaf/point, select it and click **Delete Point**. To delete all the leaves in the table, click **Delete All Points**.

6. In the **Photon Physics Tool** window, click **Save Current Machine** when you are finished setting up the rounded leaf ends.

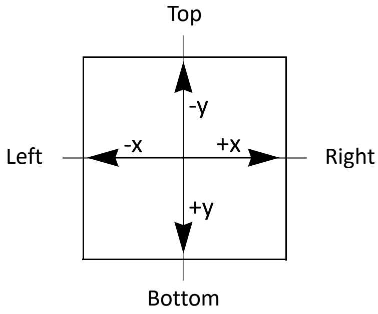
Set Leaf Parameters

1. In the **MLC Editor** window, click the **Leaves** tab.
2. Click **Add leaves** to set up the leaves for the multi-leaf collimator. The **MLC Leaf Pair Definition Window** opens.

   NOTE
   You can use the **Add leaves** option to add one leaf pair or a set of leaf pairs to an MLC. For a machine with an MLC that has leaves of varying widths, you may want to use this option multiple times—once for each set of leaf pairs of a common width. For a machine with leaves of uniform widths, you only need to add leaves once.

3. Enter the following information about the leaves to be added.
   - **Number of leaf pairs**—Specifies the number of leaf pairs to add to the MLC.

- **Center X/Y coordinate of first pair**—This is the X/Y position of the center of the first leaf pair to be added to the MLC. The X/Y position should be specified as an offset from the central axis at isocenter, as shown in the diagram below.



Beam's Eye View (from above) when the wedge tray opening faces the gantry

- **Leaf Width**—The width at SAD of the leaves to be added.
- **Minimum and Maximum Tip Positions**—The minimum and maximum tip positions (projected at isocenter) for the leaves to be added, specified in centimeters.

4 Click **Add Leaf Pairs** to add the leaves to the MLC.

5 Once you have added the leaves, you can specify the parameters for individual leaf pairs.

Select a leaf pair from the list and edit the Y position at isocenter, width, and the minimum and maximum tip positions in the fields to the right of the list. These parameters have the same functions as those described in the **MLC Leaf Pair Definition** window. If you edit the Y positions of any leaf pairs and want to re-sort the **Leaf pairs** list to be in ascending order, click **Sort leaves**.

NOTE
If you want to remove a leaf pair, select it from the list and click **Remove current leaf**. To remove all the leaves from the MLC, click **Remove all leaves**.

6 Choose an **Allow opposing adjacent leaves to overlap?** setting.

Select **Yes** for Varian and Elekta Beam Modulator machines so that the MLC leaves can interdigitate. In addition to allowing MLC leaves to overlap, interdigitation also allows the software to move the junctions between closed leaf pairs underneath the jaws during an IMRT conversion.

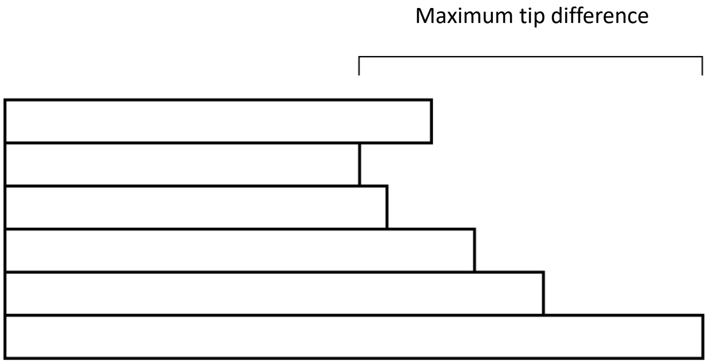
Select **No** for Siemens and other Elekta machines and any other machines that do not allow MLC leaves to interdigitate.

7 Enter the tongue and groove width at the intersection of the leaves. The software uses this value to attenuate the radiation through half of the thickness of the leaf at the overlap of the tongue and groove. (See the *Pinnacle*^{3} *Physics Reference Guide* for more information about tongue and groove width.)

8 Enter the additional interleaf leakage transmission. This value is the amount of transmission between two closed MLC leaves, and it is added to the MLC transmission in the region where the two leaves intersect. (See the *Pinnacle*^{3} *Physics Reference Guide* for more information about interleaf leakage transmission.)

9 Enter the maximum tip difference for all leaves on a side (in centimeters). This value is the maximum distance (projected at the isocenter) allowed between the most retracted leaf and the most extended leaf of a leaf bank.

The manufacturer should be able to provide values for the maximum tip difference. These differences are required for mechanical and shielding considerations. Settings you enter here are enforced during simulation, planning and IMRT conversions.



10 Enter the minimum static leaf gap (in centimeters). This value is the minimum distance (projected at the isocenter) that should be maintained when the leaves are closed while they are stationary.

11 Enter the minimum dynamic leaf gap (in centimeters). This value is the minimum distance that should be maintained between the leaves when the leaves move.

NOTE
The minimum static leaf gap and the minimum dynamic leaf gap are applied to all leaf pairs.

12 In the **Photon Physics Tool** window, click **Save Current Machine**.

Set Jaw Dependencies

1 In the **MLC Editor** window, click the **Jaw Dependencies** tab.

⚠ **CAUTION**
If you are exporting plans to a Varian linear accelerator, set the default jaw behavior to Static.

2 Set the default behavior for the jaws by selecting an option from the **Default jaws behavior** list. The specified behavior is applied only to beams with multiple control points.

- **Static**—The jaw positions are the same for all control points in a beam.
- **Variable**—The jaws conform to the MLC shape of each control point and can be different for each control point.

NOTE
For fixed jaw machines, the **Default jaws behavior** list is set to **Static** and cannot be changed.

3 Do you want the software to open an extra set of leaf pairs at the top and bottom of the exposed field automatically?

- Yes—In the **Open extra set of leaf pairs outside jaws automatically** field, select **Yes**.
- No—In the **Open extra set of leaf pairs outside jaws automatically** field, select **No**.

4 Set the maximum and minimum leaf/jaw overlap. These values determine how far under the opposing jaw an MLC leaf can extend. The actual overlap distance may vary between the minimum and maximum overlap values that you specify.

For more information on minimum and maximum leaf/jaw overlap, see the *Physical Machine Characteristics* chapter in the *Pinnacle^3 Physics Reference Guide*.

Add Photon Energies for a Machine

Before you can commission a machine, you must add the available photon energies for the machine.

1 In **Photon Physics Tool** window, click **Add** beneath the **Energy List**. The software warns you that you are about to add a new photon energy.

2 Click **OK** to continue.

3 Click **Edit** beneath the **Energy List**. The **Machine Photon Energy Editor** window opens.

4 Enter an appropriate name for the energy in the **Energy Name** field. During simulation you will use this name to select the energy.

5 Enter the energy in MV in the **Energy** field.

6 Enter the default tray factor for this energy in the **Default Tray Factor** field. During simulation this is the default value the software uses when you add a block to a beam of this energy.

7 Enter the block and tray factor for this energy in the **Default Block and Tray Factor** field. During simulation this is the default value the software uses when you add a block to a beam of this energy.

NOTE
You can disregard the **Fluence Mode ID** field because it is not applicable for the TumorLOC software.

8 In the **Allowable Dose Rates** table, enter the dose rates that you want to make available for the machine during planning. The table must contain at least two dose rates: a maximum and a minimum dose rate. Click **Insert Before** and **Insert After** to add additional dose rates to the table.

Alternatively, you can enter the maximum dose value in the **Max value** field and then click **Generate default table** to create a new table. When you generate a default table, the software creates a table with seven dose rates. The first dose rate is equal to the maximum dose value, and each subsequent dose rate is half the value of the previous dose rate (rounded down to an integer). After you create a default table, you can edit it as necessary.

9 Select the default dose rate for beams that use this energy from the **Default Dose Rate** list.

10 When you finish entering the machine energy information, click **Dismiss**.

11 In the **Photon Physics Tool** window, click **Save Current Machine**.

Commission a Machine for Simulation

After you enter the physics information for a machine, you must commission it for use in simulation. The commissioning process moves a machine from the physics machine database to the planning machine database and “stamps” the machine with the date and time of commissioning.

A commissioned machine is available only in the simulation software. If you want to make changes to a machine after commissioning, you must copy it back into the physics machine database using the **Add Machines** option, make the changes using the physics tools, and then commission the machine again.

1 In the **Photon Physics Tool** window, select the machine to be commissioned from the **Machine List** and then click **Commission**. The **Commission Machine** window opens.
2 Select **Yes** for **Photons**.
3 Type your name or initials in the **Commissioned By** field.
4 If necessary, type a description for the machine in the **Description** field.
5 Click **OK** to commission the machine.

If the machine cannot be commissioned, the **Commission Failure** window opens. See *Commission Failure* for information about correcting the problems listed in the window. Once the problems are resolved, repeat the steps in this section to commission the machine.

Commission Failure

If problems occur during the commissioning process, a list of errors appears in the **Commission Failure** window. Problems that can prevent commissioning include the following items:

- Empty **Commissioned By** field—To correct this problem, return to the **Commission Machine** window, enter your name or initials in the **Commissioned By** field, and then attempt to commission the machine again.
- Photon measured data not read in—This message appears if you did not set **Simulation only (without dose profiles)** to **Yes** in the **Machine Editor** window. To correct this problem, return to the **Machine Editor** window, click the **Misc** tab, and set **Simulation only (without dose profiles)** to **Yes**.

Delete Machines

You can delete machines from both the planning and physics machine databases using options in the physics tools.

Delete Non-Commissioned Machines

If you have created a machine but have not commissioned it, you can delete it using the **Photon Physics Tool** window.

WARNING
Once a non-commissioned machine is deleted, it cannot be restored.

1. In **Photon Physics Tool** window, select the machine that you want to delete from the **Machine List**.
2. Click **Delete** beneath the **Machine List**, and then click **Delete** again in the next window to confirm the deletion.

   Click **Dismiss** to cancel the deletion.

   NOTE
   The machine is not deleted until you save the physics data by clicking **Save All Machines** or exit the physics tool with the **Save All Machines** option set to **Yes**.

Delete Commissioned Machines

If necessary, you can remove a commissioned machine from the planning machine database.

NOTE
We strongly discourage the deletion of commissioned machines. All commissioned versions of a machine are saved in the planning machine database to allow plans to be read in and replicated with the machine used when the plan was generated.

1. In **Photon Physics Tool** window, click **Add** beneath the **Machine List**. The **Add New Machine** window opens.
2. Select **Current Commissioned Machines** to display the list of commissioned machines.
3. Select the machine you want to delete and click **Delete**. The **Confirm Current or All Versions Delete** message appears.
4. Do one of the following:
   - To delete all versions of the selected machine, click **Delete All Versions**. The **Confirm All Versions Delete** message appears. Continue to step 5.
   - To delete only the currently commissioned version of the machine, click **Delete Current Version**. The **Confirm Commissioned Machine Delete** message appears. Continue to step 6.
   - Click **Cancel** to close the message without deleting the machine.

5 Do one of the following:

- To move all versions of the machine to the **Deleted Commissioned Machines** list, click **Move All Versions to Deleted List**. All versions of the machine are moved to the **Deleted Commissioned Machines** list, and the machine is no longer accessible in the simulation software. This procedure is complete.
- To delete all versions of the machine permanently, click **Delete All Versions Permanently**. All versions of the machine you selected are deleted from the **Current Commissioned Machines** list and the **Old Commissioned Machines** list, and the machine is no longer accessible in the simulation software. This procedure is complete.

  NOTE
  We recommend that you move the machine to the **Deleted Commissioned Machines** list rather than permanently delete it. However, if you want to permanently delete the machine, we recommend that you have a full working backup of the commissioned machine so that you can restore it later, if necessary.

- Click **Cancel** to close the message without deleting the machine.

6 Do one of the following:

- To move the machine to the **Deleted Commissioned Machines** list, click **Move Machine to Deleted List**. The currently commissioned version of the machine you selected is moved to the **Deleted Commissioned Machines** list, and the machine is no longer accessible in the simulation software. The most recent old version of the machine is moved from the **Old Commissioned Machines** list to the **Current Commissioned Machines** list. This procedure is complete.
- To delete the machine permanently, click **Delete Machine Permanently**. The currently commissioned version of the machine you selected is deleted from the **Current Commissioned Machines** list, and the machine is no longer accessible in the simulation software. The most recent old version of the machine is moved from the **Old Commissioned Machines** list to the **Current Commissioned Machines** list. This procedure is complete.

  NOTE
  We recommend that you move the machine to the **Deleted Commissioned Machines** list rather than permanently delete it. However, if you want to permanently delete the machine, we recommend that you have a full working backup of the commissioned machine so that you can restore it later, if necessary.

- Click **Cancel** to close the message without deleting the machine.

Restore Deleted Commissioned Machines

When you move commissioned machines to the **Deleted Commissioned Machines** list, you cannot use them in the simulation software, but you can still access them in physics, if necessary. If an old plan uses a machine that has been deleted, and you do not have another machine in the **Current Commissioned Machines** list or the **Old Commissioned Machines** list that has the same name as the deleted machine, you cannot open the old plan unless you restore the deleted machine first. However, if your **Current Commissioned Machines** list contains a newer version of a machine that has the same name as the deleted machine, you can open the old plan.

1 In **Photon Physics Tool** window, click **Add** beneath the **Machine List**. The **Add New Machine** window opens.

2 Select **Deleted Commissioned Machines** to display a list of commissioned machines that have been deleted.

3 Select the machine you want to restore and click **Undelete**.

The machine is now available in the planning machine database. The most recent version of the machine will appear in the **Current Commissioned Machines** list, and all other versions of the machine will appear in the **Old Commissioned Machines** list.

4 Import Image Data Sets

Image data sets must be imported before you can open a plan. In most cases, image data sets are automatically imported into the **Available Images** list for the patient in the **TumorLOC Patient Directory** after the scans are complete. However, if you do not see the image data set that you expect or if your system is not set up for automatic import, you can import image data sets manually.

For information about DICOM conformance, see *DICOM Conformance* in the *Getting Started* chapter.

> **NOTE**
> If an image data set was imported automatically but you do not see the patient's name in the **TumorLOC Patient Directory** or the image data set in the **Available Images** list for the patient, either select another patient or select another image data set to force an update to the directory. The patient's name and the image data set will appear in the **TumorLOC Patient Directory**.

1. In the **TumorLOC Patient Directory**, verify that the institution that is selected in the **Institution** list is the institution that you want to use. If necessary, select a different institution from the **Institution** list.
2. Click **Import images**. The **DICOM Image Import** window opens.

   > **NOTE**
   > You must have a DICOM image data source configured for your system in order to import image data sets. See *Set Up Scanners* for information about configuring a scanner as your image data source.

3. Select the image data set that you want to import.
4. Click **Import**. The image data set that you selected appears in the **Available Images** list in the **TumorLOC Patient Directory**. The patient information associated with the image data set also appears in the window.

   If the software finds a patient in this institution that has the same first name, last name, MRN number, and date of birth as the demographic information included in image data set that you imported, then the software imports the image data set into that patient's list of available image data sets. If the software does not find a patient whose information matches that of the image data set you imported, then the software creates a new patient using the first name, last name, MRN number and date of birth information from the image data set that you imported and imports the image data set into the new patient's list of available images.

5. If you need to refresh the **Images Available for Import** list (additional image data sets have been added to your DICOM server, for example), click **Refresh**.
6. When you are finished importing images, click **Close** to close the **DICOM Image Import** window.

Transfer Image Data Sets

You can transfer image data sets from one patient to another. The patients must be located in the same institution, and the image data sets that you want to transfer cannot have any plans associated with them.

1. In the **TumorLOC Patient Directory**, select the image data set that you want to transfer from the **Available Images** list.
2. Select the patient to whom you want to transfer the image data set from the list below the **Available Images** list.
3. Click **Transfer image data set** to transfer the image data set from the current patient to the selected patient.

Delete Image Data Sets from a Patient

1. Select the patient from the patient list in the **TumorLOC Patient Directory**.
2. Select the image data set that you want to delete in the **Available Images** list for the patient.
3. Click **Delete image data set**. The image data set that you selected is removed from the **Available Images** list.

NOTE
You cannot delete an image data set if it is used by a plan.

Delete Image Data Sets from the Server

You can delete patient image data sets from the **Images Available for Import** list in the **DICOM Image Import** window.

WARNING
Deleting the image data sets from the DICOM Image Import window removes the image data sets from your network server or storage device. If you delete an image data set and then decide that you want to use it, you will have to export the image data set back to the DICOM server before you will be able to import it.

1. In the **TumorLOC Patient Directory**, click **Import images**. The **DICOM Image Import** window opens.
2. Select the image data set that you want to delete.
3. Click **Delete**. The image data set that you selected is removed from the **Images Available for Import** list.
4. If you need to refresh the **Images Available for Import** list (additional image data sets have been added to your DICOM server, for example), click **Refresh**.
5. Click **Close** to close the **DICOM Image Import** window when you are finished deleting image data sets.

5 Manage Patient Information

NOTE
If the patient that you want to use is not shown in the patient list, verify that the institution that is selected in the **Institution** list is the institution that contains the patient. If necessary, select a different institution from the **Institution** list.

Edit Patient Information

1 Select the patient from the patient list in the **TumorLOC Patient Directory** and click **Edit** under the patient list. Alternatively, you can double-click the patient in the patient list. The **Edit Patient** window opens.

2 Edit the patient information as necessary.

3 Click **Close** to save your changes.

Delete Patient Information

NOTE
Deleting a patient permanently removes patient data from the server. Patient data should be deleted only when no plans will be created for the patient or if the patient data has been backed up. For details on backing up patient data, see *Backup and Restore*.

1 Select the patient from the patient list in the **TumorLOC Patient Directory**.

To select multiple patients, hold down the **Control** key or the **Shift** key as you click on the patient names.

2 Click **Delete** under the patient list to delete the patient.

Transfer Patient Information

1 Select the patient from the patient list in the **TumorLOC Patient Directory**.

2 Select the institution to which you want to transfer the patient from the transfer institution list below the patient list.

3 Click **Transfer patient** to transfer the patient from the current institution to the selected institution.

Sort Patient Information

You can sort the patient information according to the column headings in the patient list.

For example, to sort the patients by last name, click the **Last Name** column heading. The patient list is sorted by last name in ascending order. To sort the list in descending order, click the **Last Name** column heading again.

6 Patient Plans

NOTE
If the patient that you want to use is not shown in the patient list, verify that the institution that is selected in the **Institution** list is the institution that contains the patient. If necessary, select a different institution from the **Institution** list.

Add a Plan

Once you have imported images, you can add a new plan for the patient.

1. In the **TumorLOC Patient Directory**, select the patient for whom you want to create a plan. The image data sets that are available for the patient appear in the **Available Images** list.
2. Select the image data set that you want to use. The image data set details appear in the **Image Set Details** section of the **TumorLOC Patient Directory**.
3. Click **Add plan**. A new plan is added below the image data set that you selected and the **Edit Plan Details** window opens.
4. Change the information in the **Plan Name** and **Planner** fields, as necessary. You can also select the version of software for this plan from the **Tool Version** list, if more than one version is available.
5. The default primary image data set is the image data set for which you created the plan. To change the primary image data set, select the image data set from the **Primary Image Set** list.
6. Add secondary image data sets to the plan.
   - To add one secondary image data set, select the image data set from the **Available Secondary Images** list and click **Add image data set**.
   - To select multiple image data sets, hold down the **Ctrl** key or the **Shift** key as you select the image data sets, and then click **Add image data set**.
   - To add all of the secondary image data sets, click **Add all image data sets**.

   The image data sets that you selected appear in the **Selected Secondary Images** list.

   NOTE
   You can sort the **Selected Secondary Images** list according to the column headings in the list. For example, to sort the list by the name of the image, click the **Image Name** column heading. The list is sorted by image name in ascending order. To sort the list in descending order, click the **Image Name** column heading again.

7. If necessary, you can remove secondary image data sets from the **Selected Secondary Images** list. Select the image data set that you want to remove and click **Remove image data set**. The image data set is moved back to the **Available Secondary Images** list. Hold down the **Ctrl** key or the **Shift** key to select multiple image data sets.
8. Click **TumorLOC** to open the plan, or click **Close** to close the **Edit Plan Details** window. (Your primary and secondary image data set selections are not lost if you click the **Close** button.)

NOTE
There are a few limitations to the image data sets that can be used to open a plan. If any of the following are true, you will not be able to open a plan in the simulation software using that image data set:

- The images are not DICOM-compliant
- The patient position is decubitus
- Patient position information is missing
- The image data set has been modified since the data were acquired
- The image data set is not CT
- The image data has not been reconstructed into axial slices
- The image data set contains a synthetic water phantom or synthetic data
- The number of slices, the starting Z location, or both are different between gated image data sets
- The gated image data sets were acquired from different scans

In order to work with the plan, you must open it in the planning application.

NOTE
When you open a new plan, the plan is opened in the version of software that is specified in the **Default Tool** option in the **Configuration Options** menu in **Launch Pad**. (See *Set the Default Tool* for details.) If the default software version is set to Pinnacle^3 14.0 or earlier, the plan will open in the latest version of TumorLOC that is installed on the system. If the default software version is set to a version that is more recent than Pinnacle^3 14.0, then the plan will open in that particular version of TumorLOC.

Edit Plan Details

You can edit the details for any existing plan.

1. In the **TumorLOC Patient Directory**, select the patient for whom you want to edit plan details. The image data sets and plans that are available for that patient appear in the **Available Images** list.
2. Select the plan for which you want to edit the details. The plan details appear in the **Plan Details** section of the **TumorLOC Patient Directory**.
3. Click **Edit plan details** in the **Plan Details** section. Alternatively, you can double-click the plan in the **Available Images** list. The **Edit Plan Details** window opens.
4. Update the details of the plan as necessary, and click **Close** to close the window.

Change the Primary Image Data Set

You can change the primary image data set for a plan.

NOTE
If the plan was modified in another application (for example, you opened the plan in the Pinnacle^3 Planning application and then saved it), you will not be able to change the primary image data set in the TumorLOC software.

- To change the primary image data set for a plan that has not previously been opened in the TumorLOC software, go to *New Plan*.
- To change the primary image data set for a plan that has previously been opened and saved in the TumorLOC software, go to *Existing Plan*.

New Plan

1 In the **TumorLOC Patient Directory**, select the patient that contains the plan you want to change. The image data sets and plans that are available for the patient appear in the **Available Images** list.

2 Select the plan that you want to change. The plan details appear in the **Plan Details** section of the **TumorLOC Patient Directory**.

3 Click **Edit plan details** in the **Plan Details** section. The **Edit Plan Details** window opens.

4 Select the image data set that should be used as the primary image data set from the **Primary Image Set** list. The original primary image data set is moved to the **Selected Secondary Images** list. If the new primary image data set was listed in the **Selected Secondary Images** list, the image data set is removed from the **Selected Secondary Images** list.

5 Click **Close** to close the **Edit Plan Details** window.

Existing Plan

1 In the **TumorLOC Patient Directory**, select the patient that contains the plan you want to change. The image data sets and plans that are available for the patient appear in the **Available Images** list.

2 Select the plan that you want to change. The plan details appear in the **Plan Details** section of the **TumorLOC Patient Directory**.

3 Click **Edit plan details** in the **Plan Details** section. The **Edit Plan Details** window opens.

4 Select the image data set that should be used as the primary image data set from the **Primary Image Set** list. A warning message appears indicating that the ROI contours and the placement of the POIs may change relative to the patient’s anatomy and all locked POIs will be unlocked if you continue.

5 Choose one of the following:

  - Select **No** to make no changes to the plan. The warning message disappears and no changes are made to the primary image data set selected for this plan. Click **Close** to close the **Edit Plan Details** window. This procedure is complete.
  - Select **Yes** to change the primary image data set. The original primary image data set is moved to the **Selected Secondary Images** list. If the new primary image data set was listed in the **Selected Secondary Images** list, the image data set is removed from the **Selected Secondary Images** list.

    In addition, the software opens the plan in the TumorLOC software and updates the POIs and ROIs as necessary. The software also updates beams and blocks if blocks are automatically created based on an ROI and that ROI is changed for the new primary image data set. The software saves the plan when the updates are complete.

6. Review the plan to confirm that the ROI contours, the locations of the POIs, and the locations and apertures of the beams are correct for the new primary image data set.
7. Finish the localization and simulation for this plan with the new primary image data set.

Delete a Plan

1. In the **TumorLOC Patient Directory**, select the patient that contains the plan you want to delete. The image data sets and plans that are available for the patient appear in the **Available Images** list.
2. Select the plan that you want to delete. The plan details appear in the **Plan Details** section of the **TumorLOC Patient Directory**.
3. Click **Delete plan** to delete the plan.

Open an Existing Plan

NOTE
An asterisk (*) appears next to a plan's name when the plan is locked by another user or has been modified in another application (for example, the plan was opened in the Pinnacle^3 Planning application and then saved):

- Locked plan—you will not be able to open the plan until the other user closes the plan.
- Modified plan—you will not be able to open the plan for simulation. You must open the plan in the other application to continue working with that plan.

1 In the **TumorLOC Patient Directory**, select the patient whose plan you want to open. The image data sets and plans that are available for the patient appear in the **Available Images** list.

2 Select the plan that you want to open. The plan details appear in the **Plan Details** section of the **TumorLOC Patient Directory**.

NOTE
If you are opening a plan that was created in an older version of the software, the plan is still associated with the previous software version. To use the current software for older plans, click **Edit plan details** in the **Plan Details** section and select the current software version from the **Tool Version** list.

3 Click **TumorLOC**. The plan that you selected opens in the **Simulation** window.

NOTE
When you open a plan, the **Errors Encountered During Filing** window may appear. Generally, this window appears when you create a plan in an older version of the software and then open the plan in a newer version of the software. Make sure that no commissioning errors appear. You can ignore most non-commissioning errors.

Recover a Plan

If a power failure or fatal error occurs in the software, the **Plan Recovery** window appears when you reopen the plan. Use the window to attempt to recover the last normally saved plan or the last automatically saved plan. You can review both plans before you accept and save one of them.

The software initially loads the normally saved plan. After you review the normally saved plan, choose one of the options in the **Plan Recovery** window:

- **Exit with No Changes**—Both plans are left intact and you exit the software.
- **Accept and Save Plan**—The currently loaded plan is saved and the other plan (in this case, the last automatically saved plan) is lost.
- **Review Last Auto-Saved Plan**—The software loads the last automatically saved plan, which you can review. The **Plan Recovery** window now lets you choose whether to accept and save this plan or review the last normally saved plan.

NOTE
You can switch between the two plans as many times as needed. You will not lose either plan until you accept and save one of them.

Common Tools

The following tools are always available across all the worksteps in the **Simulation** window.

Tool	Name	Function
	Move POI	Click **Move POI** to drag the current POI to the desired position in either a 2D or BEV viewing window.
☐ Crosshairs	**Crosshairs**	Click this tool to display or hide the crosshairs for a POI. This tool is located in the **Move POI** flyout tool.
	Fluoro	Click **Fluoro** to move the isocenter by panning the image in a DRR or DCR display.
	Adjust collimator 3D	Click **Adjust collimator 3D** and drag one of the axes or the jaws to rotate the collimator.
	Center beam in field	Click **Center beam in field** to center the beam in the field. The isocenter of the beam moves to the center of the field. Although the jaw positions are updated, the field size remains unchanged and the jaws are made symmetrical.
	Center beam in patient	Click **Center beam in patient** to center the beam in the patient. The isocenter of the beam moves to the center of the patient along the beam center line.
✕	**Exit**	Click **Exit** to close the **Simulation** window.
	Save	Click **Save** to save your changes to the plan.
	Set preferences	Click **Set preferences** to open the **Preferences** window. For information, see *Preferences*.
●	**Record**	Click **Record** to record a script. The tool changes to the **Stop Recording** tool after you click it. For information, see *Scripting*.
■	**Stop Recording**	Click **Stop Recording** to stop recording a script. The tool changes back to the **Record** tool after you click it.
	Manage Scripting	Click **Manage Scripting** to open the **Scripting** window. For information, see *Scripting*.

7 View Patient Data

The software allows you to display two-dimensional (2D) and three-dimensional (3D) images of patient data. This chapter explains the visualization tools that you will use to view patient data.

Maximize the Viewing Area

To expand the viewing area on screen, you can hide the panel on the left side of the screen so that the viewing windows expand into that space.

« To expand the viewing area, click the **Hide** tool. The panel is hidden, and the viewing windows expand to the left.

» To restore the panel, click the **Show** tool. The viewing windows return to their original size and the panel reappears.

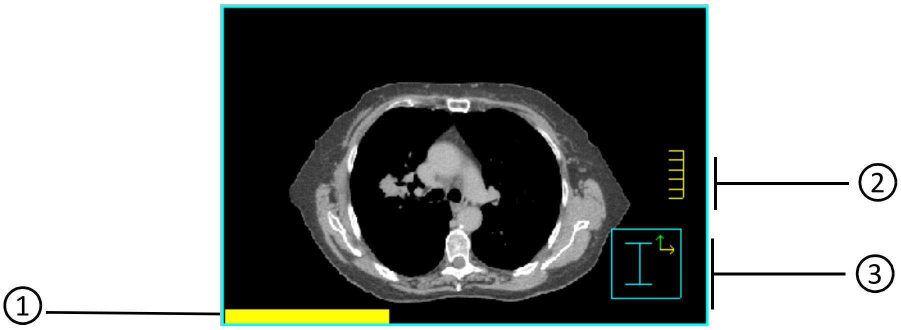
Maximize a Viewing Window

You can expand a viewing window so that it fills the entire viewing layout.

1. Right-click the viewing window that you want to expand.
2. On the menu that appears, select **Maximize Viewer**. The viewing window expands to fill the viewing area.
3. To return the viewing window to its original size, right-click the viewing window and select **Restore Viewer**.

> **NOTE**
> You can also press the **m** key to maximize or restore the viewing window.

2D Viewing Windows



1	The slice number, slice position, image data set name, and image-related information display in yellow text. For transverse images, slices are numbered from 1 starting at the end of the image set. The Z position corresponds with the scanner Z position for each slice. For sagittal and coronal images, the index number in the image data set is used as the slice number.
2	Ruler, which measures five centimeters and is scaled when the image is zoomed in and out
3	The orientation cube uses letters and arrows to indicate patient orientation. The letter in the box indicates the side of the image that is displayed: • A = Anterior • P = Posterior • S = Superior • I = Inferior • L = Left • R = Right Color-coded arrows on the box indicate patient orientation: • Green arrow is anterior-facing • Yellow arrow is left-facing • Orange arrow is superior-facing

NOTE
A change in the aspect ratio of your screen will distort the display for 2D images such that the scale in one direction is different than the scale in the other direction. However, this does not affect printed images.

Change the Display of a Viewing Window

You have several options for changing what is shown in 2D viewing windows. To access the tools, right-click a 2D viewing window and select **2D** on the menu that appears.

Menu Option	Description
Enter 3D Mode	Change the 2D viewing window to a 3D viewing window.
Next Data Set	View the next image data set. (This option is only shown if you have secondary image data sets loaded for a plan.)
Orientation	View a transverse, sagittal, or coronal image in the 2D viewing window.

Menu Option	Description
Interpolation	Select **Nearest Neighbor** or **Bi-linear**. Bi-linear interpolation takes longer to display but provides better display quality.
Zoom	Select **Fill Window**, **Double Zoom**, **Half Zoom**, or **Life Size** to change the magnification of the image. To return the magnification to the default setting, select **Fill Window**.
Choose Slice	Display a specific image in a 2D viewing window. In the window that appears, enter the number of the image you want to display.
Next Slice	View the next image in the image data set.
Previous Slice	View the previous image in the image data set.

There are several options that you can use to move through the slices and image data sets in a 2D viewing window. See *Visualization Tools* and *Keyboard Shortcuts* for information.

Set the Window and Level

You can set the window and level parameters to adjust the amount of contrast in each image set. A color scale is used to display the images. The “window” specifies the range of values to be mapped into the color scale. The “level” specifies the image value at which the range begins.

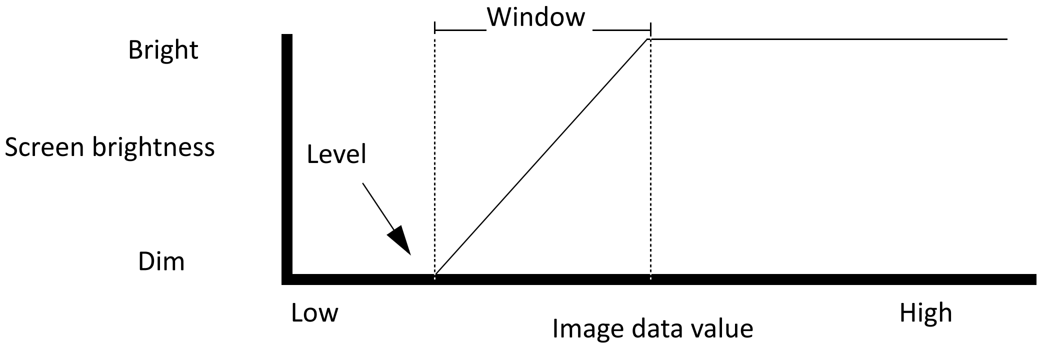


Image values below the level are set to the dimmest color. Image values above the level plus the window are set to the brightest color.

> **NOTE**
> If you have the **Middle Mouse Window/Level** preference set to **Yes**, you can use the middle mouse button in the viewing window to set the window and level. See *Preferences*.

You have several options for changing the window and level settings of a 2D viewing window.

- To use standard window and level settings, go to *Use the Presets*.
- To interactively change the window and level in the viewing window, go to step 1.

1. Right-click the 2D viewing window and select **Tools** on the menu that appears.
2. Select **Window/Level** from the **Tools** menu.
3. Drag the cursor across the viewing window to change the window and level settings. Drag the cursor left and right to change the window. Drag the cursor up and down to change the level.

Use the Presets

You can use standard window and level settings to adjust the brightness and contrast of a 2D image.

1. Right-click a 2D viewing window and select **Presets** on the menu that appears.
2. Select the preset that you want to use. The image is adjusted to the window and level settings of the preset that you chose.

Edit the Presets

You can create new presets or modify existing presets.

1. Right-click the 2D viewing window you want to modify, and select **2D** on the menu that appears.
2. Select **Edit Presets** on the **2D** menu. The **MPR Preset Editor** window opens. A list of standard preset window and level settings appears in the window.

   The window is divided into two sections:

   - The **Preset Settings** section lists the settings for the preset that is selected in the preset list. When you change values in the **Preset Settings** section of the window, the values in both the preset itself and in the current viewing window are updated.
   - The **Current Viewer Settings** section lists the settings that are being used in the viewing window in which you right-clicked. When you change values in the **Current Viewer Settings** section of the window, only the values in the current viewing window are updated; the values in the preset are not changed.
3. You have the following options to edit the presets.
   - To add a new preset, click **Add preset**. Enter the settings for the new preset. See the table that follows for descriptions of the settings.
   - To edit an existing preset, select the preset from the presets list and adjust the settings. See the table that follows for descriptions of the settings.
   - To delete a preset, select the preset from the presets list and click **Delete preset**.
   - To copy a preset, select the preset that you want to copy from the presets list and click **Copy preset**. A new preset named “Preset_1” appears in the preset list. Change the name of the preset and adjust the settings, as necessary. See the table that follows for descriptions of the settings.
   - To cancel changes that you made to the presets that came with the software and return to the original settings, click **Reset factory presets**. Presets that you created yourself are unaffected.

Field	Description
Name	The name for the preset. A default name appears here until you type a new name.
Window	Use the slider or type the value that you want to use. See *Set the Window and Level* for information about window settings.
Level	Use the slider or type the value that you want to use. See *Set the Window and Level* for information about level settings.

Field	Description
Units	Specify the window and level units: **Raw Values** (actual image data set values), **Percent of Max** (percentage of the maximum value in the image data set), or Standard Uptake Values (**SUV**). SUV units are only available when there is SUV information in Philips PET image data sets. For **Raw Values**, the range of values is zero to the maximum volume value. When you select **SUV**, the range of values becomes 0-10.

4 If you have made adjustments to the display of the current viewing window in the **Current Viewer Settings** section of the window and want to copy those settings to the current preset, click **Copy values to current preset**. The preset that is selected in the preset list is updated with the new values.

5 When you are finished editing the presets, close the window. To save your edited presets for use in future simulation sessions, click **Save & Close**. If you click **Close**, your edited presets will be saved for this plan when you save the plan but will otherwise be lost when you end the current simulation session.

Manage Annotations

You can add annotations to a 2D viewing window. To access the annotation tools, right-click a 2D viewing window and select **Tools** from the menu that appears.

Menu Option	Description
Annotate Image With Label	Add labels to 2D images. Click the viewing window at the location that you want to label. Then type the label text in the **Enter annotation** field in the window that opens.
Clear Annotation	Remove all annotations from the image.

Display the 2D Measurement Grid

You can display a measurement grid in a 2D viewing window.

NOTE
The **Show/hide grid** tools are grouped together in a flyout tool. You can access the tools by clicking the flyout arrow that appears on the right side of the tool.

1 Click **Show/hide grid** to display the grid on the current 2D viewing window.

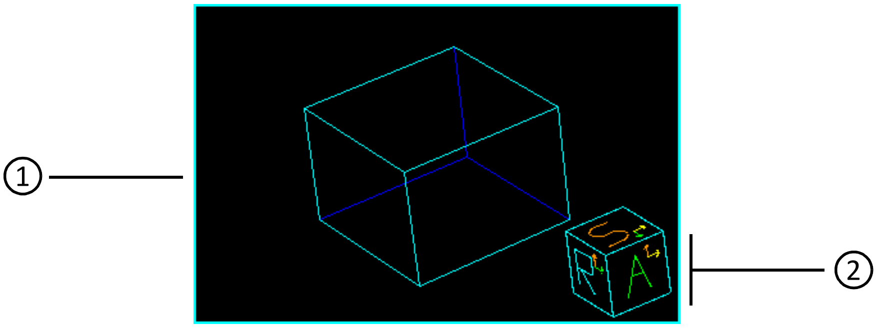
2 To change the size of the grid, click the flyout arrow to open the **Grid Size** field, and type a value in the field.

3 To hide the grid, click **Show/hide grid** again.

4 To show the measurement grid in all 2D viewing windows, right-click a 2D viewing window and select **2D** in the menu that appears. Then select **Global 2D Measurement Grid**. Click the option again to hide the grid.

NOTE
The grid size for **Global 2D Measurement Grid** is set in the **Preferences** window. See *Preferences*.

3D Viewing Windows



1	Image data set limits display as a blue cube.
2	The orientation cube uses letters and arrows to indicate patient orientation. The letter in the box indicates the side of the image that is displayed: • A = Anterior • P = Posterior • S = Superior • I = Inferior • L = Left • R = Right Color-coded arrows on the box indicate patient orientation: • Green arrow is anterior-facing • Yellow arrow is left-facing • Orange arrow is superior-facing

Change the Display of a Viewing Window

You have several options for changing what is shown in 3D viewing windows. To access the tools, right-click a 3D viewing window and select **3D** from the menu that appears.

Menu Option	Description
Enter 2D Mode	Change the 3D viewing window to a 2D viewing window.
Render	Render the image in 3D. You can also type a **r** to render the image.

Menu Option	Description
Render New Image	The following options determine when an image is rendered: • **When Requested**—The image is rendered only when you select the Render command. • **After Motion Complete**—The image is rendered after you complete any change in the orientation of the image data set. • **After Any View Change**—The image is rendered continuously, even as you make changes to the orientation of the volume. If you want to view a rendered image even while you are rotating the volume and do not care how fast or slow the software performs, you may want to choose this option. • **After Any View Change (Low-Res)**—This option only affects image data sets rendered in a surface image type, such as **Bone-Standard Quality**, **Skin-Standard Quality**, **Bone-High Quality**, or **Skin-High Quality**. The image data set is rendered as a low-resolution voxel projection while it is moved. When motion is complete, the image data set is rendered using its normal image type. If the image data set is already using a low-resolution or voxel project image type, or is being rendered as a DRR, this option works like the **After Any View Change** option. The **Render Images Automatically** preference overrides the initial setting when you open a plan. If you select a different **Render New Image** option, it becomes the current rendering method.
Image Type	Select a type of rendering. Selections include skin, bone, and digitally reconstructed radiographs of varying image qualities. High-quality methods take longer to render.
Viewpoint	Change the viewpoint for a 3D image by selecting from a number of standard views for image rendering. If you reposition the image data set so that it is no longer visible in the viewing window, choose **Move Focus to Volume Center** to reposition the center of the volume in the middle of the viewing window.
Transparent Data Set	When the patient volume is rendered using skin or bone rendering, regions of interest (ROIs) are often obscured from view because of the patient data. When you want to see the ROIs and patient data together in a 3D image, you can make the patient surface transparent.

To access the **Rotate**, **Zoom**, and **Pan** tools, right-click a 3D viewing window and select **Tools** from the menu that appears.

Menu Option	Description
Rotate	Rotate the image as if you were holding it in your hand and turning it to look at it from a different angle. With this tool selected, drag an edge of the volume limits to rotate the image.
Zoom	Change the field of view for the volume by dragging across the viewing window.
Pan	Use this tool to reposition the image within the viewing window. Drag within the window until the image is positioned as desired.
Rotate XY	Rotate the volume about the viewing coordinate system axes that extend out from the focus point in the middle of the viewing window. To rotate the volume about the y-axis, drag left or right within the viewing window. To rotate the volume about the x-axis, drag up or down.

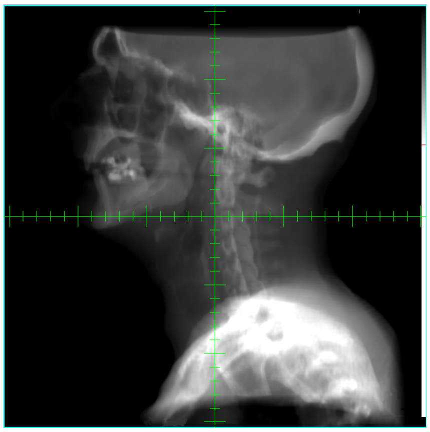
Manage Annotations

You can add annotations to a 3D viewing window. To access the annotation tools, right-click a 3D viewing window and select **Tools** from the menu that appears.

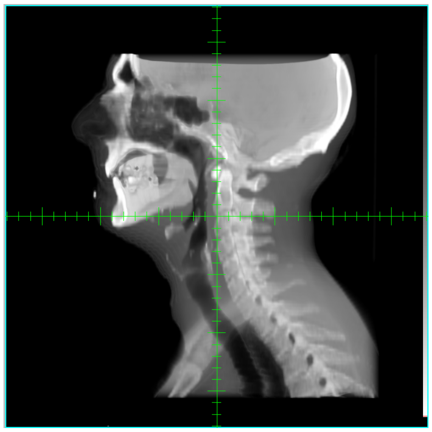
Menu Option	Description
Annotate	Label an ROI with its defined name after clicking on the ROI in a 3D viewing window. Annotations are not "linked" to the items you are labeling. For example, if you delete or rename an ROI, you must delete or rename the annotation separately.
Clear Annotation	Remove all annotations from the image.

Beam's Eye Views

Beam's eye view (BEV) displays allow you to view a projection to the isocenter plane of the patient anatomy that lies in the path of a beam. You can view volumetric images of the patient anatomy as digitally reconstructed radiographs (DRRs) or digitally composited radiographs (DCRs).



BEV DRR



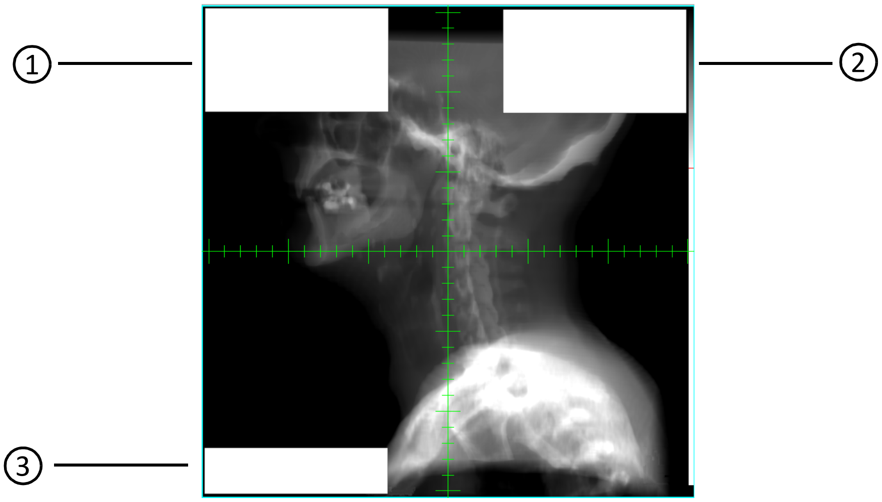
BEV DCR

1 To switch to BEV viewing mode, right-click a 3D viewing window.

2 Select **BEV** on the menu that appears, and then select either **Automatic**, a specific beam, or **None**:

   - **Automatic**—the viewing window displays a BEV of a beam that uses the current POI as its isocenter. If you change the current beam to one that uses a different isocenter, or if you change the current POI, the viewing window updates to show a BEV of a beam that uses the newly selected POI as its isocenter. (Note that the current beam is always displayed in an active BEV viewing window.)
   - <beam name>—the viewing window always displays a BEV of the beam that you select regardless of the current beam or current POI.
   - **None**—the viewing window does not display a BEV.

The BEV appears in the viewing window. It contains several annotations.



1	The patient name and SSD labels. The SSD labels indicate the beam angle with respect to the patient and are constructed from the following elements: • A—Anterior • P—Posterior • L—Left • R—Right • O—Oblique • SUP—Superior • INF—Inferior For example, an SSD label of “RAO INF” means the beam angle was right anterior oblique inferior. The label “Opp” shows the SSD value of the opposed beam.
2	Collimator angle and jaw positions. The collimator angle label indicates the following: • AP Coll—the beam is an AP beam with no couch kick • PA Coll—the beam is a PA beam with no couch kick • Lat Coll—the beam is a lateral beam with no couch kick • Coll—the default collimator label that is shown when none of the other conditions apply to the beam.
3	Name of the image data set, phases for a gated image data set, and intensity projection descriptions.

View DRRs and DCRs

BEVs are initially rendered as DRRs. You can change the image to DCRs.

1. Right-click a BEV and select **3D** on the menu that appears.
2. Select **Switch to DCR** on the **3D** menu. The image in the viewing window is rendered as a DCR.
3. To change the image back to a DRR, right-click the DCR image, select **3D** on the menu that appears, and then select **Switch to DRR** on the **3D** menu**.**

Change Rendering Settings

You have several options for rendering a BEV. To access the tools, right-click a BEV and select **3D** from the menu that appears.

Menu Option	Description
Enter 2D Mode	Change the BEV viewing window to a 2D viewing window.
Render	Render the image. You can also press **r** to render the image.
Render New Image	The following options determine when an image is rendered: • **When Requested**—The image is rendered only when you select the **Render** command. • **After Motion Complete**—The image is rendered after you complete any change in the orientation of the image data set. • **After Any View Change**—The image is rendered continuously, even as you make changes to the orientation of the volume. If you want to view a rendered image even while you are rotating the volume and do not care how fast or slow the software performs, you may want to choose this option. • **After Any View Change (Low-Res)**—This option only affects image data sets rendered in a surface image type, such as **Bone-Standard Quality**, **Skin-Standard Quality**, **Bone-High Quality**, or **Skin-High Quality**. The image data set is rendered as a low-resolution voxel projection while it is moved. When motion is complete, the image data set is rendered using its normal image type. If the image data set is already using a low-resolution or voxel project image type, or is being rendered as a DRR, this option works like the **After Any View Change** option. The **Render Images Automatically** preference overrides the initial setting when you open a plan. If you select a different **Render New Image** option, it becomes the current rendering method.

Change Window and Level Settings

You have several options for changing the window and level settings of the DRR or DCR:

- To use standard window and level settings, go to *Use Presets*.
- To use a CT to density table, go to *Use Rendering Tables*.
- To interactively change the window and level in the viewing window, go to step 1.

1 Right-click the DRR or DCR and select **Tools** on the menu that appears.

2 Select **Window/Level** from the **Tools** menu.

3 Drag the cursor across the viewing window to change the window and level settings. Drag the cursor left and right to change the window. Drag the cursor up and down to change the level.

Use Presets

1 Right-click the DRR or DCR and select **Presets** on the menu that appears.

> **NOTE**
> If **Rendering Tables** appears on the menu instead of **Presets**, then the **Rendering Mode** preference is set to **Rendering Tables**. Select **Use Presets** on the menu and return to step 1 to select a preset.

2 Select the preset that you want to use. The image is adjusted to the window and level settings of the preset that you chose.

NOTE
If you have the **Middle Mouse Window/Level** preference set to **Yes**, you can use the middle mouse button in the viewing window to set the window and level. See *Preferences*.

Edit the Presets

You can create new presets or modify existing presets.

1 Right-click the DRR or DCR and select **Presets** on the menu that appears.

2 Select **Edit Presets** on the menu that appears. The **DRR Preset Editor** window or the **DCR Preset Editor** window opens depending on the image that you selected.

The window is divided into two sections. The **Preset Settings** section lists the settings for the preset that is selected in the preset list. The **Current Viewer Settings** section lists the settings that are being used in the viewing window in which you right-clicked. When you change values in the **Preset Settings** section of the window, the values in the preset and the current viewing window are updated. When you change values in the **Current Viewer Settings** section of the window, only the values in the current viewing window are updated; the values in the preset are not changed.

3 You have several options that can be used to edit presets. See the table that follows for a description of the settings for these options.

- To add a new preset, click **Add preset**. Enter the settings for the new preset.
- To edit an existing preset, select the preset from the presets list and adjust the settings.
- To copy a preset, select the preset that you want to copy from the presets list and click **Copy preset**. A new preset named “Preset_1” appears in the preset list. Change the name of the preset and adjust the settings, as necessary.

Setting	DRR	DCR	Description
Name	X	X	The name for the preset. A default name appears here until you type a new name.
Window	X	X	This value is the window setting that is used when the software renders the BEV. When you change this value, the software renders the BEV again. Changing this value in the **Preset Settings** section changes the preset and the current viewer, while changing this value in the **Current Viewer Settings** section changes only the current viewing window.
Level	X	X	This value is the level setting that is used when the software renders the BEV. When you change this value, the software renders the BEV again. Changing this value in the **Preset Settings** section changes the preset and the current viewer, while changing this value in the **Current Viewer Settings** section changes only the current viewing window.
Contrast	X	X	This value is the contrast value. In the **Current Viewer Settings** section of the window, you must set **Auto Brightness** to **No** in order to change this value. Changing this value in the **Preset Settings** section changes the preset and the current viewer, while changing this value in the **Current Viewer Settings** section changes only the current viewing window.

Setting	DRR	DCR	Description
Brightness	X	X	This value is the brightness value. In the **Current Viewer Settings** section of the window, you must set **Auto Brightness** to **No** in order to change this value. Changing this value in the **Preset Settings** section changes the preset and the current viewer, while changing this value in the **Current Viewer Settings** section changes only the current viewing window.
Control Type	X	X	Select a control type: • **Ramp**—Voxels with CT values at the low end of the window make a lesser contribution to the image than the CT values at the upper end of the window. The relationship between the contribution of a voxel to the image and the CT value in the voxel is a linear function of the CT value, hence the name **Ramp**. **Ramp** settings are used to make DRR images that resemble traditional simulator films. • **Step**—All CT numbers above the step level contribute equally to the image. **Step** maps can be used to visualize only bone. • **Boxcar**—All CT numbers in the included range contribute equally to the image. • **Shark**—All CT numbers contribute unequally, with a central peak value. Values after the peak do not contribute to the image.
Auto Brightness	X	X	The software determines the optimal contrast and brightness settings for the current viewing window if **Auto Brightness** is set to **Yes**. When **Auto Brightness** is set to **No**, you can manually change the contrast and brightness settings for the current viewing window in the **Current Viewer Settings** section of the window.
Energy	X		This value is the beam energy, in MeVs, that will be used for generating the DRR.
Classification Bins		X	The full range of CT numbers is divided into four classification bins that you use to control the DCR. Each classification bin has a CT number range (which is set in the **Upper** and **Lower** fields) and an opacity value (which is set in the **Opacity** field). Select a classification bin to modify by clicking the radio button below the column or by clicking the shaded box in the column. After you select a bin you can adjust its settings. As you adjust the range of CT numbers for a classification bin, you can use 2D viewing windows to identify the voxels that are included in the range. Voxels included in the current classification bin are highlighted by a brown mask in 2D viewing windows. To turn off the mask, click **Disable Mask**.
Upper/Lower		X	These values are the CT numbers for the upper and lower limits of the selected classification bin. Type new values in the fields or adjust these values dynamically by dragging the upper or lower edge of the shaded box in the column. Adjust both values simultaneously by dragging the shaded box itself.
Opacity		X	This value is the opacity of the mask. Type an opacity value between 0 and 1 into the field or use the slider to adjust the opacity of the mask of the selected classification bin.
Fine Tune		X	This field lets you adjust all of the classification bins simultaneously. Type a CT number into the field or use the slider to adjust the value.

4 You can delete a preset or restore factory presets:

- To delete a preset that you created, select the preset from the presets list and click **Delete preset**. You cannot permanently delete a preset that came with the software; it will reappear in the preset list the next time you open the simulation software.

- If you made changes to any presets that came with the software, click **Reset factory presets** to restore them to their original settings. Presets that you created are unaffected.

5. If you made adjustments to the display of the current viewing window in the **Current Viewer Settings** section of the window and want to copy those settings to the current preset, click **Copy values to current preset**. The preset that is selected in the preset list is updated with the new values.
6. When you are finished editing the presets, close the window. To save your edited presets for use in future simulation sessions, click **Save & Close**. If you click **Close**, your edited presets will be saved for this plan when you save the plan, but will otherwise be lost when you end the current simulation session.

Use Rendering Tables

CT to density tables map the CT numbers to density, and the mass attenuation coefficients for these densities are used to generate the DRRs and DCRs. You can select the CT to density table that will be used to render the DRR or DCR in a viewing window.

NOTE
Creating CT to density tables specifically for generating DRRs can significantly improve image quality. See *CT Scanner Configuration* for information about creating CT to density tables.

1. Right-click the DRR or DCR and select **Rendering Tables** on the menu that appears.

NOTE
If **Presets** appears on the menu instead of **Rendering Tables**, then the **Rendering Mode** preference is set to **Presets**. Select **Use Rendering Tables** on the menu and return to step 1 to select a CT to density table to use for rendering.

2. Select the CT to density table that you want to use. The image is adjusted based on the CT to density table that you chose.

Manage Annotations

You can add annotations to a BEV. You can also preview the annotations that will be printed to film with the image. To access the tools, right-click a BEV and select **Tools** from the menu that appears.

Menu Option	Description
Annotate	Label ROIs and POIs with their defined names by clicking on the ROI or POI in the BEV viewing window. Annotations are not "linked" to the items you are labeling. For example, if you delete or rename an ROI, you must delete or rename the annotation separately.
Clear Annotation	Remove from the image all of the annotations that you added.

Menu Option	Description
Preview Annotations	Display all of the annotations that will be printed with the image. The annotations that are printed are determined by the **Image Printing** preferences that you selected. See *Preferences*. When you are finished viewing the annotations, click the tool again to hide the annotations. For the best viewing, we recommend that you maximize the viewing window when you preview the annotations. To maximize a viewing window, either right-click the window and select **Maximize Viewer**, or press the **m** key.

Room’s Eye Views

In a room’s eye view (REV), you can see the location of the patient in relationship to the gantry, accelerator, couch, and floor. This can be helpful in determining if the patient orientation is correct. However, small image data sets may be difficult to interpret given the small amount of the patient that you see in proportion to the room.

You can display REVs for each beam in the plan or you can develop multiple REVs for the same beam. Only one beam is shown per viewing window.

The geometry of the gantry, accelerator, couch, and patient is associated with the beam’s machine. When the beam geometry is modified, the REV updates appropriately. The gantry rotates, the couch rotates, and the patient shifts when the isocenter or the laser center is modified.

1. Display a 3D viewing window or beam’s eye view (BEV) viewing window.
2. Right-click the viewing window and select **REV** from the menu that appears. The **REV** menu appears.
3. Select the beam that you want to view from the **REV** menu. If you select **Current**, for example, the view is locked to the current beam. The REV appears in the viewing window.
4. To change the REV back into a standard 3D viewing window, right-click the REV, select **REV** on the menu that appears, and select **None** on the **REV** menu.

Beam Relative Views

Beam relative views (BRVs) are 2D views that are based on a beam's position, orientation, and field size. BRVs are generally oblique with respect to transverse, coronal, and sagittal patient geometry. Use BRVs to examine the spatial relationships between a beam, patient anatomy, POIs, and ROIs. BRV orientations are parallel to the central axis of the beam (back/front), parallel to the beam's x-axis, or parallel to the beam's y-axis.

BRVs are useful in several situations. For example:

- You can use BRVs for simulations involving cancers of the head and neck when a non-coplanar beam arrangement is needed. For proper field matching, you can quickly locate a projection that is sagittal or coronal to the central axis of the supraclavicular or head fields, then manipulate the gantry collimator or couch of a different beam to correctly match the divergence to a fixed beam.
- When simulating half-beam breast tangents in which the treatment couch must be angled, you can graphically match the diverging beams throughout the patient. Select the beam axial slice of the medial tangent field, then turn on the display for the lateral beam on the 2D BRV axial slice of the medial beam. Use gantry and collimator adjustments to align the lateral beam with the medial tangent beam.

1 Right-click a 2D viewing window, and select **BRV** on the menu that appears. The **BRV** menu appears.

2 Select the beam that you want to view from the **BRV** menu. The default BRV orientation is **Front/Back**. The BRV appears in the viewing window. The lines across the image represent the beam.

> **NOTE**
> For BRVs, you cannot use the POI tools to move the isocenter of the BRV's beam. The BRV image plane is determined by the isocenter.

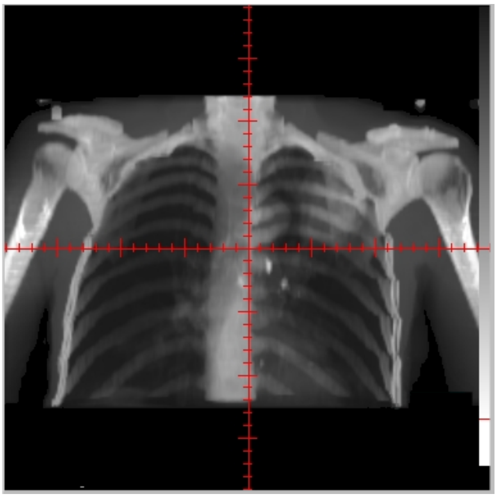
3 To select a different BRV orientation, right-click the viewing window, select **2D** on the menu that appears, select **Orientation**, and then select an orientation. You can select either **Front/Back**, the names assigned to the machine's top and bottom jaws (for example, Y1/Y2), or the names assigned to the machine's right and left jaws (for example, X1/X2).

4 To change the BRV back into a standard 2D viewing window, right-click the BRV, select **BRV** on the menu that appears, and select **None** on the **BRV** menu.

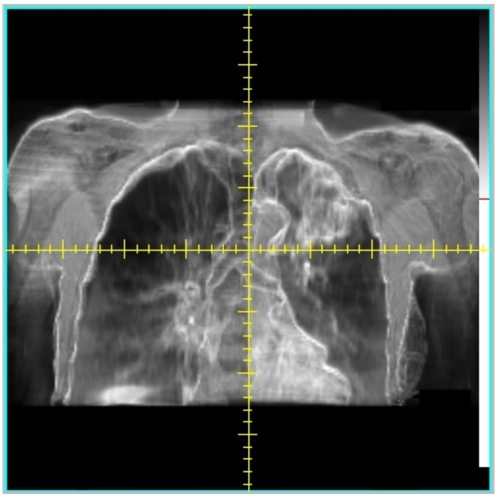
Create a Volume of Interest

The volume of interest (VOI) feature allows you to add a bounding box to a BEV DRR or DCR. The bounding box is a cube that you can adjust so that only data inside of the VOI is rendered and displayed in the viewing window. When the VOI feature is set to **Slab Mode**, the bounding box is a slab that lies perpendicular to the central axis of the beam and has a face that is parallel to the view in which you define it. The BEV VOIs are saved with the plan and are available when you reopen the plan.

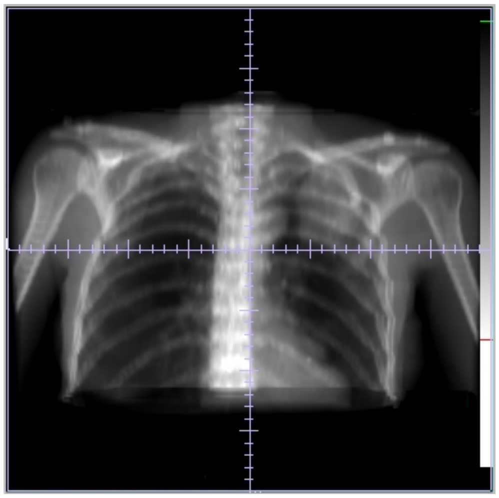
In the top two viewing windows of the example below, an anterior VOI is used to cut out unwanted voxels within the image data set. The VOI removes the sternum from the DCRs in order to obtain better visualization of the carina and bronchial bifurcation.



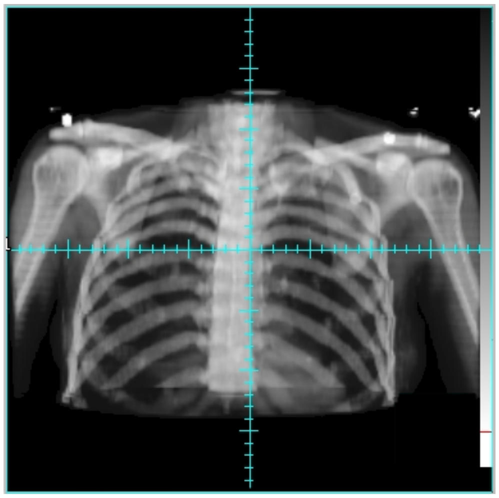
DCR with anterior VOI using
AP Ribs/Carina/ANT VOI DCR Preset



DCR with anterior VOI using
Lung AP Carina/Slab VOI DCR Preset



DRR without VOI



DCR without VOI using
Lung AP DCR Preset

1. To work efficiently with VOIs, we recommend that you use the three MPR, one 3D viewing window layout and change the 3D window to a BEV display.

   To select the three MPR, one 3D viewing window layout, click **Display Three MPR, One 3D Layout**. To set the BEV display, see *Beam's Eye Views*.

2. Right-click the BEV and select **VOI** on the menu that appears. The following menu items appear. A box is shown to the left of a menu item to indicate that the item is enabled.

Menu Option	Description
VOI Enabled	Enables or disables the VOI tool.
Adjust VOI	Creates the VOI bounding box the first time you select **Adjust VOI**. Then it allows you to change the shape of the VOI or the thickness of the slab (if **Slab Mode** is enabled).
Slab Mode	Enables or disables **Slab Mode**. When **Slab Mode** is enabled, the VOI is a slab and the **Locked to Isocenter** tool is available.
Locked to Isocenter	This tool centers the slab around the isocenter. When the slab is locked to the isocenter, the distance between the isocenter and the edges of the slab are symmetric. If you move one edge of the slab, the opposite edge of the slab moves as well. In addition, if you move the isocenter, the slab moves as well. When the slab is not locked to the isocenter, you can move the edges of the slab independently to set the slab edge locations as necessary, and the slab does not move if you move the isocenter.

3. Is the VOI tool enabled?
   - Yes—Go to step 4.
   - No—Click **VOI Enabled.** Then right-click the BEV again, select **VOI**, and go to step 4.
4. Select **Adjust VOI**. A bounding box appears in each 2D viewing window.
5. Do you want the VOI to be a slab?
   - Yes—Go to step 6.
   - No—Go to step 8.
6. Right-click the BEV and select **VOI**. Then select **Slab Mode**. The bounding box in each 2D viewing window changes from a cube to a slab with a thickness of 3 cm, and the slab is locked to the isocenter.
7. Do you want the slab to be locked to the isocenter?
   - Yes—Go to step 8.
   - No—Right-click the BEV, select **VOI**, and select **Locked to Isocenter** to disable the tool. Go to step 8.
8. To change the shape of the VOI or the thickness of the slab, click one of the 2D viewing windows. Then drag an edge of the VOI to the new location. When you release the mouse button, only the portion of the image data set within the bounding box is shown in the BEV.

Visualization Tools

Use these tools to modify the display of 2D and 3D images and obtain information about the patient data.

> **NOTE**
> Some tools are grouped together in flyout tools. You can access all of the tools in a flyout tool by clicking the flyout arrow that appears next to the tool.

Tool	Name	Function
	Scroll 2D (2D viewing windows only)	Scroll through the “stack” of transverse, sagittal, coronal, or BRV slices in a viewing window. To scroll through a stack of slices, drag left and right within the 2D viewing window. Clicking on the far left scrolls to the beginning of the series of slices. Clicking on the far right scrolls to the end of the series.
	Zoom	Increase and decrease the magnification of the image by dragging across the viewing window. Moving the mouse to the left shrinks the image. Moving the mouse to the right magnifies the image. The image remains centered in the viewing window, so you may need to use the **Pan 2D** tool to change the region of the image that is displayed.
	Box zoom 2D	Draw a box around a region of the image that you want to zoom in on. To zoom in on a particular region, drag diagonally until the region to be zoomed is within the box.
	Pan 2D	Reposition the 2D image within the viewing window. Drag within the viewing window until the image is positioned as desired.
	Reset pan/zoom	Return the image in the active viewing window to its original position and magnification.
	Go to POI	All of the viewing windows change to display the slice that is nearest to the POI that is selected in the Point workstep.
	Distance display	Measure distances on an image. As you drag, a line is drawn showing the distance being measured. The distance (in centimeters) is listed at the bottom of the image.
T	**Distance annotation**	Measure distances on an image and draw a distance indicator and label on the image. As you drag to draw a line, the line that you drew remains on the image and the distance (in centimeters) is listed on the image.
T	**Delete annotation**	Remove annotations, including distance labels, from 2D viewing windows. Select this tool and then click the annotation that you want to delete.
	Display/hide beams in 2D views	Display or hide all of the beams in the 2D viewing windows.

Tool	Name	Function
	Display/hide beams in 3D views	Display or hide all of the beams in the 3D viewing window.
	Display/hide viewer graphics	Turn on or turn off the display of the graphics in the current viewing window. Note that the orientation cube and the isocenter label are always shown in the viewing window regardless of this setting.
	Correlated pointer	Change the orthogonal slices that are displayed in the viewing windows. Drag on a viewing window until the desired slices are displayed in the other viewing windows. When the slice position lines are displayed in all three orientations, you can use this tool to quickly display the transverse, sagittal, and coronal planes that cut through structures of interest. When you are finished using the **Correlated pointer** tool, click the tool again to deactivate it. The **Scroll 2D** tool becomes active instead.
	Zoom correlated pointer 2D	Change the orthogonal slices that are displayed in the viewing windows while zooming in on a region of an image. Drag diagonally until the region to be zoomed is within the box. The region of the image that is inside the box is magnified in the transverse, sagittal, and coronal viewing windows, and the orthogonal slices that are displayed are adjusted accordingly.
	Slice position indicator	Turn on or turn off the display of the slice position in the 2D and 3D viewing windows.
123	**Show image value 2D**	Display the CT value, density, and DICOM coordinates for the point in the image where you click. The values are computed using the nearest-neighbor method.
	Show/hide grid	Turn on or turn off the display of the measurement grid in the selected 2D window.
 Grid Size 1 cm	**Grid size**	Specify the size of the grid in cm.
	Print image	Print viewing windows to paper or film. For information, see *Print Images*.
	Display one MPR, one configurable, two DRR layout	Change the layout of the viewing windows to one MPR window, one window for which you can specify the type, and two DRR windows. To set a default type to appear in the configurable viewing window, see *Preferences*.
	Display three MPR layout	Change the layout of the viewing windows to three MPR windows.
	Display three MPR, one 3D layout	Change the layout of the viewing windows to three MPR windows and one 3D window.

Tool	Name	Function
⊞	**Display three MPR, two DRR, one 3D layout**	Change the layout of the viewing windows to three MPR windows, 2 DRR windows, and one 3D window.
▷	**Play**	Play a movie of the phases of a 4D image data set. The tool changes to the **Stop** tool after you click it. See *View a Movie Using the Cine Tools*.
■ ─▮─	**Adjust speed**	Adjust the speed of the movie of the 4D phases.
□	**Stop**	Stop the movie of the 4D phases. The tool changes to the **Play** tool after you click it.

Keyboard Shortcuts

Use these keyboard shortcuts to perform various functions.

Keys	Function
n or up arrow	View next image slice.
p or down arrow	View previous image slice.
v or left or right arrows	View next image data set, including the primary image data set and intensity projection image data sets. Press **v** to view the next image data set. To scroll through image data sets, use the left and right arrow keys.
a	View transverse (axial) orientation.
s	View sagittal orientation.
c	View coronal orientation.
r	Render BEV or 3D skin.
x	Toggle between the **Scroll 2D**, **Zoom**, and **Pan 2D** tools in 2D viewing windows. Toggle between the R**otate**, **Zoom**, and **Pan** tools in 3D viewing windows.
o	Select a slice by number.
z	Set a 2D window back to the default magnification or position.
u	Increase magnification of the 2D window.
d	Decrease magnification of the 2D window.
m	Toggle the current viewing window between its maximum size within the viewing window layout and its original size.
Ctrl + **s**	Save current plan.
Ctrl + **x**	Close the **Simulation** window.
Ctrl + Shift + n	Start a new simulation session.

8 Initialize

The Initialize workstep lets you select the CT scanner that should be used for the plan and remove the couch from the patient data.

To display the Initialize workstep, click **Initialize workstep** at the top of the window.

Select a Scanner

1 Verify that the scanner chosen for this plan is correct. The scanner is displayed in the **Scanner** list in the **Setup** panel.

To view the properties of the scanner, click **View scanner properties**.

> **NOTE**
> You cannot change scanner properties from the **Scanner Information** window. These properties were set using the physics tool. For detailed information about the scanner properties, see *CT Scanner Configuration*.

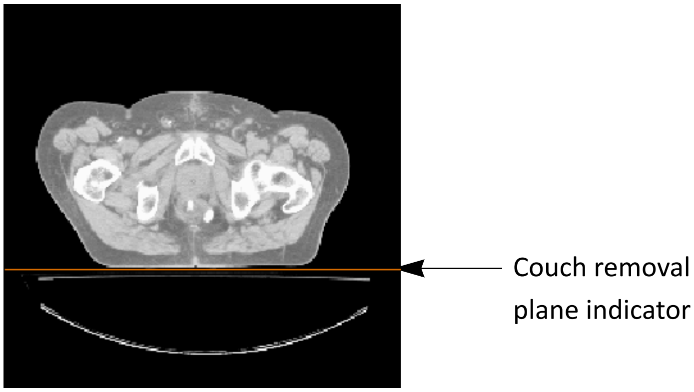
The software uses the scan information from the primary image data set to determine which scanner was used to acquire the images and selects that scanner for this plan. The name of the primary image data set is displayed at the bottom of the **Setup** panel. If the software cannot determine which scanner was used to acquire the images, then the software does not associate a scanner with the plan. You must manually select the scanner.

If the image data set is a maximum intensity projection (MIP) or a minimum intensity projection (MinIP) image data set, then the software does not associate a scanner with the plan. You must manually select the scanner for MIP and MinIP image data sets.

2 If necessary, select a different scanner from the **Scanner** list.

Remove the Couch

Because the patient CT scans include the couch, the software considers the couch to be an extension of the patient data. You can use the couch removal plane (indicated by a line in 2D images) to remove the couch from the patient data.



1 Click **Initialize workstep** to display the Initialize workstep.

2 Select **Yes** in the **Enable** field to enable the remove couch tools.

3 If the location of the couch removal plane is not shown in the viewing windows, select **Yes** in the **Display** field.

4 Click the **Move couch removal plane** tool and remove the couch by dragging the couch removal line until it is placed at the point where the patient ends and the couch top begins.

> **NOTE**
> When you are finished using the **Move couch removal plane** tool, click the tool again to deactivate it. The **Scroll** tool becomes active instead.

5 To lock the position of the couch removal plane, click **Lock**. The button image changes from unlocked to locked, and you cannot move the couch removal plane.

To unlock the position of the couch removal plane, click the button again. The button image changes from locked to unlocked, and you can move the couch removal plane.

6 If you do not want the couch removal plane to be shown in the viewing windows, select **No** in the **Display** field.

Generate an External ROI

If you set your preferences to create an external ROI the first time a plan is opened, the software automatically creates an ROI that defines the surface of the patient's skin the first time you open a plan. The ROI is named "External" in the ROI list.

> **NOTE**
> See *Preferences* for information about the external ROI preference. See *Segmentation* for information about ROIs.

The value in the **External ROI Threshold** field in the **Setup** panel is the density threshold that the software uses to differentiate between the patient and the air. Voxels that fall outside of the patient that are below this threshold are considered to be air and will not be included inside of the external ROI. The default threshold value is 0.6 g/cm^3.

In some cases you may need to change the **External ROI Threshold** value if there are artifacts outside of the patient that have a density that is greater than the default threshold value and are, therefore, considered to be part of the patient by the software. To change the **External ROI Threshold** value, type a new value in the field.

You can display the **External ROI Threshold** value in g/cm^3 or as a CT number. To change the units displayed, click **Change external ROI threshold units**.

If your preference is not set to automatically create an external ROI, or if you need to recreate the external ROI, click **Generate external ROI**.

If you do not want to use an external ROI in your plan, you can delete the external ROI from the ROI list. See *Delete an ROI* in the *Segmentation* chapter.

Create Intensity Projection Image Data Sets

You can create Maximum Intensity Projection (MIP), Minimum Intensity Projection (MinIP), and Average Intensity Projection (AIP) image data sets for 4D image data sets. MIP creates a new image data set consisting of the highest value voxels from the selected phases. MinIP creates a new image data set consisting of the lowest value voxels from the selected phases. AIP creates a new image data set consisting of the average of the voxel values from the selected phases.

1. Click **Initialize workstep** to display the Initialize workstep.
2. Click the **Image Data Sets** bar to open the **Image Data Sets** panel.
3. In the **Intensity Projection** portion of the panel, select the range of phases to be used in the intensity projection from the **Begin** and **End** lists.
4. Select the type of intensity projection that you want to create from the **Type** list.
5. Click **Calculate IP** to create the intensity projection image data set. A MIP, MinIP, or AIP image data set is created and displayed in the viewing windows. The information about the intensity projection appears within the viewing windows below the image.

   To move back and forth through the intensity projection image data set and the other image data sets one at a time, right-click a 2D viewing window and select **2D** on the menu that appears. Select **Next Data Set** to view another image data set. Select **Next Slice** or **Previous Slice** to view a different slice in the image data set. Keyboard shortcuts are also available. For information, see *Keyboard Shortcuts*.

   NOTE
   You will not be able to create an intensity projection image data set if the following are true.

   - The begin and end phase values are the same.
   - The begin and end phase values and the intensity projection type value are identical to those of an existing intensity projection image data set.

6. To delete an intensity projection image data set, select the image data set in the **Intensity Projection** list and click **Delete IP**.

   NOTE
   You can only delete an intensity projection image data set if it was created during this simulation session.

View a Movie Using the Cine Tools

If you imported a 4D image data set, you can use the cine tools to create a movie of all of the phases that are associated with the patient. You can view a movie in the active 2D or 3D viewing window.

To use the cine tools in a 2D viewing window, set the image orientation to Transverse, Sagittal, Coronal, or BRV. To use the cine tools in a 3D viewing window, render the image as a DRR or DCR. (See *Beam's Eye Views* for information about DRRs and DCRs.)

1 In the Visualization toolbar, click **Play**. The viewing window cycles through all of the phases associated with the patient. If you are creating a movie in a 3D viewing window, it may take a few minutes for all of the phases to render.

NOTE
The cine tools are grouped together in a flyout tool. You can access the tools by clicking the flyout arrow that appears on the right side of the tool.

2 After the movie has started, you can use the **Adjust speed** tool to adjust the speed of the movie. (The tool is located in the cine tools flyout tool.) Moving the slider to the left decreases the speed of the movie, and moving it to the right increases the speed of the movie.

3 Click **Stop** to stop the movie.

View Pulmonary Data

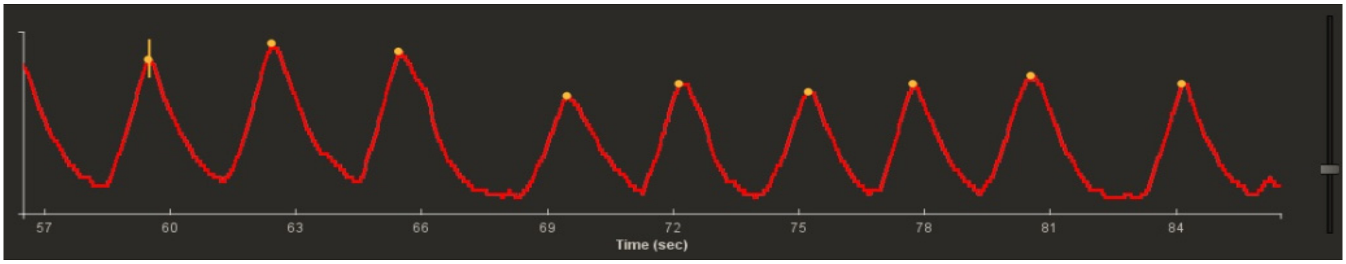
You can display both the breathing statistics and the pulmonary waveform for 4D image data sets.

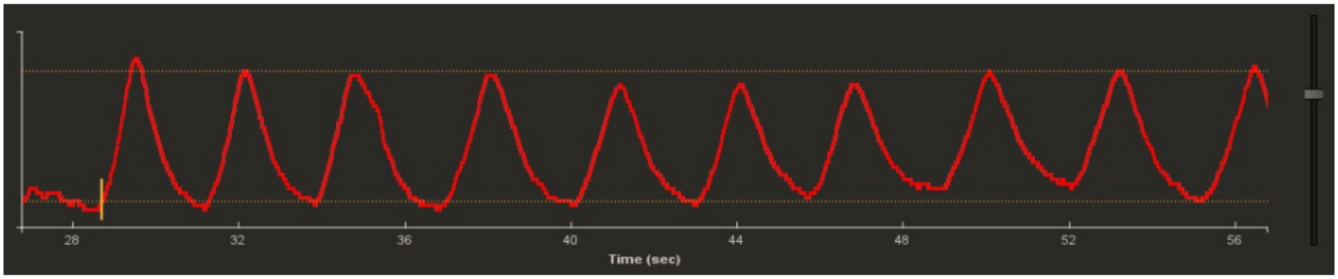
1 Click **Waveform** to open the waveform below the viewing windows.

2 Click **Show Waveform** to view the breathing waveform. A graph displays the breathing waveform for the first thirty seconds of the breathing cycle.

The white areas of the waveform indicate time when the X-ray beam was off during CT image acquisition. The red areas of the waveform indicate time when the X-ray beam was on during CT image acquisition.

If the image data set uses phased binning, dots appear on the waveform to indicate the peak points that correspond to the 0% phase (see the first graphic that follows). If the image data set uses amplitude binning, horizontal dotted lines appear on the waveform. The top line indicates the 0% phase, and the bottom line indicates the 50% phase (see the second graphic that follows).





3. To scroll through the waveform, move the scroll bar up or down. Move the scroll bar up to move from right to left in the waveform, and move the scroll bar down to move from left to right in the waveform.
4. To see the relationship between an image slice and the waveform, click a 2D viewing window to make it active. Press the left arrow key to move to the previous phase, or press the right arrow key to move to the next phase. When a slice from a 3D phase image data set is displayed, a vertical indicator line appears on the waveform to indicate the time at which the displayed slice was acquired and the point of the breathing cycle to which it corresponds. The location of the indicator line in the waveform graph is updated when you scroll through the slices of a 3D image data set for any of the phases.

   NOTE
   The image data set in the current viewing window must be from a pulmonary gated acquisition and must use phase or amplitude binning in order for the vertical indicator line to appear on the waveform.

5. Click **Zoom** to change the magnification of the waveform, and then drag the cursor across the waveform. Moving the mouse to the left decreases the magnification, and moving the mouse to the right increases the magnification.
6. Click **Reset** to return the waveform to its original position and magnification.
7. Click **Distance display** to measure time along the graph. Move the mouse over the graph to the point where you want to start your measurement, and then drag the cursor along the graph to the point at which you want to stop your measurement. As you drag the cursor, the time between the start and end points of your line is shown on the graph.
8. Click **Show Statistics**. The following breathing statistics are shown in the waveform panel.
   - **Scan Length**—The total scan time, in seconds.
   - **Breath Cycles**—The number of breaths during the scan time.
   - **Mean Breath Rate**—The mean breath rate, in breaths per minute (bpm).
   - **Breath Rate Range**—The range of the breath rates during the scan.
   - **Average Full Inhalation Level**—The average of the level of full inhale for each cycle during the scan.
   - **Average Full Exhalation Level**—The average of the level of full exhale for each cycle during the scan.
   - **Amplitude Range**—The range of the normalized breath amplitudes over the length of the scan.

- **Amplitude Standard Deviation**—The standard deviation of the normalized breath amplitudes during the scan.
- **Binning Type**—The type of binning used in the scan, either **Linear Phase** or **Amplitude**. The binning mode is selected as part of CT image reconstruction and is identified by a DICOM tag.
  - **Linear Phase** binning assumes that each peak is 0%. It breaks the distance between peaks into ten equally spaced points along the time axis and assigns a phase to each point.
  - **Amplitude** binning reduces motion artifacts. It differentiates between data that is collected during the inhale phase (the upward slope of a waveform) and the exhale phase (the downward slope of a waveform). **Amplitude** binning attempts to ensure that the breathing signal amplitude is constant within each phase across the breathing waveform.

9 Segmentation

The Segment workstep contains tools that let you add and delete regions of interest (ROIs) and select 2D and 3D display options.

To display the Segment workstep, click **Segment workstep** at the top of the **Simulation** window.

Overview

A region of interest (ROI) is a contour or set of contours that defines the limits of an area which is important in treatment planning, such as the target volume or a radiation-sensitive structure. Any number of contours can be used to define an ROI, and any number can be drawn on a single image slice. You can draw contours on transverse, sagittal, or coronal 2D images, but all contours for a single ROI should be drawn on slices with the same orientation.

The volume units (voxels) inside the ROI contours may or may not be included in the ROI volume, depending on how you define the contours. If a contour is entered within another contour, the area bounded by the two contours is included in the ROI. The gray areas in the illustration below indicate portions of the ROI that are included in the ROI volume.

The ROI contours on the left translate to the ROI volumes on the right.

Add an ROI

1 Click **Add ROI**. A new ROI appears in the list.

2 Click the **Properties** bar to open the **Properties** panel.

3 Complete the fields to define the new ROI.

Field	Description
Name	The name for the ROI. A default name appears here until you type a new name.
Color	The color in which the ROI is displayed.
2D Display	The method used to display the ROI in 2D viewing windows. See *2D Display* for information about each option.
3D Display	The method used to display the ROI in 3D viewing windows. See *3D Display* for information about each option.

4 To draw contours for the ROI, see *Draw Contours*.

Delete an ROI

1 Select the ROI that you want to delete from the ROI list.

2 Click **Delete ROI**. The software removes the ROI from the image and the ROI list.

If the ROI is used to define a block for any beams, the **ROI Dependencies** window opens when you click **Delete ROI** and the software does not delete the ROI. The **ROI Dependencies** window lists the blocks for which the ROI is used. To delete the ROI, you must delete the blocks that are defined by the ROI or use different ROIs to define those blocks.

Draw Contours

1 In the ROI list, select the ROI for which you want to draw contours.

2 Draw the contours, as needed. For information about the drawing tools, see *Tools*.

As you draw contours, the number of contours that you define appears in the **Contours** field.

3 To update the volume display for the selected ROI, click **Update** next to the **Volume** field. The volume of the selected ROI appears in the field.

Interpolate Contours

If you do not want to draw contours for an ROI on every slice of an image data set, you can use the program's interpolation features to generate contours between the contours that you drew on non-consecutive transverse slices. The individual interpolated contours that are displayed indicate where the edge of the interpolated volume intersects the transverse slices.

1 Add the ROI if you have not already done so.

2 Draw contours on at least the first and last slices that contain the ROI. The more contours that you draw within the ROI, the more accurate the interpolation will be.

3 Click **Interpolate between contours.**

4 Once the interpolated contours have been generated, you can use the ROI editing tools to move and reshape the contours. For information, see *Tools*.

5 If you are not satisfied with the results, you can click **Delete contour** to delete a single contour or **Delete all interpolated contours** to delete them all.

Reduce Points per Contour for All ROIs

If you intend to use DICOM RT to export ROIs to a system that limits the number of points in a contour, you can use this feature to reduce the number of points in all of the ROIs.

NOTE
You will not be able to undo your changes after you reduce the number of points for each contour. Make sure that the **Max Points per Contour** setting is correct before you apply your changes.

1 Click the **Properties** bar to open the **Properties** panel.

2 Type the maximum number of points that each contour should have in the **Max Points per Contour** field.

3 Click **Apply**. The software removes points, as necessary, from each contour so that each contour contains no more than the number of points that you specified.

4 To view the points in a contour, click **Select contour** and click the contour.

NOTE
The **Select contour** tool is located in the **Edit contour** flyout tool. For more information, see *Tools*.

Copy an ROI

When you create a copy of an ROI, all of the attributes of the original ROI are retained in the copy except for the ROI name and color.

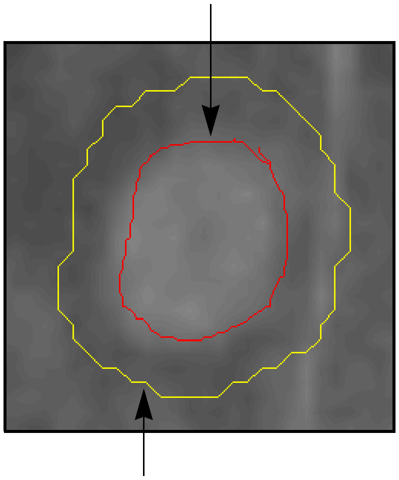
1 In the ROI list, select the ROI that you want to copy.

2 Click **Copy ROI**. The new ROI appears in the list with "_COPY" appended to its name, and it is assigned a different color from the original ROI.

Expand and Contract ROIs

You can use the expansion and contraction feature to generate the following ROIs.

- New contours based on existing ROIs, plus or minus a margin. In the example below, the software creates a new ROI by expanding the source ROI by a uniform margin of 0.5 cm.



Source ROI

Destination ROI (Source ROI + 0.5 cm)

- New contours that are combinations of existing ROIs. The existing ROIs are unaffected by this operation.

1 Click the **Autocontouring** bar to open the **Autocontouring** panel.

2 Choose one of the following.

- To quickly perform a basic expansion or contraction, go to *Quick Expansion or Contraction*.
- To expand or contract the ROI using more parameters than just a uniform margin, go to *Advanced Expansion or Contraction*.

Quick Expansion or Contraction

1 From the ROI list, select the ROI to be used as the source ROI.

2 Set the destination ROI.

- To modify an existing ROI when you expand or contract the source ROI, select **Modify Existing.**
- To create a new ROI, select **Create New.**

3 If you are modifying an existing ROI, select the ROI that you want to modify from the **Destination** list. All contours in this ROI will be replaced by new contours.

If you are creating a new ROI, type the name of the new ROI in the **Destination** field.

4 Type a value in the **Uniform Margin** field. Type a positive value to expand the source ROI, or type a negative value to contract the source ROI. The software will expand or contract the source ROI in all directions by the value that you type in this field.

5 Click **Expand/Contract ROI** to expand or contract the source ROI.

The software performs the expansion or contraction. This may take a few minutes for large volumes.

CAUTION
Review the contours to verify that they are correct for your plan.

Advanced Expansion or Contraction

1 Click **Advanced options**. The **ROI Expansion/Contraction** window opens.

2 Select the **Source** check box for the ROI to be used as the source. To combine two or more ROIs, select the **Source** check boxes for multiple ROIs.

3 If you want to prevent the new ROI from overlapping an existing one, you can define a limiting ROI by selecting one of these options.

- **Avoid Interior**—The new ROI will avoid the region inside of this ROI.
- **Avoid Exterior**—The new ROI will avoid the region outside of this ROI. For example, you can create contours for the skin surface, then select the **Avoid Exterior** check box for the patient surface ROI in order to keep the new ROI within the patient volume.

NOTE
Click **Clear All** to clear all of the check boxes in the window.

4 Set the destination ROI.
  - **Select ROI To Modify**—Select this option to modify an existing ROI when you expand or contract the source ROI. Select the ROI for which the new contours will be drawn from the list. All contours in this ROI will be replaced by new contours.
  - **Create New ROI**—Select this option to create a new ROI. Type the name for the new ROI in the **Name** field.

5 Define the margin of expansion or contraction of the source ROIs.
  - **Uniform Margin**—Select this option to expand or contract the source ROI by the same margin in all directions. Type the margin value in the **Uniform Margin** field.
  - **Variable Margin**—Select this option to expand or contract the source ROI by different margins in different directions. Type the margin values in the appropriate fields.

6 Click one of the following buttons to complete the expansion or contraction.
  - **Expand**—Expand the source ROIs by the margin.
  - **Contract**—Contract the source ROIs by the margin.

The software performs the expansion or contraction. This may take a few minutes for large volumes.

CAUTION
Review the contours to verify that they are correct for your plan.

Tools

Use the following tools to create and edit ROIs.

NOTE
Some tools are grouped together in flyout tools. You can access all of the tools in a flyout tool by clicking the flyout arrow that appears next to the tool.

Tool	Name	Function
	Create contour point by point	Define the block by “dropping” a series of points. After you click the tool, click where you want to start the contour. A small box indicates the point that you defined. Click the next point you want to add to the contour, or click and drag the point until it is positioned as desired. A line is drawn between the two points. Continue to define the remaining points in the same way. To close the contour, drop the last point of the ROI inside the box of the first point.
	Create contour freehand	Define contours by drawing a continuous line. Click and drag to draw a contour around the limits of the region until you have closed the contour. Go to the next slice on which you want to draw a contour for this ROI and repeat the steps.
	Split contour	Divide a single contour into two contours on the current ROI. To divide a contour, click and drag across the ROI.

Tool	Name	Function
	Create contour paintbrush	"Paint" an ROI on a 2D transverse slice. The tool provides contour drawing, editing, and deleting functions, depending on where you use it. After you click the tool, click and drag to paint the contour: • If you click an image where there is no contour, a new, circular contour appears. Click and drag to create a thick line; wherever you move the cursor, the circle is filled in for the ROI. • By clicking inside an existing contour, you can push out the edges. • If you click outside, but near, an existing contour, the tool functions as an eraser, and the ROI is erased wherever you move the tool. You can use this method to push in the edges. Go to the next slice on which you want to draw a contour for this ROI and repeat the process. Draw all additional contours for this ROI in the same way.
	**Paintbrush diameter**	Specify the required diameter for the **Create contour paintbrush** tool. To access this tool, click the flyout arrow that appears below the **Create contour paintbrush** tool.
	Delete contour	Remove one or more contours that are associated with the current ROI from a slice. To delete the contours, click and drag to draw a box over any contours that you want to delete that are associated with the current ROI.
	Delete all contours on current slice	Remove all of the contours that are associated with the current ROI from a transverse slice.
	Delete all contours	Remove all of the contours that are associated with the current ROI from all of the slices.
	Edit contour	Change the shape of a contour. Click the tool and then click a contour that you want to edit. The points used to create the contour appear on the perimeter of the contour. Click and drag a point until it is positioned as desired.
	Select contour	Display the points in a contour. Click the tool and then click a contour to display the points in that contour.
	Move contour	Move a contour to a new location on the same slice. Click and drag the contour to the new location.
	Scale contour	Scale a contour. Click and drag the contour left and right to scale it horizontally or up and down to scale it vertically.

Tool	Name	Function
	Autocontour current slice	Generate a single contour on a single slice automatically. The software searches to the right from where you click on the image until the first structure with values within the minimum and maximum threshold values that you specify is found. The software then automatically draws a contour around the structure. To automatically generate a contour, click the **Autocontouring** bar to open the **Autocontouring** panel. In the **Thresholds** portion of the panel, type the minimum and maximum threshold values you want to use in the **Min** and **Max** fields. Then, select the **Autocontour current slice** tool and click at an appropriate seed point in the image. If the seed point has a value within the specified range, the first structure to the right of the seed point with values outside the range is autocontoured. If the seed point has a value outside the range, the first structure to the right of the seed point with values inside the range is autocontoured.
	Autocontour all slices	Autocontour all structures on all slices. The software searches to the right from where you click on the image until the first structure with values within the minimum and maximum threshold values that you specify is found. The software then automatically draws a contour around the structure on the current slice and then generates contours on adjoining slices for any structures that are connected to the contours on the previous slice and have values within the specified range. To automatically generate a contour, click the **Autocontouring** bar to open the **Autocontouring** panel. In the **Thresholds** portion of the panel, type the minimum and maximum threshold values you want to use in the **Min** and **Max** fields. Then, select the **Autocontour all slices** tool and click at an appropriate seed point in the image. If the seed point has a value within the specified range, the first structures to the right of the seed point with values outside the range are autocontoured. If the seed point has a value outside the range, the first structures to the right of the seed point with values inside the range are autocontoured. The software then searches for the structures in adjacent slices and autocontours the structures on those slices.
	Interpolate between contours	Automatically generate contours between other contours that are not drawn on consecutive slices.
	Delete all interpolated contours	Delete all contours that were added using the **Interpolate between contours** tool.

2D Display

To select a different 2D display method for an ROI, select the ROI and make a selection from the **2D Display** list on the **Properties** panel.

- **Contour**—The ROI is shown as a line contour. The contours are only visible in the orientation used to draw contours.
- **Colorwash**—The ROI is shown only as a colorwash. Although the ROI is visible in all three orientations, you cannot manually draw contours in this display mode.
- **Poly**—A polygonal wire surface is generated for the ROI, and a contour is drawn on the 2D slices where the polygonal wire surface intersects the slice. Use this display to see a contour for the ROI on other orthogonal slices or to view an ROI on oblique slices and in multiple

image data sets. When displaying large ROIs, you may notice a significant decrease in system speed.

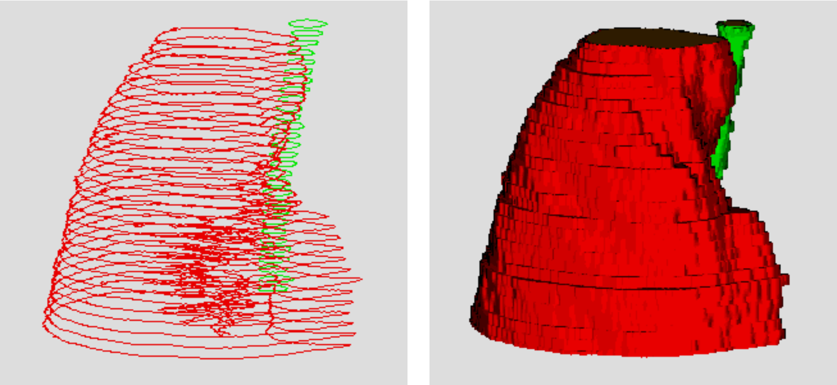
- **Off**—The ROI is not displayed in 2D images. You can draw contours with the display off, but each contour will "disappear" until you turn on the 2D display for that ROI.

3D Display

ROIs can be displayed in 3D mode with or without the patient data. The 3D display mode determines how the ROI appears in all 3D windows. For all display modes, a wireframe is used when rotating the volume and when the 3D image is not rendered.

To select a different 3D display method for an ROI, select the ROI and make a selection from the **3D Display** list on the **Properties** panel.

- **Wireframe**—Each contour in the ROI is drawn as a wireframe.



Wireframe

Surface

- **Surface**—The ROI appears as a solid surface after rendering. Use this option to generate surface displays of large ROIs.
- **Trans Surf (Transparent Surface)**—The ROI is rendered as a transparent surface. Any ROIs or other objects within or behind the transparent ROI are visible.
- **Off**—The ROI is not displayed in 3D images.

NOTE
The **Surface** and **Trans Surf** modes are not supported for variably spaced data. If you attempt to use either of these display modes with variably spaced data, a warning message is shown and the ROI is reset to **Wireframe**.

Sort ROIs

Use the following tools to sort the ROIs in the ROI list.

NOTE
The tools used to sort ROIs are grouped together in a flyout tool. You can access the tools by clicking the flyout arrow that appears below the tool.

Control	Description
AZ↓	Sort alphabetically in ascending order
ZA↓	Sort alphabetically in descending order
△	Move item up
▽	Move item down

10 Points of Interest

The Point workstep contains tools that let you add, position, and delete points of interest (POIs).

To display the Point workstep, click **Point workstep** at the top of the **Simulation** window.

Add a POI

You can display POIs in both 2D and 3D viewing windows. In 2D viewing windows:

- The intersection of the POI and the slice is displayed as a circle.
- The crosshairs on the POI and the size of the circle indicate the proximity to the center of the point.
    - If the center of the POI lies within an image slice, a complete crosshair is drawn and “Isocenter” appears in the upper right corner of the viewing window in the color of the POI.
    - If the POI does not lie directly on the slice, partial crosshairs are drawn and “Isocenter” does not appear in the viewing window.

Each BEV viewing window displays a BEV of a beam that uses the current POI as its isocenter. If you change the current POI, the viewing window updates to show a BEV of a beam that uses the newly selected POI as its isocenter.

1 Click **Add POI**. A new POI appears in the POI list.

2 To change the name of the POI, click the name of the POI in the POI list and type the new name.

3 Complete the fields to define the new POI.

Field	Description
Diameter	The diameter of the POI as it is displayed in the viewing windows.
Color	The color in which the POI is displayed.
2D Display	The method used to display the POI in 2D viewing windows.
3D Display	The method used to display the POI in 3D viewing windows.

4 If necessary, you can extend the crosshair lines to the edges of the viewing windows. To turn on or turn off the crosshair display for the POI, click the flyout arrow that appears below the **Move POI** tool. Select **Crosshairs** to turn on or turn off the crosshairs.

Position a POI

Use one of the following methods to position a POI:

- To manually move the POI, see *Manually Position a POI*.
- To automatically center a POI in an ROI, see *Automatically Position a POI*.
- To automatically place a POI at the center of the image set, see *Center POI on Image Set*.

Manually Position a POI

1 In the POI list, select the POI that you want to move.

2 Use the **Move POI** tool to drag the current POI to the desired position in either a 2D or BEV viewing window. The DICOM coordinates of the location of the POI appear in the **DICOM Coordinates** fields.

If the crosshairs are extended to the edges of the viewing window for the POI, you can drag the POI parallel to a crosshair. To move the POI only up or down, click near the POI on the horizontal crosshair and drag the POI. To move the POI only left or right, click near the POI on the vertical crosshair and drag the POI.

When you are finished using the **Move POI** tool, you must manually deactivate it by clicking the tool again. The tool does not automatically deactivate when you click another tool. When you deactivate the tool, the **Scroll** tool becomes active in 2D viewing windows and the **Zoom** tool becomes active in 3D viewing windows.

3 If necessary, type values directly into the **Left-Right**, **Ant-Post**, and **Sup-Inf** fields to adjust the location of the POI.

Automatically Position a POI

You can automatically place a POI so that it covers regions of interest (ROIs). The placement algorithm uses the smallest possible box or centroid to cover the ROIs. The POI is then placed at the center of this construct.

1 In the POI list, select the POI that you want to move.

2 Click **Autoplace POI**. The **Select Multiple ROIs** window opens.

3 Select the check box for the desired ROI from the **ROI** list. Repeat for each ROI that you want to cover.

4 Select **Box** or **Centroid** as the POI placement method.

CAUTION
Verify that the automatically placed POI is in the correct location. Change its position or diameter if necessary.

5 Click **Autoplace POI**. All viewing windows display the slice on which the POI is placed.

Center POI on Image Set

You can automatically place a POI at the center of the image set. The software calculates the total number of slices in the image set and places the POI on the slice that is closest to the center of the image set.

1 In the POI list, select the POI that you want to move to the center of the image set.

2 Click **Center POI on Image Set**. All viewing windows display the slice on which the POI is placed.

Copy a POI

When you create a copy of a POI, all of the attributes of the original POI are retained except for the POI name, POI color, and the lock setting. The new POI is not locked regardless of the lock setting of the original POI.

1 In the POI list, select the POI that you want to copy.
2 Click **Copy POI**. The new POI appears in the list with "_COPY" appended to its name, and it is assigned a different color from the original POI.

NOTE
If the preference for **Create Orthogonal Beam Pair** is set to **Yes** for subsequent POIs, then an orthogonal beam pair is created when you copy a POI. See *Preferences*.

Delete a POI

1 Select the POI that you want to delete from the POI list.
2 Click **Delete POI**. The software removes the POI from the image and the POI list.

If the POI is an isocenter for any beams, the **POI Dependencies** window opens when you click **Delete POI** and the POI is not deleted. The **POI Dependencies** window lists the beams for which the POI is the isocenter. To delete the POI, you must delete the beams that rely on that POI or specify a different isocenter for the beams.

Lock a POI

You can lock a POI to prevent it from being moved or renamed. Click **Lock POI** for the POI that you want to lock. The button image changes from unlocked to locked, and you cannot move the POI or change its name.

To unlock a POI, click the button again.

Set Slice to Current POI

When you select a POI from the POI list, the viewing windows change to display the slice that is nearest to the POI that you selected.

If you move the POI, click **Go to POI** to update the viewing windows to display the slice that is nearest to the new location of the POI.

NOTE
The **Go to POI** tool only functions in 2D viewing windows.

Sort POIs

You can sort the POIs in the POI list by clicking in the column headings. You can also use the following tools:

NOTE
The tools used to sort POIs are grouped together in a flyout tool. You can access the tools by clicking the flyout arrow that appears below the tool.

Control	Description
A↓Z	Sort alphabetically in ascending order
Z↓A	Sort alphabetically in descending order
△	Move item up
▽	Move item down

11 Beams

The Beam workstep contains tools that let you add and delete beams, set beam geometry, and define beam modifiers.

To display the Beam workstep, click **Beam workstep** at the top of the **Simulation** window.

Add a Beam

As you add beams to the plan, each beam appears in a different color. To help you associate information in the **Properties** panel with the beam display in the viewing windows, the color assigned to the beam is shown next to the beam name in the beam list.

2D images display the intersection of the beam with the slice. The limits of the beam field are indicated by a solid line. The central axis for the beam is indicated by a dashed line. When the beam is orthogonal to the image plane, the central axis position is indicated by crosshairs.

1 Click **Add beam**. A new beam appears in the list.
2 Complete the fields in the beam list to define the new beam.

Field	Description
Beam	The name for the beam. A default name appears here until you type a new name.
Isocenter	The isocenter for the beam. By default, the isocenter of the beam is the current POI. If you change the isocenter, the beam shifts so that the POI that you selected becomes the isocenter of the beam, and the viewing windows update to display beams that use the same isocenter.
2D	Display the beam in 2D viewing windows.
3D	Display the beam in 3D viewing windows.

3 In the **Properties** panel, complete the fields to finish defining the new beam.

Field	Description
Field ID	A unique identifier for the beam. The field ID information can help you identify beams after you export plan information.
Color	The color displayed for the beam.
Machine	The machine used for the beam.
Version	The version of the machine you selected. You cannot change this field.
Energy	The energy used for the beam.
Modality	**Modality** is always **Photon** for simulation. You cannot change this field.

CAUTION
Changing the SSD moves the isocenter of the beam and all attached beams. If necessary, you can use multiple isocenters to avoid this situation.

4 If necessary, you can change the SSD by typing a new value in the **SSD** field. The isocenter for the beam moves to a position corresponding to the SSD you specify.

5 You can choose to display or hide all of the beams in 2D or 3D viewing windows:

- Click **Display/hide beams in 2D views** to display or hide all of the beams in the 2D viewing windows.
- Click **Display/hide beams in 3D views** to display or hide all of the beams in the 3D viewing windows.

NOTE
When you add a new beam, the beam is always shown in the viewing windows regardless of the display or hide beam settings.

Copy and Oppose a Beam

NOTE
The copy and oppose tools are grouped together in a flyout tool. You can access the tools by clicking the flyout arrow that appears on the right side of the tool.

1 From the beam list, select the beam that you want to copy.

2 Click the copy and oppose tool that you want to use:

- **Copy beam**—A new beam whose gantry angle is equal to the selected beam is added to the plan.
- **Copy and oppose**—A new beam whose gantry angle is opposed to the selected beam is added to the plan.
- **Copy and oppose with couch**—A new beam whose gantry angle is opposed to the selected beam is added to the plan. The couch for the new beam has the same angular displacement from the default position of the couch as the selected beam, but it lies on the other side of the default position.

Delete a Beam

1 Select the beam that you want to delete from the beam list.

2 Click **Delete beam**. The software removes the beam from the image and the beam list.

Sort Beams

You can sort the beams in the beam list by clicking in the column headings. You can also use the following tools:

> **NOTE**
> The tools used to sort beams are grouped together in a flyout tool. You can access the tools by clicking the flyout arrow that appears below the tool.

Control	Description
A↓ Z	Sort alphabetically in ascending order
Z↓ A	Sort alphabetically in descending order
△	Move item up
▽	Move item down

Specify Beam Orientation and Collimation

Position the Isocenter

Use one of the following methods to position the isocenter of the current beam.

- To manually move the POI, use the **Move POI** tool to move the isocenter.
- To automatically place the isocenter in the center of the patient or the field, see *Automatically Center the Beam*.

Automatically Center the Beam

1 Select the beam whose isocenter you want to move from the beam list.

2 Center the beam.

- To center the beam in the patient, click the **Center beam in patient** tool. The isocenter of the beam moves to the center of the patient.

  NOTE
  The software uses the midpoint of the beam's central axis and the proximal and distal surfaces of the patient's skin to determine the center of the patient.

- To center the beam in the field, click the **Center beam in field** tool. The isocenter of the beam moves to the center of the field. Although the jaw positions are updated, the field size remains unchanged.

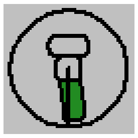
  NOTE
  The software determines the size of the field by the positions of the jaws as seen in a BEV.

Set the Beam Geometry

1 Click the **Geometry** bar in the **Beam workstep** to open the **Geometry** panel.

2 Set the angle for the couch in one of the following ways:

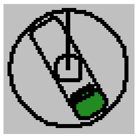
- Enter the value of the angle in degrees. The couch in the graphic moves to that value.
- Use the up and down arrows to set the angle. The couch in the graphic moves to that angle.
- Click and drag the outer portion of the couch in the graphic to the desired angle, as shown in the sample graphic below.



3 Set the angle for the gantry in one of the following ways:

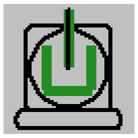
- Enter the value of the angle in degrees. The gantry in the graphic moves to that value.
- Use the up and down arrows to set the angle. The gantry in the graphic moves to that angle.

- Click and drag the outer portion of the gantry in the graphic to the desired angle, as shown in the sample graphic below.



4 Set the collimator angle (looking down from the machine at the patient) in one of the following ways:

- Enter the value of the angle in degrees. The collimator in the graphic moves to that value.
- Use the up and down arrows to set the angle. The collimator in the graphic moves to that angle.
- Click and drag the collimator in the graphic to the desired angle, as shown in the sample graphic below.



- In a BEV window, use the **Adjust collimator 3D** tool to interactively change the collimator angle. Click the **Adjust collimator 3D** tool, and click and drag one of the axes to rotate the collimator.

5 Set the jaw positions. The information in the **Jaws** portion of the **Geometry** panel indicates the current settings for the jaws.

The **Asymmetric** button indicates that the jaws are asymmetric.

The **Symmetric** button indicates that the jaws are symmetric.

To change the symmetry settings for the jaws, click the button to toggle between the two options. The button image changes to the other option to indicate the symmetry of the jaws.

6 Enter the jaw positions.

- For asymmetric jaws, enter the position of the jaw from the central axis.
- For symmetric jaws, enter the width and height of the jaws.
- In a BEV window, use the **Adjust collimator 3D** tool to interactively change the jaw positions. Click the **Adjust collimator 3D** tool, and click and drag a jaw to change its position.

7 You can synchronize the vertical jaw positions for beams that have the same isocenter and use the same machine as the current beam. When the vertical jaw positions are synchronized, changes that you make to the vertical jaw position for one beam are also made to the vertical jaw positions of all of the synchronized beams.

To synchronize the vertical jaw positions, click **Synchronize jaws**. The vertical jaw positions of all beams that use the same isocenter and machine as the current beam are set to the same value as the current beam, and the button image changes to **Do not synchronize jaws**.

To turn off the synchronization, click **Do not synchronize jaws**. The vertical jaw positions are no longer synchronized and the button image changes back to **Synchronize jaws**.

NOTE
The software will automatically remove the synchronization of the vertical jaw positions for all of the beams if you change the machine or isocenter for one of the beams that is synchronized.

8. You can oppose two existing beams. Select the beam that you want to change from the beam list, select the beam to which you want to oppose the beam from the **Oppose To** list, and click **Oppose**. The gantry angle of the beam that you selected from the beam list is changed so that it is opposed to the beam that you selected from the **Oppose To** list.

Specify a Block

When you add a block to a beam, you can manually draw the block or generate the block automatically based on a region of interest. You must use a beam's eye view (BEV) window when working with blocks.

1. Click the **Modifiers** bar to open the **Modifiers** panel.
2. To use a block, select **Yes** in the **Use Block** field.
3. Select whether to expose or block the region of interest from the **Action** list.
    - **Expose**—Treats the block as an aperture and exposes the inside of the area that is defined by the block. The rest of the field is blocked.
    - **Block**—Blocks the inside of the area that is defined by the block. The rest of the field is exposed.
4. Select the type of the block.
    - **Manual**—To manually create a block, go to *Manually Define the Block*.
    - **ROI**—To automatically create a block based on a region of interest, go to *Automatically Define the Block*.
5. To add a margin to the block, type the extra amount that should be added to each side of the block in the **Margin** field and press **Enter**. The margin that you entered is added to all sides of the block.
6. To use the AutoSurround feature, select **Yes** in the **AutoSurround Blocks** field.

    The AutoSurround feature enables the collimator jaws to automatically move to the boundaries of the blocks or to a margin around the block edge. The AutoSurround feature may be used with a block or with an MLC.

    > **NOTE**
    > The AutoSurround feature is not available for fixed jaw machines.

    When using AutoSurround with an MLC, the jaws push to either the block or the MLC-defined field, whichever is more limiting. Leaves that are above or below the block area and never touch the block are not affected.

Manually Define the Block

1. In the **Block Type** field, select **Manual**.
2. Use the following tools to create and edit the block.

Tool	Name	Function
	Create block point by point	Define the block by "dropping" a series of points. After you click the tool, click where you want to start the block. A small box indicates the point that you defined. Click the next point you want to add to the block, or click and drag the point until it is positioned as desired. A line is drawn between the two points. Continue to define the remaining points in the same way. To close the block drop the last point of the ROI inside the box of the first point.

Tool	Name	Function
	Create block paintbrush	“Paint” the block in the BEV window. The tool provides block drawing, editing, and deleting functions, depending on where you use it. After you click the tool, click and drag to paint the block: • If you click an image where there is no block, a new, circular contour appears. Click and drag to create a thick line; wherever you move the cursor, the circle is filled in for the block. • By clicking inside an existing block, you can push out the edges of the block. • If you click outside, but near, an existing block, the tool functions as an eraser, and the block is erased wherever you move the tool. You can use this method to push in the edges of the block. (The **Create block paintbrush** tool generates a large number of points to create the block. If you plan to use the **Edit block** tool to edit the block instead of using the **Create block paintbrush** tool to make your changes, we suggest that you draw the block using the **Create block point by point** tool.)
	**Paintbrush Diameter**	Specify the required diameter for the **Create block paintbrush** tool. To access this tool, click the flyout arrow that appears below the **Create block paintbrush** tool.
	Select block	Click the **Select block** tool, and then click the block to select it. The points used to create the block appear on the perimeter of the block.
	Edit block	Change the shape of a block. Click the **Edit block** tool and then click the block that you want to edit. The points used to create the block appear on the perimeter of the block. Click and drag a point until it is positioned as desired.
	Delete block	Click the **Delete block** tool to delete the block associated with the current beam.

Automatically Define the Block

1. In the **Block Type** field, select **ROI**.
2. Select the ROI to associate with the block from the **ROI** list.

CAUTION

Verify that the automatically placed block is correct for the beam. Modify the block, if necessary. You can edit an automatically generated block by changing the Block Type to Manual and then using the editing tools to adjust the shape of the block.

CAUTION

If the beam geometry is changed during automatic blocking, the software automatically reshapes the block to conform to the ROI shape.

While the block shape is correctly maintained regardless of the beam angle, the collimator jaws are not adjusted to surround the specified ROI. Check your block and adjust the field size as necessary.

Delete the Block

To delete the block, select **No** in the **Use Block** field.

Use Multi-Leaf Collimators

You can use the MLC controls to help shape the beam. You can only use multi-leaf collimators (MLCs) if an MLC for the machine is defined in the physics tool.

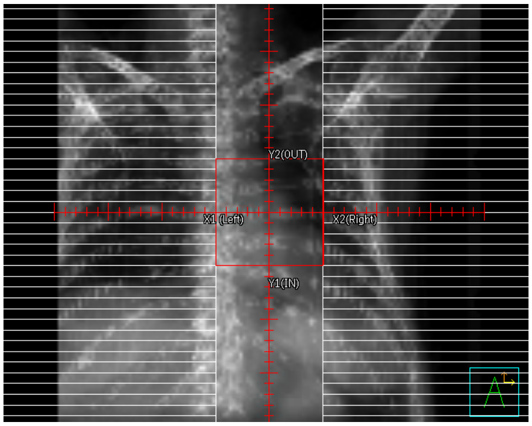
You must use a beam's eye view (BEV) window when working with MLCs in order to see the MLCs in the viewing window.

1 Click the **Modifiers** bar to open the **Modifiers** panel.

2 To use MLCs, select **Yes** in the **Use MLC** field. MLC leaves are automatically pushed to the jaw positions or to the block if a block is present in the beam.

The leaves appear as white bars in a BEV window. Use the jaw labels to help orient yourself in the BEV.

NOTE
For machines that have fixed jaws, the **Use MLC** field is set to **Yes** and cannot be changed.



WARNING
Visually verify the accuracy of your MLC settings before continuing. Incorrect MLC settings and leaf positions can result in incorrect dose.

3 Set the MLC display options.

- **Clip Leaves**—Select **Yes** to view only the section of the MLC that is within the rectangular field limits in the BEV window. When this setting is **No**, the entire MLC is displayed in the BEV window.
- **Fill Leaves**—Select **Yes** to fill in the MLC leaves with white color. When this setting is **No**, the MLC leaves are displayed with outlines.

Propagate Modifiers

You can create beam modifiers more efficiently by propagating the ROI blocking method from one beam to all of the other beams in the plan that use the same machine and isocenter.

1 Select the beam from which you want to propagate the modifiers from the beam list. The beams that use the same machine and isocenter as the selected beam appear in the **Propagate Modifiers** list.

> **NOTE**
> You cannot propagate the modifiers from a beam whose **Block Type** is set to **Manual**.

2 Click **Propagate modifiers**. The modifiers and their attributes are propagated from the selected beam to the beams in the **Propagate Modifiers** list.

12 Finalize

The Finalize workstep contains tools that let you export absolute or relative marking coordinates and plan information.

To display the Finalize workstep, click **Finalize workstep** at the top of the **Simulation** window.

Export Isocenters to a Laser System

You can export absolute or relative marking coordinates to a laser marking system. The output files are compatible with the following laser alignment systems.

- LAP CT1
- LAP CT3
- Gammex CT1
- Gammex CT3

Based on the settings that you specified in the **CT Scanner Configuration** window in the physics tool, the export files are either stored as text files in the export directory or are sent as DICOM message to an AE destination. (See *Laser Calibration Tables* in the *CT Scanner Configuration* chapter.) Your laser system must be configured to monitor the export directory and output file in order to receive the exported data.

CAUTION
Make sure that your laser systems are configured correctly so that the final patient marking is accurate. (See *Select a Scanner* in the *Initialize* chapter for information about viewing the configuration of the scanner.)

In order to export the marking coordinates to a text file, you must configure the following settings in the laser software.

- **For LAP laser system software, the couch deviations and the marking offset must be set to 0.**
- **For Gammex laser system software, the units of the coordinates in the text file must be set to “mm”.**

1 In the **Marking Mode** field, select the marking method that you want to use. The initial setting in this field is determined by the **Default Marking Mode** preference that you set. If you previously exported coordinates for this plan, the marking method that you used for that export is listed in the **Last Laser Transmission** field.

NOTE
If “--” appears in the **Last Laser Transmission** field, you have not previously sent coordinates to the laser system for this plan.

2 Choose one of the following:
  - To export the absolute positions of the isocenters, see *Absolute Marking Coordinates*.
  - To export the positions of the isocenters relative to the setup point, see *Relative Marking Coordinates*.

NOTE
Information is not displayed in the **Absolute Marking** or **Relative Marking** panels if any of the following are true.

- No isocenters are defined for this plan.
- The laser alignment system is not defined for the CT scanner that you selected.
- The laser calibration table is not defined for the CT scanner that you selected.
- A CT to density table is not defined for the CT scanner that you selected.
- The **In (toward the gantry)** setting is not defined for the CT to density table that is associated with the CT scanner that you selected.

To correct these problems, either define an isocenter for this plan or see *CT Scanner Configuration* for information about defining the CT scanner and laser calibration table.

In addition, information is not displayed in the **Absolute Marking** panel if any of the following are true.

- The image data set contains data that was reconstructed with an X/Y offset.
- The image data set was not acquired on a Philips scanner.
- The image data set was not acquired on a scanner that supports absolute marking.
- The image data set was not acquired on a couch that is compliant for use in absolute marking.
- The image data set does not specify a couch height.

Absolute Marking Coordinates

You can export the absolute positions of the isocenters in coordinates for the laser and the couch. These coordinates define how the laser and couch must be moved so that the laser crosshairs will align with the position that is marked on the patient’s skin.

1 If necessary, click **Absolute** in the **Marking Mode** field to enable the **Absolute Marking** panel.

2 Click the **Absolute Marking** bar to open the **Absolute Marking** panel. The panel shows the coordinates of the selected isocenter and the horizontal (in/out) and vertical (up/down) marking offsets.

For 3-ARM laser systems, the software displays the height of the couch at the time the image data set was acquired in the **Couch Up+/Down-** field. Confirm that the height of the couch equals this value before you mark the patient to ensure that you are marking the patient in the correct location.

3 To view the coordinates for a different isocenter, select the isocenter from the **Isocenter** list.

4 If necessary, click **Move POI** and then drag the current isocenter to a different location, or type values directly into the coordinate fields to adjust the location of the isocenter.

NOTE
For 3-ARM laser systems, you cannot change the vertical (up/down) coordinate for the couch. This value is the height of the couch at the time that the image data set was acquired and cannot be changed.

5 You can lock an isocenter to prevent it from being modified. To lock an isocenter, select it from the **Isocenter** list and click **Lock POI**. The button image changes from unlocked to locked, and you cannot modify the isocenter.

To unlock an isocenter, click the button again.

NOTE
You must lock at least one isocenter in order to export data to the laser system. Only isocenters that are locked will be sent to the laser system. If the **Warn About Unlocked Isocenters** preference is set to **Yes**, the software warns you that the plan contains unlocked isocenters when you export the data. See *Preferences*.

6 If necessary, you can extend the crosshair lines in the isocenter to the edges of the viewing windows. To turn on or off the crosshair display for the isocenter, click the flyout arrow that appears next to the **Move POI** tool. Select **Crosshairs** to turn on or turn off the crosshairs.

7 Click **Send locked isocenters to laser** to export the data for all of the isocenters that are locked. The data are exported as either a text file or DICOM according to the export settings that were defined in the physics tool. See *Laser Calibration Tables* in the *CT Scanner Configuration* chapter.

- Text file—The file is saved in the specified directory with the name that was defined in the export settings.
- DICOM—The number of images defined in the export settings are exported to the specified AE destination.

NOTE
The **Laser Export** window opens if a newer image data set has been acquired on the same scanner as the patient's primary image data set. See *Continue or Cancel the Laser Export*.

8 To generate a report, see *Generate Reports*.

Supported Laser Systems

The following are the laser systems supported by Pinnacle^3 and the number of images we recommend that you send for each system. To change the number of images that are exported, you need to change the **Image to Send** value in the export settings in the physics tool. See *Define the Export Settings* in the *CT Scanner Configuration* chapter.

Laser Controller	Number of Images
Gammex	1
LAP CARINAiso	10
LAP CARINAsim	10 or All
LAP IsoMark	1

Laser Controller	Number of Images
LAP CARINAnav	1

NOTE
While the software displays the absolute marking coordinates in cm, the coordinates are exported to the laser marking system in mm to match the unit of measure that is expected by the laser marking system.

When the coordinates are exported as a text file, all of the locked isocenters are sent to the laser. When the coordinates are exported as DICOM, only the locked isocenters that have beams associated with them are sent to the laser. Prior to DICOM export you will be asked to confirm the addition of orthogonal beam pairs to those isocenters that do not have beams associated with them.

Relative Marking Coordinates

You can export the shifts of the isocenters relative to the setup point.

1 If necessary, click **Relative** in the **Marking Mode** field to enable the **Relative Marking** panel.

2 Click the **Relative Marking** bar to open the **Relative Marking** panel. The panel shows the coordinates of the selected isocenter relative to the selected setup point.

3 Select the isocenter that should be used as the setup point from the **Setup** list.

4 If necessary, click **Move setup point** and then drag the setup point to a different location in the viewing window.

5 When you are finished adjusting the location of the setup point, click **Lock setup point** to lock the setup point so that it cannot be modified. The button image changes from unlocked to locked.

To unlock the setup point, click the button again.

NOTE
You must lock the setup point in order to export data to the laser system.

6 If necessary, you can extend the crosshair lines in the setup point to the edges of the viewing windows. To turn on or off the crosshair display for the setup point, click the flyout arrow that appears below the **Move setup point** tool. Select **Crosshairs** to turn on or turn off the crosshairs.

7 Verify that the locations of the isocenters are correct. To view the coordinates for a different isocenter, select an isocenter from the **Isocenter** list.

8 If necessary, click **Move POI** and then drag the current isocenter to a different location, or type values directly into the coordinate fields to adjust the location of the isocenter.

NOTE
For 3-ARM laser systems, you cannot change the vertical (up/down) coordinate for the couch. This value is the height of the couch at the time that the image data set was acquired and cannot be changed.

9 You can lock an isocenter to prevent it from being modified. To lock an isocenter, select it from the **Isocenter** list and click **Lock POI**. The button image changes from unlocked to locked, and you cannot modify the isocenter.

To unlock an isocenter, click the button again.

> **NOTE**
> You must lock at least one isocenter in order to export data to the laser system. Only isocenters that are locked will be sent to the laser system. If the **Warn About Unlocked Isocenters** preference is set to **Yes**, the software warns you that the plan contains unlocked isocenters when you export the data. See *Preferences*.

10 If necessary, you can extend the crosshair lines in the isocenter to the edges of the viewing windows. To turn on or off the crosshair display for the isocenter, click the flyout arrow that appears next to the **Move POI** tool. Select **Crosshairs** to either turn on or turn off the crosshairs.

11 Click **Send locked isocenters to laser** to export the data for all of the isocenters that are locked. The data are exported as a text file. The name of the file and the directory where the file is saved were defined in the physics tool. See *Laser Calibration Tables* in the *CT Scanner Configuration* chapter.

> **NOTE**
> While the software displays the relative marking coordinates in cm, the coordinates are exported to the laser marking system in mm to match the unit of measure that is expected by the laser marking system.
>
> Also, the relative marking coordinates can only be exported as a text file. The export will fail if your export settings in the physics tool specify DICOM transmission.

> **NOTE**
> The **Laser Export** window opens if a newer image data set has been acquired on the same scanner as the patient’s primary image data set. See *Continue or Cancel the Laser Export*.

12 To generate a report, see *Generate Reports*.

Generate Reports

The **Report** section of the **Absolute Marking** and **Relative Marking** panels lets you define the information that should appear in the report for the plan and then generate the report.

1 Complete the following fields as necessary to define the report.

- **Comments**—Type information that should appear in the report.
- **DICOM Coordinates**—Select this option to include the DICOM coordinates in the report. To view the coordinates, click **Show DICOM Coordinates**.
- **Shifts from First Isocenter**—For absolute marking, select this option to include the shifts from the first isocenter in the **Isocenter** list in the report. To view the shifts, click **Show shifts from first isocenter**.

NOTE

The **Shifts from First Isocenter** option is not shown in the **Relative Marking** panel. Relative marking coordinates are reported as shifts from the setup point, and these shifts are always included in relative marking report.

The initial **DICOM Coordinates** and **Shifts from First Isocenter** settings are determined by the settings you selected in the preferences. See *Preferences*.

2. To review the report prior to export or printing, click **Preview report.** The report appears in a preview window. When you are finished viewing the report, close the window.
3. To export the report to a PDF file, click **Export report**. The PDF file is saved in the export location that you specified in the preferences. See *Preferences*.

   Each file is named *MRN_YYYY-MM-DD-sim.pdf*:

   - *MRN* is the Medical Record Number.
   - *YYYY-MM-DD* is the year, month, and day that the report was exported.
   - *sim* indicates that the report is from the simulation application. This differentiates simulation report PDF files from the PDF files generated by the planning application.
4. To print the report, verify that the current printer is the appropriate printer. (The default printer is the printer that you selected in preferences. See *Preferences*.) If necessary, select a different printer from the **Available Printers** list. Then, click **Print report** to print the report.

Continue or Cancel the Laser Export

If you send marking coordinates to a laser system, the **Laser Export** window opens if the software finds a newer image data set that was acquired on the same scanner as the patient's primary image data set. Complete the procedure that follows to continue or cancel the export.

1. The **Laser Export** window lists the patient name, and the scan and date time, for the newer and primary image sets:
   - **Primary Image Set**—The image data set used by the current plan.
   - **Newer Image Set**—A recently acquired image data set that is newer than the **Primary Image Set**.
2. Compare the **Name**, **MRN**, and **Date of Birth** of the patient that is currently on the scanner table with the patient information for the **Primary Image Set** and **Newer Image Set**.
3. Do one of the following:
   - Type your initials in the **Initials** field to confirm that the correct patient is on the scanner table, and that the patient has not moved since the **Primary Image Set** was acquired. Click **OK**. The marking coordinates calculated from the patient's primary image data set are sent to the laser system.
   - If you do not want to send the marking coordinates to the laser system, click **Cancel**.

Export DICOM Plan Information

NOTE
For information about DICOM conformance, see *DICOM Conformance* in the *Getting Started* chapter.

1 Click **Finalize workstep** to display the Finalize workstep.

2 Click the **Export DICOM** bar to open the **Export DICOM** panel.

3 Complete the following fields to define the information to export.

Field	Description
RT Plan	Select **RT Plan** to export the plan information.
RT Image	**RT Image** is only available if you select **RT Plan**. Select this option to export a DRR for each beam in the plan.
Annotate Images	**Annotate Images** is only available if you select **RT Image**. Select this option to export all annotations associated with the DRRs.
RT Structure Set	Select **RT Structure Set** to export all of the ROIs associated with the image data set.
DICOM Image	Select **DICOM Image** to export image data sets in the plan. All of the image data sets are selected in the list that displays.
Local AE Title	The **Local AE Title** field shows the local node from which you will export the information. You cannot change this field.
RT Series Number	Enter a series number to associate with this export.
RT Series Description	Enter a series description to associate with this export.
Destination AE Title	Select the AE title of the remote node to which you want to export the information.
Plan Intent	Select the purpose for this export. Select **None** if you do not want to include this information in the DICOM export.

4 Click **Transmit data** to export the data that you selected.

Export a Plan for Use in Older Versions of the Pinnacle^3 Planning Software

Simulation plans created in TumorLOC software version 14.0 can only be opened in Pinnacle^3 planning software version 14.0 or newer. However, by exporting the plan via DICOM RT and then importing it into the planning software, you can use the data from a version 14.0 simulation plan in an older version of the Pinnacle^3 planning software.

1 Complete the simulation plan in the TumorLOC software.

2 In the **Export DICOM** panel, select **RT Plan** and **RT Structure Set**.

3 Specify the **RT Series Number**, **RT Series Description**, and **Destination AE Title** information as necessary.

4 Click **Transmit data** to export the RT plan and RT structures.

5 Start the Pinnacle^3 planning software.

6 Create a patient using the same patient information that you entered for the patient in the TumorLOC software.

7 Import the image data sets for that patient.

8 Add a plan for that patient, and specify the same primary image data set and secondary image data sets that you used in TumorLOC.

9 Open the plan.

10 Import the DICOM RT plan information that you exported in step 4.

11 Proceed with planning.

Print Images

> **NOTE**
> Image printers were configured for use with your simulation system at the time that your system was installed. If you need to add a printer, contact Customer Support.

You can print individual viewing windows or the entire **Simulation** window.

1. If you are printing a single viewing window, click the viewing window that you want to print.

   > **NOTE**
   > If you are printing a BEV, you can preview the annotations prior to printing. Right-click the BEV viewing window, click **Tools** on the menu that appears, and click **Preview Annotations**. The annotations that are selected to appear on the printed image appear in the viewing window. (The annotations that are shown are determined by the settings in the **Image Printing** preferences. See *Preferences* for information.)

2. Click **Print image**. The **Image Printing** window opens.
3. Verify that the selected printer is the printer that you want to use. Select a different printer from the **Printer** list, if necessary.
4. Choose one of the following.
   - If you are printing to a postscript or PDF printer, continue to step 5.
   - If you are printing to DICOM, continue to step 6.
5. Select whether to print only the active viewing window or the entire **Simulation** window.
6. Select a scaling method. Select **Fit Page** to resize the image to fill the page, or select **Resize by Life-Size Factor** and type a zoom factor for the printed image in the field. A **Resize by Life-Size Factor** value of 1 results in a life-size image.
7. To add a comment that is specific to this printed image, type a comment in the **Image Comment** field. This information will be included as an annotation on the printed image.
8. To print the image, click **Print & Close**. A message appears indicating the number of pages that will be needed to print the image. Click **Yes** to continue with the printing, or click **No** to cancel the printing and repeat this procedure to adjust the settings.

   If you click **Close**, the **Image Printing** window closes and no printout is generated.

13 Preferences

You can specify preferences for the software.

1 Click **Set preferences**. The **Preferences** window opens.

2 Select the preferences, as necessary. See the following sections for information about the preferences.

3 Choose one of the following.

- Select **Save & Close** to save these preferences for use in this simulation session and future simulation sessions.
- Select **Close** to save these preferences for use only in this simulation session. When you close this session, the preferences will revert to their previous settings.

General

Section	Title	Description
Startup Options	**Automatic Backup Increment**	Select the time interval between automatic backups. The software automatically saves all of the plan information at the time interval you specify here. These automatic backups are saved to temporary files on the server. If power to your system is disrupted or a system crash occurs, the automatic backup files can be retrieved from the server, allowing you to recover most or all of the changes made to the plan since it was last saved.
	Create External ROI	Select whether the software will automatically create an ROI at the outside patient-air threshold (the skin surface) when a plan is opened for the first time. **Yes**—The software creates an ROI at the patient skin surface and names it “External” in the ROI list. See the *Segmentation* chapter for information. **No**—The software will not automatically create the external ROI.
	Warn About Unlocked Isocenters	Select whether the software will notify you that isocenters are unlocked before you export coordinates or finalize a plan. **Yes**—The software will notify you that your plan contains isocenters that are unlocked and give you the option to continue. **No**—The software will let you export coordinates and finalize your plan without notifying you about unlocked isocenters.
	Up Arrow Advances Superior	Select the direction that the up and down arrow keys should advance through the image set. If you select **Yes** for this option, the up arrow key advances towards the patient’s superior in axial viewing windows, towards the patient’s right in sagittal viewing windows, and towards the patient’s anterior in coronal viewing windows. If you select **No** for this option, the up arrow key advances towards the patient’s inferior in axial viewing windows, towards the patient’s left in sagittal viewing windows, and towards the patient’s posterior for coronal images. The actions described above apply only to image data sets that were acquired with the patient in a head-first, supine position.

Section	Title	Description
DICOM	**DICOM Timeout**	Select the number of seconds that elapse before a DICOM RT or image export “times out.” (If a DICOM RT or image export message is sent, but a response is not received from the service class provider [SCP] within the limit you specify here, then the message “times out” and is not sent.)
	Default Destination AE Title	Select the default remote DICOM node to which you want to export DICOM information from the **Default Destination AE Title** list.
Viewer	**Default Viewer Layout**	Select the arrangement of the viewing windows. (The **Default Viewer Layout** options are grouped in a flyout tool. To access the options, click the flyout arrow that appears to the right of the current **Default Viewer Layout** icon.) Choose from the following options: One MPR viewing window, one configurable viewing window, and two DRR viewing windows Three MPR viewing windows Three MPR viewing windows and one 3D viewing window Three MPR viewing windows, two DRR viewing windows, and one 3D viewing window
	Default Window for One MPR, One Configurable, Two DRR Layout	Select the type of viewing window that will appear as the upper-right viewing window when the **One MPR, one configurable, two DRR layout** option is selected as the **Default Viewer Layout**.
Report	**Default Printer**	Select the printer that you want to use as your default printer from the **Default Printer** list.
	Export Location	Select the default destination for the PDF files that are created when you export a report. Click the browse button (...). The **Choose Directory** window opens. Browse to the directory that you want to use as the default directory for your reports, and then click **Choose**. The path to the directory appears in the **Export Location** field.
	Include DICOM Coordinates by Default	Select whether the software will automatically include the DICOM coordinates in the plan report for a new plan.
	Include Shifts from First Isocenter by Default	Select whether the software will automatically include the shifts from first isocenter in the plan report for a new plan.

Simulation

Section	Title	Description
POI Defaults	**Display POI on all Data Sets**	Select whether to display all POIs on all image data sets.
	Create Default POI	Select whether the software will automatically add a default POI to the middle of the patient volume.
Beam Defaults	**Default Machine**	Select the machine to be used as the default when beams are added to a plan. If no default is selected, the software uses the last machine loaded when you start the planning module. Subsequently added beams use the machine specified for the previous beam.
	Jaw Symmetry Mode for New Beams	When you create a new beam using a machine that allows asymmetric jaws, select whether the beam has symmetric or asymmetric jaws as a default.
	Block Crosshatch Off with MLC	Select whether the block crosshatch displays on beam's eye view (BEV) windows when the MLC is turned on. Select **Yes** to turn off the crosshatch display.
	Create Orthogonal Beam Pair	Select whether to create two orthogonal beams for the first POI or for all of the subsequent POIs. This option is applied only for new plans. Note that if you set **For First POI** to **Yes**, an orthogonal beam pair will be added to the first POI that is created in the plan, regardless of whether the software automatically creates the POI or if you manually create it.
Marking Defaults	**Default Marking Mode**	Select the default marking mode for new plans.

Image Display

NOTE
You can change the DRR and DCR settings for individual viewing windows in the **Simulation** window. See *Beam's Eye Views*.

Section	Title	Description
2D Defaults	**Window/Level Preset**	Select a default preset that should be used to set the window and level settings for new plans.
	Middle Mouse Window/Level	Select whether the middle mouse button should be set to use the window and level tool by default. If this is set to **No**, the middle mouse button uses the scroll/zoom/pan tool by default.
	2D Grid Size	Select the default resolution of the 2D measurement grid.
3D Defaults	**Render Images Automatically**	Select whether 3D images should be rendered automatically when changes are made to a 3D viewing window.

Section	Title	Description
DRR/DCR Defaults	**Render Images Automatically**	Select whether the DRR or DCR should automatically be rendered when a BEV window is created. Note that if you rendered images prior to saving the plan, those images will be rendered when you reopen the plan, regardless of this setting.
	Rendering Mode	Select the default mode for rendering DRRs and DCRs. Selecting **Presets** configures the software to use preset window and level settings to render the images. Selecting **Rendering Tables** configures the software to use a CT to density table to render the images.
	DRR/DCR Rendering Table	Select the default CT to density table to be used when displaying DRRs and DCRs. Note that this option is only available if the **Rendering Mode** is set to **Rendering Tables**.
	DRR Preset	Select the default DRR preset to use when displaying the DRR. Note that this option is only available if the **Rendering Mode** is set to **Presets**.
	DCR Preset	Select the default DCR preset to use when displaying the DCR. Note that this option is only available if the **Rendering Mode** is set to **Presets**.
	DRR Auto Brightness	Select whether automatic brightness is used when displaying the DRR.
	DCR Auto Brightness	Select whether automatic brightness is used when displaying the DCR.
	DRR/DCR Energy	Select the default energy used when generating DRRs and DCRs.
	DRR/DCR Brightness	Select the default brightness used when displaying DRRs and DCRs.

Default Colors

Title	Description
ROI (First in List)	Select the default color of the first region of interest that you create.
POI (First in List)	Select the default color of the first point that you place.
Beam (First in List)	Select the default color of the first beam that you add.
Couch Plane	Select the default color of the couch plane.
2D Grid	Select the default color of the measurement grid.

Image Printing

Section	Title	Description
	Default Image Printer	Select the printer that should be used by default for image printing from the **Default Image Printer** list.

Section	Title	Description
Image Printing Annotations	**Patient Comment**	Select whether to include text entered for this patient in the **Comment** field in the **Edit Patient** window on the printed image.
	Machine Information	Select whether to include information about the machine on the printed image.
	Beam Geometry	Select whether to include information about the beam angle on the printed image.
	Beam Modifiers	Select whether to include information about the jaw settings for the beam on the printed image.
	Isocenter Information	Select whether to include information about the isocenter on the printed image.
	Institution Information	Select whether to include information about the institution on the printed image.
Life-Size Printing	**Default Magnification Factor**	Type the default magnification factor that you want to use when scaling a viewing window for printing. A value of 1 results in a life-size image.

Image Segmentation

Title	Description
ROI 2D Display	Select the default contouring mode for an ROI in 2D viewing windows.
ROI 3D Display	Select the default contouring mode for an ROI in 3D viewing windows.
Paintbrush Diameter	Specify the default diameter for the **Create contour paintbrush** tool.

14 Scripting

The Scripting feature lets you record and play scripts of software operations.

A script executes a series of software operations when it is run. Scripts can be used for everything from repeating simple operations, such as adding an ROI or a POI, to setting up complex beams. For example, you can record a script that creates ROIs and sets their properties. Then you can run the script in each new plan to automatically create the ROIs.

NOTE
The scripts are automatically saved to the default *PinnacleSiteData/Scripts* directory. Scripts saved in any other location will be inaccessible.

If you install a new version of the TumorLOC software, you must validate all of your scripts in the new software.

Record a Script

CAUTION
Once you start recording, you cannot pause the recording, perform other actions in the planning software, and then resume recording where you left off. All mouse clicks and keyboard entries are recorded until you stop the recording. You also cannot append one script onto another, so you must record all of the steps that you want to perform in a single script or run multiple scripts separately.

1. Click **Record** and perform the operations that you want to record.
2. Click **Stop Recording** to stop the recording when you are done.
3. Type the name and description for the script in the **Scripting** window. Once a script has been recorded, you can replay the script by selecting it in the **Scripting** window.

NOTE
Script names cannot contain spaces or the following characters:

`+ ? * < > [ ] | \ ` " ' & , / ! { } ( )`

Run a Script

NOTE
Using an incorrect script may add elements to your plan that change the outcome that you are trying to achieve. Make sure you select the proper script and verify your plan after running the script.

1. Click **Manage Scripting**. The **Scripting** window opens.
2. Click the script that you want run and click **Play**.

Delete a Script

NOTE
Deleting a script will permanently remove it from the system.

1 Click **Manage Scripting**. The **Scripting** window opens.

2 Select the script that you want to remove and click **Delete**.

15 Backup and Restore

Overview

Use the backup tool in the software to back up patient and physics data. When you back up physics data, you can include commissioned and non-commissioned machines.

You can back up data to electronic media, a specific archive directory, or a UNIX file. You can manually back up the data or set up a one-time unattended backup. The software detects if a backup device is busy and waits until it is ready before performing the backup.

If you back up to electronic media, keep in mind that the media may degrade over time; consult the manufacturer's instructions for information on storage and expected shelf life.

When you do a backup, you can select multiple institutions and the patients and physics machines within those institutions. The software creates a separate backup file and report for each institution and its corresponding data.

You can back up scripts from the *PinnacleSiteData/Scripts* directory. If there are scripts with the same name, the software appends a number to the end of script to make it unique and allow back up of each script.

The software also creates a master index of the backups. You can use this master list to find and restore your data.

Use the restore tool to put the data back on your system. You can restore patient data into the same institution or a new institution. You can restore physics data into a new institution.

The software prevents you from accidentally overwriting scripts by restoring them to a location that is different from where they were originally located. The scripts are restored to a subdirectory named *script.date* (where *date* is the restore date). This subdirectory is located in the *PinnacleSiteData/* directory or in the user script directory.

Considerations

The TumorLOC software runs from either a Pinnacle^3 server or a TumorLOC server. When you back up and restore your data, you need access to that server. If you use DVD media, you need access to the DVD drive on the server. If you back up to a UNIX file, you need access to the server to move the file from the server to your long-term storage.

For UNIX backup files, we recommend that you delete the file from the server after you move the file to your long-term storage. Over time, the backup files will fill up the hard drive.

Backup

After you commission a simulation institution, it is a best practice to back up that institution. You can back up data immediately (manual) or schedule a one-time unattended backup. All backup volumes include a header file and have an index file stored on the Pinnacle^3 system. Backups to a CD or DVD include an HTML index file that you can view in a web browser.

The size of your backup depends on the files you choose to include. Be aware that plan file sizes vary depending on many factors:

- The size and resolution of your image data set (for example, water phantoms require less memory than CT image data sets)
- The number of regions of interest, points of interest, beams, beam modifiers, etc. in your plan.

NOTE
If your system has numerous processes or simulation sessions running, the CD/DVD backup may fail due to lack of system resources. Close all unnecessary processes and sessions before a CD/DVD backup.

1 From the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.

2 Click **Backup**. The **Backup** window opens.

3 In the **Backup Description** field, type a description of the backup.

This description becomes part of the header information that helps you identify and restore the backup file later.

4 For **Type Of Backup**, select **One Time Unattended** or **Manual**.

5 If you selected an unattended backup, enter the future month and day, and select the time that you want the software to perform the backup.

6 For **Backup To**, select one of these options:

- **IO Device**—Backs up data to electronic media or an archive directory. Go to step 7.
- **UNIX File**—Backs up data to a file. The software uses the file name as the volume name for the backup. Go to step 9.

7 Select the CD/DVD drive from the **Backup Device** list. **Eject CD/DVD** appears in case you need to remove a disk.

8 In the **Backup Media Volume Name** field, type the title you want assigned to the backup. Alternatively, you can click **Get Default Name** to have the software assign a name. Go to step 10.

9 Type the directory path and name of the backup file, or click **Browse** to select the location and type a name.

Backup files are stored by default in the user’s home directory.

Do not type spaces, commas, or apostrophes between characters in the file name. If you type an existing file name, the software asks you to confirm that you want to overwrite the file with the new backup.

10 For **Compression**, set whether the software should compress the file.

NOTE
Compressing data significantly increases the time it takes to back up and restore.

11 For **Print Report After Backup to**, set whether the software should print a report of the data backed up in this session.

12 If the printer you want to use is not the current printer, click **Select Printers**. The **Printer Selection** window opens. Select the printer you want to use to print the report.

13 In the pane on the left, click the arrow next to the desired institution. Separate **Patients** and **Physics** sub-directories appear.

⚠ **CAUTION**
Make sure you back up the machines associated with any patients you back up. If you do not include them in the backup, when you restore the patients the plans may be corrupted or you may not be able to open the plan.

14 Click the arrow next to **Patients** or **Physics** to display all patients or all machines. If you want to back up data for select items, click the appropriate names in the lists. Highlight scripts if you want to back them up.

Drag the cursor to make contiguous selections in a list. Hold down the **Ctrl** key as you click to make non-contiguous selections.

Use the arrow buttons between the left and right panes to move data between the current list (left) and the list of data to back up (right). Click **clear** to remove all the items from the backup list (this allows you to start the list again).

The number of megabytes you need for the backup and the device’s remaining capacity appear at the bottom of the window. If necessary, reduce the amount of data you plan to back up or delete obsolete files from your media or hard drive to accommodate the backup.

15 If you plan to back up to electronic media, insert the media in the drive. Make sure the device is on and ready to accept data.

NOTE
If another user is working in the physics or simulation tool and you attempt a backup that includes physics data or the open patients, an error message appears. You will not be able to back up the data until the other user exits the tool. Likewise, if a backup that includes physics or patient data is in progress, users cannot work with the physics or simulation tools for that institution until the backup is complete.

16 If you do not want to include computed files that may have been saved during planning, such as DRRs, select the **Exclude auto-saved computed files** check box.

17 Click **Start Backup** or **Schedule Backup**. Once the backup is complete, a window opens listing the locations and names of the backups.

NOTE
The button name changes depending on the backup method. **Start Backup** appears for manual backups and **Schedule Backup** appears for unattended backups.

18 Click **Close** to close the window. Then click **Close** to close the **Backup** window.

If you decide to cancel the unattended backup, go back to the **Backup** window and click **Cancel Unattended Backup**.

⚠ **CAUTION**
The software checks for as many failures as it can during archiving, but you should still check your backup after the procedure is finished. Use the *Master Index Maintenance* procedure to check your backup.

Fields and Buttons

The following fields and buttons are available in the windows referenced in this section.

Title	Description
Backup Description	This description becomes part of the header information that helps you identify and restore the backup file later.
Backup Device	If you choose to back up the data to a CD/DVD or archive directory, this list lets you select the type of media you are using for the backup.
Backup Media Volume Name	The name of the particular electronic media (for example: CD_001). We recommend that you label each piece of media with its volume name so it can be located when restoring data from the index. If you use a CD/DVD, the volume name will have an *.X.tar* extension where *X* is the number of the institution. One *.tar* file is created for each institution.
Backup To	The media you want to use to back up the data: a UNIX file or a different media.
Browse	Locate the directory in which you want to save the backup.
Cancel Unattended Backup	Cancel the backup you scheduled.
Clear	Remove all the items from the backup list (this allows you to start the list again).
Compression	Select **Yes** if information you are archiving should be compressed to make the file size smaller. This can significantly increase the time to back up or restore the data.
Date/Time to do backup	The month, day, and time to perform the backup.
Device Capacity	The total storage capacity of the device.
Eject CD/DVD	Open the CD/DVD tray.
Exclude auto-saved computed files	Exclude computed files from the backup.
File Name	The name of the backup file.
Get Default Name	The software assigns a volume name to the backup.
Print Report After Backup to	Select **Yes** if you want a hard copy outline of the backup after the backup is complete. If you do not print a report, you can view and print the HTML index for the backup.
Schedule Backup	Schedule the unattended backup. The backup will be performed at the selected time.
Select Printers	Choose a printer for the backup reports.
Start Backup	Start the backup.
Test Backup Integrity	Test whether the backup file is corrupted.
Total Device Space Needed	The amount of memory the current backup needs to back up all the data.

Title	Description
Type of Backup	The type of backup session you desire. A **Manual** backup starts as soon as you click the **Start Backup** button. A **One Time Unattended** backup starts at the time you set after you click the **Start Backup** button.

Restore

You can restore information by reading the header file off of the backup media or file, or using the system backup index. All backup media and files include header information. All of the backups have an index file saved on the system that outlines the content of the backup volume.

Restoring from the header file is the traditional method for restoring data. It allows you to restore data regardless of whether the information is in the index file. Restoring from the index allows you to look through records of all the backups performed on the system (unless you have removed the index records, see *Set Up Backup and Restore Defaults* in the *System Administration* chapter.

If an institution was split into multiple *.tar* files because of size, you can select all of the files and the software automatically combines them into a single institution for restoration.

When you restore an institution, the software appends “(restored)” to the institution’s name. If you restored the institution previously, the software appends “(restored)” plus a numeric value to the institution’s name. The numeric value represents the number of times you restored the institution.

Restore Using the Header File

1. From the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. Click **Restore** on the **Launch Pad** menu. The **Restore** window opens. Make sure that the **Restore From Header** tab is selected.
3. In the **Destination** field, select **Create New Institution** to restore the data to a new institution. Select **Restore into Current Institution** to restore the data into the current institution.

   NOTE
   You cannot restore physics data into an existing institution. You can restore physics data into a new institution and transfer the machines to existing institutions as required.

4. Was the data backed up in a Solaris or SunOS format?
   - Solaris—Select **Solaris Format**.
   - SunOS—Select **SunOS Format**. Choose to restore physics data or patient data. (Only physics and patient data could be backed up from the software versions that ran on SunOS.)
5. For **Restore From**, select one of these options:
   - **IO Device**—Restores data from electronic media or an archive directory. Go to step 6.
   - **UNIX File**—Restores data from a file. The **Backup/Restore File Tool** window opens. Select the file. Go to step 8.
6. Select the device from the **Backup Device** list. If you select a CD/DVD drive, **Eject CD/DVD** appears in case you need to remove a disk.
7. Are you restoring from an archive directory?
   - If yes, the **Read Header Info** window opens. Select the backups to restore and click **Read Header Info**. Go to step 8.
   - If no, go to step 8.

8. Set your header preferences:
   - Set **Add Header to Index** to **Yes** if the header information should be added to the master index.
   - Set **Read All Headers** to **Yes** to read the headers of *all* the backups on the media.

   NOTE
   The **Read All Headers** option is not available for UNIX files.

9. Click **Read Header Info**.
10. In the top pane, click the arrow next to the desired institution. **Patients**, **Physics**, and other items that can be restored appear.
11. Click the arrow next to **Patients** or **Physics** to display all patients or all machines. If you want to restore data for selected patients and physics machines, click the appropriate names in the lists of patients and machines.

    Drag the cursor to make contiguous selections in a list. Hold down the **Ctrl** key as you click to make non-contiguous selections.

    Use the **Add to List** button below the current list (top pane) and the **Remove Selected** button below the list of data to restore (bottom pane) to move data. Use the **Remove All** button to remove all the items from the restore list (this allows you to start the list again).
12. Click **Restore**. Once the restore is complete, a window opens listing the restored data.
13. Click **Close** to close the window. Then click **Close** to close the **Restore** window.

Restore Using the Index File

1. From the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. Click **Restore** on the **Launch Pad** menu. The **Restore** window opens.
3. Click the **Restore From Index** tab.
4. For **Destination**, select **Create New Institution** to restore the data to a new institution. Select **Restore into Current Institution** to restore the data into the current institution.

   NOTE
   You cannot restore physics data into an existing institution. You can restore physics data into a new institution and transfer the machines to existing institutions as required.

5. Select the way the software should display the backed-up data in the pane from the **Sort Index By** list.

   NOTE
   If you want to search the index, enter a word or numbers in the field next to the **Search Index** button. Select whether the software should search for the same case and match only the entire word. Click **Search Index** to start the search. In the list the software highlights the items that match the search criteria.

6. In the top pane, click the arrow next to the desired institution. **Patients**, **Physics**, and other items that can be restored appear.

7. Click the arrow next to **Patients** or **Physics** to display all patients or all machines. If you want to restore data for selected patients and physics machines, click the appropriate names in the lists of patients and machines.

   Drag the cursor to make contiguous selections in a list. Hold down the **Ctrl** key as you click to make non-contiguous selections.

   Use the **Add to List** button below the current list (top pane) and the **Remove Selected** button below the list of data to restore (bottom pane) to move data. Use the **Remove All** button to remove all the items from the restore list (this allows you to start the list again).

8. Click **Restore**.

   If you restore from electronic media, a window opens indicating the volume name that contains the backup files. If multiple institutions from multiple media sources are to be restored, the window opens for each media type.

   Once the restore is complete, a window opens listing the restored data.

9. Click **Close** to close the window. Then click **Close** to close the **Restore** window.

Master Index Maintenance

The maintenance features allow you to manage the master index of the backups performed on the system. The maintenance you perform is not to delete data from a backup, but to manage or remove files from the master index. The master index shows you the backed up data, the volume name (and media type), the date of the backup, the contents, and the description you entered at the time of backup.

1. From the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. Click **Restore** on the **Launch Pad** menu. The **Restore** window opens.
3. Click the **Maintenance** tab.
4. Click **View HTML Index** to launch a web browser and view the backup indices.
5. If the HTML index does not match the displayed index, click **Regenerate HTML Index Files**.
6. Select the way the software should display the backed-up data in the pane from the **Sort Index By** list.

   > **NOTE**
   > If you want to search the index, enter a word or numbers in the field next to the **Search Index** button. Select whether the software should search for the same case and match only the entire word. Click **Search Index** to start the search. In the list the software highlights the items that match the search criteria.

7. In the pane, click the arrow next to the desired institution. **Patients**, **Physics**, and other items that can be restored appear. Click the arrow next to **Patients** or **Physics** to display all patients or all machines.

8 Do you want to remove institutions from the HTML index?
   - If yes, drag the cursor to make contiguous selections in a list. Hold down the **Ctrl** key as you click to make non-contiguous selections. Go to step 9.
   - If no, go to step 10.

CAUTION
Deleting or clearing institutions removes them from the master index. You can recover the information while restoring data by reading the headers with Add Header to Index set to Yes.

9 To remove the selected institutions, click **Delete Institution(s) From Index**. To remove all information from the index files, click **Clear Entire Backup Index**.

10 Click **Close** to close the **Restore** window.

Fields and Buttons

The following fields and buttons are available in the windows referenced in this section.

Title	Description
Add Header to Index	Select **Yes** if, when the header file is read, the header information should be added to the master index. If the backup was performed on the same system, the header is already in the master index (if it was not removed as part of system administration). Use this option to restore an institution from another system or to rebuild lost index files.
Add to List	Click this button to add the highlighted record to the list of data to restore.
Backup Device	The device from which you will restore the data.
Clear Entire Backup Index	Click this button to remove all entries from the master index. This permanently deletes the selected indices unless you reread the header from the backups.
Delete Institution(s) From Index	Click this button to remove the institution records from the master list. This does not delete the actual backup.
Destination	Select **Create New Institution** to restore the data to a new institution on the current system. Select **Restore into Current Institution** to restore the data into the current institution. Physics data cannot be restored into an existing institution.
Eject CD/DVD	Click this button to open the CD/DVD tray.
Format	The backup format—SunOS and Solaris have different formats. Select **SunOS Format** for backups created in the software 3.0du6, 4.0b, or 4.0f.
Match Case	Select **Yes** to search for text exactly as you entered it.
Match Entire Word	Select **Yes** to search only for the word, not for the text within other words.
Read Header Info	Click this button to read the backup file information that is stored in the header of the file.
Regenerate HTML Index Files	Click this button to recreate the master HTML index of backups. This does not recover deleted index records.
Remove All	Click this button to remove all data from the restore list.

Title	Description
Remove Selected	Click this button to remove the highlighted record from the restore list.
Restore	Click this button to restore the selected data into a new or existing institution.
Restore From	The UNIX file or device that contains the backup file you want to restore.
Restore Patients	Select this option to restore the patients you highlighted in the list.
Restore Physics	If the backup file contains physics data, select this option to restore the physics data.
Search Index	Search through the index for the text you entered in the field to the left of the button.
Select Header File	If you are restoring from a UNIX file, click this button to browse to the file from which you will restore data.
Sort Index By	You can sort the master index by volume name, institution name, or backup date.
View HTML Index	Click this button to launch a web browser and view the backup index.

16 System Administration

Overview

This chapter explains system administration procedures that you can perform.

Configuration options

You can access configuration options that are used to perform administrative tasks. In the **TumorLOC Patient Directory**, click Settings to open the **Launch Pad** menu. Then click **Configure** to open the **Configuration Options** window.

- **Default Tool**—Select the default software version to use.
- **Select Printers**—Set up printers for use with the system.
- **Delete Images**—Delete DICOM image data sets and examine DICOM file issues.
- **SysAdmin Password**—Enter the password to enable the system administration options. This button changes to **Change Password** after you enter the password.
- **Change Password**—Change the system administration password. This button appears in place of **SysAdmin Password** after you enter the password.
- **Backup Devices**—Set up new tape drives and other backup devices.
- **Backup/Restore Conf**—Set defaults for data backup and perform backup database maintenance.
- **Institution Disk Setup**—Set up the directory “mount point” for each institution’s data.
- **Scanners**—Set up new scanners you add to the system.
- **Check Patient DB**—Check the integrity of the Launch Pad database.
- **Rebuild Patient DB**—Rebuild the patient database in Launch Pad in the event of a database corruption. The rebuild corrects all problems found by the **Check Patient DB** tool.
- **Advanced Configuration**—Open a terminal window. (This option only appears if you are connected to the TumorLOC software on the CT console.)
- **Licensing**—Enter the license key that enables your software features.
- **File Maintenance**—Limit the number of temporary files and exported files that are stored on the system.

Reconfigure Automatic Import

If you change the name of an institution that has already been set up for automatic import or add a new institution, you must reconfigure the DICOM settings on the server to enable the automatic import functionality for the institution.

Set the Default Tool

If you have multiple versions of the software installed on your system, you can select a particular version that you want to use for a specific simulation session. You can also set the default software version that should be used by new simulation sessions and the physics tool.

When you open a TumorLOC plan, the plan is opened in the version of software that is specified in the **Default Tool**. If the default software version is set to a version prior to 14.0, the plan will open in the latest version of TumorLOC that is installed on the system. If the default software version is set to version 14.0 or newer, then the plan will open in that particular version of TumorLOC.

1. In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.
3. Click **Default Tool**. The **Tool and Version** window opens. The window lists the software versions that are available on your system.
4. To select a specific version of the software for use during the current simulation session, select the version in the **Tool and Version** list.
5. Select the version of the software that you want to use as the default from the **Default** list. This version of software will be used by new simulation sessions and by the physics tool.

   NOTE
   The physics tool always uses the version of software that is set as the default software.

6. Click **Close** to save your changes and close the **Tool and Version** window.

   NOTE
   The **FG Color** and **BG Color** fields are only used in the Pinnacle^3 planning software. You do not need to change those fields for the TumorLOC software.

Use the System Administration Password

Enter the Password

To prevent unauthorized use, some system administration options are protected by a password.

1 In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2 On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.
3 Click **SysAdmin Password**.
4 Type the password in the window that opens, and then click **OK**.

The **Configuration Options** window opens. All system administration options are now available for use.

Change the Password

1 In the **Configuration Options** window, click **Change Password**. The **Change Password** window opens.
2 Type the old password and click **Continue**. The **Enter New Password** window opens.
3 Type the new password and click **Continue**. The **Verify New Password** window opens.
4 Type the new password and click **Continue**. The **Password Changed** window opens to confirm the change.
5 Click **OK**.

License the Software

Contact Customer Support for assistance in licensing your software. The following procedure outlines the basic steps that Customer Support will help you perform; Customer Support provides the license key.

1 In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.

2 On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.

> **NOTE**
> If necessary, click **SysAdmin Password** and type the system administration password to enable the system administration options.

3 Click **Licensing**. The **Licensing** window opens.

4 Click **Site Information**. The **Licensing - Site Information** window opens.

> **NOTE**
> If this is a new installation, a site name entry window opens before the **Licensing - Site Information** window opens.

5 Verify the site information with Customer Support, then click **Dismiss**.

6 Click **Key Installation**. The **Licensing - Install License** window opens.

7 Enter the license key and the application code, and then click **Install License Key**.

8 Click **Dismiss**.

9 In the **Licensing** window, click **Dismiss**.

Define Directory Mount Points for Institutions

> **NOTE**
> Only field service representatives should set up new mount points. Contact Customer Support if you have questions about mount points.

Each time you create an institution, the software automatically creates a mount point, a directory entry where patient data are saved. Think of a mount point as a “pointer” to a particular location on a disk drive.

The default mount point is adequate until the default disk drive begins to fill. If necessary, Customer Support can set up new mount points to distribute and save data to different drives. Customer Support can set separate mount points and directory paths for each institution. Click **Institution Disk Setup** in the **Configuration Options** window to view the window that is used to set up mount points.

Set Up Printers

Follow these procedures to configure your report printers.

Add Printers

1. In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.
3. Click **Select Printers**. The **Printer Selection** window opens.
4. Click **Add Printer**. The **Edit Printer** window opens.
5. Type the printer name in the **Printer Name** field.
6. To change the print command for the printer, type the new command in the **Print Command** field. The file name is automatically appended to the print command. For example, if you specify “lpr”, the command “lpr <file name>” is used. The default system text printer is always identified by “lp”.

   To add a color printer, type the following as the printer command:

   ```
   lp -c -d printname
   ```

   where `printname` is the name of the printer.
7. To choose a non-standard paper size, click **Paper Size** and select a different size from the menu that appears. **Letter** is the default paper size for the standard printer, but you can specify **Legal**, **Tabloid**, **A3**, or **A4**.
8. When you finish, click **Close**, and then click **Save Printers** in the **Printer Selection** window.

Edit Printers

1. In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.
3. Click **Select Printers**. The **Printer Selection** window opens.
4. Select the printer you need to edit from the **Available Printers** list.
5. Click **Edit Printer**. The **Edit Printer** window opens.
6. Change the printer information as necessary. For information about entering printer information, see *Add Printers*.
7. When you finish, click **Close**, and then click **Save Printers** in the **Printer Selection** window.

Delete Printers

1. In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.
3. Click **Select Printers**. The **Printer Selection** window opens.
4. Select the printer you want to delete from the **Available Printers** list, and then click **Delete Printer**. The name of the printer disappears from the list.
5. Click **Save Printers** to save your changes.

Set Up Scanners

If you add a new scanner to your system, or your system configuration changes, you need to note the addition or change in your software.

1 In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.

2 On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.

> **NOTE**
> If necessary, click **SysAdmin Password** and type the system administration password to enable the system administration options.

3 Click **Scanners** in the **Configuration Options** window. The **Scanners** window opens.

4 To install the scanner in the software, click the scanner in the **Scanner Choices** list and then click **Install**. The scanner appears in the **Installed Scanners** list.

5 To edit the scanner information, click the scanner in the **Installed Scanners** list and then click **Edit**. The **Edit IODevice** window opens.

6 Enter the appropriate information for the new scanner.
   - For DICOM3File, enter `/autoDataSets/DICOM` in the **Device** field.
   - For DICOM3CD, enter `/autoDataSets/DICOM/CD` in the **Device** field.

7 In the **Automatically delete original DICOM files after import** field, choose whether you want DICOM image files of the type you specified above to be automatically deleted from the source directory after they have been imported.

8 Click **Close** to save the information and close the window.

9 If necessary, install the next scanner as described in the previous steps.

10 Click **Close** and close the **Configuration Options** window when all of the scanners are installed.

Delete Image Data Sets

After you import image data sets, you can delete them from the source directory.

1 In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2 On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.
3 Click **Delete Images**. The **Delete Images** window opens.
4 Is the scanner for which you want to delete images selected in the **Scanner Type** list?
  - Yes—Continue to step 5.
  - No—Select the scanner in the **Scanner Type** list, then click **Reread Patient/Exam Directory**. Continue to step 5.

> **NOTE**
> If you know that image data sets have been acquired or deleted since you opened the window, click **Reread Patient/Exam Directory** to refresh the list of image sets.

5 Select the image data sets that you want to delete.
6 Click **Delete Selected Image Sets**.

Examine DICOM issues

You can examine the files in your DICOM image directory to determine which, if any, files have issues that prevent the software from importing them. You may want to examine the files for these reasons:

- You are expecting to see certain files in the list of available DICOM images, but the files do not appear in the list.
- You are performing regular maintenance on your system and you want to identify any files that cannot be imported.

1 In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2 On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.
3 Click **Delete Images**. The **Delete Images** window opens.
4 Is the scanner for which you want to examine DICOM files selected in the **Scanner Type** list?
  - Yes—Continue to step 5.
  - No—Select the scanner in the **Scanner Type** list, then click **Reread Patient/Exam Directory**. Continue to step 5.

5 Click **Examine DICOM Issues**. The **DICOM File Issues** window opens and displays a list of files. The list includes the files in the DICOM image directory that cannot be imported.
6 Select a file in the list. A description of the issue with the file displays at the bottom of the window.

> **NOTE**
> Consult your local IT staff or the vendor for the device that sent the DICOM image data set to determine how to resolve the issue with the file. If the issue cannot be resolved, you may need to acquire new images for the patient.

7 To delete a file, click **Delete Selected Files**. Or, to delete all files in the list, click **Delete All Files**. When the software prompts you to confirm the deletion, click **Yes**.

Set Up Backup Devices

If you add a new backup device to your system, or your system configuration changes, you need to make the addition or change in the software.

To back up compressed files on tapes, set up the device for compression. Usually devices that use compression have a *c* in the name. For example: */dev/rmt/0c*.

1 In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.

2 On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.

> **NOTE**
> If necessary, click **SysAdmin Password** and type the system administration password to enable the system administration options.

3 Click **Backup Devices**. The **Edit Backup/Restore IO Device** window opens.

4 Click **Add** to begin setting up the new backup device.

To edit information for an existing backup device, select it in the list of devices at the top of the window.

5 Select a default backup device from the **Default** list.

6 If you want system diagnostic messages to appear in a UNIX shell window, set the **Diagnostic Output Enabled** option to **Yes**. You must open a shell window to see the messages.

CAUTION
The software does not interface directly with HSM systems and HSM software should not be installed on your system. If you want to use an HSM system, we recommend that you set up an archive directory device (Archive Dir format). Map to an external server and directory, not a directory on your system. You should work with your system administrator to configure the HSM system to use that directory, and test the functionality of the software and the HSM system prior to performing backups.

7 In the **Format** options, select the type of backup device.

> **NOTE**
> If you have a CD/DVD writer, we recommend that you set up two backup devices: one for CDs and one for DVDs. You can set the appropriate capacity for each type of media. If you set up only one device using the DVD capacity but attempt to write to a CD, you may exceed the CD capacity and may not be able to perform a backup. The only acceptable DVD media is DVD-R.

8 Enter the information for the specific backup device. You must complete all the fields listed before you can close the window.

9 Click **Close** to save the information and close the window.

Set Up Backup and Restore Defaults

You can set the temporary directory that the software uses to compile restored data before moving it to an institution. You can also remove backup records from the database.

You can control if the HTML index of backups is updated after every backup. By default, the index is not generated after every backup.

1. In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.

> **NOTE**
> If necessary, click **SysAdmin Password** and type the system administration password to enable the system administration options.

3. Click **Backup/Restore Conf**. The **Backup/Restore Configuration** window opens.
4. Set the temporary directory or click **Browse** to navigate to the temporary directory.
5. If you want to delete the list of backup names that the software has already used, click **Delete Backup Volume DB**. The software will start over at Backup_1 for default volume names.
6. If you want the index to be generated after every backup, set **Regenerate HTML index after backups** to **Yes**.
7. Click **Close**.

Manage the Patient Database

Check the Patient Database

Use the **Check Patient DB** option to check the integrity of the database. The database sometimes may need to be resynchronized with the data repositories on your network due to manual data changes or corruption.

1. In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.

   NOTE
   If necessary, click **SysAdmin Password** and type the system administration password to enable the system administration options.

3. Click **Check Patient DB**. The software analyzes the patient database and reports the following problems if they exist.
   - Discrepancies exist between the following data in the database files versus the data on disk: number of institutions, number of patients, patient IDs, patient descriptions, number of plans, and number of image data sets.
   - The next unique institution ID is not correct, or the next unique patient ID is not correct.
   - Patients are located in the wrong directory (for example, a patient is located in the Institution directory instead of the Mount directory).
4. If necessary, use the **Rebuild Patient DB** tool described in the next section to correct the problems in the database.

Rebuild the Patient Database

CAUTION
Review all patient data and plan parameters after you rebuild the database to make sure all of the data transferred correctly.

Use the **Rebuild Patient DB** option to rebuild the database and correct all problems found by the **Check Patient DB** tool. This operation might take a while.

1. In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.

   NOTE
   If necessary, click **SysAdmin Password** and type the system administration password to enable the system administration options.

3. Click **Rebuild Patient DB** to start the rebuild process. When the process is complete, the software reports the results.

   NOTE
   If the software displays a message that it cannot completely rebuild a plan for a patient, contact Customer Support for assistance in rebuilding your database.

Specify file maintenance settings

You can limit the number of temporary plan and institution files that are stored on the system. In the **Institution and plan temporary files** section of the **File Maintenance Settings** window, the default values are 200 for the **Number of files** and 180 days for the **Age** of the files:

- When the number of files exceeds 200, the system automatically deletes the oldest temporary files to reduce the total number to 200.
- Temporary files are automatically deleted if they have been stored on the system longer than 180 days.

NOTE
The **Exported Files** section of the **File Maintenance Settings** window is used to maintain files that are transferred between Pinnacle^3 and other software applications, such as RadCalc and PlanIQ. The **Exported Files** section is not applicable to the TumorLOC software and should be ignored.

1. In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.
3. Click **SysAdmin Password**.
4. Type the system administration password in the window that opens, and then click **OK**. All system administration options are now available for use.
5. Click **File Maintenance**. The **File Maintenance Settings** window opens.
6. In the **Institution and plan temporary files** section change the default values, if necessary:
   - **Number of files**—This is the maximum number of plan and institution files that are stored by the system.
   - **Age**—This is the maximum number of days that files for a plan or institution are stored by the system.
7. Click **OK** to close the **File Maintenance Settings** window.

   The values you set for the **Number of files** and **Age** of files are applied, separately, to each plan and institution in the software. When either value is exceeded for a plan or institution, only the files for that plan or institution are automatically deleted.

Open a UNIX Terminal Window

NOTE
The **Advanced Configuration** button only appears in the **Configuration Options** window if you are connected to the TumorLOC software from the CT console. If you are using remote access to connect to the software, then you can open a UNIX terminal window from the Solaris desktop.

For some service or maintenance activities (for example, to perform system diagnostics or to update the date and time settings of the system), you need to open a UNIX terminal window. For assistance performing these activities, please contact Customer Support or your local distributor.

1. In the **TumorLOC Patient Directory**, click **Settings**. The **Launch Pad** menu appears.
2. On the **Launch Pad** menu, click **Configure**. The **Configuration Options** window opens.

   NOTE
   If necessary, click **SysAdmin Password** and type the system administration password to enable the system administration options.

3. Click **Advanced Configuration**. A UNIX terminal window opens.

Reconfigure automatic import settings

NOTE
Only software versions 14.0 and higher allow you to configure the automatic import feature with a Philips CT scanner.

The instructions that follow are used to reconfigure DICOM settings for a system that has already been set up for automatic import. To initially set up a system for automatic import, contact Customer Support or your local distributor.

To automatically import image data sets from a Philips CT scanner into the software, the server and scanner must be configured to send the image data sets to an existing institution. If you change the name of an institution that has already been set up for automatic import or add a new institution, you must reconfigure the DICOM settings on the server to enable the automatic import functionality for the institution. For more information about the automatic import feature, see *Import Image Data Sets*.

Reconfigure the DICOM settings for an Expert server

NOTE
For assistance when performing this procedure, please contact your CT service technician or Customer Support.

Complete the procedure that follows to reconfigure the DICOM settings for an Expert server.

1 Log on to the server as “`root`”.

2 Open a terminal window.

3 Type the following:

```
cd /usr/local/adacnew/DICOMStatic/bin/common
```

4 Press **Enter**.

5 At the prompt, type the following command:

```
./DICOMAddListeningAETitle -a AETitle_name -t AUTO -i
"institution_name"
```

- For `AETitle_name`, type the same AE Title that is used for the CT scanner, as it is displayed on the scanner’s console.
- For `"institution_name"`, type the name of the institution that will receive the image data sets from the CT scanner. Make sure the name of the institution is enclosed in quotation marks.

NOTE
Automatic import will not function unless the `"institution_name"` is the same as the institution that will receive the imported image data sets. For information about adding or editing an institution, see the *Institutions* chapter.

6 Press **Enter**. A directory is created on the server that is used to automatically import image data sets from the CT scanner and send them to the institution.

2 System Security and Data Privacy

Philips Healthcare recognizes that the security of Philips Healthcare products is an important part of your facility's security strategy. However, these benefits can only be realized if you implement a comprehensive, multilayered strategy (including policies, processes, and technologies) to protect information and systems from external and internal threats.

Following industry-standard practice, your strategy should address:

- physical security
- operational security
- procedural security
- risk management
- security policies
- contingency (disaster) planning

The implementation of security varies by site and may employ a number of technologies, including firewalls, virus-scanning software, and authentication technologies.

As with any computer-based system, protection must be provided so that firewalls, other security devices, or both are in place between the medical system and any externally accessible systems. The U.S.A. Veterans Administration has developed a widely used Medical Device Isolation Architecture for this purpose. Such perimeter and network defenses are essential elements in a comprehensive security strategy. Any connection of a device to a hospital network should be done with appropriate risk management for safety, effectiveness, and data and systems security. For guidance on risk management, see the IEC-80001-1 standard.

Additional security and privacy information, including MDS2 information, can be found on the Philips product security web site at www.healthcare.philips.com.

Please review Philips product security policies regarding remote service, patch management, anti-virus software, and more in the "Product Security Policy Statement" and additional information sources available through this website.

NOTE
Philips Healthcare is not responsible for the security of hospital-managed systems (desktop PCs, laptops) where Pinnacle^3 is accessed.

For specific information about security within their institutions, operators and owners can consult with the following officers at their location:

- Information Systems Security Officer
- Chief Information Officer
- HIPAA Officer (in the U.S.A.)
- Safety Officer

Regulatory Controls

Protect Patient’s Health Information

One of the most important assets to protect with security measures is the patient’s health-related information.

Many governments require that you maintain the confidentiality of this information. Therefore, strict security measures must be taken to guard this protected information.

Clinical data transferred across the network is not encrypted. See *Security Issues and Guidelines* for more information.

NOTE
Users in the U.S.A. may find guidelines at www.hhs.gov/ocr/hipaa/.

Prevent Unauthorized Device Modification

Operators of this medical equipment must permit only Philips-authorized changes to be made to the Pinnacle^3 system, either by Philips personnel or under explicit published direction from Philips.

⚠ **CAUTION**
The installation of software not authorized by Philips or not specified in the Philips system documentation may adversely affect the operation and security of the system, as well as the networks to which the system is connected. These adverse effects may not be immediately apparent to the user. Therefore, users should not install unauthorized software onto the Pinnacle^3 system.

⚠ **CAUTION**
The installed web browser on Pinnacle^3 is intended to allow access to online help only. It is not intended for casual web browsing.

Security Issues and Guidelines

Network Security

The Pinnacle^3 system must be placed on a secure local computer network that has protections against viruses and other harmful computer system intruders. Make sure the equipment is connected to a local network that uses appropriate protection, such as firewalls, network access controls, and virus scanners.

Do not use your Pinnacle^3 system to browse the Internet. Only use the Internet browsers that are provided with your Pinnacle^3 system to access the Pinnacle^3 software online help.

⚠ **CAUTION**
Connection of the system to a network that includes other equipment could result in unidentified risks to patients, users, operators, and others. You must identify, evaluate, and control these risks on-site. Changes to a network (including configuration, additional connections, disconnections, updates, and upgrades) may introduce new risks and require further analysis.

Data Transmission

The production, storage, and transfer of electronic protected health information (ePHI) is governed by HIPAA guidelines. Transferring unsecured ePHI over a network carries the risk of exposure. The following practices can help prevent inadvertent exposure of ePHI:

- Do not e-mail non-encrypted ePHI.
- Use Secure FTP to transmit non-encrypted ePHI.
- Use Secure Shell with X11-forwarding (ssh -X) instead of XDMCP to transmit non-encrypted ePHI.
- Make sure personally identifiable information is not stored in log files.

Remote Service

Philips has a global, web-based network for connecting many of your Philips systems to our advanced service resources. Remote service provides a set of tools that enables Philips Healthcare to perform service actions, entirely or partly, from a remote location. Remote service is designed to reduce system down time and improve investigation of systemic issues.

Positioning of Display Monitors

You can minimize unauthorized visual access to protected information by positioning the system’s display monitor so that it faces a wall. This prevents people from viewing protected information from doorways, hallways, and other traffic areas.

To help in limiting unauthorized visual access, an unattended session automatically locks after a set period of time. Locking does not end the session or affect patient data; it causes the screen to show the log on screen only.

Manually lock the workstation by clicking **Lock** on the **Front Panel**. Save data before concealing the screen as a safeguard.

Unlock the session by logging on to show the data on the screen.

Room Access Control

Local procedures must be put in place to limit physical access to the medical equipment in order to prevent accidental, casual, or deliberate contact by unauthorized individuals.

Access to the room containing the Pinnacle^3 system should be controlled by policy and procedures that identify who is authorized to occupy specific areas. Check with your Safety and Security Office for more information on what measures are in place or how to implement room access controls.

User Accounts

- Pinnacle^3 systems support multiple user accounts. Each user should have their own individual user account and password. Users should keep their passwords private and should not share their accounts with other users. We recommend that you use this method to manage your user accounts.
- Pinnacle^3 systems support single user sessions using a common clinical user account. We recommend that you do not use one common clinical user account for all of your users.
- System credentials (such as user name and password) must be kept confidential.

The clinical user account password should be changed from the default password.

User Name and Password Protection

Minimum user name and password standards include the following items:

- Implement strong passwords. This is the easiest and most effective method to increase security. Strong passwords consist of at least eight alphanumeric, mixed case characters, plus digits and special characters such as “@” or “*”.
- Never use words that can be found in the dictionary.
- Never post or share user names and passwords.
- Change passwords periodically.

Emergency Access

A special emergency access user account is not supported. If this is a concern, then an alternative is to provide the location of an emergency user name and password in the contingency (disaster) plan. The system is not configured to log such emergency use.

Automatic Log-Off

The system does not support automatic log-off. Users must manually log off the system.

System Hard Drive

Clinical images that reside on the system hard drive are not encrypted; therefore, it is critical to limit local access to authorized users only.

System Backup Media

The system is not intended for permanently storing sensitive patient personal information. Information should be exported to a long-term storage device as soon as possible.

The clinical data that is backed up on removable media is not encrypted and should be stored in a secure location to avoid unauthorized access.

Removable and Portable Media

When using removable media (CD-ROMs, DVDs, and USB drives), be aware of these security issues:

- Inserting removable media can introduce a virus to the medical device. It is recommended to perform a virus scan on removable media before inserting the media into the system.
- If removable media are used to store patient data, protect the information from media obsolescence by planning and performing data migrations to newer storage technologies.
- If the removable media are to be stored for safekeeping, protect the data from “fading” loss by storing it in a suitable environment and performing media renewal as recommended by the manufacturer.
- If the media containing patient data are to be discarded they must be destroyed or disabled so that the data can no longer be accessed.

CAUTION
Removable media that contains images or other medical information must be stored in a secure area that is not accessible by unauthorized individuals.

User Logging and Audit Trails

- The system records clinical user activity event logs and user audit trails used to track user access to clinical data (playback log).
- The system records a number of system-level event logs to assist with system troubleshooting and repair (message log).
- The system maintains records of user logon activity (last log).

Data Integrity Checks

- The system supports basic system-level data and database integrity checks.
- If you suspect improperly altered or destroyed clinical data, notify your local IT security office and Customer Support.

3 Physics Data Worksheets

The worksheets in this section provide checklists for the physics data required by the TumorLOC software. They list the physical description information required for the photon machines that will be used with TumorLOC. These worksheets duplicate portions of the photon physics tool windows into which the data must be entered.

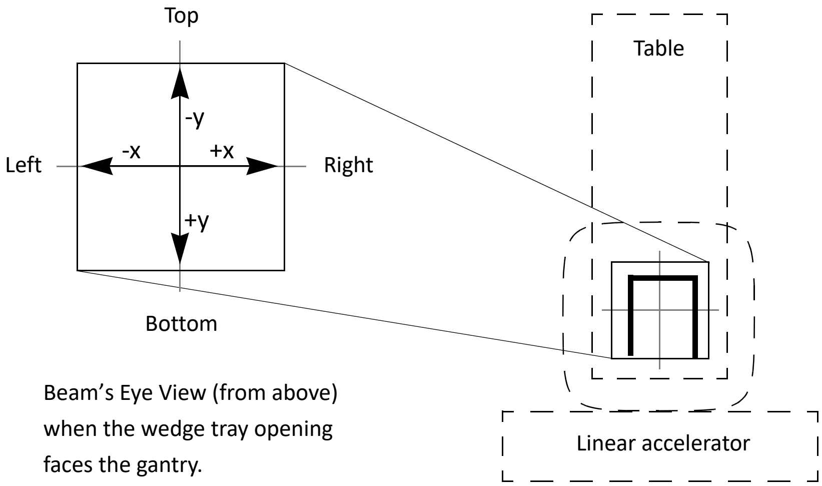
Make as many copies of the worksheets as necessary.

Machine Information - Collimator Jaws

Physicist	
Date	
Machine Name	

Collimator Jaw Information

Setting	**Left/right jaws**		**Top/bottom jaws**	
	Left	**Right**	**Top**	**Bottom**
Jaw name				
Jaw pair name				
Jaw pair thickness				
Can be asymmetric?				
Minimum position				
Maximum position				
Default position				
Decimal places				



Beam's Eye View (from above) when the wedge tray opening faces the gantry.

Machine Information - Couch & Collimator Angles

Physicist	
Date	
Machine Name	

Couch Angle Information

Setting	Value
Minimum angle	
Maximum angle	
Default angle	
Decimal places	
Couch angle when foot of table points away from gantry	
When viewed from above, is positive rotation clockwise?	

Couch position in cm	Min	Max	Default
Vertical position			
Lateral position			
Longitudinal position			

Collimator Angle Information

Setting	Value
Minimum angle	
Maximum angle	
Default angle	
Decimal places	
Collimator angle when tray opening faces gantry*	
When viewed from above, is positive rotation counterclockwise?	

*Some machines have a tray opening that never faces the gantry. Enter the angle as if you were able to rotate the tray opening to face the gantry.

Machine Information - Gantry Angles

Physicist	
Date	
Machine Name	

Gantry Angle Information

Setting	**Value**
Minimum angle	
Maximum angle	
Default angle	
Decimal places	
Gantry angle when beam points down toward floor	
Arc allowed?	
Arc rotation direction • CW or CCW • CW only • CCW only	
When facing gantry, is positive rotation counterclockwise?	
Conformal arc (yes or no)	
Machine has C-Arm?	
C-Arm maximum angle	
C-Arm decimal places	

Machine Information - Delivery Parameters

Physicist	
Date	
Machine Name	

Delivery Parameters

Setting	Value
Maximum gantry rotations (deg/sec)	
Maximum jaw speed (cm/sec)	
Maximum MLC leaf speed (cm/sec)	
Allow conformal arc?	
Allow dynamic arc?	
Dose rate delivery behavior: • Constant dose rate • Continuously variable dose rate • Binned dose rate	
Maximum gantry MU delivery (MU/deg)	
Minimum gantry MU delivery (MU/deg)	
Minimum MLC leaf MU delivery (MU/deg)	
Limit gantry acceleration?	
Maximum gantry rate change (deg/sec)	

Machine Information - Miscellaneous Machine Parameters

Physicist	
Date	
Machine Name	

Miscellaneous Machine Information

Setting	Value
Primary collimation angle (radians)	
Source to axis distance (cm)	
Source to (bottom of) flattening filter distance (cm)	
Source to (bottom of) top/bottom jaw (cm)	
Source to (bottom of) left/right jaw (cm)	
Source to (top of) block tray (cm)	
Source to image receptor	
Monitor unit decimal places (for beams)	
Monitor unit decimal places (for control points)	
Maximum MU setting	
Maximum MU per degree	
When MU exceeded: (1) Warn and limit beam MU to maximum setting (2) Warn and allow beam MU to exceed maximum	
Default block/field edge overlap (cm)	
Delivery time multiplier	

Multi-Leaf Collimator (MLC) Information

Physicist	
Date	
Machine Name	

Because an MLC typically has 20 to 40 pairs of leaves, you might want to make multiple copies of these pages to note information for each pair of leaves.

MLC Information - General

Setting	**Value**
Vendor	
Leaf motion parallel to movement of left/right jaw or top/bottom jaw?	
MLC replaces jaw?	
Source to (bottom of) MLC distance (cm)	
MLC tracks jaws? • MLC does not track jaws for open fields • MLC tracks X jaws for open fields • MLC tracks XY jaws for open fields	
MLC thickness (cm)	
Leaf position decimal places	
Bank names	
For leaf motion parallel to left/right jaw: • For the MLC leaf positions, is the Top (X2) jaw +Y or -Y? For leaf motion parallel to top/bottom jaw: • For the MLC leaf positions, is the Left (Y2) jaw +X or -X?	
MLC has rounded leaves?	
MLC has carriage?	
Is this a micro MLC?	
Name	
Manufacture code	
Applicator type: • Photon Square • Photon Rectangle • Photon Circle • Stereotactic	

MLC Information - Rounded Leaf Specifications

Rounded Leaf Tip Radius (cm)	

Leaf Position	**Offset**

Leaf Position	Offset

MLC Information - Leaves

Setting	**Value**
Allow opposing adjacent leaves to overlap?	
Tongue and groove width (cm)	
Additional interleaf leakage transmission	
Maximum tip difference for all leaves on a side (cm)	
Minimum static leaf gap (cm)	
Minimum dynamic leaf gap (cm)	

Leaf Pair	**Position (cm)**	**Width (cm)**	**Minimum tip position (cm)**	**Maximum tip position (cm)**

Leaf Pair	Position (cm)	Width (cm)	Minimum tip position (cm)	Maximum tip position (cm)

MLC Information - Jaw Dependencies

Setting	Value
Default jaws behavior (static or variable)	
Open extra set of leaf pairs outside jaws automatically?	
Maximum leaf/jaw overlap (cm)	
Minimum leaf/jaw overlap (cm)	

Photon Beam Energy Information

Physicist	
Date	
Machine Name	

Photon Beam Energy Information

Setting	**Value**
Photon energy name	
Photon energy (MV)	
Default tray factor	
Default block and tray factor	
Dose rate table (MU/min) Enter the allowable dose rates for the machine in the table cells at the right. The first value should be the maximum dose rate for the energy, and subsequent values should be monotonically decreasing.	
Default dose rate (MU/min)	

www.Philips.com/Pinnacle

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is www.philips.com/ifu.

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