PHILIPS

Pinnacle³

Planning

Reference Guide

Release 16.2 (English)

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Medical Device Directive
Pinnacle³ Radiation Therapy Planning
System is CE Marked to the Medical
Device Directive 93/42/EEC.

$C\epsilon_{0086}$

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Device Description

The Pinnacle³® Radiation Therapy Planning (RTP) software is composed of several modules including the core Pinnacle³ functionality, Syntegra™, P³IMRT®, P³MD®, and AcQSim³™. The Pinnacle³ 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.

Pinnacle³ includes networking capabilities to provide connectivity to other Pinnacle³, Syntegra, PC Access Point (remote planning), P³MD, AcQSim³, or P³IMRT workstations, input devices and output devices, as well as access to the Pinnacle³ database from any Pinnacle³ workstation available on the network. The system can be run from a single workstation but has network capability to other Pinnacle³ workstations and to both input and output devices via local area network (LAN) or wide area network (WAN). The Pinnacle³ 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 Pinnacle³ sessions run which enables display on any network accessible computer.

Installation instructions appear on the DVD insert included with the software DVD. You only need to load the software on the systems designated as the servers at your site.

To enable use of the software, a licensing key must be issued by a Customer Support representative or your local distributor. You may contact Customer Support at 1-800-722-9377 (US and Canada) or your local distributor for assistance with installation or licensing.

Intended Use

Pinnacle³ 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

Pinnacle³ Radiation Therapy Planning System is a software package intended to provide planning support for the treatment of disease processes. Pinnacle³ Radiation Therapy Planning System incorporates a number of fully integrated subsystems, including Pinnacle³ Proton, which supports proton therapy planning. The full Pinnacle³ Radiation Therapy Planning System software package provides planning support for the treatment of disease processes, utilizing photon, proton, electron and brachytherapy techniques.

Pinnacle³ 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 Pinnacle³ RTP system.

Intended Audience

This manual is written for qualified medical personnel trained as users of Pinnacle³ 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 Pinnacle³ 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.

⚠️ **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.

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.

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.

Pinnacle³ 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.

Pinnacle³ includes sample data. This information is for reference purposes only. Do not treat patients with plans based on sample machines or other sample data.

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.

Notes

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

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4

1 Introduction

The information in this guide supplements information in three other Pinnacle³ guides—the *Pinnacle³ Planning Instructions for Use*, *Classic Pinnacle³ Planning Instructions for Use*, and *AcQSim³ Instructions for Use*. The instructions for use provide the essential information for using the Pinnacle³ planning and simulation tools.

Reference information supplementing the *Pinnacle³ Physics Instructions for Use* is located in the *Pinnacle³ Physics Reference Guide*.

> **NOTE**
> Some of the options described in this guide are not available to AcQSim³ users.

The information in this guide is divided into chapters:

- Chapter 2, *Regions of Interest*, provides information on 2D autocontouring aids, ROI precision, and ROI expansion/contraction.
- Chapter 3, *Beams*, explains how to interpret machine version information in the software and how to set beam display parameters.
- Chapter 4, *Beam Modifiers*, provides reference information on wedges, beam blocks, and compensators.
- Chapter 5, *Dose*, explains how the software calculates monitor units for various modalities.
- Chapter 6, *Brachytherapy*, explains parameters for displaying brachytherapy source groups.
- Chapter 7, *Plan Evaluation Tools*, describes how the software performs NTCP and TCP calculations and provides additional information about planar dose settings.
- Chapter 8, *Plan Output*, provides details on printing plans and exporting data to Record and Verify systems.
- Chapter 9, *Scripts*, describes how to create and use HotScripts.
- Chapter 10, *Utilities*, provides information on preferences, file locations, development options, and user account administration.
- Chapter 11, *Troubleshooting and Performance*, provides troubleshooting information and tips to improve your system performance.

2 Regions of Interest

The following sections provide information on 2D autocontouring aids, ROI precision, and ROI expansion/contraction.

Autocontouring aids

If you autocontour structures, several 2D tools can assist you in determining appropriate autocontouring thresholds. You can use the **Show image value 2D** tool to display the CT value for any point in the patient data set. CT values are displayed in the bottom of the viewing window when you press the left mouse button.

When using the **Show image value 2D** tool, the CT value appears for the point in the image that corresponds to the current cursor position.
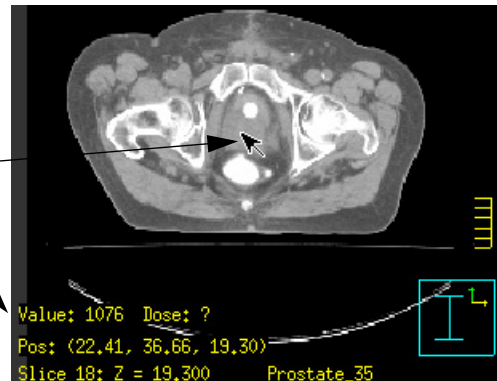
You can use the **Profile** tool to generate a profile of CT numbers across any portion of the image. To generate a profile for a structure that you want to autocontour, drag the cursor across the structure. When you release the mouse button, a window appears and shows a plot of the image values along the line that you drew. For example, the following graphic shows a profile drawn

across the lung and the resulting plot of CT values. From the plot, you can determine that the lower threshold for the lung should be approximately 500.
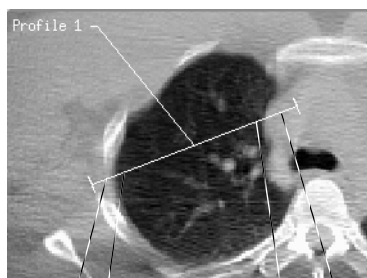
To determine the appropriate CT values for the Upper and Lower Autocontouring thresholds, select the **Profile** tool and drag the cursor across the structure to be autocontoured. A plot of CT values for each point in the profile is generated.

As you can see from the plot, the CT values for the lung fall between 90 and 450 and the CT values for the tissue around the lung are above 800. To autocontour the lung, you can select a lower threshold value between 450 and 800 and leave the upper threshold at its default value.

ROI precision

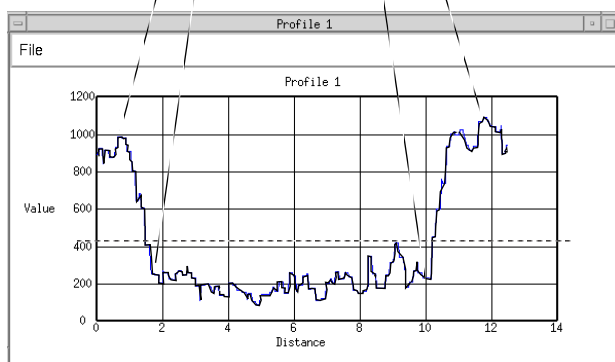ROIs have the same resolution as the data set to which they are assigned (typically the primary CT data set); thus, the ROI may have a certain coarseness. Because the ROI cannot be more precise than the data set, you can draw a tiny contour within a single data set voxel and the **Colorwash** display is just a square. The smallest possible true size for an ROI is 1 data set voxel. The software recognizes no difference among 1, 10, or any number of tiny contours drawn within a single voxel.

The **Contour** mode reflects what you draw in the software. In drawing a contour you may touch only a portion of a voxel. In **Colorwash** and **Poly** modes the whole voxel is considered part of the ROI, so the ROI may appear larger. The **Colorwash** and **Poly** modes reflect the internal representation of the ROI (how the software "sees" it), which is used for ROI statistics, volume calculations, blocks, and MLCs.

Colorwash and **Poly** modes are more accurate representations of the ROI volume than **Contour** display. **Colorwash** and **Poly** modes display the same thing, but in **Poly** mode the corners of the contours are rounded to display a smooth surface.
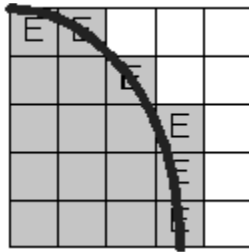
The line is the ROI as it appears in **Contour** mode.

The gray area is the ROI as it appears in **Colorwash** or **Poly** mode.

The voxels with an "E" in them represent the edge voxels (which are treated differently than the inner voxels when determining ROI volume).

ROI volume and statistics are calculated using the internal representation of the ROI (represented by the **Colorwash** and **Poly** display modes). The formula is:

ROI volume = *voxel size* x [*number of inner voxels* + (0.5 x *number of edge voxels*)]

The edge voxels are multiplied by 0.5 because voxels at the edge of a ROI typically do not have their entire volume intersected by the contour. The average volume intersected at the edge of an ROI is 0.5 voxels.

ROI expansion/contraction

This section provides information to supplement *Expand and contract ROIs* in the *Regions of Interest* chapter of the *Pinnacle³ Planning*, *Classic Pinnacle³ Planning*, and *AcQSim³ Instructions for Use*.

Evaluate ROI expansion/contraction results

Certain expansions and contractions may produce shapes that are not what you expect. Remember that ROI expansion/contraction is

• a 3D operation

• applied over the entire source ROI, and

• affected by image set resolution.

The following sections discuss each of these points.

Expansion/contraction is a 3D operation

Use 3D views or a combination of transverse, sagittal, and coronal 2D views (with the ROIs in Poly or Colorwash mode) to determine the correctness of an expansion or contraction. There are two reasons why a single 2D contour view is insufficient:

• Since the operation is 3D, parts of the source ROI that fall on other slices affect the destination ROI. This can lead to misunderstandings about what you see in 2D views.

For instance, when you expand or contract an ROI in a specific direction, it may seem as though the software has contracted or expanded the ROI in additional non-specified directions. In the example below, an elliptical ROI is expanded only in the superior and inferior directions. Note that some 2D slices through the source and destination ROIs show what appears to be right/left

and anterior/posterior expansion as well. You may mistakenly believe that the software expanded in these directions incorrectly.
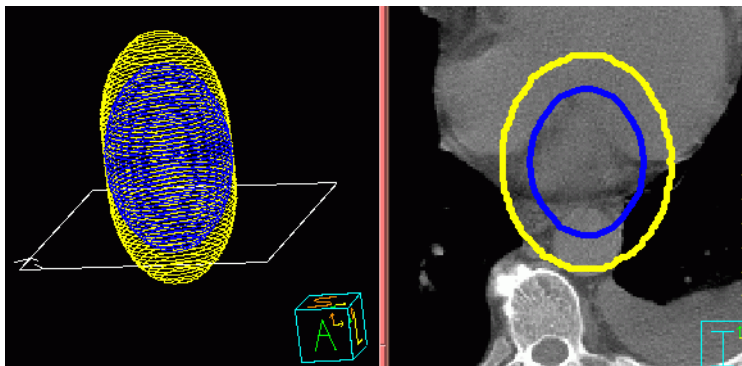
In other cases the presence of unseen structures may cause a margin to seem too large. The example below shows two 2D slices showing source and expanded ROI contours for a head/neck case. In the first slice, the expansion may seem too large in the anterior direction. However, in the second slice you can see that this is due to the influence of the nose.
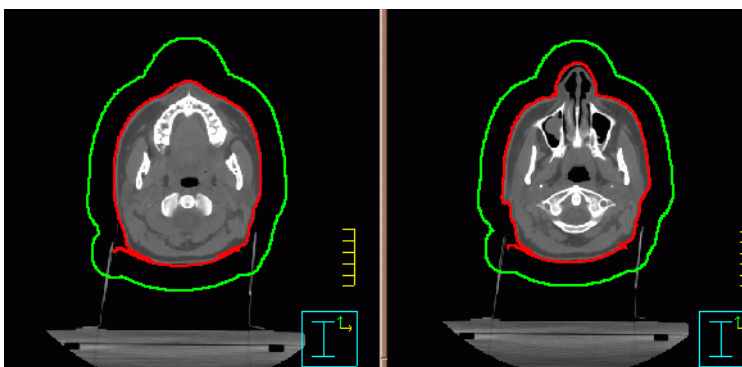
- The software computes the margin along normal vectors (imaginary lines perpendicular to the source ROI surface). Since 3D normal vectors generally do not fall in the plane of a 2D image set slice, it is not possible to measure precisely the applied margin on a 2D image set slice. A more appropriate test is verifying that the margin is never smaller than the requested margin. However, even this measurement can be affected by resolution (see *Expansion/contraction is affected by image set resolution*).

Expansion/contraction is applied over the entire source ROI

You may assume incorrectly that, for instance, an anterior expansion affects only the anterior portion of the ROI. Instead, the entire ROI is expanded in the anterior direction. Anterior is the *direction* of the expansion, not the affected portion of the ROI. There can be two unexpected results of this misunderstanding:

- You may think that when you contract or expand an ROI in a specified direction, the software contracts or expands the ROI in additional non-specified directions.

- You may find that the software expands or contracts an unintended portion of the ROI. Below are two examples of large inferior-only contraction. The arrows indicate the direction and extent of the requested contraction.

In the first example, the source ROI is a simple convex volume. The dark region in the second picture indicates the destination ROI after contraction. This is probably the result you would expect.

Orientation

Superior

Inferior

ROI after contraction (dark region)
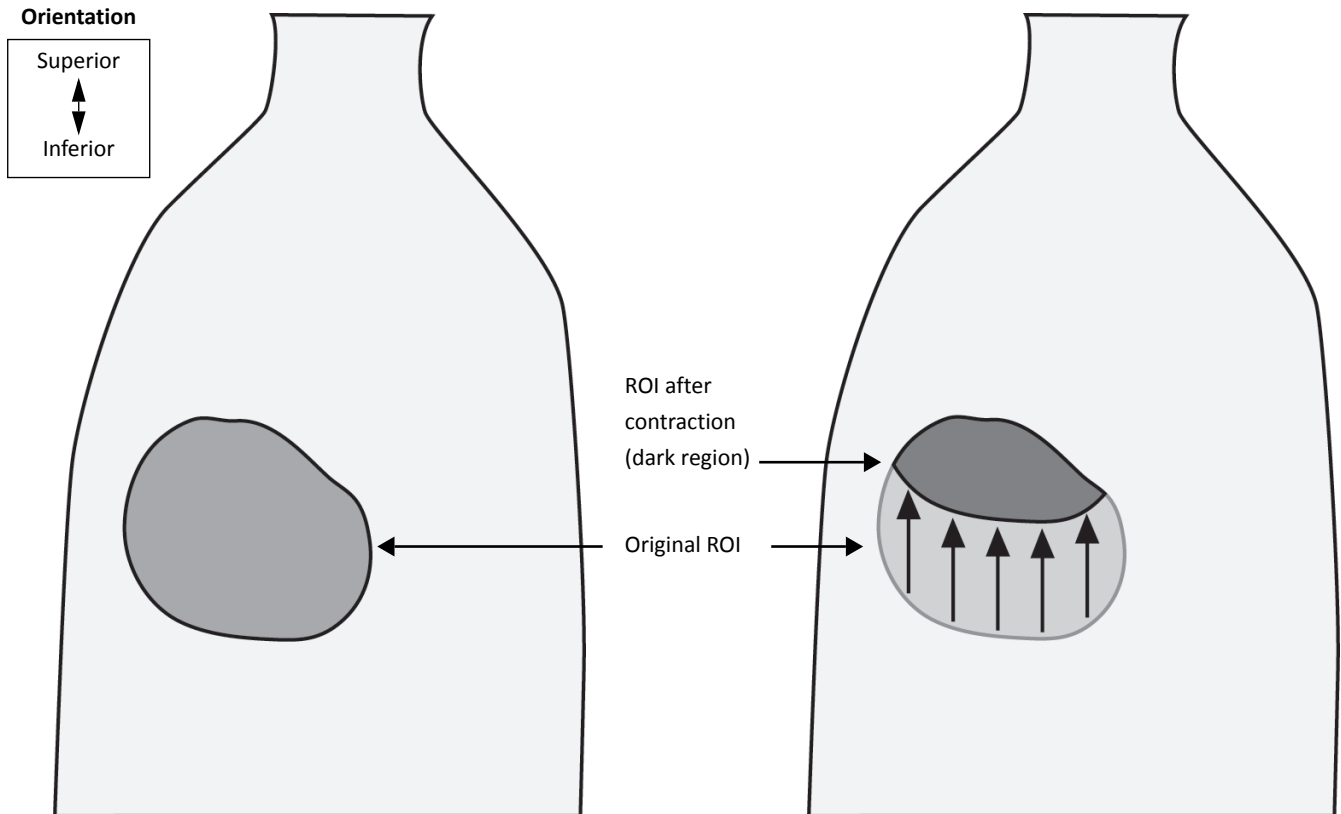
Original ROI

The second example shows a spinal cord-shaped ROI. A large inferior contraction is applied. Note that the contraction occurs over the entire ROI surface. Due to the size of the contraction and the geometry of the original shape, little of the source ROI remains in the destination ROI.

Orientation

Superior
↕
Inferior

ROI after contraction (dark region)

Original ROI
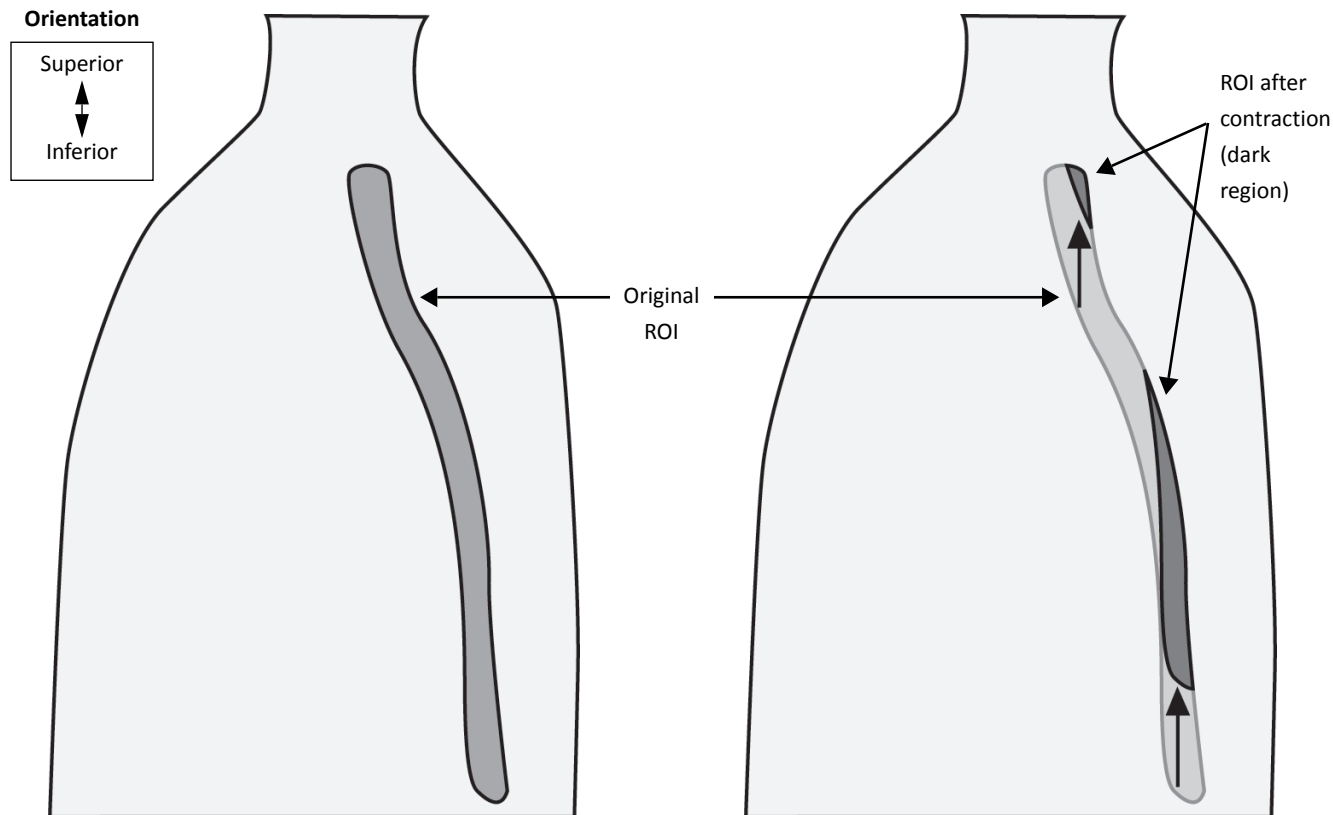
The software follows these rules because ROIs may have unusual shapes or may consist of multiple unconnected shapes. For such ROIs there are no clear "anterior" portions. As a result, the software must apply the contraction or expansion to the entire ROI.

Expansion/contraction is affected by image set resolution

Like its image set, the ROI is stored internally as a set of rectangular voxels. The size and number of voxels is constrained by the resolution of the ROI's image set. As a result, the software must translate any requested margin to the nearest number of whole voxels available to the ROI. For instance, if an ROI's image set consists of slices 4 mm thick in the superior/inferior direction, and you request a 1.5 cm superior expansion, the software applies a 1.6 cm (four voxel) superior expansion.

3 Beams

The following sections explain how to understand machine versions listed in the software, and how to set beam display parameters.

Machine versions

The **Version** field in the **External Beam Treatment Planning** window of Classic Pinnacle[3] lists the "version" of the machine you are using. To see this field in Planning or AcQSim[3], click the **Setup** tab on the **Beams** panel. New versions of machines are created when the physics information for a machine is changed and the machine is "commissioned" for planning in the software. The **Version** field displays the date and time of commissioning. Versions displayed in red indicate that the newest machine version is not being used.

When a machine is recommissioned and a new version of the machine is created, the software maintains all past versions for use in planning (unless one is deleted from the Planning Machine Database). The newest version of a machine is always used when new beams are added, but older versions are still available if you want to use an old plan with its original machine.

⚠ **CAUTION**
You can use an older version of a machine for planning. Check with your physicist to verify that you can use the older version.

If you load an old plan and a newer version of the machine is available, a message appears when you start the plan. You can use machine data from the original plan or use the newest machine data. If you use the original machine data, all calculated dose information is available. If you use the newest version, dose is invalidated.

If you use a plan with an old machine version, the version information appears in red in the Version field. This does not indicate a problem, but is merely a reminder that you are using an older machine version.

To change machine versions for a beam, select **Machine Versions** from the **Options** menu of the **External Beam Treatment Planning** window. (In Planning or AcQSim[3], you must first select **Options - Beam Spreadsheet** in the **Beams** panel to reach this window.) In the next window, select a different version and click the **OK** button.

Set the beam display parameters

You can control the 3D beam display using the **Beam Display** window. To open this window in Classic Pinnacle[3], select **Windows** - **Display Parameters** in the **External Beam Treatment Planning** window. In Planning or AcQSim[3], select **Options** - **Display Parameters** in the **Beams** panel.

All of the beam components are listed in the **Component** section of the window. To change the display options for one of the beam components, you can choose the component and then set its color. The beam components and display parameters are defined in the following sections.

Beam components

- **Blocked Field**—If a field is blocked, the software displays the edge of the blocked field. This option lets you specify the blocked field display.

- **Open Field**—Specify how to display the field defined by the collimator jaws.

- **Central Axis Crosshair**—The central axis of the beam is indicated by a cross hair. This option lets you specify how the central axis cross hair displays.

- **Wedge**—If you use a wedge, this option lets you specify the wedge display.

- **Wedge at End of Arc**—If a wedge is used with a photon arc, the wedge is displayed in the first beam of the arc and the last beam at the end of the arc. This option lets you specify how the wedge at the end of the arc is displayed.

- **Wedge Thick End Indicator**—When wedges are used, the thick end of the wedge is indicated in the beam display by a double line on the edge of the beam which passes through the thick end of the wedge. This option lets you specify how the wedge thick end indicator is displayed.

- **Compensator**—If a compensator is used for a beam, this option lets you set the compensator display options. More compensator display options can be set from the **Compensator Display Options** window.

- **Bolus**—If bolus is used, this option lets you specify how the bolus is displayed. You can specify more display options from the **Bolus Display Options** window.

- **Arc Rotation Indicator**—If an arc is used, a curve is drawn between the starting and ending beam positions to indicate the direction of rotation. This option lets you set the arc rotation indicator display options.

- **MLC Leaves**—If you use a multi-leaf collimator, this option lets you specify the display color of the MLC leaves.

- **Opening Density Matrix**—If you are licensed for P[3]IMRT, this option lets you set the display of the ODM in the IMRT window.

- **Table**, **Gantry**, **Accelerator**, **Floor**—Specify how the element appears in room's eye views. If you do not see some of the display changes you make, you should zoom in to see the data set and beam more clearly.

3D display parameters

- **Beam 3D Display**—Specifies whether the selected beam is displayed.
- **Wireframe**—When this is on, the edges of the selected beam component are displayed as a wireframe.
- **Surface Path**—When this is on, the edge of the beam is indicated on the surface of the patient when a surface image is rendered.
- **Colorwash**—Displays the intersection of the beam and patient with a colorwash.
- **Solid**—Displays the selected beam component as a solid object.
- **Transparent**—Displays the selected beam component as a transparent object.

Special modifier display options

You can specify where wedges and compensators are displayed in the beam by using the modifier display options. Click the **Modifier Display** button in the **Beam Display** window.

For each beam you can specify where the beam modifiers are displayed. You can also specify an offset from the selected display position by entering an offset distance. Negative values move the modifier closer to the beam source. Positive values move the modifier away from the beam source. This positioning has no effect on dose, it is only to help you visualize the plan.

Special beam display options

You can specify additional beam display options by clicking the **Beam Display Options** button in the **Beam Display** window.

You can specify how far to extend the beam display past the target for both static fields and for arcs. This can be useful when evaluating which beams contribute most to the dose in critical structures. You can also specify the distance from the isocenter for the display of the arc rotation indicator.

4 Beam Modifiers

The following sections provide reference information for wedges, editing beam blocks, and adding compensators manually.

Wedge orientation options

The wedge orientation icons are designed to look like the actual wedges as they appear when added to the wedge tray. The small tab shows the placement of the tab that is inserted into the machine. The available wedge orientations vary depending on orientations specified for the machine in the physics tool.

Icon	Orientation	Description
	Top to bottom	The wedge is inserted into the tray with the thick end ("heel") first.
	Bottom to top	The wedge is inserted into the tray with the thin end ("toe") first.
	Left to right	The wedge is inserted into the tray with the thin end to the right and the thick end to the left.
	Right to left	The wedge is inserted into the tray with the thin end to the left and the thick end to the right.

Beam's Eye View (from above) when the wedge tray opening faces the gantry.
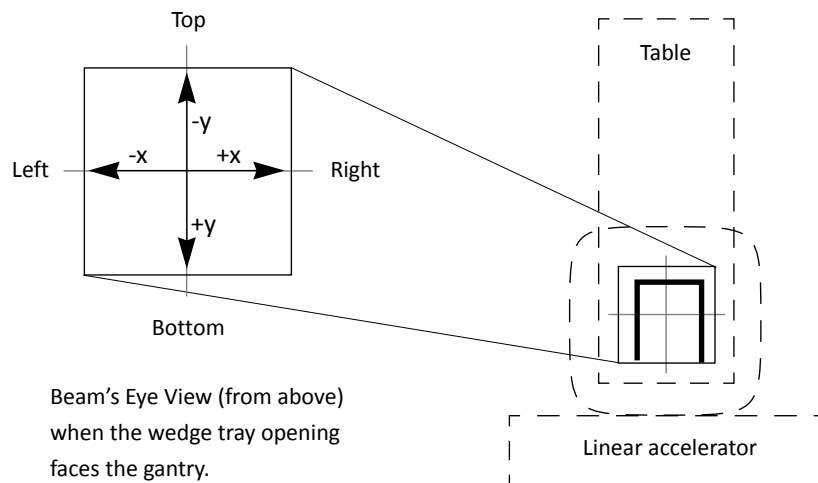
In Beam's Eye View displays, a label appears indicating which jaw the thick end is facing. These labels vary depending on the names entered in the physics tool for the jaws shown in the preceding illustration.

If you add a dynamic wedge, the software displays a "normal" wedge though the wedge shape might be different. The graphic below shows how the jaws move and the actual wedge is "shaped." The dose computation takes into account any over-travel by the jaws but to keep the display consistent, a full wedge appears.

Full wedge shape displays in software

Wedge shape used by software to compute dose

Over-travel limit of moving jaw

Treatment position of stationary jaw

Original position of stationary jaw

Moving jaw
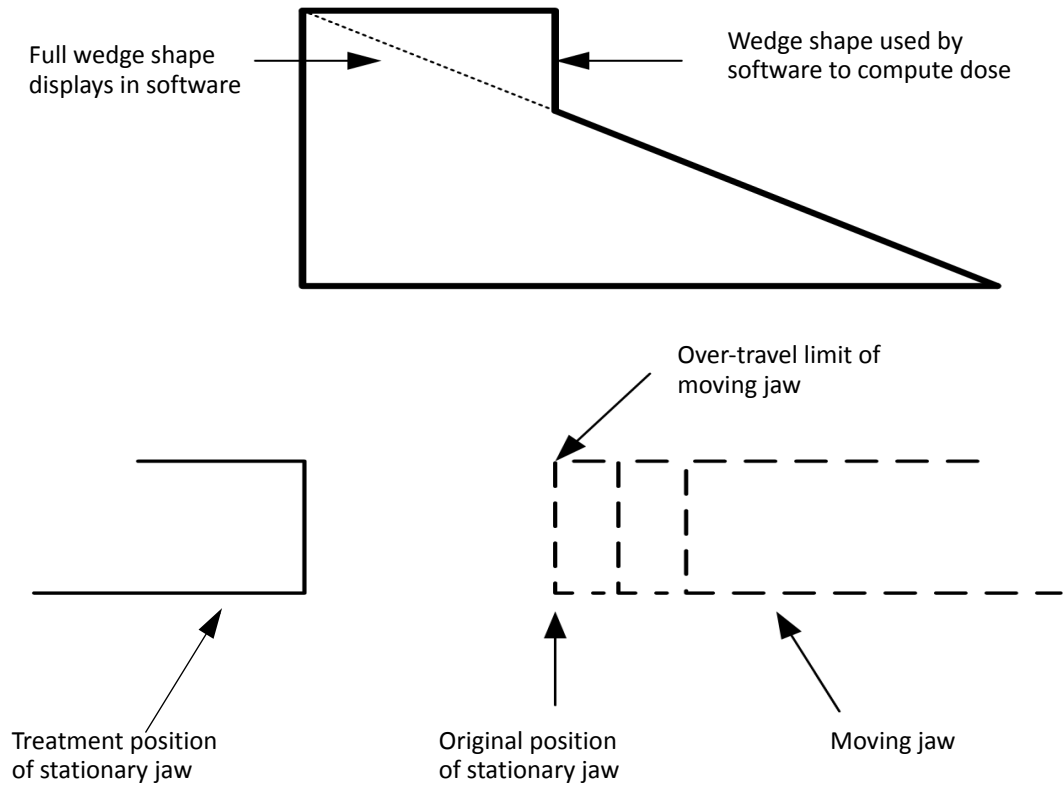
View wedge information

To display additional information about the current wedge in Classic Pinnacle[3], open the **Windows** menu on the **External Beam Treatment Planning** window, select the **Modifiers** option, and then select **Wedges**. In Planning or AcQSim[3], you can click the right mouse button on the **Wedge** field, **Angle** field, or **Orientation** field for the beam.

The **Wedge Viewer** window appears. To view additional information about a dynamic wedge from the Wedge Viewer, click the **View Vendor Data** button and the **View Angle Info** button.

Add compensators manually

You can add tissue and dose compensators to beams. The software can automatically design missing tissue and dose compensators, or, if you have another means of designing compensators, you can enter the compensator thickness array manually. The *Beam Modifiers* chapter in the *Pinnacle³ Planning*, *Classic Pinnacle³ Planning*, and *AcQSim³ Instructions for Use* describes the procedure for automatic compensator design. The procedure for manually designing a compensator is explained below.

1   Open the **Compensator Editor** window.

To open this window in Classic Pinnacle³, click the **Edit** button in the **Compensator** column of the **Modifiers** spreadsheet (in the **External Beam Treatment Planning** window). In Planning or AcQSim³, click the **Edit** button in the **Compensator** column at the bottom of the **Modifiers** tab in the **Beams** panel.

2   Select the beam for which you want to add a compensator from the **Beam** option list.

3   Set the **Use Compensator** option to **Yes**, then set the compensator attributes. These are described in the *Beam Modifiers* chapter in the *Pinnacle³ Planning*, *Classic Pinnacle³ Planning*, and *AcQSim³ Instructions for Use*.

4   Specify the following **Iterative Design** parameters.

⚠️ **CAUTION**
Do not set the depth to optimize at less than D$_{max}$.

- **Optimization Plane Depth**—Specifies the depth at which you want to optimize the dose. The depth is measured along the central axis of the beam.

- **Start With Existing Compensator**—If you set this field to **Yes**, the existing compensator design for the beam is used as a starting point for the compensator, and subsequent iterations further optimize the dose distribution at the optimization plane.

- **Type**—Select the type of compensator to be generated: missing tissue, primary dose, or full 3D dose.

5   Click the **Design Options** button to display the **Compensator Design Options** window and set the compensator design

Note that the following parameters only affect the compensator optimization.

- **Initial Compensator Thickness**—Specifies the starting thickness for the compensator design.

- **Maximum Thickness**—Sets the maximum physical thickness for the compensator. This value is also used to limit the thickness of values entered using the **Compensator Array Editor**, which is described later in this procedure.

- **Field edge border**—Sets the width of a border at the edge of the field, which defines the limits of the compensator design for the field. You can use this parameter to avoid optimizing the compensator in the penumbra region of the beam. This is applied to blocked field shapes and "flash."

- **Thickness Outside Field**—Sets the method of determining the thickness of the compensator outside the field. If you select **Mean Thickness**, the software uses the mean thickness of all compensator segments as the thickness outside the field.

If you select **Zero Thickness**, **Min Thickness**, or **Max Thickness**, the software uses zero, the minimum compensator segment thickness, or the maximum compensator segment thickness, respectively, as the thickness outside the field. If you select **Specified Thickness**, a new field appears to let you specify the thickness outside the field, in cm.

If you select the **Edge Thickness** option, the software uses the values from the closest edge of the optimized area. These values are projected out to the side of the compensator array.

When you finish setting the compensator design options, click the **Close** button to close the **Compensator Design Options** window.

6 If you know the thickness values of your compensator, you can manually enter the thicknesses by clicking the **Edit Thickness Array** button. In the **Compensator Array Editor** window, click within the grid and enter the thicknesses in the columns and rows.

If you want the column and row positions of the thickness array to be centered around zero, click **Yes** next to **Center Array at (0,0)?**.

Click the **Close** button when you finish entering thickness values.

7 Specify **Linear interpolation** or **Step interpolation** as the type of interpolation to use when resampling the compensator into the resolution of the incident fluence array.

Linear interpolation is the default selection, because most milling machines require smooth interpolation. Use **Step interpolation** when generating compensators manually (for example, coarse compensators formed using blocks of lead).

8 Did you set up a missing tissue compensator?

• If yes, click the **Create Missing Tissue Compensator** button to start the compensator optimization.

• If no, enter the number of iterations to perform for the calculation. Then click the **Calculate n Iterations** button to start the compensator optimization. During computation, the dose statistics at the computation plane depth appear in the **Plane Dose Statistics** section of the window.

9 When the calculation is done, you can set the display color and position for the compensator by clicking the **Display Options** button.

Determine the OF correction factor for a field

If you do not know the OF correction factor necessary for the compensator, you can calculate it and then enter it in the software.

1   Create the compensator and measure the Dose/MU for the beam in a water phantom using the same setup to be used for treatment.

2   Open the **Dose Computation Parameters** window.

To open this window in Classic Pinnacle[3], select **Windows** - **Dose Comp Parameters** in the **External Beam Treatment Planning** window. In Planning, select **Options** - **Dose Comp Parameters** in the **Dose** panel.

3   Set **Primary Homogeneous**, **Scatter Homogeneous**, and **Water Phantom at SSD** to **Yes**.

4   Compute the Dose/MU for the beam at the prescription point.

5   Calculate the OF Correction Factor (OF Corr) as follows:

$$\text{OF Corr} \ = \ \frac{\text{D/MU measured}}{\text{D/MU computed}}$$

6   Click the **Compensator** button. The **Compensator Editor** window appears.

7   Enter the **OF Correction Factor** and recompute the beam.

⚠ **CAUTION**
After you enter the OF Correction Factor and recompute the beam to determine the OF Correction Factor for a field, reset the Primary Homogeneous, Scatter Homogeneous, and Water Phantom at SSD dose computation options to No.

5 Dose

The following sections explain how the software performs monitor unit calculations for the various modalities and computes maximum dose.

> **NOTE**
> You cannot calculate dose in the stand-alone version of AcQSim[3].

Monitor unit calculation

Effects of dose grid geometry on dose calculation time

The time and memory required for dose computation and storage is proportional to the total number of voxels in the dose grid. The total number of voxels is affected by the dose grid resolution and the grid size.

When setting up the dose grid resolution, be aware of the trade-off between high resolution and computation time. To get better resolution, decrease the voxel size. This increases the number of voxels required to cover all the regions of interest, which in turn increases the dose computation time.

Using an unnecessarily large dose grid can also increase calculation time without yielding additional information for plan evaluation. For example, if the dose grid extends 5 cm beyond the patient in the lateral, anterior, and posterior directions, a significant percentage of dose calculation time may be wasted on the air surrounding the patient.
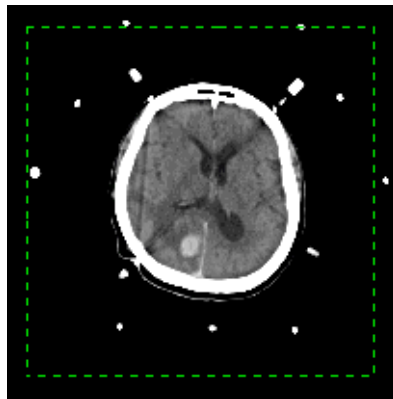
In this example, the dose grid is much larger than necessary.

Monitor unit calculations for photons

Most systems use the following equation to compute monitor units for photon beams:

$$MU = \frac{D_{presc}}{TPR \cdot OAR \cdot S_c \cdot S_p \cdot (D/MU)_{cal} \cdot (SCD/SAD)^2 \cdot T_f \cdot W_f}$$

where:

D_{presc} is the prescription dose per fraction at the prescription point, in units of cGy.

TPR is tissue phantom ratio.

OAR is the off-axis ratio.

S_c is the collimator scatter factor, which is the change in MU due to scatter from the collimator system. This factor is dependent on the field size (not including blocks).

S_p is the phantom scatter factor, which is the change in MU due to scatter from within the phantom. This factor depends on the size of the field entering the patient (including blocks).

SCD is the source to calibration point distance in units of cm.

SAD is the source to axis point distance (source to isocenter) in units of cm.

$(D/MU)_{cal}$ is the calibration dose, which is typically set to 1 cGy/MU at the reference depth in units of cGy/MU. The dose is shown in the **Monitor Units** window.

T_f is the tray transmission factor.

W_f is the wedge transmission factor.

This equation realistically applies to a water phantom with the beam normally incident on a phantom. In a real patient, most systems will scale the depth by density to look up the TPR value. Systems may also apply obliquity and patient curvature corrections.

Convolution algorithm monitor unit calculations

Because the convolution algorithm can accurately compute phantom scatter (S_p), we can use the following equation to compute dose:

$$MU = \frac{D_{presc}}{ND \cdot OF_c \cdot TTF \cdot (D/MU)_{cal}}$$

where:

D_{presc} is the prescription dose per fraction at the prescription point, in units of cGy.

ND is the Normalized Dose at the reference point.

OF_c is the computed correction factor determined during commissioning.

TTF is the total transmission factor.

$(D/MU)_{cal}$ is the dose per Monitor Unit at the calibration point.

Normalized dose is the ratio of dose per unit energy fluence at the prescription point to dose per unit energy fluence at the reference point for the calibration field (the point at which $(D/MU)_{cal}$ was measured) as determined by the convolution superposition calculation for the treatment geometry.

In a water phantom with a normally incident beam, normalized dose can be computed as follows:

$$ND = TPR \cdot OAR \cdot S_p \cdot (\text{SCD/SAD})^2$$

The raw output of the convolution dose engine is dose per unit energy fluence.

Monitor unit computation using the OF table

If you choose the **Use OF Table** option and appropriate output factors are available for the beam, the software computes absolute dose (Dose/MU) for the beam. In this case, reference point selection does not affect the dose distribution in any way. Details of the absolute dose computation are reported at the reference point. Absolute dose at the reference point can be computed as follows:

$$D_{\text{ref point}}/\text{Fraction} = MU \cdot ND \cdot OF_c \cdot TTF \cdot (D/MU)_{cal}$$

where:

MU is the monitor units per fraction.

ND is the normalized dose equal to the dose per unit incident fluence at the reference point divided by the dose per unit incident fluence at the calibration point and calibration setup (where $(D/MU)_{cal}$ was measured).

The convolution/superposition algorithm uses a head scatter model when computing the incident energy fluence. This head scatter model is intended to predict the increased output of the accelerator due to scatter in the head. During the computation of OF_p and OF_c the head scatter is

included in the OF_p. Therefore, the OF_c represents the residual effects of head scatter not included in the model. Similarly, the effects of the wedge are also included in OF_p.

Pinnacle[3] uses output factors generated using the following equation (which resembles S_c, S_p formalism):

$$OF_c \; = \; OF/\mathrm{OF}_p$$

where

> OF is the user-measured overall output factor.

> OF_p is the computed phantom output factor, which includes the head scatter model and wedge effects.

> OF_c is an internal normalization factor that will not match measured S_c values. OF_c is tabulated by equivalent square. The value used for a given field is interpolated linearly from the output factor table based on the equivalent square of the unblocked field. OF_c is also tabulated by wedge. If the beam has a wedge, an output factor for that wedge must be available.

Overriding the software's MU computation

For each beam, you can specify the dose per monitor unit to a selected point. During the monitor unit calculation for the prescription, the software uses this value to renormalize the dose distribution for the beam. In this case, Pinnacle[3] is only computing relative dose, and the accuracy is limited to the accuracy of the hand calculations or measurements used to determine the dose per monitor unit to the selected point.

Stereotactic radiosurgery monitor unit calculation

The fundamental stereotactic dose computation involves determining the dose per monitor unit D/MU (SSD, d, r, W_c) at a point from one of the stereotactic pencil beams that comprise an arc. This equation is explained in *The pencil beam dose algorithm* section in the *Pinnacle[3] Physics Reference Guide*.

Dose values in planning

Max dose in the Planning window

When you use the **Max dose point display** option in the **Planning** window, the software treats each voxel in the dose grid as having uniform dose within the boundaries of the voxel. To find the **Max dose** value, the software iterates through each voxel in the dose grid to find the voxel that has the highest dose value.

The maximum dose point is the center of the dose grid voxel that has the highest dose value.

Max dose in the ROI Statistics spreadsheet

The software defines each ROI at the resolution of the images, which is generally a finer resolution than the dose grid. (The default dose grid resolution is 0.4 cm x 0.4 cm x 0.4 cm.) Image voxels rarely align with the voxels in the dose grid.

To find the dose values that appear in the **ROI Statistics** spreadsheet, the software maps the center coordinate of each image voxel into the dose grid. The software then computes the dose value for each image voxel by linearly interpolating the dose at the image coordinate from the surrounding dose grid voxels.

As a result, the **Max** dose value reported in the **ROI Statistics** spreadsheet is almost always less than the **Max dose** reported in the **Planning** window. The magnitude of the difference depends on several factors:

- The difference between the resolution of the dose grid and the resolution of the images
- The alignment of the dose grid voxels and the image voxels
- The gradient of the dose near the maximum dose point

Dose values in the Tabular Dose Volume Histogram window

The dose values in the **Tabular Dose Volume Histogram** window are calculated the same way as the dose values in the **ROI Statistics** spreadsheet. However, the dose values are placed into discrete bins.

The dose values that appear vary depending on the bin size that you specify. If you increase the number of bins so that the bin size is reduced to 0.1 cGy, the table will display the dose values more accurately.

> **NOTE**
> You cannot exceed 10,000 bins. Therefore, you may not be able to reduce the bin size to 0.1 cGy.

Max dose in the Scorecard window

The dose values in the **Scorecard** window are calculated differently than they are in the **Planning** window, **Tabular Dose Volume Histogram** window, and **ROI Statistics** spreadsheet. For scorecards, the software calculates dose using each ROI voxel that is inside of the dose grid. Any ROI voxels outside of the dose grid are excluded from the dose calculations. Bin settings are not used to compute values in the **Scorecard** window.

Because individual ROI voxels are used to calculate dose, the dose values in the **Scorecard** window are different than the **Max dose** value in the **Planning** window and **Max** dose value in the **ROI Statistics** spreadsheet.

> **NOTE**
> Increasing the number of bins in the **Tabular Dose Volume Histogram** window can decrease the difference between values in the **ROI Statistics** spreadsheet and the **Scorecard** window.

6 Brachytherapy

The following section explains parameters for displaying brachytherapy source groups.

> **NOTE**
> You cannot perform brachytherapy in the stand-alone version of AcQSim[3].

Set source group display parameters

The brachytherapy source group display parameters are in the **Source Groups** spreadsheet of the **Brachytherapy Treatment Planning** window.

The display parameters are summarized below.

- **Display 2D**—Select **Yes** or **No** to turn the 2D display on or off for all sources in the source group.
- **Display 3D**—Select **Yes** or **No** to turn the 3D display on or off for all sources in the source group.
- **Outer Wall Color**—Choose the display color for the outer wall of the source from this option list.

  > **NOTE**
  > Make the outer wall color darker or lighter if you have trouble seeing the source on the CT image.

- **Active Length Color**—Choose the display color for the active length of the source from this option list.
- **Display Cylinder with 2D Intersection**—The intersection of the source with 2D slices can be displayed as a plus sign or as a circle surrounding the plus sign. Set the **Display Cylinder with 2D Intersection** parameter to **Yes** to display both the plus sign and the circle.

  > **NOTE**
  > This display method is slower than using only the plus sign due to the calculations required to determine the intersection. Therefore, you may want to use this display method only after you have completed your plan.

- **Display Active Length**—This option only appears for certain isotopes. Select **Yes** or **No** to turn the display of the source's active length on and off.

You can set more display parameters for sources and catheters using the **Brachytherapy Display Options** window. This window appears when you click the **Display Options** button on the **Source Groups** spreadsheet.

⚠ **CAUTION**
If you set the Distance from Slice within which to Display Catheters and Sources option to a value that is inappropriate, it will be more difficult to identify prostate implant seeds. Select an appropriate distance. We recommend +/- the distance between CT slices.

- **Distance from Slice within which to Display Catheters and Sources**—Set the 2D display cutoff distance for all catheters and sources. All catheters and sources within the specified distance of the currently displayed slice are visible. When this distance is large—for example, when you can see catheters and sources within 2 cm of the currently displayed slice—you may be able to see sources and catheters that do not actually intersect the currently displayed slice. These catheters and sources are displayed with a darker shade of their display color to indicate they do not intersect the slice. When a catheter or source intersects the current slice, the regular display color is used.

- **Highlight Current Source and Current Source Highlight Color**—Display the currently selected source with the highlight color you choose from the **Highlight Color** options menu. This option is useful when attempting to determine the source positions of specific sources.

- **Highlight Current Catheter and Current Catheter Highlight Color**—Display the current catheter with the highlight color you select from the **Highlight Color** options menu.

- **Display Current Catheter Only/Display All Catheters**—Choose whether to display all catheters or only the currently selected catheter.

7 Plan Evaluation Tools

This section provides information on biological response calculations (Källman S-model), NTCP and TCP response calculations (Lyman-Kutcher model), and planar dose settings.

> **NOTE**
> Plan evaluation tools are not available in the stand-alone version of AcQSim[3].

Biological response calculations

The **Biology** panel uses the following equations for calculating biological response probabilities. The responses are evaluated using the Källman S-model (Källman et al. 1992; Löf 2000).

> **NOTE**
> The **Biology** panel is available only if you are licensed for Biological Evaluation. If you do not have this license, you can still obtain NTCP and TCP response values for an ROI using the Lyman-Kutcher model. See *Obtain NTCP and TCP information* in this chapter.

Tumor Control Probability (TCP) calculation

The **Biology** panel allows you to calculate TCP responses for a given structure as well as a composite derived from all TCP responses.

The TCP value for a given tumor volume is calculated using the following equation:

(1)
$$P_i{}^j \; = \; e^{-\exp(e\gamma^j - \alpha^j d_i - (\beta^j d_i^2)/n)}$$

where

$P_i{}^j$ is the probability to achieve tumor control in voxel *i* for tumor *j*.

γ is the normalized slope of the dose response curve.

d_i is the dose fraction at the voxel *i*.

n is the number of fractions.

α/β is the survival curve shape parameter. The α/β ratio is approximately 3 Gy for normal tissues and 10 Gy for tumors. β and α are generated using the following equations:

(2)
$$\beta^j = \frac{e\gamma^j - (\ln \ln 2)}{(\bar{d} + (\alpha/\beta)^j)D_{50}^j}$$

(3)
$$\alpha^j = \frac{e\gamma^j - (\ln \ln 2)}{(1 + (\bar{d}/(\alpha/\beta)^j))D_{50}^j}$$

where

D_{50} is the dose level to achieve a 50% probability of tumor control.

$\bar{d}$ is approximately 2 Gy per fraction.

The composite value for all TCP responses is calculated using the following equation:

(4)
$$P_B = \prod_j P_B^j$$

where

P_B is the overall probability for benefit of the treatment by destroying all j tumors.

Normal Tissue Complication Probability (NTCP) calculation

The **Biology** panel allows you to calculate NTCP responses for a given structure as well as a composite derived from all NTCP responses.

The NTCP value for a given organ is calculated using the following equation:

(5)
$$P_I^{\,j} = \left(1 - \prod_{i \in V^{\,j}} \left[1 - (P_i^{\,j})^{s^{\,j}}\right]^{\Delta v_i^{\,j}}\right)^{1/s^{\,j}}$$

where

$P_I^{\,j}$ is the probability of causing normal tissue complication for organ j.

$s^{\,j}$ is the relative seriality of the organ j.

$P_i^{\,j}$ is calculated using equation (1).

$V^{\,j}$ is the index set for the voxels covered by organ j.

$\Delta v_i^{\,j}$ is the relative volume calculated using the following equation:

(6)
$$\Delta v_i^{\,j} = \frac{v_i^{\,j}}{\sum\limits_{i \in V^{\,j}} v_i^{\,j}}$$

The composite value for all NTCP responses is calculated using the following equation:

(7)
$$P_I = 1 - \prod_{j \in I_o} (1 - P_I^{\,j})$$

where P_I is the overall probability of injury to normal tissue.

P+ composite calculation

The P+ composite response value (Ågren et al. 1990) is generated from the combined NTCP and TCP response values. The P+ value is calculated using the following equation:

(8)
$$P_+ = P_B - P_I$$

Lyman-Kutcher model calculations

If you do not have the Biological Evaluation license, you can still obtain NTCP and TCP response values for an ROI using the Lyman-Kutcher model. This section provides the calculations used to generate these values and describes how to obtain this information in Pinnacle[3].

NTCP calculation

The software calculates NTCP for non-uniformly irradiated volumes using the histogram reduction method described by Kutcher, et al. (1991). This method reduces the volume of the non-uniformly irradiated structure to an effective volume of a uniformly irradiated structure. NTCP is calculated using the following equation:

$$NTCP_{(dose,\,volume)} = 0.5 + \frac{erf(t/(\sqrt{2}))}{2.0}$$

where

$$t = \frac{(Dose - Dose50(volume))}{(Slope \cdot Dose50(volume))}$$

Dose50(volume) = Dose50 • volume-N

N is the volume factor for the structure.

Dose50 is the dose at 50% probability of complication for the structure.

Slope is the slope factor:

$$m = \frac{1}{\sqrt{2\pi} \cdot \gamma_{50}}$$

Dose is the maximum dose to the structure.

Volume is the effective volume computed from the dose volume histogram (DVH).

The effective volume is computed from the DVH using the following equation:

$$Vol_{eff} = \frac{1}{Vol_{ref}} \sum Vol_i \cdot \left(\frac{d_i}{d_{max}}\right)^{1/N}$$

where

Vol_i is the volume of DVH bin *i*.

d_i is the dose of DVH bin *i*.

N is the volume factor specified by the user.

Vol_{Ref} is the reference volume (typically the DVH volume, but this volume can also be specified).

A database of calculated normal tissue complication probabilities is provided with the software. The data in the system database are those described by Emami, et al. (1991). You can build your own NTCP database using options in the NTCP/TCP utility. See *Obtain NTCP and TCP information* in this chapter.

TCP calculation

For tumor control probabilities, the TCP value is initially set to 1.0 (100%). For each bin in the DVH, the following computations are then performed.

- The fractional volume is computed for the bin by dividing the bin volume by the total DVH volume.
- The TCP for the bin is computed. The TCP is based only on the dose level for the bin.
- The current TCP value is multiplied by the returned TCP value raised to a power equal to the fractional volume.

The following equation is used to compute tumor control probabilities:

$$TCP_{(DVH)} = \prod_i TCP(dose_i)^{v+vol_i}$$

Obtain NTCP and TCP information

Normal Tissue Complication Probabilities (NTCP) and Tumor Control Probabilities (TCP) provide additional information for evaluating treatment plans based on the dose to critical structures and to the tumor. You can obtain NTCP and TCP response values for any structure for which a DVH has been computed.

When prior dose is included (the **Dose Display Mode** is either **Prior Dose Only** or **Current Dose and Prior Dose**), the text "Includes Prior Dose" displays on the NTCP or TCP graph. See *Assess the impact of prior dose* in the *Pinnacle³ Planning Instructions for Use*.

⚠ CAUTION
The data in the software database for calculated normal tissue complication probabilities is for reference only. We do not recommend or endorse these numbers for use in treatment decisions.

Obtain NTCP information

Pinnacle³ can calculate normal tissue complication probabilities for non-uniformly irradiated volumes using the histogram reduction method described by Kutcher, et al. (1991).

1   If a dose volume histogram for the region of interest does not exist, create one before proceeding.

2   In the **Plan Evaluation** window, select **Utilities** - **Edit NTCP/TCP**. The **NTCP/TCP Editor** appears.

3   Select the DVH for which you want to obtain an NTCP score.

> **NOTE**
> If you have your own data for NTCP calculation, you can enter your **Slope Factor** and
> **Volume Factor** to generate the NTCP curve for the selected structure. These values can
> also be saved in your custom NTCP database. See *Create your own NTCP/TCP database*.

4   Click the **Copy Parameters** button. The **TCP/NTCP Database** window appears.

5   Select either the **Custom TCP/NTCP Database** or the **System TCP/NTCP Database**.

6   Select the structure for which you want to generate a TCP or NTCP response from the list of
     structures in the database.

7   Click the **Copy Current Definition to Current DVH** button to copy the TCP or NTCP values for the
     selected structure to the currently selected dose volume histogram.

     The TCP or NTCP curve for that structure appears. Pinnacle³ calculates and displays in the
     window the effective volume for the selected dose volume histogram.

8   To update the curve to use the effective volume for the DVH, type the calculated value for the
     effective volume into the **Percent of volume covered** field.

     The NTCP value appears in the **NTCP/TCP Editor** window.

Obtain TCP information

1   If a dose volume histogram for the region of interest does not exist, create one before
     proceeding.

2   In the **Plan Evaluation** window, select **Utilities** - **Edit NTCP/TCP**. The **NTCP/TCP Editor** appears.

3   Select the DVH for which you want to obtain a TCP response value.

4   Enter the name of the structure in the **Structure** field.

5   Select **Target structure (TCP)** as the structure type.

6   Enter values in the **Dose at 50% probability** and **Slope Factor** fields. The theoretical tumor
     control probability curve appears. The TCP percentage value for the DVH appears in the
     NTCP/TCP Editor window.

Create your own NTCP/TCP database

You can use the NTCP/TCP utility to create your own database of normal tissue complication and
tumor control probabilities for the Lyman-Kutcher model.

⚠ **CAUTION**
**Enter and review these parameters carefully. Most published data does not correspond to in vivo
radiation response of normal or diseased tissue, so it is important that you do not use TCP and
NTCP as the only criteria for plan fitness.**

1   If a dose volume histogram for the region of interest does not exist, create one before
     proceeding.

2   In the **Plan Evaluation** window, select **Utilities** - **Edit NTCP/TCP**. The **NTCP/TCP Editor** appears.

3   Select the DVH for which you want to generate an entry in the Lyman-Kutcher NTCP/TCP database.

4   Select whether the structure is critical or a target.

5   Select whether to use a reference volume or the DVH Volume.

6   Enter the **Dose at 50% probability**, **Slope Factor**, and **Volume Factor** for the structure.

7   Click the **Copy Parameters** button. The **TCP/NTCP Database** window appears.

8   Select the **Custom TCP/NTCP Database** option.

9   Click the **Add Definition For Current DVH To Custom List** button to add the NTCP information for the structure to your database.

10   Click the **Cancel** button to close the **TCP/NTCP Database** window. The data is now saved in the custom TCP/NTCP database.

Planar dose settings

The Planar Dose option lets you generate the dose distribution for any beam at a given depth in a flat water phantom or the current image set. The image set and dose grid settings determine how the software generates the dose distribution. The planar dose tool computes the planar dose in cGy/MU for the selected beam. If you chose to sample the trial dose grid, the dose values in the plane are in cGy or Gy, depending on the **Dose display** setting in the **Preferences** window.

* Flat water phantom—The dose is calculated in cGy/MU at the specified plane as if the selected beam is delivered to a water phantom. You specify the SPD and SSD settings.
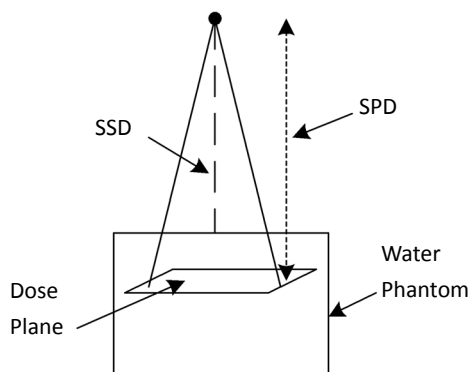
- Patient image set (**Primary data**) and **Compute beam** dose grid—The dose is calculated in cGy/MU at the specified plane as if the selected beam is delivered to the current patient image set. You specify the SPD setting.
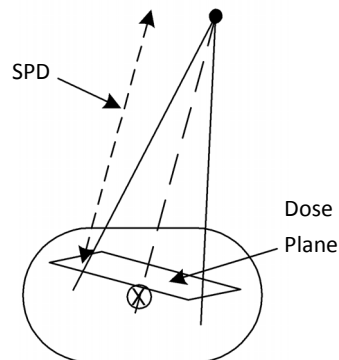
- Patient image set (**Primary data**) and **Sample trial** dose grid—The dose is determined for all beams at the specified plane as if the beams are delivered to the current patient image set. The software interpolates dose from the trial dose grid. Dose values in the plane are in cGy or Gy, depending on the **Dose display** setting in the **Preferences** window. You specify the SPD setting.
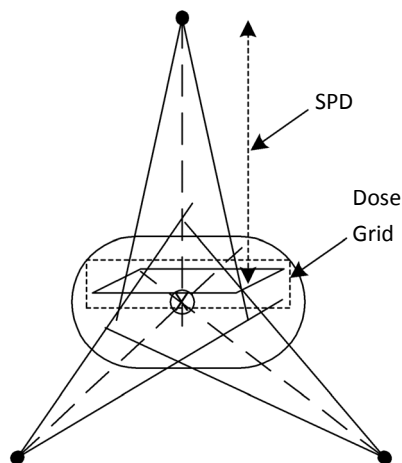
When prior dose is included, the **Dose Display Mode** (either **Prior Dose Only** or **Current Dose and Prior Dose**) displays in the **Planar Dose Computation** window. For information about assessing prior dose, see the *Calculate Dose* chapter in the *Pinnacle³ Planning Instructions for Use*.

> **NOTE**
> If you want to calculate dose to a plane that is not perpendicular to an existing beam, add a beam to the plan and give the beam a weight of zero so that it does not contribute to the dose distribution of the plan. Set the beam at the angle necessary to obtain the planar dose you want. Follow the procedure to compute dose for this beam in the *Plan Evaluation Tools* chapter in the *Pinnacle³ Planning Instructions for Use* and *Classic Pinnacle³ Planning Instructions for Use*, making sure to select the **Primary data** and **Sample trial** dose grid settings.

References

Ågren, A. K., A. Brahme, and I. Turesson. 1990. Optimization of uncomplicated control for head and neck tumors. *International Journal of Radiation Oncology, Biology, Physics* 19(4):1077-85.

Emami, B., J. Lyman, A. Brown, L. Coia, M. Goitein, J. E. Munzenrider, B. Shank, L. J. Solin, and M. Wesson. 1991. Tolerance of normal tissue to therapeutic irradiation. *International Journal of Radiation Oncology, Biology, Physics* 21(1):109-22.

Källman, P., A. Ågren, and A. Brahme. 1992. Tumor and normal tissue responses to fractionated non uniform dose delivery. *International Journal of Radiation Oncology, Biology, Physics* 62(2):249-262.

Kutcher G. J., C. Burman, L. Brewster, M. Goitein, R, Mohan. 1991. Histogram reduction method for calculating complication probabilities for three-dimensional treatment planning evaluations. *International Journal of Radiation Oncology, Biology, Physics* 21(1):137-46.

Löf, J. 2000. *Development of a general framework for optimization of radiation therapy.* Ph.D. thesis, Stockholm University.

8 Plan Output

In addition to the printing tasks described in the following paragraph, the following sections describe the information exported by Record and Verify.

Select different printers and paper sizes

From the **Printer Selection** window, you can add and delete printers, edit printer information, change paper sizes, and redirect reports to a file or a different printer.

Select printers

1   Click the **Select Printer** button in the **Trial Print Confirmation** window. The **Printer Selection** window appears.

2   Select the printer from the list of available printers.

3   Load the appropriate paper in your printer. (Click the **Edit Printer** button to change the paper size, as described in the next procedure.)

4   Click the **Close** button to return to the **Trial Print Confirmation** window and print the plan to the selected printer.

Edit printer information and change the paper size

1   Click the **Edit Printer** button in the **Printer Selection** window. The **Edit Printer** window appears.

2   To change a printer name, type a new name in the **Printer Name** field.

3   To change the print command for the printer, type the new command in the **Print Command** field. For detailed information about editing the print command, see the *System Administration* chapter in the *Launch Pad Instructions for Use*.

4   To choose a non-standard paper size, click the **Paper Size** button 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**.

5   When you finish, click the **Close** button.

Print to a Postscript file

1   Click the **Select Printer** button in the **Trial Print Confirmation** window.

2   Select **Yes** for the **Print to File** option. File name and directory options appear in the **Printer Selection** window.

3   Type a file name for the plan.

4   Choose the directory where you want to save the file.

5   To choose a non-standard paper size, click the **Paper Size** button 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**.

6   Click the **Close** button to return to the **Trial Print Confirmation** window. A Postscript file is generated and placed in the chosen directory.

Data exported by Record and Verify

The following tables list the data exported by Record and Verify. If you use the Mitsubishi format, see *Data exported by Mitsubishi DME Record and Verify*.

Plan definition data

Element	Description
Keyword	Record identifier (case insensitive)
Patient ID	Patient's primary ID number
Patient Last Name	Patient's last name
Patient First Name	Patient's first name
Patient Minitial	Patient's middle initial
Plan ID	ID of treatment plan
Plan Date	Date of plan approval
Plan Time	Time of plan approval
Course ID	Course ID number
MD Last Name	Last name of patient's radiation oncologist
MD Approve LName	Last name of radiation oncologist who approved the plan
Phy Approve LName	Last name of radiation physicist who approved the plan
Author Last Name	Last name of staff member who generated and edited the plan
RTP Mfg	The RTP manufacturer's name
RTP Model	The RTP product name
RTP Version	The RTP software version number
RTP IF Protocol	The RTP interface protocol description
RTP IF Version	The RTP interface protocol version number
CRC	16-bit cyclic redundancy check value

Prescription site data

Element	Description
Keyword	Record identifier (case insensitive)
Course ID	Course ID number
Rx Site Name	The prescription site name
Dose Spec	Where dose is specified
Dose TTL	Total dose prescribed for tx technique. When exporting data using Record and Verify, the exported dose is the reference point dose (the isocenter). If you prescribe a percentage of the reference point dose, the export data will still report 100% of the dose prescribed to the reference point.
Dose Tx	Treatment dose per fraction. When exporting data using Record and Verify, the exported dose is the reference point dose (the isocenter). If you prescribe a percentage of the reference point dose, the export data will still report 100% of the dose prescribed to the reference point.
Number of Fields	Number of fields for this technique
CRC	16-bit cyclic redundancy check value

Treatment field record data

Element	Description
Keyword	Record identifier (case insensitive)
Rx Site Name	The prescription site name
Field Name	The name of the treatment field
Field ID	Unique field identifier
Field Dose	Dose planned for this field. When exporting data using Record and Verify, the exported dose is the reference point dose (the isocenter). If you prescribe a percentage of the reference point dose, the export data will still report 100% of the dose prescribed to the reference point.
Field Monitor Units	MU planned for this field
Treatment Machine	The name of the treatment machine
Treatment Type	Arc, Dynamic, Fixed, Skip Arcs
Modality	Co-60, E/HD, Elect, Xrays
Energy	Energy of treatment beam
SAD	Source to axis distance
SSD	Source to surface distance
Gantry Angle	Gantry angle
Collimator Angle	Collimator angle
Field X Mode	Symmetric or Asymmetric. When you export a beam with independent jaws, the beam exports as asymmetric even when the jaws are positioned symmetrically.
Field X	If X mode = Asy, X = X1 + X2; if X mode = Sym, X1/X2 ignored

Element	Description
Collimator X1	The collimator X1 position
Collimator X2	The collimator X2 position
Field Y Mode	Symmetric or Asymmetric. When you export a beam with independent jaws, the beam exports as asymmetric even when the jaws are positioned symmetrically.
Field Y	If Y mode = Asy, Y = Y1 + Y2; if Y mode = Sym, Y1/Y2 ignored
Collimator Y1	The collimator Y1 position
Collimator Y2	The collimator Y2 position
Couch Angle	The couch angle
Arc Direction	The arc direction
Arc Start Angle	The arc therapy start angle
Arc Stop Angle	The arc therapy stop angle
Arc MU Degree	MU/Degree for arc therapy
Wedge	The wedge type
Dynamic Wedge	The dynamic wedge type
Block	The block code or name
Compensator	The compensator code or name
Bolus	The bolus size
CRC	16-bit cyclic redundancy check value

MLC collimator data

Element	Description
Keyword	Record identifier (case insensitive)
Field ID	Unique field identifier
MLC Type	1 = GE, 2 = Philips, 3 = Scanditronix, 4 = Siemens, 5 = Varian
MLC Leaves	Number of MLC leaves per side (maximum of 50)
MLC LP$_x$	MLC leaf position
CRC	16-bit cyclic redundancy check value

Data exported by Mitsubishi DME Record and Verify

The following tables list the data exported by Record and Verify if you used the Mitsubishi format for exporting.

Conformal Arc

Patient Data

Element	Description
Record ID	Record identifier
Patient Name	The patient's name
Patient Data 1 Sex	The patient's gender
Patient Data 1 Age	(Not supported in the software)
Patient Data 1 DOB	The patient's birth date
Patient Data 1 Site Name	The name of the patient plan
Total Number of Ports	The number of beams in the trial
Number of Leaves	The number of leaves in the multi-leaf collimator
Total Number of Records	The total number of Patient data, Treatment data, and Irradiation Field data records in the export file
Patient Data 2 Chart No.	The patient's medical record number (must be filled in)
Patient Data 2 Address	(Not supported in the software)

Treatment Data

Element	Description
Record ID	Record identifier
Port No.	The beam index + 1
Beam Source	The machine modality
Energy	The machine energy
Preset Dose	The beam monitor units
Start Angle	The gantry start angle
Stop Angle	The gantry stop angle
Field-X.X1	The right jaw in millimeters
Field-X.X2	The left jaw in millimeters
Field-Y.Y1	The top jaw in millimeters
Field-Y.Y2	The bottom jaw in millimeters
Collimator Angle	The collimator angle
Technique 1	1 = static mono-block, 2 = static multi-leaf, 3 = arc, 5 = conformal arc
Rotation Direction	The gantry rotation direction (1 = clockwise, 2 = counterclockwise)

Element	Description
Rotation Speed	(Not supported in the software)
Wedge No.	(Not supported in the software)
Tumor Dose	The dose in cGy or Gy at reference point/fraction
SSD	Source to surface distance in millimeters
Depth	If the modality is Stereotactic: SAD in millimeters - SSD in millimeters. If the modality is not Stereotactic: SPD in millimeters - SSD in millimeters.
E-Appl.	(Not supported in the software)
Accessory	The head frame accessory manufacturer name: 1 = Leksell, 2 = BRW, 3 = Fisher, Empty = Conformal Arc
Wedge Direction	The wedge orientation
Wedge Angle	If a fixed wedge is used: Wedge angle (for RTOG) specified in wedge definition. If a dynamic wedge is used: Angle specified on beam spreadsheet.
Technique 2	If the Gantry Start is not equal to the Gantry Stop, or the Couch is not 0, then 1, else blank.
Couch	(Not supported in the software)
I-Rot. Start	The couch angle
Rotation	(Not supported in the software)
C-Arm Start	The C-Arm angle
X-Appl.	The circular collimator diameter
Couch Position	(Not supported in the software)
I-Rot. Stop	(Not supported in the software)
C-Arm Stop	(Not supported in the software)
Isocenter	Supported as of Pinnacle³ release 2.2b. The laser localization of the isocenter.

Irregular Field Data

Element	Description
Record ID	Record identifier
Port No.	The beam index + 1
Step No.	The gantry angle
XL1.XL1 Opening... XLnn.XL1 Opening	Right leaf opening in millimeters
XL1.XL2 Opening... XLnn.XL2 Opening	Left leaf opening in millimeters

IMRT

Patient Data

The patient data exported is the same as that listed for conformal arc.

Treatment Data

Element	Description
Record ID	Record identifier
Port No.	The beam index + 1
Beam Source	The machine modality
Energy	The machine energy
Preset Dose	The beam monitor units
Start Angle	The gantry start angle
Stop Angle	The gantry stop angle; will appear empty in DME export if it is the same as the start angle.
Field-X.X1	(Not supported in the software)
Field-X.X2	(Not supported in the software)
Field-Y.Y1	(Not supported in the software)
Field-Y.Y2	(Not supported in the software)
Collimator Angle	The collimator angle
Technique 1	1 = static mono-block, 2 = static multi-leaf, 3 = arc, 5 = conformal arc, C = IMRT
Rotation Direction	(Not supported in the software)
Rotation Speed	(Not supported in the software)
Wedge No.	(Not supported in the software)
Tumor Dose	The dose at reference point/fraction
SSD	Source to surface distance
Depth	If the modality is Stereotactic: SAD in millimeters - SSD in millimeters. If the modality is not Stereotactic: SPD in millimeters - SSD in millimeters.
E-Appl.	The electron applicator length
Accessory	The head frame accessory manufacturer name: 1 = Leksell, 2 = BRW, 3 = Fisher, Empty = Not Stereo
Wedge Direction	The wedge orientation
Wedge Angle	If a fixed wedge is used: Wedge angle (for RTOG) specified in wedge definition. If a dynamic wedge is used: Angle specified on beam spreadsheet.
Technique 2	If the Gantry Start is not equal to the Gantry Stop, or the Couch is not 0, then 1, else blank.
Couch	(Not supported in the software)
I-Rot. Start	The couch angle
Rotation	(Not supported in the software)

Element	Description
C-Arm Start	The C-Arm angle
X-Appl.	(Not applicable for non-stereo modalities)
Couch Position	(Not supported in the software)
I-Rot. Stop	(Not supported in the software)
C-Arm Stop	(Not supported in the software)
Isocenter	(Not supported in the software)

Irradiation Field Data

Element	Description
Record ID	Record identifier
Port No.	The beam index + 1
Step No.	The gantry angle
XL1.XL1 Opening... XLnn.XL1 Opening	Right leaf opening in millimeters
XL1.XL2 Opening... XLnn.XL2 Opening	Left leaf opening in millimeters
PresetDosePerStep	Control point weight * MU
FieldX_X1	Right jaw position in millimeters
FieldX_X2	Left jaw position in millimeters
FieldY_Y1	Top jaw position in millimeters
FieldY_Y2	Bottom jaw position in millimeters
CollimatorAngle	Collimator angle

9 Scripts

The following sections explain how to use advanced HotScripts, set preferences in the software, and access development options.

Considerations when recording HotScripts

While the process of recording scripts is easy, there are some limitations you should know before you begin to create HotScripts.

- *All* of your interaction with the software will be recorded. So, if you change the gantry angle for a beam six times before settling upon the angle you want, the script sets the gantry angle to all six settings before finally leaving it at the desired setting. Therefore, you should know what you want to include in your script before you begin recording.

- If part of the script references a name taken from a text field, the script playback routine looks for an exact match (including capitalization) of the text that was scripted. For example, if you are creating a script to add beams that automatically block the ROI called "prostate," a region of interest with the name "prostate" must be available in the plan when the script is run. If the prostate has been contoured but instead called "target", the block is not added. Similarly, if you type "prosate" instead of "prostate" for the name of an ROI that is referenced in a script, the script looks for an ROI called "prosate" when the script is run.

- Script names cannot contain spaces or the following characters:

  + ? * < > [ ] | \ ` " ' & , / ! { } ( )

⚠️ **CAUTION**
We recommend that you provide notes regarding any special requirements of your scripts for the people who are using them.

- Changes to parameters in pop-up windows are applied to the current ROI, POI, or beam at the time the script is run. To make sure the change is applied correctly, make the ROI, POI or beam current in the spreadsheet and then change the parameter.

- Changes to parameters in spreadsheets will affect the ROI, POI, or beam that is in the same position in the spreadsheet as the ROI, POI, or beam that is being changed when the script is recorded. For example, if you change a parameter for the beam in the third row of the beam spreadsheet, that parameter change is applied to the beam in the third row of the spreadsheet when the script is run.

- New scripts do not appear in the **Standard Beam Plans** window until you exit the current plan and re-enter Planning mode. None of the Copy Beam options can be scripted for standard plans. To script a four-field plan, use the **Add New Beam** option four times and then modify the beam parameters as needed.

⚠️ **CAUTION**
Not all software functions can be recorded for use in scripts. You cannot record the following:

- **Tool Panel operations.**
- **3D display options for rendering.**
- **Changes to DRR options made in the Digitally Reconstructed Radiograph Specifications window.**
- **Menu selections from the Points of Interest window and the Cutplane window. However, changes to items in these windows are recorded.**
- **Responses to pop-up warning messages and Yes/No questions.**
- **Digitizer input.**
- **Changes made to values in any editable table (for example, the tables in the ROI Contour Editor and the Machine Data Editor).**

Advanced scripting

When scripts are created, they are saved as files on the computer's hard disk. The HotScripts interface provides basic scripting functions for users who want to automate simple procedures without worrying about keeping track of script files on the hard disk.

The advanced scripting options give you access to the script files. You can use the advanced scripting options to assign script files to HotScripts buttons by specifying their file names, record script files that are not assigned to HotScripts buttons, and play script files that are not assigned to HotScripts buttons.

Assign script files to HotScripts buttons using file names

If you want to assign an existing script to a HotScripts button instead of recording a new script, you can select the script by its file name using the Advanced Scripting options.

Files generated with the HotScripts recording function are saved with file names that are generated automatically. Their file names consist of the name that appears on the HotScripts button (with spaces and punctuation removed), *.Script* to identify the file as a script, and *.login* where *login* is the user login name. So, if you are logged in as "p3rtp" and you create a script called "Four Field Box," the script would be saved with the file name *FourFieldBox.Script.p3rtp*. These files should be saved in the *PinnacleSiteData/Scripts* directory. Users with Solaris 10 or later can also save the scripts in their home directory.

Scripts generated using the **Record Script File** option can be saved in any directory on the system's hard disk. Scripts that are distributed with the software are in the *PinnacleStatic/Scripts* directory, depending on the software installation.

⚠ **CAUTION**
Some scripts are automatic modeling scripts used to help physicists model a machine. Other scripts distributed with the software (for example, StereoFiveArc.Beam.Script) are dependant on machine configuration. If you run a script that sets values beyond your machine's limits, you will see error messages. Be careful when choosing a script to use when planning.

1   In the **HotScripts** window, click the **Edit** button to display the **Edit HotScript List** window.

2   Click the **Advanced** button in the **Edit HotScript List** window to display the **Advanced Scripting** window.

3   In the **HotScript name** field on the left, type an appropriate name for the HotScript.

4   If you know the file name of the script that you want to assign to the HotScripts button, type the file name (including the path) over the existing file name.

5   If you are not sure of the file name, you can search for the file by clicking the **Browse** button beside the **File** field. The **Select HotScript File** window appears.

6   Use the **Directory** list at the right to traverse the directories on your hard disk. The current directory is displayed at the top of the list. To go up one directory, double-click the double dots (**..**) in the list. To go down one directory, double-click the directory name.

You can change directories quickly using the **Public**, **System** and **Home** directory buttons. Clicking the **Public** button takes you to the directory of scripts created using the HotScripts function. Clicking the **System** button takes you to the directory of scripts that are distributed with the software. Clicking the **Home** button takes you to the home directory.

7   Select the HotScript file by typing the file name or by clicking the file name in the list of files.

8   Click the **OK** button to assign the selected script to the HotScripts button.

9   Click the **Done** button until you exit the **HotScript** windows.

Use advanced script recording

If you want to record a HotScript with a specific file name instead of the system's automatically generated file name, you can use the **Record Script File** option in the **Advanced Scripting** window. The script recording process is the same, but when you finish recording you can type a name for the script file.

This script recording option can be used to generate the beam setups, which you can recall as **Standard Plans** from the **Options** menu in the **External Beam Treatment Planning** window (Classic Pinnacle[3]) or **Beams** panel (Planning or AcQSim[3]). To be recalled as a standard plan, the scripts must be saved with the suffix *.Beam.Script* in the *PinnacleSiteData/Scripts* directory. For brachytherapy plans, use the suffix *.Brachy.Script*.

1   In the **HotScripts** window, click the **Edit** button to display the **Edit HotScript List** window.

2   Click the **Advanced** button in the **Edit HotScript List** window to display the **Advanced Scripting** window.

3   Click the **Record Script File** button to begin recording the script.

4   Perform the software operations that you want to include in your script.

5   When you finish, click the **End Recording** button to stop recording.

The **Script Save** window appears.

6   Click the **Public** button to assign the file to the default directory and then type a name for the script file in the **File Name** field. Do not include spaces in the file name. The software cannot save the script if the file name contains spaces.

All script files should have the suffix *.Script* to identify them as script files. Scripts that you want to access as standard plans should have the suffix *.Beam.Script* to identify them as user standard plans. When you click the **Public** button, the file is stored as a user standard plan in the *PinnacleSiteData/Scripts* directory.

To select the script later in the **Standard Beam Plans** window, click the **User Std Plans** button.

⚠️ **CAUTION**

We recommend that you save your scripts to the *PinnacleSiteData/Scripts* directory. (This is the default directory when recording scripts.) Scripts you save in system areas, such as *PinnacleStatic*, will be inaccessible when a new version of the software is installed.

All scripts that you create must be validated again if you install a new version of the software.

7   Click the **OK** button to save the script file. This file can be replayed using the **Play Script File** option (as described under *Use advanced script file playback*) or by assigning the file to a HotScripts button (as described under *Assign script files to HotScripts buttons using file names*).

Use advanced script file playback

You can play back script files that are not assigned to HotScript buttons using the **Script Playback** option.

1   In the **HotScripts** window, click the **Browse** button to display the **Script Playback** window.

> **NOTE**
> You can also display the **Script Playback** window by clicking the **Play Script File** button in the **Advanced Scripting** window.

2   Use the **Directory** list at the right to traverse the directories on your hard disk. The current directory is displayed at the top of the list. To go up one directory, double-click the double dots (**..**) in the list. To go down one directory, double-click the directory name.

You can change directories quickly using the **Public**, **System**, and **Home** directory buttons. Clicking the **Public** button takes you to the directory of scripts created using the HotScripts function. Clicking the **System** button takes you to the directory of scripts that are distributed with the software. Clicking the **Home** button takes you to the home directory.

3   Select the script you want and then click the **OK** button to start the script playback.

10 Utilities

The following sections describe how to set user preferences, where files are stored, how to access development options, and user accounts.

Set preferences

In the **Preferences** window you can specify separate preferences for either Classic Planning and Planning (Planning Preferences) or AcQSim³ (AcQSim³ Preferences).

> **NOTE**
> Some preferences only appear when you are licensed for certain products such as AcQSim³, Syntegra, Model-Based Segmentation, or Auto-Segmentation.

General

Title	Description
Automatic backup increment	The software automatically saves all the plan information at a time interval specified here. These automatic backups are saved to temporary files on the system's hard disk. If the power to your system is disrupted or a system crash occurs, the automatic backup files can be retrieved from the hard disk, allowing you to recover most or all of the changes made to the plan since it was last saved. This sets the time interval between automatic backups. The default value is ten minutes.
Display HotScripts window at startup	Whether the **HotScripts** window appears automatically when you start the software.
Automatically move cursor into new windows	In the software all mouse and cursor input goes to the active window. Windows are made active by moving the cursor into the window. When this option is set to **Yes**, the cursor automatically moves to new windows when they appear on the screen.
Automatically move to next field after text entry	In the software all text that is typed is entered in the active field of the active window. This option lets you set the software so that the cursor automatically moves to the next field in a window when you press the **Enter** key.
Default printer and Default color printer	The default printers for printing text output and reports from the software. Print output can still be redirected at print time.
Display Side Tools window	Whether the Side Tools window appears when you start the software.
Warn about unlocked plan	Select whether the software warns you that your plan is unlocked when you attempt to print or export it.

Title	Description
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 sets that were acquired with the patient in a head first supine position.
Automatic backup of computed files	Select whether the software when autosaving should store computed files, such as dose grid, control point dose, brachytherapy dose, DRRs, and compensators.
Default planning layout	Select whether to use Planning (single-window interface) or Classic Pinnacle³ (multi-window interface) when you click the **Planning** button in Launch Pad.
	If you select Classic Pinnacle³, click the **Initial Viewing Window Layout** button to customize the initial viewing window layout. This option is described in the *View Patient Data* chapter of the *Classic Pinnacle³ Planning Instructions for Use*.
Initial view layout	Customize the initial viewing window layout in the AcQSim³ window.
Initial beams view layout	Customize the initial viewing window layout in the **Beams** panel of the AcQSim³ window.
4 on 1 upper-right window	Set the upper-right viewing window in the Planning or AcQSim³ interface. Choose from **3D**, **2D**, or **DRR**.
Import/Export	**DICOM timeout**—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—The default remote site to which you want to export DICOM information.
	DICOM Export table shifts—For Planning, select **Yes** to export the table shift information in the RT Plan DICOM export. If you do not want to export the table shift information, select **No**.

Physics/Planning

Title	Description
Default machine	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.
Default stereo frame	The stereotactic localization frame to be used as the default when you select the Stereo Localization option for a plan. Select the stereotactic frame from the list of available frames.
Warn about computed profiles when modeling	In the physics tool, the software is designed to warn you when changes to the modeling parameters will invalidate currently computed profiles. This option allows you to specify whether you want to be warned each time profiles may be invalidated.
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.

Title	Description
Lock collimators by default	For AcQSim³, if set to **Yes**, the software locks the Y jaws for orthogonal beam pairs. If you adjust the position of the Y jaws for one orthogonal beam, the same adjustment is made to the position of the other beam's Y jaws.
Create orthogonal beam pair	For AcQSim³, when set to **Yes** for new plans, the software adds two orthogonal beams to the plan and places their isocenter at the default laser center.
Turn on AutoSurround Blocks for new beams	Turn on the **AutoSurround Blocks** feature whenever a beam is added. This feature is described in the *Beam Modifiers* chapter in the *Pinnacle³ Planning*, *Classic Pinnacle³ Planning*, or *AcQSim³ Instructions for Use*.
Block crosshatch off with MLC	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.
Reference individual 2D	Changes the behavior of the **Correlated pointer** tool. See the *Tools* chapter in the *AcQSim³ Instructions for Use* for an explanation of the tool.
Use cube volume of interest	If this is set to **Yes** and if a 3D volume of interest exists in the plan, it appears when the plan is opened. This feature works only with Philips Medical Systems image sets.
ROI Defaults	Set the following ROI preferences: • Set the diameter of the paint brush when using the **Create contour paintbrush** tool to draw an ROI on a 2D transverse slice. • Select whether clicking a mesh with a mesh tool makes it the current mesh. See the *Model-Based Segmentation* chapter in the *Pinnacle³ Planning Instructions for Use* or *AcQSim³ Instructions for Use*. • Select whether to display all ROIs on all image sets. • Select whether to display the contour outline of an ROI in a BEV. After you set this preference, all new ROIs added will display the contour outline; however, ROIs created before you set this preference remain unchanged.
POI Defaults	Select whether to display all POIs on all image sets.
Dose Display	Select whether dose is displayed in Gy or cGy and enter the number of decimal places to display throughout the software.
Dose Grid Resolution (cm)	Specify the default size of each voxel in the dose grid.

Image Display

NOTE
You can change the DRR/DCR settings for individual plans in the **Beam's Eye View Options** window. See the *View Patient Data* chapter in the *Pinnacle³ Planning*, *Classic Pinnacle³ Planning*, or *AcQSim³ Instructions for Use*.

Section	Title	Description
2D Defaults	**Interpolation**	Whether 2D images are shown with bi-linear or nearest neighbor interpolation. The interpolation method determines the smoothness of the transition between adjoining pixels. The default selection is nearest neighbor because it takes less time to display. Bi-linear interpolation makes 2D images appear smoother; we recommend that you use this method.
	Primary Window/level preset	Select a default window/level setting for primary image sets for new plans. If you choose a preset other than **Auto,** you can set additional preferences: **Window/level units**—Set the window and level units: percentage of max (maximum value in the image set), the actual image set values, or SUV values. **Window**—Set the range of values to be mapped into the color ramp. **Level**—Set the image value at which the range begins. **Color ramp function**—Set the method to use to distribute color map entries through the full range of values in the image set. The methods are: **Linear**, **Logarithmic**, **Exponential**, and **Histogram Equalization**. Note that if you change the window or level values, the selection in the **Primary Window/level preset** list changes to "--" because you are no longer using window and level values that are defined by a preset.
	2D lookup color	Set the color map for each image set. The initial default color map for the primary image set is greyscale. The initial default color map for all secondary image sets is thermal.
	Middle mouse window/level	If this is set to **Yes**, the middle mouse button uses 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.
	Link window/level by modality	Apply the window/level settings for one image to all other images that have the same modality.
	Measurement grid size	Set the default resolution of the 2D measurement grid.
3D Defaults	**Render 3D images automatically**	If this is set to **Yes**, 3D images are automatically rendered. You can override this setting for a particular 3D window by changing the **Render New Image** setting.

Section	Title	Description
DRR/DCR Defaults	**Automatically generate DRRs/DCRs**	Upon creating a BEV window, the DRR/DCR should automatically be rendered. 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.
	DRR/DCR interpolation	Select a default interpolation method for generating BEV DRRs and DCRs. **Coarse** uses nearest neighbor interpolation to generate the DRR/DCR; this option is less smooth than the other options, but faster. **Smooth** uses linear interpolation in the Z dimension only; it is smoother than **Coarse** and faster than **Smoothest**. **Smoothest** uses linear interpolation in all three dimensions, but is slower than the **Smooth** option. If necessary, you can change the interpolation method in the **Beam's Eye View Options** window.
	Apply DRR control	If this is set to **Yes**, the DRR controls for beam's eye view windows are on and the default DRR window and level are applied to the image set.
	DRR preset	Select the default DRR preset to use when displaying the DRR.
	DCR preset	Select the default DCR preset to use when displaying the DCR.
	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.
	CT to density table	Set the default CT to density table used when displaying BEVs.
	Energy	Set the default energy used when generating DRRs.
	BEV display rotation	Select a default rotation angle for BEVs. If necessary, you can change this rotation angle in the **Beam's Eye View Options** window.
	Brightness	Set the default brightness used when displaying BEVs.

Default Colors

Title	Description
ROI (first in list)	Select the default color of the first region that you contour.
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.
Laser Center	Select the default color of the laser center.
Measurement Grid	Select the default color of the measurement grid.

Film Annotation

Title	Description
Comment line	Whether the comment line appears on images printed using the DICOM print feature.
Machine information	Whether the machine information appears on images printed using the DICOM print feature.
Beam geometry	Whether the beam geometry appears on images printed using the DICOM print feature.
Beam modifiers	Whether the beam modifiers appear on images printed using the DICOM print feature.
Isocenter information	Whether the isocenter information appears on images printed using the DICOM print feature.
Institution information	Whether the institution information appears on images printed using the DICOM print feature.
Prescription information	Whether the prescription information appears on images printed using the DICOM print feature.

Image Fusion

Title	Description
Automated registration algorithm	Set the algorithm to use for automated registration of the image sets. This is only available if you are licensed for Syntegra. Options include **Local Correlation**, **Cross Correlation**, and **Normalized Mutual Information**.
Move secondary center to primary center	Whether the secondary image sets should be moved so their centers align with the primary image set's center. This is only available if you are licensed for Syntegra.
Initial view layout	The initial default view is the bank of three 2D viewing windows and one 3D viewing window. Select a different layout to use as the default.

IMRT

See the *P³IMRT Instructions for Use* for detailed descriptions of the parameters that are listed in the table below.

Title	Description
Max iterations	Set the default maximum number of times that the software should refine the optimization.
Convolution dose iteration	• For intensity modulation optimizations: The default number of iterations that the software should perform before it computes convolution dose during optimization. • For DMPO and SmartArc optimizations: The default number of iterations that the software should perform before it computes convolution dose and converts the trial to MLC segments.
Minimum segment area	Set the default minimum contiguous area that should be exposed by any MLC control point. You can set a different default value for DMPO optimizations, intensity modulation plans that use the IMFAST conversion type, and intensity modulation plans that use the K-means clustering conversion type.
Minimum segment MUs	Set the default minimum MUs required for each MLC control point. You can set a different default value for DMPO optimizations, intensity modulation plans that use the IMFAST conversion type, and intensity modulation plans that use the K-means clustering conversion type.
Minimum number of leaf pairs	Set the default minimum number of leaf pairs that should be allowed to create a segment. The software uses this value only for DMPO optimizations.
Minimum leaf end separation	Set the default minimum leaf end separation that should be allowed to create a segment. The software uses this value only for DMPO optimizations.
Beam splitting overlap distance	Set the default minimum distance that two beams should overlap if the software must split the beams. This value is approximate; the actual overlap distance after conversion may be smaller than the value that you enter.
Compute final dose	Select whether the software automatically computes dose when the conversion is complete.
Round control point MUs for Step & Shoot	Select whether the software automatically rounds the monitor units for step-and-shoot control points. If you select **Yes** for this option, the software rounds monitor units according to the precision that was set for the machine in the physics tool. If you select **No** for this option, the software does not round monitor units.
Dose engine	Select whether the software uses the **Adaptive Convolve** dose engine or the **CC Convolution** dose engine to compute final dose after optimization.
Intermediate dose engine	Select whether the software uses the **Adaptive Convolve** dose engine or the **Fast Convolve** dose engine to compute intermediate dose during optimization. The selection that you make in this field applies only to intensity modulation and DMPO optimizations. To change the default intermediate dose engine for SmartArc, see the *SmartArc* section in this chapter.
Include Auto-Planning ROIs in plan output	Select whether the ROIs that the Auto-Planning tool creates are exported via DICOM and included in the Region Of Interest Dose Statistics section of printed plan reports. If you select **No**, ROIs are not exported via DICOM. However, even if you select **No**, ROIs that are used in constraints are included in the IMRT Summary section of printed plan reports, and ROIs that have density overrides are included in the Region of Interest Density Overrides section of printed plan reports.

SmartArc

The preferences that appear in this section apply only to SmartArc plans. See the *P³IMRT Instructions for Use* for detailed descriptions of the parameters that are listed in the table below.

Title	Description
Maximum delivery time	Set the default maximum delivery time (in seconds) for a SmartArc beam. The actual treatment time may exceed this value.
Maximum leaf motion	Set the maximum distance (in centimeters) that any given leaf can move during one degree of gantry rotation.
Final gantry spacing	Select the angle spacing (in degrees) that should remain between adjacent control points after optimization.
Save dose for stored control points	Select whether you want the software to save control point dose when you exit a plan.
Compute intermediate dose	Select whether you want the software to compute intermediate dose at the convolution dose iteration.
Intermediate dose engine	Select whether the software uses the **Adaptive Convolve** dose engine or the **Fast Convolve** dose engine to compute intermediate dose during optimization.

Auto-Segmentation

See the *Auto-Segmentation* chapter of the *Pinnacle³ Planning Instructions for Use* or *AcQSim³ Instructions for Use*.

Directory paths for software files

The software saves important data to the following directories on your system:

- Institution data—Each institution's data is saved to a subdirectory named */Institution_x* in the following path: */usr/local/adacnew/Patients*.
- Patient data—Each patient's data is saved to a separate subdirectory (*/Patient_x*) beneath the institution and mount point (*/Mount_x*) to which it belongs.
- Plan data—Each plan's data is saved to a separate subdirectory (*/Plan_x*) beneath the patient to which it belongs.
- Physics data—Physics data is saved in the */Physics* directory under the */Institution_x* subdirectory.
- Scripts—Scripts that come with the software are saved in */usr/local/adacnew/Pinnacle/PinnacleStatic/Scripts*. Scripts you create are saved in */usr/local/adacnew/Pinnacle/PinnacleSiteData/Scripts*.

Pinnacle³ configuration information

You can generate a report describing your Pinnacle³ configuration, including the versions of software products (both released and beta versions, if applicable) installed on your system. After you run a script, the report appears on the screen, and if you choose, you can print the report or save it to a file by using optional flags.

1   Open an xterm window.

2   At the prompt run the following script:

```
PinnacleInfo [-cl] [-f ReportFileName] [-p|-P PrinterName]
```

Flag	Description
-c	Print the Pinnacle³ Product Compatibility Table. This table indicates which releases of various products are compatible with each other.
-l	Print the License table. This table lists the products licensed on the system.
-f	Save the report to a file. Replace *ReportFileName* with the desired file name.
-p	Print the report to a PostScript printer. The script prompts you to choose from a list of available printers.
-P	Print the report to a named PostScript printer. Replace *PrinterName* with the appropriate printer name.
-h	View help about the flags for the script.

The first page of the report appears on your screen. Press the spacebar to see the next page, or press "q" at any time to exit the report and return to a prompt.

NOTE
You can run the script as described if you are logged in with a Pinnacle[3] account (for example, p3rtp). However, if you are logged in as root, you must enter the appropriate full path for either a released or beta version of the software:

- Released: /usr/local/adacnew/PinnacleStatic/bin/common/PinnacleInfo
- Beta: /usr/local/adacbeta/PinnacleStatic/bin/common/PinnacleInfo

User accounts

For information about user accounts for your system, please consult the instructions for use for your system's server. If you need assistance, please contact Customer Support or your local distributor.

11 Troubleshooting and Performance

Pinnacle³ has many interdependent features. Some of the dependencies can slow down the planning process. This section provides tips on how to use and maintain Pinnacle³ software and workstations. It also provides tips to improve the performance problems caused by specific user options and problems caused by hardware and network issues. If you need clarification on any of these items, please contact Customer Support at 1-800-722-9377 (US and Canada) or your local distributor for assistance.

General

- Wait until other plans are finished computing in other workspaces. Although you have multiple workspaces, they are probably using the same system resources. If the processor is being used for a high-demand process, there may be little computing power (or memory) left for other functions.

- Close a plan when it is not in use. This will make more RAM available for loading new plans and may eliminate hard drive swapping. You should also close Launch Pad in other workspaces if you do not need it. This will minimize "patient in use" warnings across the network.

- Sometimes you may type or select options faster than the system can process them, which may cause the system to lock up. If this occurs, press the **Esc** key. If the system does not respond, reboot the system.

- Reboot your workstations once a week. This releases memory that does not get released when you close a plan. We recommend that you reboot the systems on Fridays. If you have too many systems to do this every week, do it every two weeks.

Launch Pad

Patient database

Do not check and repair the database if you have Launch Pad open on multiple systems.

Loading plans

- Although Pinnacle³ reports that it is **Generating high-res density grid** while loading, it is also performing other functions. These functions must be done for each trial. Delete all unnecessary trials before you save a plan, and turn off 3D visualization of beams if possible.

- If you see many machine names flash across the screen when the physics tool is loading, ask your physics group to review all of the old commissioned and old deleted machines in the physics database. Pinnacle³ performs consistency checks of all beam data when it loads the plans. If a number of machines are no longer in use, delete them to save loading time. Prior to deleting the machines, you should back up the current institution to a UNIX file or DVD.

Planning

Contour drawing

- Turn off 3D visualization of all contours, including the one being drawn. Change the 2D visualization of the current contour to "contour" only.
- Check all beams and turn off any automatic blocking for the region of interest by selecting "manual". Any previous blocks will remain. You can turn on automatic blocking after you complete the ROI.
- Remove all DVHs for the structure (available only if dose is computed). DVHs are computed as you change the plan and may slow down contouring.
- Turn off all density overrides for the structure being drawn. These densities are also assigned as you change the plan.
- Try different contouring tools to see if one works better for you.
- Use the interpolation and copy features whenever possible.
- Invalidate the dose for the beams (if possible) so that the ROI dose is not being computed as you change the plan. A quick way to invalidate dose is to reset the dose grid.

Beam manipulation

- When you change the gantry angle for a beam, Pinnacle[3] modifies the blocks in real time. Change any automatically generated blocks to "manual" if you need fine control of the rotation.
- If you do not need to see the DRR while changing a beam angle, make sure that no BEV windows are open.
- Turn off the 3D visualization of the beams. You can turn off ROIs and beams in 2D and 3D using the **Utilities** menu.
- When you copy a beam, Pinnacle[3] computes the beam as it copies it. If you want to change anything about the beam after you copy it, invalidate the dose before you copy it.

DRR

- Limit the number of open windows linked to a beam. Usually, it is only necessary to view a DRR for a beam in one or two windows. The more windows that Pinnacle[3] needs to update, the more time it takes to complete a beam function.
- The default interpolation for the DRRs is usually good enough for planning. Leave the "fast" resolution as the default—this defines the resolution when the gantry is being rotated. When the gantry stops, the DRR renders at the higher resolution for a better image.
- Increase the DRR resolution when you are sure that the plan is completed. This will improve the print quality, especially if you are using a film printer. Consider setting the resolution to 1024 at print time.

Dose computation

- The dose grid size and resolution will have the largest effect on dose computation time. Create scripts for easy changes to the dose grid resolution. Use 0.4 cm (or larger) for quick, iterative computations (such as when you are trying to determine wedge angles), and then reduce the dose grid resolution when you are ready for the final calculation. Dose grids that are larger than 0.5 cm will have a tilde (~) in front of the MUs to remind you that the dose grid is too large and printed plans will labeled with "Not for Clinical Use."

- Draw dose grids in the transverse and sagittal reconstructions with care. Only cover the ROIs, POIs, and areas where you want to see isodose lines. You do not need to cover the entire patient for scatter, because Pinnacle[3] handles this internally.

- Switching from Adaptive Convolution to Fast Convolution does not make a big difference in computation time, but it will make the plan unusable as a clinical plan.

- In the **Dose Grid Specification** window, be careful when you extend the top and bottom slices of the CT fields. If you have a full scan of the patient and there is sufficient distance between the superior and inferior edges of the beams, set these values to "zero". If your scan is too short, set these values to 5-10 cm beyond the beam edges to provide enough scatter material. Consult with your physics group for a protocol.

- If you change the laser position, dose grid, dose computation method, or couch position, you invalidate the dose. Do not compute dose if you have not set these items.

Dose evaluation (dose clouds)

- To evaluate a dose cloud, open the **Data Set Specifications** window and switch the render setting to **No** for the CT data set. When you render an image in the 3D window, the skin rendering no longer appears. Turn on the ROIs that you want to see in 3D, select the 3D rendering for the isodose cloud, and then render the image; only the ROI and isodose will be rendered. You can select how Pinnacle[3] renders a viewing window using the **Render New Image** option in the **3D** menu. You can render a viewing window after any motion, continuously, or in the default mode, which requires you to render the viewing window manually.

- Be conservative when you choose the rendering mode. If you have a complicated set of ROIs and isodoses, continuous rendering may slow the system and make it harder to adjust the viewpoint manually.

- If you know which orientation you want to view, simply select the viewpoint from the 3D window (ant/post, left/right, etc.).

DVH

- The resolution of the dose bins affects the available memory. Do not specify a high resolution until the plan is completed.

- Turn off the DVHs during IMRT optimization unless you need to watch them change while you change the plan. This will speed up optimization.

Physics

- In Pinnacle[3], you should save the machine and exit the physics tool after each modeling script is completed. Re-enter physics and run the next script. This will free memory.

- If your beam data has a very high sample rate, re-sample the data to 0.2 cm. There is usually no effect on the curve shape, and the modeling function will not have to generate as many dose error values.

- Click the **Edit** button under the **Profile List** in the **Photon Physics Tool** for every PDD and profile. If there is a problem, an error message appears: "not suitable for modeling." This means that the profile will be ignored during the automodeling process, which might skew your model for one set of field sizes over another.

- Make certain to select the correct model when you select automodeling. In the upper left corner of the **Optimization Sequencer** window, you can select the active model that is being optimized. If you do not select the intended model, you will change the parameters for the wrong model and must rerun the script on the correct model.

- In the physics tool, there is no "undo" feature. Make copies of machines when you are not sure if a modeling script will help. By making a copy of the machine, you can always delete the new version if there was no improvement and you want to return to the original model.

- Make every effort to create an accurate spectrum and electron contamination model for a machine before breaking the model into specific field sizes (if needed). Once you split the models, you will not be able to model the EC for a specific field size.

Printing

- Do not send too many jobs to the printer at once. If you believe that you have sent the print job correctly, do not send it again. This may result in many copies of the same plan or a clogged print queue. Wait for a few minutes to verify that the printing has not been delayed by other computations or excessive network traffic.

- If you cannot print, cycle the power for the printer and/or the Milan Fastport. Then try to print again.

- Pay close attention to the print confirmation window—if you expect only one page to be printed, and it tells you that six pages are required, be sure to cancel the print to find out what went wrong.

- For Physics QA, set the color of the background to white (using the built-in system scripts) to save printing time and ink. You should then autocontour phantoms at the levels at which you want to print so that you can see the edge of the phantom on the color prints.

DICOM

- If you get any errors during a DICOM RT plan export, you can click the box next to the warning for more information. This information can often help you to correct the problem yourself. If the information does not help, consult the application notes for your R&V vendor at the InCenter web site or consult the release notes.

- If you run into any time-out problems during a DICOM RT or image export, increase the **DICOM Timeout** value in the **Export** window.

Backup and restore

- Use the unattended backup feature. This allows you to select patient and physics data, and then set a time for Pinnacle³ to start the backup automatically.
- When you back up or restore multiple patients, make sure that patient files are not opened on client workstations.
- When you back up multiple patients, verify that Launch Pad is running only on the server where the backup is performed. Make sure there is new media in the drive.
- Verify that the amount of space required for the backup is appropriate for the media you have chosen.
- Verify that the plan printer is functioning properly to print the backup report.
- Make sure that the tape drive is on when the server is booted. SCSI drives need to be on before the computer is turned on to ensure recognition. Attempting to perform backups on drives that are not correctly booted may lead to failure.
- If a backup fails, try to use a new tape or DVD or different brand before calling Customer Support or your local support representative. Magnetic media can be faulty.

Workstations and networks

Preserving disk space

- IMRT and other advanced planning techniques usually take up more disk space than conventional plans. Consider deleting all unnecessary trials from the plans once you have arrived at the final clinical solutions.
- If you have a particularly large image set, consider changing the spacing of the scans at the scanner. For example, you can use 1 cm slices superior and inferior to the area of interest, and 0.5 cm slices where you need more resolution. To maintain image continuity, use the same slice thickness as the slice spacing (for example, 10 mm x 10 mm and 5 mm x 5 mm, as opposed to 10 mm spacing with 5 mm thickness).
- Original CT, MR, and PET images are stored on the same drive as the patient data and physics data. However, you can delete these images once you have imported them into a patient file. (A copy of the image set is retained with the patient so you can export it later if necessary.)
- Once a week use the command "df -k" in a UNIX terminal or xterm window to assess the hard drive space on your system. The */files* directory stores your raw images, and the */PrimaryPatientData* directory stores the patients and physics data. The */export* directory is where the Pinnacle³ software resides, as well as the data you have saved to the p3rtp home directory (*/home/p3rtp*) and its subdirectories.
- Remove old RTOG export files, MLC files, screen capture files, and any other data that is not needed on the system.

Memory considerations

- Pinnacle[3] performs best with 8 GB RAM or more. It will run on less, but you may notice slower performance. To check the amount of RAM on your system, open a UNIX terminal or xterm window and type the following command:

  ```
  # prtconf | grep Memory
  ```

  Check the amount of memory in megabytes (1024 megabytes = 1 gigabyte of RAM).

- An IMRT optimization requires a minimum of 2 GB RAM per plan.

- A SmartArc optimization requires x86 hardware (such as the System 810X or SmartEnterprise) and a minimum of 4 GB RAM per plan. However, we recommend that the system have at least 16 GB RAM and two CPUs for optimal performance.

- To check the amount of memory being used by the system, use the "`top`" command in a UNIX terminal or xterm window. A list of active processes appears. The amount of RAM required for each process is listed, along with the amount of RAM the active processes are using. If you see that a large amount of RAM is installed, but only a few KB are available, too many processes are running at once. Use the "`q`" command to quit from the "`top`" program (may not be available on all systems).

- Pinnacle[3] allows you to work on more than one patient at the same time on the same workstation. However, each plan that is in use requires system resources and may degrade performance. Newer systems have more than one CPU, can hold large amounts of RAM, and support 64-bit and multi-threaded processing, all of which greatly improve performance when multiple workspaces are in use. If your system supports multi-threaded processing, you can type "`prstat -a`" in an xterm window to monitor the memory usage of Pinnacle[3] processes.

64-bit and multi-threaded processing

Pinnacle[3] 9 or later software that is installed on x86 hardware (such as the System 810X or SmartEnterprise) allows 64-bit and multi-threaded processing.

- 64-bit processing allows the software to address large portions of RAM (more than 4 GB) in order to solve larger problems. As a result, very large plans should be able to run completely in RAM without accessing the hard disk.

- Multi-threaded processing allows the software to break up certain computational tasks (such as machine modeling, photon dose computation, planar dose computation, and IMRT optimization) into smaller tasks that can be performed at the same time. The software automatically finds the optimal number of tasks to use based on the capabilities of the hardware in your system.

Network issues

- To verify the speed of the network, type the following command:

  ```
  # dladm show-dev
  ```

  The network cards are set for autonegotiation for network speed. The minimum speed for a LAN is 100 Mbps full duplex.

- On a wide-area network you may see a significant slowdown and NFS errors may appear in the */var/adm/messages* file. This happens if a wide-area directory is shared between sites, the host computer is shut off, or there is a problem with the WAN connection. If the network connection cannot be restored or if the host computer cannot be turned on again, open a UNIX terminal window and type "`rm wide`". This removes the link to the host computer and prevents the NFS failures from slowing down the system. Contact Customer Support or your local support representative to re-establish the link and help you determine the problem.

System administration

⚠️ **WARNING**
It is critical that the server be turned on first, and then the clients.

- Use the "`dmesg`" command in a UNIX terminal or xterm window to look for obvious errors or warnings.

- You can also check for errors by going to the */var/adm* directory and typing "`view messages`". Press **Shift+G** to view the most recent entries at the bottom of the file, and then use the up arrow to scroll through the file. When you finish, type "`:q`". Examine this file for any obvious errors or warnings. You can ignore these errors: bootp, sendmail, ring buffer and serial.

- Use the "`uptime`" command on all systems. You can also type "`rup`" on each LAN system to see how long it has been up and running.

- Routinely use the "`df -k`" command to assess the available hard drive space on the system. No partition should exceed 75% of capacity if possible. The planning will slow down if */PrimaryPatientData* becomes too full.

- Use an uninterruptible power supply (UPS) on each workstation to protect it from power surges and power loss. For a single workstation and monitor, a 1400VA UPS is the minimum recommended capacity. Keep in mind that the external hard drives and tape drives should also be on the UPS, because they are part of the SCSI chain.

- Do not plug printers into the UPS.

- Periodically, use the test feature of the UPS to verify proper functionality. Malfunctioning or underrated UPSs can contribute to many forms of system instability, usually in the form of "panics" or system crashes and lockups. (Panics are system messages that prevent the system from booting or running the OS and usually indicate hardware problems.)

- If you note a client with a longer uptime (longer than that of other clients), shut the system down (clients first, then the server) and reboot in the proper order.

- SCSI devices must always be turned on before the server. These devices include external hard drives, tape drives, and film scanners. If you turn on these devices after the server has been booted they may not work properly.

PHILIPS