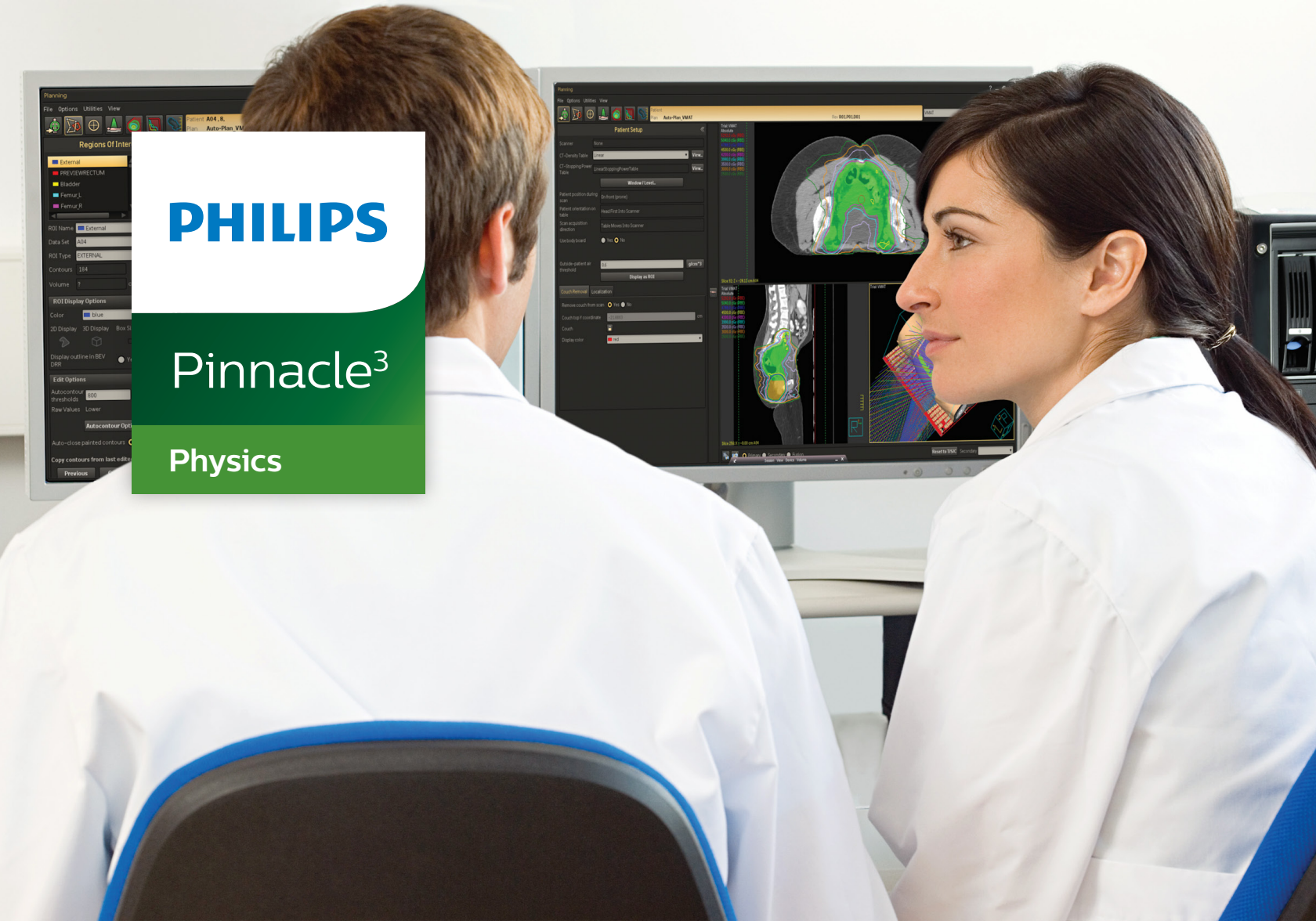

Instructions for Use

Release 16.4 (English)

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

CE 2797

Device Description

The Pinnacle³® Radiation Therapy Planning (RTP) software is composed of several modules including the core Pinnacle³ functionality, Syntegra™, P³IMRT®, 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, 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. The expected service lifetime of the software is five (5) years.

To enable use of the software, a license key must be issued by the installer after software installation has been completed. If you have any software issues, please contact your service representative: Customer Support (1-800-722-9377 for US and Canada), your local Philips Customer Service provider, or your local Distributor. Beginning with Pinnacle³ 16.4, you will need to provide your service representative with the equipment ID assigned to your software kit. Your equipment ID can be found in the **About** window and is used to direct your call to the appropriate service personnel.

Intended Use

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.

Minimum Requirements

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

Professional

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

Network

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

Third-Party Software

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

Smart Enterprise (Cluster Server Nodes)

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

Smart Enterprise (Application Servers)

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

Notes

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

Use of Symbols in Labeling

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

General Device Warnings

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

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

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

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

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

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

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

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

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

This software product is a Medical Device.

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

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

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.

1 Introduction

The *Pinnacle³ Physics Instructions for Use* describes measured beam requirements, physics data importing and entry, and physics tool usage. You can use the following tools:

- **CT to Density Table**—Map CT numbers for your CT scanner to physical density values for use during dose calculation.
- **CT to Stopping Power Table**—If you are licensed for proton treatment planning, map CT numbers for your CT scanner to relative stopping power values for use during dose calculation.
- **External Beam Physics**—Use the Photon Physics tool, the Stereo Physics tool, and the Electron Physics tool to enter and edit machine information, enter measured beam data, and adjust the beam model parameters. If you are licensed for Proton treatment planning, you can also use the Proton Physics tool to enter and edit proton machine information, import measured beam data, and adjust beam model parameters.
- **Brachytherapy Physics**—Enter brachytherapy isotope information and generate dose lookup tables for the isotopes.
- **Brachytherapy Simulators**—Create and commission simulator machines used for brachytherapy simulator film reconstruction.

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

Access the Pinnacle³ physics tools

The physics tools are available from the main Physics Tools window after you enter a valid password.

1 Start the Pinnacle³ software.

2 In the **Launch Pad** menu, click the Institutions button. The **Select Institution** window appears.

3 In the **Select Institution** window, select the institution for which you want to enter or edit the physics data.

4 In the **Launch Pad** menu, click the **Physics** button.

5 At the next prompt, enter the physics tool password and click the **OK** button.

> **NOTE**
> The default password is “physics”. To change the password, see the next section.

6 When you enter the correct password, the **Physics Tools** window appears. Click the button for the tool you want to use.

Details for using each of the physics tools are described in the following chapters.

Change the physics tool password

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

1 Click the **Change Password** button on the **Physics Tools** window.

2 In the resulting window, type the old password and click the **Continue** button.

3 At the next prompt, enter the new password and click the **Continue** button.

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

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

DICOM conformance

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

Van Dyk criteria

For photon external beam treatment plans, Pinnacle^3 uses a 3D convolution superposition dose calculation algorithm, as described by T. Rock Mackie, Ph.D. and others. This model computes the dose from first principles and uses a limited set of measurements to fit the model to the measured data. Corrections are made in the model for patient surface irregularities, voxel-by-voxel CT density tissue inhomogeneities, phantom and head scatter, and beam-shaping devices such as bolus, wedges, blocks, multi-leaf collimators, and compensators. Photon convolution is in accordance with the recommendations of T.R. Mackie, J.W. Scrimger, and J.J. Battista, "A convolution method of calculating dose for 15-MV x rays," *Medical Physics* 12(2):188-196 (1985).

For electron beams, Pinnacle^3 uses a standard pencil beam dose calculation algorithm. The algorithm is based on the work of K.R. Hogstrom, M.D. Mills, and P.R. Almond. The work is summarized in "Electron beam dose calculations," *Physics in Medicine and Biology* 26:445-459 (1981).

For brachytherapy, Pinnacle^3 provides two methods of calculating dose. One method uses a standard dose calculation algorithm based on the work of Cassell and Meisberger. Using a Sievert Integral, the system calculates dose distributions for brachytherapy sources. The work is summarized in "A fundamental approach to the design of a dose-rate calculation program for use in brachytherapy," *The British Journal of Radiology* 56:113-119 (1983). The second method is the TG43 calculation method, which uses the TG43 dose formalism of Nath, et al. in "Dosimetry of interstitial brachytherapy sources: Recommendations of the AAPM Radiation Therapy Committee Task Group No. 43." *Medical Physics* 22(2):209-234 (1995).

For proton therapy, Pinnacle^3 calculates dose using the Bragg Peak model as described in "An analytical approximation of the Bragg curve for therapeutic proton beams," T. Bortfeld, *Med. Phys.* 24:2024-2033 (1997), and the pencil beam algorithm described in "A pencil beam algorithm for proton dose calculations," L. Hong, et al, *Physics in Medicine and Biology* 41: 1305-1330 (1996).

The acceptance criteria are in accordance with the recommendations of Van Dyk, et al. in "QA of Treatment Planning Computers," *Int. J. Rad. Onc. Biol, & Physics*, Vol 26. The acceptance criteria of Pinnacle^3 photon beam, electron beam, brachytherapy, and proton treatment plans are specified in the following tables as millimeters of isodose line displacement or as percentages of maximum dose. In many cases, the performance of Pinnacle^3 exceeds these criteria.

NOTE
Percentages in the tables that follow are percentages of the central ray normalization dose.

NOTE
The data in the tables that follow represent a combination of random and systematic uncertainties at approximately the 67% confidence level (one standard deviation). In many cases, the performance of Pinnacle³ exceeds these criteria.

Photon Beam	Criterion
Homogenous, Unblocked	
Central ray data (except buildup region)	2%
High dose region - small dose gradients	3%
Large dose gradients (>30%/cm)	4 mm
Low dose region - small dose gradients	3%
Inhomogeneity Correction	
Central ray (slab geometry, in region of electron equilibrium)	3%
Anthropomorphic with electronic equilibrium Off axis, contour correction, inhomogeneities, or irregular fields (blocks and shields)	
High dose region - small dose gradients	4%
Large dose gradients (>30%/cm)	4 mm
Low dose region - small dose gradients	3%

Electron Beam	Criterion
Homogenous, Unblocked	
Central ray data	2%
High dose region - small dose gradient	4%
Large dose gradients (>30%/cm)	4 mm
Low dose region - small dose gradients	4%
Inhomogeneity Correction (slab geometry, in region of electron equilibrium)	
Central ray	5%
Anthropomorphic with electronic equilibrium Contour correction, inhomogeneities, or irregular fields (blocks and shields)	
High dose region - small dose gradient	7%
Large dose gradients (>30%/cm)	5 mm
Low dose region - small dose gradients	5%

Brachytherapy	Criterion
Single point source - distance 0.5 cm to 5 cm	5%
Single line source - points along the source normal to the central 80% of the active length of the source, distance 0.5 cm to 5 cm from source axis in regions not affected by ends of source.	5%

Proton Beam	Criterion
Anthropomorphic with electronic equilibrium	
High dose region - small dose gradient	5%
Large dose gradients (>30%/cm)	5 mm
Low dose region - small dose gradients	5%

2 CT Scanner Configuration

To configure a CT scanner, click the **Scanner Configuration** button in the **Physics Tools** window. The **CT Scanner Configuration** window appears. In this window, you can define CT to density tables and configure CT scanners. If you are licensed for AcQSim³, you can also define the laser calibration tables in this window. If you are licensed for proton treatment planning, you define CT to stopping power tables in this window.

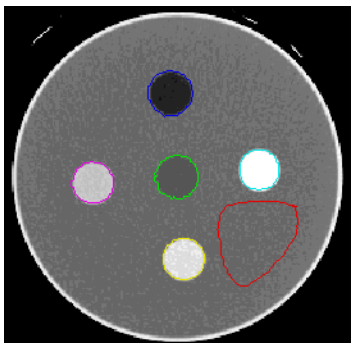
NOTE
When you click the **Save** button in the **CT Scanner Configuration** window, the information in all of the tabs is saved.

Obtain the CT mapping information

Before you define a CT to density table, you can obtain the CT numbers for materials of known densities by scanning a CT calibration phantom. You can then read the image set into Pinnacle³ to determine the CT numbers to enter in a CT to density table.

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

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



Next, contract the ROIs to ensure that they are completely within the material boundaries and calculate statistics on them to determine the average CT number for each material type. You can then enter this value with the corresponding physical density value in the CT to Density Table physics tool. For more information on working with ROIs, see the *Regions of Interest* chapter in the *Pinnacle³ Planning Instructions for Use*.

For information about obtaining the CT mapping information for relative stopping power, which is required for proton treatment planning, see *CT to stopping power tables*.

CT to density tables

The mass density information inherent in the patient CT images is used to account for tissue inhomogeneities in Pinnacle³ photon, electron, and proton dose calculations. For every CT scanner used to obtain patient images for treatment planning, you must scan a CT calibration phantom with known physical densities, determine the CT numbers associated with those densities, and enter a table that maps the CT numbers to the appropriate densities.

During planning, Pinnacle³ reads in the CT numbers and then determines the density for each voxel of the patient using the selected CT to Density table. The density is used to look up mass attenuation coefficients and is used for density scaling during superposition.

Pinnacle³ uses mass attenuation coefficient tables stored for several material types in determining the TERMA distribution in heterogeneous media. Each material-specific table is stored with its physical density. The mass attenuation coefficient for each density in the CT volume is then determined through linear interpolation between the materials closest in physical density. This allows Pinnacle³ to account for the different material types that may be present in the treatment volume.

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

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

To help you learn the software while you obtain the required physics data, Pinnacle³ includes a default CT to Density table with a set of simplified mappings. For more information, see *Default CT to density table*.

Default CT to density table

If you start Pinnacle³ in planning mode with no CT to density tables defined, the software automatically creates a default, linear table called Linear DRR Table. The table is only valid for generating DRRs, not for dose computation.

In physics mode, Pinnacle³ creates a CT to density table called Physics Table. This table is always assigned to the plan/trial when in physics and is used for all DRR generation. The table is valid for dose computation and has the same values as the Linear DRR Table:

CT Number	Density (g/cm³)
0	0.000
1000	1.000
21410	21.410

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

NOTE
When you compute dose in the physics tool, the software uses the Physics Table as the CT to density table. This table is based on a water phantom, meaning that for CT number = 1,000, the density is 1.0 g/cm^3. If your measured data for modeling uses a different CT to density table, the measured and computed profiles may not match. (Note that for ease of calculation, the Pinnacle^3 software adds a value of 1000 to each CT number as measured on the CT scanner.)

Add or edit a CT to density table

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

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

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

1 In the **CT Scanner Configuration** window, select the **CT to Density Tables** tab.
2 Do you want to add a new table or edit an existing table?
   - Add a new table—Click the **Add Table** button. A new table appears in the **CT to Density Tables** list.
   - Edit an existing table—In the **CT to Density Tables** list, select the table that you want to edit.
3 In the **Name** field, type a name for the CT to density table.
4 Select whether the table will be used for DRRs only or for both DRRs and dose computation.
5 For the **In (toward the gantry)** direction, select the **+Y** or **-Y** coordinate for laser export.

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

6 Select the X coordinates for laser export.

   X coordinates (Right/Left) for AcQSim^3 laser export can be reversed from other CT simulation systems. In AcQSim^3, +X is to the right as you are standing at the foot of the table facing the gantry, while in other CT simulation systems +X is to the left. As a result, you must choose +X or -X as the right (toward gantry) direction for laser export so that the X coordinates in AcQSim^3 will match the X coordinates of other CT simulation systems.

NOTE
The X coordinate for Gammex lasers must be positive to the right as you are standing at the foot of the table facing the gantry. As a result, when you export laser localization coordinates for Gammex lasers, Pinnacle^3 always exports +X for the X coordinate regardless of the selection that you make for the X coordinate when you commission the CT to density table.

7 Set the default for isocenter shift display by clicking the **Display Isocenter Shift As** option list and selecting **Laser**, **Table**, or **Patient**. In the planning and AcQSim^3 software, the **Display shift as** option in the **Beam Isocenter** window defaults to the setting you choose here.

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

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

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

10 Click the **Save** button.

Delete a CT to density table

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

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

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

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

CT to stopping power tables

You must be licensed for proton treatment planning to use this feature.

For proton treatment planning, you must define a CT to stopping power table in addition to the CT to density table. The density and stopping power information is used in Pinnacle^3 proton dose calculations to account for tissue inhomogeneities. Calibrations must be made for both. The CT to stopping power table contains the conversion from the CT number to the relative stopping power.

$$\text{Relative Stopping Power} = \frac{\rho_m S_m}{\rho_w S_w}$$

where ρ is density, S is mass stopping power, m is material, and w is water. The CT to stopping power table should contain CT values starting from 0 and must contain at least 10 points.

We recommend that you create CT to density and CT to stopping power calibration tables for each scanner kVp used to generate patient images for treatment planning with protons because the data in each table will vary depending on the specific scanner kVp setting.

> **NOTE**
> The relative stopping power information entered in the CT to stopping power table is critical for correct dose calculations. Failure to specify the CT to stopping power table for the CT scanner used to obtain treatment planning images may result in erroneous dose calculations.

To calibrate your CT scanner numbers with the appropriate stopping power, follow the procedure used by your facility. You can find additional guidance in published literature, such as U. Schneider, E. Pedroni, and A. Lomax, “The calibration of CT Hounsfield units for radiotherapy treatment planning,” *Phys. Med. Biol.* 41:111-124 (1996).

For information about creating CT to density tables, see *CT to density tables*.

Default CT to stopping power table

If you start Pinnacle^3 in planning mode with no CT to stopping power tables defined, the software automatically creates a default, linear table called Linear Stopping Power Table. The table is only valid for calculating range and modulation, not for dose computation.

In physics mode, Pinnacle^3 creates a CT to stopping power table called Physics Stopping Power Table. This table is always assigned to the plan/trial when in physics and is used during model validation. The table has the same values as the Linear Stopping Power Table:

CT Number	Stopping Power
0	0.000
100	0.100
500	0.500
1000	1.000
2000	2.000

CT Number	Stopping Power
3100	3.100
3400	3.400
3700	3.700
6790	6.790
21410	21.410

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

NOTE
When you compute dose in the Proton Physics tool as part of model validation, the software uses the Physics Table as the CT to density table and the Physics Stopping Power Table as the CT to stopping power table. These tables are based on a water phantom, meaning that for CT number = 1,000, the density is 1.0 g/cm^3 and the relative stopping power is 1.0. If your measured data for modeling uses a different CT to density table, a different CT to stopping power table, or both, the measured and computed profiles may not match. (Note that for ease of calculation, the Pinnacle^3 software adds a value of 1000 to each CT number as measured on the CT scanner.)

Add or edit a CT to stopping power table

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

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

When you enter CT to stopping power table information, you must enter the relative stopping power for the phantom materials as a function of the CT number.

1 In the **CT Scanner Configuration** window, select the **CT to Stopping Power Tables** tab.
2 Do you want to add a new table or edit an existing table?
   - Add a new table—Click the **Add Table** button. A new table appears in the **CT to Stopping Power Tables** list.
   - Edit an existing table—In the **CT to Stopping Power Tables** list, select the table that you want to edit.
3 In the **Name** field, type a name for the CT to stopping power table.
4 If you are adding a new table, click the **Insert After** button to add the first row to the table. Then click the **Insert Before** or **Insert After** buttons to insert new rows before or after the currently selected row. The CT to stopping power table must contain at least 10 rows.

5 Type the CT numbers and their corresponding relative stopping power values in ascending order, and make sure that all of the CT values are positive. The first entry in the table must be a CT number value of 0 and a relative stopping power value of 0.

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

6 Click the **Save** button.

7 Repeat this procedure, as necessary, to create a CT to stopping power table for each scanner kVp that you use to generate patient images for treatment planning.

Delete a CT to stopping power table

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

2 Select the CT to stopping power table that you want to delete.

3 Click the **Delete Selected CT to Stopping Power Table** button to delete the table.

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

AcQSim³ laser calibration tables

You must be licensed for AcQSim³ to use this feature.

In the **Laser Settings** tab of the **CT Scanner Configuration** window, you can set up laser calibration tables for use with AcQSim³. Laser calibration tables allow you to set the difference between the center of the field of view and the horizontal and vertical position of the lasers.

For Philips image sets that are sent to the Pinnacle³ system via DICOM, you can select the calibration table for the laser system you used, and the software recalculates the coordinates to account for the offset. Laser calibration tables are unique to each institution and each CT scanner. Therefore, if you have multiple institutions or multiple scanners, you must set up tables for each one.

Add or edit a laser calibration table

1 In the **CT Scanner Configuration** window, select the **Laser Settings** tab.

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

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

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

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

5 Click the **Save** button.

Delete a laser calibration table

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

2 Select the laser that you want to delete.

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

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

Define the Export Settings

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

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

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

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

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

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

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

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

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

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

CT scanners

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

Add or edit a CT scanner

To perform this procedure, you need the manufacturer name and model name of the CT scanner exactly as it appears in the DICOM file for any image set that is created using the scanner. You also need the kVp at which the scanner operates, especially if the scanner operates at more than one kVp. If a DICOM station name has been defined for the scanner, you will need that information as well.

If you do not know the exact manufacturer name, model name, DICOM station name, or kVp of the scanner, you can find the information in Pinnacle[3]. Import an image set that was scanned using the CT scanner, then enter planning and select **Utilities** - **Data Sets** in the **Planning** window. The **Data Set Specifications** window appears.

The manufacturer name, model name, DICOM station name, and kVp of the scanner appear in the lower left corner of the **Data Set Specifications** window. Write these values down exactly as they appear, including capitalization and symbols.

> **NOTE**
> The kVp and DICOM station name information are not required as part of CT scanner configuration; however, we recommend that you define the kVp for the scanner.
>
> If a CT scanner operates at more than one kVp, you should configure a separate CT scanner for each kVp value at which the scanner can operate. Each scanner must have a unique name, but the manufacturer name and model name should be the same for each kVp configuration. The CT to density table should be different for each kVp configuration.
>
> Proton range and dose are strongly dependent on CT number to stopping power calibration. In addition, the calibration will vary according to scanner protocol, in particular the tube potential (kVp) used in acquiring the CT images. Specific tables must be created for each tube potential in use for images used in dose calculation.

1 In the **CT Scanner Configuration** window, select the **CT Scanners** tab.

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

- Add a new scanner—Click the **Add Scanner** button. A new scanner appears in the **CT Scanners** list.
- Edit an existing scanner—Select the scanner that you want to edit in the **CT Scanners** list.

3 In the **Scanner Name** field, type a name for the scanner. The name of the CT scanner should be related to the specific configuration or scanner. During planning, this name is used to define the scanner used for image acquisition.

4 Select the CT to density table that you want to associate with the selected CT scanner.

5 If you are licensed for proton treatment planning, select the CT to stopping power table that you want to associate with the selected CT scanner.

6 If you are licensed for AcQSim^3, select the laser calibration table that you want to associate with the selected scanner.

7 Select the laser alignment system that you want to associate with the selected CT scanner.

8 Information that you enter in the remaining fields on the CT Scanners tab is used by the software to identify the scanner configuration when you import an image set. It is not mandatory that you define this information, but any information that you do define will be used by the software to assign a CT scanner to a plan when the scanner information matches the data in the primary image set that is used in the plan.

   Type the manufacturer name and model name of the scanner.

9 If you want to define the station name, select **Use Station Name** and type the station name in the field.

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

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

11 Click the **Save** button.

Delete a CT scanner

1 In the **CT Scanners** tab, click the **Delete Scanner** button. The **Delete CT Scanner Confirm** window appears.

2 Select the scanner that you want to delete.

3 Click the **Delete Selected CT Scanner** button to delete the scanner.

3 Working with Machines and the Machine Database

In Pinnacle³, the physics information for all external beam treatment modalities is organized in a machine database you create using the Photon, Stereotactic Radiosurgery, and Electron Physics tools. The database consists of all the linear accelerators that are available for an institution. The information stored for a machine includes its physical characteristics, treatment modalities, the energies for each modality, the beam model or dose lookup table for each beam, and measured beam data.

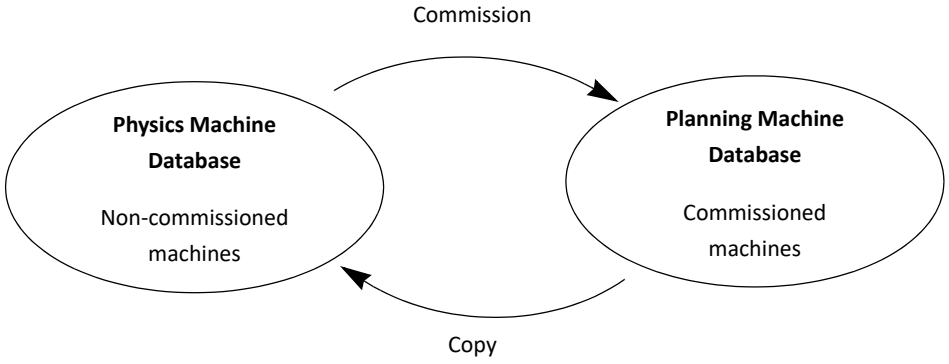
If you are licensed for proton treatment planning, you can also create proton machines using the Proton Physics tool.

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

The Pinnacle³ machine databases

Pinnacle³ maintains two machine databases:

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



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

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

When plans created with an old version of the machine are read into the planning software, you are given the option of retaining the dose information as computed by the old version, or updating to the new machine version and losing the dose computation information.

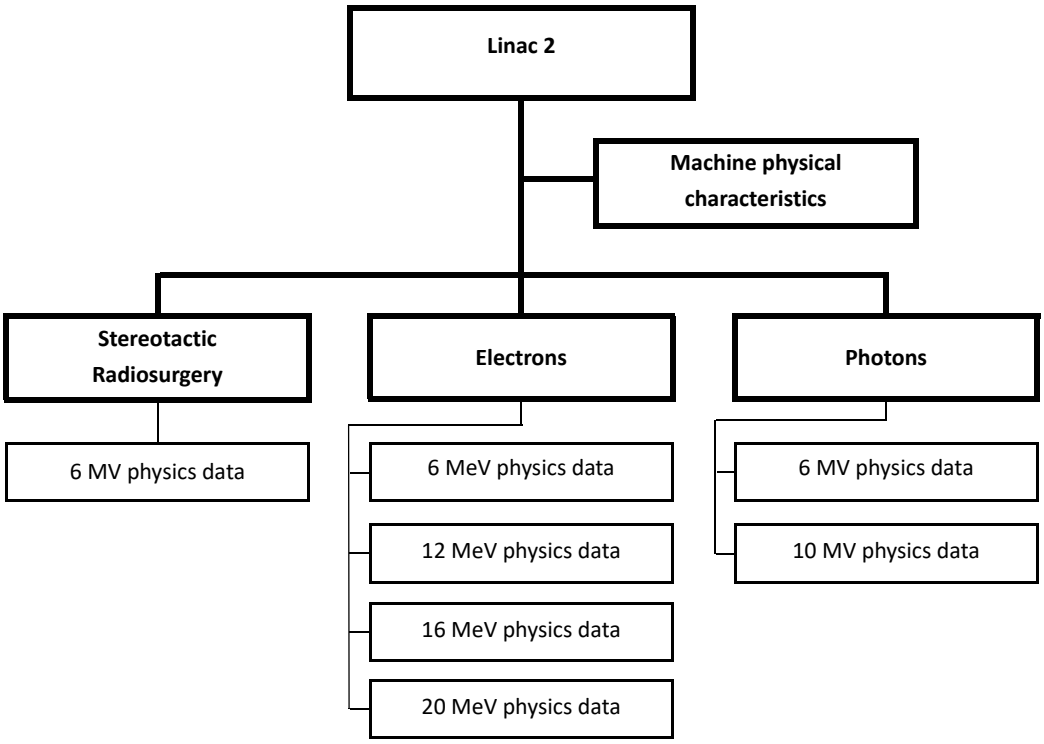
Machine data organization

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

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

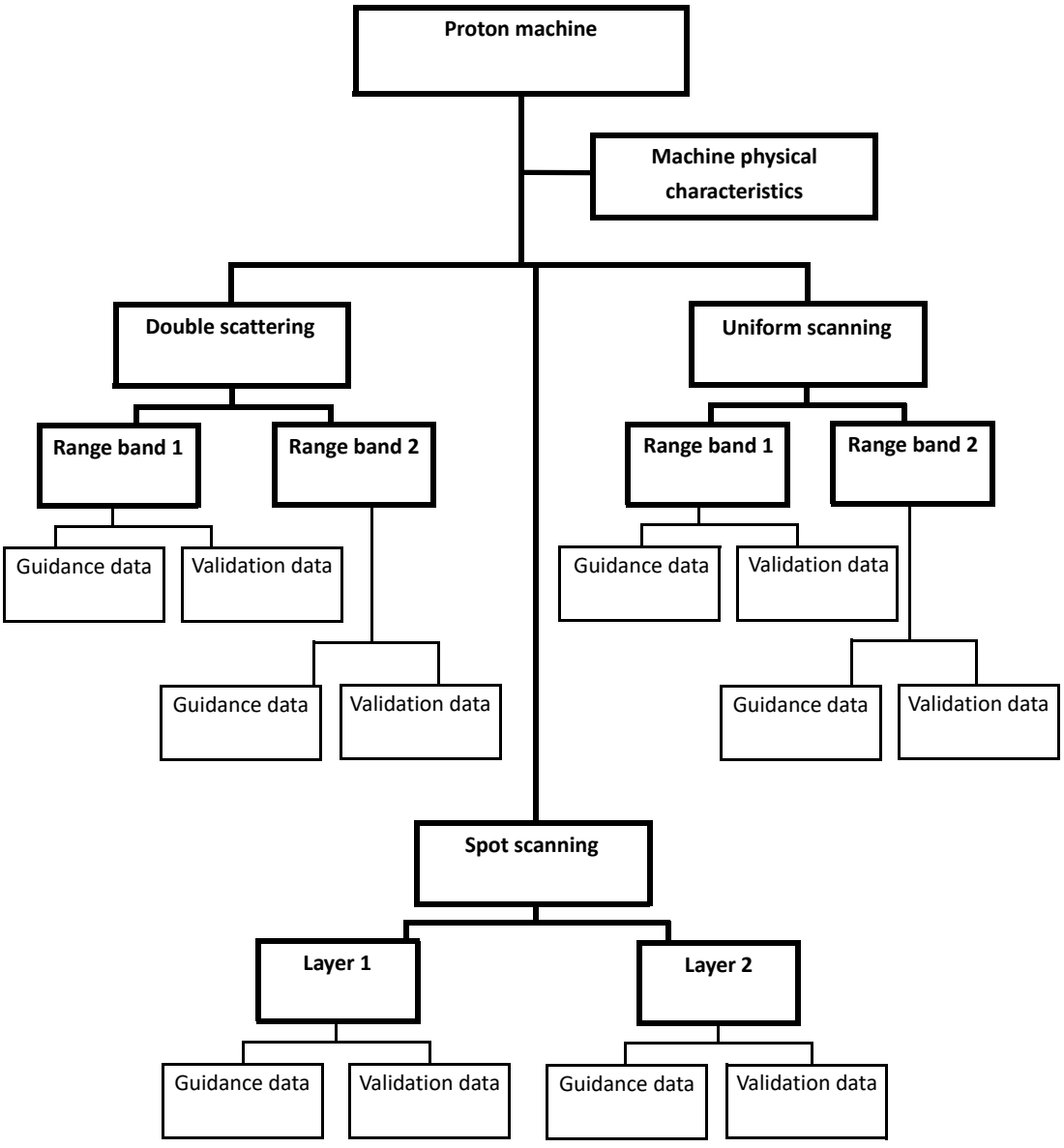
After entering the machine characteristics, use the Photon, Stereotactic Radiosurgery, and Electron Physics tools to set up energies for each modality, enter or import the measured physics data for each beam energy, and generate a beam model (for photon and electron beams) or a dose lookup table (for stereo beams). Use the Proton Physics tool to define range bands, import measured data for each range band, and generate modulation tables.

The following graphic provides an example of machine information organization for photon, stereotactic, and electron machine data.



The following graphic is an example of machine information organization for proton machine data. Guidance data are measured profiles that are used to model the range bands for double scattering

and uniform scanning or the layers for spot scanning. Guidance data includes Bragg peak, half beam blocked, open beam, and fluence profiles for double scattering and uniform scanning. It includes integral depth dose (IDD) profiles and in-air lateral fluence profiles for spot scanning. Validation data are measured depth dose and cross beam profiles that are used to validate the model of the machine.



Machine data and new versions of Pinnacle³ software

When you install a new version of Pinnacle³ software, be sure to review the release notes and determine the impact of the new software on existing physics machines and isotopes. If the new software requires you to recommission or remodel machines or isotopes, you should create a new institution in which you can remodel and recommission machines without affecting an institution

that is currently in use for clinical work. We recommend that you create the new institution by backing up the physics data for an existing institution and then restoring the data to a new institution.

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

1 Open Launch Pad.

2 In the **Launch Pad** menu, click the **Institutions** button.

3 Select the new institution from the list of available Institutions.

4 Click the **Dismiss** button.

5 In the **Launch Pad** menu, click the **Configure** button.

6 In the **Configuration Options** window, click the **Default Tool** button. The **Tool and Version** window appears.

7 Select the new version of Pinnacle³ software from the **Tool and Version** list.

8 In the **Launch Pad** menu, click the **Physics** button to open the physics tool.

When you have completed this physics session, be sure to exit Launch Pad after you close the physics tool. Exiting Launch Pad resets the software version to the default version. You will avoid accidentally creating plans with the non-default software version in the non-default institution by exiting Launch Pad and then reopening it before you continue planning.

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

NOTE
The planning tool will only recognize machines and isotopes that were commissioned in the same or previous version of the physics tool. Therefore, plans combining machines or isotopes that were commissioned in different Pinnacle³ versions must be opened using the latest version of the machines or isotopes needed for the plan. Some version changes, notably versions 7.4f and above, cannot combine machines from versions 7.0g and below in the same plan due to the requirement of remodeling the machines in version 7.4f.

9 When you are ready to use the new version of Pinnacle³ software clinically, select the new version of the software from the **Default** option list in the **Tool and Version** window so that the new version is the default planning and physics software.

4 Photon, Stereotactic, and Electron Machine Definition

This chapter describes how to create, delete, and commission photon, stereotactic, and electron machines for use in treatment planning.

WARNING
The accuracy of the treatment planning dose calculation depends on the quality of the data entered in the physics tool. If the quality of this data is poor, or if the computed dose is not verified with measured data, the dose calculation may be inaccurate.

Add machines to the physics database

NOTE
Although the examples in this chapter use the Photon Physics tool to create the machine and enter its characteristics, you can use the Stereo Physics tool or Electron Physics tool as well.

1 Click the **Photon Physics Tool** button in the **Physics Tools** window. The **Photon Physics Tool** window appears.

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

2 Click the **Add** button beneath the **Machine List**. The **Add New Machine** window appears.

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

- **Old Commissioned Machines** are old versions of current machines.
- **Deleted Commissioned Machines** are commissioned machines that have been deleted from the planning machine database. However, they are not deleted completely from the system. If necessary, you can reproduce dose distributions from calculations using a deleted machine.
- **Sample Machines** can be used to experiment with the physics tools when you first receive your system and to perform quality assurance tests.
- **Commissioned Brachytherapy Simulators** are versions of simulators that have been commissioned for brachytherapy. Typically, you would not use simulators as a basis for creating external beam treatment machines.

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

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

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

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

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

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

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

   For each machine, you must enter the physical description, as described in the following section. You must also enter the physics information for all modalities on the machine and then commission it for use in treatment planning.

Enter the physical machine characteristics

After adding a machine using one of the physics tools, you need to enter information for the machine's physical characteristics and the wedges used on the machine. You can use the worksheets in *Physics Data Worksheets* to record the machine description information.

Much of the machine information is not specific to treatment modality. Therefore, machines you add in one physics tool are available in the others; you do not need to re-enter the information for each modality.

Required physical description information

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

- Collimator jaw attributes, including whether the jaws can be independent and the minimum, maximum, and default jaw position settings.
- Source to axis distance, source to jaw distances, and monitor unit limits.
- Couch attributes, gantry attributes, and collimator attributes, including the minimum, maximum, and default angles and the calibration angle and direction of positive rotation.
- Multi-leaf collimator (MLC) attributes, including the source to MLC distance, the leaf pair geometry, minimum and maximum leaf positions, rounded leaf ends, and travel speed.
- Stereotactic collimator data, if the machine is used for stereotactic radiosurgery.
- Wedge type, density, and physical profile for wedges available on the machine. You must also enter jaw limits when using the wedge and possible wedge orientations.
- The proper jaw and MLC orientations and labels.

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

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

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

The tabs located near the top of the window let you display information about the jaw, couch, collimator, and gantry angles and other general machine parameters. The Photon, Electron, and Stereo energy lists at the bottom of the window show the energies that are available for each modality on the machine. Add energies using the Photon, Electron, and Stereo Physics tools.

3 Enter the machine name and select a machine type.

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

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

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

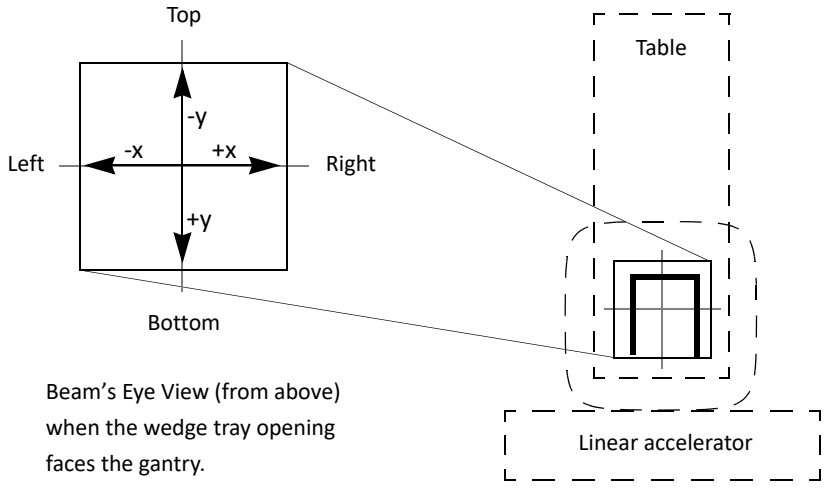
WARNING
If you enter information incorrectly in the Machine Editor window, Pinnacle³ may report incorrect output during treatment planning.

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

Enter jaw information

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

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



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

1 Specify the following jaw information.

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

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

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

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

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

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

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

Enter couch information

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

2 Specify the following couch information.

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

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

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

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

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

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

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

  NOTE
  The couch position values are in the IEC Table Top coordinate system and represent the exact values that are sent in the DICOM export. Unlike most of the other values entered into the **Machine Editor** window, you do not enter the values seen inside the treatment room, but must first convert to IEC coordinates. Please refer to your treatment table's documentation for specific information.

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

Enter collimator information

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

2 Specify the following collimator information.

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

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

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

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

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

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

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

Enter gantry information

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

2 Specify the following gantry information.

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

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

4 Specify the direction of positive rotation when facing the gantry from the foot of the couch by selecting **Yes** or **No** next to **When facing gantry, is positive rotation counterclockwise?**. This information is used to translate the gantry angles to the coordinate system used in the Pinnacle^3 software.

5 Does your machine have a C-Arm?

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

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

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

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

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

Enter delivery information

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

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

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

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

5 Do you want to enable conformal arc beams?

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

6 Do you want to enable dynamic arc beams?

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

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

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

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

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

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

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

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

11 Does the machine limit the gantry acceleration?

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

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

Enter High-Dose Technique information

Set the parameters on the **High-Dose** tab only if your machine requires a High-Dose Technique confirmation for the beam.

1 Click the **High-Dose** tab in the **Machine Editor** window.

2 Set the **Set High-Dose Technique MU thresholds** field to **Yes**. The High-Dose Technique parameters appear in the window.

3 Enter the maximum MU setting for a High-Dose Technique beam.

4 In the **When High-Dose Technique MU limit exceeded, warn and** field, specify the behavior of the system when the maximum monitor unit setting is exceeded.

- If you select the **Limit beam MU to maximum setting** option, the actual monitor units required for a prescription are not displayed. Instead, the maximum monitor unit setting is displayed. The dose that is displayed is proportional to the limited MUs.
- If you select the **Allow beam MU to exceed maximum** option, the software will allow the beam to exceed the maximum MU setting you defined so that the MU displayed will be the actual MU required for the prescription.

5 Enter the **High-Dose Technique MU thresholds** for the beam types that the machine allows.

Obtain the MU threshold value for each beam type from the vendor for the machine.

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

> **NOTE**
> If the machine uses High-Dose Technique, the **When MU limit exceeded, warn and** field on the **Misc** tab (for standard beams) is set to **Allow beam MU to exceed maximum** and cannot be changed. In addition, we recommend that you consider setting the **Maximum MU setting** value on the **Misc** tab to the same value as the lowest High-Dose Technique MU threshold. See *Enter other general machine parameters*.

In planning, when the MUs for a beam exceed the High-Dose Technique MU for that beam type, the value “SRS” is displayed in the High-Dose Technique tag (300A,00C7) in the DICOM export.

In planning, the MU value displays with a yellow border when the MU value exceeds the maximum MU value for a standard beam, and with a red border when the MU value exceeds the maximum MU value for a High-Dose Technique beam. The printed plan report, however, does not indicate specifically that a beam uses High-Dose Technique.

> **NOTE**
> In the irregular field calculator, the software uses the maximum MU setting for standard beams, not High-Dose Technique beams.

Enter other general machine parameters

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

2 Specify the following information.

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

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

  NOTE
  For fixed jaw machines, there is only one source to (bottom of) jaw distance field. The source to jaw distances are used to determine the most limiting collimating device when computing the scatter field. For the Elekta Beam Modulator machine, the millstone will generally be the most limiting collimating device (with the MLC). Therefore, use the distance to the bottom of the millstone for the Elekta Beam Modulator machine.

- **Source to (bottom of) left/right jaw**—This value is the distance (in centimeters) from the source to the bottom of the collimators for the Left/Right jaw pair.
- **Source to (top of) block tray**—This value is the distance (in centimeters) from the source to the top of the block tray.
- **Source to image receptor**—This value is the distance (in centimeters) from the source to the image receptor.
- **Simulation only (without dose profiles)**—Specify whether the machine will be commissioned as a simulation-only machine. If you set this option to **Yes**, you will not be able to compute dose with this machine. Use this option to commission machines for AcQSim^3.

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

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

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

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

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

  If you select the **Allow beam MU to exceed maximum** option, the software will allow the beam to exceed the maximum MU setting you defined so that the MU displayed will be the actual MU required for the prescription.

  NOTE
  If the machine uses High-Dose Technique, this field is set to **Allow beam MU to exceed maximum** and cannot be changed. Verify that the **Maximum MU** setting value is appropriate. See *Enter High-Dose Technique information*.

- **Default block/field edge overlap (cm)**—This value is the margin of overlap that should exist between a block and the edge of the field. This sets the default value that appears in the **Export** window of the planning software.
- **Delivery time multiplier**—This is the default value that is used to calculate the maximum delivery time for each beam in a treatment plan. We recommend that you enter a default value based on the type of plan you deliver most often. As needed, you may change the default value for a beam during treatment planning.

  NOTE
  You can enter a value from 1 to 5 for the **Delivery time multiplier**.

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

Enter multi-leaf collimator information

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

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

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

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

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

Set general parameters

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

2 Specify the MLC vendor.

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

CAUTION
If you specify that the MLC leaves should replace one pair of jaws, Pinnacle³ will assume that pair of jaws does not exist when calculating dose only if the Use MLC? option is set to Yes. The jaws will appear in the software and on plan reports, but Pinnacle³ will not include them in any calculations.

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

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

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

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

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

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

NOTE
The jaws listed in the **MLC tracks jaws?** option list are relative to the Pinnacle³ MLC orientation, so the X jaw option always corresponds to the jaw to which the MLC is parallel. For example, if leaf motion is parallel to the top/bottom jaw and you select the **MLC tracks X jaws for open fields** option, the MLC will always track the top/bottom set of jaws.

NOTE
For machines in which the MLC replaces jaws, setting the MLC to not track the jaws is equivalent to setting the MLC to track the X jaw because the MLC is the X jaw in Pinnacle³.

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

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

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

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

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

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

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

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

12 Select **Yes** for **Is this a micro MLC?** if your MLC is a micro MLC.

If you select **Yes**, the **Name**, **Manufacture code**, and **Applicator type** fields appear. Enter information in these fields to define the micro MLC.

13 In the **Physics Tool** window, click the **Save Current Machine** button.

Set up rounded leaf ends

You can set up a table that describes the offset of the MLC to accommodate the difference between the actual leaf position and the Pinnacle³ leaf position (the leaf position on the accelerator readout). See the *Pinnacle³ Physics Reference Guide* for more information about leaf position.

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

For Varian, the leaf offset data can be found in the MLCTABLE.TXT file on the MLC controller. The data is also available in the Varian sample machine provided with the Pinnacle³ software. The offset values in the Pinnacle³ Leaf Offset Calibration table can be derived from the MLCTABLE.TXT file by taking the values in the second column of the table in the MLCTABLE.TXT file and subtracting the values in the first column. The leaf positions in the **Leaf Offset Calibration** table should be the values in the second column of the table in the MLCTABLE.TXT file.

For Elekta, the leaf offset data are available in the Elekta sample machines provided with the Pinnacle³ software. See *Add machines to the physics database* for information about adding a sample machine to the database.

1 On the **General** tab, click the **Rounded Leaf End Specs** button. The **Rounded Leaf End Specification** window appears.

2 Enter the radius of curvature for the rounded leaf end in the **Rounded Leaf Tip Radius** field. For detailed information about the radius of curvature, see the *Physical Machine Characteristics* chapter in the *Pinnacle³ Physics Reference Guide*.

3 To have the software enter default values for the table, click the **Create Default Table** button.

4 To edit the values in the table, click in the cell you need to edit and enter a value in the field above the table.

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

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

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

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

Set leaf parameters

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

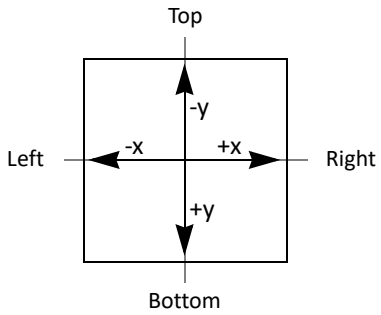
2 Click the **Add leaves** button to set up the leaves for the multi-leaf collimator. The **MLC Leaf Pair Definition Window** appears.

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

3 Enter the following information about the leaves to be added.

- **Number of leaf pairs**—Specifies the number of leaf pairs to add to the MLC.

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



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

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

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

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

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

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

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

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

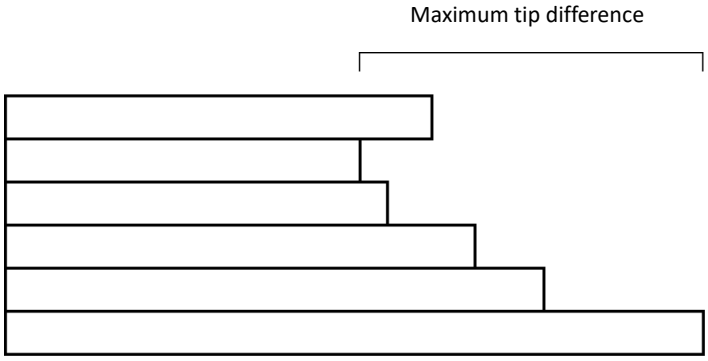
Select **No** for Siemens and other Elekta machines and any other machines that do not allow MLC leaves to interdigitate.

7 Enter the tongue and groove width at the intersection of the leaves. The software uses this value to attenuate the radiation through half of the thickness of the leaf at the overlap of the tongue and groove. (See the *Pinnacle³ Physics Reference Guide* for more information about tongue and groove width.)

8 Enter the additional interleaf leakage transmission. This value is the amount of transmission between two closed MLC leaves, and it is added to the MLC transmission in the region where the two leaves intersect. (See the *Pinnacle³ Physics Reference Guide* for more information about interleaf leakage transmission.)

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

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



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

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

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

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

Set jaw dependencies

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

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

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

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

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

3 Do you want the software to open an extra set of leaf pairs at the top and bottom of the exposed field automatically?
   - Yes—In the **Open extra set of leaf pairs outside jaws automatically** field, select **Yes**.
   - No—In the **Open extra set of leaf pairs outside jaws automatically** field, select **No**.

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

   For more information on minimum and maximum leaf/jaw overlap, see the *Physical Machine Characteristics* chapter in the *Pinnacle³ Physics Reference Guide*.

Verify MLC setup

You should verify the MLC setup before you commission the machine.

1 Without exiting the physics tool, click the **Beams** button in the **Pinnacle Main Menu**. The **External Beam Treatment Planning** window appears.
2 From the **Options** menu, select **Add New Beam**.
3 Click the **Modifiers** tab to open the **Modifiers** spreadsheet.
4 In the **Modifiers** spreadsheet, click the **Blocks** button. The **Beam Blocks** window appears.
5 Click the **Add Block** button.
6 Attempt to set up various fields that violate the MLC limitations.
7 Set the **Use MLC option** to **Yes** to see the MLC leaves in the field.
8 Click the **MLC Options** button to open the **Beam MLC Leaf Position Editor** window.
9 On the **Display Options** tab, set the **Clip leaves** option to **No** so you can see all the MLC leaves for the machine.
10 Verify that the system satisfies all of the MLC limitations.

Enter Record & Verify information

NOTE
You do not need to perform this procedure if you use DICOM RT to transfer your plans.

If you will export data to a Record and Verify (R & V) system, you must assign the proper R & V jaw settings and MLC orientations to the respective machine jaws in Pinnacle^3.

1 Click the **R & V Config** button on the **Machine Editor** window. The **R & V Configuration** window appears.

2 Click the **Yes** button to enable R & V for the machine and display the rest of the window.

The MLC options at the bottom of the window do not appear unless the machine has an MLC.

3 Select which R & V jaw should map to each Pinnacle^3 and machine jaw, for the top, bottom, left, and right jaws.

Pinnacle^3 refers to the **Left**, **Right**, **Top**, and **Bottom** jaws when the collimator angle is such that the tray opening faces the gantry, as indicated by the graphic in the center of the window. Use this graphic for orientation as you specify the R & V jaws.

If your institution uses different terminology when referring to these jaw positions, you specified your own labels for the **Jaw Names** in the **Machine Editor** window described earlier in this chapter. These custom **Machine** labels are shown with the Pinnacle^3 labels for each of the jaws.

4 Use the **Output bank** and **Output leaf pair** fields to specify the order in which the MLC leaves should be exported to the R & V system.

5 For an Elekta MLC, the **Export MLC Leaf Positions as relative to the Central Axis?** option appears. If you select **Yes**, the MLC positions will be exported as relative to the central axis rather than in the coordinate system of the linear accelerator.

6 After specifying the jaw and MLC settings, validate your R & V configuration by clicking the **Setup R & V Test Plan** button at the bottom of the window.

Pinnacle^3 creates a test plan and opens a window of instructions to help you validate your configuration against the R & V system and linear accelerator.

7 Perform the following steps to complete the validation.

a Verify the jaw settings in the **External Beam Treatment Planning** window, which appears when you click the **Setup R & V Test Plan** button.

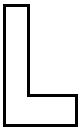
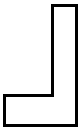
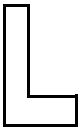
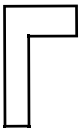
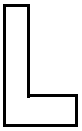
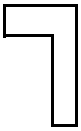
b Export the plan to the R & V system using the **Export** window that appears. If you need help performing the export, see the *Export* chapter of the *Pinnacle^3 Planning Instructions for Use*. Confirm that the plan information at the R & V system console is the same as the information you set up in Pinnacle^3.

c Verify the MLC shape in the beam's eye view (BEV) of the **Beam Blocks** window, which also appears when you click the **Setup R & V Test Plan** button. Print the BEV at a 1.0 scale by clicking the **Print BEV Using x:1 Scale** button in the **Beam Blocks** window, then place the BEV printout under the linear accelerator to verify that the two are aligned.

8 If necessary, re-orient the MLC leaves in the R & V Configuration window to match the linear accelerator.

For example, if the MLC is oriented so that the leaves move left and right, and then you reversed the leaf banks, the MLC might appear flipped on the linear accelerator, as shown in the following illustrations.

To orient the MLC leaves so that the configuration in the BEV matches that on the linear accelerator, take the corrective action listed in the table.

If the MLC has this appearance on the BEV:	And the MLC has this appearance on the linear accelerator:	Take the following corrective action:
		Switch the bank setting in the **Output bank** field of the **R & V Configuration** window.
		Change the setting in the **Output leaf pair** field of the **R & V Configuration** window.
		Switch the settings in BOTH the **Output bank** field and the **Output leaf pair** field.

9 When you finish defining the R & V configuration, click the **Dismiss** button.

NOTE
If you want to use Record and Verify, you cannot commission the machine without entering the manufacturer code for every wedge orientation you use. Instructions for defining wedges are included later in this chapter.

10 In the **Physics Tool** window, click the **Save Current Machine** button.

Enter electron cone information

You must define the electron cones to be used with each machine.

1 Click the **Electron Cones** button on the **Machine Editor** window. The **Electron Applicator List** window appears.

2 Click the **Add** button. A cone is added to the list with a default name of *ElectronApplicator_x*.

3 Click the **Edit** button. The **Electron Cone Editor** window appears.

4 Change the default name and set the cone's width and length.

The width is parallel to left/right jaws. The length is parallel to top/bottom jaws.

5 Enter the manufacturer code to identify the electron cone for Record & Verify exporting.

6 Click the **Dismiss** button to return to the **Electron Applicator List** window.

Repeat steps 2-6 for each cone for this machine.

7 When you finish, click the **Dismiss** button to close the **Electron Applicator List** window.

8 In the **Physics Tool** window, click the **Save Current Machine** button.

Enter stereotactic collimator information

If the machine is used for stereotactic radiosurgery, you must specify the circular collimators that are available.

1 Click the **Stereo Collimators** button on the **Machine Editor** window. The **Stereo Collimator List** window appears.

2 Click the **Add** button to add a new collimator to the list.

3 To edit the information for the selected collimator, click the **Edit** button. The **Stereo Collimator Editor** window appears.

4 Enter a **Name** for the collimator:

- For an Aktina cone, type a name that effectively describes the cone.
- For all other collimators, type the Applicator ID. Obtain the Applicator ID from the vendor for the machine.

5 Set the **Applicator ID** field:

- For the **Aktina Cone** option, located toward the bottom of the **Stereo Collimator Editor** window, select **Yes**. The **Applicator ID** field is automatically updated with “Aktina SRS”.
- For all other collimators, the **Applicator ID** field is automatically updated with the Applicator ID you typed in the **Name** field.

NOTE
The DICOM tag for the Applicator ID is 300A,0108.

6 Enter the diameter and the jaw settings for the collimator. The jaw settings are used in the planning software to automatically set the jaw positions and cannot be edited while planning.

7 Enter the **Accessory Code** for the collimator. Obtain the Accessory Code from the vendor for the machine.

NOTE
The DICOM tag for the Accessory Code is 300A,00F9.

8 Click the **Dismiss** button to close the **Stereo Collimator Editor** window.

9 In the **Physics Tool** window, click the **Save Current Machine** button.

Enter tolerance table information

Detailed tolerance table information is stored on the record and verify system or the treatment machine. Because a machine may use several tables, you can configure multiple tables that correspond to the tables on the machine.

1 Click the **Tolerance Tables** button on the **Machine Editor** window. The **Tolerance Table List** window appears.

2 Click the **Add** button. A table is added with a default name of *TolTable_x*.

3 Click the **Edit** button. The **Tolerance Tables Editor** window appears.

4 Change the default name and set the tolerance table number such that it corresponds to the appropriate tolerance table for the machine.

5 Click the **Dismiss** button to return to the **Tolerance Table List** window.

6 Repeat steps 2-5 for each tolerance table for the machine. Each tolerance table must have a unique name and number.

7 When you finish, click the **Dismiss** button to close the **Tolerance Table List** window.

8 In the **Physics Tool** window, click the **Save Current Machine** button.

Define physical wedges for a machine

After you enter the machine physical description, you are ready to enter wedge information for the available wedges on the machine. The following information is required:

- Wedge angle, material, length, and density
- Source to wedge distance
- Possible wedge orientations
- Jaw limits when using the wedge
- Physical wedge profile

To ensure a proper profile, use the manufacturer's specification drawings as well as the measurements you take from the wedges themselves.

CAUTION
Only mono-density wedges are supported in Pinnacle³. Using multiple-density wedges can result in incorrect dose calculations.

NOTE
For information on adding dynamic wedges, see *Define dynamic wedges for a machine*.

1 Select the machine for which you want to enter information from the **Machine List** in the **Photon Physics Tool** window.
2 Click the **Edit** button beneath the **Machine List**. The **Machine Editor** window appears.
3 Click the **Wedges** button on the **Machine Editor** window. The **Wedge List** window appears.

From this window, you can add wedges to the list of available wedges, select wedges to be edited, and delete wedges.

To add a wedge, click the **Add Wedge** button. A wedge named "Wedge_1" is added to the list. You can edit the wedge name in the **Wedge Editor** window.

To delete a wedge, click the **Delete Wedge** button. In the window that appears, select the wedge and click the **Delete Selected Wedge** button.

Edit a wedge

1 Click the **Edit Wedge** button in the **Wedge List** window. The **Wedge Editor** window appears.

(For a diagram that shows the wedge orientation to the beam, see *Enter jaw information* in this chapter.)

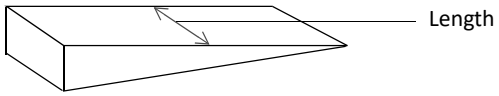
2 Enter the wedge information in the top section of the window.
- **Name**—Enter a unique name for the wedge. Use this name to select the wedge later during planning.
- **Virtual/Dynamic**—Select **Yes** if the wedge is a virtual/dynamic wedge. For information about adding dynamic wedges, see *Define dynamic wedges for a machine*.

NOTE
For fixed jaw machines, the **Virtual/Dynamic** field is set to **No** and cannot be changed. Dynamic and virtual wedges are not allowed for fixed jaw machines.

- **Can be used as Motorized Wedge**—Select **Yes** if the wedge is a motorized wedge. For information about adding motorized wedges, see *Define motorized wedges for a machine*.
- **Wedge Angle**—Enter an angle for the wedge.
- **Material**—Type the name of the wedge material in this field.

CAUTION
Pinnacle³ handles wedge densities of up to 20.00 g/cm³.

- **Density**—Enter the wedge material density in g/cm³.
- **On Top of Mounting Tray?**—Specify whether the wedge is on top of the mounting tray.
- **Source to Wedge Distance**—Enter the distance in centimeters from the source to the flat side/base of the wedge.
- **Length**—Enter the measured length of the wedge in centimeters.



Specify the possible wedge orientations and, if you want, enter your own labels for the wedge orientations.

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.

If you plan to export data to a Record and Verify system, you must enter manufacturer wedge codes for each orientation in the **Manufacturer Code** fields.

NOTE
If you want to use Record and Verify, you cannot commission the machine without entering the manufacturer code for every wedge orientation.

3 Specify the jaw limits for the wedge, in centimeters, in each of the possible orientations. Type the limits in the **Left**, **Right**, **Top**, and **Bottom Jaw Limit** fields.

4 To enter the physical profile for the wedge, click the **Wedge Physical Profile** button at the bottom of the **Wedge Editor** window. The **Machine Wedge Physical Profile Editor** window appears.

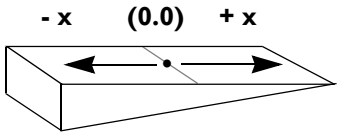
5 If you are creating a profile, create the rows and fields for the table.

Click the **Ins After** button to add the first row to the table. Then click the **Ins Before** and **Ins After** buttons to insert new rows before and after the currently selected row, respectively.

CAUTION
If you are using dimensions from the wedge manufacturer, verify their accuracy by doing a few measurements.

6 Enter the wedge profile in the table.

The profile is defined by the offset (in centimeters) from the central axis and the wedge thickness (in centimeters) at that point. The offset is measured out from the central axis of the beam, which has an offset value of 0.0. The offsets measured from the central axis to the heel of the wedge must be negative. The offsets measured from the central axis to the toe of the wedge must be positive.

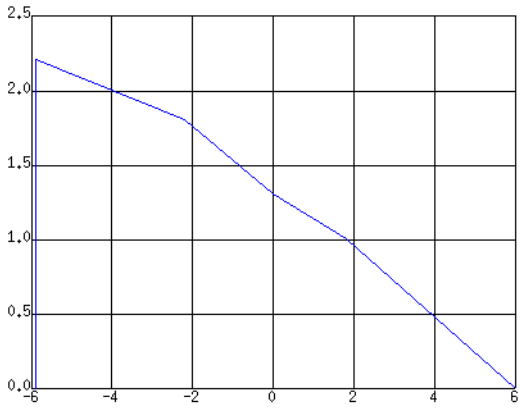


You must fulfill the following requirements when entering the wedge profile:

- Enter the wedge profile values starting with the heel of the wedge and ending with the toe.
- The profile must include at least three data points.
- To define the thickness of the heel of the wedge, you should enter the first offset value twice: once with a thickness of 0.0 and again with the measured thickness. In other words, the first two offset values (x) must be equal.
- After the first value, the offset values must be increasing and the thickness values must be nonincreasing.
- The last thickness value (y) must be zero.

The following illustration shows the wedge profile for a 30-degree wedge.

Offset (cm)	Thickness (cm)
-5.90	0.00
-5.90	2.20
-2.20	1.80
0.00	1.30
1.80	1.00
6.00	0.00



NOTE
Do not close the curve by entering the starting value (in this case, -5.90, 0.0) again at the end of the list.

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

7 When you finish entering the profile values, click the **Dismiss** button in the **Wedge Profile Editor** window.

The system checks that the wedge has been entered correctly. If the criteria listed in step 6 are not met, the system warns you about problems with the wedge.

8 Click the **Dismiss** button in the **Wedge Editor** window to close the wedge editor.

9 Click the **Dismiss** button in the **Wedge List** window to close the wedge list.

10 Click the **Dismiss** button in the **Machine Editor** window to close the window.

11 In the **Physics Tool** window, click the **Save Current Machine** button to save the wedge data.

Define dynamic wedges for a machine

This section explains how to set up dynamic wedges in the Pinnacle^3 Photon Physics tool. A dynamic wedge is a device that delivers wedge-shaped photon dose distributions using computer-controlled dose delivery synchronized to collimator motion.

CAUTION
Dynamic wedges were not available until software version 5.0g. If you add dynamic wedges to machines that were commissioned before version 5.0g and save the information in a software version previous to 5.0g, the dynamic wedges will not work. Other information in the older machines could be corrupted as well.

Before setting up a dynamic wedge, you need to add or select the appropriate machine in the physics tool. For more details, see *Add machines to the physics database* earlier in this chapter. The machine you select must have photon energies.

Before you set up dynamic wedges for the first time, it may be helpful to read the section on dose computation with dynamic wedges in the *Photon Beam Physics & Measured Data Requirements* chapter of the *Pinnacle^3 Physics Reference Guide* to help you understand how Pinnacle^3 computes dose with dynamic wedges.

Define dynamic wedges

After you have entered the machine physical description, including photon energies, you are ready to enter information for the dynamic wedges that are available on the machine. The following dynamic wedge information is required:

- Machine energies that use dynamic wedges
- Wedge vendor, such as Varian or Siemens
- Transmission factor
- Possible wedge orientations
- Jaw limits when using the wedge
- Vendor-specific wedge parameters, such as a Golden ST table for Varian, and a calibration constant and linear attenuation coefficient for Siemens

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

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

3 Click the **Wedges** button on the **Machine Editor** window. The **Wedge List** window appears.

From this window, you can add wedges to the list of available wedges, select wedges to be edited, and delete wedges.

To add a wedge, click the **Add Wedge** button. A wedge named “Wedge_1” is added to the list. You can edit the wedge name later in the **Wedge Editor** window.

To delete a wedge, click the **Delete Wedge** button. In the window that appears, select the wedge and click the **Delete Selected Wedge** button.

Edit a wedge

1 Click the **Edit Wedge** button in the **Wedge List** window. The **Wedge Editor** window appears.

2 Enter a unique name for the wedge in the **Name** field. Use this name to select the wedge later during planning.

3 Click **Yes** next to **Virtual/Dynamic**. The top section of the **Wedge Editor** changes to display dynamic wedge settings.

4 Click the **Add Energy** button to make a machine energy available to the dynamic wedge. A list of available machine energies appears.

5 Select the energy you want to add and click the **Add Energy** button. The energy you selected is added to the **Current Energy** option list in the **Wedge Editor** window.

6 Enter the remaining dynamic wedge information.

- **Delete Energy**—To delete an energy, click this button. The **Dynamic Wedge Energy Delete** window appears. Select the energy you want to delete and click the **Delete Selected Energy** button.
- **Current Energy**—Use the menu to select a wedge energy to edit.
- **Vendor**—Select the name of the wedge vendor. **Varian** is selected by default.
- **Transmission Factor**—The transmission factor is the percentage (expressed as a decimal fraction) of the energy that is not blocked by the jaw.

  The transmission factor range is 0.0 to 0.10. The larger values within this range have a “flattening” effect on the profile. You can adjust the transmission factor after you compute the profile, then recompute if necessary.

7 Edit the vendor-specific dynamic wedge data. If you selected **Siemens** as the vendor, go to the next step to edit data for a Siemens dynamic wedge. Go to step 9 to edit data for a Varian dynamic wedge.

8 If you selected **Siemens** as the vendor, click the **Edit Siemens Wedge Data** button in the **Wedge Editor**. The **Vendor Specific Data** window appears.

Define the following settings in the **Vendor Specific Data** window:

- **Current Energy**—Select the energy for the wedge.
- **Linear Attenuation Coefficient**—See your Siemens literature for an explanation of this coefficient and to determine what to enter in this field.
- **Calibration Constant—**See your Siemens literature for an explanation of this constant and to determine what to enter in this field.
- **Min. and Max. Jaw Speed**—Enter the minimum and maximum jaw speeds in units of mm/s.
- **Min. and Max. Dose Rates—**Enter four settings: the minimum and maximum dose rates when the accelerator is in the low dose rate mode, and the minimum and maximum dose rates when the accelerator is in the high dose rate mode. Enter all values in units of MU/min.

When you finish, click the **Dismiss** button. Then go to step 14 of this procedure.

9 If you selected **Varian** as the vendor, you can import and edit a Golden ST table for the dynamic wedge. Click the **Edit Golden ST Table** button in the **Wedge Editor** to display the **Vendor Specific Data** window. Use the **Current Energy** list field to change the energy you want to edit.

10 Specify the minimum deliverable monitor units for the energy in the **Minimum Deliverable Monitor Units** field.

11 Click the **Import** button and select a Golden ST table from the resulting list, then click **OK**. A table appears and displays the relative dose for each collimator position, relative to the central axis.

12 After importing the profile, you can edit it using the following controls:

- Use the **Ins Row After** and **Ins Row Before** buttons to insert a new row after or before the currently selected row. You can use either button to add the first row to the table.
- Click the **Delete Row** button to remove the selected row from the profile.
- Click the **Initialize Table** button to create a default table with collimator positions from -20 cm to 10 cm incremented by 1 cm. The dose for each is zero.
- To edit a collimator position or dose value, select it in the table and then enter a new value in the **Value** field.

13 When you finish editing the profile values for each energy, click the **Dismiss** button to return to the **Wedge Editor**.

14 Click the **Define Wedge Angles** button to define wedge angles. The **Wedge Angle Editor** window appears.

Wedge angles for planning must be between 0 and 80 degrees. You can define two types of angles:

- **Discrete**—If you select **Discrete** angles, a list of allowed angles appears. You can add angles to the list using the **Add A New Angle** field. To delete an angle from the list, select it and then click the **Delete Angle** button. The angles you specify will then be available in Planning mode.
- **Continuous**—If you select the **Continuous** angle type, the list of allowed angles disappears. In Planning mode, you will then be able to enter any dynamic-wedge angle between the minimum and maximum angle settings you define.

After defining the angles you want, specify the minimum and maximum allowable wedge angles, and then click **Dismiss** to return to the **Wedge Editor**.

15 Specify the possible wedge orientations and, if desired, enter your own labels for the wedge orientations. For descriptions of wedge orientations, see *Define physical wedges for a machine*.

16 If you plan to export data to a Record and Verify system, you must enter manufacturer wedge codes for each orientation in the **Manufacturer Code** fields. For dynamic wedges, you must enter a base name and include a % sign in the name. Upon export, the % will be replaced with the angle of the wedge.

> **NOTE**
> If you want to use Record and Verify, you cannot commission the machine without entering the manufacturer code for every wedge orientation.

17 Specify the jaw limits for the wedge, in centimeters, in each of the possible orientations. Type the limits in the **Left**, **Right**, **Top** and **Bottom Jaw Limit** fields.

18 Click the **Dismiss** button in the **Wedge Editor** window to close the wedge editor.

19 Click the **Dismiss** button in the **Wedge List** window to close the wedge list.

20 Click the **Dismiss** button in the **Machine Editor** window to close the window.

21 In the **Physics Tool** window, click the **Save Current Machine** button to save the wedge data.

Compute the dynamic wedge profile

After you have defined the dynamic wedge, you can compute the profile. You must import and compute profiles or you cannot commission the wedges and machine.

> **NOTE**
> You can only compute the dynamic or virtual wedge model if the open field model is complete or a sample model is loaded.

1 Click the **Model** button in the **Photon Physics Tool** window.

The **Photon Model Editor** window and the **Machine Data Model** window appear.

2 Click **Compute Profiles** in the **Machine Data Model** window.

The wedge profiles appear.

3 Set the **Compute** option for all profiles to **Yes** and then click the **Compute Profile(s)** button to start the computation.

If necessary, you can return to the **Wedge Editor** window and adjust the transmission factor after you compute the profile. If you adjust the transmission factor, you must recompute the profile.

Define motorized wedges for a machine

Define a motorized wedge just as you would a fixed wedge in the **Wedge Editor** window, with three exceptions.

- You must enter the maximum wedge angle of the motorized wedge in the **Wedge Angle** field.
- You must allow only the wedge orientation that is physically possible for a motorized wedge with your machine.
- You must select **Yes** for the **Can be used as Motorized Wedge** field.

After commissioning, this wedge will be available for use as a motorized wedge.

CAUTION
Be sure to select No in the Allowed column for the wedge orientations that are not allowed by your machine. If you allow wedge orientations that are not physically possible on your machine, you could create plans that cannot be delivered.

NOTE
If you plan to use both fixed and motorized wedges, we recommend that you define multiple wedges and name each wedge appropriately to reflect the wedge type (fixed or motorized).

NOTE
The computation of the synthesized wedge angle is based on the **Wedge Angle** value. Make sure this angle is correct before you commission the machine.

WARNING
If you expect to export plans that contain motorized wedges, be sure to include beams with motorized wedges in your validation of export. The validation should include all allowed wedge orientations, different MLC positions, and square and rectangular fields. This will help ensure that your beams have been modeled properly.

Synthesized wedge angle

The formula used to compute the synthesized wedge angle is:

$$\tan\theta_S = F \cdot \tan\theta_n$$

where:

θ_n = the angle of the wedge field

θ_S = the angle of the synthetic wedge field

$$F = \frac{D_w}{D_o + D_w}$$

where D_w (the wedge field dose) and D_o (the open field dose) are the relative doses to water at the calibration SSD and depth for the specified field size and are given by:

$$D_w = MU_w \cdot OF_w$$
$$D_o = MU_o \cdot OF_o$$

and OF_w and OF_o are the relative output factors entered in the physics tool.

Test non-commissioned machines from within the planning software

Many quality assurance tests require the use of tools that are available only in the Pinnacle^3 planning software. If you want to run quality assurance tests from the planning software on uncommissioned machines, follow the steps below.

WARNING
This option is for quality assurance purposes only. Do not use non-commissioned physics machines for planning.

1 Enter the planning software with the data set you want to use for testing.

2 Click the **Beams** button at the top of the **Planning** window to display the **Beams** panel to the left of the viewing windows.

3 Select **Options** - **Beam Spreadsheet** to open the **External Beam Treatment Planning** spreadsheet.

4 Select **Options** - **Load Physics Machines** in the **External Beam Treatment Planning** spreadsheet.

5 At the next prompt, click the **Load Physics Machines** button. Pinnacle^3 loads the machines that are in the physics machine database into the planning machine database. All currently uncommissioned machines are available in the planning software until you exit.

6 Exit the software when you finish testing the uncommissioned machines.

Commission a machine for planning

After you enter the physics information for all modalities and energies on a given machine and model the profiles, you must commission it for use in treatment planning.

The commissioning process moves a machine from the physics machine database to the planning machine database and “stamps” the machine with the date and time of commissioning.

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

1 In the **Photon**, **Electron**, or **Stereotactic Radiosurgery Physics Tool** window, select the machine to be commissioned from the **Machine List** and then click the **Commission** button. The **Commission Machine** window opens.

2 Select the modalities for which you want to commission the machine.

> **NOTE**
> For fixed jaw machines, the **Electrons** and **Stereo** modalities are set to **No** and cannot be changed. You cannot commission electron or stereo energies for fixed jaw machines.

3 Type your name or initials in the **Commissioned By** field.

4 Type a description for the machine in the **Description** field (optional).

5 Click the **OK** button to commission the machine.

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

Commission failure

If problems occur during the commissioning process, a list of errors appears in the **Commission Failure** window. Problems that can prevent commissioning include, but are not limited to:

- Empty **Commissioned By** field—To correct this problem, return to the **Commission Machine** window, enter your name or initials in the **Commissioned By** field, and then attempt to commission the machine again.
- Uncomputed output factors—To correct this problem, return to the appropriate physics tool, compute the output factors for all energies on the machine, and then attempt to commission the machine again.

  NOTE
  The software allows you to commission the machine if you have uncomputed output factors. However, the software cannot compute MUs in planning if you do not compute output factors.

- Jaw setting violations—A machine that has output factors or measurement geometries with jaw setting violations.
- Uncomputed profiles—During modeling, all profiles for all modalities should be computed and compared with the measured data. When a machine is commissioned, the software reports any uncomputed profiles.

  While all profiles should be computed, you can commission machines with uncomputed profiles if necessary. Follow these guidelines:

  – For photons, all profiles may be uncomputed at the time of commissioning, as long as you have obtained models for all energies which yield a good fit between measured and computed data.
  – For electrons, compute at least one profile for each energy.
  – For stereotactic radiosurgery, compute at least one profile for each cone size.

  To correct the problem, return to the **Photon**, **Electron** or **Stereotactic Radiosurgery Model** window and compute all uncomputed profiles. Then, attempt to commission the machine again. The list of uncomputed profiles is not updated automatically when profiles are computed again. To update the list, click the **Update List** button.

  We recommend that you do not commission a machine unless all of the profiles are computed.

  NOTE
  Use two scripts in the System scripts directory to compute all electron and stereotactic profiles: ComputeAllElectronProfiles.Script and ComputeAllStereoProfiles.Script. To run these scripts, click the **Browse** button in the **HotScripts** window to go to the System scripts directory, select the script, and click the **OK** button.

Delete machines

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

Delete non-commissioned machines

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

WARNING
Once a non-commissioned machine is deleted, it cannot be restored. All measured data associated with the machine is deleted with the machine.

1 Click the **Photon Physics Tool** button in the **Physics Tools** window. The **Photon Physics Tool** window appears.

2 Select the machine you want to delete from the **Machine List**.

3 Click the **Delete** button beneath the **Machine List**, and then click the **Delete** button again in the next window to confirm the deletion.

Click the **Dismiss** button to cancel the deletion.

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

Delete commissioned machines

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

NOTE
We strongly discourage the deletion of commissioned machines. All commissioned versions of a machine are saved in the planning machine database to allow plans to be read in and replicated with the machine used when the plan was generated. If a machine is deleted, you cannot subsequently read in the plan and view the dose as it was calculated when the plan was generated.

1 Open a physics tool by clicking the **Photon Physics Tool**, **Stereo Physics Tool**, or **Electron Physics Tool** button.

2 Click the **Add** button beneath the **Machine List**. The **Add New Machine** window appears.

3 Select the **Current Commissioned Machines** button to display the list of commissioned machines.

4 Select the machine you want to delete and click the **Delete** button. The **Confirm Current or All Versions Delete** message opens.

5 Do one of the following:

- To delete all versions of the selected machine, click the **Delete All Versions** button. The **Confirm All Versions Delete** message opens. Continue to step 6.

- To delete only the currently commissioned version of the machine, click the **Delete Current Version** button. The **Confirm Commissioned Machine Delete** message opens. Continue to step 7.
- Click the **Cancel** button to close the message without deleting the machine.

6 Do one of the following:

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

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

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

7 Do one of the following:

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

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

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

Restore deleted commissioned machines

When you move commissioned machines to the **Deleted Commissioned Machines** list, you cannot use them in planning, but you can still access them in physics, if necessary. If an old plan uses a

machine that has been deleted, and you do not have another machine in the **Current Commissioned Machines** list or the **Old Commissioned Machines** list that has the same name as the deleted machine, you cannot open the old plan unless you restore the deleted machine first. However, if your **Current Commissioned Machines** list contains a newer version of a machine that has the same name as the deleted machine, you can open the old plan, but you must recompute dose.

1 Open a physics tool by clicking the **Photon Physics Tool**, **Stereo Physics Tool**, or **Electron Physics Tool** button.

2 Click the **Add** button beneath the **Machine List**. The **Add New Machine** window appears.

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

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

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

5 Importing and Entering Measured Beam Data

NOTE
If you are commissioning the machine as a simulation-only machine, you do not need to follow the procedures in this chapter. You only need to enter the machine parameters as described in the *Photon, Stereotactic, and Electron Machine Definition* chapter and commission the machine.

This chapter describes how to import measured data into the selected physics tool, how to manually enter measured data, and how to use the Profile tools to edit measured data.

You can import measured photon, electron, or stereotactic radiosurgery data files from Scanditronix Wellhöfer, Multidata, XL-Plan, TG23, and Pinnacle Full ASCII formats. The tools for entering or importing measured data are the same for photon, electron, or stereotactic radiosurgery data.

For proton measured data, Pinnacle^3 supports the IBA RFA-300 ASCII data file format that is produced by Omni-Pro Accept and a CSV data file format that is produced by Omni-Pro Incline acquisition software. For information about which file format is supported for which types of measured data, see the *Proton Beam Physics & Physics Utilities* chapter.

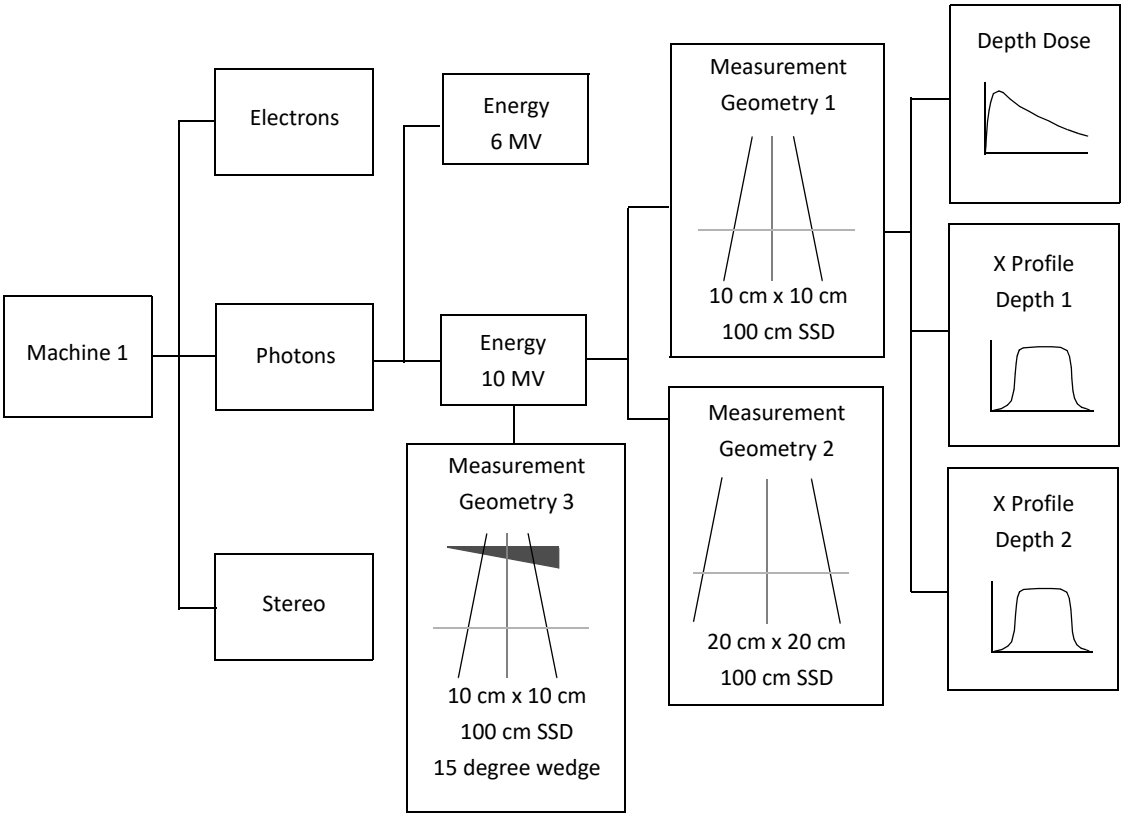
NOTE
When importing data using Scanditronix Wellhöfer programs, you may use the legacy Wellhöfer 600 or 700 series ASCII format. If you are using OmniProAccept, you must use Pinnacle Full ASCII format.

For information on the measured beam data required for each modality, see the *Pinnacle^3 Physics Reference Guide*.

WARNING
The accuracy of the treatment planning dose calculation depends on the quality of the data entered in the physics tool. If the quality of this data is poor, or if the computed dose is not verified with measured data, the dose calculation may be inaccurate.

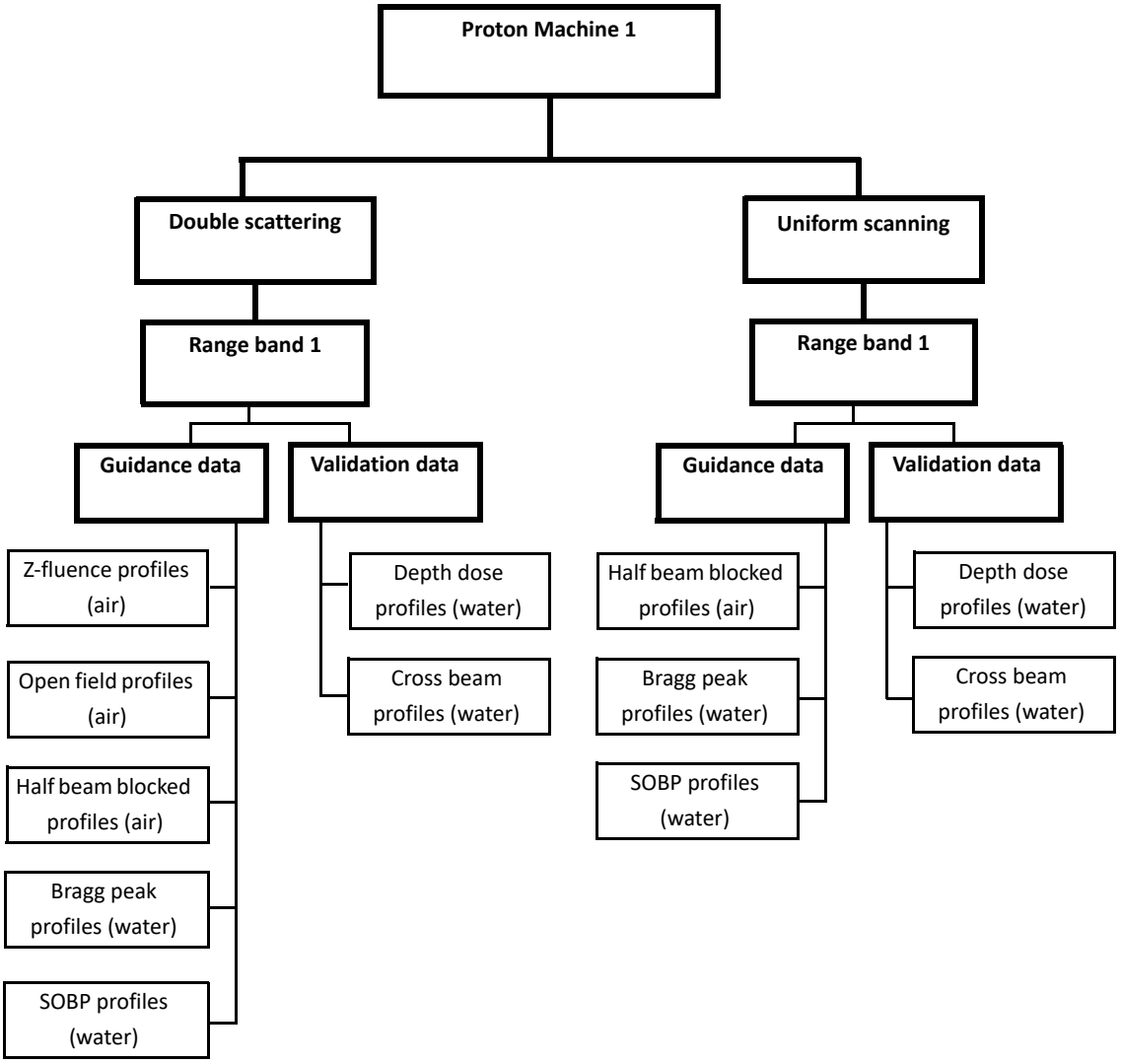
Machine data organization

Measured machine data for photon, stereotactic, and electron beams are organized in the machine database by energy and measurement geometry, as shown in the graphic below.



In the Physics Tool windows, the **Measurement Geometry List** indicates the measurement geometries for the measured data files associated with the current energy. The **Profile List** indicates the measured profiles that have been entered or imported for the selected measurement geometry. The selected machine, energy, measurement geometry, and profile are highlighted in the lists.

Measured machine data for proton machines are organized in the machine database by delivery type (double scattering and uniform scanning). Data are further organized by range band for double scattering and uniform scanning, as shown in the graphic below. Guidance data are measured profiles that are used to model the range bands or layers. Validation data are measured profiles that are used to validate the model of the machine.



In the **Proton Physics Tool** window, the **Measurement Setting List** indicates the measurement settings for the measured validation data files that are associated with the range band. The **Profile List** indicates the measured profiles that have been imported for the selected measurement setting.

Import measured data files

> **NOTE**
> You do not import proton measured data in the same way that you import photon, stereotactic, and electron measured data. Information about importing measured data for the proton modality is included in the *Proton Beam Physics & Physics Utilities* chapter.

You have two options for importing measured data files for photon, stereotactic, and electron data. The option you should use depends on the type of measured data file.

- Use the **Import Profiles** button in the Physics Tool windows to import profiles and sets of profiles for Scanditronix Wellhöfer, MultiData, XLPlan, TG23, or Pinnacle Full ASCII.
- Import simple ASCII and Scanditronix Wellhöfer files from the **Profile Editor** window.

Since the import tools are essentially the same for the photon, stereotactic, and electron modalities, the process is described in a general fashion in this chapter. The examples use the Photon Physics tool, but the process is the same for importing electron and stereotactic radiosurgery data.

NOTE
If the width of the measured data profile that you import does not match the width of the open field for the machine, the software ignores the profile when you model the machine.

NOTE
When importing data using Scanditronix Wellhöfer programs, you may use the legacy Wellhöfer 600 or 700 series ASCII format. If you are using OmniProAccept, you must use Pinnacle Full ASCII format.

Copy files to or from removable media

Before you can import measured data files into the physics tools, you should copy them into a directory on the computer's hard disk. This section describes how to copy data from removable media to the computer's hard disk.

The following UNIX commands are useful when working with directories.

Command	Description
`mkdir directory`	Creates a directory beneath the current directory with the name you enter.
`cd directory`	Moves you to the specified directory. If the directory is not a subdirectory beneath the current directory, the directory name should be preceded with a forward slash: `cd /home/files/rtp.`
`cd ..`	Moves you to the directory directly above the current directory.
`pwd`	Displays the name of the current directory.
`ls -l`	Lists the contents of the current directory. (This is a long list, including whether the item is a file or directory, the ownership, and read/write/execute privileges.)
`cp file1 file2`	Copies the file(s) from one location (*file1*) to another (*file2*). When copying directories and files, use a -r switch with the command (`cp -r`). See *Copy a file from removable media to the system's hard disk* for more details.

First, you should create directories for the data on the system's hard disk. You can then copy your files to these directories.

Make a new directory on the hard disk drive

1 Open an xterm window from the root menu either by clicking the right mouse button on the screen background or clicking on the terminal icon in the desktop tool bar.

2 To create the directory for the machine, type:

`mkdir machinename`

where *machinename* is the name you enter for your machine.

3 To move to the directory you created, type:

`cd machinename`

4 If you want to create separate subdirectories for the data for each energy, type the following command for each energy:

`mkdir energy1`

After creating a directory for the files on the system's hard disk, you can transfer the files into the new directory.

Copy a file from removable media to the system's hard disk

1 Connect the removable drive to the USB port on the workstation.

2 In an xterm window, type:

```
cd /rmdisk/unnamed_rmdisk
```

3 To list the contents of the drive, type:

```
ls -l
```

4 Go to the directory where you want to place the measured data.

```
cd machinename/energy1
```

5 Make sure you are in the correct directory by typing:

```
pwd
```

The system should respond with the appropriate directory.

```
/home/p3rtp/machinename/energy1
```

6 You can copy one file at a time to the current directory, or you can copy a set of files to the current directory.

Items to copy	Command
All files and subdirectories	`cp -r /rmdisk/unnamed_rmdisk/* .`
All files	`cp /rmdisk/unnamed_rmdisk/* .`
Specific subdirectory	`cp -r /rmdisk/unnamed_rmdisk/subdirectoryname .`
Specific file	`cp /rmdisk/unnamed_rmdisk/filename .`

7 To make sure the data has been copied to the current directory, type:

```
ls -l
```

8 Type `exit` then press **Enter** to close the xterm window.

Copy files to removable media

1 Connect the removable drive to the USB port on the workstation.

2 In an xterm window, type:

```
cd /rmdisk/unnamed_rmdisk
```

3 Type the following in the xterm window:

```
cp /directorypath/filename .
```

where *directorypath* is the path to the directory where the file is located and *filename* is the name of the file. Don't forget to type a space and a dot at the end of the command.

For example:

```
cp /home/p3rtp/jones.mlc .
```

4 Type `ls` to verify that the file was successfully copied to the removable drive.

5 Type `exit` then press **Enter** to close the xterm window.

Import Scanditronix Wellhöfer, Multidata, Pinnacle Full ASCII, or TG23 format files

NOTE
You do not import proton measured data in the same way that you import photon, stereotactic, and electron measured data. Information about importing measured data for the proton modality is included in the *Proton Beam Physics & Physics Utilities* chapter.

When using the Scanditronix Wellhöfer, Multidata, Pinnacle Full ASCII or TG23 data formats, the data for multiple measurements taken with the same measurement geometry are stored in a single file. The following procedure describes how to import this type of measured data file.

NOTE
Pinnacle^3 automatically detects the file type. You do not need to select the file format.

NOTE
Scanditronix Wellhöfer 600 and 700 and Multidata files cannot be imported in their default binary format. They must be saved as ASCII files. For more information, contact Customer Support (request application notes 2000-08 and 2000-09). If you have a newer version of one of these products, contact your vendor to see if the version supports Pinnacle Full ASCII formats.

1 Go to the appropriate physics tool for the type of data you are importing.

2 Click the **Import Profiles** button in the **Physics Tool** window. The **Import Profiles** window appears.

3 Use the **Directory** list at the right to locate directories and measured data files on your hard disk.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home Directory** button.

4 Select the files you want to import.

- To select multiple files that are contiguous in the directory list, hold down the **Shift** key and select the first and last files. All files in between are selected as well.
- To select multiple files that are not contiguous in the directory list, hold down the **Control** key and select the files you want to import.

5 Select importing options depending on the data format you are using:

- If you are importing profiles from Scanditronix Wellhöfer, you can select whether you want to reverse the crossplane X and Y mapping. This option toggles the behavior between importing into X profiles versus Y profiles, and vice versa.
- If you are importing profiles from Multidata, you can turn on the interpretation of the files in grid format.
- If you are importing profiles from XLPlan (XL-Plan-PC), you must select **Yes** for **Fault Tolerant Import** and specify the machine energy for which you are importing profiles.

6 Click the **OK** button to import the selected files. The **Confirm Profile Import** window appears.

7 Select **Yes** next to **Apply Modifications to all Profiles in List** if you want changes that you make to be applied to all of the profiles in the measurement geometry. (Changes to the **Profile depth** field are only applied to the current profile, regardless of this setting.)

8 If necessary, change the profile type in the **Type** option list.

It is very important that you set up the machine collimator angle the way it is defined in Pinnacle^3 so that the automodeler can function properly. The collimator must be rotated to the default collimator angle as defined in Pinnacle^3 or the X and Y profiles will not be properly selected during automodeling.

If your data was collected using a collimator angle that is not the default angle, change the default angle to match the angle used during data collection so that your profiles can be modeled properly. (See *Enter collimator information* in the *Photon, Stereotactic, and Electron Machine Definition* chapter to change the collimator angle.) To use the original default collimator angle for planning, change the collimator angle back to the original setting after modeling but before commissioning.

9 Review and revise the profiles in the confirmation window and delete profiles that you do not want to import into the physics tool.

To delete a profile, select it in the list of profiles and then click the **Delete Selected Profile** button. To cancel the file import, click the **Cancel** button.

> **NOTE**
> When importing photon profiles with wedges, you may need to select the wedge that was used to obtain the profile from the **Wedge** option list. If a wedge name does not appear for the wedged data, define the wedge before you import the data. See the *Photon, Stereotactic, and Electron Machine Definition* chapter for information about defining wedges.
>
> When importing photon profiles with dynamic wedges, you can specify the angle of the wedge. If you are using a physical wedge, then its angle is fixed and you cannot change it.

This procedure is written assuming you are importing photon profiles, but the process is the same if you are importing electron or stereotactic profiles with one exception. Instead of selecting a wedge, select an electron cone when importing electron profiles, and select a stereotactic applicator when importing stereotactic profiles.

10 If a profile was measured with the MLC in the field, select **Yes** next to **Profile includes user defined MLC**. The **Closed MLC leaf offset from CAX** and **MLC Rectangle** fields appear.

The **Closed MLC leaf offset from CAX** field lets you define how far from the central axis the closed leaf gap is pushed. A positive value pushes the closed leaves toward the jaw that is listed to the right of the field. A negative value pushes the closed leaves away from the jaw listed to the right of the field.

The **MLC Rectangle** fields let you enter the X and Y positions for the MLC. The MLC positions are included with the profile information at the top of the window.

NOTE

The **Profile includes user defined MLC** option only appears if the machine has an MLC. For fixed jaw machines, the option is set to **Yes** and cannot be changed.

If you change these values after you compute profiles, you will invalidate the computed profiles for the measurement geometry.

Pinnacle^3 displays a warning message if you enter an MLC value that violates the machine parameters, and the value is set to the closest value that does not violate the parameters. Be sure to enter MLC values that are valid for your machine. The warning message will also appear if machine parameters are changed so that the MLC values violate the new parameters.

11 When you finish reviewing the profiles, click the **Import Profiles** button to import the profiles.

12 Click the **Save All Machines** button in the **Physics Tool** window to save the measured data you just imported.

Enter measurement geometries for ASCII file import or manual measured data entry

NOTE
You do not import proton measured data in the same way that you import photon, stereotactic, and electron measured data. Information about importing measured data for the proton modality is included in the *Proton Beam Physics & Physics Utilities* chapter.

If you are importing data files using the Import Data option or entering data using the data editor, you must first define the setup information for the dose measurements in the **Measurement Geometry List**. The measurement geometry describes the machine and water tank configuration for one set of measurements. It includes the collimator size and the SSD.

1 Go to the appropriate physics tool for the type of data you are importing.

2 Click the **Read Measured Data** button beneath the **Measurement Geometry List** to read the measured data associated with the current energy.

Any measured data that has been entered and saved for the current energy is shown in the **Measurement Geometry List** and **Profile List**.

NOTE
If you are importing Scanditronix Wellhöfer, MultiData, XLPlan, TG23, ARM, PTW, or any other scanning system that can export Pinnacle Full ASCII measured data files, you do not need to add measurement geometries as described in the following steps. The measurement geometries are automatically detected by the file import function.

After the measured data has been read in, the **Read Measured Data** button is replaced by **Add**, **Edit**, and **Delete** buttons and the **Compute All** button (for photon geometries).

3 Click the **Add** button beneath the **Measurement Geometry List** to add a measurement geometry to the list.

4 To edit the measurement geometry, click the **Edit** button. The **Machine Data Profile Geometry** window appears.

5 In the **SSD** field, enter the SSD used for the measurement.

6 Enter the field size by specifying the left, right, top, and bottom jaw settings.

7 If you are importing stereotactic radiosurgery profiles, select the collimator size instead of the field size. Then continue to step 11.

8 If you are importing electron profiles, select the electron cone size and set the exposed field size instead of selecting the field size. Then continue to step 11.

9 If you are importing profiles for wedged fields, select the wedge and specify the orientation used to obtain the wedge. If you are using a dynamic wedge, you can also specify its angle. The angle is fixed for physical wedges.

NOTE
It is important to select the correct wedge orientation for the profiles. If you compute profiles during the modeling process and notice that the modeled wedge profile

appears to be an open field, the wedge orientation may have been specified incorrectly in the previous window.

10 If a measurement geometry should include an MLC, select **Yes** next to **User defined MLC rectangle**. The **Closed MLC leaf offset from CAX** and **MLC Rectangle** fields appear.

The **Closed MLC leaf offset from CAX** field lets you define how far from the central axis the closed leaf gap is pushed. A positive value pushes the closed leaves toward the jaw that is listed to the right of the field. A negative value pushes the closed leaves toward the jaw that is opposite the one listed to the right of the field.

The **MLC Rectangle** fields let you enter the X and Y positions for the MLC. The MLC information is included with the profile information at the top of the window.

NOTE
The **User defined MLC rectangle** option only appears if the machine has an MLC. For fixed jaw machines, the option is set to **Yes** and cannot be changed.

If you change these values after you compute profiles, you will invalidate the computed profiles for the measurement geometry.

Pinnacle^3 displays a warning message if you enter an MLC value that violates the machine parameters, and the value is set to the closest value that does not violate the parameters. Be sure to enter MLC values that are valid for your machine. The warning message will also appear if machine parameters are changed so that the MLC values violate the new parameters.

CAUTION
Verify that the measurement geometries are correct before saving the data.

11 When you have specified the measurement geometry, click the **Dismiss** button.

NOTE
Each measurement geometry can have any number of profiles associated with it. If the same measurement geometry was used for a number of measurements, you only need to enter the geometry once.

12 To delete a measurement geometry, select it from the **Measurement Geometry List** and click the **Delete** button beneath it.

Import simple ASCII measured data files

NOTE
You do not import proton measured data in the same way that you import photon, stereotactic, and electron measured data. Information about importing measured data for the proton modality is included in the *Proton Beam Physics & Physics Utilities* chapter.

You can import measured data from ASCII or Scanditronix Wellhöfer ASCII data files. The data should reside on the treatment planning system hard disk before you read the data into the Machine Data Editor.

NOTE
When importing data using a Scanditronix Wellhöfer program, you may use the legacy Wellhöfer 600 or 700 series ASCII format.

1 Go to the appropriate physics tool for the type of data you are importing.

2 If you have not already done so, add the measurement geometries used to collect the data to the **Measurement Geometry List**. This procedure is described in *Enter measurement geometries for ASCII file import or manual measured data entry*.

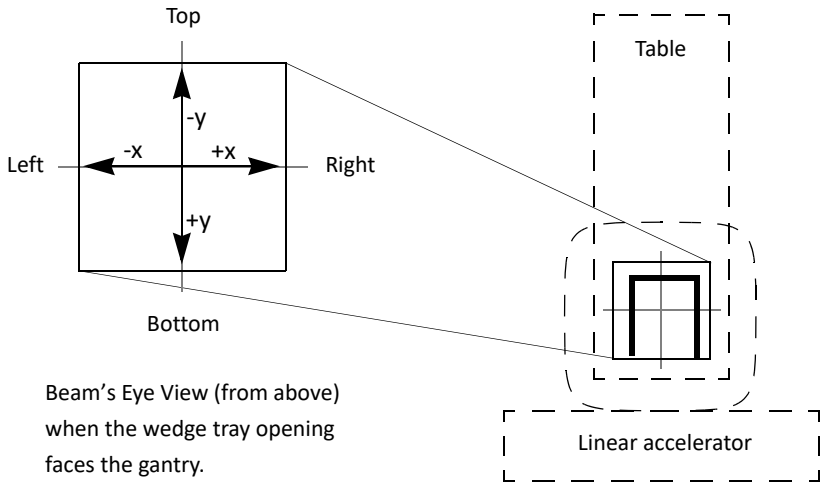
3 From the **Measurement Geometry List**, select the measurement geometry that was used to obtain the data.

4 To add a new profile to the list, click the **Add** button beneath the **Profile List**. A new profile is added to the list of dose profiles.

5 To display the **Machine Data Editor** window, click the **Edit** button beneath the **Profile List**.

6 Select the profile type from the **Type** option list.

If you are entering a depth dose profile that was not measured on the central axis, enter the axis offset(s) for the data in the **Left/Right Offset** and **Bottom/Top Offset** fields. The offsets are measured out from the central axis, as shown below.



If you are entering an X or Y profile, you must specify the profile depth. If the profiles were not measured through the central axis, you must specify an offset value. For X profiles that were measured off-axis, you must specify the Bottom/Top offset. For Y profiles that were measured off-axis, you must specify the Left/Right offset. These offsets for X and Y profiles are measured out from the central axis as shown above.

7 Click the **Import Data** button in the **Machine Editor** window. The **Machine Data Import** window appears.

8 Use the **Directory** list on the right side of the window to locate the directories and measured data files on your hard disk.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home** button.

You can use the **Search Pattern** option to search for specific files in a directory. For example, you could type *pdd** in the **Search Pattern** field to list only the files that start with “pdd”. Type an asterisk (*) to list all files in the current directory.

9 Select the file you want to import from the list of available files.

10 Select either the ASCII or Wellhöfer file format from the **Import File Type** option list.

11 Click the **OK** button to import the selected file.

NOTE
For details on the ASCII file format, see the *Pinnacle³ Physics Reference Guide*.

Manual entry of measured data files

NOTE
If you are working with proton measured data, please see the *Proton Beam Physics & Physics Utilities* chapter. Manual entry of measured data is different for proton data.

You can enter measured data profiles manually by typing the values in the profile data editor.

1 Go to the appropriate physics tool for the type of data you are entering.

2 From the **Measurement Geometry List**, select the measurement geometry that was used to obtain the data.

3 To add a new profile to the list, click the **Add** button beneath the **Profile List**. A new profile is added to the list of dose profiles.

4 To display the **Machine Data Editor** window, click the **Edit** button beneath the **Profile List**.

5 If you are creating a profile, take the following steps:

   a Create the rows and fields for the table. Use either the **Ins Before** button or **Ins After** button to add the first row to the table. Click the same buttons to insert new rows before and after the currently selected row, respectively.

   b Enter the depth or offset value, in centimeters, in the left field and the measured dose in the right field. After you enter the second value, the graph appears to the right of the table.

   c To enter profile values, click the field you want to edit, then type the value in the field that appears above the table. Click the green check mark next to the field or press **Enter** to accept the value you typed. Click the red **x** to cancel the change.

   d To delete a point, click in either the **Offset** or **Measured** field for that point and click the **Delete** button. To delete all the points in the profile, click the **Delete All Points** button.

6 To adjust the high dose/low dose gradient regions of the profile, click the **Modify Gradient Threshold** button and specify the high dose gradient threshold value. The **Profile Problems** window appears.

   NOTE
   The **Modify Gradient Threshold** button does not appear if there is a problem with the profile. Instead, a warning message and the **View Problems** button appear. See *Evaluate measured data for automodeling* in the *Photon Beam Physics & Physics Utilities* chapter for information about the **View Problems** button and how to correct problems with profiles.

7 When you finish entering the measured data for the profile, click the **Dismiss** button to return to the **Photon Physics Tool** window.

8 To delete a profile, select the profile you want to delete from the **Profile List** and click the **Delete** button beneath it.

9 Click the **Save All Machines** button in the **Photon Physics Tool** window to save the measured data you just entered.

Edit measured data files

NOTE
For information about editing measured data files for protons, see the *Proton Beam Physics & Physics Utilities* chapter.

You can edit measured data profiles to correct for problems in the data using the Machine Data Editor and the Profile tools.

1 Go to the appropriate physics tool for the type of data you are editing.

2 From the **Measurement Geometry List**, select the measurement geometry of the profile you want to edit.

3 Select the profile you want to edit from the **Profile List**.

4 Click the **Edit** button beneath the **Profile List**. The **Machine Data Editor** window appears.

5 To edit the profile values, click the field you want to edit, then type the value in the field that appears above the table. Click the green check mark next to the field or press **Enter** to accept the value you typed. Click the red **x** to cancel the change.

6 Change the **Type** option, if necessary. It is important that the **Type** option be set correctly so that the in-plane and cross-plane effective source size model parameters are modeled correctly. See *Import Scanditronix Wellhöfer, Multidata, Pinnacle Full ASCII, or TG23 format files* for more information about the Type option.

7 If you want to print the profile, see *Print profile* for instructions.

8 When you finish entering the measured data for the profile, click the **Dismiss** button to return to the **Physics Tool** window.

9 Click the **Save All Machines** button in the **Physics Tool** window to save the measured data you just entered.

Use Profile tools

You can also use the Profile tools to edit the measured data. You can smooth the data, center or invert the profile, or reposition the profile.

1 From the **Measurement Geometry List**, select the measurement geometry of the profile you want to edit.

2 Select the profile you want to edit from the **Profile List**.

3 Click the **Edit** button beneath the **Profile List**. The **Machine Data Editor** window appears.

4 Click the **Profile Tools** button to display the **Profile Tools** window.

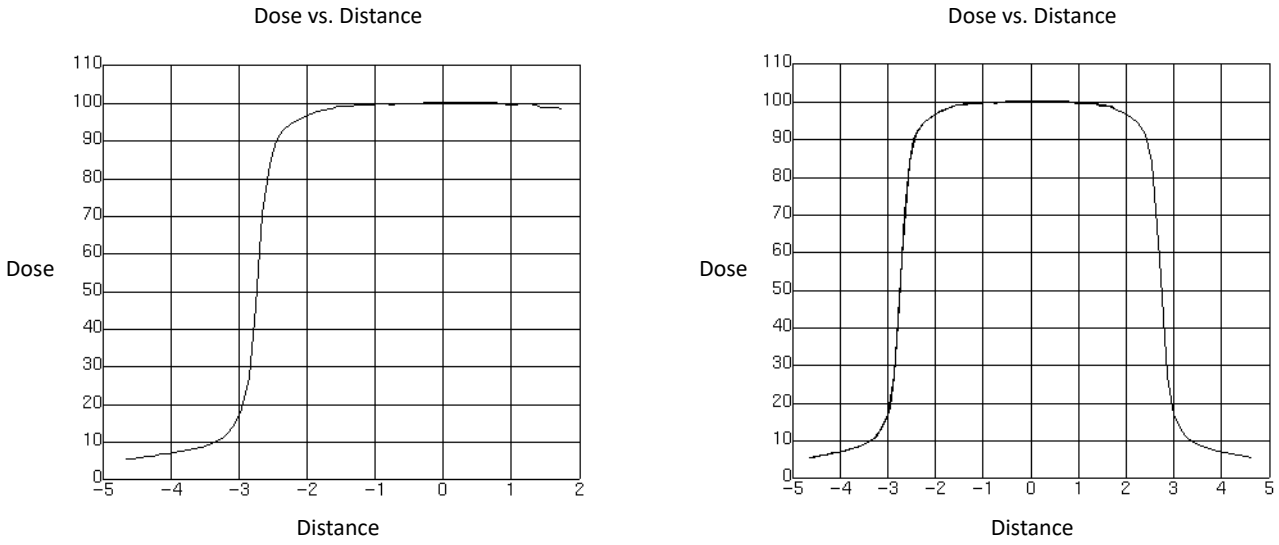
The options available in this window change depending on the type of profile selected in the **Profile List**.

CAUTION
The filtering tools for editing a profile also smooth the high gradient regions. Excessive smoothing can adversely affect the data integrity.

5 Select **Yes** next to the **Apply Filter to All...** option if you want the changes you make to be applied to all of the profiles of that type in the measurement geometry.

6 Use the following tools to edit the profile:

- The filtering tools smooth out noisy data. The **Noise Window Width** specifies the noise window for the filter, and the **Magnitude Cutoff** is used to truncate the filter.
- The **Mirror** button lets you mirror the data around the central axis. This function is useful when you do not have enough data in a cross-axis profile. For instance, if a profile is incomplete because of the water phantom limits, use the **Mirror** button to create a complete profile, as shown below.



- The **Re-Sample** button lets you resample the measured data at a different resolution. Specify the resolution in the Re-Sample Resolution field.
- The **Scroll** buttons let you manually reposition the data on the X axis.
- The **Center Profile** button centers the profile on the X axis.
- The **Invert X** button inverts the profile on the X axis.
- The **Scale** and **Offset** buttons let you scale or offset the profile on the X or Y axis by the amount you specify in the fields.

7 If necessary, you can restore the profiles to their original settings. Click the **Restore Original Curve** button to restore the current profile, or click the **Restore All Original Curves** button to restore all of the profiles in the measurement geometry.

Save edited data profiles to a new file

If you use the Machine Data Editor or the Profile tools to edit the measured data, you can save the edited data to a file.

1 Click the **Export Data** button in the **Machine Data Editor** window. The **Machine Data Export** window appears.

2 Specify the directory where you want to save the data, type a name for the file, and click the **OK** button.

Print profile

1 In the **Machine Data Editor** window, click the **Print Plot** button. The **Print Profile Plot Confirmation** window appears. The current printer is listed as the Selected Printer.

2 Click the **Print** button to print to the selected printer. To select a different printer, click the **Select Printer** button, select a different printer, and click the **Dismiss** button. Then click the **Print** button.

6 Photon Beam Physics & Physics Utilities

This chapter describes the photon beam physics modeling process, the modeling parameters associated with the Collapsed Cone Convolution Superposition dose model, and dose calculation.

The process of adding machines and entering the general machine data is covered in the *Working with Machines and the Machine Database* chapter. The process of importing and entering measured data is described in the *Importing and Entering Measured Beam Data* chapter.

WARNING
The accuracy of the treatment planning dose calculation depends on the quality of the data entered in the physics tool. If the quality of this data is poor, or if the computed dose is not verified with measured data, the dose calculation may be inaccurate.

The photon model parameters

The **Photon Model Editor** window groups the photon model parameters based on the regions of the dose profiles where their effects are most apparent. To open the **Photon Model Editor** window, in the **Photon Physics Tool** window click the **Model** button.

For information about the Collapsed Cone Convolution Superposition dose model and the photon model parameters and how changes to those parameters affect the model, see the *Photon Beam Physics & Measured Data Requirements* chapter in the *Pinnacle³ Physics Reference Guide*.

Photon beam modeling

After you create a machine and enter or import all of the measured beam data for a photon energy on that machine, you can begin the beam modeling process for that photon energy.

Because the Pinnacle³ photon dose algorithm is model-based rather than measurement-based, the software uses the imported measured data only for comparison with the dose profile it calculates for the same measurement geometry. By iteratively adjusting the dose model parameters and evaluating the quality of the match between the measured and computed depth doses and profiles, you can create a dose model which accurately characterizes the output of your machine.

Pinnacle³ provides you with various levels of control over the modeling process. You can manually model a beam by iteratively changing the parameters and reviewing the resulting dose distributions, or you can use the automatic modeling options to let the software optimize the parameters.

You can also use both the manual and automatic options during the modeling process. For example, you can manually adjust a parameter until the profile looks reasonable and then choose to use an optimization script to “fine-tune” that parameter.

> **NOTE**
> The software does not provide the ability to revert to previous photon model parameter settings. You should keep a record of the parameter settings used each time you compute the profiles so that you can revert to previous settings if the new settings worsen the match between the computed and measured curves.

A library of models is available for various machines and energies. These models can be used as a starting point for the model optimization process to decrease the length of time required for modeling.

> **NOTE**
> Whether you are modeling your beam using the automodeling options or manually modeling the beam, it is a good idea to use a model from the model library as a starting point.

While individual institutions may determine their own acceptance criteria for their modeled data, we recommend using the criteria outlined by Van Dyk, et al., in their publication titled, “Commissioning and quality assurance of treatment planning computers.”

Add photon energies for a machine

Before you can begin the modeling process, you must add the available photon energies for the machine.

1 Click the **Photon Physics Tool** button in the **Physics Tools** window. The **Photon Physics Tool** window appears.

2

3 Click the **Add** button beneath the **Energy List** in the **Photon Physics Tool** window. The software warns you that you are about to add a new photon energy.

4 Click the **OK** button to continue.

5 Click the **Edit** button beneath the **Energy List** in the **Photon Physics Tool** window. The **Machine Photon Energy Editor** window appears.

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

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

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

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

10 Select the fluence-shaping mode for this energy from the **Fluence Mode ID** option list:

- **None**—A fluence mode ID is not assigned to this energy.
- **Flattening Filter Free (FFF)**—The software appends “FFF” to the name in the **Energy Name** field to indicate that this energy uses the Flattening Filter Free fluence mode ID.
- **Stereotactic Radiosurgery (SRS)**—The software appends “SRS” to the name in the **Energy Name** field to indicate that this energy uses the Stereotactic Radiosurgery fluence mode ID.

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

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

12 In the **Default Dose Rate** option list, select the default dose rate for beams that use this energy.

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

14 Click the **Save All Machines** button in the **Photon Physics Tool** window to save the energy information before proceeding.

After you create the photon energies for the machine, you should import the measured beam data for those energies. The process for importing measured beam data is described in the *Importing and Entering Measured Beam Data* chapter.

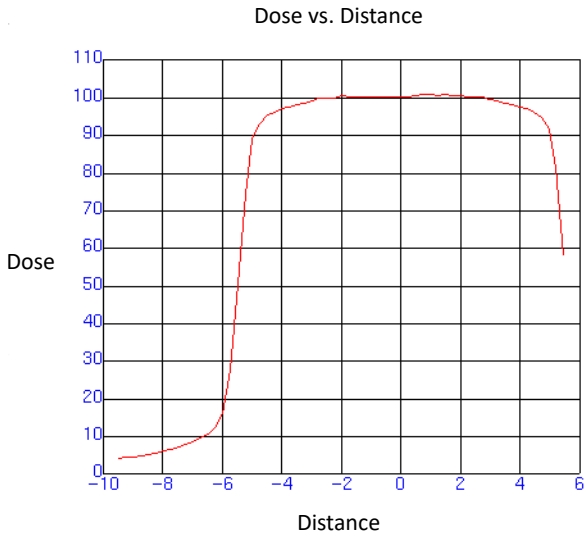
Evaluate measured data for automodeling

Before you begin the modeling process, you should evaluate the measured data you imported to determine whether it is suitable for automodeling. If there are problems with the data, you may need to use the Profile tools to correct the problems or you may need to remeasure your data.

> **NOTE**
> It is a good idea to use the following procedure to evaluate your data even if you are not using the automodeling functions. You will obtain a better model if the rules used to evaluate the data for automodeling are also used when manually modeling the data.

1 In the **Photon Physics** window, click the **Edit** button under the **Profile List**. The **Machine Data Editor** window appears.

If there is a problem with the data that will create problems during automodeling, a message appears in red at the bottom of the window. To see the cause of the problem, click the **View Problems** button for a description of the problem and an indication of how the problem can be fixed. For instance, in the example below, the data does not extend into the tails in the +X direction of the profile. This could be fixed by using the **Mirror** option in the Profile tools to mirror the data around the central axis.



2 Leave the **Machine Data Editor** open and also open the **Photon Physics Tool** window so that you can see both the **Photon Physics Tool** window and the lower half of the **Machine Data Editor** at the same time.

3 Select the first measurement geometry in the **Measurement Geometry List**.

4 Select each profile in the **Profile List** and determine whether there is a problem with the profile.

> **NOTE**
> Any profile that is unsuitable for automodeling will not be evaluated for automodeling.

5 If there is a problem with the profile, determine the cause of the problem and, if possible, correct the problem using the Profile tools. For more details about the Profile tools, see the *Importing and Entering Measured Beam Data* chapter.

6 Repeat steps 3-5 for each measurement geometry and measured profile.

Once you have determined that your measured data is acceptable, you can begin the modeling process as described in the following sections.

Import a model from the model library

The Model Library lets you access stored photon models for various types of machines. The models are defined for a given machine type and energy. They can be used as a starting point for the modeling process for your machine.

Whether you are modeling your beam using the automodeling options or by manually modeling the beam, it is a good idea to use a model from the Model Library as a starting point.

CAUTION
The machine models in this library are intended to be used as a starting point for generating a model for your machine. Do not use these models without first comparing the computed profiles generated with these models to your measured profiles.

1 In the **Photon Physics Tool** window, select the machine and energy for which you want to copy a model.

2 Click the **Model** button. The **Photon Model Editor** window appears.

3 Click the **Access Model Library** button. The **Photon Model Library** window appears.

4 Select the machine type and energy from the model library on the right side of the window. A description of the model appears in the top of the window.

5 Click the **Copy From Library To Current Model** button to copy the model parameters.

6 Click the **Dismiss** button to close the **Photon Model Library** window.

Before adjusting any of the model parameters, compute the profiles for all measurement geometries as described in the following section.

Compute depth doses and X and Y profiles

By comparing computed depth doses and X and Y profiles against the measured depth doses and profiles for your machine, you can determine how well the software model matches your beam. Generally, you have to adjust the beam spectrum and the photon model parameters and recompute the profiles a number of times before you obtain a good match between the measured and computed depth doses and dose profiles.

1 In the **Photon Physics Tool** window, select the measurement geometry for which you want to compute the depth dose and/or profile(s).

2 Click the **Model** button. The **Photon Model Editor** window and the **Machine Data Model** window appear.

3 Depending upon the field size for which you are computing profiles and the resolution of the measured data, you may want to adjust the size of the phantom to reduce computation time and increase the resolution of the fluence grid to eliminate the effects of aliasing in the computed profiles. The phantom size and fluence grid fields are located on the **Phantom** tab of the **Photon Model Editor** window.

   The fluence grid resolution can be increased to 0.2 cm to reduce or eliminate the “stair step” effect apparent in computed profiles for small field sizes.

   When the fluence grid resolution is increased and the default water phantom size (50 cm x 50 cm) is used, a large amount of memory is required for computation, and the system may be unable to complete the calculation without running out of memory. To remedy this, decrease the phantom size as much as possible to decrease the total number of voxels in which the fluence must be computed. For example, if you are computing profiles for a 4 cm x 4 cm field and you have a profile measured at 20 cm, you can decrease the **Lateral** size to 20 and the **Depth** to 30.

   NOTE
   The fluence grid resolution should not be coarser than 0.4 cm.

4 When you are done modeling and are ready to compute output factors, set the **Phantom Size Lateral** and **Depth** values back to larger values (we recommend 50 cm x 50 cm). If output factors are computed with a phantom that is too shallow or too narrow, the scatter can be underestimated during dose computation.

5 In the **Machine Data Model** window, click the **Compute Profiles** button. The **Compute Profiles** window appears.

6 Select the profiles you want to compute.

   Use the **Yes/No** buttons to choose whether to compute each profile. To reduce computation time, you may want to limit the number of profiles you compute at any one time by selecting **Yes** for only those profiles you need for comparison.

7 Click the **Compute Profiles** button. When the computation is complete, the profiles appear in the **Machine Data Model** window.

NOTE
If you try to compute a profile for an invalid field size, a message appears. Field sizes may be invalid because the values entered for jaw limits, jaw limit precision, or the wedge-specific jaw limits do not allow for the specified measurement geometry. If this happens, you must fix the error before proceeding by correcting the measurement geometry or the machine limits.

8 To see one of the profiles in more detail, click the **Detail** button. The **Profile Statistics** window displays the measured and computed profiles.

You can change the profile that appears by selecting a different geometry from the **Geometry** option list or a different profile from the **Profile** option list.

You can enter a value in the **Connect at** field based on the profile type:

- For depth dose curves, you can select the point at which the measured and computed profiles are connected by specifying a depth in the **Connect at** field. Typically this should be set to 10 cm.
- For cross beam profiles, you can select the point at which the measured and computed profiles are connected by specifying a position in the **Connect at** field. Typically, you should set the value to 0 cm (central axis) or, for asymmetric fields, normalize the plot to the center of the field.

NOTE
It is important set the **Connect at** field to the appropriate normalization point for asymmetric fields if you plan to use an automodeling sequence on the profile.

The machine data comparison table lists the measured and computed dose for each depth or point in the profile and lists the absolute difference and the percent error between the measured and computed values. The absolute difference is computed using the following equation:

$$Diff = Computed\ dose - Measured\ dose$$

The percent error for profiles is computed using the following equation.

$$\%\ Error = \frac{Computed\ dose - Measured\ dose}{Central\ axis\ dose} \cdot 100\%$$

The percent error for a depth dose is computed using the following equation:

$$\%\ Error = \frac{Computed\ dose - Measured\ dose}{Maximum\ depth\ dose} \cdot 100\%$$

In addition, errors are reported for regions of the depth doses and cross beam profiles that correspond to the parameter set regions. The **Mean Error**, **Mean Square Error**, and **Standard Deviation** can be used to assess the overall fit in a particular region. The **Length** for that region indicates the total “length” of the profiles that were used to obtain the error values.

9 Determine whether there is a good match between the computed and measured profiles by comparing them and assessing the difference, percent error, and distance to agreement between the measured and computed dose. Guidelines on evaluating the match are provided in the following sections.

   If the two curves match well, repeat this procedure for the next measurement geometry.

   If the two curves do not match well, adjust the spectrum or the photon model parameters and recompute the profile. The following sections describe how to adjust the spectrum or the photon model parameters.

10 When you finish modeling the beam, click the **Save Current Machine** button to save the modeled beam data.

Optimize the photon model parameters using the automodeler

Pinnacle[3] provides an automodeling tool that can optimize the photon model parameters for you. Use the automodeler to generate a model for you or to fine-tune a model that you created.

The following questions and answers give you an idea of how to use the automodeler. The rest of this section explains the automodeling process and sequences in detail.

1 Is this a new beam or one with old models?
   - If new, copy in a model from the model library and then compute all fields.
   - If old, reduce the models to a single model for all beams and then compute all fields.

2 Does the model look good?
   - If yes, you do not need to use the automodeling sequences. Skip the rest of these steps.
   - If the model needs a great deal of improvement, tune the entire model. For example, use the **E_TuneAllInSections** sequence.

3 Do the depth dose curves look good for open fields?
   a If the depth dose curves need improvement, run the **FineTuneECAndSpectrum** sequence.
   b Next, check the buildup. If the buildup needs improvement, run the **FineTuneECInParallel** or **FineTuneECInSections** sequence.

4 Do the cross-beam profiles look good for open fields?

   If the profiles need improvement, run the **FineTuneCrossBeam** sequence.

5 Do the wedged fields look good?
   - If the wedged fields need a great deal of improvement, split off the models for wedges and run the **FineTuneAllForWedge** sequence on the appropriate models. Next, check the wedge profiles. If the profiles need some improvement, run the **FineTuneModifierScatter** sequence.
   - If the wedges look adequate but could be improved, run the **FineTuneModelForOpenAndWedgedFields** sequence. Next, check the wedge profiles. If the profiles need improvement, split off the models for wedges and run the **FineTuneAllForWedge** sequence. When you finish, check the wedge profiles again. If the profiles still need improvement, run the **FineTuneModifierScatter** sequence.

See the *Pinnacle[3] Physics Reference Guide* for information about the automodeling sequences.

Prepare to use the automodeler

Before using the automodeler to generate a model, you should do the following:

- **Evaluate your measured data.** Make sure it is suitable for automodeling using the procedure in *Evaluate measured data for automodeling*. Cross-beam profiles must have at least 2.0 cm outside the field to be used for automodeling. If your current profiles do not reach this distance, you may want to remeasure them. The profile editor can be used to add points outside the field; however, this is not recommended unless you know the correct values.

NOTE
Profiles that are unsuitable for automodeling will not be used in any optimization sequences.

- **Check the resolution of your measured profiles.** A measurement resolution of 0.20 cm is recommended. You can use data measured with higher resolutions, but the automodeler will be slower. If the measurement resolution of your data is less than 0.10 cm, you can change it using the **Resample** option in the **Profile Tools** window. The use of lower-resolution data (greater than 0.20 cm) can result in poor models and inaccurate results. Resampling to a finer resolution yields no improvements because no information is added. Automodeling of the electron contamination cross-beam parameter is possible only if the data set contains cross-beam profiles at a depth below the maximum depth of electron contamination. We recommend that you include a d_{max} profile in your data set. If no d_{max} profiles exist, set the Off-Axis Coefficient (OAC) to zero. (Electron contamination is homogeneous.)

WARNING
If you use the FineTuneModelForFieldSize sequence, do not adjust the C_1, C_2, and C_3 variables. For information on these variables, see the *Photon Beam Physics & Measured Data Requirements* chapter in the *Pinnacle³ Physics Reference Guide*.

WARNING
C_1, C_2, and C_3 are used to produce a function of field size. They should be the same for each model when the models have been created for each field size.

If you have photon models that are in the same wedge group but have different field sizes, you cannot assign different values for C_1, C_2, and C_3. It causes problems in the interpolation over field size for the different field-size specific models.

Improve the speed of automodeling

You can decrease the amount of time required for automodeling in a number of ways:

- The amount of data to be analyzed affects the time needed for automodeling. Using more field sizes than recommended in the *Pinnacle³ Physics Reference Guide* has the greatest impact on automodeling time because a TERMA (Total Energy Released per unit Mass) computation must be performed for each field size throughout the process. If you have measured both X and Y profiles, you should include these in the modeling data set.

CAUTION
If you have measured only X or only Y profiles, the automodeler will only optimize the Effective Source Size in the direction of the measured profiles. In such cases, you must manually change the source size for the direction in which you have not measured profiles to match the computed value for the other. Also, it is important that the orientation of the X and Y profiles be set correctly so that the in-plane and cross-plane effective source size model parameters are modeled correctly.

- If you have substantially more measurement geometries than you want to use for automodeling, make a copy of your current machine in the Photon Physics tool. Delete any undesired field sizes from the machine copy and begin automodeling. When you finish

modeling, copy the model to the original machine using the Model Library, compute all profiles, and compare the model-generated profiles against all your measured profiles.

- Dismiss the model window (the window that shows the measured and computed profiles) before starting any optimization sequence. Having this window open during optimization can significantly delay the process. Reopen the window to compute profiles and evaluate the model.

Generate a model with the automodeler

Before you begin modeling with the automodeler, you should complete the following initial steps to make the process easier.

- Copy a model from the model library to the current model or select an initial energy spectrum for modeling.

CAUTION
If the exact energy for your machine is not available, select the spectrum with the nominal energy closest to, but greater than, your beam's nominal energy. You must select a spectrum that has non-zero entries in the energy bin of the highest expected energy. For example, for an 18 MV beam you would use a spectrum that does not have zero for the 20 MV spectrum entry.

- If you have loaded part of a machine model from a previous version of software, you should begin by deleting ALL models except the **All Field Sizes** model.
- Specify the **Max Depth** parameter on the **Buildup** tab of the **Photon Model Editor** window. The **Max Depth** defines the maximum depth receiving electron contamination dose. The recommended starting values are d_{max} plus 1.0 to 1.5 cm for lower energies (4-8 MV) and d_{max} plus 2.0 cm for higher energies.
- The connection depth of the depth dose profiles is important during automodeling of the electron contamination. This depth should be between 5 cm and 10 cm, and roughly 2 cm beyond the maximum depth of electron contamination dose. The connection depth is set in the **Profile Statistics** window and is set for each depth dose independently.

Once you have completed these initial steps, you are ready to start the automodeling process.

1 In the **Photon Physics Tool** window click the **Model** button. The **Photon Model Editor** window appears.

2 Click the **Auto-Modeling** button. If you have not used the automodeling option before, the **Select Optimization Sequence** window appears.

3 Select a sequence from the list of optimization sequence files and then click the **OK** button to load the sequence. These sequences optimize specific parameters of the model.

NOTE
Use the automodeling sequences that are appropriate to the situation. A common mistake is to use a sequence intended for all field sizes on a model intended to be used for a single field size. We recommend that you start with a single model for all open fields and one for each of your wedges.

For a complete list of sequences, see the *Photon Beam Physics & Measured Data Requirements* chapter in the *Pinnacle³ Physics Reference Guide*.

4 After you select a sequence, specify automodeling options in the **Optimization Sequencer** window that appears.

The **Optimization Sequencer** window gives you access to these automodeling options:

- **State**—View the currently selected state or select a state.
- **Save Machine on State Transition**—Specify whether to save the automodeling results after each step in the sequence is completed.
- **Tolerance Scale Factor**—Override the normal tolerance value for the current state. If a given step is not yielding acceptable results, this value may be decreased and the state optimized again. Generally, this value does not need to be changed.
- **Start Optimization**—Starts the optimization for the current sequence.
- **Optimize Current State**—Optimizes the currently selected state.
- **Load New Optimization Sequence**—Select a new optimization sequence.
- **View Parameter Status and View Selected Data**—View information about the status of the automodeling process. For more information, see *View information about the automodeling process*.

5 Click the **Start Optimization** button. The software runs through the optimization process and generates an optimized model using the measured data available.

NOTE
If you are using a cone radius model instead of arbitrary fluence, examine the cone radius of the model after the automodeler is finished. If necessary, return the cone radius to a more realistic value, then recompute the profiles and continue automodeling to improve any remaining deficiencies in the model.

NOTE
If absolutely necessary, you can cancel any optimization sequence while it is running. You can then save either the model you used at the beginning of the sequence or the best fit obtained during optimization of the current state.

If you have measured only X or only Y profiles, the automodeler may generate different X and Y values for the **Effective Source Size**. If this happens, manually change the source size for the direction in which you have not measured profiles to match the computed value for the other.

View information about the automodeling process

During the automodeling process, you can review the status of the parameters by clicking the **View Parameter Status** button on the **Optimization Sequencer** window. If the parameter is being adjusted during the current stage of the automodeling process, **true** appears in the **Optimizing** column.

You can also determine which profiles are being used at each stage of the optimization process by clicking the **View Selected Data** button. The **Selected Data** window appears and displays each profile with a symbol to its left. These symbols are described in the table below.

Symbol	Indicates
+	The profile is being used for the current stage of automodeling.
-	The profile is not being used for the current stage of automodeling.
*	The profile is not suitable for automodeling.

Automodeling for wedged fields

Once you have a satisfactory model for the open field sizes, you can model the wedged fields. Repeat the following steps for each wedge.

1 If the wedges need a great deal of improvement, split off the models for wedges and run the **FineTuneAllForWedge** sequence.

2 Check the wedge profiles.

- If the profiles need improvement, run the **FineTuneModifierScatter** sequence.
- If the wedges look adequate but could be improved, run the **FineTuneModelForOpenAndWedgedFields** sequence.

3 Check the wedge profiles. If the profiles need improvement, split off the models for wedges and run the **FineTuneAllForWedge** sequence.

4 Check the wedge profiles. If the profiles still need improvement, run the **FineTuneModifierScatter** sequence.

> **NOTE**
> If you have measured only X or only Y profiles, the automodeler may generate different X and Y values for the **Effective Source Size**. If this happens, manually change the source size for the direction in which you have not measured profiles to match the computed value for the other.

Manually optimize the photon model parameters

All of the parameters may also be manually specified and adjusted. The following sections describe how to manually adjust the photon model parameters for a beam.

Beam modeling sequence overview

1 Select the initial spectrum to use for your beam and leave the other model parameters at their default values. Be sure to turn off the **Electron Contamination** parameters before adjusting the spectrum.

2 Compare the measured and computed depth doses and adjust the spectrum first for the 10 cm x 10 cm field size until there is a reasonably good match and then repeat this step for all field sizes. Ignore the match in electron contamination region.

> **NOTE**
> It may be difficult to get very close matches until some of the other parameters have been set to approximately correct values, so do not spend too much time attempting to get a perfect match.

3 Do a coarse adjustment of the **Out of Field** parameters using cross-beam profiles for all field sizes and depths. Adjust the **Gaussian Height**, **Gaussian Width**, and **Jaw Transmission** factors until the fit is within 5% in the tails of the cross-beam profiles.

4 Do a coarse adjustment of the **In Field** parameters using large field sizes at depths of 5 cm and greater. Adjust the **Off-Axis Softening**, **Fluence Increase/cm**, and **Cone Radius** parameters until the fit is within 5% in the high dose/low dose-gradient region of the profiles.

5 Do a coarse adjustment of the **Effective Source Size** using all cross-beam profiles at depths of 5 cm and greater. Evaluate the fit between the measured and computed profiles in the high dose-gradient region of the profiles.

6 Repeat steps 2 through 5 to fine-tune these parameters.

7 Turn on the **Electron Contamination** and set the **Max Depth** parameter to the depth at which the electron contamination no longer has an effect (typically 1 to 2 cm below d_{max}).

8 Use one of the automodeling sequences to adjust the **Electron Contamination** parameters.

9 Reset the **Phantom Size** to 50 cm x 50 cm and set the **Fluence Grid Resolution** to 0.4 cm.

10 Compute all profiles and all field sizes and compare the match for all profiles.

Once you have a model for all open field sizes, use that model as a starting point for the wedged fields and follow the same procedure as that described above.

Select the initial spectrum for beam modeling

If you are not using a model from the model library as a starting point, you have to select an initial spectrum for modeling. A number of published and interpolated spectra are available in the software. Select a spectrum of the same energy as your beam if one is available. If the exact energy is not available, select the spectrum with the nominal energy closest to but greater than your beam's nominal energy.

1 Select the machine and energy for which you want to model the beam from the **Machine List** and **Energy List**.

2 In the **Photon Physics Tool** window click the **Model** button. The **Photon Model Editor** and the **Machine Data Model** windows appear.

3 On the **Depth Dose** tab in the **Photon Model Editor** window, click the **Published Spectra** button. The **Published Photon Spectra** window appears.

4 Select the spectrum with the correct energy for the beam you are modeling and then click the **Copy into current spectrum** button. The spectrum appears on the **Depth Dose** tab in the **Photon Model Editor** window.

Model the spectrum

You model the spectrum by comparing computed and measured open field depth dose curves and adjusting the spectrum until the shape of the two curves matches well. You have to compare the measured and computed open field depth doses for the 5 cm x 5 cm, 10 cm x 10 cm, 20 cm x 20 cm, 30 cm x 30 cm, 20 cm x 5 cm, and 5 cm x 20 cm field sizes. Also include 40 cm x 40 cm or the largest possible field size. You should also compute and compare any additional open field depth doses you measured.

1 Start to model the beam spectrum by computing the depth dose profile for a 10 cm x 10 cm field size.

> **NOTE**
> For information on how to select and compute profiles, refer to the *Compute depth doses and X and Y profiles* section.

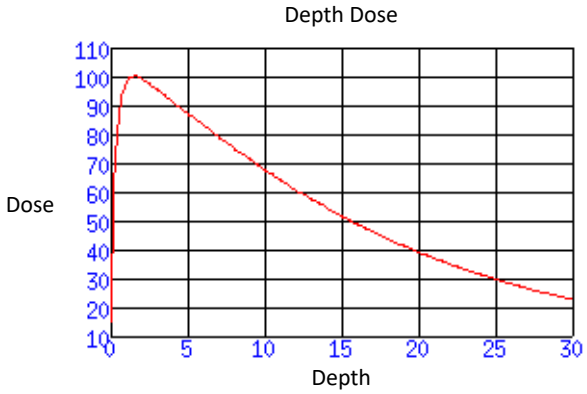
2 In the **Machine Data Model** window click the **Detail** button. The **Profile Statistics** window appears with a detailed view of the computed and measured depth doses.

3 In the **Connect at** field, specify a depth of 10 cm for connecting the measured and computed depth dose curves.

4 Compare the computed depth dose to the measured depth dose.

Because the **Electron Contamination** parameters should be used to handle the electron contamination region, you should compare the shape of the curves starting at 1 to 2 cm deeper

than the measured d_{max} dose. For example, if you were comparing a computed profile to the measured depth dose shown below, you should ignore the region up to 3 cm.



WARNING
Do not adjust the low energy photons in the spectrum to improve the match in the electron contamination region. If you adjust the spectrum so that the computed and measured depth doses match well in the electron contamination region, incorrect dose calculations may result.

5 If the shape of the computed and measured curves does not match well, adjust the beam spectrum by increasing or decreasing the number of relative photons for energies in the region of the spectrum that does not match well.

If the Depth Doses do not match at

- **Deeper Depths**—If the tail of the computed depth dose curve is higher than the tail of the measured depth dose, adjust the spectrum by decreasing the relative number of photons for high energies. If the tail of the computed depth dose curve is lower than the tail of the measured depth dose, adjust the spectrum by increasing the relative number of photons for high energies.
- **Intermediate Depths**—If the tails match well but the middle of the computed depth dose curve is higher than the middle of the measured depth dose, adjust the spectrum by decreasing the relative number of photons for middle range energies. If the tails match well but the middle of the computed depth dose curve is lower than the middle of the measured depth dose, adjust the spectrum by increasing the relative number of photons for middle range energies.

CAUTION
You cannot arbitrarily add energies to the beam spectrum; you must select energies that correspond to available dose-spread kernels. The default spectra are filled with all possible valid energies up to the nominal energy. If you have measured the spectrum on your machine and want to enter your own data, you must make certain that the spectrum is sampled into the correct energy bins. If it is not, you have to re-sample the spectrum such that you conserve mean-energy.

To change the number of relative photons for an energy, in the Beam Energy Spectrum table click in the field you want to edit. Then click in the field that appears above the table and type

in the value. Click the green check mark or press **Enter** to accept the value you typed. Click the red “x” to cancel the change to the value of the current field.

6 Recompute the depth dose and evaluate whether the change improved or degraded the fit between the measured and computed depth doses. Repeat steps 4 and 5 until the shape of the computed depth dose closely matches the shape of the measured depth dose for the field.

7 Repeat steps 2-6 for all open field depth dose profiles available.

NOTE
It is sometimes difficult to achieve the desired match between measured and computed dose profiles before the other model parameters have been set to approximately correct values. For example, the depth dose fit can be affected by both the off-axis softening parameter and the fluence increase per centimeter. Therefore, you should not spend a great deal of time trying to get a perfect fit the first time. Get it as close as possible without extreme effort for the first attempt, then tune the other parameters and revisit the spectrum again.

Model the in field photon model parameters

To access the in field photon model parameters, click the **In Field** tab in the **Photon Model Editor** window.

The flattening filter attenuation changes both the photon fluence and the distribution of the photon energies as functions of off-axis distance. You can model the change to photon fluence using either cone radius or arbitrary profile. You can model the change to the distribution of the photon energies with the **Spectral Off-Axis Softening Factor** parameter. See the *Photon Beam Physics & Measured Data Requirements* chapter of the *Pinnacle³ Physics Reference Guide* for more information.

> **NOTE**
> If you change the flattening filter attenuation **Modeled As** option from **Cone** to **Arbitrary Profile** or vice versa, the change does not affect all of the models in the current energy. The change only affects models that have the same wedge state as the current model (for example, all open field models if the current model is an open field or all 30 degree wedge models if the current model is a 30 degree wedge).

Arbitrary profile

The arbitrary profile option lets you create a non-linear fluence profile.

1 Select **Arbitrary Profile** from the **Modeled As** option list. The **Edit Fluence Filter Profile** window appears. A default arbitrary profile appears in the window.

> **NOTE**
> If the **Arbitrary Profile** option was already selected in the **Modeled As** option list, the **Edit Fluence Filter Profile** window does not open automatically. Click the **Arbitrary Profile Editor** button to open the window.

2 Review the arbitrary profile, and edit the profile, if necessary.

Use the **Ins Before** and **Ins After** buttons to add points to the profile. Click in the cells in the table to edit values for the points. (Enter **Radius** values in cm.) Use the delete buttons to delete points from the profile.

To add many points to the profile at once, enter the number of points you want the profile to contain in the **Number of points** field and click the **Create Arbitrary Profile** button. The new profile appears in the window. (The previous profile is overwritten.) The default profile is linear with a slope of 0.6% per cm.

> **NOTE**
> For each point in the profile, the radius must be 0 cm–50 cm and the incident fluence value must be 0.25–1.5 or you will not be able to compute dose.

3 On the **In Field** tab, adjust the **Limit Profile Edge for Auto-Modeling by** value, if necessary. The default value is 0.5 cm. This value moves the boundary between the penumbra and the high dose region toward the central axis of the profile to remove data points that might be included

from the penumbra. This adjustment is applied to all cross beam profiles for all measurement geometries and only affects automodeling of the arbitrary fluence profile.

4 Automodel the profile using the arbitrary profile states in the E_TuneAllInSection sequence.

5 Review the automodeled profile and adjust the points, if necessary.

6 When you finish, click the **Save All Machines** button in the **Photon Physics Tool** window to save the modeled data.

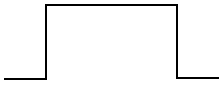
Cone radius

Select **Cone** from the **Modeled As** option list to display the cone radius fields.

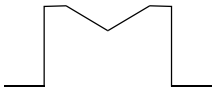
The **Fluence Increase/cm** controls the rate of increase in the relative energy fluence as the off-axis distance increases until you reach the cone radius. The off-axis distance is measured in the isocentric plane orthogonal to the beam.

The model assumes the initial relative energy fluence profile is flat across the field. If the profile is not flat, you can use the **Fluence Increase/cm** parameter to define the rate of change in the fluence profile as a function of distance from the central axis.

The effect of the **Fluence Increase/cm** parameter is to change the angle of a cone which is removed from the relative energy fluence to mimic the effects of the flattening filter.



Initial relative energy fluence profile



Increasing the Fluence Increase/cm increases the cone angle

Decreasing the Fluence Increase/cm decreases the cone angle

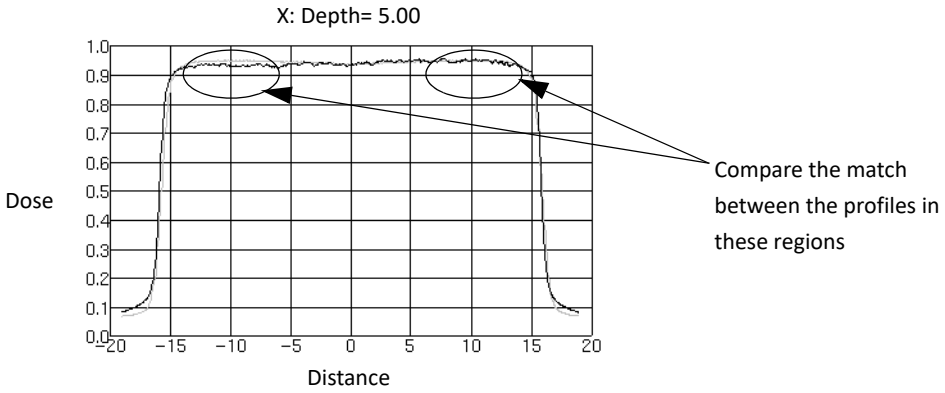
The **Cone Radius** parameter sets the radius from the central axis after which you see no additional increase or decrease to the magnitude of the fluence. Once the cone radius is reached, the relative fluence is held constant and no longer increases or decreases.

The incident fluence per centimeter is tuned using X and Y profiles for a large field size (30 cm x 30 cm or larger). This parameter affects dose profiles in a similar fashion across all depths.

1 Begin with the **Fluence Increase/cm** set to zero.

2 Compute X and Y profiles for a large field size (at least 30 cm x 30 cm) at 5 cm, 10 cm, and 20 cm deep and compare the computed and measured profiles.

NOTE
Do not use d_{max} profiles when modeling the incident fluence.



For the first approximation, observe the percent error in the highlighted region illustrated above, using the **Detail** window and all depths for which profiles are available. Then use the following equation to calculate the fluence increase per centimeter:

$$\text{Fluence Inc/cm} = (\%\text{error} / \text{x cm}) \cdot (1/100\%)$$

Where *x* is a representative distance off of the central axis as observed on the graph axis, and *%error* is a representative error observed in the regions highlighted above. When using this equation, ignore values that are outside the cone radius.

3 If the profiles do not match well, iteratively adjust the **Fluence Increase/cm** until you obtain a good match between the computed and measured profiles.

4 To set the cone radius you need to identify break-points in the profile. If cone radius needs to be set, you will see a clearly defined peak in the profile well before the shoulder region. Set this parameter to the off axis distance of the clearly defined peak if it is present. Otherwise, do not modify the cone radius.

5 When you finish, click the **Save All Machines** button in the **Photon Physics Tool** window to save the modeled data.

Adjust the off-axis softening factor

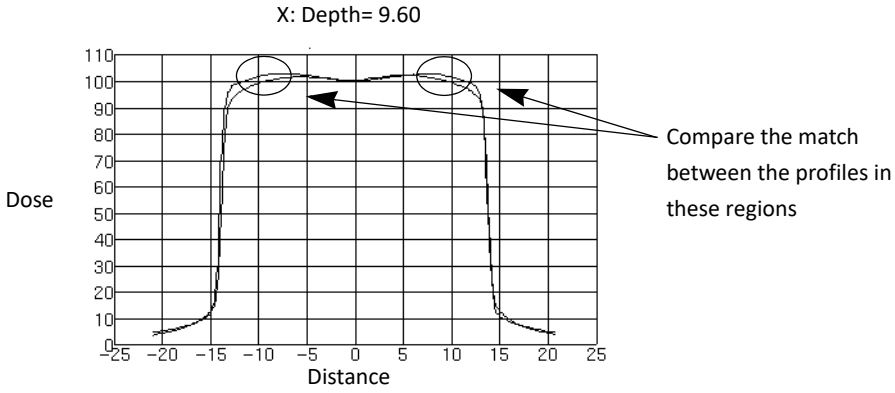
The off-axis softening factor “softens” the beam as the distance from the central axis increases. Softening refers to a decrease in the number of high energy photons relative to low energy ones and is primarily caused by photon absorption in the flattening filter.

When the off-axis softening factor is set to a positive value, the mean-energy decreases as the off-axis angle increases. (The exact values of the mean-energy can be seen by clicking the **View Off Axis Softening** button.) This decreased mean-energy is most apparent in the increased relative dose in the low dose-gradient, high-dose region away from the central axis near the surface. As you increase the off-axis softening factor, you increase the size of the horns observed in cross-beam profiles near the surface.

The effects of beam softening are not linear regarding the TERMA calculation, and therefore you should tune this parameter first before trying to adjust the **Fluence Increase/cm** parameter. It is useful to set the fluence increase parameter to zero, and then adjust the off-axis softening factor until a similar error is observed at all depths for a large field in a region around 10 cm away from the central axis. It does not matter whether the error observed is positive or negative. If it is constant, it can be corrected using the linear parameter **Fluence Increase/cm**.

> **NOTE**
> You have to compute profiles for the largest field you have measured at approximately 5 cm, 10 cm, and 20 cm depths.

1 Compute the profiles at 5 cm, 10 cm, and 20 cm depths using a **Fluence Increase/cm** of 0 and a **Spectral Off-Axis Softening Factor** of 12.

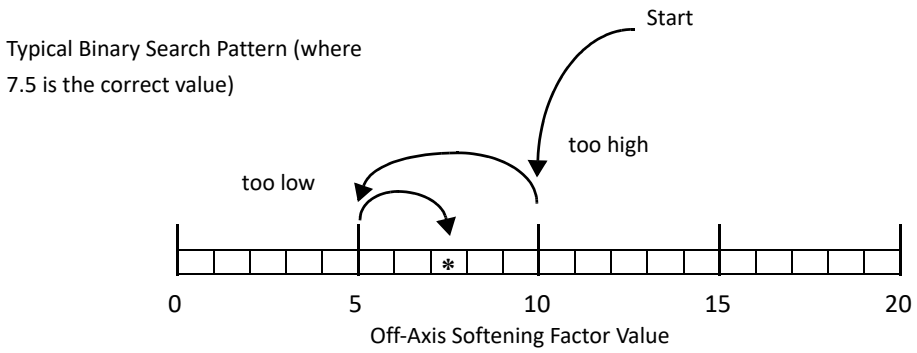


2 Observe the error between the measured and computed curves in the regions highlighted in the illustration above. The goal is to obtain constant error rather than an exact match. The error can be positive or negative, as long as it is similar for all three depths.

3 If the error is not similar, adjust the off-axis softening factor and recompute.

If the computed value is lower than the measured data at shallow depths and higher than the measured data at greater depths, increase the off-axis softening factor. If the computed values are high at shallow depths and low at greater depths, decrease the off-axis softening factor.

This parameter typically has values between 0 and 20. Changes to this parameter can be made by factors of 2. For the best results try a binary search where the search space is repeatedly split, as is illustrated below.



NOTE
Currently, the software does not provide the ability to revert to previous photon model parameter settings. You should keep a record of the parameter settings used each time you compute the profiles so that you can revert to previous settings if the new settings worsen the match between the computed and measured curves.

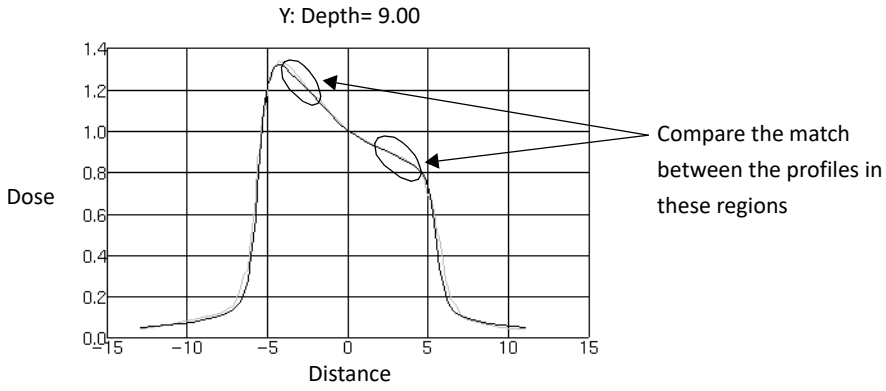
4 Repeat steps 2 and 3 for the given field size at all depths until you observe a constant error between the measured and computed profiles in the region illustrated in step 1.

Set the wedge/compensator scatter factor

The **Wedge/Compensator Scatter Factor** lets you adjust the amount of scatter produced from a given wedge. Typical values for the wedge scatter factor are: 0.5 for Varian machines and 0.2 for Elekta machines with an internal wedge. See the *Photon Beam Physics & Measured Data Requirements* chapter of the *Pinnacle³ Physics Reference Guide* for more information.

1 On the **In Field** tab in the **Photon Model Editor** window, set the **Wedge/Compensator Scatter Factor** to 0.5.

2 Compute dose profiles for the 30 cm x 30 cm field at all depths and compare the computed and measured profiles. Compare the match between the profiles in the low dose-gradient, high-dose region.



NOTE
If the computed profiles appear as if no wedge is present in the beam, it is due to an incorrect physical description of the wedge or to an improper wedge orientation in the current measurement geometry. You must identify the problem and fix it before proceeding.

Also, if you have problems getting the profiles to fit, verify that the central axis of the beam is 0 as characterized in the **Machine Wedge Physical Profile Editor** window. See the *Working with Machines and the Machine Database* chapter.

3 If the profiles do not match well, adjust the wedge scatter factor and recompute the dose profiles until you obtain a good match between the computed and measured profiles.

Model the out of field photon model parameters

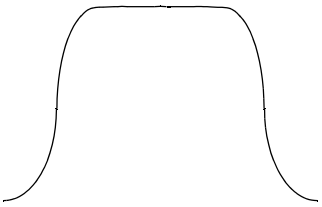
The penumbra and tails of the profiles are modeled with the **Out of Field** model parameters. The **Effective Source Size** parameters model the shape of the penumbra. The **Flattening Filter Scatter Source** parameters model the shape of the tails of the cross-beam dose profiles. The **Transmission Factors** parameters model the jaw or MLC transmission factors and adjust the height of the tail section of the profiles. You can model the jaws with one or two transmissions depending on whether or not the thicknesses are the same.

To access the out of field photon model parameters, click the **Out of Field** tab in the **Photon Model Editor** window. (See the *Photon Beam Physics & Measured Data Requirements* chapter of the *Pinnacle³ Physics Reference Guide* for more information about the Out of Field parameters.)

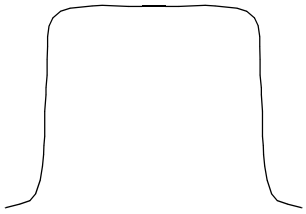
Set the effective source size

The software uses the effective source size for modeling the penumbra of a beam by blurring the incident fluence model. The effective source size should be tuned after getting acceptable matches between computed and measured data both inside and outside the field in the low dose-gradient regions.

Both X and Y profiles for a number of field sizes tune the effective source size. Changing the effective source size affects the shape of both the shoulders and the base of the X and Y profiles. Increasing the effective source size makes the shoulders and base of the profiles rounder. Decreasing the effective source size makes the shoulders and base of the profiles more square.



Use a larger effective source size to make the shoulders and base of the profiles more round

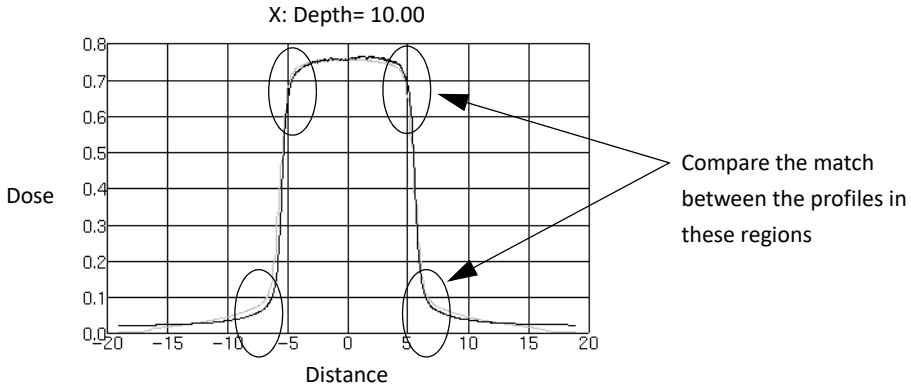


Use a smaller effective source size to make the shoulders and base of the profiles more square

Because the effective source size is linked to X and Y profiles, it is important that the collimator angle was in the correct orientation during data collection. Verify the orientation using the collimator graphic shown in the **Confirm Profile Import** window (see the *Importing and Entering Measured Beam Data* chapter). If your data was collected using a collimator angle that is not the default angle as defined in Pinnacle³, change the default angle to match the angle used during data collection so that your profiles can be modeled properly. (See *Enter collimator information* in the *Working with Machines and the Machine Database* chapter to change the collimator angle.) To use the original default collimator angle for planning, change the collimator angle back to the original setting after modeling but before commissioning.

1 In the **Photon Model Editor** window, reset the source size to 0.2 cm in the X (perpendicular to gantry axis) and Y (parallel to gantry axis) fields.

2 Compute X and Y profiles for the largest field at 10 cm depth and compare the computed and measured profiles. Compare the match between the measured and computed profiles in both the shoulders and the base of the high gradient region.

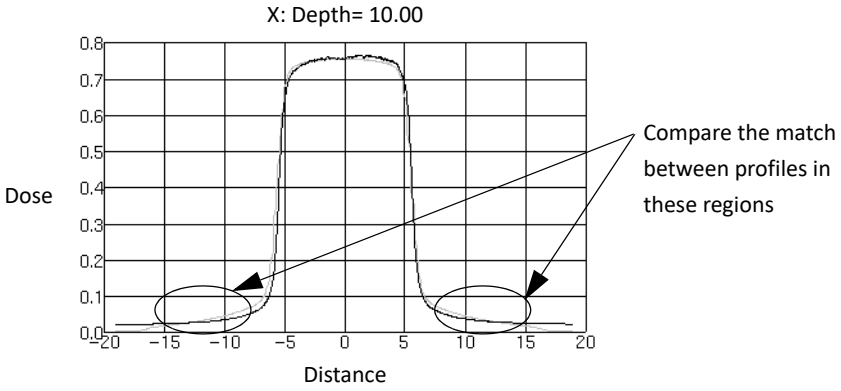


3 If the profiles do not match well, iteratively adjust the **Effective Source Size** until you obtain a good match between the computed and measured profiles.

Set the flattening filter scatter source

The **Flattening Filter Scatter Source** parameters control the model of the photon scatter from the flattening filter. This scatter is most visible in the tails of the cross-axis scans, but the software model takes this contribution into account across the entire beam. The scatter also affects the output factors. The software models this photon scatter source as a Gaussian curve. See the *Photon Beam Physics & Measured Data Requirements* chapter in the *Pinnacle³ Physics Reference Guide* for more information.

1 Compare the match between the tails of the measured and computed cross-axis scans.



2 If the profiles do not match well, iteratively adjust the Gaussian height and Gaussian width until you obtain a good match between the computed and measured profiles.

The **Gaussian Height** parameter defines the fraction of the central axis energy fluence that is due to the flattening filter scatter when the collimator jaws are wide open.

The **Gaussian Width** parameter specifies the width (in centimeters) of the Gaussian curve used to model the flattening filter scatter source.

Set the transmission factors

Compare the match between the tails of the measured and computed cross-axis scans (as shown in the graphic in the *Set the flattening filter scatter source* section). If the profiles do not match well, iteratively adjust the transmission factors following the procedure in this section until you obtain a good match between the computed and measured profiles.

> **NOTE**
> If you modify any of the transmission values, you invalidate the profiles for that model. Transmission factors cannot be edited for interpolated models.

1 Select an **XY Jaw Transmission Equal** option.

If you select **Yes**, you can enter one jaw transmission for both pairs of jaws. If you select **No**, you can enter a transmission for the top/bottom pair and the right/left pair.

> **NOTE**
> The **XY Jaw Transmission Equal** option does not appear for fixed jaw machines.

> **NOTE**
> If you set **MLC Replaces Jaws** to **Yes** in the MLC Editor, you can only set a single jaw transmission.

> **NOTE**
> If you change the **XY Jaw Transmission Equal** option, the change does not affect all of the models in the current energy. The change only affects models that have the same wedge state as the current model (for example, all open field models if the current model is an open field or all 30 degree wedge models if the current model is a 30 degree wedge).

2 Enter a jaw transmission value (0.001-0.200). The jaw transmission specifies the fraction of the energy fluence transmitted through the jaws. This models the actual jaw transmission.

3 Enter an MLC transmission value (0.001-1.000). The MLC transmission specifies the fraction of the energy fluence transmitted through the MLC leaves.

> **NOTE**
> The **MLC Transmission** field only appears if the machine has an MLC. You must enter a valid MLC transmission factor before commissioning. The MLC transmission cannot be edited during planning.

Model the electron contamination

Pinnacle^3 accounts for the electron contamination in a beam by adding electron dose to the photon dose. The electron dose is modeled as a modified exponential curve.

The electron contamination parameters control the amount of electron dose that is added, the maximum depth where the electrons have an effect, the rate of electron dose fall-off with respect to depth and the change in electron contamination with field size.

To access the electron contamination parameters, click the **Buildup** tab in the **Photon Model Editor** window.

1 Because the electron contamination region is a high dose gradient region, you should use a fine grid resolution when modeling the electron contamination parameters. A fine grid resolution allows you to see the effects of changes in the parameters on a greater number of points in the region, thus making it easier to determine the correct parameter settings. To make sure that you do not exceed the limits of the system's memory when calculating profiles, click the **Phantom** tab and set the **Modeling Geometry Options** so that the water phantom size is relatively small (for example, 20 cm x 20 cm) and use a **Fluence grid resolution** of 0.15 cm–0.2 cm for the calculation. Then, click the **Buildup** tab to display the electron contamination parameters.

2 Estimate the maximum depth of the electron contamination by adding 1.0 to the computed d_{max} value in a depth dose curve. Enter that value in the **Max Depth** field and compute the depth dose.

3 Select the EC Surface Dose parameter by observing the error between the computed and measured depth dose profiles at 0.25 cm depth. Convert the error from a percentage to a fraction. For example, if there is a 30% error, enter an **EC Surf Dose** parameter of 0.3.

4 Compute the depth dose for the given field size. Once the profiles are computed, observe the match between the measured and computed profiles and adjust the parameters.

   If the computed surface dose is too high, lower the EC Surface Dose value. If the computed surface dose is too low, increase the EC Surface Dose value.

5 Once the EC Surface Dose and Maximum Depth parameters appear to be about right, tune the **Depth Coefficient** parameter until the curves match well at a depth that is about half of the depth defined by the Maximum Depth parameter.

6 The remaining parameters are best tuned by using the automodeling parameters. Go to the automodeler and select one of the EC Optimization sequences to obtain the best fit for the Depth Fraction, Scale Fraction and C_1, C_2, and C_3 parameters.

Model the off-axis electron contamination

The Off-Axis Coefficient electron contamination parameter accounts for the decrease in the effects of the electron contamination as you move off-axis. Pinnacle^3 models this effect using a Gaussian curve (with radial symmetry). The Off-Axis Coefficient parameter controls the width of this Gaussian curve. When the Off-Axis Coefficient is set to 0, the Gaussian curve is flat. Increasing the value of this parameter allows you to shape the electron contamination dose magnitude; when set to a value of 50 or greater, the Gaussian curve becomes very narrow, effectively applying electron contamination only to the central axis.

CAUTION
The Off-Axis Coefficient parameter should not be adjusted until all other modeling is complete. Changing the Off-Axis Coefficient to any value other than zero while modeling at deeper depths may interfere with proper adjustment of the Fluence Increase/cm and Off-Axis Softening Factor parameters.

1 On the **Buildup** tab in the **Photon Model Editor** window, set the Off-Axis Coefficient to 0.

2 Compute X and Y profiles for the largest field size at d_{max} and compare the computed and measured profiles in the “tails” or “feet” of the profiles. You should also see some change inside the field for large field sizes.

3 If the profiles do not match well, iteratively adjust the Off-Axis Coefficient until you obtain a good match between the computed and measured profiles. Increasing the Off-Axis Coefficient lowers the tails. Decreasing it raises the tails.

Generate models for multiple field sizes

If you are unable to generate a single model that provides acceptable results for all field sizes, you can create multiple models for a beam energy. The **Model List** option allows you to generate models for multiple field sizes.

CAUTION
Create multiple models only if you cannot achieve acceptable matches between measured and computed dose profiles for the full range of field sizes.

When you use multiple models, the software interpolates models for intermediate field sizes. Therefore, if it is necessary to create multiple models, create and optimize a model for the smallest field size and a model for the largest field size. Once models exist for the smallest and largest field sizes, you can compare measured and computed profiles for intermediate field sizes and determine how well the interpolated models work for those field sizes. If you need more than two models for a given geometry, try to keep the parameters monotonic.

The interpolated models are marked with an asterisk in the **Model** field in the **Photon Model Editor** window. You cannot edit interpolated models. To edit the model parameters for an intermediate field size, you must create a model for that field size.

When using automodeling, some sequences should not be used for energies with multiple models. For more details on automodeling sequences, see the *Photon Beam Physics & Measured Data Requirements* chapter in the *Pinnacle³ Physics Reference Guide*.

1 From the **Measurement Geometry List**, select the field size for which you want to create a model.

2 In the **Photon Model Editor** window click the **Model List** button. The **Photon Model List** window appears. The interpolated model for the current field size has an asterisk.

3 To create a model for the field size, click the **Create New Model** button. A model is created using a copy of the interpolated parameters (if only one model exists, the parameters for that model are copied).

4 If you want to create a model that is specific to a wedge, you can copy the model to a wedge by clicking the **Copy to Wedge** button. From the window that appears, choose the wedge to which you want to copy the model, and then click the **OK** button.

> **NOTE**
> When copying a model to a wedge, ALL models for the current energy are copied, even if wedge profiles do not exist for those field sizes.

5 After you create a model for a given field size, complete the modeling process for the new model.

If you want to delete a model from the model list, select the model and then click the **Delete Current Model** button in the **Photon Model List** window.

Model dynamic wedges

1 Begin with a well-modeled open field.

2 Click the **Model** button in the **Photon Physics Tool** window. The **Photon Model Editor** and the **Machine Data Model** window appear.

3 Compute the profiles for the dynamic wedge using the open field. Click **Compute Profiles** in the **Machine Data Model** window. The wedge profiles appear.

4 Return to the **Wedge Editor** window and adjust the transmission factor to match the angle of the dose distribution profiles at all depths. If you adjust the transmission factor, you must recompute the profile.

   The transmission factor is the percentage of the energy that is not blocked by the wedge. The larger values within this range have a “flattening” effect on the profile.

5 Continue modeling as with physical wedges. Create a wedge-specific model only if necessary.

Validate the compensator dosimetry

In the planning tool the dose computation for compensators uses the “open-field” model. To validate the relative dosimetry for compensators, we recommend that you create a wedge-shaped compensator and measure cross-beam profiles and central axis depth dose for it in the Photon Physics tool prior to commissioning the machine.

1 Create a wedge-shaped compensator, but do not exceed the wedge limitations in Pinnacle^3.

2 Acquire measured data for validation. For information on the necessary data, see the *Photon Beam Physics & Measured Data Requirements* chapter of the *Pinnacle^3 Physics Reference Guide*.

3 In the Photon Physics tool, select the machine you want to use to validate the compensator and click the **Edit** button beneath the **Machine List**. The **Machine Editor** window appears.

4 In the **Machine Editor** window, click the **Wedges** button. The **Wedge Editor** window appears.

5 Create a wedge that is an accurate representation of the compensator (the shape, density, etc.). The wedge should use the “open-field” model; in other words, do not specify a wedge-specific model for the compensator.

   Design the wedge with the density of material that you will typically use for creating the compensator, and use a thickness range that you expect to use clinically. See *Define physical wedges for a machine* in the *Working with Machines and the Machine Database* chapter for information.

6 Import the measured data. Use the procedures in the *Importing and Entering Measured Beam Data* chapter.

7 Compute the profiles and validate the dosimetry. Use the procedures in *Compute depth doses and X and Y profiles* and *Set the wedge/compensator scatter factor*.

   You can modify the **Wedge/Compensator Scatter Factor** to adjust the gradient in the computed dose profiles. The scatter factor for open field will be used with the compensator. If the factor differs greatly between the compensator and other wedges, you may need to create separate models for the wedged fields.

CAUTION
After successful modeling, you should delete the wedge to avoid accidental use in Planning mode.

Print physics models

1 In the **Photon Model Editor** window, click the **Print** button. The **Photon Model Print Confirmation** window appears.

2 Select **Current Model** to print a report for only the current model, or select **All Models** to print a report for each model in the current geometry.

3 Click the **Print** button to print to the selected printer. To select a different printer, click the **Select Printer** button, select a different printer, and click the **Dismiss** button. Then click the **Print** button.

Photon beam output factor computation

After you model the beam shape, compute the output factors for the beam. To compute the output factors for a beam of a specific energy, enter the calibration output factor measurement and the relative output factor measurements. In addition to the open beam output factor computations, calculate the relative output factors for all wedged fields.

> **NOTE**
> When computing output factors, use as small a fluence grid as possible. The fluence grid used for computation is defined in the models.

For information on how Pinnacle^3 uses output factors and handles head scatter, see the *Photon Beam Physics & Measured Data Requirements* chapter in the *Pinnacle^3 Physics Reference Guide*.

Enter measured relative output factor data for open fields

1 In the **Photon Physics Tool** window, click the **Output Factors** button. The **Photon Output Factors** window appears.

> **NOTE**
> For fixed jaw machines, the **Edit Calibration Geometry** button appears beneath the **calibration point** paragraph in the **Photon Output Factors** window. Before computing output factors, go to *Calibration geometry for fixed jaw machines* to define the MLC geometry of the calibration field.

2 Enter the depth (in centimeters) at which the calibration output factor measurement and the relative output factor measurements were taken.

3 Enter the source to calibration point distance (in centimeters) used for the calibration output factor measurement.

4 Enter the dose per monitor unit at the calibration point.

5 To add field sizes to the list of measurement field sizes, click the **Add** button beneath the field sizes list.

6 To edit the measurement geometry and enter the relative output factor for the currently selected field size, click the **Edit** button. The **Photon Output Factor Measurement Geometry** window appears.

> **NOTE**
> If the MLC is set to track the XY jaws and the MLC leaves would violate the machine constraints if they were pushed, a warning is displayed at the bottom of this window.
>
> For fixed jaw machines, the **Closed MLC leaf offset from CAX** field and **MLC Rectangle** geometry fields appear below the **Angle** field. See *Import Scanditronix Wellhöfer, Multidata, Pinnacle Full ASCII, or TG23 format files* in the *Importing and Entering Measured Beam Data* chapter for information about these fields.

7 Enter the measurement geometry in the top, bottom, left and right jaw fields.

> **NOTE**
> For fixed jaw machines, you cannot edit the jaw positions.

8 If a wedge was used for the measurement, select the wedge from the **Wedge** option list and specify the wedge orientation. If you are using a dynamic wedge, you can also specify its angle. The angle is fixed for physical wedges.

9 Enter the **Relative Output Factor** for the field.

The **Relative Output Factor** for an open field is calculated using the equation:

$$\text{Relative Output Factor} = \frac{Dose_{FS}}{Dose_{CFS}}$$

where $Dose_{FS}$ is the measured dose for the given field size and $Dose_{CFS}$ is the measured dose for the calibration field.

The relative output factor for a wedged field is calculated using the equation:

$$\text{Relative Output Factor} = \frac{Dose_{WFS}}{Dose_{CFS}}$$

where $Dose_{WFS}$ is the measured dose for the given wedged field size and $Dose_{CFS}$ is the measured dose for the open calibration field.

> **NOTE**
> The ratio is not the wedge factor because $Dose_{CFS}$ is the fixed open calibration field dose.

10 From the **Photon Output Factors** window, select a new field size from the **Measurement Field Sizes** list and repeat steps 7-9 for each remaining field size.

11 When you are finished editing all of the field sizes, click the **Dismiss** button in the **Photon Output Factor Measurement Geometry** window.

Calibration geometry for fixed jaw machines

For fixed jaw machines, you must define the geometry of the calibration field before you compute output factors.

> **NOTE**
> The calibration field defined in this section is used only for output factor computation, not modeling. This field size is used as the reference field size for output factor computations. We recommend 10.4 x 10.4 for the Elekta Beam Modulator machine.

1 Click the **Edit Calibration Geometry** button in the **Photon Output Factors** window. The **Calibration Geometry Editor** window appears.

2 Enter the geometry values in the **MLC Rectangle** fields, or click the **Compute default calibration geometry** button to have the software compute values so that the calibration field is as close to

10 cm x 10 cm as possible. The **Equivalent square of MLC rectangle (cm)** value updates after you enter the values. The field size must be a minimum of 4 cm.

NOTE
The calibration field must be symmetric. As you enter values, the software adjusts the corresponding values as necessary to keep the field symmetric.

3 When you have defined the geometry, click the **Dismiss** button.

Compute output factors for photon beams

After entering all of the measured output factor data for a beam, you must compute the relative output factors for the beam.

1 In the **Photon Output Factors** window, click the **Compute** button. The **Photon Output Factor Computation** window appears.

CAUTION
Pinnacle³'s OF_c and OF_p are not the same as collimator scatter factor (S_c) and phantom scatter factor (S_p) defined in *The Physics of Radiation Therapy* (Khan, 1994). OF_c represents the field-size dependent correction factor for head scatter that is not accounted for in Pinnacle³'s head model.

2 Click the **Compute** button. The software computes the OF_p and OF_c for each field size.

CAUTION
If the output factors are less than 0.95 for a 3 cm x 3 cm field or greater than 1.05 for a 30 cm x 30 cm field, we recommend that you measure point doses for several MLC collimated fields to verify that the dose is accurate in fields where the MLC is highly collimated relative to the jaws (for example, a 35 cm x 35 cm jaw field with a 10 cm x 10 cm MLC field). If there are significant dose errors, the head scatter model is probably not correct or there are errors in the measured data. Return to the *Set the flattening filter scatter source* section and change the Gaussian height and width parameters to adjust the head scatter model.

> **NOTE**
> If you try to compute a field size that is invalid, the message **Jaw limits or wedge limits could not be set** appears. Field sizes may be invalid because the values entered for jaw limit precision or the wedge limits do not allow for the specified measurement geometry.

3 If the machine has a wedge, you can plot the output factors by wedge and wedge angle. Select a wedge from the **Plot OF for** option list. If you select a dynamic wedge, you can also specify a wedge angle.

4 If you want to print the table, click the **Print** button. In the **Output Factor Print Confirmation** window, click the **Print** button to print to the selected printer. (To select a different printer, click the **Select Printer** button, select a different printer, and click the **Dismiss** button. Then click the **Print** button.)

5 Click the **Dismiss** button to return to the **Photon Output Factors** window.

6 Click the **Dismiss** button in the **Photon Output Factors** window to return to the **Photon Physics Tool** window.

7 To save the computed output factors, click the **Save All Machines** button in the **Photon Physics Tool** window.

Validate models

You should validate your beam models, particularly the output factors, by comparing Pinnacle^3 calculations with measurements. Use fields that are similar to those you are likely to treat. This is especially important with IMRT (both forward planning and inverse planning), which can involve the use of very small, heavily blocked fields. Ideally, this validation should be done before you commission the machine. Specifically, use the planar dose tool to validate the modeling of the MLC characteristics (tongue and groove, rounded leaf end, leaf offset table, and interleaf leakage). Refer to the *Plan Evaluation Tools* chapter in the *Pinnacle^3 Planning Instructions for Use* for more information.

References and recommended reading

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Mackie, T.R., A.F. Bielajew, D.W.O. Rogers, and J.J. Battista. 1988. Generation of photon energy deposition kernels using the EGS Monte Carlo code. *Phys. Med. Biol.* 33(1):1-20.

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Van Dyk, J., R.B. Barnett, J.E. Cygler, and P.C. Shragge. 1993. Commissioning and quality assurance of treatment planning computers. *International Journal of Radiation Oncology, Biology and Physics* 26(2):261-273.

7 Electron Physics & Physics Utilities

CAUTION
You cannot commission electron energies for fixed jaw machines.

This chapter describes the Pinnacle^3 electron dose algorithm and the Electron Physics tool. The required electron measured data are described in the *Pinnacle^3 Physics Reference Guide*.

The process of adding machines and entering the general machine data is covered in *Working with Machines and the Machine Database*. The process of importing and entering measured data is described in the *Importing and Entering Measured Beam Data* chapter.

WARNING
The accuracy of the treatment planning dose calculation depends on the quality of the data entered in the physics tool. If the quality of this data is poor, or if the computed dose is not verified with measured data, the dose calculation may be inaccurate.

Electron dose algorithm

The electron dose calculation uses the Hogstrom pencil-beam algorithm (Hogstrom, 1981, 1984 and 1987). The algorithm uses a combination of measured data and model parameters that characterize the electron beam physics. After you determine the appropriate electron model parameters, you can generate dose lookup tables, which are used for dose calculation.

Use the Electron Physics tool

Use the Electron Physics tool to add electron energies for a machine, generate the dose lookup table for each energy, and enter electron output factors. Once you enter electron physics data for all energies on a machine, you can add physics information for the other modalities on the machine and then commission it for planning.

Add electron energies for a machine

You add and edit the electron energies for the selected machine using the **Add** and **Edit** buttons in the **Electron Physics Tool** window.

1 Click the **Electron Physics Tool** button in the **Physics Tools** window. The **Electron Physics Tool** window appears.

2 Click the **Add** button beneath the **Energy List**, then click the **OK** button in response to the warning that appears.

3 Click the **Edit** button beneath the **Energy List**. The **Machine Electron Energy Editor** window appears.

4 Type an appropriate name for the energy in the **Energy Name** field. During planning, this name is used to select the energy.

5 Specify the energy in MeV in the **Energy** field.

6 Enter the cutout material photon transmission factor that you measured for this electron energy. This parameter determines how much of the photon dose is transmitted through the cutout material. The value is used as the default transmission factor during planning.

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

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

8 In the **Default Dose Rate** option list, select the default dose rate for beams that use this energy.

9 When you finish entering the energy information, click the **Dismiss** button.

10 Click the **Save Current Machine** button in the **Electron Physics Tool** window to save the energy information you just entered.

Model electron beam data

For each energy and cone size, a beam description file is generated based on the measured data you import and the model you define using the Electron Physics tool. Before modeling an electron energy, you must import the depth dose and cross-axis profile measurements in water for each cone size, as described in the *Electron Physics & Data Requirements* chapter of the *Pinnacle³ Physics Reference Guide*.

Electron beam modeling is simpler than photon beam modeling. There is only one electron model for all field sizes, and electron modeling requires the interactive adjustment of only two parameters. You measure or calculate the other model parameters from the measured data, as described in the *Pinnacle³ Physics Reference Guide*. The electron model parameters are described below.

- **Incident Energy** ($E_{p,0}$)—most probable incident electron energy. It is computed from the practical range of electrons (R_p) using the Markus relation:

  $E_{p,0}(MeV) = (1.919 \bullet R_p) + 0.722$

  The software can calculate the incident energy for you if you enter R_p, or you can calculate incident energy yourself.

- **Photon Contamination Measurement Depth**—used for modeling the dose due to contaminating photons. The depth should be R_p + 2 cm.
- **Calibration Setup SSD (actual)**—setup source to surface distance.
- **Calibration Virtual SSD**—standard distance from the point of the virtual source to the surface at which the water phantom used to measure beam input data is irradiated. For a complete description of how the virtual SSD is determined, see the *Electron Physics & Data Requirements* chapter of the *Pinnacle³ Physics Reference Guide*.
- **Drift Distance (for Setup SSD)**—specifies the distance from the downstream edge of the beam-defining collimator to the surface of the phantom or patient at the standard treatment distance.
- **Sigma-theta-x (angular scattering variance)**—characterizes the angular scattering of electrons in air. It can be calculated from the 80% - 20% penumbra, as described by Hogstrom (1981, 1987). For a complete description of the calculation, see the *Electron Physics & Data Requirements* chapter of the *Pinnacle³ Physics Reference Guide*.

Two parameters are adjusted to fit the computed data with your measured data: the Off-Axis Ratios and the FMCS (Water Scatter Correction Factor). Because the FMCS is difficult to determine for low-energy beams, it is best to model the high-energy beams for a given machine first and use the FMCS determined for the high-energy beams for all energies.

- **Off-Axis Ratios**—For each cone size, you must enter off-axis ratios, which allow you to shape the incident fluence and compensate for beam asymmetries. The off-axis ratios are defined at a depth of $R_{90}/2$ (R_{90} is the depth on the central axis at which dose has decreased to 90% of the maximum dose), which should be used as a reference when tuning these values. In particular, the ratio of measured to computed dose at a point off the central axis is the ratio you enter in the table. For guidelines for tuning off-axis ratios, see the *Electron Physics & Data Requirements* chapter in the *Pinnacle³ Physics Reference Guide*.
- **FMCS (scatter correction factor)**—corrects for the angular scattering of electrons in the computation medium relative to air. The FMCS is applied to the angular scattering power of the reference medium in the calculation. Qualitatively, this parameter makes the dose spread out more or less in the patient.

1 In the **Electron Physics Tool** window, select the machine and energy for the beam to be modeled from the **Machine List** and **Energy List**.

2 Select a measurement geometry from the **Measurement Geometry List**.

3 Click the **Model** button to open the **Electron Model Parameters** window and the **Machine Electron Model** window.

4 Compute the incident energy using the Markus relation, based on assumptions made in the electron dose engine.

To have Pinnacle³ compute the incident energy for you, click the **Compute from Practical Range** button and enter the practical electron range value (R_p) in the appropriate field.

The incident energy and the photon contamination measurement depth are automatically calculated using the practical electron range you enter. Click the **Copy Computed Parameters to Model** button to copy the values to the model parameter window, and then click the **Dismiss** button to close it.

5 If you do not have measured profiles that match the computed photon contamination measurement depth (R_p + 2 cm), change the value in the **Photon Contamination Measurement Depth** field to match your measured data. For the physics tool to work properly, this depth *must* be R_p + 1 cm or deeper.

If you choose this depth incorrectly, your adjustments of the remaining electron model parameters may not achieve the desired effect on the resulting dose. In the worst-case scenario, you will be unable to fit the calculated data to the measured data. If you do not have this data, measure it before proceeding.

NOTE
You must measure photon contamination profiles for all field sizes of a given energy at the same depth. If there are only small differences in profile depth, you should select a single depth. You can specify a common depth for each profile using the electron profile editor.

Only X profiles should be entered in the **Photon Contamination Measurement Depth** field. Y profiles are ignored, and a warning is displayed when you compute profiles.

6 Enter the following values in the **Electron Model Parameters** window:
- The calibration setup SSD. (This is the actual SSD.)
- The calibration virtual SSD. For a description of how to compute the virtual SSD, see the *Electron Physics & Data Requirements* chapter of the *Pinnacle³ Physics Reference Guide*.
- The drift distance for setup SSD that you measured.
- The value you calculated for sigma-theta-x (angular scattering variance).
- Set the FMCS to 1.0 for now. Do not change this parameter until the other parameters have been correctly adjusted.

7 Add the field sizes for the model by clicking the **Add** button beside the **Square Fields** list. Create entries for a range of field sizes including the field sizes with which you plan to treat.

8 Click the **Edit Size and Ratio** button. The **Cone Ratios** window appears.

9 Enter the cone size for each entry you added to the list, but leave the off-axis ratios at 1.00 for now. Then click the **Dismiss** button.

10 Set the phantom size so that the **Lateral** dimension is just large enough to cover the largest cone size and the **Depth** is at least R_p + 5 cm.

11 Compute profiles for all available measurement geometries.

To compute the profiles, first select the measurement geometry in the **Electron Physics Tool** window. Then click the **Compute Profiles** button in the **Machine Electron Model** window. The **Compute Profiles** window appears. Set the **Compute** option for all profiles to **Yes** and then click the **Compute Profile(s)** button to start the computation.

NOTE
To run a script that computes all electron profiles for all geometries, start the scripting utility, choose the **Browse** option in the **HotScripts** window, go to the **System** scripts directory, and select **ComputeAllElectronProfiles.Script**.

NOTE
The profile is computed using the full lateral dimension entered in the **Electron Model Parameters** window. However, for phantoms with a lateral dimension greater than 30 cm, the dose computation is limited to 30 cm (distance of +/- 15 cm).

12 Assess and adjust the profiles as needed in the **Machine Electron Model** window. For detailed information about adjusting parameters, see the *Electron Physics & Data Requirements* chapter in the *Pinnacle³ Physics Reference Guide*.

13 To print profile plots, click the **Print Profile Plots** button in the **Machine Electron Model** window, and then click **Print** in the **Electron Profile Print Confirmation** window.

14 When you finish, return to the **Electron Physics Tool** window and click the **Save Current Machine** button to save the computed dose lookup tables.

Electron beam output factor entry

Monitor units are calculated in the planning tool only if the SSD and field size for the beam do not exceed the range of setup geometries (SSD and field size) for measured output factors entered in the Electron Physics tool.

After setting the parameters and calculating the dose lookup tables, you must enter the output factors for the beam. Measured output factors depend on the cone size, square field size, and SSD (the depth is always d_{max}). We recommend that you measure output factors for your clinical range of SSDs in 5-cm increments for each cone size, at exposed field sizes of 2 cm, 3 cm, 4 cm, 6 cm, 8 cm, 10 cm, and your maximum field size. The maximum field size for each cone is the cone size. For example, if your range of SSDs is 100-120 cm, you would measure output factors at 100, 105, 110, 115, and 120 SSD.

All relative output factors are relative to the calibration condition, and we recommend that you measure the factors at the depth of maximum dose (d_{max}). The software uses as the calibration condition the measured output factor from your 10 cm x 10 cm cone using a 10 cm x 10 cm cutout, at an SSD=100 cm and depth=d_{max}.

For more information about output factors, see the *Electron Physics & Data Requirements* chapter in the *Pinnacle³ Physics Reference Guide*.

1 Click the **Output Factors** button at the bottom of the **Electron Physics Tool** window. The **Electron Output Factors** window appears.

2 Enter the calibration depth (in centimeters) at which the reference output factor measurement was taken.

3 Enter the source to calibration point distance (in centimeters) used for the reference output factor measurement.

4 Enter the dose per monitor unit (cGy/MU) at the calibration point.

5 To add field sizes to the list of measurement field sizes, click the **Add** button beneath the list. A new field size with a default geometry of 10 x 10 is added to the list.

   The fields you add must be square.

6 To edit the measurement geometry and enter the relative output factor for the currently selected field size, click the **Edit** button. The **Electron Output Factor Measurement Geometry** window appears.

7 Enter the SSD and the measurement depth for the measurement geometry in the appropriate fields.

8 Select an electron cone.

9 In the **Exposed Field Size (Cutout Shape)** fields, enter the exposed field size limits for the measurement.

10 Enter the **Relative Output Factor** for the field.

11 In the **Electron Output Factors** window, select a new field size from the **Measurement Field Sizes** list and repeat steps 7-10 for each remaining field size.

12 When you finish entering output factor data, click the **Dismiss** button in the **Electron Output Factor Measurement Geometry** window.

Compute output factors

After entering all of the measured output factor data, you must compute the output factors.

1 In the **Electron Output Factors** window, click the **Compute** button. The **Electron Output Factor Computation** window appears.

2 Click the **Compute** button. The **Compute Output Factor Confirmation** window appears.

3 In the **Compute Output Factor Confirmation** window, click the **Compute** button. The software computes the OF_p and OF_c for each field size, and then it fills in the table when all the output factors are computed.

4 To change the output factors plotted on the graph, select different cone sizes from the **Cone Size** option list and different SSDs from the **SSD** option list.

5 If you want to print the output factor table, click the **Print** button. In the **Output Factor Print Confirmation** window, click the **Print** button to print to the selected printer. (To select a different printer, click the **Select Printer** button, select a different printer, and click the **Dismiss** button. Then click the **Print** button.)

6 Click the **Dismiss** button to close the **Electron Output Factor Computation Window**.

7 In the **Electron Output Factors** window, click the **Dismiss** button to return to the **Electron Physics Tool** window.

8 In the **Electron Physics Tool** window, click the **Save Current Machine** button to save the output factor information you entered.

9 Commission the machine using the process described in *Working with Machines and the Machine Database*.

References and recommended reading

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Hogstrom, K.R. 1987. Evaluation of electron pencil beam dose calculation. *Radiation Oncology Physics 1986* (AAPM Monograph 15) ed. J.G. Kereiakes, H.R. Elson, and C.G. Born. New York: American Institute of Physics. 532-557.

8 Stereotactic Radiosurgery Physics & Physics Utilities

CAUTION
You cannot commission stereotactic energies for fixed jaw machines.

This chapter describes the Stereotactic Radiosurgery Physics tool.

The process of adding machines and entering the general machine data is covered in *Working with Machines and the Machine Database*. The process of importing and entering measured data is described in the *Importing and Entering Measured Beam Data* chapter.

WARNING
The accuracy of the treatment planning dose calculation depends on the quality of the data entered in the physics tool. If the quality of this data is poor, or if the computed dose is not verified with measured data, the dose calculation may be inaccurate.

For information on the Pinnacle^3 stereotactic radiosurgery dose algorithm, see the *Pinnacle^3 Physics Reference Guide*.

Use the Stereotactic Physics tool

Use the Stereo Physics tool to add stereotactic energies for a machine, import or enter measured stereotactic data, generate the dose lookup table for each energy, and enter stereotactic output factors. Once you enter the information for all energies on a given machine, you can add physics information for the other modalities on the machine and then commission it for planning.

For information on importing the measured beam data, see the *Importing and Entering Measured Beam Data* chapter.

Add stereo energies for a machine

You can add and edit stereotactic radiosurgery energies for the selected machine using the **Add** and **Edit** buttons in the **Stereo Physics Tool** window.

1 Click the **Stereo Physics Tool** button in the **Physics Tools** window. The **Stereotactic Radiosurgery Physics Tool** window appears.

2 Click the **Add** button beneath the **Energy List**, then click the **OK** button in response to the warning that appears.

3 Click the **Edit** button beneath the **Energy List**. The **Machine Stereo Energy Editor** window appears.

4 Type an appropriate name for the energy in the **Energy Name** field. During planning, this name is used to select the energy.

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

6 Select the fluence-shaping mode for this energy from the **Fluence Mode ID** option list:

- **None**—A fluence mode ID is not assigned to this energy.
- **Flattening Filter Free (FFF)**—The software appends “FFF” to the name in the **Energy Name** field to indicate that this energy uses the Flattening Filter Free fluence mode ID.
- **Stereotactic Radiosurgery (SRS)**—The software appends “SRS” to the name in the **Energy Name** field to indicate that this energy uses the Stereotactic Radiosurgery fluence mode ID.

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

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

8 In the **Default Dose Rate** option list, select the default dose rate for beams that use this energy.

9 When you finish entering the energy information, click the **Dismiss** button.

10 Click the **Save Current Machine** button in the **Stereotactic Radiosurgery Physics Tool** window to save the energy information you just entered.

Enter stereo output factor information

You must enter relative output factor information for each collimator used with each energy on a machine. Output factors are computed when the beam is modeled.

1 Click the **Output Factors** button at the bottom of the **Stereotactic Radiosurgery Physics Tool** window. The **Stereo Output Factors** window appears.

2 Enter the **Dose/MU in Air** measured for a 10 cm x 10 cm open field.

3 Enter the **Back Scatter Factor** for a 10 cm x 10 cm open field.

4 For each collimator, enter the relative output factor and the back scatter factor. The relative output factor ($OF(W_c)$) is calculated using the equation

$$OF(W_c) = \frac{D(d_{max}, W_c)}{D(d_{max}, 10 \times 10)}$$

where W_c is the collimator size at isocenter.

NOTE
You can interpolate the collimator back scatter factor by clicking the **Interpolate BSF from 10x10 BSF** button.

The interpolated back scatter factor is calculated using the equation

$$BSW(W_c) = 1 + \frac{W_c}{dia_{eq}}(BSF_{10 \times 10} - 1)$$

where the equivalent diameter dia_{eq} of a circular field size equal in area to 10 cm x 10 cm is given by the equation (dia_{eq} = 11.28 for l = 10)

$$dia_{eq} = \left(\frac{2 \cdot l}{\sqrt{\pi}}\right) = 1.128 \cdot l$$

5 When you finish entering the stereotactic output factor information for the current energy, select another energy from the **Energy List** in the **Stereotactic Radiosurgery Physics Tool** window and repeat steps 2–4 for each remaining energy.

6 When you finish entering stereotactic output factor data, click the **Dismiss** button.

7 In the **Stereotactic Radiosurgery Physics Tool** window, click the **Save Current Machine** button to save the output factor information you just entered.

Stereotactic radiosurgery lookup table calculation

The stereotactic radiosurgery dose calculation is based on interpolating dose from tabular, circular field dose distributions in water. For each energy and collimator size, a dose lookup table is generated based on the measured data you import. After you import the required measured data for a collimator size for a particular energy, you must generate the dose lookup tables for that beam.

After you generate all lookup tables for a machine, you can commission the machine for use in the treatment planning software.

1 In the **Stereotactic Radiosurgery Physics Tool** window, select the machine and energy for the beam to be modeled from the **Machine List** and **Energy List**.

2 Select a measurement geometry for the collimator you want to model.

> **NOTE**
> The required scan data are 80 SSD and 100 SSD. No other distances can be used. If you have an 80 SAD machine, you will not be able to use the stereotactic planning module.

3 Click the **Model** button to open the **Stereotactic Radiosurgery Model** window.

4 In the **Stereotactic Radiosurgery Model** window, click the **Compute Profiles** button. The **Compute Profiles** window appears and lists the profiles for the current measurement geometry.

5 Select **Yes** for all profiles to be used to generate the dose table and click the **Compute Profile(s)** button.

The status of the computation is displayed in the **Status** field at the bottom of the screen. When the computation is complete, the profiles appear in the **Stereotactic Radiosurgery Model** window.

> **NOTE**
> To run a script that computes all stereotactic profiles for all geometries, start the scripting utility, choose the **Browse** option in the **HotScripts** window, go to the **System** scripts directory, and select **ComputeAllStereoProfiles.Script**.

6 To see a profile in more detail, click the **Detail** button. The **Stereo Data Comparison** window displays the measured and computed profiles.

7 To print profile plots, click the **Print Profile Plots** button in the **Stereotactic Radiosurgery Model** window, and then click **Print** in the **Stereo Profile Print Confirmation** window.

8 When you finish, return to the **Stereotactic Radiosurgery Physics Tool** window and click the **Save Current Machine** button to save the computed dose lookup tables.

9 Repeat this procedure for all stereotactic beams available on the machine, and then commission the machine using the process described in *Working with Machines and the Machine Database*.

9 Brachytherapy Physics

This chapter describes the required source characteristic data for the Pinnacle³ brachytherapy dose algorithm. It also explains the brachytherapy data entry tools.

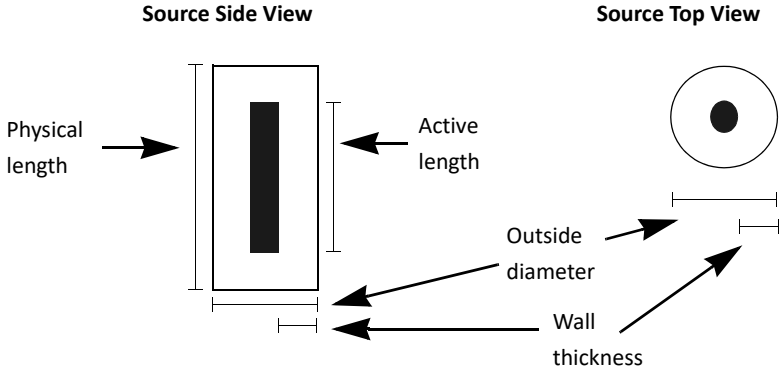
For information on dose computation, see the *Brachytherapy Physics* chapter in the *Pinnacle³ Physics Reference Guide*.

Required source data

WARNING
All brachytherapy sources used to treat patients should have a NIST-traceable calibration. In 1999, NIST implemented a new calibration standard for I-125 (Nycomed Amersham models 6711 and 6702, and North American Scientific models 3631 A/S and 3631 A/M), and Pd-103 (Theraseed Model 200). Failure to take this into account when entering source data could result in incorrect dose calculations. Details are provided in the references (Williamson et al, 1999 and Williamson et al, 2000).

For each source you want to add to the source library, you must enter the source data summarized below. This data is then used to generate the isotope lookup table used in the planning calculations.

- Source name.
- Source type (point source or line source).
- Lookup table computation method (Geometric or TG43).
- Source dimensions shown below (physical length, active length, outside diameter, and wall thickness). The units for the dimensions can be millimeters or centimeters. For point sources, these dimensions are used only for display purposes.



- Source half life and half life units (hours, days, months, or years).
- Coefficients for the tissue correction function. If the source is a line source, you must also enter source and wall linear absorption coefficients.

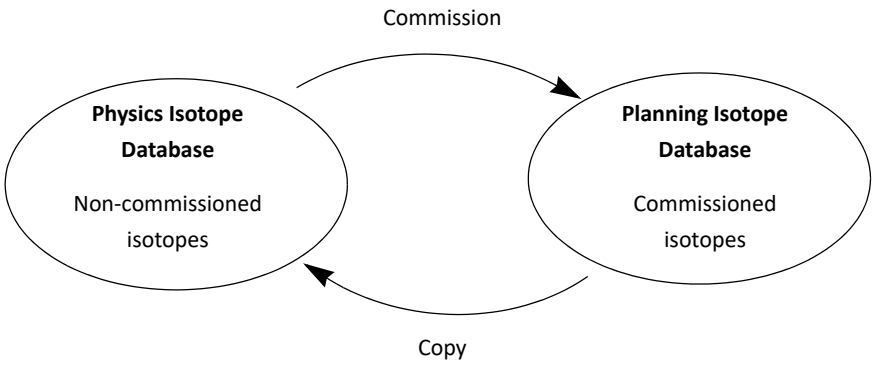
- The dose normalization can be specified by one of the following combinations:
  - dose rate, exposure rate constant, and air exposure to dose conversion factor
  - dose rate, air kerma rate, and air exposure to dose conversion factor
  - exposure rate constant, rad to Roentgen conversion factor, and exposure rate/dose
  - air kerma rate, rad to Roentgen conversion factor, and exposure rate/dose

The dose information required for lookup table computation varies depending on the computation method selected.

- For Geometric computation, you must enter coefficients for the Meisberger polynomial. If the source is a line source, you must also enter source and wall linear absorption coefficients.
- For TG43 computation, you must enter or compute the geometry function, the radial dose function (polynomial coefficients), and the anisotropy function. These functions are described in the *Brachytherapy Physics* chapter of the *Pinnacle³ Physics Reference Guide*.

Brachytherapy isotope databases

In the same way that machines are created in the external beam physics tools and then commissioned for use in planning, isotopes are created in the Brachytherapy Physics tool and then commissioned for use in planning. Two isotope databases are maintained: the physics isotope database and the planning isotope database.



When an isotope is commissioned, it is removed from the physics isotope database, added to the planning isotope database, and “stamped” with the date and time of commissioning. This stamp identifies the version of the isotope. All plans include information about the version of the isotope used to create them.

To make changes to an isotope after it has been commissioned, you must copy it back into the physics isotope database, make the changes using the Brachytherapy Physics tool, and then recommission the isotope. The new version is then available in the planning isotope database.

Use the Brachytherapy Physics tool

Use the Brachytherapy Physics tool to enter the brachytherapy isotope characteristics and generate the dose lookup table for each isotope. You must generate dose tables for a source before it can be commissioned for use in planning.

To enter the Brachytherapy Physics tool, click the **Brachy Isotopes** button in the **Physics Tools** window. The **Brachytherapy Physics Tool** window appears.

Add isotopes to the Brachytherapy Physics tool

You can add and define isotopes using the Brachytherapy Physics tool.

1 Click the **Add Isotope** button at the bottom of the **Brachytherapy Physics Tool** window. The **Add New Isotope** window appears.

   You can add a new isotope or copy an existing one to the **Physics Tool Isotope** list from the **Available Isotopes** list, which shows non-commissioned and commissioned isotopes.

2 To copy an existing isotope into the physics tool for modification, first select whether the isotope is in the non-commissioned, commissioned, or deleted list by clicking the appropriate option button. From the updated list of isotopes, select the one you want to copy and click the **Copy Selected** button. The isotope is copied into the physics isotope database.

   If you want to copy an isotope from a different institution or installation, click the **Locate** button and use the **Isotope Locator** window to find the isotope on the system's hard disk. For details on using the locator window, see *Add machines to the physics database* in the *Working with Machines and the Machine Database* chapter.

3 To create an isotope, click the **Create Default** button in the **Add New Isotope** window. A new isotope with the name Isotope_1 is added to the list of isotopes in the Brachytherapy Physics tool.

4 Type a name for the source in the **Name** field.

5 Specify whether the source is a point source or a line source.

6 In the **Units** option list, select the units for the source dimensions.

7 Specify the source dimensions. If the source is a point source, the dimensions you enter here are used when the source is displayed. They are not used in point source dose calculations.

8 Specify the source half life in the **Half Life** field, and select the half life units from the option list.

9 Choose the dose normalization method. You can use a **Dose Rate Constant**, **Air Kerma Rate Constant**, or **Exposure Rate Constant**. (To select the **Air Kerma Rate Constant** or **Exposure Rate Constant**, select the appropriate units.)

To normalize using a **Dose Rate Constant**, set **Use Dose Rate Constant** to **Yes**, and enter the dose rate constant for the source in cGy/hr/U.

For the **Geometric** method, to use either the **Air Kerma Rate Constant** or the **Exposure Rate Constant**, set **Use Dose Rate Constant** to **No**. Select the units to be used for normalization, and enter the normalization value. The label for this parameter (**Air Kerma Rate Constant** or **Exposure Rate Constant**) changes depending on the selected units.

When not using the **Dose Rate Constant**, you must also specify the **Exposure to Dose Conversion Factors** for tissue (f_{med}) and air (W/e). When using the **Dose Rate Constant**, you must enter the **Exposure to Dose Conversion Factor** for air (W/e) and the **Exposure Rate Constant**.

10 Enter the appropriate dose information as described in the following sections.

Enter source data

Enter the physics data required for lookup table computation using the data sheets in the bottom portion of the **Brachytherapy Physics Tool** window. For sources using the Geometric method, you need to enter tissue correction function information (i.e., Meisberger coefficients) before computing the dose lookup tables. For line sources, you also have to enter linear absorption coefficients.

The TG43 computation method allows you to enter additional dose information for sources so that the dose formalism described in the report of the AAPM Task Group No. 43 can be used for the lookup table computation. In addition to the radial dose function that is entered for both computation methods, the TG43 computation method uses a Geometry function and an Anisotropy function in the lookup table computation. For details on how these functions affect the source dose computation, see the *Brachytherapy Physics* chapter in the *Pinnacle³ Physics Reference Guide*.

CAUTION
We recommend that you perform acceptance tests for your TG43 isotopes to confirm the dose calculations within the software.

Enter source dose data for the Geometric computation method

1 Click the **Tissue Correction** tab.

2 Specify the first bin center, the bin size, and the number of bins for the tissue correction calculation.

- The first bin center is the center of the lowest bin. It determines the radius at which the calculation starts. All bin centers are defined from this origin.
- The bin size is the width of all bins, and specifies the spatial resolution of the calculation.
- The number of bins defined in the bin structure determines the radius.

3 Enter the Meisberger polynomial coefficients in the appropriate fields. When setting up tissue correction functions, enter polynomial coefficients so that the computed tissue correction function will have a positive value. A value of zero indicates that a given coefficient is not to be used.

4 If the source is a line source, you must specify the source and wall linear absorption coefficients. Click the **Lookup Table** tab to display the **Lookup Table** window, and enter the source and wall linear absorption coefficients and units.

Enter source dose data for the TG43 computation method

1 Click the **Geometry Function** tab. You can compute or manually enter data for the Geometry function using either Cartesian or polar coordinates. If you switch between Cartesian and polar coordinates, parameters might be adjusted automatically to fit within allowable limits.

You can specify the first bin center, bin size, and number of bins. For explanations of these parameters, see the *Enter source dose data for the Geometric computation method* section.

CAUTION
If you manually enter TG43 geometry factors, Pinnacle³ will automatically normalize them to be 1 at a distance of 1 cm from the center of the source. This function is indicated by the following equation, which appears when you manually enter TG43 geometry factors: G(r, theta)/G(1 cm, 90 deg).

You can find geometry function data for sources in several publications.

2 Click the **Radial Function** tab. You can compute the radial dose function data from the polynomial coefficients or manually enter it. Specify the first bin center, the bin size, and the number of bins for the calculation.

If you are computing the radial dose function, enter the polynomial coefficients in the appropriate fields.

If you enter zero for a coefficient, it is not used in the computation. If you enter coefficients that create a value other than 1 at a 1 cm radius, the software normalizes all the values, scaling them to have 1 at a 1 cm radius.

If you are manually entering radial dose function data, select the item you want to edit and type the value in the field above the **Radial Dose Function** table.

3 Click the **Anisotropy Function** tab. The data you must enter for the Anisotropy function depends on whether the source is a point source or a line source.

For line sources, you must specify whether you want to enter the data using Cartesian or polar coordinates. You must also specify the first bin center, the bin size, and the number of bins for the data. To enter the anisotropy data itself, select the cell in the table that you want to edit and enter the value in the field above the left corner of the table.

For point sources, you must specify the anisotropy data in polar coordinates. Select whether to use the Anisotropy Constant (scalar) or the Radial Anisotropy Factor. If you use the Anisotropy Constant, you need only enter the scalar value for the anisotropy function. If you use the Radial Anisotropy Factor, you must enter the first bin center, the bin size, and the number of bins for the data.

NOTE
Make sure after you enter the anisotropy function that you press the **Enter** key. This ensures that the value is entered into the software. If you do not press the **Enter** key, you have only changed the function without making the software relate it to the lookup tables.

Compute lookup tables

After you have entered the source information, you must compute the lookup table for the isotope. The Anisotropy and Geometry lookup tables must extend to 90 degrees before you can compute the lookup table.

For the Geometric lookup table, the table stores the “shape” of the dose. This table is calculated using the summation:

$$\frac{1}{N}\sum_{i}^{N} e^{(-\mu_s d_s - \mu_f d_f)} \cdot ((T(d_l))/d_i^{\,2})$$

1 Click the **Lookup Table** tab to display the **Lookup Table** window.

2 Specify the bin size and the number of bins in the Y and Z directions (the Z direction is along the central axis of the source). The bin size specifies the resolution of the lookup table, and the number of bins determines the extent of the lookup table.

   The value of the lowest bin is applied down to zero regardless of the lower bin limit or extent. Zero is applied above the limit of the highest bin.

   For the best dose accuracy, the maximum bin size cannot exceed 0.300 cm. When using small dose bins, you should increase the number of bins to make sure you can compute the dose at least 10 cm from the source.

3 Click the **Compute Lookup Table** button to compute the lookup table.

4 When the lookup table has been computed, click the **Save Isotopes** button at the bottom of the **Brachytherapy Physics Tool** window to save the source and dose lookup information for the isotope you just computed.

Add a source to permanent inventory

You can create an inventory for sources that are stored permanently in your source vault. When these sources are selected for use in planning, the source strength is calculated automatically from the calibration date entered in the inventory spreadsheet. Any number of sources can be added to inventory for a single isotope, and the source strength, strength units, and calibration date can be specified for each source.

NOTE
The Inventory function does not manage the quantity of each source.

1 Select the isotope type for which you want to add sources to inventory.

2 Click the **Inventory** tab in the **Brachytherapy Physics Tool** window to display the Inventory setup options.

3 Click the **Add New Source** button beneath the **Calibrated Source List** to add a new source to inventory.

4 In the **Name** field, type a name for the source.

5 Select the **Source Strength Units** from the list of units.

6 Enter the measured source strength in the **Source strength** field.

7 Enter the calibration date for the source in the format YYYY-MM-DD HH:MM:SS (Year-Month-Date Hour:Minute:Second).

Delete isotopes

You can delete isotopes from both the planning isotope database and the physics isotope database using options in the Brachytherapy Physics tool.

Delete an isotope from the brachytherapy physics database

1 Select the isotope you want to delete in the Brachytherapy Physics tool.

2 Click the **Delete Isotope** button at the bottom of the window.

To make the deletion permanent, you must save the isotope database using the **Save Isotopes** button at the bottom of the **Brachytherapy Physics Tool** window.

Delete an isotope from the brachytherapy planning database

1 Click the **Add** Isotope button at the bottom of the **Brachytherapy Physics Tool** window. The **Add New Isotope** window appears.

2 Click the **Commissioned Isotopes** option button to list the currently commissioned isotopes.

3 Select the isotope you want to delete from the list of available isotopes, then click the **Delete** button.

Commission isotopes

After you enter all the physics information for an isotope, you “commission” it for use in treatment planning.

When an isotope is commissioned, it is moved from the physics isotope database to the planning isotope database and given a unique identifier consisting of the date and time of commissioning. This commissioned isotope will be available only in the treatment planning software. If you want to make changes to an isotope after commissioning it, you must copy it back into the physics isotope database, make the changes using the physics tool, and recommission the isotope.

1 Select the isotope you want to commission in the Brachytherapy Physics tool.

2 Click the **Commission** button. The **Commission Isotope** window appears.

3 Enter your name and a description of the isotope, then click the **OK** button to commission it.

WARNING
After commissioning a brachytherapy isotope, verify the accuracy of the dose calculation before clinical use.

References and recommended reading

Cassell, K.J. 1983. A fundamental approach to the design of a dose-rate calculation program for use in brachytherapy. *The British Journal of Radiology* 56:113-119.

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Meisberger, L.L., R.J. Keller, and R.J. Shalek. 1968. The effective attenuation in water of the gamma rays of gold 198, iridium 192, cesium 137, radium 226, and cobalt 60. *Radiology* 90:953-957.

Nath, R., L.L Anderson, G. Luxton, K.A. Weaver, J.F. Williamson, and A.S. Meigooni. 1995. Dosimetry of interstitial brachytherapy sources: Recommendations of the AAPM Radiation Therapy Committee Task Group No. 43. *Medical Physics* 22(2):209-234.

Williamson et al, 1999. Guidance to users of Nycomed Amersham and North American Scientific, Inc., I-125 Interstitial Sources: Dosimetry and calibration changes: Recommendations of the American Association of Physicists in Medicine Radiation Therapy Committee Ad Hoc Subcommittee on Low-Energy Seed Dosimetry. *Medical Physics* 26(4): 570-573.

Williamson, et al, 2000. Recommendations of the American Association of Physicists in Medicine on ^{103}Pd interstitial source calibration and dosimetry: Implications for dose specification and prescription. *Medical Physics* 27(4): 634-642.

10 Brachytherapy Simulator Machines

If your clinic routinely uses simulators to obtain films for brachytherapy planning, you may want to create brachytherapy simulator machines to simplify brachy source reconstruction in Pinnacle^3.

In brachytherapy planning, use the brachytherapy film reconstruction option to select a simulator machine and enter the simulator couch, gantry, and collimator angles that were used to obtain the films. (See the *Brachytherapy Treatment Planning* chapter in the *Classic Pinnacle^3 Planning Instructions for Use* for information about simulator film reconstruction.) You can then reconstruct brachytherapy sources from non-orthogonal films. For example, you can use a brachytherapy simulator to create isocentric stereo-shift films. This chapter describes how to create and commission brachytherapy simulator machines.

> **NOTE**
> Brachytherapy simulator machines are not used for virtual simulation. They are only available for simulator film reconstruction in the brachytherapy planning software. The linear accelerators that are defined as physics machines should be used for virtual simulation.

Create brachytherapy simulator machines

You create brachytherapy simulator machines using the Brachytherapy Simulator tool, which is available from the Pinnacle^3 **Physics Tools** window.

1 Open the physics tools.

2 Click the **Brachytherapy Simulators** button in the **Physics Tools** window. The **Brachytherapy Simulator Machines** tool appears.

3 To add a simulator machine, click the **Add** button beneath the **Machine List**. The **Add New Simulator** window appears.

In the **Add New Simulator** window, you can create a brachytherapy simulator by copying one of the physics machines (**Non-Commissioned** or **Commissioned**), a sample machine, or a commissioned brachytherapy simulator to the **Available Machines** list. You can also create a brachytherapy simulator using the **Create Default** option. If you copy a physics machine, only the machine limits and angles are copied.

4 To copy a machine to the **Available Machines** list, select the machine and click the **Copy Selected** button. To create a brachytherapy simulator, click the **Create Default** button.

Set up brachytherapy simulator machines

You define brachytherapy simulator machines by entering their jaw, gantry, collimator, couch limits, and characteristics.

1 Select the machine from the **Machine List** in the **Brachytherapy Simulator Machines** window.

2 Click the **Edit** button beneath the **Machine List**. The **Simulator Editor** window appears.

3 Enter the machine information in the **Simulator Editor** window. For information about the fields in the **Simulator Editor** window, see *Enter the physical machine characteristics* in the *Working with Machines and the Machine Database* chapter.

Enter couch, gantry, and collimator angle information

Use the following procedure to set the limits for couch, gantry, and collimator movement on the brachytherapy simulator. For each of these machine components, you must enter a calibration setup angle and a direction of rotation. This information is used to automatically translate your brachytherapy simulator machine angles to the coordinate system used in Pinnacle^3.

1 Click the **Couch Angles** button in the bottom right corner of the **Simulator Editor** window to display the **Couch Angle Parameters** window.

2 Specify the couch angle parameters. For information on the fields in the **Couch Angle Parameters** window, see *Enter the physical machine characteristics* in the *Working with Machines and the Machine Database* chapter.

3 When you finish, click the **Dismiss** button in the **Couch Angle Parameters** window.

4 Click the **Collimator Angles** button in the bottom right corner of the **Simulator Editor** window to display the **Collimator Angle Parameters** window.

5 Specify the collimator angle parameters. For information on the fields in the **Collimator Angle Parameters** window, see *Enter the physical machine characteristics* in the *Working with Machines and the Machine Database* chapter.

6 When you finish, click the **Dismiss** button in the **Collimator Angle Parameters** window.

7 To enter gantry settings, click the **Gantry Angles** button in the bottom right corner of the **Simulator Editor** window. The **Gantry Angle Parameters** window appears.

8 Enter the gantry angle parameters. For information on the fields in the **Gantry Angle Parameters** window, see *Enter the physical machine characteristics* in the *Working with Machines and the Machine Database* chapter.

9 When you finish, click the **Dismiss** button in the **Gantry Angle Parameters** window.

10 Once you have entered the brachytherapy simulator machine information, you can either save the simulator in the physics tool by clicking the **Save All Machines** button, or you can commission the machine.

Commission brachytherapy simulator machines

Once you define the machine information for a brachytherapy simulator, you can commission it for use in brachytherapy film reconstruction.

1 Select the machine you want to commission from the **Machine List** in the **Brachytherapy Simulator Machines** window.

2 Click the **Commission** button. The **Commission Machine** window appears.

3 Type your name in the **Commissioned By** field. You must enter a name in order to commission the brachytherapy simulator.

4 Type a description for the machine in the **Description** field.

5 Click the **OK** button to commission the brachytherapy simulator.

11 Proton Machine Definition

This chapter describes how to create proton machines for use in treatment planning. If you are not licensed for proton treatment planning, you will not be able to access the Proton Physics tools.

WARNING
The accuracy of the treatment planning dose calculation depends on the quality of the data entered in the physics tool. If the quality of this data is poor, or if the computed dose is not verified with measured data, the dose calculation may be inaccurate.

Add proton machines to the physics database

1 Click the **Proton Physics Tool** button in the **Physics Tools** window. The **Proton Physics Tool** window appears.

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

2 Click the **Add** button beneath the **Machine List**. The **Add New Machine** window appears.

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

- **Old Commissioned Machines** are old versions of current machines.
- **Deleted Commissioned Machines** are commissioned machines that have been deleted from the planning machine database. However, they are not deleted completely from the system. If necessary, you can reproduce dose distributions from calculations using a deleted machine.

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

4 From the updated list of available machines, select the one that you want to copy and click the **Copy Selected** button. The machine is copied into the Physics Tool **Machine List** for modification.

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

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

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

After you confirm that you are copying the correct machine, you are asked if you want to copy it to the commissioned list or the non-commissioned list. This option is available only when you copy a commissioned machine, and it is useful when you create a patient plan in one institution and then must transfer the patient to a different institution for later treatment. You can import the commissioned machine that you used to create the original plan into the institution where the patient will be treated.

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

For each machine, you must enter the physical description, as described in the following section. You must also enter the physics information for each delivery type and then commission it for use in treatment planning.

Enter the physical machine characteristics

After adding a machine, you need to enter information for the machine's physical characteristics. You can use the worksheets in the *Pinnacle³ Physics Instructions for Use* to record the machine description information.

> **NOTE**
> While the majority of the physical characteristics that you must define for the machine apply to all of the delivery types, some of the physical characteristics only apply to a specific delivery type (for example, they are necessary for the double scattering and uniform scanning delivery types). Unless it is specifically noted in these instructions, you should assume that the information is applicable to all of the delivery types.

You must enter the following physical description parameters for your machine. Enter all angles and settings using your machine's coordinate system.

- Couch attributes, including the minimum, maximum, and default angles.
- Gantry attributes, including minimum and maximum angles and whether continuous or discrete gantry angles are allowed.
- Nozzle components, including nominal source to axis distance, magnet to isocenter distance, minimum and maximum distance from isocenter to the virtual block tray, the delivery types that are supported, and whether full plateau delivery is supported.
- Snout attributes, including shape and dimensions; and compensator thickness and aperture slab information.
- Imaging devices, including angle, SAD, and energy.
- Other machine information, including the maximum MU setting and the point level settings for the pristine peak range, the proximal and distal edges of the SOBP, and the integral depth dose.

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

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

The tabs located near the top of the window let you display information about the couch, gantry, nozzle, snout, imaging device, and other machine parameters.

3 Type the machine name in the **Machine name** field at the top of the window.

The machine name is the name that is used in the treatment planning software to identify the machine, so the machine name must be unique. If you plan to use DICOM RT to export plans, limit the machine name to 16 characters or less.

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

WARNING
If you enter information incorrectly in the Machine Editor window, Pinnacle³ may report incorrect output during treatment planning.

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

Enter couch information

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

2 Specify the following couch information.

- **Decimal places**—This value is the number of decimal places that are allowed on this machine when setting the couch angle.
- **Minimum angle**—This value is the minimum couch angle that is allowed by the machine. Enter the angle in the field or rotate the couch in the graphic.
- **Maximum angle**—This value is the maximum couch angle that is allowed by the machine. Enter the angle in the field or rotate the angle in the graphic.

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

- **Default angle**—This value is the couch angle used when a beam is added using this machine.

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

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

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

5 In the **Proton Physics Tool** window, click the **Save Current Machine** button to save your changes.

Enter gantry information

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

2 Specify whether continuous or discrete gantry angles are allowed by clicking the appropriate option button.

- **Continuous**—The gantry can be set at any angle within a range of angles that is defined by minimum and maximum angle values. Continue to *Continuous gantry angles*.
- **Discrete**—The gantry can only be set at specific angles that are defined during machine commissioning. Continue to *Discrete gantry angles*.

Continuous gantry angles

1 Specify the following gantry information.

- **Decimal places**—This value is the number of decimal places that can be used on this machine when setting the gantry angle.
- **Minimum angle**—This value is the minimum gantry angle that can be achieved by the machine. Enter the angle in the field or rotate the green gantry in the graphic.
- **Maximum angle**—This value is the maximum gantry angle that can be achieved by the machine. Enter the angle in the field or rotate the red gantry in the graphic.
- **Default angle**—This value is the gantry angle used when a beam is added using this machine.

2 In the **Gantry angle when beam points down toward floor** field, type the angle of the gantry when the beam is aimed straight down at the floor. This field is located above the graphic on the **Gantry** tab. This information is used to translate the gantry angles to the coordinate system used in the Pinnacle^3 software. The angle you enter is represented by the blue gantry in the graphic.

3 Specify the direction of positive rotation when facing the gantry from the foot of the couch by selecting **Yes** or **No** next to **When facing gantry, is positive rotation counterclockwise?**. This information is used to translate the gantry angles to the coordinate system used in the Pinnacle^3 software.

4 In the **Proton Physics Tool** window, click the **Save Current Machine** button to save your changes.

Discrete gantry angles

1 In the **Decimal places** field, type the number of decimal places that can be used on this machine when setting the gantry angle.

2 To add discrete angles for this machine, you must create a discrete angle list. Click the **Insert After** button to add the initial row. Then click the **Insert Before** or **Insert After** buttons to add additional rows.

3 Enter the angle values.

To enter a value, click the row you want to edit, then type the value in the **Angle** field that appears above the table. Click the green check mark next to the field or press **Enter** to accept the value. Click the red **x** to cancel the change.

The smallest angle you enter is represented by the green gantry in the graphic, and the largest angle you enter is represented by the red gantry.

4 In the **Default angle** option list, select the angle that you want to use as the default gantry angle when this machine is used in planning.

5 To delete a row from the **Angle** list, click the row you want to delete and click the **Delete Row** button.

6 In the **Gantry angle when beam points down toward floor** field, type the angle of the gantry when the beam is aimed straight down at the floor. This field is located above the graphic on the **Gantry** tab. This information is used to translate the gantry angles to the coordinate system used in the Pinnacle^3 software. The angle you enter is represented by the blue gantry in the graphic.

7 Specify the direction of positive rotation when facing the gantry from the foot of the couch by selecting **Yes** or **No** next to **When facing gantry, is positive rotation counterclockwise?**. This information is used to translate the gantry angles to the coordinate system used in the Pinnacle^3 software.

8 In the **Proton Physics Tool** window, click the **Save Current Machine** button to save your changes.

Enter nozzle component information

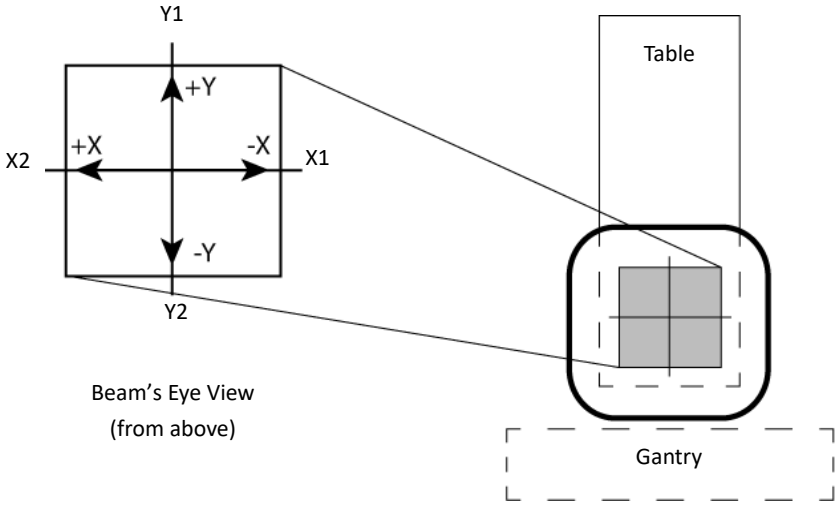
1 Click the **Nozzle Components** tab in the **Proton Machine Editor** window. The nozzle component information appears in the window.

2 Specify the nominal source to axis distance.

3 Specify whether the machine supports double scattering or uniform scanning by clicking the **Yes** or **No** option buttons in the **Delivery type** field.

> **NOTE**
> The only delivery types that will be available to you are those for which you are licensed.

4 If you specified that uniform scanning is allowed for this machine, type the distance from the magnets to the isocenter in the **Magnet to isocenter distance** fields. The X magnet scans the proton beam in the Pinnacle³ X direction, and the Y magnet scans the proton beam in the Pinnacle³ Y direction as shown in the image that follows.



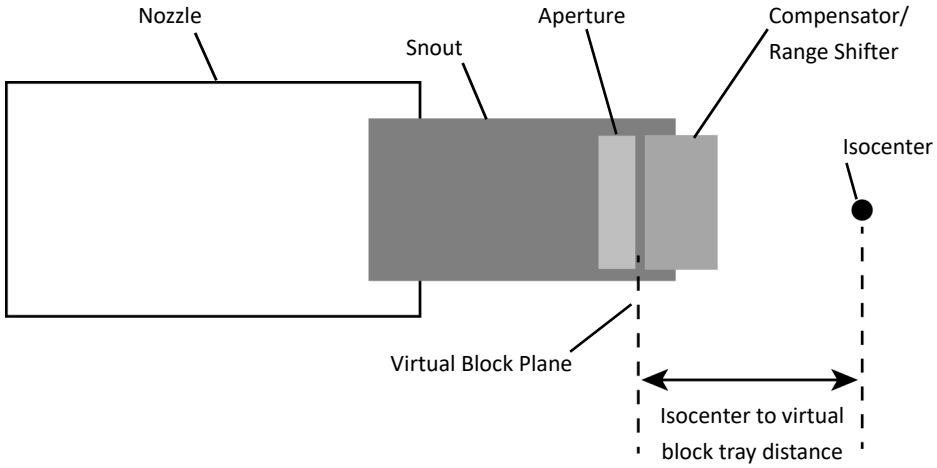
5 For double scattering and uniform scanning delivery types, if the machine supports full plateau delivery, choose whether to enable it for this machine by clicking the **Yes** or **No** option button in the **IBA full plateau support** field.

- **Yes**—Full plateau delivery is enabled for this machine and will be available for use in planning. Full plateau delivery means that the 100% dose level for a delivered SOBP extends to the patient surface in a beam's dose calculation when the full plateau option is selected in planning for that beam.
- **No**—Full plateau delivery will not be available for use in planning, and full modulation delivery will be used instead. Full modulation means that the user-defined dose level for the proximal edge of a delivered SOBP extends to the patient surface in a beam's dose calculation. This user-defined dose level is based on the modulation table. For example, if the user defines a dose level for the proximal edge of 95%, then 95% of plateau dose extends to the patient surface in a beam's dose calculation.

6 Type the minimum and maximum distance from the isocenter to the virtual block tray (as shown in the image that follows) in the appropriate fields. The virtual block tray is the same reference plane as is defined by the DICOM standard.

NOTE
Pinnacle³ defines the snout position as the distance from the isocenter to the virtual block tray. Also, Pinnacle³ assumes that the compensator or range shifter is directly downstream and adjacent to the virtual block tray.

If your machine does not support a moveable snout (for example, the isocenter to virtual block tray distance is fixed), set the minimum and maximum distances from the isocenter to the virtual block tray values so that they are equal.



7 In the **Proton Physics Tool** window, click the **Save Current Machine** button to save your changes.

Enter snout information

1 Click the **Snout** tab in the **Proton Machine Editor** window. The snout information appears in the window.

2 Click the **Add** button to add a new snout.

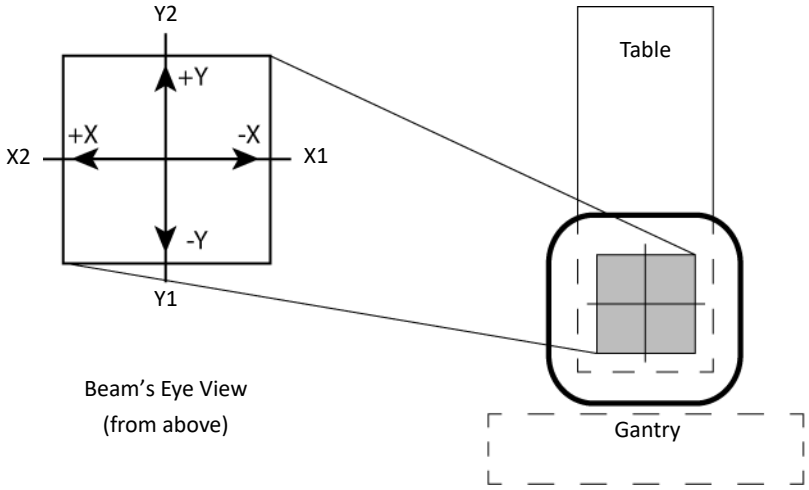
3 In the **Name** field, type a name for the snout. Each snout must have a unique name.

4 In the **ID** field, type an ID for the snout. The ID is used internally by the software to identify the snout, so the snout ID must be unique.

5 Specify whether the snout is circular or rectangular by selecting the appropriate option.

6 Do one of the following:

- If you specified that the snout is circular, type the diameter of the snout.
- If you specified that the snout is rectangular, type the X and Y dimensions of the snout based on the Pinnacle[3] beam coordinate system as shown in the image that follows.



7 Type the thickness of the unmilled compensator in the **Unmilled compensator thickness** field.

NOTE
You can define multiple snouts to support different unmilled compensator thicknesses. For example, you can define one 10 cm snout for an unmilled compensator thickness of 5 cm and a second 10 cm snout for an unmilled compensator thickness of 10 cm. When you define multiple snouts, you have more flexibility when selecting snouts and compensator thicknesses during planning.

8 Type the thickness of each aperture slab in the **Slab thickness** field. The calculated maximum and maximum override values for the slab appear in the **Maximum Supported Range** table.

NOTE
In the **Calculated Maximum** field of the **Maximum Supported Range** table, the software displays the maximum range that can be stopped per material based on the number of slabs and the slab thickness values that you entered. If necessary, you can override the maximum range with a value that is less than or equal to the maximum calculated value.

The **Calculated Maximum** and **Maximum Override** values for the slab only appear in the **Maximum Supported Range** table if at least one aperture material is present.

9 Type the maximum number of aperture slabs allowed by the machine for that snout in the **Maximum number of slabs** field.

10 To arrange the list of snouts in alphabetical order, click the **Sort** button.

11 To delete a snout, select the snout in the **Snouts** list and click the **Delete** button.

12 In the **Proton Physics Tool** window, click the **Save Current Machine** button to save your changes.

Define compensator and aperture materials

The materials that are available in planning for use in compensators and apertures are commissioned as part of the machine data.

1 Click the **Snout** tab in the **Proton Machine Editor** window. The snout information appears in the window.

2 Click the **Material Definition** button on the **Snout** tab. The **Beam Modifier Property Definition** window opens. The window contains two tabs: **Compensator** and **Aperture**. Use these tabs to define the compensator and aperture materials. See the *Compensator materials* and *Aperture materials* sections for instructions.

3 When you finish defining the materials, click the **Dismiss** button to close the window.

Compensator materials

The compensator materials that you define in the Proton Physics tool are used to design appropriate compensator shapes in planning to produce the required dose distributions. The material definitions ensure that appropriate material is used and that accurate thicknesses are produced during compensator milling.

Add a new compensator material

1 Click the **Compensator** tab in the **Beam Modifier Property Definition** window.

2 Click the **Add** button. The **Compensator Material Editor** window opens.

3 Complete the **Name** and **ID** fields.

4 Type the value for the stopping power relative to water.

5 Type the minimum thickness of a compensator that is created with this material.

6 Type a default value for the diameter of the milling tool. In planning, this value will be used as the initial diameter for the milling tool for this compensator material.

7 Click the **OK** button to save the information and add the new material to the compensator **Material List**.

Edit an existing compensator material

> **NOTE**
> You must recommission the machine if you change the definition of a material after you commissioned the machine.

1 Click the **Compensator** tab in the **Beam Modifier Property Definition** window.

2 In the **Material List**, select the name of the material that you need to edit.

3 Click the **Edit** button. The **Compensator Material Editor** window opens.

4 Change the values as necessary.

5 Click the **OK** button to save your changes.

Set a default compensator material

1 Click the **Compensator** tab in the **Beam Modifier Property Definition** window.

2 In the **Material List**, select the name of the material that you want to set as the default.

3 Click the **Set As Default** button. The **Default compensator material** field updates with the name of the material that you selected.

Delete a compensator material

> **NOTE**
> If you want to delete a compensator material after you have commissioned the machine, you must recommission the machine. Also, if you delete a compensator material that is used by a compensator in a plan, you must recreate that compensator with another material.

1 Click the **Compensator** tab in the **Beam Modifier Property Definition** window.

2 In the **Material List**, select the name of the material that you want to delete.

3 Click the **Delete** button.

Aperture materials

The aperture materials that you define in the Proton Physics tool are used by the planning tool to ensure that apertures are milled using the appropriate materials.

The software supports the use of a single, static aperture per beam. For the double scattering beams and uniform scanning beams, the software automatically adds a default aperture to each beam after you select a target ROI.

> **NOTE**
> Be sure to define aperture slabs whose combined total thickness is sufficient to stop the protons that have the highest available range for a given field size. Insufficient aperture thickness can cause dose delivery errors. In planning, the software will not let you select an aperture that is not thick enough to stop the beam and will prevent you from computing dose.

Add a new aperture material

1 Click the **Aperture** tab in the **Beam Modifier Property Definition** window.

2 Click the **Add** button. The **Aperture Material Editor** window opens.

3 Complete the **Name** and **ID** fields.

4 Type the value for the stopping power relative to water.

5 Type the minimum value for the diameter of the milling tool.

6 Type a default value for the diameter of the milling tool. In planning, this value will be used as the initial diameter for the milling tool for this aperture material.

7 Click the **OK** button to save the information and add the new material to the aperture **Material List**.

Edit an existing aperture material

> **NOTE**
> You must recommission the machine if you change the definition of a material after you commissioned the machine.

1 Click the **Aperture** tab in the **Beam Modifier Property Definition** window.
2 In the **Material List**, select the name of the material that you need to edit.
3 Click the **Edit** button. The **Aperture Material Editor** window opens.
4 Change the values as necessary.
5 Click the **OK** button to save your changes.

Set a default aperture material

1 Click the **Aperture** tab in the **Beam Modifier Property Definition** window.
2 In the **Material List**, select the name of the material that you want to set as the default.
3 Click the **Set As Default** button. The **Default aperture material** field updates with the name of the material that you selected.

Delete an aperture material

> **NOTE**
> If you want to delete an aperture material after you commissioned the machine, you must recommission the machine. Also, if you delete a material that is used by an aperture in a plan, you must recreate that aperture with another material.

1 Click the **Aperture** tab in the **Beam Modifier Property Definition** window.
2 In the **Material List**, select the name of the material that you want to delete.
3 Click the **Delete** button.

Enter imaging device information

In order to generate setup DRR images, you must define the X-ray imaging devices in the treatment room. This information is used by the planning software to generate setup DRRs.

> **NOTE**
> The software only supports those imaging devices whose axes lie in the plane that is traced by the proton beam as it rotates. Out-of-plane imaging devices are not supported. You can generate DRRs out-of-plane by using an appropriate combination of imaging device axis angle and table angle position to generate the necessary imaging device axis relative to the patient.

Continuous X-ray imaging device

Follow this procedure if you use an X-ray imaging device that can rotate through a range of angles (for example, from 0 to 359 degrees). Continuous devices typically move in tandem with the gantry.

1 Click the **Imaging Devices** tab in the **Proton Machine Editor** window. The imaging device information appears in the window.
2 Click the **Add** button.
3 Type a name for the imaging device.
4 Select **Continuous** in the **Angle Mode** field.
5 Type the pairing angle value.

   The pairing angle is the angle at which the axis of the X-ray imaging device is located when the proton gantry is at 0 degrees.

6 Type the SAD and energy values.
7 If necessary, repeat steps 2-6 to add more continuous X-ray imaging devices.
8 To sort the **Imaging Devices** list in alphabetical order, click the **Sort** button.
9 In the **Proton Physics Tool** window, click the **Save Current Machine** button to save your changes.

Fixed X-ray imaging device

Follow this procedure if you use an X-ray imaging device that is fixed to the room coordinate system.

1 Click the **Imaging Devices** tab in the **Proton Machine Editor** window. The imaging device information appears in the window.
2 Click the **Add** button.
3 Type a name for the imaging device.
4 Select **Fixed** in the **Angle Mode** field.
5 Type the angle in the **Angle** field.

   If your imaging device is orthogonal to the axis of gantry rotation, type a value of 90 in the **Angle** field.

6 Type the SAD and energy values.

7 If necessary, repeat steps 2-5 to add more fixed X-ray imaging devices.

8 To sort the **Imaging Devices** list in alphabetical order, click the **Sort** button.

9 In the **Proton Physics Tool** window, click the **Save Current Machine** button to save your changes.

Enter other general machine parameters

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

2 Specify the following monitor unit information:

- **Monitor Unit decimal places for beams**—The software uses this value to round the monitor units for beams. The software rounds the monitor units after you calculate dose in Planning.

  If you set the decimal places to 0, the software rounds the number of monitor units to a whole number, which may result in differences between the monitor units in Pinnacle^3 and hand-computed monitor units.

- **Maximum MU setting**—This value is the maximum allowable monitor unit setting per beam for a machine.

- **When MU limit exceeded, warn and**—Specify the behavior of the system when the maximum monitor unit setting is exceeded.

  – If you select the **Limit beam MU to maximum setting** option, the actual monitor units required for a prescription are not displayed. Instead, the maximum monitor unit setting is displayed.

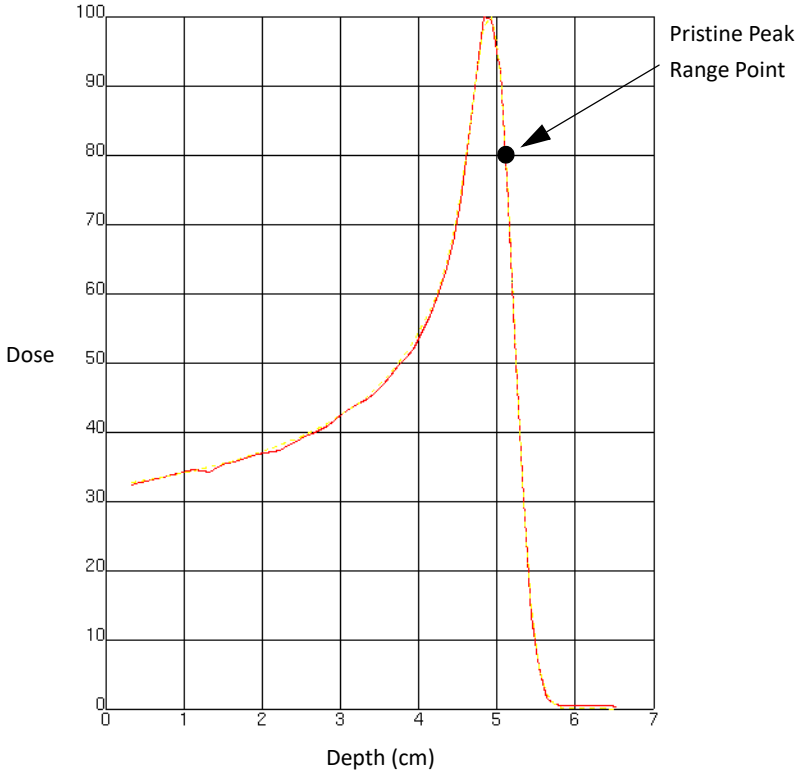
  – If you select the **Allow beam MU to exceed maximum** option, the software will allow the beam to exceed the maximum MU setting you defined so that the MU displayed will be the actual MU required for the prescription.

3 Specify the point level values.

4 In the point level fields, specify the percentage of the full scale that will represent the depth of the distal edge of the pristine peak and the depths of the proximal and distal edges of the SOBP for this machine. These point levels are used for indication only (for example, as the levels on graphs). They are not used in any of the fitting functions nor are they used in the determination of any of the model parameter values.

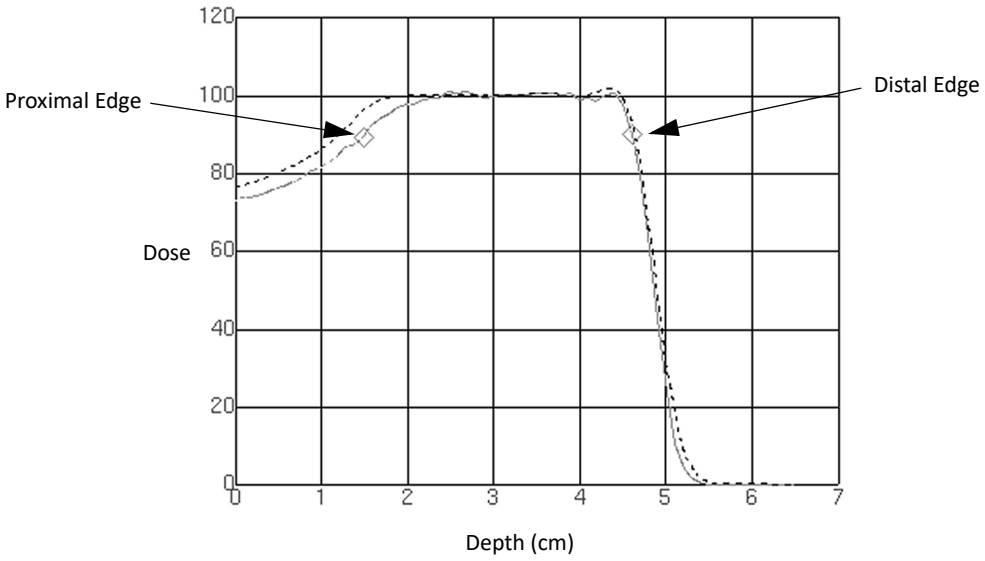
> **NOTE**
> Profiles that you import into the software must satisfy your institution's own definition of point levels for both Bragg peak and spread-out Bragg peak profiles. For example, if your institution's defined Bragg peak point level is 90%, then when plotted, a measured Bragg peak in water of range 5 g/cm^2 should have its 90% level at 5.00 cm +/- your institution's tolerance.
>
> All of an institution's point levels are implicitly contained in both the profile data and the resulting profile fit parameters. For example, when a Bragg peak for a set range of 5 g/cm^2 in the example above is fit, the resulting fit parameters are connected to a 5.00 g/cm^2 range defined at the 90% level, independent of the definitions that you typed into the model settings in the software.

- In the **Pristine Peak Range Point Level** field, type the value that you want to use to report the distal edge depth of the pristine peak. The following graphic shows a pristine peak depth of approximately 5.2 cm at an 80% level.



- In the **SOBP Proximal Edge Point Level** and **SOBP Distal Edge Point Level** fields, type the values that you want to use to report the proximal and distal edge depths of the SOBP. These values are percentages that the software uses to determine the associated depth for the different peak edges. The depths are not used in any of the modeling calculations, but are used for display and evaluation purposes. The following graphic shows a proximal edge depth

of approximately 1.5 cm and a distal edge depth of approximately 4.6 cm, both at a 90% level.



5 If you have enabled the Uniform Scanning delivery type for the machine, a field appears on the **Misc** tab that lets you choose whether to export the setting sequence for range modulators during planning. Specify your export preference in the field.

6 If you have enabled the Double Scattering delivery type for the machine, fields appear on the **Misc** tab that let you choose whether to export the setting sequences for lateral spreading devices and range modulators during planning. Specify your export preferences in the appropriate fields.

7 In the **Physics Tool** window, click **Save Current Machine** to save your changes.

12 Proton Beam Physics & Physics Utilities

NOTE
The information in this chapter is only applicable if you are licensed for proton treatment planning.

This chapter describes the proton beam physics modeling process. The process of adding machines and entering the general machine data is covered in the *Proton Machine Definition* chapter.

WARNING
The accuracy of the treatment planning dose calculation depends on the quality of the data entered in the physics tool. If the quality of this data is poor, or if the computed dose is not verified with measured data, the dose calculation may be inaccurate.

Select delivery type

You can commission a machine to use the double scattering or uniform scanning delivery types depending on the proton licenses that you purchased. Each delivery type has unique parameters and must be modeled separately from the others.

1 In the **Proton Physics Tool** window, select a delivery type from the **Delivery Type** list.

2 Continue to *Add range bands* to model the double scattering and uniform scanning delivery types.

Add range bands

A proton machine's total available deliverable range is divided into intervals, or range bands. The dose model parameter values are determined separately for each defined range band and, when appropriate, are modeled as a linear function of the range for each range band. This parameter linearization model produces calculated dose that agrees with measurements taken for beams of any arbitrary range value within a given range band.

This approach is as accurate as the linear variation of model parameters is with range. Range bands that span different machine options or configurations may not be accurate due to different hardware being inserted in the nozzle. In general, as the range band width increases, you should check for non-linear behavior, and, if necessary, reduce the width of the range band.

Before you can begin modeling, you must add range bands for the appropriate delivery types. Dose calculation in proton planning is only available for range and modulation values that are within the range bands that you define. For example, if you do not define a range band for ranges of 5–10 cm, you will not be able to compute dose for ranges in that interval.

Add range bands for double scattering

1 In the **Proton Physics Tool** window, click the **Add** button beneath the **Range Band List**. The software warns you that you are about to add a new proton range band.

2 Click the **OK** button. The **Range Band Parameters** window opens.

3 Type a name for the new range band in the **Range Band** field if you do not want to use the default name.

4 Type the ID of the range modulation wheel for this range band in the **Modulator ID** field.

   The ID value is defined by the manufacturer of your machine.

5 Type the IDs of the scatterers in the appropriate fields. The ID value is defined by the manufacturer of your machine.

   These IDs are sent with the RT-Ion data and must match the value that both the R&V system and the delivery machine expect.

6 Type the minimum and maximum range values for this range band in the **Range** field.

7 Type the minimum and maximum modulation values for this range band in the **Modulation** field.

8 Type the minimum and maximum field radius values for this range band in the **Field Radius** field.

   NOTE
   In planning, if overlapping range bands are present, the software automatically chooses the range band that has the smallest minimum field radius.

9 Click the **OK** button to save your changes and close the window.

10 Click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes to the machine.

11 Choose one of the following:

- Repeat this procedure, as needed, to add all of the necessary range bands for double scattering.
- Continue to *Model double scattering parameters* to model the new range band, and then return to create additional range bands.

Add range bands for uniform scanning

1 In the **Proton Physics Tool** window, click the **Add** button beneath the **Range Band List**. The software warns you that you are about to add a new proton range band.

2 Click the **OK** button. The **Range Band Parameters** window opens.

3 Type a name for the new range band in the **Range Band** field if you do not want to use the default name.

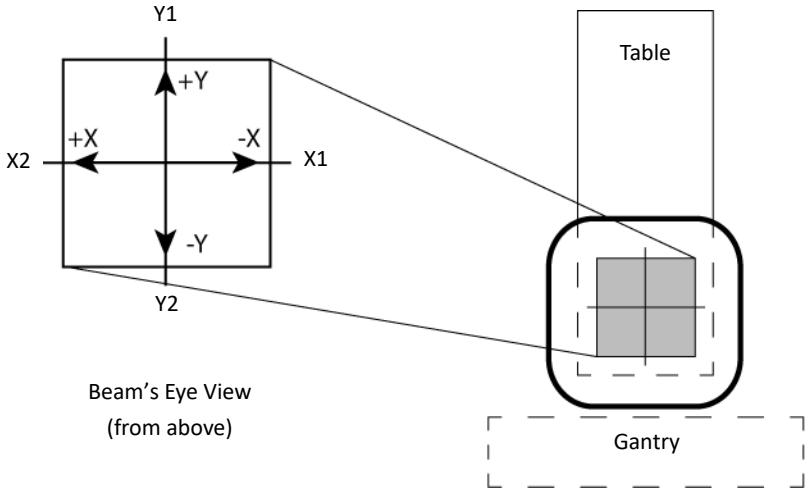
4 Type the ID of the range modulation wheel for this range band in the **Modulator ID** field.

The ID value is defined by the manufacturer of your machine.

5 Type the minimum and maximum range values for the range band in the **Range** field.

6 Type the minimum and maximum modulation values for the range band in the **Modulation** field.

7 Type the minimum and maximum X and Y field radius values for the range band in the **X Field Radius** and **Y Field Radius** fields with respect to the Pinnacle³ beam coordinate system shown below.



8 Click the **OK** button to save your changes and close the window.

9 Click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes to the machine.

10 Choose one of the following:

- Repeat this procedure, as needed, to add all of the necessary range bands for double scattering.
- Continue to *Model uniform scanning parameters* to model the new range band, and then return to create additional range bands.

Define a virtual water phantom for double scattering and uniform scanning

For each range band, you must define a virtual water phantom for the software to use to calculate dose profiles. These dose profiles will then be compared to measured dose profiles when you validate your models.

1 Click the **Model Settings** button in the **Proton Physics Tool** window. The **Model Settings window** opens.

2 Select a range band for which you want to define a virtual water phantom from the **Range Band** option list.

3 Type the lateral, depth, and resolution dimensions of the virtual water phantom. The dimensions do not have to match those of the water phantom that you use when collecting data, but the dimensions must be large enough to encompass the largest measured profile.

4 Repeat steps 2 and 3 until you have defined virtual water phantoms for all of the range bands.

5 Click the **Dismiss** button to close the window.

6 Choose one of the following:

- Continue to *Model double scattering parameters* to model double scattering range bands.
- Continue to *Model uniform scanning parameters* to model uniform scanning range bands.

Model double scattering parameters

After you have created the range bands for the machine, you must model the range bands. The section describes how to model double scattering range bands. For information about modeling uniform scanning range bands, see *Model uniform scanning parameters*.

1 In the **Proton Physics Tool** window, select **Double Scattering** from the **Delivery Type List**.

2 From the **Range Band List**, select the range band that you want to model.

3 Click the **Model** button. The **Proton Model Editor** window opens. Continue to *Model effective SAD in air for double scattering*.

Model effective SAD in air for double scattering

You must import at least three fluence profiles measured in air for each range band in order to model the Effective SAD.

For fluence profiles, Pinnacle^3 supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software. Be sure that your profiles are in the proper file format before you import them.

> **NOTE**
> Data in an IBA RFA-300 ASCII data file are in units of mm. Pinnacle^3 displays units in cm and computes values in units of cm. Pinnacle^3 converts the data from mm to cm when you import the data file.

For each range band, we recommend that you include fluence measurements that were taken between zero and the maximum range of the range band. The measurements that are taken below the minimum range of the range band are used to more accurately fit the effective SAD as a linear function of the set range.

> **NOTE**
> The software assumes that the beam is traveling in the positive Z direction; reverse your data to make it compatible with the direction of the beam, if necessary.

1 Select the **Effective SAD** tab in the **Proton Model Editor** window. The effective SAD profile information appears.

2 Click the **Import** button below the **Profile List** to import the fluence profiles. The **Proton Machine Profile Import** window opens.

3 Use the **Directory** list at the right to locate directories and measured data files on your hard disk.

   The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home** button.

4 Select one or more files to import.
   - To select multiple files that are contiguous in the directory list, hold down the **Shift** key and select the first and last files. All files in between are selected as well.
   - To select multiple files that are not contiguous in the directory list, hold down the **Control** key and select the files that you want to import.

5 Click the **OK** button. The imported fluence profile appears in the **Profile List**, and the initial normalization factor and effective SAD values for the selected profile are listed in the **Profile Fitting Parameters** section of the tab.

6 Repeat steps 2-5 until you have imported all of the necessary fluence profiles.

7 To view or edit the contents of an imported profile, go to *View and edit fluence profile data*.

8 In the **Range in Phantom** field in the **Profile Fitting Parameters** section of the tab, type the range for each profile in the **Profile List**. The range value must be unique for each profile.

   To switch from one profile to another, select the file name in the **Profile List**.

   NOTE
   The range value that you type in the **Range in Phantom** field should be the set range that was used when the measured data in the imported file was collected. Set range is the range that the beam would have in water after it exits the machine.

9 Perform an inverse square fit to the imported fluence measurements.
   - To perform the fit for one profile, select the profile from the **Profile List** and click the **Fit Current Profile Parameters** button.
   - To perform the fit for all of the profiles in the **Profile List**, click the **Fit All Profile Parameters** button.

   The fitted values for the file that is highlighted in the **Profile List** appear in the **Fitted Value** fields on the **Effective SAD** tab for both the **Effective SAD** and the **Normalization Factor**. In addition, the **ZFluence Fluence Comparison** window opens. The imported data is shown in red on the graph, the current computed data is shown in yellow, and previously computed data is shown in black.

10 Evaluate the fitted values.
   - The red and yellow curves on the graph should be aligned with each other.
   - You can verify that the fitted value for the **Normalization Factor** is a reasonable value. In the **ZFluence Fluence Comparison** window, scroll through the data in the table and find the row for a depth as close to 0.00 cm as possible. If the process of fitting the profile was successful, the **Measured** value in that row should closely match the value that is displayed in the **Normalization Factor Fitted Value** field on the **Effective SAD** tab.

11 If necessary, you can adjust the fitted values to get better alignment between the computed and measured fluence profiles. On the **Effective SAD** tab, iteratively change the values in the **Normalization Factor Fitted Value** and **Effective SAD Fitted Value** fields. When you type a new value, the data shown in the **ZFluence Fluence Comparison** window is updated.

   Adjust the fitted values until the measured and computed fluence profiles are aligned as much as possible.

12 To view the previously computed data (the data as it was prior to the last time the profiles were fitted) without invalidating or optimizing the current computed data, click the **View** button under **Profile Fitting Parameters** section.

> **NOTE**
> The **View** button is only active if you have fitted the profile parameters.

13 If you need to return the data and computed profiles to their original settings, select the profile that you want to reset from the **Profile List** and click the **Reset Fit** button on the **Effective SAD** tab. The values in the **Fitted Value** fields are set back to 0, and the data shown in the **ZFluence Fluence Comparison** window is returned to the original values.

> **NOTE**
> The **Reset Fit** button is only active if you manually change a value in one of the fitted value fields.

14 When you are finished fitting all of the fluence profiles, click the **Dismiss** button to close the **ZFluence Fluence Comparison** window.

15 On the **Effective SAD** tab, click the **Fit Range Band Parameters** button to linearly fit the effective SAD as a function of set range for the fluence profiles. The software computes the slope and intercept values for the effective SAD and displays them in the **Range Band Fitting Parameters** section of the tab.

16 You can evaluate the fitting of the range band by calculating the effective SAD using the range band slope and intercept values that are computed by the software. Calculate the following:

$$\text{Effective SAD} = \text{Slope} \cdot \text{Range} + \text{Intercept}$$

The effective SAD value that you calculate should closely match the effective SAD value that is shown in the **Profile Fitting Parameters** section of the tab. If you are not satisfied with the fitting, repeat the profile fitting for a given range band, manually adjusting the fit parameters or addressing deficient measured data as necessary.

> **NOTE**
> We recommend that you use a spreadsheet tool to plot the effective SAD fit parameter values versus the range values in order to evaluate how well your data were fit.

17 When you are satisfied with the modeling of the effective SAD for this range band, click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

18 Continue to *Model virtual SAD in air for double scattering*.

View and edit fluence profile data

1 Select the profile from the **Profile List** on the **Effective SAD** tab and click the **View** button. The **Proton Z Fluence Plot** window opens. The profile data and plot are shown in the window.

2 If necessary, you can adjust the values in the table. To change a value, click the table cell that you want to edit, and then type the new value in the field that appears above the table. When you type in the field, a green check mark and a red **x** appear next to the field. Click the green check mark or press **Enter** to accept the value. Click the red **x** to cancel the change. Click the

Insert Before or **Insert After** buttons to insert new rows before or after the currently selected row.

3 To change the profile that is shown in the window, select the profile from the **Profile** option list in the **Proton Z Fluence Plot** window.

4 To normalize the y-axis of the plot to 1.0 instead of the raw maximum value, set the **Normalize** field above the plot to **Yes**.

5 When you are finished viewing the data, click the **Dismiss** button to close the **Proton Z Fluence Plot** window.

Model virtual SAD in air for double scattering

You must import at least three measurement files of open field beams for each range band in order to compute the virtual SAD. Each measurement file that you import must contain at least three profiles at different depth positions in air for the set range of the machine at the time that the measurements were collected. These profiles that are grouped together within a file are referred to as a profile group in the software. The software fits the profiles within a profile group to determine the virtual SAD parameter value for the associated range value.

For measurement files of open field beams, Pinnacle^3 supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software. Be sure that your profiles are in the proper file format before you import them.

> **NOTE**
> Data in an IBA RFA-300 ASCII data file are in units of mm. Pinnacle^3 displays units in cm and computes values in units of cm. Pinnacle^3 converts the data from mm to cm when you import the data file.

1 Select the **Virtual SAD** tab in the **Proton Model Editor** window. The virtual SAD information appears.

2 Click the **Import** button below the **Profile Group List** to import the measurement files. The **Proton Machine Profile Import** window opens.

3 Use the **Directory** list at the right to locate directories and measured data files on your hard disk.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home** button.

4 Select one or more files to import.

- To select multiple files that are contiguous in the directory list, hold down the **Shift** key and select the first and last files. All files in between are selected as well.
- To select multiple files that are not contiguous in the directory list, hold down the **Control** key and select the files you want to import.

5 Click the **OK** button. The imported file appears in the **Profile Group List**.

Each measurement file that you import contains multiple profiles. The profiles are listed in the **Profile** option list in the **Profile Fitting Parameters** section of the tab. The normalization factor

and FWHM/2 (Half Width Half Maximum) values that are listed below the **Profile** option list pertain to the current profile. To view data for a different profile, select the profile from the **Profile** option list.

6 Repeat steps 2-5 until you have imported all of the necessary profiles.

7 To view or edit the contents of an imported file, go to *View and edit open field beam profile data*.

8 In the **Range in Phantom** field in the **Profile Group Parameters** section of the tab, type the range for each file in the **Profile Group List**. The range value must be unique for each file.

To switch from one file to another, select the file name in the **Profile Group List**.

NOTE
The range value that you type in the **Range in Phantom** field should be the set range that was used when the measured data in the imported file was collected. Set range is the range that an open field beam should have in water after it exits the machine.

9 Perform a fit of the imported profiles.

- To perform a fit for one file, select the file from the **Profile Group List** and click the **Fit All Profiles in Current Group** button.
- To perform a fit for all of the files in the **Profile Group List**, click the **Fit All Profiles in All Groups** button.

When you click a button, the following actions occur:

- The fitted values for the current profile appear in the **Normalization Factor Fitted Value** and **FWHM/2 Fitted Value** fields on the **Virtual SAD** tab.
- The software computes the slope, intercept, and virtual SAD values and displays them in the **Profile Group Parameters** section of the **Virtual SAD** tab.
- The **Proton Virtual SAD Fit Comparison** window opens. A plot for each profile contained in the current profile is shown in the window. The imported data is shown in red on each graph, the current computed data is shown in yellow, and previously computed data is shown in black.

10 Evaluate the fitted profiles.

- The red and yellow curves on each graph should be aligned with each other.
- You can verify that the fitted value for the FWHM/2 is a reasonable value. Click the **Detail** button in the **Proton Virtual SAD Fit Comparison** window. Then find the rows in the table, both left and right of the central axis, that contain a measured dose as close to 50% of maximum as possible. Add together the X position values for those two rows and divide the sum by 2. If the process of fitting the profile was successful, the result should closely match the value that is displayed in the **FWHM/2 Fitted Value** field on the **Virtual SAD** tab.

11 If necessary, you can adjust the fitted values for the profiles to get better alignment between the computed and measured profiles. On the **Virtual SAD** tab, select the profile that you want to adjust from the **Profile** list. Then, iteratively change the values in the **Normalization Factor Fitted Value** and **FWHM/2 Fitted Value** fields. When you type the new values, the profile shown in the **Proton Virtual SAD Fit Comparison** window for the selected profile is updated.

Adjust the fitted values until the measured and computed profiles are aligned as much as possible. Then click the **Fit All Profiles in Current Group** button to recompute the slope, intercept, and Virtual SAD values.

12 You can verify that the virtual SAD value is accurate by calculating virtual SAD using the calculated slope and intercept values

$$\text{Virtual SAD} = \text{Slope} \cdot Z + \text{Intercept}$$

where Z is the distance from the isocenter. The virtual SAD value that you calculate should closely match the virtual SAD value shown in the **Profile Group Parameters** section of the tab. If you are not satisfied with the fitting, fit the profiles again.

13 To view the previously computed data (the data as it was prior to the last time the profiles were fitted) without invalidating or optimizing the current computed data, click the **View** button.

NOTE
The **View** button is only active if you have fitted the profile parameters.

14 If you need to return the data and computed profiles to their original settings, click the **Reset Fit** button on the **Virtual SAD** tab. The values in the **Fitted Value** fields are set back to 0, and the data shown in the Proton **Virtual SAD Fit Comparison** window is returned to the original values.

NOTE
The **Reset Fit** button is only active if you manually change a value in one of the fitted value fields.

15 Do one of the following:

- If you clicked the **Fit All Profiles in Current Group** button in step 9 and have other files to fit, select another file from the **Profile Group List** on the **Virtual SAD** tab and click the **Fit All Profiles in Current Group** button to perform a fit of that file. Then, return to step 10 to evaluate the fitted profiles.
- If you clicked **Fit All Profiles in All Groups** button in step 9 and need to evaluate other fitted profiles, select another file from the **Profile** option list in the **Proton Virtual SAD Fit Comparison** window. Then return to step 10 to evaluate the fitted profiles in that profile group.
- If you have evaluated the fitted profiles for all of the measurement files that you imported, continue to step 16.

16 Click the **Dismiss** button to close the **Proton Virtual SAD Fit Comparison** window.

17 Click the **Fit Range Band Parameters** button to perform a linear fit for the virtual SAD as a function of range. The software computes the slope and intercept of the virtual SAD and displays the values in the **Range Band Fitting Parameters** section of the tab.

18 You can evaluate the fitting of the range band by calculating the virtual SAD using the range band slope and intercept values computed by the software. Calculate the following:

$$\text{Virtual SAD} = \text{Slope} \cdot \text{Range} + \text{Intercept}$$

The virtual SAD value that you calculate should closely match the virtual SAD value shown in the **Profile Group Parameters** section of the tab. If you are not satisfied with the fitting, fit the profiles and the range bands again.

NOTE
We recommend that you use a spreadsheet tool to plot the virtual SAD fit parameter values versus the range values in order to evaluate how well your data were fit.

19 When you are satisfied with the modeling of the virtual SAD for this range band, click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

20 Continue to *Model effective source size in air for double scattering*.

View and edit open field beam profile data

1 Select a file from the **Profile Group List** on the **Virtual SAD** tab and click the **View** button. The **Proton Virtual SAD Plot** window opens. A plot for each profile contained in the file is shown in the window.

2 Click the **Detail** button to view the data for each profile. The **Virtual SAD Details** window opens. The profile data and plot are shown in the window.

3 If necessary, you can adjust the values in the table. To change a value, click the field that you want to edit, then type the new value in the field that appears above the table. When you type in the field, a green check mark and a red **x** appear next to the field. Click the green check mark or press **Enter** to accept the value. Click the red **x** to cancel the change. Click the **Insert Before** or **Insert After** buttons to insert new rows before or after the currently selected row.

4 To change the profile that is shown in the window, select a profile from the **Position** option list near the top of the window.

5 When you are finished viewing the data, click the **Dismiss** button to close the **Virtual SAD Details** window. Then click the **Dismiss** button to close the **Proton Virtual SAD Plot** window.

Model effective source size in air for double scattering

You must import at least three measurement files of half beam blocked fields for each range band in order to compute the effective source size. Each measurement file that you import must contain at least three profiles at different depth positions in air for the set range of the machine at the time that the measurements were collected. These profiles that are grouped together within a file are referred to as a profile group in the software. The software fits the profiles within a profile group to determine the effective source size parameter value for the associated range value.

For measurement files of half beam blocked fields, Pinnacle^3 supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software. Be sure that your profiles are in the proper file format before you import them.

NOTE
Data in an IBA RFA-300 ASCII data file are in units of mm. Pinnacle^3 displays units in cm and computes values in units of cm. Pinnacle^3 converts the data from mm to cm when you import the data file.

For each range band, we recommend that you include measurements of half beam blocked fields that were taken between zero and the maximum range of the range band. The measurements that are taken below the minimum range of the range band are used to more accurately fit the effective source size as a linear function of the set range.

1 Select the **Effective Source Size** tab in the **Proton Model Editor** window. The effective source size information appears.

2 Click the **Import** button below the **Profile Group List** to import the measurement files. The **Proton Machine Profile Import** window opens.

3 Use the **Directory** list at the right to locate directories and measured data files on your hard disk.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home** button.

4 Select one or more files to import.

- To select multiple files that are contiguous in the directory list, hold down the **Shift** key and select the first and last files. All files in between are selected as well.
- To select multiple files that are not contiguous in the directory list, hold down the **Control** key and select the files that you want to import.

NOTE
If you are selecting multiple files for import at one time, make sure that all of the files that you select are blocked on the same side (left or right).

5 Specify if the half beam in the selected file is blocked on the left or right by clicking the **Left** or **Right** option button in the **Blocked** field.

6 Click the **OK** button. The imported file appears in the **Profile Group List**.

Each measurement file that you import contains profiles. The profiles are listed in the **Profile** option list in the **Profile Fitting Parameters** section of the tab. The **Normalization Factor** and **Sigma** values listed below the **Profile** option list pertain to the current profile. To view data for a different profile, select the profile from the **Profile** option list.

7 Repeat steps 2-6 until you have imported all of the necessary measurement files.

8 To view or edit the contents of an imported file, or to adjust the offset prior to performing the linear fit, go to *View and edit half beam blocked profile data*.

9 In the **Range in Phantom** field in the **Profile Group Parameters** section of the tab, type the range for each file in the **Profile Group List**. The range value must be unique for each file.

To switch from one file to another, select the file name in the **Profile Group List**.

NOTE
The range value that you type in the **Range in Phantom** field should be the set range that was used when the measured data in the imported file was collected. Set range is the range that the beam would have in water after it exits the machine.

10 Perform a linear fit of the imported profiles.

- To perform a fit for one file, select the file from the **Profile Group List** and click the **Fit All Profiles in Current Group** button.
- To perform a fit for all of the files in the **Profile Group List**, click the **Fit All Profiles in All Groups** button.

When you click a button, the following actions occur:

- The fitted values for the current profile appear in the **Normalization Factor Fitted Value** and **Sigma Fitted Value** fields on the **Effective Source Size** tab.
- The software computes the slope, intercept, and effective source size values for the current profile and displays them in the **Profile Group Parameters** section of the **Effective Source Size** tab.
- The **Proton Half Beam Profile Plot** window opens. A plot for each profile contained in the current profile is shown in the window. The imported data is shown in red on each graph, the current computed data is shown in yellow, and previously computed data is shown in black.

11 Evaluate the fitted profiles. The red and yellow curves on each graph should be aligned with each other, and the correct side of the profile should be fitted (the left side is fitted for a left-blocked profile, or the right side is fitted for a right-blocked profile).

12 If the edge of the asymmetric block was not located at 0 cm when the profiles were measured, change the value in the **Offset** field to define where the edge of the asymmetric block was located. The profiles shift according to the value that you enter.

> **NOTE**
> A block edge is located at 0 cm when the 50% level of the edge of the block is at 0 cm.

13 If necessary, you can adjust the fitted values for the profiles to get better alignment between the computed and measured profiles. On the **Effective Source Size** tab, select the profile that you want to adjust from the **Profile** option list. Then, iteratively change the values in the **Normalization Factor Fitted Value** and **Sigma Fitted Value** fields. When you type the new values, the profile shown in the **Proton Half Beam Profile Plot** window for the selected profile is updated.

Adjust the fitted values until the measured and computed profiles are aligned as much as possible. Then click the **Fit All Profiles in Current Group** button to recompute the slope, intercept, and **Effective Source Size** values.

14 You can verify that the effective source size value is accurate by calculating effective source size using the nominal SAD for the machine and the computed slope and intercept values:

$$\text{Effective Source Size} = \text{Slope} \cdot Z + \text{Intercept}$$

where Z is the distance from the isocenter. The effective source size value that you calculate should closely match the effective source size value that is shown in the **Profile Group Parameters** section of the tab. If you are not satisfied with the fitting, fit the profiles again.

15 To view the previously computed data (the data as it was prior to the last time the profiles were fitted) without invalidating or optimizing the current computed data, click the **View** button.

NOTE
The **View** button is only active if you have fitted the profile parameters.

16 If you need to return the data and computed profiles to their original settings, click the **Reset Fit** button on the **Effective Source Size** tab. The values in the **Fitted Value** fields are set back to 0, and the data shown in the **Proton Half Beam Profile Plot** window is returned to the original values.

17 Do one of the following:

- If you clicked the **Fit All Profiles in Current Group** button in step 10 and have other files to fit, select another file from the **Profile Group List** on the **Effective Source Size** tab and click the **Fit All Profiles in Current Group** button to perform a linear fit of that file. Then, return to step 11 to evaluate the fitted profiles.
- If you clicked **Fit All Profiles in All Groups** button in step 10 and need to evaluate other fitted profiles, select another file from the **Profile** option list in the **Proton Half Beam Profile Plot** window. Then return to step 11 to evaluate the fitted profiles in that profile group.
- If you have evaluated the fitted profiles for all of the measurement files that you imported, continue to step 18.

18 Click the **Dismiss** button to close the **Proton Half Beam Profile Plot** window.

19 Click the **Fit Range Band Parameters** button to perform a linear fit for the effective source size as a function of set range. The software computes the slope and intercept of the effective source size and displays the values in the **Range Band Fitting Parameters** section of the tab.

20 You can evaluate the fitting of the range band by calculating the effective source size using the range band slope and intercept values computed by the software. Calculate the following:

$$\text{Effective Source Size} = \text{Slope} \cdot \text{Range} + \text{Intercept}$$

The effective source size value that you calculate should closely match the effective source size value that is shown in the **Profile Group Parameters** section of the tab. If you are not satisfied with the fitting, fit the profiles and the range bands again.

NOTE
We recommend that you use a spreadsheet tool to plot the effective source size fit parameter values versus the range values in order to evaluate how well your data were fit.

21 When you are satisfied with the modeling of the effective source size for this range band, click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

22 Continue to *Model pristine peak for double scattering*.

View and edit half beam blocked profile data

1 Select a file from the **Profile Group List** on the **Effective Source Size** tab and click the **View** button. The **Proton Half Beam Profile Plot** window opens. A plot for each profile that is contained in the file is shown in the window.

2 Click the **Detail** button to view the data for each profile. The **Proton Half Beam Details** window opens. The profile data and plot are shown in the window.

3 If necessary, you can adjust the values in the table. To change a value, click the field that you want to edit, then type the new value in the field that appears above the table. When you type in the field, a green check mark and a red **x** appear next to the field. Click the green check mark or press **Enter** to accept the value. Click the red **x** to cancel the change. Click the **Insert Before** or **Insert After** buttons to insert new rows before or after the currently selected row.

4 If the edge of the asymmetric block was not located at 0 cm when the profiles were measured, change the value in the **Offset** field to define where the edge of the asymmetric block was located. The profiles shift according to the value that you enter.

5 To change the profile that is shown in the window, select a profile from the **Position** option list near the top of the window.

6 When you are finished viewing the data, click the **Dismiss** button to close the **Proton Half Beam Details** window. Then click the **Dismiss** button to close the **Proton Half Beam Profile Plot** window.

Model pristine peak for double scattering

You must import at least three Bragg peak measurement files in order to complete the modeling of the pristine peak for each range band.

For Bragg peak measurements, Pinnacle^3 supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software and a CSV data file format that is produced by OmniPro-Incline software. Be sure that your profiles are in the proper file format before you import them.

The software normalizes the measured and fitted profiles to 100 relative dose units. Thus the fitting algorithm is sensitive to the peak dose of the profile. Before you import data, please be sure to accurately determine the peak dose while you are measuring the pristine peak to ensure an accurate fitting process.

> **NOTE**
> You cannot model the pristine peak for a range band until you have modeled the effective SAD for that range band. The software uses the effective SAD to remove the inverse square dependence from the Bragg peak prior to fitting.
>
> Data in an IBA RFA-300 ASCII data file are in units of mm. Pinnacle^3 displays units in cm and computes values in units of cm. Pinnacle^3 converts the data from mm to cm when you import the data file.

1 Select the **Pristine Peak** tab in the **Proton Model Editor** window. The pristine peak information appears.

2 Click the **Import** button below the **Profile List** to import the Bragg peak measurements. The **Proton Machine Profile Import** window opens.

3 Use the **Directory** list at the right to locate directories and measured data files on your hard disk.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home** button.

4 Select one or more files to import.

- To select multiple files that are contiguous in the directory list, hold down the **Shift** key and select the first and last files. All files in between are selected as well.
- To select multiple files that are not contiguous in the directory list, hold down the **Control** key and select the files that you want to import.

5 Click the **OK** button. The imported file appears in the **Profile List**. The initial **RZero**, **SigmaZero**, **Epsilon**, and **SigmaOne** values are listed in the **Profile Fitting Parameters** section of the tab.

- **RZero** is the fitting parameter that represents the range from the model for the depth dose distribution of the Bortfeld Bragg peak. The **RZero** parameter equals the water equivalent distance of the distal 80% value of the Bragg peak.
- **SigmaZero** and **SigmaOne** are two parameters that represent the width of the Gaussian range straggling, where **SigmaOne** adds a depth dependence to the model.
- **Epsilon** is the fitting parameter from the Bortfeld Bragg peak depth dose distribution model representing the fraction of primary fluence contributing to the “tail” of the energy spectrum.

6 Repeat steps 2-5 until you have imported all of the necessary Bragg peak measurement files.

7 To view or edit the contents of an imported file, go to *View and edit Bragg peak profiles*.

8 In the **Range** and **Nominal SSD** fields, type the range and nominal SSD for each profile in the **Profile List**. The range value must be unique for each profile.

To switch from one profile to another, select the file name in the **Profile List**.

> **NOTE**
> The values that you type are the set range and the nominal SSD that were used when the measurement was performed. The nominal SSD is the physical distance from the water surface to the nominal source.

9 In the **Measurement Depth Offset** field, type the measurement offset value.

This field allows you to shift the profile in the z direction. This may be necessary if the measured depth dose profiles are shifted due to materials in the field (for example, the walls of the water tank or ion chamber). If the data was corrected for these items prior to import, the value in the **Measurement Depth Offset** field should be 0.

10 Perform a fit of the imported Bragg peak measurements.

- To perform a fit for one file, select the file from the **Profile List** and click the **Fit Current Profile Parameters** button.
- To perform a fit for all of the files in the **Profile List**, click the **Fit All Profile Parameters** button.

The fitted values for the file that is highlighted in the **Profile List** appear in the **RZero Fitted Value**, **SigmaZero Fitted Value**, **Epsilon Fitted Value**, and **SigmaOne Fitted Value** fields on the **Pristine Peak** tab. In addition, the **Pristine Peak Fitting Comparison** window opens. The measured Bragg peak data, Bragg peak profile, and the **% Error** plot are shown in the window. In the Bragg peak profile, the imported data is shown in red, the current computed data is shown in yellow, and previously computed data is shown in black.

NOTE
The fitting algorithm for the modeling parameters of the individual curves may fall into a local minima. The computed curves may not optimally match the measured data, or the fitting algorithm may find a solution that is not linearly correlated to other fitting results within the same range band. If this occurs, adjust the **Init Value** of one or more of the fitting parameters, fit the profiles again, and evaluate the results again. With regard to fitting the pristine peak, failure to correct this issue may cause unwanted tilting or sharp distal peaks in the SOBP fitting, especially with ranges that approach the minimum of the range band.

11 Evaluate the fitted profiles.
- The red and yellow curves on each graph should be aligned with each other.
- You can verify that the fitted value for RZero is a reasonable value. In the **Pristine Peak Fitting Comparison** window, scroll through the data in the table and find the row for a measured distal dose as close to 80% as possible. If the profile fitting process was successful, the depth value in that row should closely match the value that is displayed in the **RZero Fitted Value** field on the **Pristine Peak** tab.

12 If necessary, you can adjust the fitted values for the Bragg peaks to get better alignment between the computed and measured profiles. On the **Pristine Peak** tab, iteratively change the values in the **RZero**, **SigmaZero**, **Epsilon**, and **SigmaOne Fitted Value** fields. When you type the new values, the data shown in the **Pristine Peak Fitting Comparison** window is updated.

Adjust the fitted values until the measured and computed profiles are aligned as much as possible.

13 To view the previously computed data (the data as it was prior to the last time the profiles were fitted) without invalidating or optimizing the current computed data, click the **View** button under **Profile Fitting Parameters** section.

NOTE
The **View** button is only active if you have fitted the profile parameters.

14 To return the data and profiles to their original values, click the **Reset Fit** button on the **Pristine Peak** tab. The values in the **Fitted Value** fields are set back to 0, and the data shown in the **Pristine Peak Fitting Comparison** window is returned to the original values.

NOTE
The **Reset Fit** button is only active if you manually change a value in one of the fitted value fields.

15 Repeat steps 10-12 until you have fitted all of the Bragg peak measurement files that you imported.

16 Click the **Dismiss** button to close the **Pristine Peak Fitting Comparison** window.

17 Click the **Fit Range Band Parameters** button. The software computes the slope and intercept of RZero, SigmaZero, Epsilon, and SigmaOne and displays the values in the **Range Band Fitting Parameters** section of the tab.

18 You can evaluate the fitting of the range band by calculating the RZero value using the range band RZero slope and intercept values computed by the software. Calculate the following:

$$\text{RZero Fitted Value} = \text{RZero Slope} \cdot \text{Range} + \text{RZero Intercept}$$

The value that you calculate should closely match the value shown in the **RZero Fitted Value** field in the **Profile Fitting Parameters** section of the tab. If you are not satisfied with the fitting, fit the profiles and the range bands again.

NOTE
We recommend that you use a spreadsheet tool to plot each fit parameter value versus the range value in order to evaluate how well your data were fit.

19 If you want to evaluate the Bragg peak model, go to *Evaluate the Pristine Peaks*.

20 When you are satisfied with the modeling of the pristine peaks for this range band, click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

21 Continue to *Model spread-out Bragg peak components*.

View and edit Bragg peak profiles

1 Select the profile from the **Profile List** on the **Pristine Peak** tab and click the **View** button. The **Proton Pristine Plot** window opens. The profile data and plot are shown in the window.

2 If necessary, you can adjust the values in the table. To change a value, click the field that you want to edit, and then type the new value in the field that appears above the table. When you type in the field, a green check mark and a red **x** appear next to the field. Click the green check mark or press **Enter** to accept the value. Click the red **x** to cancel the change. Click the **Insert Before** or **Insert After** buttons to insert new rows before or after the currently selected row.

3 To change the profile that is shown in the window, select the profile from the **Profile** option list in the **Proton Pristine Plot** window.

4 When you are finished viewing the data, click the **Dismiss** button to close the **Proton Pristine Plot** window.

Evaluate the Pristine Peaks

When you have finished modeling the pristine peaks, you can evaluate the Bragg Peak model for this range band.

1 In the **Pristine Peak** tab, click the **Evaluation** button. The **Pristine Peak Evaluation** window opens.

2 To evaluate the ability of the model to plot a Bragg peak for any range within the range band, type the nominal SSD in the **Nominal SSD** field and a range value in the **Range** field. A Bragg peak for the range that you entered appears in the window.

3 To evaluate the model against measured depth dose data, click **Yes** in the **Test with measurement** field.

4 If the file that you plan to import contains multiple depth dose profiles, type the number of the profile that you want to use in the **Index** field.

NOTE
Individual profiles are indexed starting at 0, not 1.

5 Click the **Import** button. The **Proton Machine Test Profile Import** window opens.

6 Use the **Directory** list at the right to locate directories and measured data files on your hard disk.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home** button.

7 Select a file to import.

8 Click the **OK** button. The measured data appears in the window. In the Bragg peak profile, the imported data is shown in red and the current computed data is shown in yellow.

9 In the **Index** field, enter the value of the index that was used when the measured depth dose data was collected.

10 In the **Measurement Depth Offset** field, enter the value of the offset that was used when the measured depth dose data was collected.

11 In the **Nominal SSD** field, enter the nominal SSD that was used when the measured depth dose data was collected.

12 In the **Range** field, enter the range that was used when the measured depth dose data was collected.

13 Review the fit of the profiles.

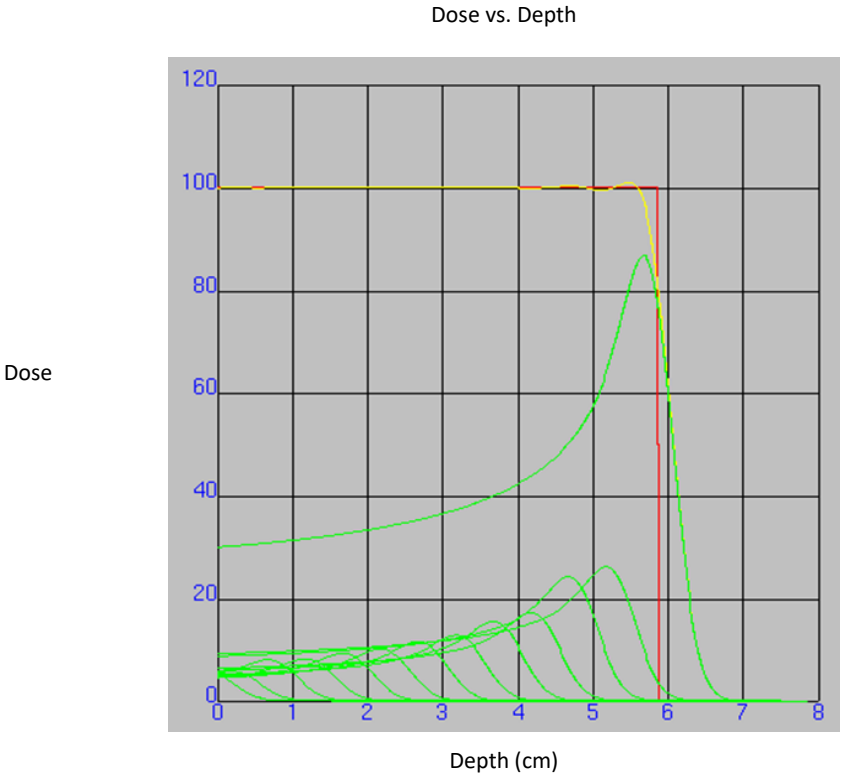
- If you are satisfied with the fit, click the **Dismiss** button to close the **Pristine Peak Evaluation** window. This procedure is complete.
- If the measured and computed profiles are not well aligned, click the **Dismiss** button to close the **Pristine Peak Evaluation** window and model the pristine peaks for the range band again.

Model spread-out Bragg peak components

NOTE
You must complete the modeling of the effective SAD, the virtual SAD, the effective source size, and the pristine peak before you model the spread-out Bragg peak (SOBP) components. Information from those models is necessary for the successful modeling of an SOBP.

When you model the components of the fully-modulated SOBP (see the graph below), you are establishing the information needed to build the SOBP functions for each range band. These specific SOBP functions need to reproduce the respective SOBPs delivered by the proton machine. (A fully-modulated SOBP is one in which the range equals the modulation. Ideally, the dose is completely flat from a depth of 0 cm to a depth equal to the range.) During modeling, you will

optimize the weights of the components necessary to build an appropriate SOBP function for the range band.



Pullback defines the position of a pristine peak relative to another pristine peak. The positions are determined using a specified level on the distal edge, for example 90% of peak maximum. An SOBP is composed of pristine peak components. A pullback interval is the distance in g/cm^2 between each two adjacent components in the SOBP. The cumulative pullback is the distance between a given component and the most distal component in the SOBP.

1 Select the **SOBP Components** tab in the **Proton Model Editor** window.

2 In the **Pullback Interval** field, type a pullback interval from 0.1–2.0 g/cm^2. We suggest a starting value that is close to the 80-80% width of a Bragg peak at the maximum range of the range band.

3 Click the **Populate Weight Table** button. The software creates the SOBP component weight table.

Each row in the table represents information for a single SOBP component. The number of components is determined by the maximum range values divided by the pullback interval. The first component has a default pullback interval of 0.00 g/cm^2. The pullback interval and the cumulative pullback for each component are both listed in the table. The weights are equal for all components in this initial table.

4 If necessary, you can adjust the values in the table. To change a value, click the field that you want to edit, then type the new value in the field that appears above the table. When you type

in the field, a green check mark and a red **x** appear next to the field. Click the green check mark or press **Enter** to accept the value. Click the red **x** to cancel the change. Click the **Insert Before** and **Insert After** buttons to add additional rows to the table.

5 You can lock the components in the weight table so that the optimization process does not change the weight value for that component. A value of 0 in the **Lock** column means that the row is not locked, and a value of 1 means that the row is locked.

- To lock all of the rows in the table, click the **Yes** button in the **Lock all rows?** field.
- To lock only certain rows in the table, type the number 1 in the **Lock** column for those rows. The optimization will not change the values in the locked rows but may change values in the unlocked rows as necessary to obtain the best optimization results.

NOTE
Locking a row only prevents the optimization process from changing the weight value in that row. You can manually change the values in all of the rows whether or not they are locked.

6 When you are satisfied with the values in the weight table, click the **Optimize** button to optimize the weights of the components that you have defined. The software displays the components and the computed SOBP in a graph when the optimization is complete.

NOTE
The goal of the optimization algorithm is for the sum of the component curves to be 100% at each depth (or 1.0 if the graph is normalized) from the surface to the maximum range of the range band. A weight is the maximum height (amplitude) of a Bragg peak component, and the weights of all of the components are not normalized to the first component or to the sum of all of the weights.

NOTE
Depending on the number of entries in the weight table and the depth of the range band, the optimization of the weight table can take 30 seconds or more to complete. The deeper the range band, the more time it will take to complete the optimization.

NOTE
If the weight table becomes invalid after you have optimized it (for example, you change one of the modeling parameters), the word **Invalid** appears on the tab next to the **Optimize** button.

7 Click the **Details** button to view a detailed display of the computed 1-dimensional SOBP function. The **SOBP Details** window opens. The table that appears in the window contains the differences between the computed SOBP and the 100% dose values for each pullback interval. (The 100% dose values are represented by the red line on the graph so that you can compare the dose values of the computed SOBP with the 100% dose values. The red line extends from 0 to the maximum range of the range band on the x-axis, and it is located at 100% dose on the y-axis. The current computed data is shown in yellow on the graph, and previously computed data is shown in black. The components are shown in green.)

8 Review the components and the SOBP. The SOBP in the graph should be as flat as possible. If necessary, you can iteratively change the data and optimize the table until you are satisfied with the results. Possible changes include the following:

- Click the **Optimize** button more than once to optimize the existing values again.
- Adjust the weight values of certain components and lock those rows.
- Change the pullback interval to obtain a flatter SOBP function. For example, a pullback interval of 0.7 g/cm^2 may produce a flatter SOBP function than a value of 0.5 g/cm^2.

NOTE
If you change the pullback interval, click the **Populate Weight Table** button to recreate the SOBP component weight table.

9 When you are satisfied with the modeling of the SOBP components for this range band, continue to *Model the modulation table for double scattering*.

Model the modulation table for double scattering

NOTE
Before you can create a cumulative weight table, you must complete the optimization of the SOBP component weight table on the **SOBP Components** tab.

The modulation table represents the sum of the component weights that is required to generate an SOBP of a given modulation for the range band. The modulation table also contains an entry for a partial shining factor for each modulation.

In planning, the modulation table is used to determine how Pinnacle^3 should compute the SOBP function necessary to cover the target that is assigned to that beam. If an entry for a specific modulation is not present in the table, the software will interpolate the cumulative weight between modulations that are commissioned to generate the proper SOBP.

You must import at least three SOBP depth dose profiles measured in water for each range band in order to complete the modeling of the modulation table.

NOTE
When you import the measured data, we recommend that you include measured SOBPs with ranges that approach the minimum range of the range band in order to verify the accuracy of the computed SOBPs across the entire range band.

For SOBP depth dose profiles, Pinnacle^3 supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software and a CSV data file format that is produced by OmniPro-Incline software. Be sure that your profiles are in the proper file format before you import them.

NOTE
Data in an IBA RFA-300 ASCII data file are in units of mm. Pinnacle^3 displays units in cm and computes values in units of cm. Pinnacle^3 converts the data from mm to cm when you import the data file.

The minimum number of SOBP depth dose profiles required for modeling is three, but we recommend that you import more than three to create a more accurate modulation table. More SOBP depth dose profiles will produce better interpolation results.

1 Select the **Modulation Table** tab in the **Proton Model Editor** window.

2 Click the **Import** button below the **Profile List**. The **Proton Machine Profile Import** window opens.

3 Use the **Directory** list at the right to locate directories and measured data files.

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, click the directory name in the list. To return to your home directory, click the **Home** button.

4 Select one or more files to import.

- To select multiple files that are contiguous in the directory list, hold down the **Shift** key and select the first and last files. All files in between are selected as well.
- To select multiple files that are not contiguous in the directory list, hold down the **Control** key and select the files that you want to import.

5 Click the **OK** button. The imported files appear in the **Profile List**.

6 Repeat steps 2-5 until you have imported all of the necessary measured depth dose profiles.

7 To view or edit the contents of an imported profile, go to *View and edit depth dose profile data*.

8 After you import all of the depth dose profiles, you must fit the profiles that are computed by the software to the measured profiles. Select the first file to fit from the **Profile List** on the **Modulation Table** tab.

9 Enter a range value in the **Range** field.

10 Type the modulation and nominal SSD values in the **Modulation** and **Nominal SSD** fields. The values that you specify must be the values that were set at the machine when the measured data were collected.

After you enter the nominal SSD value, the software computes and displays the initial number of pullbacks and initial cumulative weight required for the range and modulation that you specified. These components are shown in a table when you press the **Enter** key after you type the modulation value for the profile.

NOTE
The software will prevent you from creating the modulation table unless the first profile in the **Profile List** has a modulation that is equal to the minimum modulation of the range band within +/-0.01 g/cm^2 and the last profile in the **Profile List** has a modulation that is equal to the maximum modulation of the range band within +/-0.01 g/cm^2.

NOTE
The modulation value is the modulation that the beam would exhibit if it were in water. The software assumes that each imported SOBP curve meets your facility's defined levels for distal and proximal edge locations. Importing data that do not meet this requirement may lead to errors in calculated dose.

11 In the **Measurement Depth Offset** field, type the measurement offset value.

This field allows you to shift the profile in the z direction. This may be necessary if the measured depth dose profiles are shifted due to materials in the field (for example, the walls of the water tank or ion chamber). If the data were corrected for these items prior to import, the value in the **Measurement Depth Offset** field should be 0.

12 Click the **Evaluate SOBP with 1D Calculation** button to display the computed and measured SOBP. The **Evaluate SOBP** window opens. The imported SOBP data is shown in red on the graph, the current computed data is shown in yellow, and the previously computed data is shown in black.

The proximal edge depth and distal edge depth values are shown on the graph with diamond-shaped markers when **Show Edge Depth Markers** field is set to **Yes**. The measured values are shown with red markers and the computed values are shown with yellow markers. The markers show levels that are defined in the **Model Settings** window and are intended to show your facility's definitions of these levels. See *Define a virtual water phantom for double scattering and uniform scanning*.

NOTE
You may notice unwanted tilting or distinct, sharp distal peaks of the computed SOBPs when you compare them to the measured SOBPs with ranges that approach the minimum range of the range band. This may occur if the pristine peak fitting parameters for **SigmaOne**, **Epsilon**, and **SigmaZero** vary too much across the range band. To mitigate the problem, return to the **Pristine Peak** tab and manually reduce the slope of the **SigmaOne**, **Epsilon**, and **SigmaZero** fitting parameters by adjusting the fitted values of each profile to an average value across the range band. (Do not change the **RZero** value.) Changing these parameters may reduce the accuracy of the fit for the individual pristine peaks, but may also remove the tilting and sharp distal peak of the computed SOBPs in the **Modulation** tab. Alternatively, you could split this range band into finer bands in an attempt to reduce the tilting and sharp distal peaks.

13 To normalize the profiles at a specific depth, enter the depth value in the **Connect curves at depth (cm)** field. The value that you enter becomes the point at which the measured and computed profiles are connected.

For best results, connect the curves in a region of the profiles that is relatively flat.

14 To include the SOBP components in the graph, click the **Yes** button in the **Show Components** field.

15 To include the edge depth markers in the graph, click the **Yes** button in the **Show Edge Depth Markers** field.

16 To normalize the y-axis of the plot to the modulation mean instead of the maximum plateau value, set the **Normalize to modulation mean** field above the plot to **Yes**.

17 To adjust the proximal edge of the computed profile to get better agreement between the computed and measured profiles, iteratively change the **Cumulative Weight** value until the profiles are more closely aligned.

18 To adjust the proximal shoulder of the computed SOBP profile, change the **Partial Shining Factor** value.

19 Repeat steps 17-18 until you are satisfied with the agreement of the computed and measured profiles.

20 Click the **Details** button to view details of the 1-dimensional SOBP. The **Evaluate 1D Details** window opens. The table that appears in the window contains the following data: depth in cm, the measured and computed dose at each depth, and the difference, error percentage, and distance to agreement between the measured and computed dose. The window also contains a

plot of the current profile. The imported data is shown in red on the graph, the current computed data is shown in yellow, and the previously computed data is shown in black.

21 Choose one of the following options:

- If you need to generate another entry for the modulation table, select a file from the **Profile List** on the **Modulation Table** tab and return to step 9.
- If you are finished generating entries in the modulation table, continue to step 22.

22 Click the **Transfer All to Modulation Table** button on the **Modulation Table** tab to generate the modulation table. Then click the **Display Weight vs. Modulation Plot** button to view the modulation table and graph.

23 To view the cumulative weight value for any modulation in the graph, enter a modulation value in the **Modulation** field. The software determines the intermediate modulation values through quadratic interpolation.

24 When you are satisfied with the modulation table, continue to *Validate the model for double scattering*.

> **NOTE**
> The modulation table will be invalidated if you change any of the associated depth dose profiles or the profile parameters, which include the range, modulation, nominal SSD, partial shining factor, and cumulative weight.

View and edit depth dose profile data

1 Select the profile from the **Profile List** on the **Modulation Table** tab and click the **View** button. The **SOBP Profile Plot** window opens. The profile data and plot are shown in the window.

2 If necessary, you can adjust the values in the table. To change a value, click the table cell that you want to edit, and then type the new value in the field that appears above the table. Click the green check mark next to the field or press **Enter** to accept the value. Click the red **x** to cancel the change. Click the **Insert Before** or **Insert After** buttons to insert new rows before or after the currently selected row.

3 To change the profile that is shown in the window, select the profile from the **Profile** option list in the **SOBP Profile Plot** window.

4 To normalize the y-axis of the plot to 1.0 instead of the raw maximum value, set the **Normalize** field above the plot to **Yes**.

5 When you are finished viewing the data, click the **Dismiss** button to close the **SOBP Profile Plot** window.

Validate the model for double scattering

When you are finished modeling the machine, you must validate the accuracy of your model by comparing at least one computed longitudinal (depth) dose profile or lateral (cross beam) profile against measured depth dose profiles and cross beam profiles for each range band.

NOTE
We recommend that you validate multiple depth dose and cross beam profiles against a measured profile in water phantom.

Add or edit measurement settings

Before you import measured data that will be used to validate the model, you must define the geometry specific to that measurement by making entries in the **Measurement Setting List**. Each range band has its own **Measurement Setting List**, and each entry in the list contains one or more profiles, each of which share a common setup and machine geometry.

1 Go to the **Proton Physics Tool** window.

2 Select **Double Scattering** from the **Delivery Type List**.

3 Select a range band from the **Range Band List**.

4 Do you want to add a new measurement setting or edit an existing measurement setting?

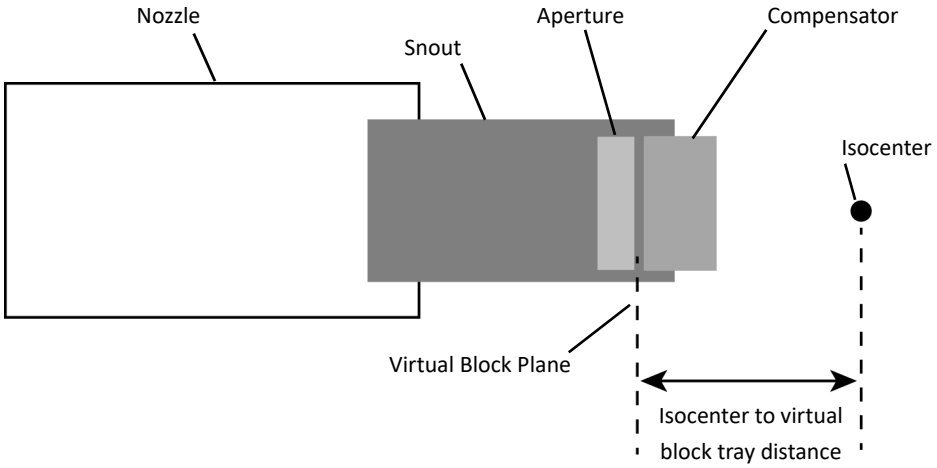
- To add a new measurement setting, click the **Add** button beneath the **Measurement Setting List**. The **Proton Data Measurement Setting** window opens.
- To edit an existing measurement setting, select the measurement setting from the **Measurement Settings List**, and click the **Edit** button beneath the **Measurement Setting List**. The **Proton Data Measurement Setting** window opens.

5 Complete the fields in the **Machine Delivery Settings** and **Field Setup** sections of the window with the values that were used when the measured data that you will associate with this measurement setting were collected.

After you specify the range, modulation, snout position and nominal SSD, the software computes the size of the field and displays the data in the **Physical Size** fields. The software also computes the estimated size of the beam at isocenter based on the virtual SAD and displays the data in the **Isocenter Size** fields. If you change the field size, the software recomputes the beam size at isocenter and updates the values in the **Isocenter Size** fields.

NOTE
The range, modulation, snout position, and nominal SSD values that you specify must be the values that were set at the machine when the measured data were collected. The imported profiles should match your facility's definitions for range and modulation expected from those machine settings and measurement in water.

Pinnacle³ defines the snout position as the distance from the isocenter to the virtual block tray as shown in the graphic that follows.



CAUTION
Verify that the measurement settings are correct before you save the data.

6 When you have specified the measurement settings, click the **Dismiss** button.

NOTE
Each measurement setting can have any number of profiles associated with it. If the same measurement settings were used for a number of measurements, you only need to enter the measurement settings once.

7 Click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

8 To delete a measurement setting, select the measurement setting from the **Measurement Setting List** and click the **Delete** button beneath the list. Then click the **OK** button in the **Confirm Measurement Setting Delete** window.

If you delete a measurement setting, click the **Save Current Machine** button to save your changes.

Add or edit profiles

Once measurement settings are saved, you can import the profiles associated with the settings.

For depth dose profiles, Pinnacle³ supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software and a CSV data file format that is produced by OmniPro-Incline software. For cross beam profiles, Pinnacle³ supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software. Be sure that your profiles are in the proper file format before you import them.

NOTE
Data in an IBA RFA-300 ASCII data file are in units of mm. Pinnacle³ displays units in cm and computes values in units of cm. Pinnacle³ converts the data from mm to cm when you import the data file.

1 In the **Measurement Setting List**, select the measurement setting for which you want to import profiles.

2 Do you want to add a new profile or edit an existing profile?
- To add a new profile, go to step 3.
- To edit an existing profile, go to step 7.

3 Click the **Add** button beneath the **Profile List**. The **SOBP Dose Profile Import** window opens.

4 Use the **Directory** list at the right to locate directories and measured data files in the file system.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home** button.

5 Select the files you want to import.
- To import a single file, select that file from the list of files.
- To select multiple files that are contiguous in the directory list, hold down the **Shift** key and select the first and last files. All files in between are selected as well.
- To select multiple files that are not contiguous in the directory list, hold down the **Control** key and select the files you want to import.

6 Click the **OK** button to import the selected files. New profiles are added to the **Profile List**.

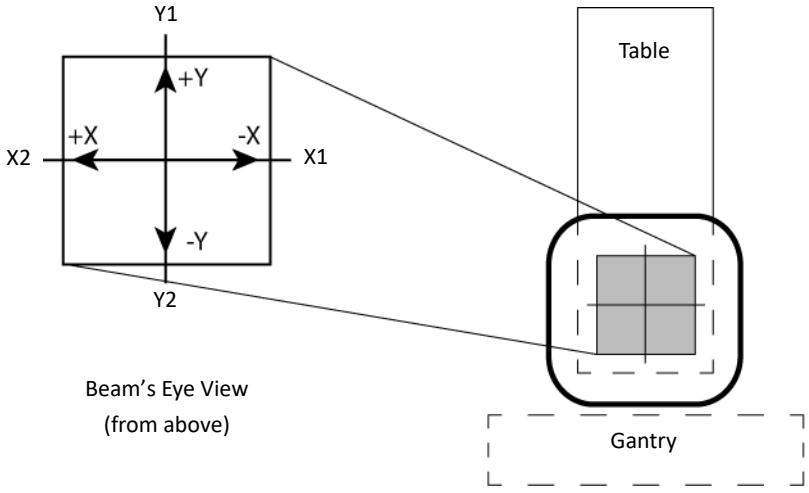
NOTE
If a file that you import contains multiple profiles, each profile is added to the **Profile List**.

7 Select the profile that you want to edit from the **Profile List** and click the **Edit** button beneath the **Profile List**. The **Proton Data Editor** window opens.

8 Verify that the profile type is correct in the **Type** option list. Change the profile type, if necessary.

9 Choose one of the following:
- If the profile that you are editing is a depth dose profile that was not measured on the central axis, enter the axis offsets for the data in the **Left/Right Offset** and **Bottom/Top Offset** fields. The offsets are measured out from the central axis as shown in the graphic that follows.
- If the profile that you are editing is a cross beam profile, you must specify the profile depth in the **Profile Depth** field. If the profiles were not measured through the central axis, you must specify an offset value. For X profiles that were measured off-axis, you must specify the Bottom/Top offset. For Y profiles that were measured off-axis, you must specify the

Left/Right offset. These offsets for X and Y profiles are measured out from the central axis as shown in the graphic that follows.



10 Review the profile. If necessary, you can manually edit the data. For more information, see *Edit data manually*.

11 If you want to replace the profile that you are currently reviewing, you can import a profile from the **Proton Data Editor** window. Click the **Import Data** button. The **Proton Machine Profile Import window** opens.

Use the **Directory** list at the right to locate the directory and the file that you want to import. Then select the file from the list of files and click OK to import the file.

NOTE
The software only imports a single file and a single profile if you import from the **Proton Data Editor** window. If the file you choose to import contains multiple profiles, the software only imports the first profile in the file.

12 When you are finished reviewing this profile, click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

13 Repeat steps 2-12 until you have imported all of the necessary profiles for this measurement setting.

14 Click the **Dismiss** button to close the **Proton Data Editor** window.

15 To delete a profile from the measurement setting, select the profile from the **Profile List** and click the **Delete** button beneath the **Profile List**. Then click the **OK** button in the **Confirm Profile Delete** window.

If you delete a profile, click the **Save Current Machine** button to save your changes.

Compute profiles

By comparing computed depth dose and cross beam profiles against the measured depth dose and cross beam profiles for the machine, you can evaluate the accuracy of the model's dose calculation.

If the agreement between the profiles does not satisfy your defined action levels, you may have to adjust the proton model parameter values and recompute the profiles to obtain good agreement.

1 From the **Measurement Settings List** in the **Proton Physics Tool** window, select the measurement setting for which you want to compute profiles.

2 Click the **Model Validation** button. The **Machine Proton Model Window** opens.

3 In the **Machine Proton Model Window**, click the **Compute Profiles** button. The **Compute Profiles Window** opens.

4 Select the profiles you want to compute.

Use the **Yes**/**No** buttons to choose whether to compute each profile. To change a button from **Yes** to **No**, click the button.

5 Click the **Compute Profile(s)** button. When the computation is complete, the profiles appear in the **Machine Proton Model Window**.

> **NOTE**
> Dose is computed in physics assuming that the beam is always perpendicular to the water phantom regardless of the gantry angles that have been defined for the machine.

6 To view detailed information about a profile, click the **Details** button. The **Machine Proton Comparison Window** opens. The window displays the measured and computed profiles for the selected profile.

If the measurement setting contains more than one profile, you can change the profile that is shown in the window by selecting a different profile from the **Profile** option list in the **Machine Proton Comparison** window.

The machine data comparison table lists the measured and computed dose for each depth or point in the profile and lists the absolute difference and the percent error between the measured and computed values. The absolute difference is computed using the following equation:

$$Diff = Computed\ dose - Measured\ dose$$

The percent error for cross beam profiles is computed using the following equation:

$$\%\ Error = \frac{Computed\ dose - Measured\ dose}{Central\ axis\ dose} \cdot 100\%$$

The percent error for depth dose profiles is computed using the following equation:

$$\%\ Error = \frac{Computed\ dose - Measured\ dose}{Maximum\ profile\ dose} \cdot 100\%$$

7 Compare the computed and measured profiles and assess the difference, percent error, and distance to agreement to determine if these values meet your institution's acceptance criteria for agreement.

If the agreement meets the criteria, repeat this procedure for the next profile in the Profile option list.

If the agreement does not meet the criteria, adjust the proton model parameters and recompute the profile.

> **NOTE**
> If you make adjustments to the model parameters, you will invalidate the modeling for the SOBP components and the modulation table.

8 To normalize the profiles at a specific depth, enter the depth value in the **Connect curves at (cm)** field and select **Yes** in the **Normalize** field. The value you enter becomes the point at which the measured and computed profiles are connected.
   - For best results, connect the curves in a region of the profiles that is relatively flat.
   - For cross beam profiles, use a value of 0 cm to connect the curves at the central axis, or, for asymmetric profiles, connect the curves at the center of the field.

9 Click the **Save Current Machine** button to save your changes.

10 Choose one of the following:
   - To create another measurement setting, return to *Add or edit measurement settings*.
   - If you are finished validating all of your range bands, go to *Commission a machine for planning* to commission the machine.

Edit data manually

You can edit measured data profiles to correct for problems in the data using the **Proton Data Editor** window and the **Profile** tools.

1 From the **Measurement Setting List**, select the measurement setting of the profile that you want to edit.

2 From the **Profile List**, select the profile that you want to edit.

3 Click the **Edit** button beneath the **Profile List**. The **Proton Data Editor** window opens.

4 To edit the profile values, click the field in the data table that you want to edit, then type the value in the field that appears above the table. Click the green check mark next to the field or press **Enter** to accept the value that you typed. Click the red **x** to cancel the change.

5 Change the **Type** option, if necessary.

   If you change the **Type** option, you must also change the **Profile Depth**, **Left/Right Offset**, and **Bottom/Top Offset** values, as appropriate.

6 When you finish editing the measured data for the profile, click the **Dismiss** button to return to the **Proton Physics Tool** window.

7 Click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

Use Profile tools

You can also use the **Profile** tools to edit the measured data. You can smooth the data, center or invert the profile, or reposition the profile.

> **NOTE**
> These tools are not intended to compensate for inadequate data collection or for low-quality (noisy) data. Some tools, such as filtering tools, can round the edges of the profile and, consequently, influence the resulting fit parameter values. In this situation, the determined values may not be accurate.

1 From the **Measurement Setting List**, select the measurement setting of the profile you want to edit.

2 From the **Profile List**, select the profile you want to edit.

3 Click the **Edit** button beneath the **Profile List**. The **Proton Data Editor** window opens.

4 Click the **Profile Tools** button. The **Proton Profile Tools** window opens.

The options available in this window change depending on the type of profile selected in the **Profile List**.

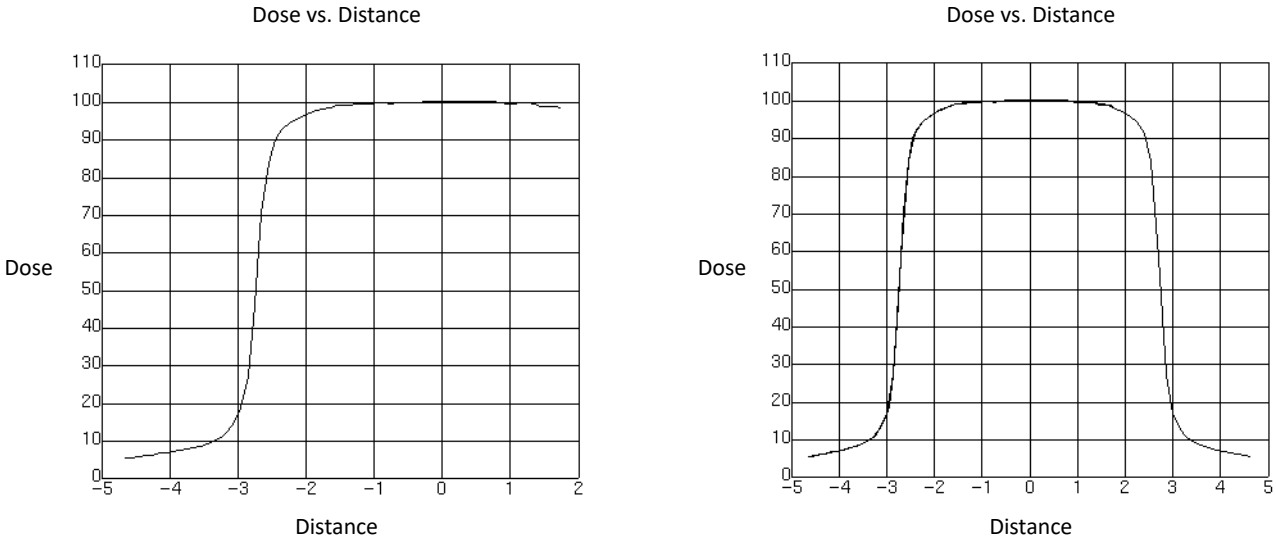
CAUTION
The filtering tools for editing a profile also smooth the high gradient regions. Excessive smoothing can adversely affect the data integrity.

5 Select **Yes** next to the **Apply Filter To All** option if you want the changes you make to be applied to all of the profiles of that type in the measurement setting.

6 Use the following tools to edit the profile:

- The filtering tools smooth out noisy data. The **Noise Window Width** specifies the noise window for the filter, and the **Magnitude Cutoff** is used to truncate the filter.
- For cross beam profiles, the **Mirror** button lets you mirror the data around the central axis. This function is useful when you do not have enough data in a cross beam profile. For

instance, if a profile is incomplete because of the water phantom limits, use the **Mirror** button to create a complete profile, as shown in the image that follows.



- The **Re-Sample** button lets you resample the measured data at a different resolution. Specify the resolution in the **Re-Sample Resolution** field.
- The **Scroll** buttons let you manually reposition the data on the X axis.
- The **Center Profile** button centers the profile on the X axis.
- The **Invert X** button inverts the profile on the X axis.
- The **Scale** and **Offset** buttons let you scale or offset the profile on the X or Y axis by the amount you specify in the fields.

7 If necessary, you can restore the profile to its original settings. Click the **Restore Original Curve** button to restore the current profile, or click the **Restore All Original Curves** button to restore all of the profiles in the measurement setting.

Save edited data profiles to a new file

If you use the **Proton Data Editor** or the **Profile** tools to edit the measured data, you can save the edited data to a file.

1 Click the **Export Data** button in the **Proton Data Editor** window. The **Proton Profile Export** window appears.

2 Specify the directory where you want to save the data, type a name for the file, and click the **OK** button.

3 Click the **Cancel** button to close the **Proton Profile Export** window.

Model uniform scanning parameters

After you have created the range bands for the machine, you must model the range bands. The section describes how to model uniform scanning range bands. For information about modeling double scattering range bands, see *Model double scattering parameters*.

1 In the **Proton Physics Tools** window, select **Uniform Scanning** from the **Delivery Type List**.

2 From the **Range Band List**, select the range band that you want to model.

3 Click the **Model** button. The **Proton Model Editor** window opens.

There is nothing for you to model on the **Effective SAD** tab or the **Virtual SAD** tab, so continue to *Model effective source size in air for uniform scanning*.

Model effective SAD in air for uniform scanning

The **Effective SAD** tab for uniform scanning range bands displays the midpoint of the X and Y magnet distances to isocenter that were entered in the machine settings when the machine was defined. This value is used for the Effective SAD and cannot be edited.

Model virtual SAD in air for uniform scanning

The **Virtual SAD** tab for uniform scanning range bands displays the X and Y magnet distances to isocenter that were entered in the machine settings when the machine was defined. These values are used for the respective Virtual SADs and cannot be edited.

Model effective source size in air for uniform scanning

You must import at least three measurement files of half beam blocked fields for each range band in order to compute the effective source size. Each measurement file that you import must contain at least three profiles at different depth positions in air for the set range of the machine at the time that the measurements were collected. These profiles that are grouped together within a file are referred to as a profile group in the software. The software fits the profiles within a profile group to determine the effective source size parameter value for the associated range value.

For measurement files of half beam blocked fields, Pinnacle^3 supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software. Be sure that your profiles are in the proper file format before you import them.

> **NOTE**
> Data in an IBA RFA-300 ASCII data file are in units of mm. Pinnacle^3 displays units in cm and computes values in units of cm. Pinnacle^3 converts the data from mm to cm when you import the data file.

For each range band, we recommend that you include measurements of half beam blocked fields that were taken between 0 and the maximum range of the range band. The measurements that are taken below the minimum range of the range band are used to more accurately fit the effective source size as a linear function of the set range.

1 Select the **Effective Source Size** tab in the **Proton Model Editor** window. The effective source size information appears.

2 Is the source size symmetric?

- If yes, click the **Yes** button below the **Is source size symmetric** field.
- If no, specify the profiles that you want to model by clicking the **X** or **Y** button below the **Is source size symmetric** field.

3 Click the **Import** button below the **Profile List** to import the measurement files. The **Proton Machine Profile Import** window opens.

4 Use the **Directory** list at the right to locate directories and measured data files on your hard disk.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home** button.

5 Select one or more files to import.

- To select multiple files that are contiguous in the directory list, hold down the **Shift** key and select the first and last files. All files in between are selected as well.
- To select multiple files that are not contiguous in the directory list, hold down the **Control** key and select the files that you want to import.

> **NOTE**
> If you are selecting multiple files for import at one time, make sure that all of the files that you select are blocked on the same side (left or right).

6 Specify if the half beam in the selected file is blocked on the left or right by clicking the **Left** or **Right** option button in the **Blocked** field.

7 Click the **OK** button. The imported file appears in the **Profile List**.

Each measurement file that you import contains profiles. The profiles are listed in the **Sub Profile** list in the **Profile Fitting Parameters** section of the tab. The normalization factor and Sigma values listed below the **Profile** option list pertain to the current profile. To view data for a different profile, select the profile from the **Sub Profile** list.

8 Repeat steps 3-7 until you have imported all of the necessary measurement files.

9 To view or edit the contents of an imported file, or to adjust the offset prior to performing the linear fit, go to *View and edit half beam blocked profile data*.

10 In the **Range in Phantom** field in the **Half Beam Profile Parameters** section of the tab, type the range for each file in the **Profile List**. The range value must be unique for each file.

To switch from one file to another, select the file name in the **Profile List**.

> **NOTE**
> The range value that you type in the **Range in Phantom** field should be the set range that was used when the measured data in the imported file was collected. Set range is the range that the beam would have in water after it exits the machine.

11 Perform a linear fit of the imported profiles.

- To perform a fit for one file, select the file from the **Profile List** and click the **Fit All Profiles in Current Group** button.
- To perform a fit for all of the files in the **Profile List**, click the **Fit All Profiles in All Groups** button.

When you click a button, the following actions occur:

- The fitted values for the current profile appear in the **Normalization Factor Fitted Value** and **Sigma Fitted Value** fields on the **Effective Source Size** tab.
- The software computes the slope, intercept, and effective source size values for the current profile and displays them in the **Half Beam Profile Parameters** section of the **Effective Source Size** tab.
- The **Proton Half Beam Profile Plot** window opens. A plot for each profile contained in the current profile is shown in the window. The imported data is shown in red on each graph, the current computed data is shown in yellow, and previously computed data is shown in black.

12 Evaluate the fitted profiles. The red and yellow curves on each graph should be aligned with each other, and the correct side of the profile should be fitted (the left side is fitted for a left-blocked profile, or the right side is fitted for a right-blocked profile).

13 If the edge of the asymmetric block was not located at 0 cm when the profiles were measured, change the value in the **Offset** field to define where the edge of the asymmetric block was located. The profiles shift according to the value that you enter.

> **NOTE**
> A block edge is located at 0 cm when the 50% level of the edge of the block is at 0 cm.

14 If necessary, you can adjust the fitted values for the profiles to get better alignment between the computed and measured profiles. On the **Effective Source Size** tab, select the profile that you want to adjust from the **Profile** option list. Then, iteratively change the values in the **Normalization Factor Fitted Value** and **Sigma Fitted Value** fields. When you type the new values, the profile shown in the **Proton Half Beam Profile Plot** window for the selected profile is updated.

Adjust the fitted values until the measured and computed profiles are aligned as much as possible. Then click the **Fit All Profiles in Current Group** button to recompute the slope, intercept, and Effective Source Size values.

15 You can verify that the effective source size value is accurate by calculating effective source size using the nominal SAD for the machine and the computed slope and intercept values:

$$\text{Effective Source Size} = \text{Slope} \cdot Z + \text{Intercept}$$

where Z is the distance from the isocenter. The effective source size value that you calculate should closely match the effective source size value that is shown in the **Half Beam Profile Parameters** section of the tab. If you are not satisfied with the fitting, fit the profiles again.

16 To view the previously computed data (the data as it was prior to the last time the profiles were fitted) without invalidating or optimizing the measurement computations, click the **View** button in the **Half Beam Profile Parameters** section.

> **NOTE**
> The **View** button is only active if you have fitted the profile parameters.

17 If you need to return the data and computed profiles to their original settings, click the **Reset Fit** button on the **Effective Source Size** tab. The values in the **Fitted Value** fields are set back to 0, and the data shown in the **Proton Half Beam Profile Plot** window is returned to the original values.

18 Do one of the following:

- If you clicked the **Fit All Profiles in Current Group** button in step 11 and have other files to fit, select another file from the **Profile List** on the **Effective Source Size** tab and click the **Fit All Profiles in Current Group** button to perform a linear fit of that file. Then, return to step 12 to evaluate the fitted profiles.
- If you clicked **Fit All Profiles in All Groups** button in step 11 and need to evaluate other fitted profiles, select another file from the **Profile** option list in the **Proton Half Beam Profile Plot** window. Then return to step 12 to evaluate the fitted profiles in that profile group.
- If you have evaluated the fitted profiles for all of the measurement files that you imported, continue to step 19.

19 Click the **Dismiss** button to close the **Proton Half Beam Profile Plot** window.

20 Click the **Fit Range Band Parameters** button to perform a linear fit for the effective source size as a function of set range. The software computes the slope and intercept of the effective source size and displays the values in the **Range Band Fitting Parameters** section of the tab.

21 You can evaluate the fitting of the range band by calculating the effective source size using the range band slope and intercept values computed by the software. Calculate the following:

$$\text{Effective Source Size} = \text{Slope} \cdot \text{Range} + \text{Intercept}$$

The effective source size value that you calculate should closely match the effective source size value that is shown in the **Half Beam Profile Parameters** section of the tab. If you are not satisfied with the fitting, fit the profiles and the range bands again.

> **NOTE**
> We recommend that you use a spreadsheet tool to plot the effective source size fit parameter values versus the range values in order to evaluate how well your data were fit.

22 If the source size is not symmetric and you have not modeled this range band for both the X and Y profiles, select the direction that you still need to model from the **Is source size symmetric** field and return to step 3 in this procedure.

23 When you are satisfied with the modeling of the effective source size for this range band, click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

24 Continue to *Model pristine peak for uniform scanning*.

View and edit half beam blocked profile data

1 Select a file from the **Profile List** on the **Effective Source Size** tab and click the **View** button. The **Proton Half Beam Profile Plot** window opens. A plot for each profile that is contained in the file is shown in the window.

2 Click the **Detail** button to view the data for each profile. The **Proton Half Beam Details** window opens. The profile data and plot are shown in the window.

3 If necessary, you can adjust the values in the table. To change a value, click the field that you want to edit, then type the new value in the field that appears above the table. When you type in the field, a green check mark and a red **x** appear next to the field. Click the green check mark or press **Enter** to accept the value. Click the red **x** to cancel the change. Click the **Insert Before** or **Insert After** buttons to insert new rows before or after the currently selected row.

4 If the edge of the asymmetric block was not located at 0 cm when the profiles were measured, change the value in the **Offset** field, in the **Proton Half Beam Details** window, to define where the edge of the asymmetric block was located. The profiles shift according to the value that you enter.

5 To change the profile that is shown in the window, select a profile from the **Position** option list near the top of the window.

6 When you are finished viewing the data, click the **Dismiss** button to close the **Proton Half Beam Details** window. Then click the **Dismiss** button to close the **Proton Half Beam Profile Plot** window.

Model pristine peak for uniform scanning

You must import at least three Bragg peak measurement files in order to complete the modeling of the pristine peak for each range band.

For Bragg peak measurements, Pinnacle^3 supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software and a CSV data file format that is produced by OmniPro-Incline software. Be sure that your profiles are in the proper file format before you import them.

The software normalizes the measured and fitted profiles to 100 relative dose units. Thus the fitting algorithm is sensitive to the peak dose of the profile. Before you import data, please be sure to accurately determine the peak dose while you are measuring the pristine peak to ensure an accurate fitting process.

> **NOTE**
> Data in an IBA RFA-300 ASCII data file are in units of mm. Pinnacle^3 displays units in cm and computes values in units of cm. Pinnacle^3 converts the data from mm to cm when you import the data file.

1 Select the **Pristine Peak** tab in the **Proton Model Editor** window. The pristine peak information appears.

2 Click the **Import** button below the **Profile List** to import the Bragg peak measurements. The **Proton Machine Profile Import** window opens.

3 Use the **Directory** list at the right to locate directories and measured data files on your hard disk.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home** button.

4 Select one or more files to import.

- To select multiple files that are contiguous in the directory list, hold down the **Shift** key and select the first and last files. All files in between are selected as well.
- To select multiple files that are not contiguous in the directory list, hold down the **Control** key and select the files that you want to import.

5 Click the **OK** button. The imported file appears in the **Profile List**. The initial **RZero**, **SigmaZero**, **Epsilon**, and **SigmaOne** values are listed in the **Profile Fitting Parameters** section of the tab.

- **RZero** is the fitting parameter that represents the range from the model for the depth dose distribution of the Bortfeld Bragg peak. The **RZero** parameter equals the water equivalent distance of the distal 80% value of the Bragg peak.
- **SigmaZero** and **SigmaOne** are two parameters that represent the width of the Gaussian range straggling, where **SigmaOne** adds a depth dependence to the model.
- **Epsilon** is the fitting parameter from the Bortfeld Bragg peak depth dose distribution model representing the fraction of primary fluence contributing to the “tail” of the energy spectrum.

6 Repeat steps 2-5 until you have imported all of the necessary Bragg peak measurement files.

7 To view or edit the contents of an imported file, go to *View and edit Bragg peak profiles*.

8 In the **Range** and **Nominal SSD** fields, type the range and nominal SSD for each profile in the **Profile List**. The range value must be unique for each profile.

To switch from one profile to another, select the file name in the **Profile List**.

> **NOTE**
> The values that you type are the set range and the nominal SSD that were used when the measurement was performed. The nominal SSD is the physical distance from the water surface to the nominal source.

9 In the **Measurement Depth Offset** field, type the measurement offset value.

This field allows you to shift the profile in the z direction. This may be necessary if the measured depth dose profiles are shifted due to materials in the field (for example, the walls of the water tank or ion chamber). If the data was corrected for these items prior to import, the value in the **Measurement Depth Offset** field should be 0.

10 Perform a fit of the imported Bragg peak measurements.

- To perform a fit for one file, select the file from the **Profile List** and click the **Fit Current Profile Parameters** button.
- To perform a fit for all of the files in the **Profile List**, click the **Fit All Profile Parameters** button.

The fitted values for the file that is highlighted in the **Profile List** appear in the **RZero Fitted Value**, **SigmaZero Fitted Value**, **Epsilon Fitted Value**, and **SigmaOne Fitted Value** fields on the **Pristine Peak** tab. In addition, the **Pristine Peak Fitting Comparison** window opens. The measured Bragg peak data, Bragg peak profile, and the **% Error** plot are shown in the window. In the Bragg peak profile, the imported data is shown in red, the current computed data is shown in yellow, and previously computed data is shown in black.

NOTE
The fitting algorithm for the modeling parameters of the individual curves may fall into a local minima. The computed curves may not optimally match the measured data, or the fitting algorithm may find a solution that is not linearly correlated to other fitting results within the same range band. If this occurs, adjust the **Init Value** of one or more of the fitting parameters, fit the profiles again, and evaluate the results again. With regard to fitting the pristine peak, failure to correct this issue may cause unwanted tilting or sharp distal peaks in the SOBP fitting, especially with ranges that approach the minimum of the range band.

11 Evaluate the fitted profiles.
   - The red and yellow curves on each graph should be aligned with each other.
   - You can verify that the fitted value for **RZero** is a reasonable value. In the **Pristine Peak Fitting Comparison** window, scroll through the data in the table and find the row for a measured distal dose as close to 80% as possible. If the profile fitting process was successful, the depth value in that row should closely match the value that is displayed in the **RZero Fitted Value** field on the **Pristine Peak** tab.

12 If necessary, you can adjust the fitted values for the Bragg peaks to get better alignment between the computed and measured profiles. On the **Pristine Peak** tab, iteratively change the values in the **RZero**, **SigmaZero**, **Epsilon**, and **SigmaOne Fitted Value** fields. When you type the new values, the data shown in the **Pristine Peak Fitting Comparison** window is updated.

   Adjust the fitted values until the measured and computed profiles are aligned as much as possible.

13 To view the previously computed data (the data as it was prior to the last time the profiles were fitted) without invalidating or optimizing the measurement computations, click the **View** button in the **Profile Fitting Parameters** section.

NOTE
The **View** button is only active if you have fitted the profile parameters.

14 To return the data and profiles to their original values, click the **Reset Fit** button on the **Pristine Peak** tab. The values in the **Fitted Value** fields are set back to 0, and the **Pristine Peak Fitting Comparison** window is closed.

NOTE
The **Reset Fit** button is only active if you manually change a value in one of the fitted value fields.

15 Repeat steps 10-12 until you have fitted all of the Bragg peak measurement files that you imported.

16 Click the **Dismiss** button to close the **Pristine Peak Fitting Comparison** window.

17 Click the **Fit Range Band Parameters** button. The software computes the slope and intercept of **RZero**, **SigmaZero**, **Epsilon**, and **SigmaOne** and displays the values in the **Range Band Fitting Parameters** section of the tab.

18 You can evaluate the fitting of the range band by calculating the **RZero** value using the range band RZero slope and intercept values computed by the software. Calculate the following:

$$RZero\text{Fitted Value} = RZero\text{Slope} \cdot \text{Range} + RZero\text{Intercept}$$

The value that you calculate should closely match the value shown in the **RZero Fitted Value** field in the **Profile Fitting Parameters** section of the tab. If you are not satisfied with the fitting, fit the profiles and the range bands again.

> **NOTE**
> We recommend that you use a spreadsheet tool to plot each fit parameter value versus the range value in order to evaluate how well your data were fit.

19 If you want to evaluate the Bragg peak model, go to *Evaluate the Pristine Peaks*.

20 When you are satisfied with the modeling of the pristine peaks for this range band, click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

21 Continue to *Model spread-out Bragg peak components*.

View and edit Bragg peak profiles

1 Select the profile from the **Profile List** on the **Pristine Peak** tab and click the **View** button. The **Proton Pristine Plot** window opens. The profile data and plot are shown in the window.

2 If necessary, you can adjust the values in the table. To change a value, click the field that you want to edit, and then type the new value in the field that appears above the table. When you type in the field, a green check mark and a red **x** appear next to the field. Click the green check mark or press **Enter** to accept the value. Click the red **x** to cancel the change. Click the **Insert Before** or **Insert After** buttons to insert new rows before or after the currently selected row.

3 To change the profile that is shown in the window, select the profile from the **Profile** option list in the **Proton Pristine Plot** window.

4 When you are finished viewing the data, click the **Dismiss** button to close the **Proton Pristine Plot** window.

Evaluate the Pristine Peaks

When you have finished modeling the pristine peaks, you can evaluate the Bragg Peak model for this range band.

1 In the **Pristine Peak** tab, click the **Evaluation** button. The **Pristine Peak Evaluation** window opens.

2 To evaluate the ability of the model to plot a Bragg peak for any range within the range band, type the nominal SSD in the **Nominal SSD** field and a range value in the **Range** field. A Bragg peak for the range that you entered appears in the window.

3 To evaluate the model against measured depth dose data, click **Yes** in the **Test with measurement** field.

4 If the file that you plan to import contains multiple depth dose profiles, type the number of the profile that you want to use in the Index field.

> **NOTE**
> Individual profiles are indexed starting at 0, not 1.

5 Click the **Import** button. The **Proton Machine Test Profile Import** window opens.

6 Use the **Directory** list at the right to locate directories and measured data files on your hard disk.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home** button.

7 Select a file to import.

8 Click the **OK** button. The measured data appears in the window. In the Bragg peak profile, the imported data is shown in red and the current computed data is shown in yellow.

9 In the **Measurement Depth Offset** field, type the measurement offset value.

This field allows you to shift the profile in the z direction. This may be necessary if the measured depth dose profiles are shifted due to materials in the field (for example, the walls of the water tank or ion chamber). If the data was corrected for these items prior to import, the value in the **Measurement Depth Offset** field should be 0.

10 In the **Nominal SSD** field, enter the nominal SSD that was used when the measured depth dose data was collected.

11 In the **Range** field, enter the range that was used when the measured depth dose data was collected.

12 Review the fit of the profiles.

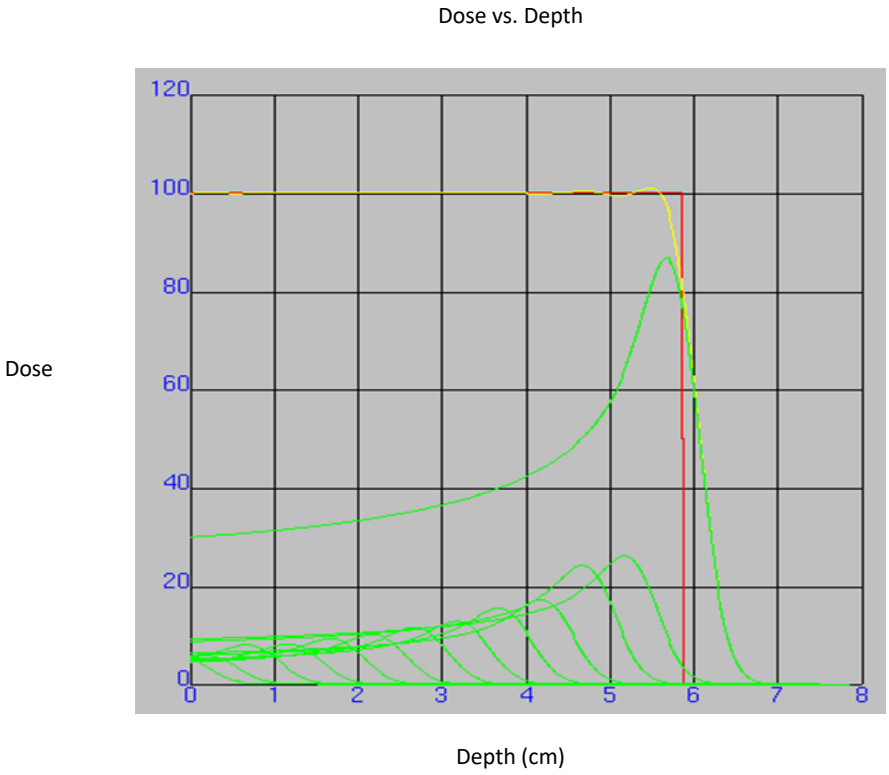
- If you are satisfied with the fit, click the **Dismiss** button to close the **Pristine Peak Evaluation** window. This procedure is complete.
- If the measured and computed profiles are not well aligned, click the **Dismiss** button to close the **Pristine Peak Evaluation** window and model the pristine peaks for the range band again.

Model spread-out Bragg peak components

> **NOTE**
> You must complete the modeling of the effective source size and the pristine peak before you model the spread-out Bragg peak (SOBP) components. Information from those models is necessary for the successful modeling of an SOBP.

When you model the components of the fully-modulated SOBP (see the graph below), you are establishing the information needed to build the SOBP functions for each range band. These specific SOBP functions need to reproduce the respective SOBPs delivered by the proton machine. (A fully-modulated SOBP is one in which the range equals the modulation. Ideally, the dose is

completely flat from a depth of 0 cm to a depth equal to the range.) During modeling, you will optimize the weights of the components necessary to build an appropriate SOBP function for the range band.



Pullback defines the position of a pristine peak relative to another pristine peak. The positions are determined using a specified level on the distal edge, for example 90% of peak maximum. An SOBP is composed of pristine peak components. A pullback interval is the distance in g/cm^2 between each two adjacent components in the SOBP. The cumulative pullback is the distance between a given component and the most distal component in the SOBP.

1 Select the **SOBP Components** tab in the **Proton Model Editor** window.

2 In the **Pullback Interval** field, type a pullback interval from 0.1–2.0 g/cm^2. We suggest a starting value that is close to the 80-80% width of a Bragg peak at the maximum range of the range band.

3 Click the **Populate Weight Table** button. The software creates the SOBP component weight table.

   Each row in the table represents information for a single SOBP component. The number of components is determined by the minimum and maximum range values divided by the pullback interval. The first component has a default pullback interval of 0.00 g/cm^2. The pullback interval and the cumulative pullback for each component are both listed in the table. The weights are equal for all components in this initial table.

4 If necessary, you can adjust the values in the table. To change a value, click the field that you want to edit, then type the new value in the field that appears above the table. When you type in the field, a green check mark and a red **x** appear next to the field. Click the green check mark or press **Enter** to accept the value. Click the red **x** to cancel the change. Click the **Insert Before** and **Insert After** buttons to add additional rows to the table.

5 You can lock the components in the weight table so that the optimization process does not change the weight value for that component. A value of 0 in the **Lock** column means that the row is not locked, and a value of 1 means that the row is locked.

- To lock all of the rows in the table, click the **Yes** button in the **Lock all rows?** field.
- To lock only certain rows in the table, type the number 1 in the **Lock** column for those rows. The optimization will not change the values in the locked rows but may change values in the unlocked rows as necessary to obtain the best optimization results.

NOTE
Locking a row only prevents the optimization process from changing the weight value in that row. You can manually change the values in all of the rows whether or not they are locked.

6 When you are satisfied with the values in the weight table, click the **Optimize** button to optimize the weights of the components that you have defined. The software displays the components and the computed SOBP in a graph when the optimization is complete.

NOTE
The goal of the optimization algorithm is for the sum of the component curves to be 100% at each depth (or 1.0 if the graph is normalized) from the surface to the maximum range of the range band. A weight is the maximum height (amplitude) of a Bragg peak component, and the weights of all of the components are not normalized to the first component or to the sum of all of the weights.

NOTE
Depending on the number of entries in the weight table and the depth of the range band, the optimization of the weight table can take 30 seconds or more to complete. The deeper the range band, the more time it will take to complete the optimization.

NOTE
If the weight table becomes invalid after you have optimized it (for example, you change one of the modeling parameters), the word **Invalid** appears on the tab next to the **Optimize** button.

7 Click the **Details** button to view a detailed display of the computed 1-dimensional SOBP function. The **SOBP Details** window opens. The table that appears in the window contains the differences between the computed SOBP and the 100% dose values for each pullback interval. (The 100% dose values are represented by the red line on the graph so that you can compare the dose values of the computed SOBP with the 100% dose values. The red line extends from 0 to the maximum range of the range band on the x-axis, and it is located at 100% dose on the y-axis. The current computed data is shown in yellow on the graph, and previously computed data is shown in black. The components are shown in green.)

8 Review the components and the SOBP. The SOBP in the graph should be as flat as possible. If necessary, you can iteratively change the data and optimize the table until you are satisfied with the results. Possible changes include the following:

- Click the **Optimize** button more than once to optimize the existing values again.
- Adjust the weight values of certain components and lock those rows.
- Change the pullback interval to obtain a flatter SOBP function. For example, a pullback interval of 0.7 g/cm^2 may produce a flatter SOBP function than a value of 0.5 g/cm^2.

NOTE
If you change the pullback interval, click the **Populate Weight Table** button to recreate the SOBP component weight table.

9 When you are satisfied with the modeling of the SOBP components for this range band, continue to *Model the modulation table for uniform scanning*.

Model the modulation table for uniform scanning

NOTE
Before you can create a cumulative weight table, you must complete the optimization of the SOBP component weight table on the **SOBP Components** tab.

The modulation table represents the sum of the component weights that is required to generate an SOBP of a given modulation for the range band.

In planning, the modulation table is used to determine how Pinnacle^3 should compute the SOBP function necessary to cover the target that is assigned to that beam. If an entry for a specific modulation is not present in the table, the software will interpolate the cumulative weight between modulations that are commissioned to generate the proper SOBP.

You must import at least three SOBP depth dose profiles measured in water for each range band in order to complete the modeling of the modulation table.

NOTE
When you import the measured data, we recommend that you include measured SOBPs with ranges that approach the minimum range of the range band in order to verify the accuracy of the computed SOBPs across the entire range band.

For SOBP depth dose profiles, Pinnacle^3 supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software and a CSV data file format that is produced by OmniPro-Incline software. Be sure that your profiles are in the proper file format before you import them.

NOTE
Data in an IBA RFA-300 ASCII data file are in units of mm. Pinnacle^3 displays units in cm and computes values in units of cm. Pinnacle^3 converts the data from mm to cm when you import the data file.

The minimum number of SOBP depth dose profiles required for modeling is three, but we recommend that you import more than three to create a more accurate modulation table. More SOBP depth dose profiles will produce better interpolation results.

1 Select the **Modulation Table** tab in the **Proton Model Editor** window.

2 Click the **Import** button below the **Profile List**. The **Proton Machine Profile Import** window opens.

3 Use the **Directory** list at the right to locate directories and measured data files.

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, click the directory name in the list. To return to your home directory, click the **Home** button.

4 Select one or more files to import.

- To select multiple files that are contiguous in the directory list, hold down the **Shift** key and select the first and last files. All files in between are selected as well.
- To select multiple files that are not contiguous in the directory list, hold down the **Control** key and select the files that you want to import.

5 Click the **OK** button. The imported files appear in the **Profile List**.

6 Repeat steps 2-5 until you have imported all of the necessary measured depth dose profiles.

7 To view or edit the contents of an imported profile, go to *View and edit depth dose profile data*.

8 After you import all of the depth dose profiles, you must fit the profiles that are computed by the software to the measured profiles. Select the first file to fit from the **Profile List** on the **Modulation Table** tab.

9 Verify that the nominal SSD value shown in the **Nominal SSD** field is accurate for this file. (When you import the file, the software uses data from the file to fill the nominal SSD value.) If necessary, type a new nominal SSD value in the field.

10 Type the modulation and range values in the **Modulation** and **Range** fields. The values that you specify must be the values that were set at the machine when the measured data were collected.

After you enter the modulation value, the software computes the initial number of pullbacks and the initial cumulative weight required for the range and modulation that you specified. These components are shown in a table when you press the **Enter** key after you type the modulation value for the profile.

NOTE
The software will prevent you from creating the modulation table unless the first profile in the **Profile List** has a modulation that is equal to the minimum modulation of the range band within +/-0.01 g/cm^2 and the last profile in the Profile List has a modulation that is equal to the maximum modulation of the range band within +/-0.01 g/cm^2.

NOTE
The modulation value is the modulation that the beam would exhibit if it were in water. The software assumes that each imported SOBP curve meets your facility's defined levels for distal and proximal edge locations. Importing data that do not meet this requirement may lead to errors in calculated dose.

11 In the **Measurement Depth Offset** field, type the measurement offset value.

This field allows you to shift the profile in the z direction. This may be necessary if the measured depth dose profiles are shifted due to materials in the field (for example, the walls of the water

tank or ion chamber). If the data were corrected for these items prior to import, the value in the **Measurement Depth Offset** field should be 0.

12 Click the **Evaluate SOBP with 1D Calculation** button to display the computed and measured SOBP. The **Evaluate SOBP** window opens. The imported SOBP data is shown in red on the graph, the current computed data are shown in yellow, and previously computed data are shown in black.

The proximal edge depth and distal edge depth values are shown on the graph with diamond-shaped markers. The measured values are shown with red markers and the computed values are shown with yellow markers. The markers show levels that are defined in the **Model Settings** window and are intended to show your facility's definitions of these levels. See *Define a virtual water phantom for double scattering and uniform scanning*.

NOTE
You may notice unwanted tilting or distinct, sharp distal peaks of the computed SOBPs when you compare them to the measured SOBPs with ranges that approach the minimum range of the range band. This may occur if the pristine peak fitting parameters for **SigmaOne**, **Epsilon**, and **SigmaZero** vary too much across the range band. To mitigate the problem, return to the **Pristine Peak** tab and manually reduce the slope of the **SigmaOne**, **Epsilon**, and **SigmaZero** fitting parameters by adjusting the fitted values of each profile to an average value across the range band. (Do not change the **RZero** value.) Changing these parameters may reduce the accuracy of the fit for the individual pristine peaks, but may also remove the tilting and sharp distal peak of the computed SOBPs in the **Modulation** tab. Alternatively, you could split this range band into finer bands in an attempt to reduce the tilting and sharp distal peaks.

13 To normalize the profiles at a specific depth, enter the depth value in the **Connect curves at depth (cm)** field. The value that you enter becomes the point at which the measured and computed profiles are connected.

For best results, connect the curves in a region of the profiles that is relatively flat.

14 To include the SOBP components in the graph, click the **Yes** button in the **Show Components** field.

15 To include the edge depth markers in the graph, click the **Yes** button in the **Show Edge Depth Markers** field.

16 To normalize the y-axis of the plot to the modulation mean instead of the maximum plateau value, set the **Normalize to modulation mean** field above the plot to **Yes**.

17 To adjust the proximal edge of the computed profile to get better agreement between the computed and measured profiles, iteratively change the **Cumulative Weight** value until the profiles are more closely aligned.

18 Click the **Details** button to view details of the 1-dimensional SOBP. The **Evaluate 1D Details** window opens. The table that appears in the window contains the following data: depth in cm, the measured and computed dose at each depth, and the difference, error percentage, and distance to agreement between the measured and computed dose. The window also contains a plot of the current profile. The imported data is shown in red on the graph, the current computed data is shown in yellow, and the previously computed data is shown in black.

19 Choose one of the following options:

- If you need to generate another entry for the modulation table, select a file from the **Profile List** on the **Modulation Table** tab and return to step 9.
- If you are finished generating entries for the modulation table, continue to step 20.

20 Click the **Transfer All to Modulation Table** button on the **Modulation Table** tab to generate the modulation table. Then click the **Display Weight vs. Modulation Plot** button to view the modulation table and graph.

21 To view the cumulative weight value for any modulation in the graph, enter a modulation value in the **Modulation** field. The software determines the intermediate modulation values through quadratic interpolation.

22 When you are satisfied with the modulation table, continue to *Validate the model for uniform scanning*.

> **NOTE**
> The modulation table will be invalidated if you change any of the associated depth dose profiles or the profile parameters, which include the range, modulation, nominal SSD, and cumulative weight.

View and edit depth dose profile data

1 Select the profile from the **Profile List** on the **Modulation Table** tab and click the **View** button. The **SOBP Profile Plot** window opens. The profile data and plot are shown in the window.

2 If necessary, you can adjust the values in the table. To change a value, click the table cell that you want to edit, and then type the new value in the field that appears above the table. Click the green check mark next to the field or press **Enter** to accept the value. Click the red **x** to cancel the change. Click the **Insert Before** or **Insert After** buttons to insert new rows before or after the currently selected row.

3 To change the profile that is shown in the window, select the profile from the **Profile** option list in the **SOBP Profile Plot** window.

4 To normalize the y-axis of the plot to 1.0 instead of the raw maximum value, set the **Normalize** field above the plot to **Yes**.

5 When you are finished viewing the data, click the **Dismiss** button to close the **SOBP Profile Plot** window.

Validate the model for uniform scanning

When you are finished modeling the machine, you must validate the accuracy of your model by comparing at least one computed longitudinal (depth) dose profile or lateral (cross beam) profile against measured depth dose profiles and cross beam profiles each range band.

> **NOTE**
> We recommend that you validate multiple depth dose and cross beam profiles. We also recommend that you validate both the X profiles and Y profiles, especially if the model includes an asymmetric source size.

Add or edit measurement settings

Before you import measured data that will be used to validate the model, you must define the geometry specific to that measurement by making entries in the **Measurement Setting List**. Each range band has its own **Measurement Setting List**, and each entry in the list contains one or more profiles, each of which share a common setup and machine geometry.

1 Go to the **Proton Physics Tool** window.

2 Select **Uniform Scanning** from the **Delivery Type List**.

3 Select a range band from the **Range Band List**.

4 Do you want to add a new measurement setting or edit an existing measurement setting?

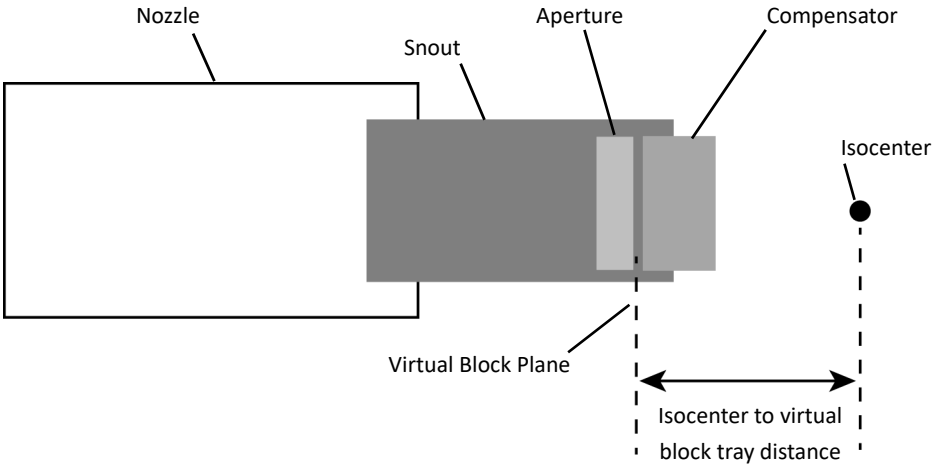
- To add a new measurement setting, click the **Add** button beneath the **Measurement Setting List**. The **Proton Data Measurement Setting** window opens.
- To edit an existing measurement setting, select the measurement setting from the **Measurement Settings List**, and click the **Edit** button beneath the **Measurement Setting List**. The **Proton Data Measurement Setting** window opens.

5 Complete the fields in the **Machine Delivery Settings** and **Field Setup** sections of the window with the values that were used when the measured data that you will associate with this measurement setting were collected.

After you specify the range, modulation, snout position and nominal SSD, the software computes the size of the field and displays the data in the **Physical Size** fields. The software also computes the estimated size of the beam at isocenter based on the virtual SAD and displays the data in the **Isocenter Size** fields. If you change the field size, the software recomputes the beam size at isocenter and updates the values in the **Isocenter Size** fields.

> **NOTE**
> The range, modulation, snout position, and nominal SSD values that you specify must be the values that were set at the machine when the measured data were collected. The imported profiles should match your facility's definitions for range and modulation expected from those machine settings and measurement in water.

Pinnacle³ defines the snout position as the distance from the isocenter to the virtual block tray as shown in the graphic that follows.



CAUTION
Verify that the measurement settings are correct before you save the data.

6 When you have specified the measurement settings, click the **Dismiss** button.

NOTE
Each measurement setting can have any number of profiles associated with it. If the same measurement settings were used for a number of measurements, you only need to enter the measurement settings once.

7 Click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

8 To delete a measurement setting, select the measurement setting from the **Measurement Setting List** and click the **Delete** button beneath the list. Then click the **OK** button in the **Confirm Measurement Setting Delete** window.

If you delete a measurement setting, click the **Save Current Machine** button to save your changes.

Add or edit profiles

Once measurement settings are saved, you can import the profiles associated with the settings.

For depth dose profiles, Pinnacle³ supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software and a CSV data file format that is produced by OmniPro-Incline software. For cross beam profiles, Pinnacle³ supports the IBA RFA-300 ASCII data file format that is produced by OmniPro-Accept software. Be sure that your profiles are in the proper file format before you import them.

NOTE
Data in an IBA RFA-300 ASCII data file are in units of mm. Pinnacle^3 displays units in cm and computes values in units of cm. Pinnacle^3 converts the data from mm to cm when you import the data file.

1 In the **Measurement Setting List**, select the measurement setting for which you want to import profiles.

2 Do you want to add a new profile or edit an existing profile?
- To add a new profile, go to step 3.
- To edit an existing profile, go to step 7.

3 Click the **Add** button beneath the **Profile List**. The **SOBP Dose Profile Import** window opens.

4 Use the **Directory** list at the right to locate directories and measured data files in the file system.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (**..**) in the list. To go down one directory, click the directory name in the list. To return to your home directory, click the **Home** button.

5 Select the files you want to import.
- To import a single file, select that file from the list of files.
- To select multiple files that are contiguous in the directory list, hold down the **Shift** key and select the first and last files. All files in between are selected as well.
- To select multiple files that are not contiguous in the directory list, hold down the **Control** key and select the files you want to import.

6 Click the **OK** button to import the selected files. New profiles are added to the **Profile List**.

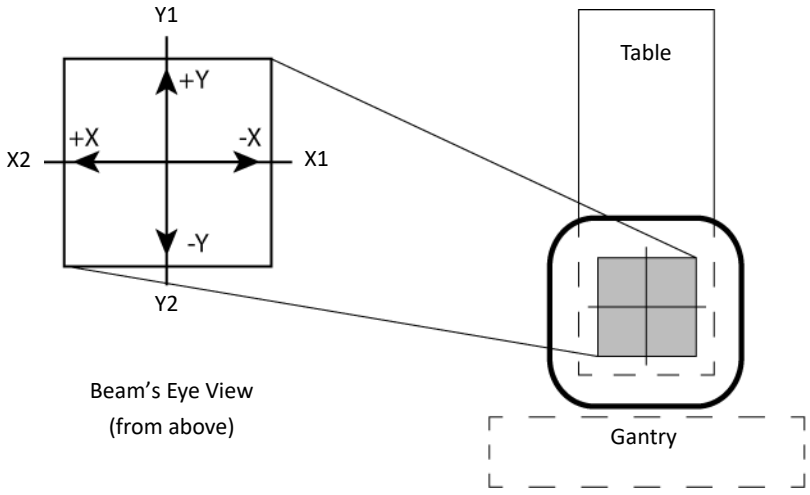
NOTE
If a file that you import contains multiple profiles, each profile is added to the **Profile List**.

7 Select the profile that you want to edit from the **Profile List** and click the **Edit** button beneath the **Profile List**. The **Proton Data Editor** window opens.

8 Verify that the profile type is correct in the **Type** option list. Change the profile type, if necessary.

9 Choose one of the following:
- If the profile that you are editing is a depth dose profile that was not measured on the central axis, enter the axis offsets for the data in the **Left/Right Offset** and **Bottom/Top Offset** fields. The offsets are measured out from the central axis as shown in the graphic that follows.
- If the profile that you are editing is a cross beam profile, you must specify the profile depth in the **Profile Depth** field. If the profiles were not measured through the central axis, you must specify an offset value. For X profiles that were measured off-axis, you must specify the Bottom/Top offset. For Y profiles that were measured off-axis, you must specify the

Left/Right offset. These offsets for X and Y profiles are measured out from the central axis as shown in the graphic that follows.



10 Review the profile. If necessary, you can manually edit the data. For more information, see *Edit data manually*.

11 If you want to replace the profile that you are currently reviewing, you can import a profile from the **Proton Data Editor** window. Click the **Import Data** button. The **Proton Machine Profile Import** window opens.

Use the **Directory** list at the right to locate the directory and the file that you want to import. Then select the file from the list of files and click **OK** to import the file.

> **NOTE**
> The software only imports a single file and a single profile if you import from the **Proton Data Editor** window. If the file you choose to import contains multiple profiles, the software only imports the first profile in the file.

12 When you are finished reviewing this profile, click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

13 Repeat steps 2-12 until you have imported all of the necessary profiles for this measurement setting.

14 Click the **Dismiss** button to close the **Proton Data Editor** window.

15 To delete a profile from the measurement setting, select the profile from the **Profile List** and click the **Delete** button beneath the **Profile List**. Then click the **OK** button in the **Confirm Profile Delete** window.

If you delete a profile, click the **Save Current Machine** button to save your changes.

Compute profiles

By comparing computed depth dose and cross beam profiles against the measured depth dose and cross beam profiles for the machine, you can evaluate the accuracy of the model's dose calculation.

If the agreement between the profiles does not satisfy your defined action levels, you may have to adjust the proton model parameter values and recompute the profiles to obtain good agreement.

1 From the **Measurement Settings List** in the **Proton Physics Tool** window, select the measurement setting for which you want to compute profiles.

2 Click the **Model Validation** button. The **Machine Proton Model Window** opens.

3 In the **Machine Proton Model Window**, click the **Compute Profiles** button. The **Compute Profiles Window** opens.

4 Select the profiles you want to compute.

Use the **Yes**/**No** buttons to choose whether to compute each profile. To change a button from **Yes** to **No**, click the button.

5 Click the **Compute Profile(s)** button. When the computation is complete, the profiles appear in the **Machine Proton Model** Window.

> **NOTE**
> Dose is computed in physics assuming that the beam is always perpendicular to the water phantom regardless of the gantry angles that have been defined for the machine.

6 To view detailed information about a profile, click the **Details** button. The **Machine Proton Comparison Window** opens. The window displays the measured and computed profiles for the selected profile.

If the measurement setting contains more than one profile, you can change the profile that is shown in the window by selecting a different profile from the **Profile** option list in the **Machine Proton Comparison** window.

The machine data comparison table lists the measured and computed dose for each depth or point in the profile and lists the absolute difference and the percent error between the measured and computed values. The absolute difference is computed using the following equation:

$$Diff = Computed\ dose - Measured\ dose$$

The percent error for cross beam profiles is computed using the following equation:

$$\%\ Error = \frac{Computed\ dose - Measured\ dose}{Central\ axis\ dose} \cdot 100\%$$

The percent error for depth dose profiles is computed using the following equation:

$$\%\ Error = \frac{Computed\ dose - Measured\ dose}{Maximum\ depth\ dose} \cdot 100\%$$

7 Compare the computed and measured profiles and assess the difference, percent error, and distance to agreement to determine if these values meet your institution's acceptance criteria for agreement.

   If the agreement meets the criteria, repeat this procedure for the next profile in the **Profile** option list.

   If the agreement does not meet the criteria, adjust the proton model parameters and recompute the profile.

   NOTE
   If you make adjustments to the model parameters, you will invalidate the modeling for the SOBP components and the modulation table.

8 To normalize the profiles at a specific depth, enter the depth value in the **Connect curves at (cm)** field and select **Yes** in the **Normalize** field. The value you enter becomes the point at which the measured and computed profiles are connected.
   - For best results, connect the curves in a region of the profiles that is relatively flat.
   - For cross beam profiles, use a value of 0 cm to connect the curves at the central axis, or, for asymmetric profiles, connect the curves at the center of the field.

9 Click the **Save Current Machine** button to save your changes.

10 Choose one of the following:
   - To create another measurement setting, return to *Add or edit measurement settings*.
   - If you are finished validating all of your range bands, go to *Commission a machine for planning* to commission the machine.

Edit data manually

You can edit measured data profiles to correct for problems in the data using the **Proton Data Editor** window and the Profile tools.

1 From the **Measurement Setting List**, select the measurement setting of the profile that you want to edit.

2 From the **Profile List**, select the profile that you want to edit.

3 Click the **Edit** button beneath the **Profile List**. The **Proton Data Editor** window opens.

4 To edit the profile values, click the field in the data table that you want to edit, then type the value in the field that appears above the table. Click the green check mark next to the field or press **Enter** to accept the value that you typed. Click the red **x** to cancel the change.

5 Change the **Type** option, if necessary.

   If you change the **Type** option, you must also change the **Profile Depth**, **Left/Right Offset**, and **Bottom/Top Offset** values, as appropriate.

6 When you finish editing the measured data for the profile, click the **Dismiss** button to return to the **Proton Physics Tool** window.

7 Click the **Save Current Machine** button in the **Proton Physics Tool** window to save your changes.

Use Profile tools

You can also use the Profile tools to edit the measured data. You can smooth the data, center or invert the profile, or reposition the profile.

> **NOTE**
> These tools are not intended to compensate for inadequate data collection or for low-quality (noisy) data. Some tools, such as filtering tools, can round the edges of the profile and, consequently, influence the resulting fit parameter values. In this situation, the determined values may not be accurate.

1 From the **Measurement Setting List**, select the measurement setting of the profile you want to edit.

2 From the **Profile List**, select the profile you want to edit.

3 Click the **Edit** button beneath the **Profile List**. The **Proton Data Editor** window opens.

4 Click the **Profile Tools** button. The **Proton Profile Tools** window opens.

The options available in this window change depending on the type of profile selected in the **Profile List**.

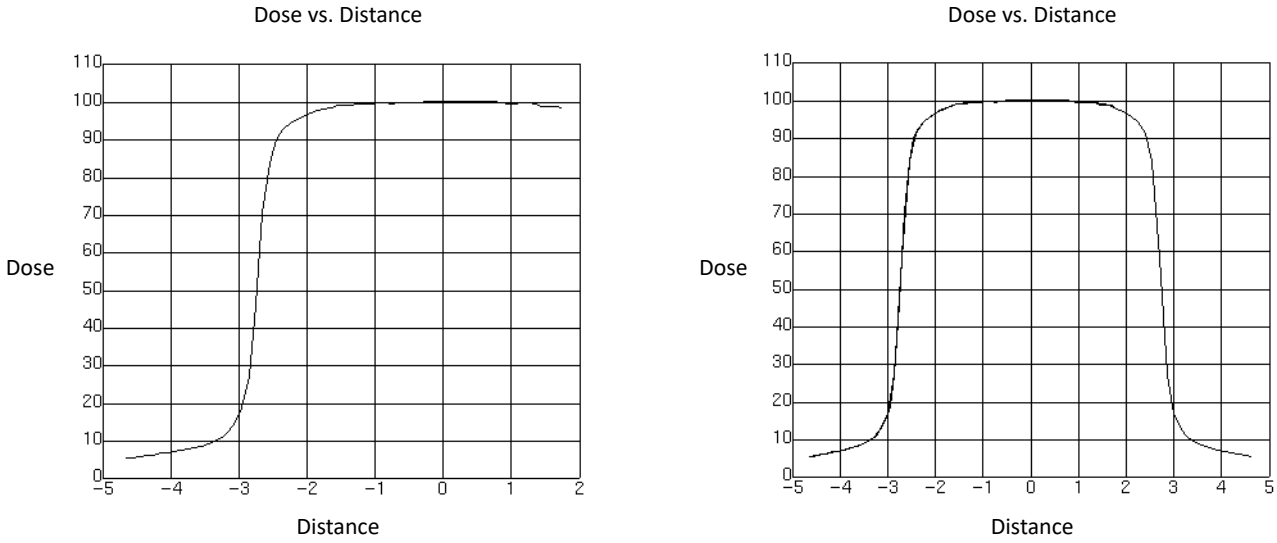
CAUTION
The filtering tools for editing a profile also smooth the high gradient regions. Excessive smoothing can adversely affect the data integrity.

5 Select **Yes** next to the **Apply Filter To All** option if you want the changes you make to be applied to all of the profiles of that type in the measurement setting.

6 Use the following tools to edit the profile:

- The filtering tools smooth out noisy data. The **Noise Window Width** specifies the noise window for the filter, and the **Magnitude Cutoff** is used to truncate the filter.
- For cross beam profiles, the **Mirror** button lets you mirror the data around the central axis. This function is useful when you do not have enough data in a cross beam profile. For

instance, if a profile is incomplete because of the water phantom limits, use the **Mirror** button to create a complete profile, as shown in the image that follows.



- The **Re-Sample** button lets you resample the measured data at a different resolution. Specify the resolution in the **Re-Sample Resolution** field.
- The **Scroll** buttons let you manually reposition the data on the X axis.
- The **Center Profile** button centers the profile on the X axis.
- The **Invert X** button inverts the profile on the X axis.
- The **Scale** and **Offset** buttons let you scale or offset the profile on the X or Y axis by the amount you specify in the fields.

7 If necessary, you can restore the profile to its original settings. Click the **Restore Original Curve** button to restore the current profile, or click the **Restore All Original Curves** button to restore all of the profiles in the measurement setting.

Save edited data profiles to a new file

If you use the **Proton Data Editor** or the Profile tools to edit the measured data, you can save the edited data to a file.

1 Click the **Export Data** button in the **Proton Data Editor** window. The **Proton Profile Export** window appears.

2 Specify the directory where you want to save the data, type a name for the file, and click the **OK** button.

3 Click the **Cancel** button to close the **Proton Profile Export** window.

Print proton physics model

1 In the **Proton Model Editor** window, click the **Print** button. The **Proton Model Print Confirmation** window opens.

2 Confirm that the selected printer is the printer that you want to use.

To select a different printer, click the **Select Printer** button, select a different printer, and click the **Dismiss** button.

3 Click the **Print** button.

Commission a machine for planning

After you enter machine and physics information for all delivery types for a given machine, model the profiles, and validate the models, you must commission the machine for use in treatment planning.

The commissioning process moves a machine from the physics machine database to the planning machine database and “stamps” the machine with the date and time of commissioning.

A commissioned machine is available only in the treatment planning software. If you want to make changes to a machine after commissioning, you must copy it back into the physics machine database using the Add Machines option, make the changes using the proton physics tools, and recommission the machine.

1 In the **Proton Physics Tool** window, select the machine to be commissioned from the **Machine List** and then click the **Commission** button. The **Commission Proton Machine** window opens.

2 Select the delivery types for which you want to commission the machine by clicking the **Yes** or **No** buttons in the **Double Scattering** and **Uniform Scanning**.

> **NOTE**
> The **Yes** and **No** buttons do not appear for a delivery type if you did not enable that delivery type when you entered the machine data.

3 Type your name or initials in the **Commissioned By** field.

4 Type a description for the machine in the **Description** field (optional).

5 Click the **OK** button to commission the machine.

If problems occur during the commissioning process, a list of errors appears in the **Commission Failure** window. Correct the problems listed in the window, and then repeat the steps in this section to commission the machine.

Delete proton machines

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

Delete non-commissioned machines

WARNING
Once a non-commissioned machine is deleted, it cannot be restored. All measured data associated with the machine is deleted with the machine.

1 Click the **Proton Physics Tool** button in the **Physics Tools** window. The **Proton Physics Tool** window appears.

2 Select the machine you want to delete from the **Machine List**.

3 Click the **Delete** button beneath the **Machine List**, and then click the **Delete** button again in the next window to confirm the deletion.

Click the **Dismiss** button to cancel the deletion.

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

Delete commissioned machines

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

> **NOTE**
> We strongly discourage the deletion of commissioned machines. All commissioned versions of a machine are saved in the planning machine database to allow plans to be read in and replicated with the machine used when the plan was generated. If a machine is deleted, you cannot subsequently read in the plan and view the dose as it was calculated when the plan was generated.

1 Click the **Proton Physics Tool** button in the **Physics Tools** window. The **Proton Physics Tool** window appears.

2 Click the **Add** button beneath the **Machine List**. The **Add New Machine** window appears.

3 Select the **Current Commissioned Machines** button to display the list of commissioned machines.

4 Select the machine you want to delete and click the **Delete** button. The **Confirm Current or All Versions Delete** message opens.

5 Do one of the following:

- To delete all versions of the selected machine, click the **Delete All Versions** button. The **Confirm All Versions Delete** message opens. Continue to step 6.
- To delete only the currently commissioned version of the machine, click the **Delete Current Version** button. The **Confirm Commissioned Machine Delete** message opens. Continue to step 7.
- Click the **Cancel** button to close the message without deleting the machine.

6 Do one of the following:

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

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

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

7 Do one of the following:

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

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

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

Restore deleted commissioned machines

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

1 Click the **Proton Physics Tool** button in the **Physics Tools** window. The **Proton Physics Tool** window appears.

2 Click the **Add** button beneath the **Machine List**. The **Add New Machine** window appears.

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

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

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

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13 Physics Data Worksheets

The worksheets in this section provide checklists for the physics data required by the Pinnacle^3 treatment planning system.

The machine description worksheets list the physical description information required for the machines. These worksheets duplicate portions of the physics tool windows into which the data must be entered. Details on the machine physical description information can be found in the *Physical Machine Characteristics* chapter of the *Pinnacle^3 Physics Reference Guide*.

The measured data worksheets summarize the measured data required for each treatment modality. These worksheets can be used as checklists when measuring machine data to make sure that you measure all of the data required for each modality. Detailed descriptions of the measured data requirements can be found in the chapters of this manual that cover each modality. The worksheets list the data which must be collected for each measurement geometry for each energy on every machine.

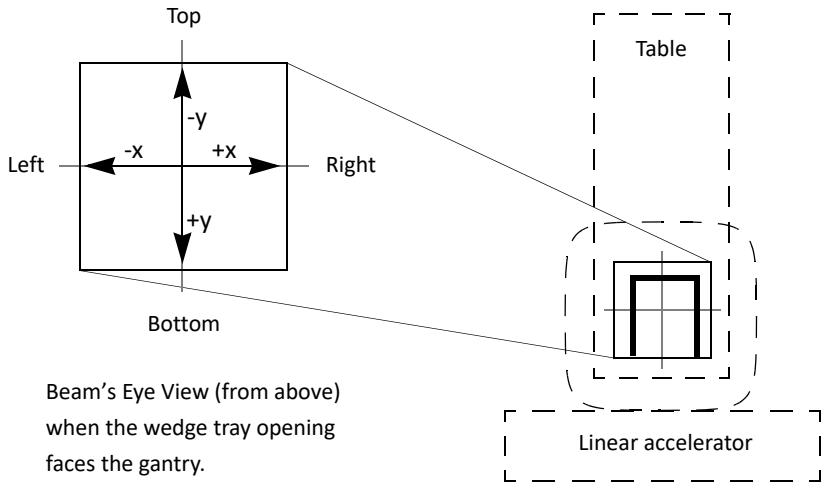
Make as many copies of the worksheets as necessary.

Machine information - collimator jaws

Physicist	
Date	
Machine Name	

Collimator jaw information

Setting	**Left/right jaws**		**Top/bottom jaws**	
	Left	**Right**	**Top**	**Bottom**
Jaw name				
Jaw pair name				
Jaw pair thickness				
Can be asymmetric?				
Minimum position				
Maximum position				
Default position				
Decimal places				



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

Machine information - couch & collimator angles

Physicist	
Date	
Machine Name	

Couch angle information

Setting	**Value**
Minimum angle	
Maximum angle	
Default angle	
Decimal places	
Couch angle when foot of table points away from gantry	
When viewed from above, is positive rotation clockwise?	

Couch position in cm	**Min**	**Max**	**Default**
Vertical position			
Lateral position			
Longitudinal position			

Collimator angle information

Setting	**Value**
Minimum angle	
Maximum angle	
Default angle	
Decimal places	
Collimator angle when tray opening faces gantry*	
When viewed from above, is positive rotation counterclockwise?	

*Some machines have a tray opening that never faces the gantry. Enter the angle as if you were able to rotate the tray opening to face the gantry.

Machine information - gantry angles

Physicist	
Date	
Machine Name	

Gantry angle information

Setting	**Value**
Minimum angle	
Maximum angle	
Default angle	
Decimal places	
Gantry angle when beam points down toward floor	
Arc allowed?	
Arc rotation direction • CW or CCW • CW only • CCW only	
When facing gantry, is positive rotation counterclockwise?	
Conformal arc (yes or no)	
Machine has C-Arm?	
C-Arm maximum angle	
C-Arm decimal places	

Machine information - delivery parameters

Physicist	
Date	
Machine Name	

Delivery parameters

Setting	Value
Maximum gantry rotations (deg/sec)	
Maximum jaw speed (cm/sec)	
Maximum MLC leaf speed (cm/sec)	
Allow conformal arc?	
Allow dynamic arc?	
Dose rate delivery behavior: • Constant dose rate • Continuously variable dose rate • Binned dose rate	
Maximum gantry MU delivery (MU/deg)	
Minimum gantry MU delivery (MU/deg)	
Minimum MLC leaf MU delivery (MU/deg)	
Limit gantry acceleration?	
Maximum gantry rate change (deg/sec)	

Machine information - High-Dose Technique parameters

Physicist	
Date	
Machine Name	

CAUTION
When you enable High-Dose Technique, the When MU limit exceeded, warn and field on the Misc tab is set to Allow beam MU to exceed maximum for standard beams, and the value cannot be changed. Please verify that the Maximum MU setting for standard beams on the Misc tab is set to the appropriate value.

High-Dose Technique machine information

Setting	Value
Set High-Dose Technique MU thresholds?	
High-Dose Technique maximum MU setting	
When High-Dose Technique MU exceeded: (1) Warn and limit beam MU to maximum setting (2) Warn and allow beam MU to exceed maximum	

High-Dose Technique MU thresholds

Beam Type	Threshold Value
Static beam	
Arc beam	
Conformal Arc beam	
Step & Shoot MLC beam	
Dynamic Arc beam	

Machine information - miscellaneous machine parameters

Physicist	
Date	
Machine Name	

CAUTION
When you enable High-Dose Technique, the When MU limit exceeded, warn and field is set to Allow beam MU to exceed maximum for standard beams, and the value cannot be changed. Please verify that the Maximum MU setting for standard beams is set to the appropriate value.

Miscellaneous machine information

Setting	Value
Primary collimation angle (radians)	
Source to axis distance (cm)	
Source to (bottom of) flattening filter distance (cm)	
Source to (bottom of) top/bottom jaw (cm)	
Source to (bottom of) left/right jaw (cm)	
Source to (top of) block tray (cm)	
Source to image receptor	
Monitor unit decimal places (for beams)	
Monitor unit decimal places (for control points)	
Maximum MU setting	
Maximum MU per degree	
When MU exceeded: (1) Warn and limit beam MU to maximum setting (2) Warn and allow beam MU to exceed maximum	
Default block/field edge overlap (cm)	
Delivery Time Multiplier	

Multi-leaf collimator (MLC) information

Physicist	
Date	
Machine Name	

Because an MLC typically has 20 to 40 pairs of leaves, you might want to make multiple copies of these pages to note information for each pair of leaves.

MLC information - General

Setting	**Value**
Vendor	
Leaf motion parallel to movement of left/right jaw or top/bottom jaw?	
MLC replaces jaw?	
Source to (bottom of) MLC distance (cm)	
MLC tracks jaws? • MLC does not track jaws for open fields • MLC tracks X jaws for open fields • MLC tracks XY jaws for open fields	
MLC thickness (cm)	
Leaf position decimal places	
Bank names	
For leaf motion parallel to left/right jaw: • For the MLC leaf positions, is the Top (X2) jaw +Y or -Y? For leaf motion parallel to top/bottom jaw: • For the MLC leaf positions, is the Left (Y2) jaw +X or -X?	
MLC has rounded leaves?	
MLC has carriage?	
Is this a micro MLC?	
Name	
Manufacture code	
Applicator type: • Photon Square • Photon Rectangle • Photon Circle • Stereotactic	

MLC information - Rounded Leaf Specifications

Rounded Leaf Tip Radius (cm)	

Leaf Position	**Offset**

Leaf Position	Offset

MLC information - Leaves

Setting	Value
Allow opposing adjacent leaves to overlap?	
Tongue and groove width (cm)	
Additional interleaf leakage transmission	
Maximum tip difference for all leaves on a side (cm)	
Minimum static leaf gap (cm)	
Minimum dynamic leaf gap (cm)	

Leaf Pair	Position (cm)	Width (cm)	Minimum tip position (cm)	Maximum tip position (cm)

Leaf Pair	Position (cm)	Width (cm)	Minimum tip position (cm)	Maximum tip position (cm)

MLC information - Jaw dependencies

Setting	Value
Default jaws behavior (static or variable)	
Open extra set of leaf pairs outside jaws automatically?	
Maximum leaf/jaw overlap (cm)	
Minimum leaf/jaw overlap (cm)	

Machine information - wedges

Physicist	
Date	
Machine Name	

Wedge information

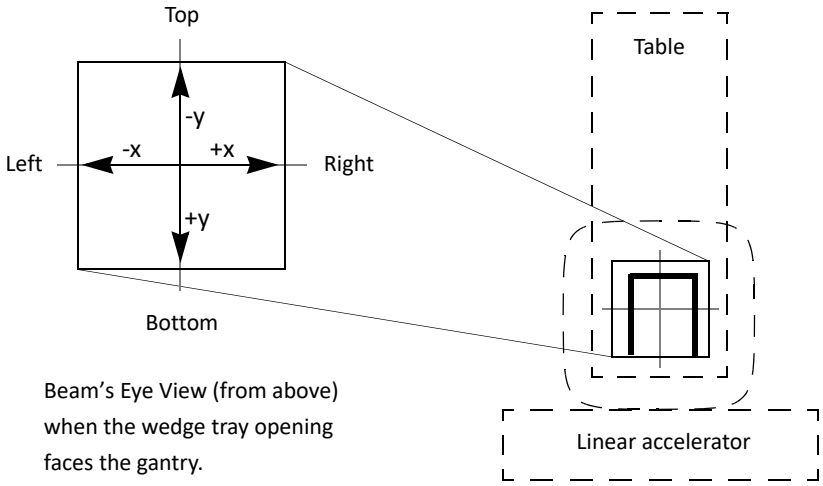
You only need to provide values for the type of wedge you are using (physical or dynamic). You can make copies of this page, if necessary, if you will be using multiple wedges.

Type of Wedge	Setting	Value
Physical wedge	Name	
	Can be used as motorized wedge?	
	Wedge angle	
	Wedge Material	
	Density (gm/cm^3)	
	Wedge on top of mounting tray?	
	Source to wedge distance (cm)	
	Length (cm)	
Dynamic wedge - Siemens	Wedge energy (MV)	
	Transmission factor	
	Linear attenuation coefficient	
	Calibration constant	
	Minimum and maximum jaw speeds (mm/s)	
	Minimum & maximum dose rates in low dose mode (MU/min)	
	Minimum & maximum dose rates in high dose mode (MU/min)	
Dynamic wedge - Varian	Wedge energy (MV)	
	Transmission factor	
	Minimum deliverable monitor units (Varian wedges only)	
	Minimum angle allowed	
	Maximum angle allowed	

Regardless of whether you are using physical wedges or dynamic wedges, you should also fill out the following table.

Orientation	Allowed?	Label	Manufacturer Code	Jaw Limits in cm			
				Left	Right	Top	Bottom
							
							
							
							

The Left, Right, Top and Bottom jaw labels in the above table refer to the jaws indicated in the following illustration.



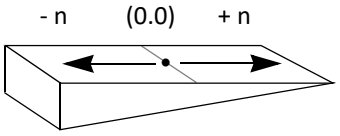
Beam's Eye View (from above) when the wedge tray opening faces the gantry.

Machine information - wedges

Physicist	
Date	
Wedge Name	

Wedge physical profile

The profile is defined by the offset (in centimeters) from the central axis and the wedge thickness (in centimeters) at that point. The offset is measured out from the central axis, which has an offset value of 0.0. The values for the offsets measured from the central axis to the heel of the wedge should be negative. The values for the offsets measured from the central axis to the toe of the wedge should be positive.



When the wedge profile values are entered in the software, the values for the thick end of the wedge must be entered first. To define the thickness of the heel of the wedge, the first offset value should be entered twice: once with a thickness of 0.0 and again with the measured thickness. The thickness does not include any base on which the wedge is mounted.

Central Axis Offset	Thickness

Machine information - record and verify system

Physicist	
Date	
Machine Name	

Record and verify information

Setting	Value
Enable R & V for this machine? (Yes or No)	
Top jaw coordinate	
Bottom jaw coordinate	
Left jaw coordinate	
Right jaw coordinate	
MLC leaf bank output order (Left bank is first or last?)	
MLC leaf pair output order (Leaf pair 1 is first or last?)	

Machine information - electron cones

Physicist	
Date	
Machine Name	

Electron cones

Print additional copies of this worksheet for additional electron cones.

Setting	Value
Electron cone name	
Manufacturer code	
Width	
Length	

Setting	Value
Electron cone name	
Manufacturer code	
Width	
Length	

Setting	Value
Electron cone name	
Manufacturer code	
Width	
Length	

Setting	Value
Electron cone name	
Manufacturer code	
Width	
Length	

Machine information - stereotactic collimators

Physicist	
Date	
Machine Name	

Stereotactic radiosurgery collimators

Name	Diameter (cm)	Accessory Code	X1	X2	Y1	Y2

Machine information - tolerance tables

Physicist	
Date	
Machine Name	

Tolerance tables

Table Name	Table Number

Photon beam energy information

Physicist	
Date	
Machine Name	

Photon beam energy information

Setting	**Value**
Photon energy name	
Photon energy (MV)	
Default tray factor	
Default block and tray factor	
Dose rate table (MU/min) Enter the allowable dose rates for the machine in the table cells at the right. The first value should be the maximum dose rate for the energy, and subsequent values should be monotonically decreasing.	
Default dose rate (MU/min)	

Photon beam measured data worksheet 1: Open field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Field Size	5 cm x 5 cm
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam measured data worksheet 2: Open field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Field Size	10 cm x 10 cm
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam measured data worksheet 3: Open field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Field Size	20 cm x 20 cm
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam measured data worksheet 4: Open field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Field Size	20 cm x 5 cm
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam measured data worksheet 5: Open field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Field Size	5 cm x 20 cm
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam measured data worksheet 6: Open field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Field Size	30 cm x 30 cm
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam measured data worksheet 7: Open field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Field Size	40 cm x 40 cm (or largest field size)
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam measured data worksheet 8: MLC field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Jaw Size	20 cm x 20 cm
MLC Field Size	2 cm x 2 cm
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam measured data worksheet 9: MLC field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Jaw Size	20 cm x 20 cm
MLC Field Size	3 cm x 3 cm
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam measured data worksheet 10: MLC field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Jaw Size	20 cm x 20 cm
MLC Field Size	5 cm x 5 cm
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam measured data worksheet 11: MLC field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Jaw Size	20 cm x 20 cm
MLC Field Size	10 cm x 10 cm
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam measured data worksheet 12: MLC field

Physicist	
Date	
Machine Name	
Energy	
Wedge/Modifier? (Y/N)	
Description	
Jaw Size	20 cm x 20 cm
MLC Field Size	15 cm x 15 cm
SSD	100
Recommended resolution for profiles	0.20 cm

⑦	Profile Type	Depth	X Offset*	Y Offset*	Resolution	File Name
	Depth Dose	0–25 cm				
	X Profile	5 cm				
	Y Profile	5 cm				
	X Profile	10 cm				
	Y Profile	10 cm				
	X Profile	20 cm				
	Y Profile	20 cm				
	X Profile	d_{max}				
	Y Profile	d_{max}				

* If depth dose profile is not measured on the central axis.

Photon beam output factors worksheet

Physicist	
Date	
Machine Name	
Energy	

Reference output factor measurement

Setting	Value
Field size, MLC defined (for fixed jaw machines, if applicable)	
Calibration point depth (cm)	
Source to calibration point distance (cm)	
Dose/MU at calibration point (cGy/MU)	

Note: Calibration point depth of 10 cm is strongly recommended. Do not use a calibration point depth of d_{max}.

Relative output factor measurements

Depth (cm): same as calibration point depth

Field Size (cm^2)	Relative Output Factor

Wedged field output factors worksheet

Physicist	
Date	
Machine Name	
Energy	

Wedged field output factor measurements

Wedge	

Field Size (cm^2)	**Relative Output Factor**

The relative output factor for a wedged field is calculated using the equation

$$OF = \frac{Dose_{WFS}}{Dose_{CFS}}$$

where $Dose_{WFS}$ is the measured dose for the given wedged field size and $Dose_{CFS}$ is the measured dose for the open calibration field. Note that the ratio is *not* the wedge transmission factor because $Dose_{CFS}$ is the fixed open calibration field dose.

WARNING
The wedge transmission factor cannot be substituted for the wedged field output factors. Using the wedge transmission factor instead of wedged field output factors will result in incorrect monitor unit calculations.

Stereotactic radiosurgery energy information

Physicist	
Date	
Machine Name	

Stereotactic radiosurgery energy information

Setting	Value
Stereotactic energy name	
Stereotactic energy (MV)	
Dose rate table (MU/min) Enter the allowable dose rates for the machine in the table cells at the right. The first value should be the maximum dose rate for the energy, and subsequent values should be monotonically decreasing.	
Default dose rate (MU/min)	

Stereotactic radiosurgery measured data worksheet

Physicist	
Date	
Machine Name	
Collimator Size (cm)	
Recommended resolution for profiles	0.20 cm

Profiles Measured with SSD = 80 cm

✓	Profile Type	Depth	Resolution	File Name
	Depth Dose	0–30 cm		
	X Profile	1 cm		
	X Profile	5 cm		
	X Profile	10 cm		
	X Profile	15 cm*		
	X Profile	20 cm		
	X Profile	25 cm		
	X Profile	30 cm		

Profiles Measured with SSD = 100 cm

✓	Profile Type	Depth	Resolution	File Name
	Depth Dose	0–30 cm		
	X Profile	1 cm		
	X Profile	5 cm		
	X Profile	10 cm		
	X Profile	15 cm*		
	X Profile	20 cm		
	X Profile	25 cm		
	X Profile	30 cm		

* Profiles at these depths are not required but are recommended for increased accuracy.

Stereotactic radiosurgery output factors worksheet

Physicist	
Date	
Machine Name	
Energy	

10 cm x 10 cm reference field measurements

Setting	Value
Dose/MU in air (cGy/MU)	
Back scatter factor	

Collimator-specific measurements

Collimator (cm)	Relative Output Factor	Back Scatter Factor

ROF (W_c)—The relative output factor for collimator diameter W_c.

$$ROF(W_c) = \frac{\text{Reading at } d_{max}(W_c)}{\text{Reading at } d_{max}(10 \times 10)}$$

Electron beam energy information

Physicist	
Date	
Machine Name	

Electron beam energy information

Setting	**Value**
Electron energy name	
Electron energy (MV)	
Default cutout material transmission factor	
Dose rate table (MU/min) Enter the allowable dose rates for the machine in the table cells at the right. The first value should be the maximum dose rate for the energy, and subsequent values should be monotonically decreasing.	
Default dose rate (MU/min)	

Electron beam measured data worksheet 1

Physicist	
Date	
Machine Name	
Energy	

Depth Dose Measurement for Determining the Practical Range

⑦	Profile Type	Depth	Cone Size	File Name
	Depth Dose	SSD=SAD	Largest available	

Depth Dose Measurements with SSD = SAD

⑦	Profile Type	Depth	Cone Size	File Name
	Depth Dose	R_p + 5 cm		
	Depth Dose	R_p + 5 cm		
	Depth Dose	R_p + 5 cm		
	Depth Dose	R_p + 5 cm		
	Depth Dose	R_p + 5 cm		
	Depth Dose	R_p + 5 cm		
	Depth Dose	R_p + 5 cm		
	Depth Dose	R_p + 5 cm		
	Depth Dose	R_p + 5 cm		

Depth dose measurements in water must be made for each scanned square field, otherwise the software cannot compute the profile.

Electron beam measured data worksheet 2

Physicist	
Date	
Machine Name	
Energy	

The following profiles must be measured with a water phantom setup SSD = SAD. For quality assurance, the same set of profiles should be measured at extended SSDs (for example, 105, 110, 115, and 120 for an SAD = 100 machine).

SSD	

⑦	**Profile Type**	**Depth**	**File Name**
	X Profile	1/2(R_{90})	
	Y Profile	1/2(R_{90})	
	X Profile	R_{90}	
	X Profile	R_{70}	
	X Profile	R_{50}	
	X Profile	R_p + 2 cm	

Electron beam measured data worksheet 3

Physicist	
Date	
Machine Name	
Energy	

The following profiles must be measured in air. These profiles do not need to be imported into Pinnacle[3].

Cone Size	

⑦	**Profile Type**	**SSD**		**File Name**
	X Profile	SSD = SAD		
	Y Profile	SSD = SAD		
	X Profile	SSD = SAD + 5		
	Y Profile	SSD = SAD + 5		
	X Profile	SSD = SAD + 10		
	Y Profile	SSD = SAD + 10		
	X Profile	SSD = SAD + 15		
	Y Profile	SSD = SAD + 15		
	X Profile	SSD = SAD + 20		
	Y Profile	SSD = SAD + 20		

Electron beam measured data worksheet 4

Physicist	
Date	
Machine Name	
Energy	
Drift Distance (cm)*	

*Drift Distance is the distance between the collimator and the surface of the phantom for the standard setup SSD.

Cutout Material Photon Transmission Factor

Determine the photon dose transmitted through the cutout material. The ratio of the blocked field dose to the open field dose is the cutout material photon transmission factor.

$$\text{Cutout material transmission factor} = \frac{Dose_{R_p + 2\,cm}\ \text{blocked field}}{Dose_{R_p + 2\,cm}\ \text{open field}}$$

⑦	Profile Type	Setup	Depth	Dose
	Point Dose	10 cm x 10 cm open field, SSD =SAD	R_p + 2 cm	
	Point Dose	10 cm x 10 cm blocked field, SSD = SAD	R_p + 2 cm	

Electron beam measured data worksheet 5

Physicist	
Date	
Machine Name	
Energy	

Off-Axis Ratio Worksheet

Energy	
Cone Size	
Profile (X or Y)	

Position	Measured Value	Computed Value	Off-axis Ratio

Electron output factors worksheet 1

Physicist	
Date	
Machine Name	
Energy	

NOTE
The field sizes listed on this worksheet are the recommended sizes for a standard set of electron output factors. If necessary, collect data for smaller field sizes to accommodate smaller output factors in the individual cones.

Reference output factor measurement

Setting	Value
Calibration point depth (cm)	
Source to calibration point distance (cm)	
Dose/MU at calibration point (cGy/MU)	

Relative output factor measurements

Depth (cm): Same as calibration point depth.

NOTE
You may want to measure a SSD less than 100 cm (98 cm, for example). Patient curvature or other factors can cause the SSD can be slightly less than 100 cm, and MUs will not be calculated in these situations unless you have measured an SSD less than 100 cm.

SSD (cm)	Cone Size (cm)	Field Size (cm)	Relative Output Factor Nominal Energies (MeV)					
			6	9	12	15	18	20
100	6 x 6	2 x 2						
		3 x 3						
		4 x 4						
		6 x 6						
	10 x 10	3 x 3						
		4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
	15 x 15	3 x 3						
		4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
	20 x 20	4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
		18 x 18						
		20 x 20						
	25 x 25	4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
		18 x 18						
		20 x 20						
		25 x 25						

SSD (cm)	Cone Size (cm)	Field Size (cm)	Relative Output Factor Nominal Energies (MeV)					
			6	9	12	15	18	20
105	6 x 6	2 x 2						
		3 x 3						
		4 x 4						
		6 x 6						
	10 x 10	3 x 3						
		4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
	15 x 15	3 x 3						
		4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
	20 x 20	4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
		18 x 18						
		20 x 20						
	25 x 25	4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
		18 x 18						
		20 x 20						
		25 x 25						

SSD (cm)	Cone Size (cm)	Field Size (cm)	Relative Output Factor Nominal Energies (MeV)					
			6	9	12	15	18	20
110	6 x 6	2 x 2						
		3 x 3						
		4 x 4						
		6 x 6						
	10 x 10	3 x 3						
		4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
	15 x 15	3 x 3						
		4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
	20 x 20	4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
		18 x 18						
		20 x 20						
	25 x 25	4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
		18 x 18						
		20 x 20						
		25 x 25						

SSD (cm)	Cone Size (cm)	Field Size (cm)	Relative Output Factor Nominal Energies (MeV)					
			6	9	12	15	18	20
115	6 x 6	2 x 2						
		3 x 3						
		4 x 4						
		6 x 6						
	10 x 10	3 x 3						
		4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
	15 x 15	3 x 3						
		4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
	20 x 20	4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
		18 x 18						
		20 x 20						
	25 x 25	4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
		18 x 18						
		20 x 20						
		25 x 25						

SSD (cm)	Cone Size (cm)	Field Size (cm)	Relative Output Factor Nominal Energies (MeV)					
			6	9	12	15	18	20
120	6 x 6	2 x 2						
		3 x 3						
		4 x 4						
		6 x 6						
	10 x 10	3 x 3						
		4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
	15 x 15	3 x 3						
		4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
	20 x 20	4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
		18 x 18						
		20 x 20						
	25 x 25	4 x 4						
		6 x 6						
		8 x 8						
		10 x 10						
		12 x 12						
		15 x 15						
		18 x 18						
		20 x 20						
		25 x 25						

Machine information - couch angles (protons)

Physicist	
Date	
Machine make and model	

Couch angle information

Setting	**Value**
Decimal places	
Minimum angle	
Maximum angle	
Default angle	
When viewed from above, is positive rotation clockwise?	
Couch angle when foot of table points away from gantry	

Couch position in cm	**Min**	**Max**	**Default**
Vertical position			
Lateral position			
Longitudinal position			

Machine information - gantry angles (protons)

Physicist	
Date	
Machine make and model	

Gantry angle information - continuous

Setting	Value
Decimal places	
Minimum angle	
Maximum angle	
Default angle	
When facing gantry, is positive rotation counterclockwise?	
Gantry angle when beam points down toward floor	

Gantry angle information - discrete

Setting	Value
Decimal places	
Angles:	
Default angle	
When facing gantry, is positive rotation counterclockwise?	
Gantry angle when beam points down toward floor	

Machine information - nozzle components (protons)

Physicist	
Date	
Machine make and model	

Nozzle components

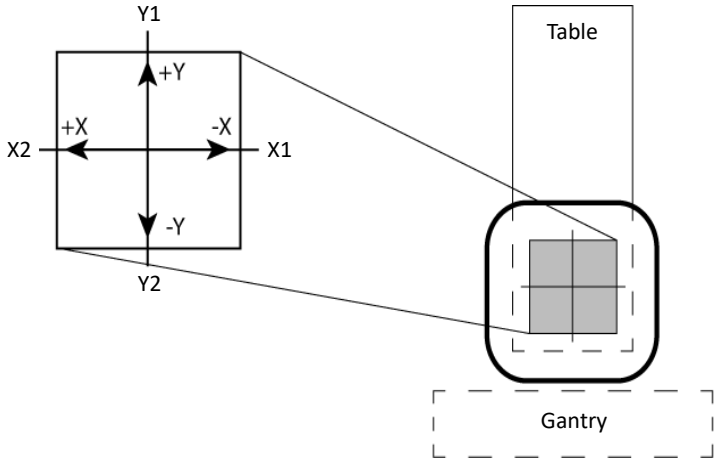
Setting	**Value**
Nominal source to axis distance	
Delivery type: • Double scattering • Uniform scanning	
Magnet to isocenter distance • X magnet (cm) • Y magnet (cm)	
Full plateau delivery supported	
Minimum distance from isocenter to virtual block tray (cm)	
Maximum distance from isocenter to virtual block tray (cm)	

Machine information - snout (protons)

Physicist	
Date	
Machine make and model	

Snout

Setting	Value
Name	
ID	
Circular: Diameter (cm) Rectangular: • X (cm) • Y (cm)	
Unmilled compensator thickness (cm)	
Slab thickness (cm)	
Maximum number of slabs	



Compensator material (double scattering and uniform scanning)

Setting	Value
Name	
ID	
Stopping power relative to water	
Minimum compensator thickness (cm)	
Default milling tool diameter (cm)	

Aperture material (double scattering and uniform scanning)

Setting	Value
Name	
ID	
Stopping power relative to water	
Minimum milling tool diameter (cm)	
Default milling tool diameter (cm)	

Machine information - imaging devices (protons)

Physicist	
Date	
Machine make and model	

Imaging device - fixed or continuous

Setting	Value
Name	
Angle mode: Fixed or Continuous • Fixed: Angle (deg) • Continuous: Pairing angle (deg)	
SAD (cm)	
Energy (kV)	

Machine information - miscellaneous machine parameters (protons)

Physicist	
Date	
Machine make and model	

Miscellaneous machine information

Setting	Value
Monitor unit decimal places for beams	
Maximum MU setting	
When MU limit exceeded, warn and: (1) Limit beam MU to maximum setting (2) Allow beam MU to exceed maximum	
Pristine peak range point level (%)	
SOBP proximal edge point level (%)	
SOBP distal edge point level (%)	

Z-fluence profile measured data worksheet (double scattering)

Physicist	
Date	
Machine make and model	

Setting		**Value**
Range	Minimum	
	Maximum	
Modulation	Minimum	
	Maximum	
Modulator ID		
Range band name		

⑦	**Name of the Profile**	**Range**

Open field profile measured data worksheet (double scattering)

Physicist	
Date	
Machine make and model	

Setting		**Value**
Range	Minimum	
	Maximum	
Modulation	Minimum	
	Maximum	
Modulator ID		
Range band name		

⑦	**Name of the Profile**	**Energy (MeV)**	**Measurement Plane (cm)**			

Half beam blocked profile measured data worksheet (double scattering and uniform scanning)

Physicist	
Date	
Machine make and model	

Setting		**Value**
Range	Minimum	
	Maximum	
Modulation	Minimum	
	Maximum	
Modulator ID		
Range band name		

⑦	**Name of the Profile**	**Range Band**

⑦	**Name of the Profile**	**Range Band**

Pristine peak depth dose measured data worksheet (double scattering and uniform scanning)

Physicist	
Date	
Machine make and model	

Setting		**Value**
Range	Minimum	
	Maximum	
Modulation	Minimum	
	Maximum	
Modulator ID		
Range band name		

⑦	**Name of the Profile**	**Range**

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