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Eclipse Algorithms Reference
Guide Eclipse

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Abstract	*Eclipse Algorithms Reference Guide* provides reference information about the algorithms supported in Eclipse, version 13.0.
	This document is the English-language original.
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Chapter 1   Introduction

This guide assumes that you are familiar with Microsoft® Windows. Before you begin using the application, read your Microsoft Windows documentation to become familiar with the Windows environment.

Intended Audience for This Document

This guide is written mainly for physicists or any other users responsible for commissioning, configuring and validating beam data.

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

Eclipse should only be used by qualified medical professionals.

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

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

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

WARNING: Acceptance tests done during installation are not adequate measures for clinical acceptance of the system. You need to separately commission each algorithm and beam data with additional tests.

Visual Cues

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

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

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

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

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

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

Related Publications

- *Treatment Planning for External Beam - Eclipse Reference Guide*—Provides background information and detailed instructions for creating external treatment plans.
- *Beam Configuration Reference Guide*—Provides reference information and procedures for beam data configuration required for performing dose calculation for external treatment plans.

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3. Choose an option:
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What is New in Eclipse Algorithms

Eclipse algorithms contain the following changes. In addition to the items included below, there are several minor enhancements:

- In IRREG Planning, point dose is now calculated using the Anisotropic Analytical Algorithm (AAA).
- The Pencil Beam Convolution (PBC) and Generalized Gaussian Pencil Beam (GGPB) algorithms are no longer released in this version. For information on these algorithms, refer to *Eclipse Algorithms Reference Guide* for Eclipse version 11.0.

Chapter 2 General About Eclipse Algorithms

Using Eclipse Configured Beam Data

Eclipse Beam Data, available only for the AAA and Acuros XB algorithms, is valid for Varian Clinac 21/23EX Series medical linear accelerators and other Clinacs conforming to the beam specifications detailed in Sections 1.0 and 2.0 of Clinac 21/23EX Equipment Specification (Document RAD 4205), the Clinac iX Accelerator Specifications (Document RAD 9510), the Trilogy Accelerator Specifications (Document RAD 9515), and Clinac Beam Matching (Document RAD 2055). These include all Clinac iX accelerators, all Trilogy accelerators, Clinac 2100C/CD/EX accelerators with Serial Number 865 or later and Clinac 2300CD/EX accelerators with Serial Number 146 or later. For older machines that have been upgraded to EX specifications, it is necessary to confirm that the part number of the 6-MV photon-field-flattening filter is P/N 1103282.

Compare the dosimetric beam data acquired from the treatment machine at the site to the dosimetric beam data used in the configuration of the preconfigured beam data and ensure that the variations do not exceed user tolerance. If variations exceed the tolerance, use the dosimetric beam data acquired at the site for calculation algorithm configuration.

Eclipse Algorithms and CT Image Data

The CT image data is handled differently in different Eclipse dose calculation algorithms. The HU values in the image are converted either to electron density, mass density or proton stopping power depending on the type of plan and algorithm used. The conversion is done following CT calibration curves configured in Beam Configuration. Multiple CT scanners can be configured in the system and each CT scanner has its own set of calibration curves.

For each CT scanner the following curves are available:

- Electron Density: This curve is used by the AAA and MRDC algorithms to convert HU values to relative electron density.

- Mass Density: This curve is used by the Acuros XB and eMC algorithms to convert HU values to mass density. From the derived mass density, Acuros XB and eMC determine the material composition of voxels in the image. For more information on the mass density to material conversion method employed by Acuros XB, see Chapter 6, "CT to Material Mapping," on page 140. For more information on the mass density to material conversion method employed by eMC, see Chapter 8, "Preprocessing the Absorber CT Volume," on page 178.

- Proton Stopping Power: This curve is used by the PCS algorithm to convert HU values to Proton Stopping Power (relative to water). For more information, refer to *Proton Algorithm Reference Guide*.

To achieve accurate dose calculations, it is essential to define a valid CT calibration curve for each CT scanner in Beam Configuration. For each CT image imported into the system, the CT scanner name in the image header is compared with CT scanners stored in the database. If a match is found, the custom CT calibration curve is used for all dose calculations. If a matching CT scanner is not found, you need to manually define the CT scanner to use for the image series. All used CT calibration curves must be approved. For instructions on approving a CT calibration curve, refer to *Beam Configuration Reference Guide*.

Calibration curves are defined up to a certain maximum HU value. You can modify these curves and extend their defined range of HU values. It is possible that HU values found in CT images are higher than the maximum HU value for which the calibration curves are defined. For instructions on modifying CT calibration curves, refer to *Beam Configuration Reference Guide*.

To verify that the CT calibration curve is correctly configured, take a CT image of the calibration phantom, import it in the system and check that the values shown by the Physical Property tool are correct. (For information on the Physical Property tool, refer to *Treatment Planning for External Beam - Eclipse Reference Guide*.)

The table describes how the Eclipse algorithms handle HU values that fall outside the range covered by the CT calibration curves.

Table 1 Eclipse Algorithms and CT Image Data

Algorithm	How CT Image Data is Handled
AAA	The AAA algorithm truncates all HU values higher than the maximum HU value defined in the CT calibration curve to the maximum electron density value. A warning is shown in the DCF status window and logged in the field calculation notes when such a situation occurs. Additionally, the maximum electron density modeled in AAA is 15. Electron densities larger than that are truncated to the maximum value (that is, the value 15 is used).
Acuros XB	The Acuros XB algorithm stops the calculation if an HU value in the CT image is higher than or equal to the maximum HU value defined in the CT calibration curve. The volume spanned by CT image pixels whose mass density (derived either from the HU value in the image or assigned to a structure) exceeds the maximum mass density of the materials used in automatic conversion (3.0 g/cm^3) is calculated. If this volume is higher than a user defined maximum volume for automatic material assignment to high density artifacts, the calculation is prevented until a material is assigned via a structure. For smaller volumes, automatic conversion to a user defined material takes place. This is to prevent incorrect material assignment to a significant volume of a high density material.
MRDC	The MRDC algorithm truncates all HU values higher than the maximum HU value defined in the CT calibration curve to the maximum electron density value. MRDC does not give any warning message if truncation is done. In addition, for speed and memory reasons, electron density values are binned so that for each calculation voxel the MRDC uses a density value averaged over a small subvolume, typically 4x4x4 voxels.
eMC	The eMC algorithm truncates all HU values higher than the maximum HU value defined in the CT calibration curve to the maximum mass density value. A warning is shown in the DCF status window and logged in the field calculation notes when such a situation occurs.

Accuracy of Eclipse Dose Calculation Algorithms

The following information is provided as a reference indicating the methods used to evaluate Eclipse algorithm accuracy. The information is provided as an example, more comprehensive set of data is needed for testing the accuracy for clinical use.

Accuracy of the dose calculation algorithms is evaluated by comparing measured data against the calculation results obtained in the same field geometry and the same MU values. Accuracy evaluation measurements and the beam data that is used for configuring dose calculation algorithms must be obtained from the same machine so that between the measurements machine sustains the same calibration and identical beam properties.

Algorithms' accuracy is quantified in terms of gamma error. Gamma error is defined as the shortest distance in four dimensional space where the relative dose represents the fourth dimension. For gamma metric, the unit of the distance and the dose are rescaled: dose is in units of a percent of the maximum dose, and the distance in units of given number of mm. For example, with gamma scale 3% and 3 mm, gamma error smaller than 1 guarantees that at that point dose difference is no more than 3%, or the distance to agreement no more than 3 mm. Dose calculation accuracy goal defined by the gamma error scale is considered to be fulfilled when gamma error value for 95% of the examined measurement points is no more than 1.

The accuracy goal is evaluated separately for two regions (sets of measurement points): the high dose region consists of measurement points with higher dose than 20% of the maximum measured dose. The global region consists of measurement points higher than 3% of the maximum dose in our example case. It is further required that the gamma error in this example exceeds the value 1.67.

In the following, dose comparison examples are shown for depth dose curves measured for static fields with SSD = 100 cm. The table below summarizes the field geometries and gamma error scales stating the algorithms' accuracy in these conditions. Comparison results are shown in the figures below, source of the measured data is indicated before each figure.

Table 2 Accuracy of Eclipse Dose Calculation Algorithms

Algorithm	Field setup	Gamma error scale	Figure
AAA	Open field, 10 cm X 10 cm, SSD = 100 cm	2%, 2 mm	Figure 1
Acuros XB	Open field, 10 cm X 10 cm, SSD = 100 cm	2%, 2 mm	Figure 2
CDC	20 mm conical collimator, SSD = 100 cm	2%, 1 mm	Figure 3
eMC	Applicator field, 10 cm x 10 cm, SSD = 100 cm	2%, 2 mm[a]	Figure 4

a. Note that typically the eMC accuracy is 3%. For more information, see Chapter 8, Section "Known Limitations of the eMC Algorithm" on page 195.

Dose is calculated with AAA using calculation resolution 0.25 cm. Depth dose curve is measured on Elekta SL18 in water phantom with ionization chamber IC15.
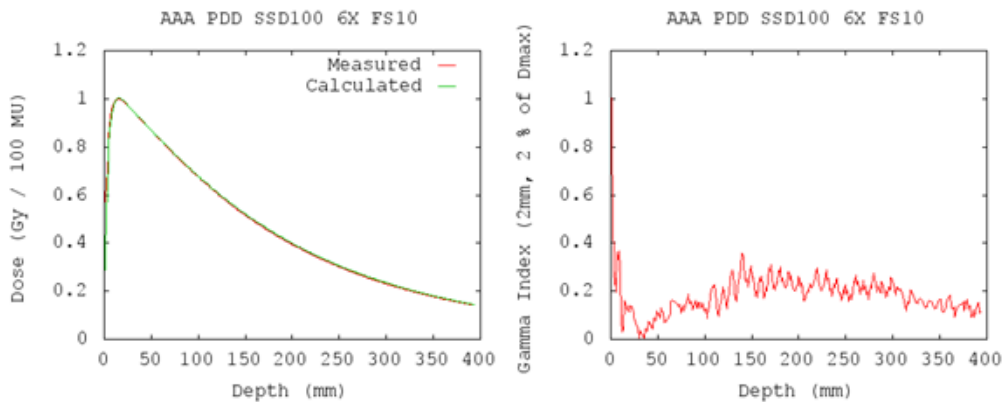
Figure 1   Depth dose curve comparison for AAA

Dose is calculated with Acuros XB using calculation resolution 0.25 cm. Depth dose curve is measured on Elekta SL18 in water phantom with ionization chamber IC15.
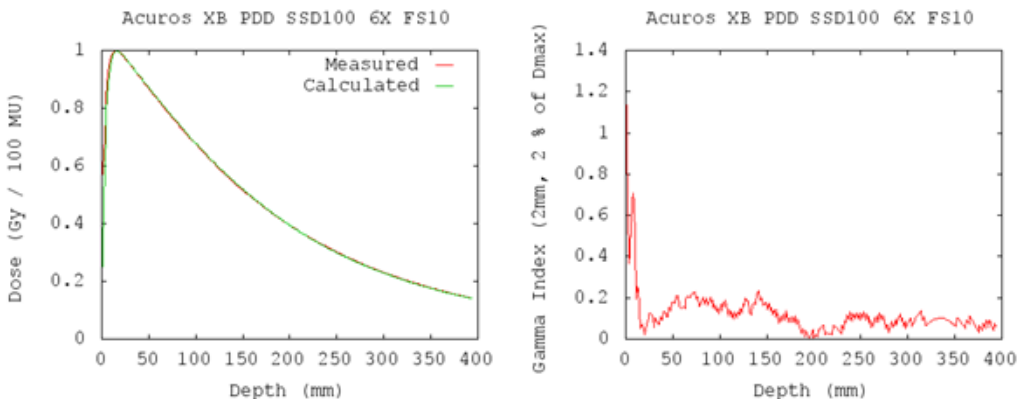
Figure 2   Depth dose curve comparison for Acuros XB

Dose is calculated with CDC using calculation resolution 0.1 cm and fine grid setting. Depth dose curve is measured on Varian TrueBeam in water phantom with SRS Diode and ionization chamber CC01-IC.
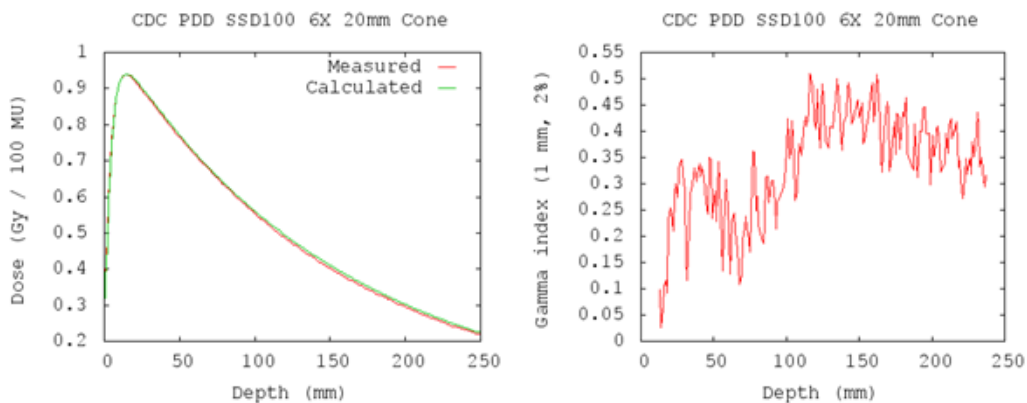
Figure 3   Depth dose curve comparison for CDC

Dose is calculated with eMC using the following calculation options: calculation resolution 0.25cm, accuracy 1, no smoothing. Depth dose curve is measured on Varian TrueBeam in water phantom with ionization chamber IC15.
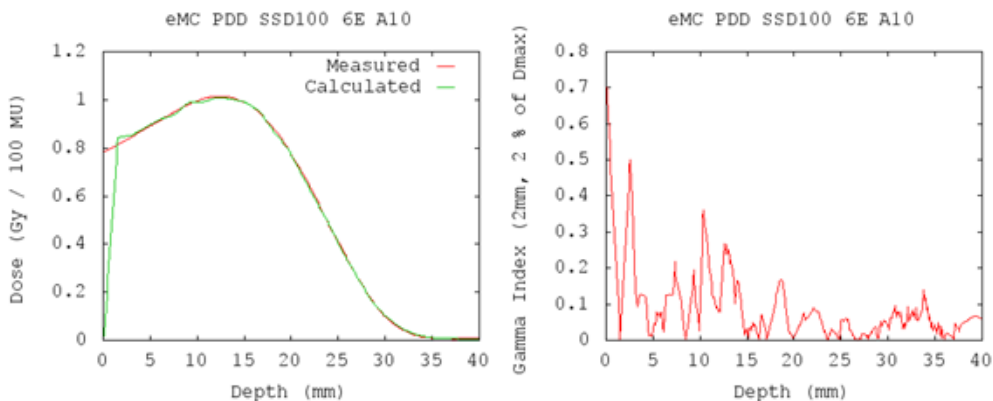
Figure 4   Depth dose curve comparison for eMC

Volume I   AAA and Acuros XB Dose Distribution
             Calculation Algorithms

Chapter 3   Implementation of AAA and Acuros XB in Eclipse

The AAA and Acuros XB dose calculation algorithms are separately licensed features in Eclipse. The photon beam source model, used by AAA and Acuros XB, is configured in Beam Configuration. The resolution of the dose calculation grid can be selected in the range of 1–5 mm for AAA and 1–3 mm for Acuros XB during treatment planning in Eclipse External Beam Planning.

The dose calculation in External Beam Planning with the AAA and Acuros XB fully supports the use of beam modifiers, such as blocks, hard wedges, dynamic wedges, compensators, MLCs and Intensity Modulated Radiation Therapy (IMRT) with Dynamic MLC (DMLC). The algorithms also support calculation of VMAT fields (Volumetric Modulated Arc Therapy), and account for patient support devices (for example couch structures) and bolus linked to a field in the dose calculation. Dose inside a bolus is visualized, but dose inside support structures is not visualized. The AAA and Acuros XB process all pixels outside the body, including those in contoured structures, as air, except for bolus and patient support devices.

The dose calculation in IRREG Planning with AAA supports the use of open fields, fields with blocks, fields with static MLC, fields with hard wedges and fields with dynamic wedges (Elekta Motorized Wedges and Elekta OmniWedges are not supported). Acuros XB cannot be used in IRREG Planning. In IRREG, AAA calculates the dose at a given point based on SSD and depth information. The result corresponds to a water phantom measurement at that point with the field perpendicular to the phantom surface which is assumed to be flat. In the case of several fields, the contribution of each field to a given point is calculated independently and added to the total dose at that point. In the case of several points, this is repeated for each point.

For information on how to select a calculation model for dose calculation in Eclipse, refer to *Treatment Planning for External Beam - Eclipse Reference Guide*. For information on configuring the source model, see Chapter 4, "Configuration of Photon Beams," on page 55. For information on using Beam Configuration, refer to the online help system or *Beam Configuration Reference Guide*.

Monitor Unit Calculation

The calculation of MU is based on output factor measurements performed for different field sizes in a certain reference geometry (see Chapter 4, "Output Factor Geometry," on page 102), and calibration calculations made for the reference field size.

The change in the output factor as a function of field size is caused by changes in phantom scatter, head scatter and collimator backscatter into the monitor chamber. The phantom and head scatter effects are accounted for by the photon beam source model and the volumetric dose calculation algorithm (AAA or Acuros XB). The remaining change in the output factors is assumed to be caused by collimator backscatter. It is estimated from the measured output factor table as shown in the equation.

Eq. 1

$$\mathrm{CBSF}(X,Y) = \frac{\mathrm{OF}_{\mathrm{ref}}}{\mathrm{OF}(X,Y)} \times \frac{D'(X,Y)}{D'_{\mathrm{ref}}}$$

where

$\mathtt{X,Y}$	=	Collimator settings ($\mathtt{X = X_2 - X_1}$, $\mathtt{Y = Y_2 - Y_1}$)
$\mathtt{CBSF(X,Y)}$	=	Collimator back-scatter factor for an open field with same collimator settings.
$\mathtt{OF_{ref}}$	=	Output factor table value for reference field size. The value is normally 1.0. The reference field size is given by the parameter *Absolute dose reference field size*, defined in the AAA and Acuros XB Parameters (see Table 12 on page 71).
$\mathtt{OF(X,Y)}$	=	Output factor table value for field size $\mathtt{X,Y}$.
$\mathtt{D'(X,Y)}$	=	Dose at the reference point calculated by the AAA or Acuros XB for the field size $\mathtt{X,Y}$ and the reference geometry when ignoring the effect of collimator back scatter.
$\mathtt{D'_{ref}}$	=	Dose calculated by the AAA or Acuros XB for the reference conditions in the reference geometry (Chapter 4, "Output Factor Geometry," on page 102) when ignoring the effect of collimator back scatter.

The reference field geometry used in the measurement of the output factor table is indicated by the Source-Phantom Distance parameter defined in the output factor table in Beam Configuration (see Table 5

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on page 59). The reference point depth from the surface of the phantom is given by the Detector depth from phantom surface parameter, also defined in the output factor table.

The final MU are calculated from the prescribed dose, plan normalization, field weight, field normalization and a normalization factor determined by the dose calculation algorithm. The normalization factor determined by the AAA and Acuros XB is the MU value for 1 Gy to 100% of the current field. AAA and Acuros XB calculate the monitor units at the normalization point MU_{norm} for open field, hard wedge, Enhanced Dynamic Wedges and physical compensators as in the equation:

Eq. 2

$$MU_{norm} = CBSF(X,Y) \times \left(\frac{MU_{calib}}{D_{calib}}\right) \times \left(\frac{D_{ref}}{D_{norm}(X,Y)}\right) \times \frac{1}{WCF(X,Y)}$$

where

$CBSF(X,Y)$ = Collimator back-scatter factor for an open field with same collimator settings (see Equation 1 on page 31).

In case of treatment units where MLC defines the field size (for example Elekta), the collimator back-scatter factor is calculated based on the effective field size in X and Y direction instead of the collimator jaw settings (X, Y).

MU_{calib} = User-defined value of parameter Reference Dose In MU At Calibration Depth. (For hard wedges, this parameter is read from the wedge parameters. See Chapter 4, "Hard Wedge Parameters," on page 77.)

D_{calib} = User-defined value of parameter Reference Dose In Gy At Calibration Depth. (For hard wedges, this parameter is read from the wedge parameters. See Chapter 4, "Hard Wedge Parameters," on page 77.)

D_{ref} = Dose calculated by the AAA or Acuros XB for the reference conditions (see Chapter 4, "Output Factor Geometry," on page 102) at the calibration depth, which is the value of the Absolute Dose Scaling Factor parameter. (For hard wedges, this parameter is read from the wedge parameters.)

$D_{norm}(X,Y)$ = Dose calculated by the AAA or Acuros XB at the field normalization point, based on the selected field normalization method.

$WCF(X,Y)$ = Wedge correction factor for hard wedge field with the collimator jaw settings (X,Y).

In case the field contains a block or an MLC, the wedge correction factor is calculated based on the effective field size in X and Y direction instead of the collimator jaw settings (X, Y).

Reference dose calculation is similar to MU calculation. AAA and Acuros XB calculate a reference dose factor as in the following equation. The reference dose (Ref. D) shown in the Info Window is

calculated from this reference dose factor by taking into account the prescribed dose, plan normalization, field weight, field normalization and a normalization factor determined by the dose calculation algorithm. Note that the reference dose is not calculated if the central axis is outside the field aperture, or at the boundary of field aperture, or if the central axis is blocked by an MLC or block. It is also not calculated for an arc field or when the plan dose calculation mode is used for Acuros XB.

Eq. 3

$$\text{Ref\_dose} = \frac{D_{d_{\max}}}{D_{\text{norm}}}$$

where

$D_{d_{\max}}$ =   Maximum dose along the central axis

In the case of an IMRT field, the LMC calculates the field MU. For this, the LMC needs from the AAA or Acuros XB the MUGY10 parameter and the collimator back-scatter factor for an open field. For information on the LMC and MU calculation for IMRT fields, see Chapter 10, Section "MU Calculation in the LMC" on page 255. For information on how the collimator back-scatter factor is defined in the AAA, see Equation 1 on page 31.

Normalization

The normalization modes used in the AAA and Acuros XB for volumetric dose calculation can be selected in Beam Configuration in the Calculation Options of the calculation model. The selected field normalization mode is used for all fields, with a few exceptions. If the result of using the selected normalization mode will be unacceptable, or if the mode cannot be used for a field, another field normalization type is automatically selected for that field.

The table describes the field normalization modes available, and the cases where the selection is automatically changed.

Table 3 Field Normalization Methods in AAA and Acuros XB

Norm. Mode	Meaning	Exceptions
No field normalization	Field dose is normalized to 100% at 1Gy/100MU.	*IMRT field:* Normalization method is automatically changed to *IMRT field normalization*.
100% to isocenter	Field dose is normalized to 100% at the isocenter.	*Isocenter in air / isocenter covered by block / low dose[*] at isocenter:* The dose is normalized to a point on the isocenter plane that has the highest dose. If the dose at that point is low, the normalization method is changed to *100% to field central axis Dmax*. [*]Dose at isocenter is considered low if it is lower than 10% of the maximum field dose. For fields that are not components of Elekta Motorized Wedge or Elekta OmniWedge, the dose is also considered low if it is lower than 50% of the maximum dose on the isocenter plane.
		Fixed SSD field: Normalization method is changed to *100% to field central axis Dmax*.
		IMRT field: Normalization method is automatically changed to *IMRT field normalization*.
		VMAT field and AAA or Acuros XB: Normalization method is automatically changed to *No field normalization*.
		Acuros XB and plan dose calculation (non-IMRT fields): Normalization method is automatically changed to *No field normalization*.

Table 3 Field Normalization Methods in AAA and Acuros XB

Norm. Mode	Meaning	Exceptions
100% to field central axis Dmax	Field dose is normalized to 100% at the dose maximum along the CAX.	*Entire CAX in air / CAX covered by a block / low dose*[**] *along the CAX:* Normalization method is changed to *100% to field Dmax*. [**] Dose lower than 10% of the maximum field dose.
		IMRT field: Normalization method is automatically changed to *IMRT field normalization*.
		Arc fields and AAA or Acuros XB: Normalization method is automatically changed to *No field normalization*.
		Acuros XB and plan dose calculation: Normalization method is automatically changed to *No field normalization*.
100% to field Dmax	Field dose is normalized to 100% at the field dose maximum.	*Low dose in entire field:* Normalization method is changed to *No field normalization*.
		IMRT field: Normalization method is automatically changed to *IMRT field normalization*.
		Arc fields and AAA or Acuros XB: Normalization method is automatically changed to *No field normalization*.
		Acuros XB and plan dose calculation: Normalization method is automatically changed to *No field normalization*.

Table 3 Field Normalization Methods in AAA and Acuros XB

Norm. Mode	Meaning	Exceptions
IMRT field normalization	For IMRT fields, Monitor Unit calculation is performed by the Leaf Motion Calculator (LMC). The AAA normalizes the field dose to be compatible with the MU calculated by the LMC. For more information on MU calculation for IMRT fields, see Chapter 12, Section "MU Calculation in the LMC" on page 385.	This normalization method cannot be selected in Beam Configuration. It is automatically selected by the AAA and Acuros XB algorithms for IMRT fields.
		Acuros XB and plan dose calculation: Normalization method is automatically changed to *No field normalization*.

The figure describes how the user-selected field normalization mode *100% to isocenter* is changed by the AAA and Acuros XB if the mode is not applicable to the field.
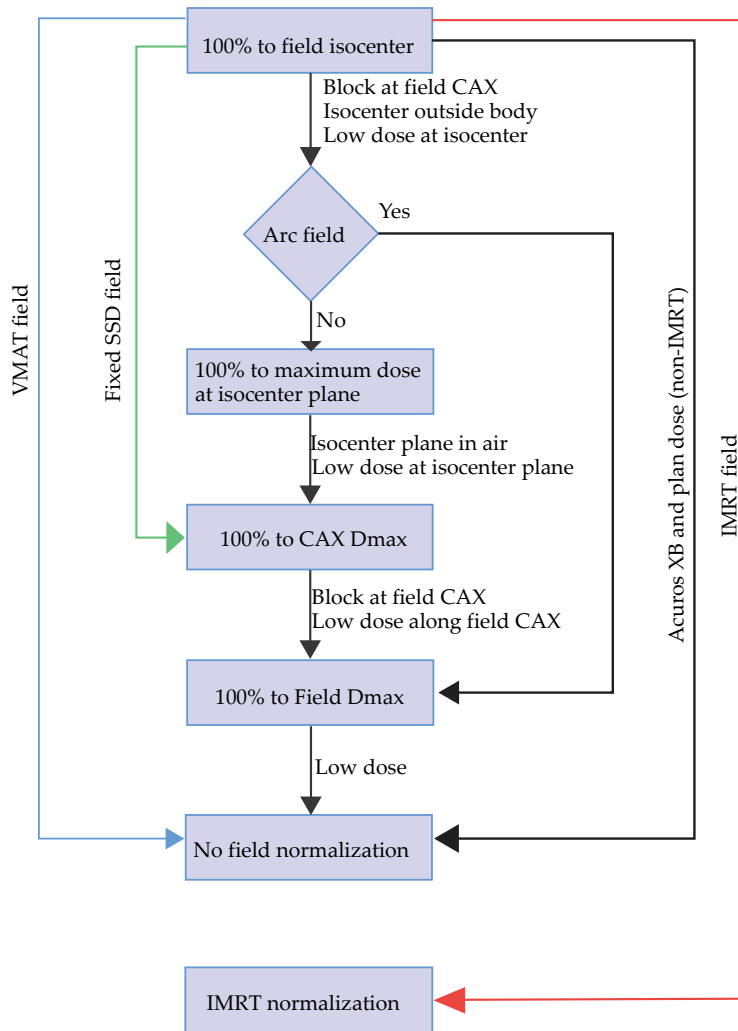
Figure 5   Selection of Field Normalization in AAA and Acuros XB

Calculation Options

The following calculation options can be configured for AAA and Acuros XB:

- Calculation grid
- Heterogeneity correction
- Field normalization
- Angular resolution in conformal arc and VMAT calculations
- Dose reporting mode (Acuros XB only)
- Plan dose calculation (Acuros XB only)
- Automatic high density material (Acuros XB only)
- Maximum automatic high density volume in cm^3 (Acuros XB only)

Default calculation options are defined in Beam Configuration. Angular resolution in conformal arc and VMAT calculations is defined in DCF settings.

Calculation grid. The calculation grid value for AAA can be any value between 1 and 5 mm, and for Acuros XB any value between 1 and 3 mm. When using small grid sizes (smaller than 2 mm), the size of the dose matrices may lead to a shortage of computer memory resources.

During dose calculation, AAA calculates the dose first into a divergent dose matrix. The width of the divergent dose matrix depends on the jaw positions. An additional margin is added in order to calculate also the low dose tail resulting from head scatter and phantom scatter. This margin depends on the field size and the selected calculation resolution. The default margin size is 12 cm. However, the margin is reduced so that the number of calculation points at isocenter plane does not exceed 74000, that is:

$$\frac{(FS\_X + 2 \times M) \times (FS\_Y + 2 \times M)}{(h \times h)} \leq 74000$$

where:

FS_X	=	Field size in cm in X-direction.
FS_Y	=	Field size in cm in Y-direction.
M	=	Size of the additional margin in cm. The margin is always at least 7 cm.
h	=	Calculation grid size in cm.

Thus, for AAA the divergent dose matrix, as well as the input fluences (2D fluence for primary source, 3D fluences for second source, electron contamination and wedge scatter) extend 7-12 cm beyond the field edge at the isocenter plane. For Acuros XB, the same margin is used as in AAA for the input fluences. However, as the dose deposition is done in the Cartesian coordinate system covering the entire calculation volume (as opposed to the divergent system for AAA), the phantom scatter may extend further out in Acuros XB than in AAA, where the dose attains zero value outside the margin.

Within each image plane, the resolution of the dose calculation corresponds to the defined grid size. With AAA, the corner of one of the voxels in the dose matrix that is sent back to Eclipse client after dose calculation is located in a point, whose DICOM X and Y coordinates are the same as the DICOM X and Y coordinates of the isocenter of the first field in the plan. If the isocenter is outside the calculation volume, this is true for the dose grid mesh extended outside the calculation volume.

With Acuros XB, if the pixel size of the image slices is, within 0.01 mm, the same as the calculation grid size, or the calculation grid size divided or multiplied by an integer, the dose matrix that is sent back to the Eclipse client is aligned with the image, and the calculation grid size is automatically modified (by adding or subtracting 0.01 mm or less) so that the exact match is obtained. That is, a dose voxel boundary coincides with an image pixel boundary whenever possible. If this is not possible, the center of one of the voxels in the dose matrix that is sent back to Eclipse client after dose calculation is located in a point, whose DICOM X and Y coordinates are the same as the DICOM X and Y coordinates of the isocenter of the first field in the plan. If the isocenter is outside the calculation volume, this is true for the dose grid mesh extended outside the calculation volume.

In the axis perpendicular to the image slices, AAA and Acuros XB adapt the grid resolution to ensure that the dose is always calculated exactly on the image slices. If the slice thickness is larger than the defined grid size, AAA and Acuros XB may calculate the dose on dose planes between the image slices. If the slice spacing is smaller than the defined grid size, AAA and Acuros XB may skip calculating the dose on some slices. For image slice thickness `IS`, AAA and Acuros XB calculate `IS/n...IS/3`, `IS/2`, `IS`, `IS × 2`, `IS × 3...IS × n` and sets the dose plane spacing to the value closest to the defined grid size. For examples, see the figure. Note that when the slice separation is

larger than the defined grid size, AAA and Acuros XB also produce an internal image with smaller slice separation. When the slice thickness is divided by an even number according to the above procedure, one of these extra slices will be located exactly in the middle between two original slices, and therefore a possible sharp boundary in the original (phantom) image will be "blurred" due to an extra slice with an intermediate density.
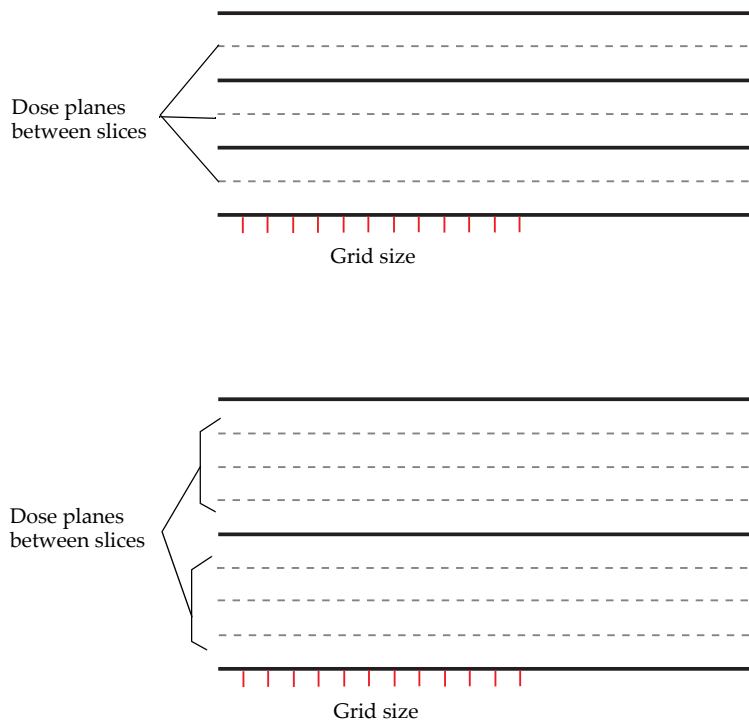
Figure 6 Grid Size and Dose Matrix Resolution in AAA and Acuros XB

Heterogeneity correction. Heterogeneity correction can be on or off:

- On—Heterogeneity inside the Body is taken into account in the dose calculation.
- Off—The whole Body is treated as water. However, bolus and support structures, if any, use their specific CT values.

Field normalization. See "Normalization" on page 34.

Angular resolution in conformal arc and VMAT calculations. This option specifies the angular resolution in degrees for arc field calculations. It integrates the existing machine control points into beams placed along the arc at the defined interval. For conformal arc and VMAT fields, *OFF* means that the beams used to calculate the arc coincide to the machine control points. For standard arc fields, *OFF* means that the angular resolution is 5 degrees.

This option is defined either in global or local DCF calculation settings (choose **Tools > Workstation Configuration > Settings for Distributed Calculation Framework**, and either global or local settings).

For information on configuration of beam data, refer to *Beam Configuration Reference Guide*.

Dose reporting mode. This option defines whether Acuros XB reports dose to medium or dose to water. The Acuros XB transport calculation is identical regardless of the selected reporting mode, only the post-processing step is different. In both cases, the energy dependent fluence calculated by Acuros XB is multiplied by a response function to get the local dose. For dose to water, the same response function (that of water) is used everywhere. For dose to medium, the dose response of the material in the output grid voxel is used. For more information on dose to water and dose to medium, see Chapter 6, Section "Fluence to Dose Conversion" on page 137.

Plan dose calculation. This option defines whether the plan dose is calculated. Plan dose calculation can be on or off.

Plan dose calculation **on** - The total dose from all the fields in the plan is calculated with one Acuros XB run. With this option, only one dose matrix per plan is obtained, whereas the field dose matrices are not calculated.

Plan dose calculation **off** - The individual field doses are calculated in separate Acuros XB runs. With this option, the field dose matrices are obtained in addition to the plan dose matrix. This allows, for example, the modification of field weights without the need to re-calculate the plan dose with Acuros XB.

If field doses are not needed, and a single machine is available to perform the dose calculation, it is faster to calculate a plan with multiple fields with plan dose calculation **on**. For RapidArc plans with

multiple arcs, however, calculating with plan dose calculation **off** may decrease calculation time when more than one computer is available through the DCF. In such cases, each arc will be calculated on a separate machine, enabling the parallelization of both the source model and the ray tracing of the sources into the patient. Since both these components scale linearly with the number of fields, they can become significant for RapidArc plans with multiple arcs.

Acuros XB plan dose calculation occurs only when:

- the plan dose calculation option is set on, and
- the plan has more than one field, and
- all fields in the plan use the same treatment unit, particle type, energy and primary fluence mode, and
- none of the fields in the plan have either a motorized wedge or an OmniWedge, and
- dose calculation has not been requested for fixed reference point values (Calculate Dose with Preset Values dialog), and
- the plan is not a verification plan, and
- all fields in the plan are IMRT fields, or all fields in the plan are VMAT fields, or there are no IMRT fields and no VMAT fields in the plan.
- If there is a bolus in the plan, it must be assigned to all fields in the plan.

When plan dose calculation is on, the field normalization used will be *no field normalization*. For IMRT fields, the normal IMRT normalization is used. As a consequence, the field MU will be proportional to the field weights. Therefore, calculating the same plan with plan dose calculation on and with plan dose calculation off may result in different field MU and therefore different plan dose distributions. When plan dose calculation is used, the desired MU are known in advance, with the possible exception of an overall normalization factor. You can then either calculate the volume with preset values and define the desired MU, or define field weights proportional to the desired MU in the Info Window.

Automatic high density material. This option defines the material assigned automatically to high density pixels in the image, for which no material has been manually assigned. The volume where the automatic assignment of a high density material is made is limited by

the calculation option *Maximum automatic high density volume in cm*^{3}. When the automatic material assignment is made, the default density of each material is used. This option can be changed in Beam Configuration.

Table 4 Automatic High Density Materials

Material ID	Description
Bone	Material name[a]: Bone. Default density 1.85 g/cm^3.
Muscle_Skeletal	Material name: Muscle Skeletal. Default density 1.05 g/cm^3.
Stainless_Steel	Material name: Stainless Steel. Default density 8.00 g/cm^3.
Ti6Al4V_ELC	Material name: Titanium alloy. Default density 4.42 g/cm^3.

a. Note that material IDs are always the same, but material names change depending on the localized language.

High density pixels are pixels whose mass density (derived from the HU value in the image) exceeds the maximum mass density of the materials used in automatic conversion (3.0 g/cm^3). For the list of materials for automatic CT to material conversion, see "CT to Material Mapping" on page 140.

Maximum automatic high density volume in cm^3**.** This option defines the maximum volume where the automatic assignment of a high density material can be made. This option can be changed in Beam Configuration.

Chapter 4   Photon Beam Source Model

The photon beam source model is used only by the AAA and Acuros XB dose calculation algorithms. When configuring the Acuros XB, beam data configured for AAA can be imported and reconfigured with the Acuros XB configuration program and vice versa. For information on AAA, see Chapter 5, "Anisotropic Analytical Algorithm (AAA) for Photons," on page 113. For information on Acuros XB, see Chapter 6, "Acuros External Beam Algorithm (Acuros XB) for Photons," on page 124.

Dosimetric comparison of Acuros XB to AAA and eMC can be found in the literature[1].

Clinical Beam Modeling of Photon Beams

An accurate parameterized model of the radiation output of medical linear accelerators was developed by using previously published results from Monte Carlo simulations of the treatment unit head. For each clinical beam, the parameters of the model are modified to construct a customized phase-space specific to the clinical beam to be modeled. The clinical beam is represented using a photon beam source model, which has the following main components, or sources: primary photon source, second photon source, electron contamination source, and photons scattered from the hard wedge (wedge scatter source). The sources are characterized by a number of parameters derived in the configuration of the source model. For more information, see "Configuration of Photon Beams" on page 55.

The broad clinical beam is divided into finite-sized beamlets β, as illustrated in the figure. Beamlet size is a function of the calculation grid size. Additionally, the separate photon and electron components each have a different beamlet intensity.

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1. Dosimetric comparison of AcurosXB deterministic radiation transport method with Monte Carlo and model-based convolution methods in heterogeneous media. Han et al., Med. Phys. 38 (5), 2651 May 2011.
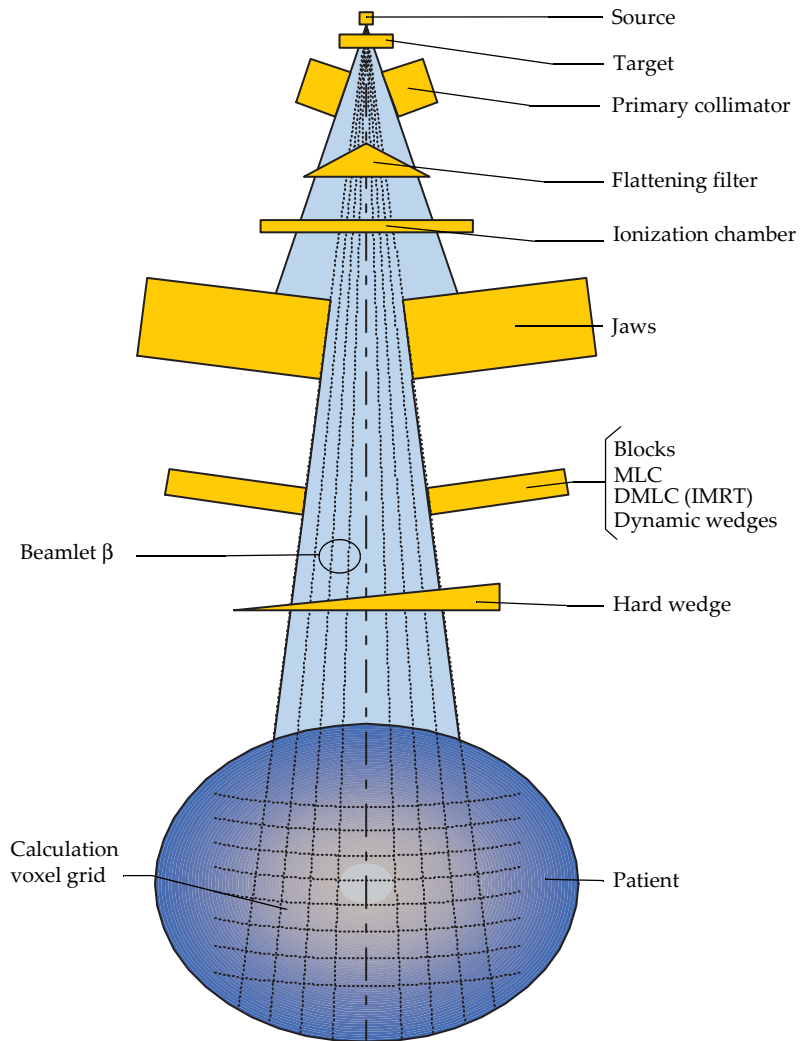
Figure 7   Treatment Unit Components, Broad Beam Division

Primary Source

In the photon beam source model, the primary source is a point source located at the target plane. The physical effects of the finite size of the primary source are modeled by the effective target spot size parameters (for more information on the parameters, see"AAA and Acuros XB Parameters" on page 71). The source models the bremsstrahlung photons created in the target that do not interact in the

The labels in Figure 7 are:
- Source
- Target
- Primary collimator
- Flattening filter
- Ionization chamber
- Jaws
- Blocks / MLC / DMLC (IMRT) / Dynamic wedges
- Beamlet β
- Hard wedge
- Calculation voxel grid
- Patient

treatment unit head. The initial photon spectra after the target on the beam central axis were simulated with BEAMnrc using realistic target materials and thicknesses. Beam hardening in the flattening filter is modeled by attenuating the initial spectrum by a radially varying amount of the flattening filter material. Separate energy spectra for every fanline of the broad beam are derived from the mean energy curve (see Figure 9 on page 50). The non-uniform photon energy fluence is modeled by a radially varying intensity profile curve (see Figure 10 on page 50).

Second Source

The second source is a Gaussian plane source located at the bottom plane of the flattening filter. It models the photons that result from interactions in the accelerator head outside the target (primarily in the flattening filter, primary collimators and secondary jaws). As a result of the lower location of the second source, radiation from the second source diverges more than radiation from the primary source; hence the effect is most noticeable outside the beam defined by the primary source. The second source modeling has been disabled for flattening filter free (FFF) beams, since the most important source of scattered radiation is not present in the beamline. The second source modeling has been disabled also for hard wedges, except for the Elekta motorized wedge.

Electron Contamination

Electron contamination component describes the dose deposited in the build-up region not accounted for by the primary and extra-focal photon components. Electron contamination is also used to model photon contamination (photons created in electron interactions). Electron contamination is modeled with a depth-dependent curve that describes the total amount of electron contamination dose at a certain depth. The parameters for electron contamination for hard wedges are configured in Beam Configuration.

Photon Scatter from Wedge

Each point in the wedge acts as an auxiliary scatter source. The intensity of scatter radiation from each point is assumed to be proportional to the amount of primary radiation hitting that point. The

scatter radiation is assumed to have a slightly forward-directed directional distribution. This model is implemented with a dual Gaussian model, where the width of the Gaussian kernel increases with the distance from the wedge.

Modeling of the Primary Source

Phase Space Model

The beam is modeled using physics-based parameters. These parameters give a description of the phase space of the particles comprising the treatment beam. A model based on physics-based parameters enables accurate dose calculation in conditions that are different from the measurement conditions, which is a different approach from that of semi-empirical models. The model requires only minimal technical information about the construction of the treatment unit head. The parameters of the model can be easily and quickly adapted to an individual accelerator.

For a specific beam with a static gantry angle, modulated by jaws and possibly a static or dynamic MLC, the source model generates a phase space, which is sent to the dose calculation algorithm. Physical jaws are assumed to have zero transmission, except for Elekta virtual wedge calculation, for which jaw transmission needs to be defined in Beam Configuration. The phase space consists of a primary source phase space and one or more non-primary source phase spaces. The primary phase space consists of a two-dimensional energy fluence grid and a two-dimensional grid of spectra. The non-primary phase space consists of a three-dimensional energy fluence grid (that is, a two-dimensional energy fluence grid that varies with distance from source) and a single spectrum. For an arc field, the source model calculates several static beam phase spaces.

Photon Energy Spectrum

Dose calculation algorithms for photon beams require information about the energy spectrum of the primary photons in the beam. The initial photon spectra were determined for a generic machine from

Monte Carlo simulations of the bremsstrahlung spectrum of the electrons impinging on the target. The figure shows an example of an initial photon spectrum for a 6 MV beam.
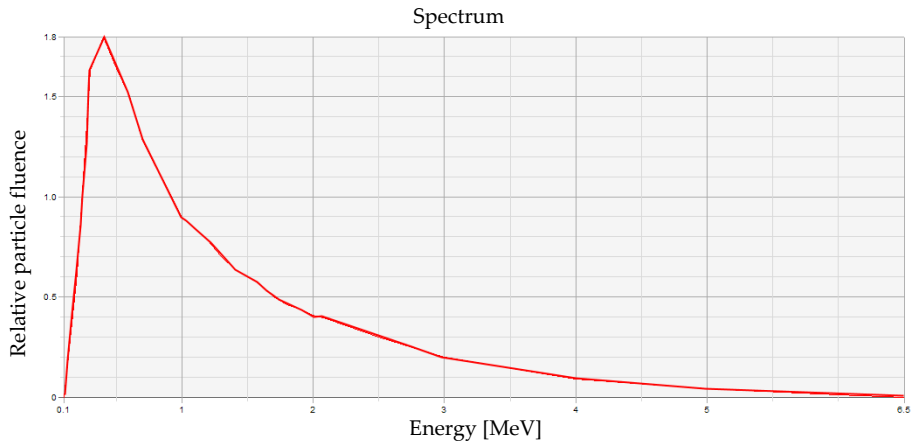
Spectrum

Figure 8   Example of 6 MV Photon Spectrum

Mean Energy

Another important parameter that affects the energy spectrum used by the source model is the *mean energy* as a function of the radius from the beam CAX. An example of the mean radial energy for a 6 MV beam is given in the figure. This curve is used by the source model to determine the beam hardening effect of the flattening filter on the photon spectrum. Based on the mean energy curve and the user-specified flattening filter material, the source model determines the energy spectrum of the beam as a function of radial distance from the beam CAX. For flattening filter free (FFF) beams, the mean radial energy curve models the off-axis variation in the initial bremsstrahlung spectrum.
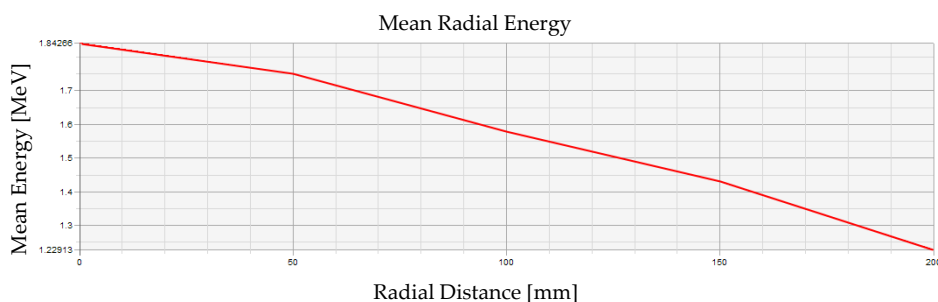
Figure 9   Example of the Mean Energy as a Function of Distance from the CAX of a 6 MV Photon Beam

Intensity Profile

The intensity of the photon beam varies slightly across the treatment field. The varying photon fluence is modeled with the help of a parameter called the *intensity profile* curve. The intensity profile is computed as the photon energy fluence (number × energy of photons) as a function of the radial distance from the CAX.

The figure shows an example of the intensity profile for a 18 MV beam:
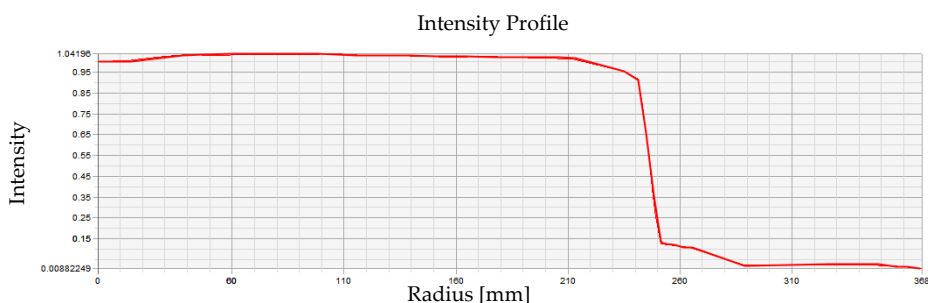
Figure 10   Example of Intensity Profile of an 18 MV Beam

The figure shows an example of the intensity profile for a 10 MV flattening filter free beam:

Eclipse Algorithms Reference Guide
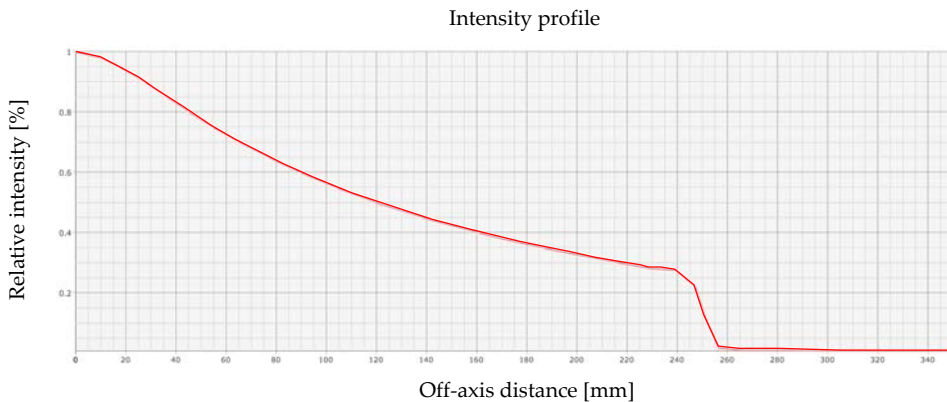
Figure 11   Example of Intensity Profile of a 10 MV Flattening Filter Free Beam

Modeling of the Second Source

Extra-focal photon radiation (all photons emerging from outside the target) is modeled using a finite-size second source located at the bottom surface of the flattening filter. This virtual source is called the *second source*. The second source has a Gaussian intensity distribution. Its energy fluence distribution is wider than that of the primary source, since it is located closer to the patient in the beamline. The energy fluence is also blurred near the fluence edges because of its finite size.

Second Source Energy Fluence

The second source fluence at an arbitrary plane is computed by adding the contributions from each element of the source for each pixel in the destination fluence array. The contributions vary depending on whether the beam ray hits the collimator jaws or MLC leaves. This calculation models both the upper and lower edge of the collimator jaws, but the MLC as a single plane. The contribution is scaled by the Gaussian weight of the source element, by the inverse square of the distance between the elements at the source and destination planes, and by the cosine of the ray angle.

Second Source Parameters

The second source model includes a spectrum whose energy axis is scaled to obtain a given mean energy. Off-axis variation in the second source spectrum is not modeled. The weight of the second source compared to the primary photon source, the width of the Gaussian at the source plane, and the mean energy are free parameters derived as described in "Configuration Program for Photon Beams" on page 88. The distance from the target to the second source and the distances from target to each collimating device are read from the library at the beginning of the configuration. These parameters are defined in the configuration according to the machine geometry, and are not changed during the optimization process. The distance parameters can be modified by the user to make them match with the actual treatment machine before beginning the configuration.

Modeling of the Electron Contamination

The electron contamination is modeled with a depth-dependent curve that describes laterally integrated electron contamination dose at different depths. Acuros XB requires additionally an energy spectrum for the contamination electrons. It is determined by fitting a set of monoenergetic electron depth doses to the depth-dependent curve.

The shape of the electron fluence is obtained as a convolution of the aperture shape and a 2D sum-of-Gaussians kernel. The second Gaussian component has a smaller effective sigma, and it allows the photon beam source model to better model the electron scattering that occurs in air.

The figure shows an example of the electron contamination curve.
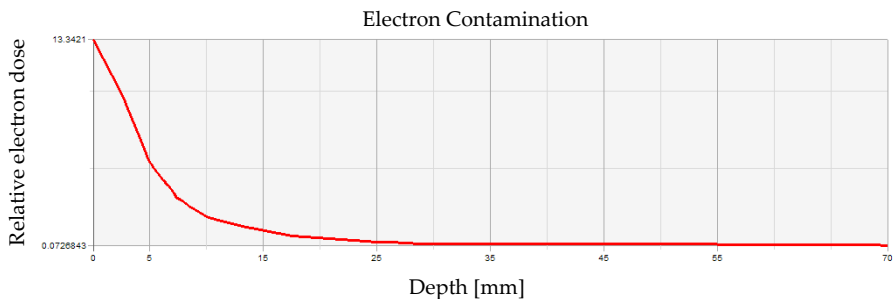
Figure 12   Example of Electron Contamination Curve

Beam Modifiers in the Treatment Beam Model

Most beam modifying accessories affect only the beam fluence used in dose calculation. Blocks, trays and MLCs employ a user-defined transmission factor to model the radiation transmitted through the accessory. Compensators, Dynamic Wedges and IMRT fields also modify the fluence of the beam. The head scatter effects are taken into account by using a finite size second source located at the bottom surface of the flattening filter (see "Modeling of the Second Source" on page 51). The contribution of the contaminating electrons also depends on the photon beam fluence shape.

Hard wedges modify the fluence and the spectral characteristics of the beam. The configuration program determines these effects from the depth dose and profile measurements for several field sizes. The wedge scatter effects are derived simultaneously to the above effects during the beam configuration. The user-defined wedge material and the wedge transmission derived during configuration process are used to determine the 2D energy spectrum after the wedge from the configured open field energy spectrum.

Physical compensators (also referred as standard compensators, as opposed to dynamic beam compensation with MLC) modify the fluence and the spectral characteristics of the beam. The fluence is modified based on the thickness matrix of the compensator and the effective linear attenuation coefficients (EAC). The compensator scatter is taken into account by utilizing field size dependent EACs determined by the configuration program. If a block is placed under the compensator in a treatment beam, the equivalent field size calculation for defining the EAC value ignores all blocks, even if some of them reside above the compensator. In this case, no blocks are taken into account for compensator scatter and a warning is given in the calculation log. The compensated beam spectrum is hardened according to the compensator thickness and user-defined compensator material properties.

The EAC values are used in dose calculation by AAA or Acuros XB. The linear attenuation factor configured for a dosimetric material in Beam Configuration is used by Eclipse client to calculate compensator thickness matrix based on the transmission matrix created by PBC. The

linear attenuation factor should correspond to the average calculated EAC value for the given configured compensator material in Beam Configuration.

Note: *For dose calculation and field visualization, External Beam Planning models photon treatment unit collimators as a system of X and Y jaws together with blocks or MLC. In the case of Siemens treatment units, this model is not entirely accurate, because the MLC device replaces the collimator X jaws.*

Known Limitations of the AAA and Acuros XB Algorithms

AAA and/or Acuros XB dose calculation algorithms have the following known limitations:

AAA accuracy in lung. For 4 MV to 6 MV energies and field sizes larger than or equal to 5x5 cm^2, AAA tends to underestimate the dose in lung and overestimate the dose in water-equivalent tissue after the lung. For 6 MV, the errors are smaller than 3% of the field CAX dose maximum. However, error from local dose can become significantly larger, if the local dose is small relative to the dose maximum.

For 10 MV to 20 MV energy modes and field sizes smaller than or equal to 5x5 cm^2, AAA tends to overestimate the dose in lung. The errors become larger as the field size decreases and the lung density decreases. For 18 MV and 3x3 cm^2 field, the maximum error in lung with density 1.85 g/cm^3 is approximately 7% of the field dose maximum.

Accuracy of AAA and Acuros XB for static MLC fields. For 18 MV, AAA and Acuros XB tend to underestimate the dose at shallow depths for certain static MLC shapes. At 3 cm depth, the error can reach 3% of the local dose.

For 6 MV, AAA and Acuros XB may underestimate the dose at large depths (larger than or equal to 20 cm) for certain static MLC shapes. The errors are more pronounced for elongated (for example H-shaped) openings. The errors can reach up to ~4% of the local dose.

Accuracy of AAA and Acuros XB for hard wedges. Accuracy is typically within 3% of dose maximum or 3 mm in the areas of high dose gradients. Larger errors can be observed in the build-up region for low (4 MV) and high (18 MV and 20 MV) nominal energies. For high

energy photon beams, larger dose differences may also be observed outside the field edge for large field sizes (larger than or equal to 15x15 cm^2).

Configuration of Photon Beams

Monte Carlo simulations of the radiation generated by treatment head were used to determine the fundamental medical linear accelerator model used in the photon beam source model. The model parameters are adapted for each clinical beam by the source model configuration program. These parameters determine a customized phase space that defines the fluence and energy spectrum specific to each treatment unit and energy.

The input of the source model configuration program consists of specific measured beam data and parameter values that are either defined by the user or read in from the parameter library. The parameters describe the measurement geometry and the physical characteristics of the beam.

The measured beam data files can be imported into Eclipse for the source model configuration, or you can use Varian Eclipse Beam Data. For information on the configuration, see "Configuring Photon Beams in Beam Configuration" on page 104.

This section describes the parameters and beam data measurements required for the configuration, the way the source model configuration program works, the configuration and measurement geometries for the source model, provides step-by-step instructions for configuring the photon beam source model in Beam Configuration, and describes how the configured source model data can be evaluated.

For detailed information on using Beam Configuration, refer to the Eclipse online help system or *Beam Configuration Reference Guide*. For information on how to select a calculation model for dose calculation in Eclipse, refer to *Treatment Planning for External Beam - Eclipse Reference Guide*.

Note: *When performing measurements and configuring the photon beam source model, notice the following:*

- *The instructions for beam data measurements are recommendations only. Varian Medical Systems is not responsible for incorrect measurements or inaccurate configuration resulting from erroneous measurements.*

- *Clinical physicists responsible for the measurements must always use their own judgment in deciding the level of acceptable accuracy of the measurements in relation to the calculations, and find the compromises needed for each specific accelerator as far as measurements are concerned.*

- *It is important to configure the system so that it corresponds to the characteristics of the treatment machine. Wedges must be configured with particular care.*

- *Periodically perform follow-up measurements and compare with the dosimetric beam data used for configuring the beam. If fluctuations are large and the configured beam data no longer represents the average beam delivered by the machine, reconfigure the beam data using the newer dosimetric beam data.*

- *Measure all dosimetric beam data in as stable conditions as possible.*

- *Perform all measurements as accurately as possible. However, the source model configuration program is able to recover from small measurement errors in the input files, such as small lateral shifts (tolerance +/- 2.5 mm) or noise.*

- *Use the same file naming conventions in beam data measurements (input files) and in Beam Configuration (Therapy Unit name), and name the input files so that it is easy to match the beam data to the treatment unit during the configuration process.*

- *Perform the effective point of measurement correction. The source model does not perform this correction automatically, and neglecting this correction will shift the measured dose maximum positions. This will result in an error in the electron contamination model.*

- *When measuring profiles, especially for large field sizes, use the available width of the phantom as efficiently as possible. Avoid measuring near the walls of the phantom: missing water volume near the point of*

measurement also implies missing scatter in the profiles. Instead of using measurement points close to the phantom wall, reposition the phantom so that the full width of the measured profile fits well inside the phantom.

- *It is recommended to use an ionization chamber for all beam data measurements for the source model.*

Small Field Support

Note: *If measurements for very small field sizes are included in the beam data, the selected detector needs to be suitable for the measurement of small fields. The positioning of the phantom and detector needs to be done carefully.*

Beam Data Configuration

A single beam data containing both small and large field measurements is expected to produce accurate results for all field sizes. There is no need to create separate models for the calculation of small and large field sizes.

Recommended Measurements for Open Beam

Measure the following for small fields:

- Depth dose curves and profiles from 3x3 cm^2 up to maximum field size deliverable with the machine (for example 40x40 cm^2).

  The measurement set must contain field sizes at least up to 10x10 cm^2.

  Inclusion of measurements for smaller field sizes than 3x3 cm^2 does not have a significant impact on the calculated beam data parameters. Beam model should be accurate even though the measurement data does not contain very small field sizes (1x1 cm^2 and 2x2 cm^2). Note also, that depth dose curve and profile measurements for field sizes smaller than 2x2 cm^2 are ignored by the configuration program.

- Diagonal profiles for the maximum field size.
- Output factors from 3x3 cm^2 up to the maximum field size deliverable with the machine.

  Output factors for field sizes 1x1 cm^2 and 2x2 cm^2 can be included, if desired. However, these will not affect the calculation results for small MLC collimated fields in treatment units, where MLC is located below the jaws (for example Varian). This is because the

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backscatter in these cases is determined from the size of the jaw opening. If small jaw-collimated fields are used in the treatments, the inclusion of output factor measurements for these field sizes may improve the accuracy.

Tuning of the effective spot size parameters

The beam data includes parameters `Effective target spot size in X-direction` and `Effective target spot size in Y-direction`, which have a significant effect on the calculated absolute dose level for very small field sizes (<= 1x1 cm^2) and for the shape of the calculated penumbra for all field sizes.

These parameters should be manually adjusted for each treatment unit based on high-resolution measurements (such as film). After changing the parameter value, attention should be paid on the agreement in the absolute dose level for small field sizes and on the penumbra region for all field sizes.

For more information on the effective spot size parameters, see "AAA and Acuros XB Parameters" on page 71.

Beam Data Measurements for Photon Beams

The photon beam source model needs specific measured beam data for performing dose distribution calculations. All beam data must be measured under the same setup conditions (see Figure 13 on page 101).

Required Source Model Beam Data Measurements for Open Fields

To be able to configure the source model correctly for open fields, measure at least the data listed in the following table and import it to Beam Configuration. Perform beam data measurements for open fields as follows:

- Measure depth dose curves and profiles using the *same field sizes*. The effective measurement point correction must be applied to the measured depth dose curves before importing the data in Beam Configuration.

- All profile measurements can be performed at the X- or the Y-axis.

- Use a single *Source Phantom Distance (SPD) between 70–140 cm* for all measurements.

Configuration program for the photon beam source model may use only a subset of the measured field sizes. For details, see "Adaptation of Measurements in the Configuration" on page 90.

The mandatory open field measurements for the Elekta Beam Modulator differ slightly from the other open field measurements of the photon beam source model. For more information, see "Required Measurements for Elekta Beam Modulator" on page 66.

Table 5 Open Field, Mandatory Beam Data Measurements

Measured Parameter	Scan Axis / Depth	Field Size in cm²
Depth dose curves[a]	CAX	Field sizes smaller than 10 x 10[b]
		10×10
		Intermediate field size(s)
		Largest field size
Profiles[a,c]	d_{max}, 5 cm, 10 cm, 20 cm, 30 cm depth[d]	Field sizes smaller than 10 x 10[b]
		10×10
		Intermediate field size(s)
		Largest field size
Diagonal profile	d_{max}, 5 cm, 10 cm, 20 cm, 30 cm depth[d]	Largest field size

Table 5 Open Field, Mandatory Beam Data Measurements

Measured Parameter	Scan Axis / Depth	Field Size in cm²
Output factors	5 cm depth ≤ 15 MV 10 cm depth for > 15 MV	See Table 6 on page 61

a. The same set of field sizes for depth dose curve and profile measurements should be used. Measurements for field sizes that appear only in either the depth dose curve measurements or the profile measurements are excluded from configuration.

b. It is mandatory to include depth dose and profile measurements for at least two valid field sizes smaller than 10 x 10 cm^2.

c. Measure profiles at least 35 mm past the 50% of the CAX point.

d. These are recommended depths. Also other depths may be used. A field size is considered valid if it contains at least three valid profile measurements and a valid depth dose curve measurement.

The following table lists the open field sizes for which the output factor measurements are performed. Optional field sizes are on grey background. Perform output factor measurements as follows:

■ The correct *measurement depth is 5 cm or 10 cm, depending on the energy*. Do not perform the output factor measurements at the d_{max}.

■ Measure the output factor for each field size with the *same SPD and detector depth*. Changing the detector depth (for instance, to match the d_{max} of each field size) is not allowed.

■ Indicate the field sizes in centimeters to have them displayed correctly in Beam Configuration.

■ Note that it is not necessary to measure every field size combination. However, make the measurements in such a way as to allow completion of the entire table by linear interpolation between measured values. This interpolation can be done automatically in Beam Configuration (refer to *Beam Configuration Reference Guide*). For information on the selection of field sizes for collimator backscatter, see "Adaptation of Measurements in the Configuration" on page 90.

■ Usually it is not necessary to measure output factors for fields smaller than 2 cm in any direction, because such small apertures are typically delimited by the multileaf collimator instead of the collimator jaws. However, if these are measured, extra care should be taken in selecting the measurement device and performing the

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measurements. If the jaw field size is smaller than the smallest field size used for output factor measurement, a warning that MU may be incorrect is displayed in the calculation log when calculating the final dose in External Beam Planning.

The table shows the field sizes for open field output measurements when the smallest field size is 3 x 3 cm and the largest field size is 40 x 40 cm.

Table 6 Field Sizes for Open Field Output Factor Measurements

		Width (FX)							
		3	5	7	10	15	20	30	40
Height (FY)	3	3×3	3×5	3×7	3×10	3×15	3×20	3×30	3×40
	5	5×3	5×5	5×7	5×10	5×15	5×20	5×30	5×40
	7	7×3	7×5	7×7	7×10	7×15	7×20	7×30	7×40
	10	10×3	10×5	10×7	10×10	10×15	10×20	10×30	10×40
	15	15×3	15×5	15×7	15×10	15×15	15×20	15×30	15×40
	20	20×3	20×5	20×7	20×10	20×15	20×20	20×30	20×40
	30	30×3	30×5	30×7	30×10	30×15	30×20	30×30	30×40
	40	40×3	40×5	40×7	40×10	40×15	40×20	40×30	40×40

In addition to the output factors for different field sizes, additional parameters are used to determine the geometry of the output factor measurements (see "Output Factor Parameters" on page 85).

Each value in the output factor table indicates the ratio of the measured dose at the detector depth for each measured field size and the dose at the detector depth for the reference field size, when using the reference MU. For information on output factor formats, see Appendix D on page 337.

Measurements for Absolute Point Doses

The configuration of Elekta Beam Modulator requires measurements of absolute point doses for a set of asymmetrical fields. These values are used by the configuration program to optimize the Mean Radial Energy, Intensity Profile and second source parameters by minimizing the gamma error.

This data type is recommended for all Elekta machines. For all other machine vendors and models, absolute point dose data is optional.

The absolute point doses supported by the source model configuration program can be imported into Beam Configuration in a separate measurement file. You need to manually create the file for the import. To enable Beam Configuration to read the file, it must use a specified file format. For information on the file format and example files, see Appendix C on page 326.

For each measured field, the table indicates the asymmetrical jaw positions (X1, X2, Y1, Y2) in millimeters, the detector position (X, Y, Z) in millimeters and the measured point dose at the detector in cGY/MU.

The recommended set of measurements is the following.

- One small field size (for instance, 4×4 cm^2) located at the extreme positions of the open collimator jaws in the X- and Y-directions, and in a few locations in between the extremes.
- One larger field size (for instance, 10×10 cm^2) located at the extreme positions of the open collimator jaws in the X- and Y-directions and in a few middle positions.

The recommended measurement geometry is the following:

- Source-to-Phantom Distance (SPD) = 950 mm
- Detector depth (Z) = 50 mm. The depth increases from the phantom top surface towards the floor. Additional measurements at other depths can also be used.
- Detector position (X, Y, Z) is entered in orthogonal coordinates. The origin of the coordinate system is at the surface of the phantom, at beam central axis.

Asymmetrical jaw positions are indicated in the IEC 61217 scale.

Required Measurements for Wedge Fields

The minimum set of measured data required for physical wedge fields to correctly configure the photon beam source model is described in the table.

Table 7 Wedge Field, Required Beam Data Measurements

Measured Parameter	Scan Axis	Field Size in cm²	Status
Depth doses[a]	CAX	4×4	Recommended
		10×10	Recommended
		15×15	Recommended for wedges of width 20 cm
		20×20	Recommended for wedges of width 30 cm
		Max.square field size	Mandatory
		Max. field size to both directions[b]	Recommended
Output factors[c]	5 cm depth ≤ 15 MV 10 cm depth for > 15 MV	See Table 6 on page 61	Mandatory
Profiles[a,d]	d_{max}, 5 cm, 10 cm, 20 cm, 30 cm depth	4×4	Recommended
		10×10	Recommended
		15×15	Recommended for wedges of width 20 cm
		20×20	Recommended for wedges of width 30 cm
		Max. square field size	Mandatory
		Max. field size to both directions[b]	Recommended
Longitudinal profile[a]	d_{max}, 5 cm, 10 cm, 20 cm, 30 cm depth	Max.square field size *or* Max. field size to both directions[b]	Mandatory at one depth (e.g. 5 cm); Recommended at other depths

a. The largest field size in depth doses, profiles and longitudinal profiles can be either the maximum square field size or the maximum field size to both directions. However, the largest field size must be the same in all of the measurement types.

b. The field size must not be specified in terms of the equivalent field size for source model configuration. The field size can be specified in w2CAD either, for example, as `%FLSZ 400*200` or `%FLSZ 200*400`. The order must be the same for all of the measurement types (PDD, profiles). Note that if wedge field sizes larger than the maximum square field are calculated, and the "max field size to both directions" data is not present in Beam Configuration, a warning of possibly deteriorated dose calculation accuracy is shown in the calculation notes.

c. The required wedge position for all output factor measurements is collimator rotation = 0°. Output factors can be measured with any wedge rotation.

d. All measured wedge profiles have to be measured in the same direction, that is, either the dose increases from left to right in all profiles, or the dose increases from right to left in all profiles. Mixing both types of profiles is not allowed.

Optional Measurements for Wedge Fields

In addition to the measurements listed in Table 7 on page 63, optional measurements may be performed for configuring wedges for the source model. The optional measurements are needed for running the last configuration step for wedges (configure wedge correction factors for different SSDs). Performing the last configuration step improves the accuracy for short and long SSDs for wedged fields. This is achieved by modifying the electron contamination and wedge scatter components based on the additional measurements.

The optional measurements are the following:

- Measured wedge depth doses for SSD = 80 cm and SSD = 120 cm
- Absolute point doses at different SSD—Needed if the wedge depth doses for different SSDs are imported.

Measured Wedge Depth Doses

Wedge depth doses can be measured for SSD = 80 cm and SSD = 120 cm.

To Define Measured Wedge Depth Doses

1. Measure the wedge depth doses for 1–5 field sizes, which are the same field sizes or a subset of the field sizes as used for the default SPD (as specified in "General Parameters" on page 70). Use the same field sizes for both SSDs.

2. To be able to import the curves, edit the w2CAD file. Change the depth dose type from `WDD` either to `WDD_SSD80` or `WDD_SSD120`.

3. In the Beam Configuration Context Window, select a wedge.

4. To import the measured depth doses for the selected wedge, choose **Import > Measured Wedge Depth Doses for SSD 80 cm** or **Import > Measured Wedge Depth Doses for SSD 120 cm**.

Absolute Point Doses at Different SSDs

The absolute point doses at different SSDs are needed if the wedge depth doses for different SSDs are imported into Beam Configuration. The absolute point doses at different SSDs are given in a table (see below), which contains the SSD and measured dose in cGy/MU for each field size.

To Define Absolute Point Doses at Different SSDs

1. To add a blank table, in the Context Window, select a wedge and then choose **Insert > New Absolute point doses at different SSDs**.

2. In the blank table, for each measurement (Meas<n>), type the SSD, field size in X-direction (FSX), field size in Y-direction (FSY) and the measured dose (for either SSD = 800 mm or SSD = 1200 mm). For an example, see the figure below.

	SSD [mm]	FSX [mm]	FSY [mm]	Dose [c...
Meas1	800.000	40.000	40.000	0.998
Meas2	800.000	100.000	100.000	1.130
Meas3	800.000	300.000	300.000	1.283
Meas4	800.000	300.000	400.000	1.303
Meas5	1200.0...	40.000	40.000	0.483
Meas6	1200.0...	100.000	100.000	0.526
Meas7	1200.0...	300.000	300.000	0.586
Meas8	1200.0...	300.000	400.000	0.596
Meas9	0.000	0.000	0.000	0.000
Meas10	0.000	0.000	0.000	0.000

1. Values for measurements performed for 4 field sizes and SSD = 800. **2.** Values for measurements performed for 4 field sizes and SSD = 1200. **3.** Cells of field sizes for which no measurement has been made.

If you have measured fewer than 5 field sizes, type "0.0" in the extra cells.

3. In the Parameter View below the table, define the detector depth in millimeters and the wedge orientation.

Required Measurements for Compensator Fields

Point dose measurements for compensators are required for five different square field sizes (for example, 2 cm, 5 cm, 10 cm, 20 cm and 30 cm), with and without a slab of compensator material inserted into the beam. In addition, the compensator thickness must be defined in compensator parameters. Each of these point dose measurements must be performed in the same measurement geometry, for example, SSD = 95 cm and depth = 5 cm. It is recommended to perform the measurements deeper than the depth of the dose maximum. For clarity, it is also recommended to deliver the same amount of MU in each point dose measurement.

Field sizes used in measurements should span the range of field sizes used in treatment. Measured point dose data, field sizes and measurement geometry are defined in a table in Beam Configuration.

To Define Point Dose Data and Field Sizes for Compensators

1. In the Context Window, select **Measured compensator data**.

2. In the **FS[mm]** column, type the field sizes in millimeters.

3. In the **Open[cGy/MU]** column, type the measured point doses for the open fields in cGy/MU.

4. In the **Comp[cGy/MU]** column, type the measured point doses for the fields with the flat compensator in cGy/MU.

5. In the Parameter View below the table, define the measurement source-phantom distance and measurement depth in millimeters.

Required Measurements for Elekta Beam Modulator

Open Field Measurements for the Elekta Beam Modulator

The table lists the open field measurements required for the configuration of the Elekta Beam Modulator.

The required field sizes are determined by the width of the Elekta Beam Modulator leaves (4 mm). Example field sizes:

- FX direction: 2.4, 3.2, 4.0, 5.6, 8.0, 10.4, 12.0, 16.0 and 21.0 cm
- FY direction: 2.4, 3.2, 4.0, 5.6, 8.0, 10.4, 12.0, 16.0 cm.

Table 8 Elekta Beam Modulator, Mandatory Open Field Measurements

Measured Parameter	Scan Axis/Depth	Field Size in cm²
Depth dose curves[a]	CAX	Field sizes smaller than 10.4×10.4[b]
		10.4×10.4
		Intermediate field size(s)
		21.0×16.0 (largest rectangular field size)[c]
Profiles[a,d]	d_{max}, 5 cm, 10 cm, 20 cm, 30 cm depth[e]	Field sizes smaller than 10.4×10.4[b]
		10.4×10.4
		Intermediate field size(s)
		21.0×16.0 (largest rectangular field size)[c]
Diagonal profile[f]	d_{max}, 5 cm, 10 cm, 20 cm, 30 cm depth[e]	21.0×16.0 (largest rectangular field size)[c]

a. The same set of field sizes for depth dose curve and profile measurements should be used. Measurements for field sizes that appear only in either the depth dose curve measurements or the profile measurements are excluded from configuration.

b. It is mandatory to include depth dose and profile measurements for at least two valid field sizes smaller than 10.4 x 10.4 cm².

c. The measurement of the largest rectangular field size must be recorded in this order in the w2CAD file (the correct syntax is %FLSZ 210*160).

d. Measure profiles at least 35 mm past the 50% of the CAX point.

e. These are recommended depths. Also other depths may be used. A field size is considered valid if it contains at least three valid profile measurements and a valid depth dose curve measurement.

f. The diagonal profile shall always be measured along the direction from one field corner to the other field corner. In case of Elekta Beam Modulator, the angle between diagonal and cross-line profile will differ from 45 degrees, since the maximum field size is not a square.

Output Factor Measurements for the Elekta Beam Modulator

The output factors for the Elekta Beam Modulator can be imported into Beam Configuration in a separate file. To enable Beam Configuration to read the file, it must use a specified file format. For information on the file format and example files, see Appendix D on page 337.

The table lists the field sizes to be used for the output factor measurements for the Elekta Beam Modulator.

Table 9 Field Sizes for Output Factor Measurements for Elekta Beam Modulator

		Width (FX) in IEC 61217 Scale								
		2.4	3.2	4	5.6	8	10.4	12	16	21
Height (FY) in IEC 61217 Scale	2.4	2.4 × 2.4	2.4 × 3.2	2.4 × 4	2.4 × 5.6	2.4 × 8	2.4 × 10.4	2.4 × 12	2.4 × 16	2.4 × 21
	3.2	3.2 × 2.4	3.2 × 3.2	3.2 × 4	3.2 × 5.6	3.2 × 8	3.2 × 10.4	3.2 × 12	3.2 × 16	3.2 × 21
	4	4 × 2.4	4 × 3.2	4 × 4	4 × 5.6	4 × 8	4 × 10.4	4 × 12	4 × 16	4 × 21
	5.6	5.6 × 2.4	5.6 × 3.2	5.6 × 4	5.6 × 5.6	5.6 × 8	5.6 × 10.4	5.6 × 12	5.6 × 16	5.6 × 21
	8	8 × 2.4	8 × 3.2	8 × 4	8 × 5.6	8 × 8	8 × 10.4	8 × 12	8 × 16	8 × 21
	10.4	10.4 × 2.4	10.4 × 3.2	10.4 × 4	10.4 × 5.6	10.4 × 8	10.4 × 10.4	10.4 × 12	10.4 × 16	10.4 × 21
	12	12 × 2.4	12 × 3.2	12 × 4	12 × 5.6	12 × 8	12 × 10.4	12 × 12	12 × 16	12 × 21
	16	16 × 2.4	16 × 3.2	16 × 4	16 × 5.6	16 × 8	16 × 10.4	16 × 12	16 × 16	16 × 21

Wedge Field Measurements for the Elekta Beam Modulator

The table lists the required wedge field measurements for the Elekta Beam Modulator.

Table 10 Required Wedge Field Measurements for Elekta Beam Modulator

Measured Parameter	Scan Axis	Field Size in cm²	Status
Depth dose curves	CAX	3.2×3.2	Recommended
		5.6×5.6	Recommended
		8.0×8.0	Recommended
		10.4×10.4	Recommended
		16×16	Mandatory
		21×16 (largest rectangular field size)[a]	Recommended
Output factors[b]	5 cm depth	See Table 9 on page 68	Mandatory
Profiles	d_{max}, 5 cm, 10 cm, 20 cm, 30 cm depth	3.2×3.2	Recommended
		5.6×5.6	Recommended
		8.0×8.0	Recommended
		10.4×10.4	Recommended
		16×16	Mandatory at 10 cm depth; Recommended at other depths
Longitudinal profile	d_{max}, 5 cm, 10 cm, 20 cm, 30 cm depth	21×16 (16×16 is also allowed)	Mandatory at 5 cm depth; Recommended at other depths

a. The measurement of the largest rectangular field size must be recorded in this order in the w2CAD file (the correct syntax is `%FLSZ 210*160`).

b. The required wedge position for all output factor measurements is collimator rotation = 0°. Output factors can be measured with any wedge rotation.

Configuration Parameters for Photon Beams

Beam Configuration uses measured beam data and a number of parameter values for calculating the configured beam data. Part of these parameter values are read from RT Administration, part from the parameter files of the algorithm.

If you are using Varian Eclipse Beam Data without any modifications to the parameter values or without using your own measured beam data, you only need to enter the absolute dosimetry parameters ("AAA and Acuros XB Parameters" on page 71 and "Hard Wedge Parameters" on page 77) and verify the parameters contained in the data; no changes are required unless the parameter values are clearly incorrect.

General Parameters

The photon beam source model requires that the following general treatment unit parameters are either read from RT Administration or defined in Beam Configuration. Some default values are read from the Data Type Specification file of the algorithm. When configuring the source model, verify that the parameters read from RT Administration are correct, and ensure that no required parameters are missing.

General Parameters read from RT Administration:

- Nominal energy in MV

    The nominal energy can be specified either according to BJR-11 or BJR-17 specifications, and both lead to equally accurate results in the dose calculations. The nominal energy according to BJR-11 specification is assumed to be equal to the energy of the monoenergetic electron beam that hits the target, thereby producing bremsstrahlung photons. The spectrum of these photons has been precalculated by Monte Carlo simulation for all available nominal energies and is stored in the machine data library. The nominal energies according to BJR-17 are internally mapped to those of BJR-11.

Table 11 BJR-11 and BJR-17 energies

BJR-11	BJR-17
6 MV	6 MV
10 MV	10 MV

Table 11 BJR-11 and BJR-17 energies

BJR-11	BJR-17
15 MV	16 MV
18 MV	23 MV
20 MV	25 MV

- Default source-phantom distance for depth dose and profile measurements, expressed in cm

  Define the SPD used in the actual beam data measurements in Beam Configuration.
- Source-axis distance expressed in cm

General Parameters defined in Beam Configuration:

- Therapy unit name
- Radiation type (must be "photon")
- Vendor
- Source-to-phantom distance used during the beam data measurements, expressed in cm
- Smallest open beam size in X and Y directions
- Largest open beam size in X and Y directions.

  For the Elekta Beam Modulator, set the maximum size in X-direction to 21 cm, and the maximum size in the Y-direction to 16 cm.
- Number of profiles (minimum 3, maximum 5 profiles)
- 1st–5th profile depth in cm

AAA and Acuros XB Parameters

The AAA and Acuros XB require defining the following parameters in Beam Configuration.

Table 12 AAA and Acuros XB Parameters

Parameter	Description
Absolute dose reference field size [mm]	Size of the reference field used in configuration, expressed in millimeters. Usually, this should be the same size that was used to normalize the measured output factor table (that is, the field size for which the output factor = 1.0).

Table 12 AAA and Acuros XB Parameters

Parameter	Description
Absolute dose calibration depth [mm]	Depth of the reference point used in configuration, expressed in millimeters. The recommended depth for 6 MV, 10 MV and 15 MV is 50 mm, and the recommended depth for 18 MV and 20 MV is 100 mm. (For an illustration of the geometry, see Figure 15 on page 103.)
Absolute dose calibration source-phantom distance	Distance between the source and the surface of the phantom (SPD) used during the absolute dose calibration, expressed in millimeters. (For an illustration of the geometry, see Figure 15 on page 103.)
Reference dose at calibration depth [Gy]	Absolute dose in water for the reference field size at the reference point at the calibration depth, expressed in Gray. *Do not introduce a "dose to muscle" correction with Acuros XB. When the dose to medium calculation option is selected, Acuros XB reports dose to muscle, and any other medium. If values with a "dose to muscle" correction are used in Beam Configuration, then a double correction will be done in the dose distributions.*
Reference MU at calibration depth [MU]	MU given to produce the reference dose for calibration.
Machine type	Type of treatment unit. AAA and Acuros XB support several types of treatment units. This parameter also specifies the nominal energies supported for the selected treatment unit. The energies available depend on the particular treatment unit.
Effective target spot size in X-direction (IEC61217)[mm]	Models the broadening of the penumbra in X-direction[a]. The modeling is done by applying a Gaussian smoothing to the energy fluence of primary photons. This parameter equals the width of the Gaussian distribution in the X-direction (IEC 61217 scale) at isocenter plane, expressed in millimeters.
Effective target spot size in Y-direction (IEC61217)[mm]	Models the broadening of the penumbra in Y-direction[a]. The modeling is done by applying a Gaussian smoothing to the energy fluence of primary photons. This parameter equals the width of the Gaussian distribution in the Y-direction (IEC 61217 scale) at isocenter plane, expressed in millimeters.

Table 12 AAA and Acuros XB Parameters

Parameter	Description
Leaf transmission for Elekta Beam Modulator	*Elekta Beam Modulator only.* Relative MLC leaf transmission for the Elekta Beam Modulator head design. This parameter is used only in the configuration of the dose calculation algorithm, and not in dose calculation. The MLC parameters for forward dose calculation are defined as dosimetric data in RT Administration (**Radiation and Imaging Devices** workspace **> MLC** tab).
Open field profile measurement direction (IEC61217)	Direction of open field profile measurements in IEC 61217 scale. Possible values are "Collimator X" and "Collimator Y".

a. In addition to the finite size of the bremsstrahlung target, also the beam limiting devices may contribute to the effects modeled. For example, rounded MLC leaf tips can be modeled using an elliptic effective target spot size. As a result, different values for the effective target spot size may be necessary for MLC-limited and jaw-limited fields. In the case of IMRT fields, one should also consider that Smart LMC takes the rounded leaf tips into account in fluence calculation, whereas other LMC algorithms do not. Also note that because the effective target spot size is defined in the collimator coordinate system, it cannot be used to accurately describe an elliptic focal spot at the target plane.

Defining the Machine Type Parameter

The selected machine type has an effect on certain parameters that are retrieved from the machine data library when the first configuration step for open beam is run. These parameters can be manually modified after this step before starting the actual configuration process. Specifically, the selection has an effect on the distances of second source, jaws and MLC from the target (specified in Open Beam Parameters) and on the initial spectrum used in the configuration. See the table for distance values defined in the machine data library for different treatment unit types.

The selected machine model has a limited effect on the way the configuration process works. It affects, for example, the checks done to ensure that mandatory input data is available. The selection also affects the way the collimator backscatter factor (CBSF) is determined during forward dose calculation. For treatment units where the MLC is the topmost collimator (Elekta), the CBSF is determined based on

the MLC opening. For treatment units where the jaws are the topmost collimator (Varian, Siemens), the CBSF is determined based on the jaw opening.

If the machine model used is not found from the list, but is supported by the algorithm, select the closest model or Generic. Then, check the distance parameters listed in the table and the spectrum before starting the actual configuration process.

It should be noted that the distance of hard wedge from target varies for different treatment unit types. The correct value needs to be specified in the Hard Wedge Parameters or in Elekta Motorized Wedge (MW) Parameters.

Table 13 Distance Values for Different Treatment Unit Types Defined in the Machine Data Library

	Varian	Elekta	ElektaBM	Siemens
Distance of second source from target [mm]	125	158	151.5	94.6
Distance of Y-jaw top surface from target [mm]	280	431	376	197
Distance of Y-jaw bottom surface from target [mm]	358	509	468	275
Distance of X-jaw top surface from target [mm]	367	396	479.9	283
Distance of X-jaw bottom surface from target [mm]	445	426	522.7	359
Distance of MLC from target [mm]	509	336	425.3	283

Adjusting Target Spot Parameters

The *Effective target spot size in the X- and Y-direction* parameters are not automatically optimized. Instead, these parameters should be manually adjusted based on the characteristics of the individual treatment unit.

The spot size parameters have significant effect on the calculated absolute dose for very small fields (width less than 1 cm in either x- or y-direction) and on the calculated profiles in the penumbra region for all field sizes. Hence, the spot size parameters can be adjusted by matching measurements and calculations in these situations.

However, for both types of measurements, extra care should be taken when selecting the measurement device to avoid artefacts arising, e.g., from volume averaging effects. Film, for example, could be used for these types of measurements.

For AAA and Varian treatment units, a spot size parameter value of 0 mm can be used. For AAA and Elekta Beam Modulator treatment units, a value around 2.5 mm has been found to be appropriate for 6 MV energy mode in the collimator X direction. For Acuros XB and Varian treatment units, a value of 1 mm is suggested. However, in all cases, fine-tuning of the spot size parameter values can be performed based on matching measurements and calculations.

Open Beam Parameters

The photon beam source model requires defining open beam parameters in Beam Configuration to model extra-focal radiation of the open beam. The open beam parameters are read from the machine parameter library (see "Machine Parameter Library for Photon Beams" on page 85.) The values read from the library can also be edited manually.

The table uses the jaw names in accordance with the IEC 61217 standard.

Table 14 Open Beam Parameters

Parameter	Description
Distance of second source from primary source [mm]	Distance between the virtual secondary source and the primary source, expressed in millimeters. The distance is defined by the treatment head geometry. The beam emerging from the secondary source is more divergent than the beam from the primary source. The secondary source is a virtual radiation source, located by default at the same distance as the bottom plane of the flattening filter (see also "Clinical Beam Modeling of Photon Beams" on page 45 and "Beam Modifiers in the Treatment Beam Model" on page 53).

Table 14 Open Beam Parameters

Parameter	Description
Distance of Y-jaw top surface from target [mm]	Distance between the primary source and top surface of the collimator Y-jaw, expressed in millimeters. The distance is defined by the treatment head geometry. If the distance changes with jaw opening, use the distance where the jaw is as close to the central axis as possible. This parameter affects the sharpness of the penumbra of a beam from the secondary source.
Distance of Y-jaw bottom surface from target [mm]	Distance between the primary source and bottom surface of the collimator Y-jaw, expressed in millimeters. The distance is defined by the treatment head geometry. If the distance changes with jaw opening, use the distance where the jaw is as close to the central axis as possible. This parameter affects the sharpness of the penumbra of a beam from the secondary source.
Distance of X-jaw top surface from target [mm]	Distance between the primary source and top surface of the collimator X-jaw, expressed in millimeters. The distance is defined by the treatment head geometry. If the distance changes with jaw opening, use the distance where the jaw is as close to the central axis as possible. This parameter affects the sharpness of the penumbra of a beam from the secondary source.
Distance of X-jaw bottom surface from target [mm]	Distance between the primary source and bottom surface of the collimator X-jaw, expressed in millimeters. The distance is defined by the treatment head geometry. If the distance changes with jaw opening, use the distance where the jaw is as close to the central axis as possible. This parameter affects the sharpness of the penumbra of a beam from the secondary source.
Distance of MLC from target [mm]	Distance between the primary source and the MLC device, expressed in millimeters. The distance is defined by the treatment head geometry. If the distance changes with jaw opening, use the distance where the leaves are as close to the central axis as possible. If the MLC has rounded leaf tips, use the distance to the middle of the leaves. For double focused MLCs where the leaf tip is not rounded, use the distance to the top surface of the leaves. This parameter affects the sharpness of the penumbra of a beam from the secondary source.

Table 14 Open Beam Parameters

Parameter	Description
Size of second source [mm]	Size of the secondary source, expressed in millimeters. Defines the size of the Gaussian shaped source distribution, defined at the source plane. The formula for the distribution is: $$k(x,y;\sigma) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2 + y^2}{2\sigma^2}}$$ where σ is the size parameter. This determines the shape and range of secondary source effect, and the field size from which this effect is seen. Typical value range 20–80 mm.
Relative intensity of second source	Intensity of the radiation emerging from the secondary source in relation to the primary source. Affects the magnitude of the profiles in the tail regions in particular. Typical value range 0.02–0.10.
Mean energy of second source [MeV]	Mean energy of the radiation emerging from the secondary source, expressed in megaelectronvolts. Determines the depth dose curve of the second source. The energy is typically lower than the mean energy of the primary source. Typical value is approximately 1.0 MeV.

Hard Wedge Parameters

The hard wedge (or fixed wedge) parameters include the following:

Table 15 Hard Wedge Parameters

Parameter	Description
Wedge length [mm]	Maximum wedge size in the longitudinal wedge direction, expressed in millimeters. Usually this value is 400 mm.
Wedge width [mm]	Maximum wedge size in the lateral wedge direction (direction which the thin edge of the wedge points to), expressed in millimeters. Usually this value is 150, 200 or 300 mm.
Wedge angle [degrees]	Wedge angle used by the configuration program to determine wedge scatter parameters. It also automatically determines the wedge angle based on the measured wedge profiles.

Table 15 Hard Wedge Parameters

Parameter	Description
Wedge material [Fe, Cu, Pb]	Wedge material ■ Fe = Iron ■ Cu = Copper ■ Pb = Lead.
Wedge orientation in output factor table (IN/OUT/LEFT/RIGHT)[a]	Wedge orientation in the output factor table measurements, expressed in relation to the treatment unit: ■ IN = thin edge points in (IEC 61217 wedge filter coordinate system: 0°) ■ OUT = thin edge points out (IEC 61217 wedge filter coordinate system: 180°) ■ LEFT = thin edge points left (IEC 61217 wedge filter coordinate system: 270°) ■ RIGHT = thin edge points right (IEC 61217 wedge filter coordinate system: 90°)
Reference dose for hard wedge at calibration depth [Gy]	Absolute dose in water at the reference point at the calibration depth and field size at SSD, expressed in Gray.
Reference MU for hard wedge at calibration depth [MU]	MU given to produce the reference dose for calibration.
Distance of wedge from primary source [mm]	Distance of wedge from primary source.
Relative intensity of wedge scatter source	Relative intensity of the scatter source of the wedge.
Mean energy of wedge scatter source [MeV]	Mean energy of the radiation emerging from the wedge scatter source, expressed in megaelectronvolts.

a. Notice that the LEFT and RIGHT wedge orientations are reversed in w2CAD and IEC 61217.

Enhanced Dynamic Wedge (EDW) Parameters

The Enhanced Dynamic Wedge (EDW) parameters include the following:

Table 16 EDW Parameters

Parameter	Description
Size of second source [mm]	Size of the secondary source, expressed in millimeters. For more details, see Table 14 on page 75.
Relative intensity of second source	Relative intensity of the radiation emerging from the secondary source. For more details, see Table 14 on page 75.
Mean energy of second source [MeV]	Mean energy of the radiation emerging from the secondary source, expressed in megaelectronvolts. For more details, see Table 14 on page 75.

These parameters are copied from the open field parameters by running the configuration step **Copy second source parameters from open field**.

Elekta Motorized Wedge (MW) Parameters

The Elekta motorized wedge (MW) parameters include the following:

Table 17 MW Parameters

Parameter	Description
Wedge length [mm]	Maximum wedge size in the longitudinal wedge direction, expressed in millimeters. Usually this value is 400 mm.
Wedge width [mm]	Maximum wedge size in the lateral wedge direction (direction which the thin edge of the wedge points to), expressed in millimeters. Usually this value is 150, 200 or 300 mm.
Wedge material [Fe, Cu, Pb]	Wedge material ■ Fe = Iron ■ Cu = Copper ■ Pb = Lead.

Table 17 MW Parameters

Parameter	Description
Wedge orientation in output factor table (IN/OUT/LEFT/RIGHT)[a]	Wedge direction in the output factor table measurements, expressed in relation to the treatment unit: ■ IN = thin edge points in (IEC 61217 wedge filter coordinate system: 0°) ■ OUT = thin edge points out (IEC 61217 wedge filter coordinate system: 180°) ■ LEFT = thin edge points left (IEC 61217 wedge filter coordinate system: 270°) ■ RIGHT = thin edge points right (IEC 61217 wedge filter coordinate system: 90°)
Reference dose for hard wedge at calibration depth [Gy]	Absolute dose in water at the reference point in the calibration geometry defined for the open field, expressed in Gray.
Reference MU for hard wedge at calibration depth [MU]	MU given to produce the reference dose for calibration.
Size of second source [mm]	Size of the secondary source, expressed in millimeters, as defined in Table 14 on page 75.
Relative intensity of second source	Intensity of the radiation emerging from the secondary source in relation to the primary source. For more details, see Table 14 on page 75.
Mean energy of second source [MeV]	Mean energy of the radiation emerging from the secondary source, expressed in megaelectronvolts. For more details, see Table 14 on page 75.
Distance of wedge from primary source [mm]	Distance of wedge from primary source, expressed in millimeters.
Relative intensity of wedge scatter source	Relative intensity of the scatter source of the wedge.
Mean energy of wedge scatter source [MeV]	Mean energy of the scatter source of the wedge, expressed in megaelectronvolts.

a. Notice that the LEFT and RIGHT wedge orientations are reversed in w2CAD and IEC 61217. For motorized wedges, only the IN direction is possible.

Elekta Virtual Wedge Parameters

Elekta Virtual Wedges (EVW) are similar to Varian Enhanced Dynamic Wedges (EDW) and Siemens Virtual Wedges (SVW) in that the angled dose distribution is produced by moving a collimator jaw. In this case, only the backup diaphragm, which moves in the same direction as the MLC leaves, can be moved.

An EVW field is one of the components that form Elekta OmniWedge fields. These components are the following:

- Open field component
- Elekta Virtual Wedge component
- Elekta Motorized Wedge field component

Elekta OmniWedge fields containing a wedge in arbitrary directions and angles are produced[2] by the combination of the different components. The backup diaphragm has a finite transmission, whose value depends on the energy mode.

Table 18 Elekta Virtual Wedge Parameters

Parameter	Description
Transmission of Backup diaphragm [1]	Transmission (between 0 and 1) of the backup diaphragm. This value has to be manually adjusted for each energy mode to obtain a good match between the calculated and measured EVW fields. Good starting points are the following: ■ 4X—Start at 0.09 ■ 6X—Start at 0.10 ■ 15X—Start at 0.12

Configuring Elekta OmniWedge

To configure Elekta OmniWedge, you need to add wedges both in RT Administration and Beam Configuration. For more information about using RT Administration, refer to *RT Administration Reference Guide*. For more information about using Beam Configuration, refer to *Beam Configuration Reference Guide*.

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2. For more information on the Elekta OmniWedge, refer to M.H. Phillips et al.: Dynamic and omni wedge implementation on an Elekta SL linac. Med. Phys. 27, 1623—1634, 2000.

To Configure Elekta OmniWedge

1. In *RT Administration*, create a New Dynamic Wedge for the Elekta treatment unit. In the Dynamic Wedge Properties dialog box, select the **Enhanced** check box.

2. Create a New Standard Wedge. In the Standard Wedge Properties dialog box, select the **Omniwedge** check box and the **Motorized** check box.

3. In addition to the above wedges, you can also create a second New Standard Wedge. In the Standard Wedge Properties dialog box, select the **Motorized** check box. The two motorized wedges will have different limits for jaw positions.

4. In *Beam Configuration*, create a Motorized Wedge and an Enhanced Dynamic Wedge.

5. Match and assign the wedge add-ons. Match the Enhanced Dynamic Wedge to the wedge that has the **Enhanced** check box selected in RT Administration.

Siemens Virtual Wedge Parameters

With Siemens Virtual Wedges (SVW), like Varian Enhanced Dynamic Wedges (EDW), the angled dose distribution is created by moving the collimators during beam-on.[3] Although the source model configuration program does not need the virtual wedge parameters, they are used in dose calculation to produce the angled dose distribution.

In treatment planning, virtual wedges are used in the same way as an EDW. Eclipse is capable of calculating virtual wedge angles of 0–60°. The source model is able to calculate the virtual wedge in both the FX and FY-directions, but this may not be possible for the accelerator.

The Siemens Virtual Wedge parameters include the following:

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3. For a more detailed discussion on Siemens Virtual Wedge, refer to J. P. C. van Sant-voort: Dosimetric evaluation of the Siemens Virtual Wedge. Phys Med Biol 43, 2651–2663, 1998.

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Table 19 SVW Parameters

Parameter	Description
Effective linear attenuation coefficient [1/cm]	Effective linear attenuation coefficient (supplied by Siemens) of the virtual wedge for the nominal beam energy. Fluence across the field can be expressed with the formula $g(x) = e^{c \cdot \mu \cdot x \cdot \tan\alpha}$, where c = attenuation correction factor, μ = effective linear attenuation coefficient, x = position away from the central axis and α = desired wedge angle. The unit is 1/cm.
Attenuation correction factor	Correction factor (supplied by Siemens) to accurately specify the linear attenuation for the specific accelerator and energy. The same attenuation factor has to be configured for the virtual wedge as is used in the accelerator.
Maximum overtravel for X-jaws [mm]	Used for calculating the size of the gap for larger fields when using a FX-direction virtual wedge. This parameter is 5 mm smaller than the normal overtravel distance, meaning that the overtravel of the virtual wedge in the FX direction is by default 15 mm. You can check the overtravel in your Siemens treatment machine and change the value in Beam Configuration accordingly.
Maximum overtravel for Y-jaws [mm]	Used for calculating the size of the gap for larger fields when using a FY-direction virtual wedge. This parameter is 5 mm smaller than the normal overtravel distance, meaning that the overtravel of the virtual wedge in the FY direction is by default 95 mm.
Minimum gap [mm]	Before delivering a field using a virtual wedge, the dynamic jaw is moved close to the opposing static jaw. When the beam is turned on, the jaws remain static for the first few MU to create a sharper edge at the toe of the wedge. The minimum gap defines the minimum width of the gap left between the jaws before the delivery of the field.

Compensator Parameters

The parameters required by compensator configuration are listed in the table.

Table 20 Compensator Parameters

Parameter	Description
Attenuation curve for compensator material	The attenuation curve for a compensator material. If `Brass`, `Cerrobend`, `Al` or `Cu` are selected, the corresponding default attenuation curve is used. For any other attenuation curves, also the attenuation curve data must be imported using the Read from file command.
Attenuation curve data	A user-defined attenuation curve data for the compensator. Define the full path to the data file for importing the user-defined attenuation curve data. The data is read from the file when the compensator configuration is performed. Once the data is read from the file, this text box is cleared. The attenuation curve data file must be a text file containing two columns separated by a space. The first column is for the energy (in MeV), the second column is for the mass attenuation coefficient μ/ρ (in cm^2/g). For each energy value, only one mass attenuation value is allowed. For an example of the attenuation curve data file, see Appendix C on page 336. The mass attenuation curve data can be obtained from: http://www.nist.gov/pml/data/xraycoef/index.cfm
Compensator mass density [g/cm^3]	Mass density of the compensator. This affects the beam hardening properties of the compensator.
Compensator thickness [mm]	Thickness of the flat compensator used in configuration measurements, expressed in millimeters.
Source-to-compensator tray distance [mm]	Distance from the source to the compensator tray, expressed in millimeters. The value has to match the source-to-tray distance value shown in the Slot section of the Compensator Properties dialog box.
Compensator mounting position	The value can be either `PATIENT_SIDE` or `SOURCE_SIDE`. In the Tray section of the Compensator Properties dialog box, the values are: ■ Selected *Above tray* check box: `SOURCE_SIDE`. ■ Unselected *Above tray* check box: `PATIENT_SIDE`.
Beam hardening correction factor for EAC [1/cm^2]	Beam hardening correction factor (bhcf) is an optional parameter to modify EACs for compensator thickness values that deviate from the configuration thickness. By default the value is 0.0.

The compensator modifies the fluence as:

Eq. 4 $a = b \times \exp[-c \times [d + e \times (c - f)]]$

where

a	=	Fluence with compensator at (x, y)
b	=	Fluence without compensator at (x, y)
c	=	Compensator thickness at (x, y), expressed in cm
d	=	Effective attenuation coefficient (EAC) for the given field size interpolated from the calculated EAC values defined in Beam Configuration, expressed in 1/cm
e	=	Beam hardening correction factor for EAC, expressed in $1/cm^2$
f	=	Thickness of the flat compensator used in configuration measurements, expressed in cm

Output Factor Parameters

In addition to the output factors for different field sizes (Table 6 on page 61), the following parameters are used in Beam Configuration to determine the geometry used in the output factor measurements:

■ Source-Phantom Distance [mm]—Distance from the treatment unit source to the surface of the phantom during the output factor measurements.

■ Detector depth from phantom surface [mm]—Distance from the surface of the phantom to the dose detector during the output factor measurements.

Note: *In order for Beam Configuration to be able to handle non-integer centimeter field sizes, the output factors for the Elekta Beam Modulator head must be imported with the **Import > Output Factors for Elekta Beam Modulator** command.*

Machine Parameter Library for Photon Beams

The installation of AAA and Acuros XB includes a library containing parameters that describe the treatment unit type and energy. These parameters are used in and have a significant effect on the optimization of machine parameters. The parameters may also contain initial guesses for some treatment unit parameters.

The library parameters are used as input in the configuration, and the parameter values read from the library are shown in Beam Configuration. The parameter values read from the library may be different for different manufacturers and energies.

The source model machine parameter library contains initial guesses for the following machine parameters:

- Photon energy spectrum
- Mean radial energy
- Location of the virtual second source, the X and Y collimator jaws and the MLC device
- Intensity, energy and size of the virtual second source
- Material of the flattening filter (The material is None for flattening filter free beams)

Parameters in Varian Eclipse Beam Data

Absolute Dosimetry Parameters

The table describes the absolute dosimetry parameters used for the Varian Eclipse Beam Data. The absolute dose reference field size, source-phantom distance and depth must not be modified. The reference dose at calibration depth and Reference MU at calibration depth parameters must be adjusted to reflect the machine specific calibration.

The Varian Eclipse Beam Data defines the output factor table in the isocentric field geometry. It is recommended to use this same geometry for the configuration of absolute dosimetry, in which case the following parameter values should be used for all energies:

Table 21 Absolute Dosimetry Parameters

Parameter	Energy	Value
Absolute Dose Calibration Source-Phantom Distance [mm]	6, 10, 15 MV, 6 MV SRS	950
	18, 20 MV	900
Absolute Dose Reference Field Size [mm]	6, 10, 15 MV, 6 MV SRS	100
	18, 20 MV	100

Table 21 Absolute Dosimetry Parameters

Parameter	Energy	Value
Absolute Dose Calibration Depth [mm]	6, 10, 15 MV, 6 MV SRS	50
	18, 20 MV	100
Reference Dose At Calibration Depth [Gy]	6, 10, 15, 18, 20 MV, 6 MV SRS	To be measured
Reference MU At Calibration Depth [MU]	6, 10, 15, 18, 20 MV, 6 MV SRS	To be set

Wedges in Varian Eclipse Beam Data

Varian Eclipse Beam Data for photon beams contains 13 sets of measurement data for each energy mode: one set of measurements for the open field and one set for each of the 12 different wedges. However, the Varian Eclipse Beam Data for the stereotactic high dose rate 6 MV energy mode (6 MV SRS) does not contain any data for wedges.

The characteristics of the data are the following:

- Open field: Identified with code 00
- Wedge:
    - Treatment units equipped with an MLC have two slots (upper and lower slot), and a separate wedge for each slot
    - Treatment units without an MLC have one slot
    - Wedge size for the 15 and 30 degree wedges: 20 and 30 cm in the wedge direction, 40 cm in longitudinal direction. The sizes of the 45 and 60 degree wedges in the wedge direction are always 20 and 15 cm, respectively.

The table lists the wedge angles and sizes corresponding to the identification codes used in the Eclipse Beam Data, grouped into six different wedge sets.

Table 22 Eclipse Beam Data Wedge Angles, Sizes and Codes

MLC Units			Non-MLC Units		
Angle	Size	Wedge Code	Angle	Size	Wedge Code
Upper Wedge Set (20 cm)			20 cm Wedge Set		
15°	20	01	15°	20	01
30°	20	02	30°	20	02
45°	20	03	45°	20	03
60°	15	04	60°	15	04
Upper Wedge Set (30 cm)			30 cm Wedge Set		
15°	30	09	15°	30	09
30°	30	10	30°	30	10
45°	20	03	45°	20	03
60°	15	04	60°	15	04
Lower Wedge Set (20 cm)					
15°	20	05			
30°	20	06			
45°	20	07			
60°	15	08			
Lower Wedge Set (30 cm)					
15°	30	11			
30°	30	12			
45°	20	07			
60°	15	08			

Configuration Program for Photon Beams

The optimization process used by the photon beam data configuration program is particularly suitable for model-based algorithms such as the AAA and Acuros XB. The photon beam source model uses a set of parameters (see "Machine Parameter Library for Photon Beams" on

page 85) to describe the beam characteristics, and, consequently, the calculated dose distribution in a water phantom. The photon beam configuration program optimizes these parameters to match the calculated distribution with the (processed) measured distribution as accurately as possible.

The optimization process uses an objective function that consists of two terms:

- Total gamma error[4] for the calculated data points with respect to the measured curves (primary term). This error measure is usable in both low and high dose gradient regions. The gamma error measure is defined by two scaling constants, the distance axis unit (3 mm by default) and the relative dose axis unit (1% by default) (for more information, see "Evaluating Gamma Error Histograms" on page 112).

- Penalty term (secondary term) to, for instance, filter out noise from the profile and the mean energy curve, or to dampen the effects of certain measurement artifacts. The penalty function consists of penalties for noise, an increasing mean energy curve and an increasing intensity profile (outside the field edge), and for unphysical second source parameters.

The total objective function is a mapping from the parameter set to a single real number. This objective function can be given to a standard multi-dimensional optimization routine that returns the set of parameters giving (approximately) the minimum of the objective function. The source model configuration program uses Powell's method[5] in the multi-dimensional optimization, and a simple, fast quadratic optimization for single-dimensional line searches inside Powell's method.

Due to their nature, parameters related to electron contamination are excluded from the optimization process. They are optimized separately from the other parameters. In practice, all regions in the dose distribution with a significant effect from contaminating electrons are initially excluded from the first optimization round, and

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4. Daniel A. Low, William B. Harms, Sasa Mutic, and James A. Purdy, A technique for the quantitative evaluation of dose distributions. Med. Phys. 25 (5), 656–661 (1998).

5. M. J. D. Powell: An efficient method for finding the minimum of a function of several variables without calculating derivatives. Comp. J. 7 (2), 155–162 (1964).

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the electron contamination parameters are optimized after that. Finally, the optimization process is restarted using full measurement data to reach consistency.

Adaptation of Measurements in the Configuration

Prior to the optimization of the machine parameters, the source model configuration program verifies the measured beam data and adapts the measured values if possible. You can review the adapted and original measurements in the Beam Data workspace of Beam Configuration (see "Evaluating the Configured Source Model Data" on page 110).

The source model configuration program performs the following detections and adaptations in the following order:

- *No measured diagonal profiles:* Optimization stops, you are prompted to import diagonal profiles.
- *Mandatory field sizes not measured:* Configuration stops.
- *Depth dose curves or profiles saturate into a constant value before the measurement ends:* These values are removed.
- *Depth dose curves or profiles drop to zero before the measurements end:* These values are removed from the measurements.
- *Profiles measured deeper than the corresponding depth dose curve:* Depth dose curve is extrapolated to the required depth. A notification is issued.
- *X-coordinate of the 50% value deviates from the assumed field edge position:* Profiles with a deviation > 2.5 mm are ignored, and a warning is issued. Otherwise the profile is shifted by the required amount.

    For flattening filter free beams, the field edge position is detected from the location of the maximum gradient of the profile.

- *Profile tails missing from the measurements:*
    - Tails of both profile halves missing (measurements past the X-coordinate corresponding to the 50% value on the Y-axis)— Profile excluded from the configuration. A warning message is issued.
    - Tail of one profile missing—Longer profile half is included in the configuration.
    - Both profile halves fully measured—Maximum gamma error between the profile halves is calculated. Profiles with gamma error exceeding 1.0 are ignored, and a warning is issued. Otherwise, the optimization uses the average of the profile halves.
- *Incorrectly positioned detector* (leading to missing scatter in the central field region): A notification is issued. The profile is ignored at, for instance, r < 10 cm.

    This does not apply to flattening filter free beams.
- *Too large dose outside the field in profile tail region:* Due to the use of an incorrect detector, for instance, the dose outside the field edge may become unphysically large and affect the second source intensity parameter. In this case, a notification is issued.
- *Selection of field sizes used when optimizing the source model parameters:* The configuration program may use only a subset of the measured field sizes for depth dose curves and profiles when optimizing the source model parameter values. If the input data contains more field sizes than in the list of preferred field sizes below, the configuration program selects input field sizes that are closest to the preferred field sizes. Otherwise, all input field sizes are used in the configuration. Field sizes smaller then 20 mm are ignored.

    Preferred field sizes in Acuros XB configuration:

Machine	Field Sizes in mm						
Elekta Beam Modulator	24.0	40.0	56.0	80.0	104.0	160.0	210.0
Novalis	20.0	30.0	40.0	60.0	80.0	100.0	
Other machine types	20.0	40.0	60.0	100.0	200.0	400.0	

Preferred field sizes in AAA configuration:

Machine	Field Sizes in mm								
All machines	20.0	30.0	40.0	60.0	80.0	100.0	150.0	200.0	250.0
	300.0	350.0	400.0						

■ *Selection of field sizes for the collimator backscatter table for Elekta Beam Modulator:* To select the X- and Y-field sizes for the CBSF table for the Elekta Beam Modulator, the field sizes found in the output factor table are used if there are less than 9 X-field sizes and 8 Y-field sizes. However, field sizes smaller than 24 mm in either X- or Y- direction are not selected. If the number of field sizes in output factor table is greater, the field sizes closest to the field sizes in the the following list are selected from the output factor table.

Preferred X-field sizes in mm (IEC61217)	24.0	32.0	40.0	56.0	80.0	104.0	120.0	160.0
	210.0							
Preferred Y-field sizes in mm (IEC61217)	24.0	32.0	40.0	56.0	80.0	104.0	120.0	160.0

■ *Selection of field sizes for collimator backscatter table for machines other than Elekta Beam Modulator:* The field sizes from the following list that are between the smallest and the largest field size found from the output factor are selected.

Field Sizes in mm								
20.0	30.0	50.0	70.0	100.0	150.0	200.0	300.0	400.0

In addition, the smallest field size in the output factor table is added in case it differs by 5 mm or more from the otherwise smallest field size in the list. Also, the largest field size in the output factor table is added in case it differs by 50 mm or more from the otherwise largest field size in the list.

For severe errors in the measurement data, a notification is issued about the error, the severity of the error, and whether the corresponding curve was ignored in the configuration. Warnings are also issued if the maximum field size in both directions is not used for wedge fields.

Source Model Configuration Steps

Measurements for all field sizes are used in the configuration process to determine the optimal parameter values. The steps are shown in the Calculate Beam Data dialog box, in which you select the items to be calculated. (For more information on the step file, refer to *Beam Configuration Reference Guide*.)

You can perform all of the configuration steps at once (complete configuration) or any selected steps one at a time for the selected add-on. You can modify the initial guesses for the machine parameters fetched from the library in the configuration parameters (see "Configuration Parameters for Photon Beams" on page 70) or by using the Curve Editor in Beam Configuration.

The source model beam data is calculated for each add-on separately in configuration steps.

Note: *The calculation of configured beam data in Beam Configuration modifies the values of some of the parameters. The configured Mean radial energy, Intensity profile and Second source parameters are retained as initial values if the configuration is performed several times (unless the parameters are re-fetched from the library).*

Configuration Steps for Open Field

The source model beam data is calculated for the open field add-on in the following configuration steps:

- Get parameters from machine data library.

  Creates initial guesses for the configuration. Mean radial energy, intensity profile, second source parameters, electron contamination, and spectrum are set to machine-specific default values. These values are not yet configured to match the measurements.

- Configure open beam (complete configuration).
  This is the recommended method.

  Optimizes the Mean Radial Energy, Intensity Profile and second source parameters by minimizing the gamma error, configures Electron Contamination curve and Sigmas, and calculates the absolute dose parameters and the CBSF table.

- Partial configuration steps 1–5.

  Each of the partial configuration steps can be run either one at a time or as a sequence to consume less of your computer memory. Selecting all of the partial configuration steps produces the same result as running the first configuration step only.

  - Partial configuration 1 (optimization phase I).
  - Partial configuration 2 (optimization phase II).
  - Partial configuration 3 (optimization phase III).
  - Partial configuration 4 (absolute dosimetry).
  - Partial configuration 5 (CBSF table).

- Calculate error histogram.

The following parameters must be defined and the following measured data imported before performing the configuration steps:

- General Parameters (nominal energy, source-axis distance, source-phantom distance)
- Parameters: Absolute dose parameters, machine type, target spot parameters, leaf transmission (for Elekta Beam Modulator)
- Open Beam Parameters (automatically fetched from the library if not found)
- Measured diagonal profiles (DPR)
- Measured depth doses (OPD)

- Measured profiles (OPP)
- Output factor table, or Output factor table for Elekta Beam Modulator
- Absolute point doses

  Required for Elekta Beam Modulator, recommended for all Elekta machines, optional for other machine models and vendors
- Spectrum (automatically fetched from the library if not found)
- Intensity Profile (fluence map)

  Can be obtained by running the configuration step "Get machine parameters from library". This step uses the shallowest measured diagonal profile as an initial guess.
- Mean radial energy

  Can be obtained by running the configuration step "Get machine parameters from library")
- Electron Contamination

  Can be obtained by running the configuration step "Get machine parameters from library". This step creates an initial guess which attenuates from the surface value 1e-15 to value 0 at the depth of 8 cm.

Configuration Steps for Hard Wedges

All open field configuration steps must be performed before configuring wedges.

The source model beam data is calculated for the hard wedge add-ons in the following configuration steps:

- Configure hard wedge (all steps)

  Optimizes the relative intensity and energy of the wedge scatter source and the wedge transmission curve, and calculates the absolute dose parameters and the CBSF table.
- Configure wedge transmission, scatter and electron contamination
- Configure absolute dosimetry
- Configure wedge correction factor table
- *Optional:* Configure wedge correction factors for different SSDs

The following parameters must be defined and the following measured data imported before performing the wedge configuration steps:

- Hard wedge parameters (see Table 15 on page 77)
- Measured wedge depth doses (WDD)
- Measured wedge profiles (WDP)
- Measured wedge longitudinal profile (WLP)
- Measured output factor table for the wedge
- *Optional:* Measured depth doses for different SSDs and a point dose measurement in absolute scale for each curve. These affect electron contamination and wedge scatter.

Configuration Steps for Compensators

All open field configuration steps must be performed before configuring compensators.

The source model beam data for compensator add-ons is calculated in a single configuration step:

- Configure physical compensator

The following parameters must be defined and the following measured data must be entered before performing the compensator configuration:

- Compensator parameters (see Table 20 on page 84)
- Compensator calibration measurements: Point doses for five square fields with and without a slab of compensator material as explained in "Required Measurements for Compensator Fields" on page 66.

Data Generated in the Configuration

Beam Data Generated for Open Fields

The source model configuration program generates the following data for open field add-ons:

- Mean radial energy curve
- Intensity profile curve
- Spectrum
- Electron contamination curve and parameters for the electron contamination fluence kernel (see Equation 16 on page 122):

- Electron contamination curve—Describes both electron and photon contamination (photon scatter from contaminant electrons or collimator leaves).
- Sigma parameters—Sigma0 and Sigma1 smoothing factors (size of the Gaussian) for the electron contamination, Relative fraction of Sigma0 parameter

  The exact values of the electron contamination sigma parameters are sensitive to changes in the dose calculation algorithm and fluctuations in the measured depth dose curves. Thus, the sigma values may change between the algorithm versions.

- Gamma error histograms
  - PDD before dmax—Histogram of gamma error values of depth dose curves before the dose maximum, expressed as a percentage of the measurement points.
  - PDD after dmax—For measurement points in the depth dose curve after the dose maximum.
  - Profile in Flat Region—For lateral and diagonal profiles before the field edge.
  - Profile in Field Edge—For lateral and diagonal profiles in the field edge.
  - Profile Outside Field Edge—For lateral and diagonal profiles outside the field edge.

- Processed measured diagonal profiles: Profiles possibly modified by the configuration program. Some curves may be removed (original curves remain intact).

- Processed measured depth doses: Curves possibly modified by the configuration program. Some curves may be removed (original curves remain intact).

- Processed measured profiles: Profiles possibly modified by the configuration program. Some curves may be removed (original curves remain intact).

- Calculated diagonal profiles: Profiles for the same depths as the measured diagonal profiles.

- Calculated depth doses for all measured field sizes.

- Calculated profiles for all measured field sizes and depths.

- Collimator back-scatter factor table: Radiation scattered back towards the ionization chamber.

- Open Beam parameters: Second source size, intensity, and energy.
- Model parameters: Calculated absolute dose scaling factor.

Beam Data Generated for Wedge Fields

The source model configuration program generates the following data for hard wedge and motorized wedge add-ons:

- Wedge parameters
  - Calculated absolute dose in water (Gy) at the calibration depth.
  - *Elekta Motorized Wedge only:* Second source size, energy and intensity
  - Wedge scatter source intensity
  - Energy of the wedge scatter source
- Wedge transmission curve: Relative amount of incident photons that transport through the wedge without interacting.
- Wedge electron contamination: Separate electron contamination parameters for the wedge
- Wedge correction factors: Corrects the error between the measured and calculated output factors.
- Wedge correction factors for SSD: Created, if the last optional configuration step is performed. Contains scaling factors for electron contamination and wedge scatter as a function of SSD.

Enhanced Dynamic Wedges have one configuration step, which copies the second source parameters from open field.

Siemens Virtual Wedges do not require configured beam data.

For hard wedges, the MU/Gy factor is determined based on separate user-defined hard wedge values for the absolute dose at the reference point and the MU used.

Beam Data Generated for Elekta Motorized Wedge

The source model configuration program generates the following data for Elekta motorized wedge:

- Calculated MW parameters: Calculated absolute dose in water (Gy) at the calibration depth.
- Wedge transmission curve: Relative amount of incident photons that transport through the wedge without interacting.
- Wedge correction factors: Corrects the error between the measured and calculated output factors.

Beam Data Generated for Compensators

The source model configuration program generates the following data for compensator:

- Calculated EACs for five square field sizes.
- The mass attenuation coefficient curve.

EACs are calculated as follows:

Eq. 5

$$EAC = -\frac{1}{f}\log\left(\frac{ad}{bc}\right)$$

where

a	=	Measured dose of a compensator field, expressed in cGy/MU
b	=	Calculated dose of an open field, but using compensator beam hardening, expressed in cGy/MU
c	=	Measured dose of an open field, expressed in cGy/MU
d	=	Calculated dose of an open field, expressed in cGy/MU
f	=	Thickness of the flat compensator used in configuration measurements, expressed in cm

Absolute Dosimetry Parameters

For open fields, Beam Configuration calculates how much dose is deposited at the reference point used in the configuration geometry (not using normalization). In addition to this, the MU/Gy factor used by Eclipse to calculate the MU for each field (see Chapter 3, "Monitor Unit Calculation," on page 31), is determined based on user-defined values for the absolute dose at the reference point and the MU used.

The source model configuration program calculates the following AAA and Acuros XB parameters, and wedge parameters:

Table 23 Calculated AAA and Acuros XB Parameters

Parameter	Calculated for	Description
Absolute Dose Scaling Factor	Open field Hard wedge Elekta Motorized Wedge	Is used to define the relationship between the dose calculated by the algorithm and the absolute calibration reference conditions. *Non-modifiable.*

Configuration and Measurement Geometries for Photon Beams

The following phantom geometries are used in the photon beam source model configuration:

- Measurement geometry for measuring the depth dose and profiles
- Output factor table geometry for the configuration of CBSF table
- Absolute dosimetry geometry for the configuration of MU calculation

Measurement Geometry

Figure 13 on page 101 defines the measurement geometry for profiles and depth doses.
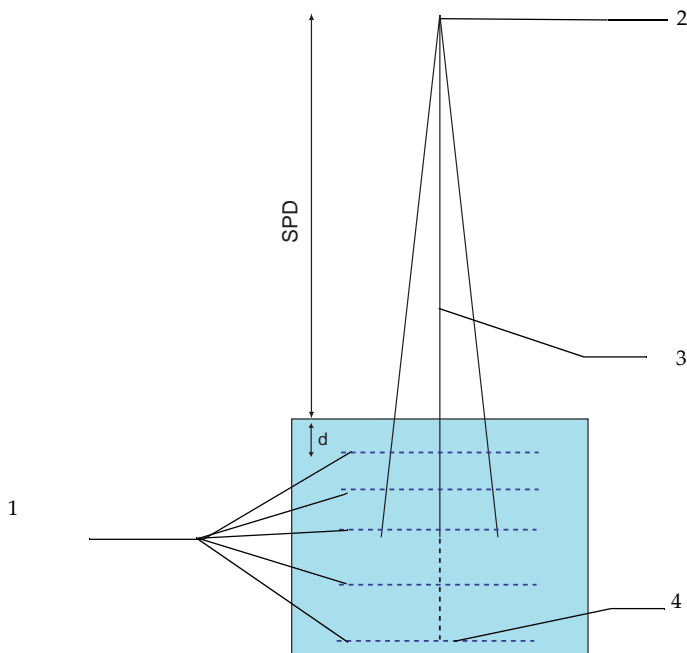
1. Profile measurement depths. **2.** Focus. **3.** CAX. **4.** Depth dose measurement.

Figure 13   Profile Measurement Geometry

In the profile measurement geometry,

- SPD is the Source-Phantom Distance in General Parameters in Beam Configuration (see "General Parameters" on page 70).
- Measurement depths (d) are the 1st to 5th profile depths in General Parameters (see "General Parameters" on page 70).

Output Factor Geometry

Figure 14 on page 102 defines the expected geometry for output factor measurements.
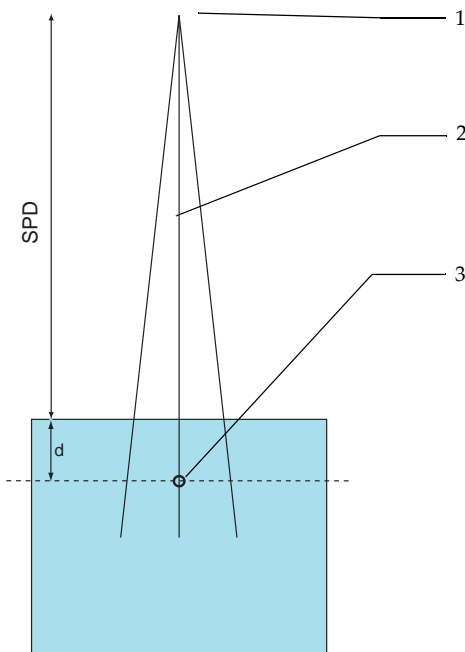
1. Focus. **2.** CAX. **3.** Measurement point.

Figure 14   Output Factor Geometry

In the output factor geometry,

- SPD is the Source-Phantom Distance in the output factor table. The isocenter location depends on the SAD.
- Measurement depth (d) is the Detector Depth in the output factor table (see "Output Factor Parameters" on page 85).
- Reference field size is the value of the Absolute Dose Reference Field Size parameter in the AAA and Acuros XB Parameters (see "AAA and Acuros XB Parameters" on page 71).

Absolute Dosimetry Geometry

Figure 15 on page 103 defines the geometry for the configuration of the absolute dosimetry.
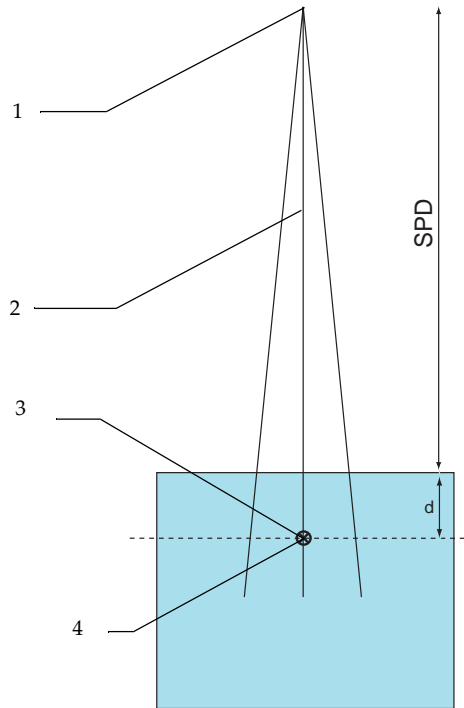
1. Focus. **2.** CAX. **3.** Isocenter. **4.** Measurement point.

Figure 15   Absolute Dosimetry Geometry

For the absolute dosimetry configuration,

- Measurement depth (d) is the value of the Absolute Dose Calibration Depth parameter in the AAA and Acuros XB parameters.
- Reference field size is the value of the Absolute Dose Reference Field Size parameter in the AAA and Acuros XB Parameters.

Configuring Photon Beams in Beam Configuration

The source model for AAA and Acuros XB can be configured by importing measured beam data into Eclipse, or by using CadPlan or Eclipse beam data, or by using Varian Eclipse Beam Data. Acuros XB can also be configured by importing the configured AAA beam data and reconfiguring, and vice versa.

Configuring the AAA or Acuros XB by Importing Measured Beam Data

Measured beam data can be imported into Beam Configuration in ASCII format (w2CAD beam data), CadPlan format (data previously configured in CadPlan), or Eclipse beam data.

To Configure the AAA or Acuros XB Using Measured ASCII Beam Data

1. In Beam Configuration, go to the Beam Data workspace. For instructions on how to use the Beam Configuration, refer to the Eclipse online help system or *Beam Configuration Reference Guide*.

2. Add new beam data.

   The Parameters file of the algorithm is read.

3. Verify the validity of the treatment unit parameters, model parameters and other parameters. For more information on the parameters, see "General Parameters" on page 70.

4. In the Focus window, right-click an add-on and choose **Import > Measured <nn>**.

5. In the **Look in** list box of the dialog box that opens, navigate to the folder containing the files to be imported and click **OK** to start the import.

   If you notice errors in the measured data, stop the import process. Trace the source of the error to a problem in the measured data, and correct the measured data before resuming the import procedure.

6. Repeat steps 4 and 5 for each type of measured beam data to be imported.

7. When you have added all necessary measured beam data, calculate the configured beam data by doing one of the following:

   a. To calculate the configured beam data for all add-ons in a therapy unit, go to the Focus window, select the therapy unit and then choose **Beam Data > Calculate All Beam Data**.

   b. To calculate the configured beam data for each individual add-on at a time, go to the Focus window, select each add-on for which you wish to calculate configured beam data, and choose **Beam Data > Calculate Beam Data**. Then, in the Calculate Beam Data dialog box, select the check boxes of each item you wish to calculate.

   Remember to save and approve your configured beam data. Validate the configured beam data in the Beam Analysis workspace. If you need to continue the configuration after validating the data, unapprove the data first. For instructions for approving, validating and unapproving beam data, refer to Beam Configuration Reference Guide.

To Configure the AAA or Acuros XB Using CadPlan Beam Data

Note: *Use this method to import the measured beam data of an existing configured PBC model for the configuration of the AAA or Acuros XB.*

1. In Beam Configuration, go to the Beam Data workspace. For instructions on how to use Beam Configuration, refer to the Eclipse online help system or *Beam Configuration Reference Guide*.

2. Add new beam data.

   The Parameters file of the algorithm is read.

3. Verify the validity of the treatment unit parameters, model parameters and other parameters. For more information on the parameters, see "General Parameters" on page 70.

4. In the Focus window, right-click an add-on and choose **Insert > New Measured <nn>**.

5. Repeat step 4 for each type of measured beam data.

6. In the Focus window, right-click a measured beam data item and choose **Import CadPlan Measurement Data File**.

7. In the **Look in** list box of the dialog box that opens, navigate to the folder containing the files to be imported, select the beam data file and click **Open**.

8. Repeat steps 6 and 7 for each type of measured beam data.

9. When you have imported all necessary measured beam data, calculate the configured beam data for the add-ons.

    a. In the Focus window, click each add-on for which you wish to calculate configured beam data, choose **Beam Data > Calculate Beam Data**.

    b. In the Calculate Beam Data dialog box, select the check boxes of each item you wish to calculate.

    Remember to save and approve your configured beam data. Validate the configured beam data in the Beam Analysis workspace. If you need to continue the configuration after validating the data, unapprove the data first. For instructions for approving, validating and unapproving beam data, refer to Beam Configuration Reference Guide.

To Configure the AAA or Acuros XB Using Existing Eclipse Beam Data

1. In Beam Configuration, go to the Beam Data workspace. For instructions on how to use Beam Configuration, refer to the Eclipse online help system or *Beam Configuration Reference Guide*.

2. Add new beam data.

    The Parameters file of the algorithm is read.

3. Verify the validity of the treatment unit parameters, model parameters and other parameters. For more information on the parameters, see "General Parameters" on page 70.

4. In the Focus window, select the treatment unit and then choose **File > Import > Eclipse Beam Data**.

5. To navigate to the directory containing the Eclipse beam data, click **Browse**. The active directory is shown in the Eclipse data box.

    Navigate to the level of general data files of the calculation model. This level is above the folders containing the configured beam data files. For instance, the general data folder may be named "AAA", and the configured data folders below it "000", "001", "002", and so on. You should navigate to the folder named "AAA" in this example.

6. In the list box on the left, select the data set containing the Eclipse beam data to import.

7. In the Into beam data box, define a name for the beam data.

8. Click **OK**.

   The Eclipse beam data appears in the Context window.

9. Match and assign the add-ons.

10. When you have imported all necessary measured beam data, calculate the configured beam data for the add-ons.

    a. In the Focus window, click each add-on for which you wish to calculate configured beam data, and choose **Beam Data > Calculate Beam Data**.

    b. In the Calculate Beam Data dialog box, select the check boxes of each item you wish to calculate.

    Remember to save and approve your configured beam data. Validate the configured beam data in the Beam Analysis workspace. If you need to continue the configuration after validating the data, unapprove the data first. For instructions for approving, validating and unapproving beam data, refer to Beam Configuration Reference Guide.

Configuring the Acuros XB Using AAA Beam Data

When configuring the Acuros XB, you can either start from the measured beam data as explained above, or import the existing AAA beam data and reconfigure.

To Configure the Acuros XB Using AAA Beam Data

1. Import the AAA beam data for Acuros XB by choosing **File > Import > Eclipse Beam Data**.

2. Select the **Open Field** and choose **Beam Data > Calculate Beam Data**.

3. Select each wedge one at a time and choose **Beam Data > Calculate Beam Data**, if applicable.

Configuring the AAA or Acuros XB
Using Varian Eclipse Beam Data

Varian Eclipse Beam Data is provided by Varian at the installation of the calculation algorithm. Using this beam data, you only need to do minimal manual configuration in Beam Configuration to match and assign your add-ons (open field, wedges and Enhanced Dynamic Wedge). You can also modify the beam data manually.

If you are using Varian Eclipse Beam Data without any modifications to the parameter values or without using your own measured beam data, you only need to enter the absolute dosimetry parameters ("AAA and Acuros XB Parameters" on page 71 and "Hard Wedge Parameters" on page 77) and verify the parameters contained in the beam data; no changes are required unless the parameter values are clearly incorrect.

The preconfigured Varian Eclipse Beam Data for AAA and Acuros XB were acquired with a Wellhofer IC-10 ionization chamber following standard protocols used at the Varian factory for verification of specifications. This is documented in "Varian High Energy Clinac Machine Configuration and Beam Tuning Specification for the CadPlan Preload Beam Data". However, the percent depth doses in the preconfigured beam data are corrected for the effective depth of measurement by shifting them 1.8 mm closer to the surface.

Varian Eclipse Beam Data is representative for a Varian high energy clinac accelerator conforming to the specifications detailed in Sections 1.0 and 2.0 of "Clinac 21/23EX Equipment Specification" (RAD 4205) and "Clinac Beam Matching" (RAD 2055).

The data is valid only for:

- 2100-series (C, CD, EX, etc.) S/N 865 or higher
- 2300-series (CD, EX) S/N 146 or higher
- All iX and Trilogy

Compare the dosimetric beam data acquired from the treatment machine at the site with the dosimetric beam data used in the configuration of the preconfigured beam data, and ensure that the variations do not exceed the user tolerance. If variations exceed the tolerance, use the dosimetric beam data acquired at the site for calculation algorithm configuration.

To Configure the AAA or Acuros XB Using Varian Eclipse Beam Data

1. In Beam Configuration, go to the Beam Data workspace. For instructions on how to use Beam Configuration, refer to the Eclipse online help system or *Beam Configuration Reference Guide*.

2. Add new beam data.

   The Parameters file of the algorithm is read.

3. Verify the validity of the treatment unit parameters, model parameters and other parameters. For more information on the parameters, see "General Parameters" on page 70.

4. In the Focus window, right-click the treatment unit and then select **Import Eclipse Data** to add Varian Eclipse Beam Data.

5. Navigate to the directory on the server where the beam data is installed (normally
   ```
   \\<Server name>\DCF$\client\PreconfiguredBeamData\
   Anisotropic Analytical Algorithm (<version number>)
   ```
) and
   ```
   \\<Server name>\DCF$\client\PreconfiguredBeamData\
   Acuros External Beam (<version number>)
   ```
)

6. Select the desired beam data and click **OK**.

7. Match and assign the add-ons.

   The Varian Eclipse Beam Data identifies wedges in a particular way. To correctly match and assign your wedges, see "Parameters in Varian Eclipse Beam Data" on page 86.

   a. To match the wedges, select the check box of a hard wedge in the ID column, and then click **Single**.

   b. In the Automatically Match Add-On Data dialog box, go to the Match list, select the degree corresponding to the selected hard wedge, and then click **OK**.

   c. Repeat A. and B. for each hard wedge you want to configure.

   d. To match an Enhanced Dynamic Wedge, click EW in the ID column, go to the Automatic Match box and click **Single**.

   e. Click **Close**.

   Remember to save and approve your configured beam data. Validate the configured beam data in the Beam Analysis workspace. If you need to continue the configuration after validating the data, unapprove the data first. For instructions for approving, validating and unapproving beam data, refer to Beam Configuration Reference Guide.

To Modify AAA or Acuros XB Beam Data Configured
Using Varian Eclipse Beam Data

1. In the Focus window, select **Parameters** under the treatment unit that contains your configured Varian Eclipse Beam Data.

2. To modify the absolute dosimetry parameters, click on the cell of the parameter to be modified and type in your new parameter value.

3. Calculate the configured beam data for the add-ons.

   a. In the Focus window, click each add-on for which you wish to calculate configured beam data, and choose **Beam Data > Calculate Beam Data**.

   b. In the Calculate Beam Data dialog box, select the check boxes of each item you wish to calculate.

   Remember to save and approve your configured beam data. Validate the configured beam data in the Beam Analysis workspace. If you need to continue the configuration after validating the data, unapprove the data first. For instructions for approving, validating and unapproving beam data, refer to Beam Configuration Reference Guide.

Evaluating the Configured Source Model Data

The configured source model data for AAA and Acuros XB can be visually verified in Beam Configuration.

Evaluating Electron Contamination Curve for Open Beam and Hard Wedges

The source model configuration program produces the electron contamination curve and the Sigma parameters related to this curve.

The electron contamination curve defines the values to be added to the non-normalized results of the dose calculation at each depth. Electron contamination is also used to model photon contamination (photons created in electron interactions). The electron contamination curve is defined by value pairs (<depth in mm>, <laterally integrated electron contamination dose>). The depth values should always be positive and in an ascending order. The electron contamination curve usually peaks at appr. 0.5 mm at the surface, and falls rapidly close to zero within approximately 50 millimeters (depending on the energy).

The Sigma parameters are smoothing factors for the electron contamination. The value of the Sigma parameters are always positive, and the value range is wide. Large values produce less electron contamination for small field sizes and spread the electron contamination more in the lateral direction. The coefficient c_0 specifies the relative weight of the first Gaussian, which is always between 0 and 1.

Evaluating Back-Scatter Factor Table

The back-scatter factor table contains the back-scatter factors for the same field sizes as output factor measurements. The horizontal rows define the field size in the X-direction (positive); columns define the field size in the Y-direction (positive). These values are > 1 for field sizes smaller than the reference field size, and < 1 for larger field sizes (always positive).

Evaluating Wedge Transmission Curve

The wedge transmission curve is defined by value pairs (<distance in mm on wedge axis>, <relative wedge transmission>). The maximum value on the curve is scaled to 1.0, and the relative wedge transmission values are > 0. The distance values can be negative or positive, but they are always in ascending order.

Evaluating the Energy Spectrum

The energy spectrum curve is usually peaked at very low energies. The curve is defined by value pairs (<energy in MeV>, <particle fluence>). The curve is fetched from the machine library. You can check that the highest energy in the curve corresponds to the nominal energy. This curve is not modified during the configuration process.

Evaluating the Radial Energy

The radial energy curve determines the average energy curve of photons after the flattening filter, which attenuates low-energy components of the spectrum. Usually the energy decreases smoothly when moving from the field central axis (radial distance 0.0 mm) to the field edge. The mean radial energy curve is defined by value pairs (<radial distance at SAD in mm>, <energy in MeV>), in which the values are positive and in an ascending order.

Evaluating Gamma Error Histograms

Evaluating gamma error histograms is available only for AAA. Using the fully configured source model, the gamma error[6] is calculated for each processed measurement curve by comparing it with calculated points. For this purpose, the measured and calculated curves are superimposed to the same graph, in which the X-axis corresponds to position (mm) and the Y-axis to relative dose (%) as in Figure 16 on page 112.
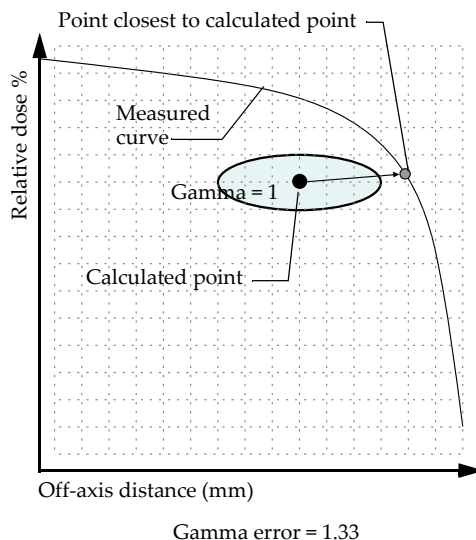
Gamma error = 1.33

Figure 16   Definition of Gamma Error Norm

In the figure, the continuous line represents the measured profile, the black dot and the grey dot indicating the calculated point and the point closest to it on the measured curve, respectively. For the gamma metric, the unit of measurement of the off-axis distance is 3 (mm), and the unit of measurement of the relative dose difference is 1 (%). The area surrounding the calculated point in which the calculated gamma norm is 1 or smaller is shown with an ellipse. The resulting gamma error is approximately 1.33.

For at least 99% of the measurement points in the Varian Eclipse Beam Data for the AAA, the gamma error norm is lower than 1.0.

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6. Daniel A. Low, William B. Harms, Sasa Mutic, and James A. Purdy, A technique for the quantitative evaluation of dose distributions. Med. Phys. 25 (5), 656–661 (1998).

Chapter 5   Anisotropic Analytical Algorithm (AAA) for Photons

About the Anisotropic Analytical Algorithm (AAA)

The AAA is a 3D pencil beam convolution/superposition algorithm that uses separate Monte Carlo derived modeling for primary photons, scattered extra-focal photons, and electrons scattered from the beam limiting devices. The lateral dose deposition characteristics are modeled with six exponential curves. The functional shapes of the fundamental physical expressions in the AAA enable analytical convolution, which significantly reduces the computational time.

The AAA was originally conceived by Dr. Waldemar Ulmer[7,8,9] and Dr. Wolfgang Kaissl[10,11]. The development of the algorithm culminated in the publication of the triple-Gaussian photon kernel model in 1995[8].

Before being implemented in Eclipse, the AAA approach has been applied to stereotactic radiation therapy planning[12]. The implementation of the AAA in Eclipse continues the research and development of the algorithm and is based on the earlier work by Ulmer and Kaissl.

Important improvements have been made to the AAA dose calculation algorithm in the areas of treatment unit and tissue heterogeneity modeling, and increasing the accuracy of the scattered dose calculation[13].

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7. Max-Planck-Institut für Biophysik, Göttingen, Germany.

8. Ulmer W, Harder D: A Triple Gaussian Pencil Beam Model for Photon Beam Treatment Planning, 2. Med. Phys. 5 (1995) 25–30.

9. Ulmer W, Harder D: Applications of a Triple Gaussian Pencil Beam Model for Photon Beam Treatment Planning, 2. Med. Phys. 6 (1996) 68–74.

10. Varian Medical Systems Imaging Laboratory GmbH, Baden, Switzerland.

11. Ulmer W and Kaissl W: The inverse problem of a Gaussian convolution and its application to the finite size of the measurement chambers/detectors in photon and proton dosimetry, Phys. Med. Biol. 48 (2003) 707–727.

12. Ulmer W, Brenneisen W: Application of an Analytical Pencil Beam Model to Stereotactic Radiation Therapy Planning, Journal of Radiosurgery, Vol 1, No.3, 1998.

The AAA accounts for tissue heterogeneity anisotropically in the entire three-dimensional neighborhood of an interaction site, by using photon scatter kernels in multiple lateral directions (see "Scatter Kernels" on page 115). The final dose distribution is obtained by the superposition of the dose calculated with photon and electron convolutions.

Dose Calculation in the Anisotropic Analytical Algorithm (AAA)

The clinical implementation of the AAA is divided into two:

- Photon beam source model—Determines the fundamental physical parameters required for the actual dose calculation (see Chapter 4, "Modeling of the Primary Source," on page 48 and Chapter 4, "Modeling of the Second Source," on page 51).[14]
- Dose calculation algorithm—Calculates the dose deposition using the fundamental physical parameters. These parameters characterize the particle fluences and energy spectra of the photons and electrons comprising the clinical beam (see "Volumetric Dose Calculation" on page 117).[15]

Patient Scatter Model

The patient scatter model is used in depositing the dose inside the patient, while phase-space parameters give the description of the treatment beam upstream of the patient. The full treatment beam entering the patient is divided into finite-sized beamlets, each of which is modeled using several monoenergetic scatter kernels.

13. Tillikainen L, Helminen H, Torsti T, Siljamäki S, Alakuijala J, Pyyry J and Ulmer W: A 3D pencil beam based superposition algorithm for photon dose calculation in heterogeneous media, Phys. Med. Biol. 53 (2008) 3821–3839.

14. Tillikainen L, Siljamäki S, Helminen H, Alakuijala J and Pyyry J: Determination of parameters for a multiple-source model of megavoltage photon beams using optimization methods, Phys. Med. Biol. 52 (2007) 1441–1467.

15. Tillikainen et al.: A 3D pencil-beam-based superposition algorithm for photon dose calculation in heterogeneous media, Phys. Med. Biol. 53 (2008) 3821–3839.

Scatter Kernels

The scatter kernels describe the phantom-scatter effects for different beam qualities. The EGSnrc[16] Monte Carlo code was used to compute scatter kernels for monoenergetic pencil beams in water. A polyenergetic scatter kernel is constructed as a weighted sum of the monoenergetic scatter kernels. During the 3D dose calculation these kernels are scaled according to the densities of the actual patient tissues determined from the CT images.

Beamlets

The figure shows the geometrical definitions of the coordinates referring to a single beamlet β on the X–Z plane, with the Y-axis pointing outwards from the paper. The coordinates are defined in two coordinate systems:

- Patient coordinate system
- Beamlet coordinate system

The coordinates of the calculation point (P) in the figure are $(\tilde{x}, \tilde{y}, \tilde{z})$ in the patient coordinate system, and (x,y,z) in the beamlet coordinate system. The depth coordinate z is measured from the intersection point of the central fanline and the skin in the beamlet coordinate system.

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16. NRCC Report PIRS-701: The EGSnrc Code System: Monte Carlo Simulation of Electron and Photon Transport, I. Kawrakow and D.W.O. Rogers; Nov 7, 2003.
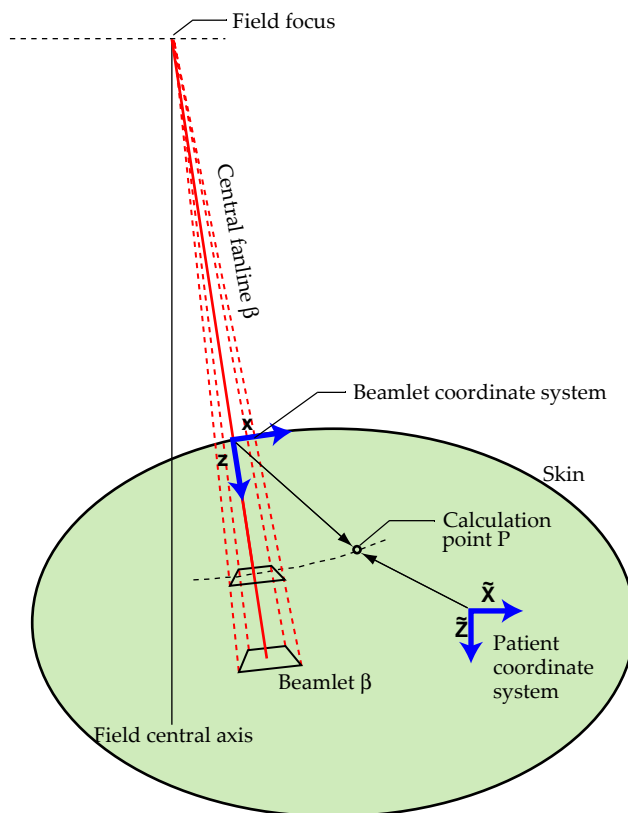
Figure 17 Coordinates in Patient Coordinate System and Beamlet Coordinate System on X–Z Plane

The broad clinical beam is divided into finite-size beamlets β. The side length of the beamlet corresponds to the resolution of the calculation grid on the isocenter plane.

The dose calculation is based on the convolutions over the beamlet cross-sections separately for the primary photons, extra-focal photons (second source), scatter from hard wedges, and for electrons contaminating the primary beam. The dose is convolved by using the physical parameters defined for every beamlet β.

All depth-dependent functions used in the beamlet convolutions are computed along the central fanline of the beamlet using the depth coordinate z. Lateral dose scattering due to photons and electrons is defined on the spherical shell perpendicular to the central fanline of the beamlet. The AAA makes the assumption that the dose resulting

from photon and electron scatter can be calculated by a division into two main directions, which are the lateral and the depth scatter. As can be seen in the figure, the lateral calculation plane has a spherical shape, where the center of the sphere is located in the field focus. The use of spherical coordinate systems allows us to use more uniform models of the pencil beams across the broad beam.

The dose to an arbitrary calculation point $(\tilde{X}, \tilde{Y}, \tilde{Z})$ in the patient is obtained by summing up the dose contributions of all individual beamlets β of the broad beam in the final global superposition.

Volumetric Dose Calculation

For volumetric dose distribution calculation, the patient body volume is divided into a matrix of 3D calculation voxels based on the selected calculation grid (see Figure 7 on page 46). The geometry of the calculation voxel grid is divergent, aligning the coordinate system with the beam fanlines. Every calculation voxel is associated with the mean electron density ρ that is computed from the patient CT images according to a user-specified calibration curve. The maximum allowed value for electron density in AAA is 15. Electron densities larger than that are truncated to the maximum value (that is, value of 15 is used).

Note: *When a beam traverses lung tissue, the AAA tends to overestimate dose at the lung-soft tissue interface, where the beams exits the lung and enters soft-tissue again. The effect is more pronounced as the interface depth increases.*

Convolution Models

The 3D dose distribution is calculated from separate convolutions for the primary photon source, second photon source, wedge scatter source and contaminating electron source. The convolutions are performed for all finite-sized beamlets that comprise the clinical broad beam. The final dose distribution is obtained by a simple superposition of the individual beamlet contributions.

Photon Dose Calculation

The photon beam attenuation is modeled with an energy deposition density function $I_\beta(z, \rho)$. The photon scatter is modeled with a scatter kernel $K_\beta(x, y, z)$ that defines the lateral energy scattering. Both functions I_β and K_β are defined individually for each beamlet β. The

primary and extra-focal photons are calculated in the same way, with the exception of their spectral composition and the position and size of the focal spot.

The dose convolution in the AAA is performed in terms of energy. In comparison with dose-based convolution, which is more common, energy convolution allows the energy to be conserved more accurately even in more complex heterogeneous convolutions. The energy is converted to dose using the scaled-water approximation.

The energy distribution resulting from an arbitrary beamlet β due to photons in a sufficiently large homogenous neighborhood is calculated by the following formula:

Eq. 6

$$E_{ph,\beta}(\tilde{X},\tilde{Y},\tilde{Z}) = \Phi_\beta \times I_\beta(z,\rho) \times K_\beta(X,Y,Z)$$

In the convolution, the calculation point $(\tilde{X},\tilde{Y},\tilde{Z})$ is represented by (x,y,z) relative to the origin of the beamlet coordinate system. The photon fluence Φ_β is assumed to be uniform over the small cross-section of beamlet β.

The energy deposition function $I_\beta(z,\rho)$ denotes the area integral of the deposited energy over the sphere surface of the pencil beam at depth z.

Eq. 7

$$I_\beta(z) = \iint h_\beta(t,v,z) \ dt \ dv$$

where

h_β =   poly-energetic pencil beam kernel derived from Monte Carlo simulations

The energy deposition function $I_\beta(z,\rho)$ accounts for tissue heterogeneity by employing the concept of radiological scaling. This is performed by setting $I_\beta(z,\rho) = I_\beta(z') \cdot \dfrac{\rho(0,0,z)}{\rho_{water}}$, where the radiological depth z' is defined as:

         Eclipse Algorithms Reference Guide

Eq. 8

$$Z' = \int_0^z \frac{\rho(0,0,t)}{\rho_{water}} dt$$

where

ρ = electron density

The photon scatter kernel $K_\beta(x,y,z)$ is composed of the weighted sum of six exponential functions as shown in Equation 9 on page 119. Here we assume a homogeneous phantom; the effect of lateral heterogeneities is discussed in "Lateral Density Scaling of the Photon Scatter Kernels" on page 120.

Eq. 9

$$K_\beta(x,y,z) = \sum_{k=0}^{5} c_k(z') \frac{1}{r} e^{-\mu_k r}$$

where

$$r = \sqrt{x^2 + y^2}$$

and z' is defined as in Equation 8 on page 119.

Here z' is used instead of z to take into account the effect of heterogeneity between the calculation point and the beamlet entry point in the scatter properties of the pencil beam.

The exponential kernels are characterized with the decay constants μ_k. The factors c_k define the weights for the exponential kernels and ensure the unity normalization of the total kernel energy. The parameters $c_k(z')$ of the polyenergetic scatter kernel $K_\beta(x,y,z)$ are determined by doing a least squares fit of the basis functions $\frac{1}{r} e^{-\mu_k r}$ to the Monte Carlo derived pencil beam scatter kernels. The constants μ_k are chosen such that $1/\mu_k$ vary from 1 to 100 mm with equal logarithmic intervals.

Note that although the equation above implies that there is a singularity at $r = 0$, the actual integral is two-dimensional and does not diverge.

Lateral Density Scaling of the Photon Scatter Kernels

Density scaling of the individual pencil beams is done by scaling the energy at each location by the average density between the calculation point and the origin of the pencil beam.

In practice, this is done by dividing the kernel of the following equation into a finite number (16) of rays that emerge from the origin. Distribution of absorbed energy at a location K_β(x,y,z) in presence of heterogeneity is then calculated as:

Eq. 10

$$K_\beta(x,y,z) = \frac{\rho(x,y,z)}{\rho_{water}} \sum_{k=0}^{5} c_k(z') \frac{1}{r} e^{-\mu_k r_d(x,y,z)}$$

where

$$r_d(x,y,\rho) = \int_R \frac{\rho(\vec{t})}{\rho_{water}} \left|d\vec{t}\right| \times \frac{z'}{z}$$

r_d	=	Radiological distance from kernel origin (0,0,z) to (x,y,z) along ray R that passes through (x,y).
$\frac{z'}{z}$	=	Ratio correcting for the diverging coordinate system.

Heterogeneity History Correction of the Photon Scatter Kernels

Using the previous formulas would result in an overtly abrupt estimation of the changes in scatter conditions at the borders of heterogeneities in slab-like phantoms. This is avoided by moving the energy distribution in the depth direction using a one-dimensional scatter kernel. This takes care of the gradual changes of the scatter conditions after the heterogeneity borders. But since this transform would result in moving the dose deeper, this is pre-compensated by applying the reverse transform to the poly-energetic pencil beam kernel h_β(x,y,z).

The one-dimensional scatter kernel k_z(z) is of the following form:

Eq. 11

$$k_z(z) = \sum_{i=1}^{2} c_i \frac{1}{\mu_i} e^{-\mu_i z}$$

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The parameters μ_i and c_i are determined using optimization methods such that the I_β function calculated for the pre-compensated pencil beam kernel h'_β in Equation 14 on page 121 does not have any build-up.

The one-dimensional convolution of energy $E_{ph,\beta}$ is then defined as:

Eq. 12
$$E'_{ph,\beta}(x,y,z) = E_{ph,\beta}(x,y,z) \otimes k_z(z)$$

where

$\otimes$ =   Convolution operator

In the presence of heterogeneities, the convolution kernel is scaled by the local electron density as follows:

Eq. 13
$$k_z(z) = \frac{\rho(z)}{\rho_{water}} \sum_{i=1}^{2} c_i \frac{1}{\mu_i} e^{-\mu_i z'}$$

where

$\rho(z)$ =   Local electron density
z' =   Radiological distance from the kernel origin

The pre-compensation to the poly-energetic pencil beam kernel $h_\beta(x,y,z)$ is of the following form:

Eq. 14
$$h'_\beta(x,y,z) = h_\beta(x,y,z) \otimes inv(k_z(z))$$

where

$inv(k_z(z))$ =   Deconvolution kernel derived from $k_z(z)$

The above formulations result in a modified pencil beam $h'_\beta(x,y,z)$, which replaces the original $h_\beta(x,y,z)$ in "Photon Dose Calculation" on page 117. The heterogeneity history correction method has been defined so that it has no effect in the absence of heterogeneities.

Contaminating Electrons

The primary photon beam is contaminated with electrons originating mainly in the flattening filter, collimating jaws and air. If beam modifiers are used, the modifiers may absorb most of the electrons in

the open beam, but the modifier itself becomes a secondary source of contaminating electrons. In general, electron contamination depends strongly on the beam energy and the field size.

The energy distribution resulting from an arbitrary beamlet β due to the contaminating electrons is calculated by the following equation:

Eq. 15

$$E_{cont,\beta}(\tilde{X},\tilde{Y},\tilde{Z}) = \Phi_{cont,\beta} \times I_{cont,\beta}$$

In the above equation, the calculation point $(\tilde{X},\tilde{Y},\tilde{Z})$ is represented by (x,y,z) in the beamlet coordinate system. The electron fluence $\Phi_{cont,\beta}$ and the energy deposition function $I_{cont,\beta}$ are assumed to be uniform over the cross-section of beamlet β. In the presence of heterogeneities, the energy deposition function is scaled in a similar way as the I_β function for photons.

The fluence of the contaminating electrons is determined by convolving photon fluence with a sum-of-Gaussians kernel $K_{fl,e}$.

Eq. 16

$$K_{fl,e}(x,y) = \sum_{K=0}^{1} C_{cont,k} \frac{1}{2\pi\sigma^2_{cont,k}} \exp\left[-\frac{x^2+y^2}{2\sigma^2_{cont,k}} \right]$$

The parameters c_k specify the relative weights of the two Gaussian components where $c_1 = 1-C_0$

The energy deposition density function $I_{cont,\beta}(z,\rho)$ for the contaminating electrons is determined from the measured data and tabulated as a function of the depth z.

Superposition

The absorbed energy $E(\tilde{X},\tilde{Y},\tilde{Z})$ at an arbitrary calculation point in the patient is obtained by a superposition of the separate energy contributions from the primary photons (ph1) (Equation 6 on page 118), extra-focal photons (ph2) (Equation 6 on page 118), and contaminating electrons (Equation 15 on page 122) from all individual beamlets denoted by index β:

Eq. 17

$$E(\tilde{X},\tilde{Y},\tilde{Z}) = \sum_{\beta} (E_{ph1,\beta}(\tilde{X},\tilde{Y},\tilde{Z}) + E_{ph2,\beta}(\tilde{X},\tilde{Y},\tilde{Z}) + E_{cont,\beta}(\tilde{X},\tilde{Y},\tilde{Z}))$$

Conversion to Dose

As a final step, the absorbed energy distribution is converted to a dose. An assumption is made that the different heterogeneities can be modeled as scaled water. Electron densities are used to convert the energy to dose instead of mass density. The final dose is given by:

Eq. 18

$$D(\tilde{X},\tilde{Y},\tilde{Z}) = c\,E(\tilde{X},\tilde{Y},\tilde{Z}) \cdot \frac{\rho_{\text{water}}}{\rho(\tilde{X},\tilde{Y},\tilde{Z})}$$

where c handles the unit conversion from J/m^3 to Gy.

Chapter 6   Acuros External Beam Algorithm (Acuros XB) for Photons

About the Acuros External Beam Algorithm (Acuros XB)

The Acuros XB algorithm was developed to provide accurate and rapid dose calculations for external photon beam radiotherapy treatments ranging from 4 MV to 25 MV, with calculation grid voxel sizes ranging from 1 to 3 mm. In external photon beam radiotherapy, heterogeneities introduced by materials such as lung, air, bone and implants may significantly influence the dose distribution in the patient, especially in the presence of small or irregular fields. Through solving the linear Boltzmann transport equation (LBTE), Acuros XB directly accounts for the effects of these heterogeneities.

Dose Calculation with Acuros XB Algorithm

The LBTE is the governing equation that describes the macroscopic behavior of radiation particles (neutrons, gamma-rays, electrons, etc.) as they travel through and interact with matter. For a given volumetric domain of matter, subject to a radiation source, the solution to the LBTE would give an 'exact' description of the dose within the domain. However, since closed form, or analytic, solutions to the LBTE can only be obtained for a few simplified problems, the LBTE must be solved in an open form, or non-analytic, manner.

There are two general approaches to obtaining open form solutions to the LBTE. The first approach is the widely known Monte Carlo method, which stochastically predicts particle transport through media by tracking a statistically significant number of particles through successive random interactions. Although Monte Carlo methods do not explicitly solve the LBTE, they do indirectly obtain the solution to this equation. The second approach is to explicitly solve the LBTE using numerical methods[17]. Methods used to explicitly solve the LBTE are relatively new to the medical physics community, where

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17. Lewis EE, Miller WF, "Computational methods of neutron transport", Wiley, New York, 1984.

Monte Carlo and correction based algorithms, which employ pre-calculated Monte Carlo dose kernels, have generally been used for dose calculation.

Both Monte Carlo and explicit LBTE solution methods are convergent. That is, with sufficient refinement both approaches will converge on the same solution. The achievable accuracy of both approaches is equivalent and is limited only by uncertainties in the particle interaction (cross-section) data and uncertainties in the problem being analyzed.

However, in practice, neither Monte Carlo nor explicit LBTE solution methods are exact, and both methods produce errors. In Monte Carlo, errors are stochastic, and result from simulating a finite number of particles. When Monte Carlo methods employ certain techniques to accelerate solution times, however, systematic errors may also be introduced. In explicit LBTE solution methods, errors are primarily systematic, and result from discretization of the solution variables in space, angle, and energy. Additionally, differences may also result from the treatment of charged particle coulomb interactions, which are generally approximated in both Monte Carlo and explicit LBTE solution methods.

In both Monte Carlo and explicit LBTE solution methods, a trade-off exists between speed and accuracy. Reduced computational time may be achieved when less stringent accuracy criteria are specified, and vice versa.

Overview of Calculation Steps

The Acuros XB dose calculation proceeds according to the following steps:

- Step 1: Creating the physical material map.
- Step 2: Transporting the components of the photon beam source model (primary photon source, secondary photon source and electron contamination source) into the patient.
- Step 3: Transporting the scattered photon fluence in the patient.
- Step 4: Transporting the electron fluence in the patient.
- Step 5: Calculating the desired dose mode (dose to medium, or dose to water).

The following figure describes the steps in the Acuros XB calculation process:

```
                    ┌───────────────────────────────┐
                    │                               │
                    │   Photon Beam Source Model    │
                    │                               │
                    └───────────────────────────────┘
           │                    │                      │
    $q^{\gamma}_{primary}$  $q^{\gamma}_{secondary}$  $q^{e}_{contaminant}$
           ▼                    ▼                      ▼
                    ┌───────────────────────────────┐
                    │      Step 2. Ray Tracing of   │
                    │      Beams into the Patient   │
                    └───────────────────────────────┘
                    │                              │
              $q^{\gamma\gamma}_{unc}$        $q^{\gamma e}_{unc}$
                    │                              │
                    ▼                         $q^{ee}_{unc}$
       ┌───────────────────────────┐              │
       │   Step 3: Scattered Photon│              │
       │   Fluence Calculation     │              │
       └───────────────────────────┘              │
                    │                              │
              $q^{\gamma e}_{coll}$                │
                    ▼                              ▼
                    ┌───────────────────────────────┐
                    │     Step 4: Collided Electron │
                    │     Fluence Calculation       │
                    └───────────────────────────────┘
                                  │
                            $\Psi^{e}_{coll}$
                                  ▼
                    ┌───────────────────────────────┐
                    │     Step 5: Dose Calculation  │
                    └───────────────────────────────┘
                                  │
                           $D_W$ or $D_M$
                                  ▼
                    ┌───────────────────────────────┐
                    │            Eclipse            │
                    └───────────────────────────────┘
```
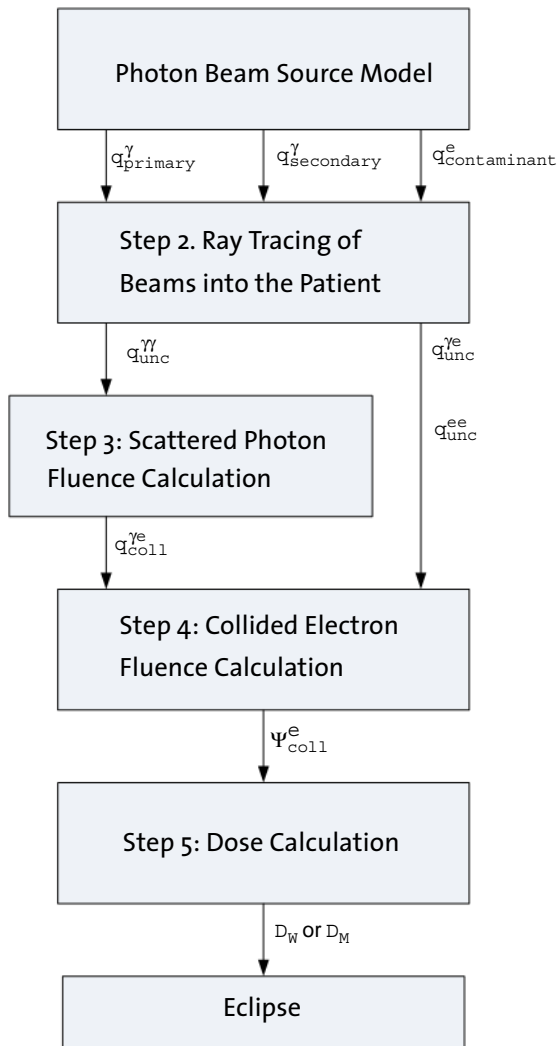
Figure 18   Acuros XB Calculation Steps

where:

$q^{\gamma}_{\text{primary}}$	=	Primary photon source (from Photon Beam source model)
$q^{\gamma}_{\text{secondary}}$	=	Secondary photon source (from Photon Beam source model)
$q^{e}_{\text{contaminant}}$	=	Electron contamination source (from Photon Beam source model)
$q^{\gamma\gamma}_{\text{unc}}$	=	First scattered photon source (produced from primary and secondary photon sources)
$q^{\gamma e}_{\text{unc}}$	=	First scattered electron source (produced from primary and secondary photon sources)
q^{ee}_{unc}	=	First collided electron source (produced from electron contamination source)
$q^{\gamma e}_{\text{coll}}$	=	Collided electron source (produced from scattered photon interactions)
Ψ^{e}_{coll}	=	Angular electron fluence
D_W	=	Dose to water
D_M	=	Dose to medium

Acuros XB is described in more detail in the following sections. For information on the Photon Beam source model, see Chapter 4, "Photon Beam Source Model," on page 45. For more information on calculation options, see Chapter 3, "Implementation of AAA and Acuros XB in Eclipse," on page 30.

Background of the Acuros XB Algorithm

The impetus behind the development of explicit LBTE solution methods in general was to provide a rapid alternative to Monte Carlo simulations, which often require long calculation times. Similarly, many of the methods contained within Acuros XB were originally developed in a prototype solver as part of research in the X-Division of Los Alamos National Laboratories. The prototype solver developed at Los Alamos National Laboratories, called Attila, was co-authored by the founders of Transpire, Inc[18, 19].

Transpire, Inc. established an exclusive licensing agreement to commercialize the prototype Attila solver and, since 2002, has continually developed it for commercial use as a general purpose radiation transport software product. Attila has been extensively validated for a broad range of applications, including publications presenting the application of Attila towards external photon beam dose calculations[20, 21]. Acuros XB builds upon many of the methods in Attila, but represents a ground-up solver rewrite in which the methods were adapted and optimized for external photon beam dose calculations.

18. Wareing TA, McGhee JM, Morel JE, Pautz SD, "Discontinuous Finite Element Sn Methods on Three-Dimensional Unstructured Grids", Nucl. Sci. Engr., Volume 138, Number 2, July 2001.
19. Wareing TA, Morel JE, McGhee JM, "Coupled Electron-Photon Transport Methods on 3-D Unstructured Grids", Trans Am. Nucl. Soc., Washington D.C., Vol 83, 2000.
20. K. Gifford, J. Horton, T. Wareing, G. Failla, F. Mourtada, "Comparison of a finite-element multigroup discrete-ordinates code with Monte Carlo for radio-therapy calculations", Phys. Med. Biol., May 2006, 7;51(9):2253-65.
21. O. Vassiliev, T. Wareing, I. Davis, J. McGhee, D. Barnett, J. Horton, K. Gifford, G. Failla, U. Titt, F. Mourtada, "Feasibility of a multigroup deterministic solution method for three-dimensional radiotherapy dose calculations", Int J Radiat Oncol Biol Phys., Sep 2008, 1;72(1):220-7.

Acuros XB Solution Methods

For a spatial domain with volume, v, and surface, δv, Acuros XB solves the time-independent three-dimensional system of coupled Boltzmann transport equations (LBTE), which are given by (for brevity the dependent variables have been suppressed in the equations):

Eq. 19
$$\hat{\Omega} \cdot \vec{\nabla} \Psi^{\gamma} + \sigma_t^{\gamma} \Psi^{\gamma} = q^{\gamma\gamma} + q^{\gamma}$$

Eq. 20
$$\hat{\Omega} \cdot \vec{\nabla} \Psi^e + \sigma_t^e \Psi^e - \frac{\partial}{\partial E} S_R \Psi^e = q^{ee} + q^{\gamma e} + q^e$$

Eq. 21
$$\vec{r} \in V, \ \hat{\Omega} \in 4\pi, \text{ and } E > 0$$

where

Ψ^{γ}	=	Angular photon fluence (or flux if not time integrated), $\Psi^{\gamma}(\vec{r},E,\hat{\Omega})$, as a function of position, $\vec{r} = (x,y,z)$, energy, E, and direction, $\hat{\Omega} = (\mu,\eta,\zeta)$
Ψ^e	=	Angular electron fluence, $\Psi^e(\vec{r},E,\hat{\Omega})$
$q^{\gamma\gamma}$	=	Photon-to-photon scattering source, $q^{\gamma\gamma}(\vec{r},E,\hat{\Omega})$, which is the photon source resulting from photon interactions
q^{ee}	=	Electron-to-electron scattering source, $q^{ee}(\vec{r},E,\hat{\Omega})$, which is the electron source resulting from electron interactions
$q^{\gamma e}$	=	Photon-to-electron scattering source, $q^{\gamma e}(\vec{r},E,\hat{\Omega})$, which is the electron source resulting from photon interactions
q^{γ}	=	External photon source, $q^{\gamma}(E,\hat{\Omega})$. This source term represents all photons coming from the machine source model.
q^e	=	External electron source, $q^e(E,\hat{\Omega})$. This source term represents all electrons coming from the machine source model.
σ_t^{γ}	=	Macroscopic photon total cross section, $\sigma_t^{\gamma}(\vec{r},E)$, units of cm^{-1}
σ_t^e	=	Macroscopic electron total cross section, $\sigma_t^e(\vec{r},E)$, units of cm^{-1}
S_R	=	Restricted collisional plus radiative stopping power, $S_R(\vec{r},E)$

Equation 19 and Equation 20 on page 129 solve for the photon and electron transport, respectively. Equation 19 and Equation 20 are subject to all possible standard boundary conditions on surface, δv. In Acuros XB, all external surfaces have vacuum or non-reentrant boundary conditions applied:

Eq. 22 $\qquad \Psi^\gamma = 0$, for $\hat{\Omega} \cdot \vec{n} < 0$,

Eq. 23 $\qquad \Psi^e = 0$, for $\hat{\Omega} \cdot \vec{n} < 0$

where

$\vec{n}$ $\qquad$ = $\qquad$ Normal vector to surface δv, pointing outward normal from the computational grid boundary.

The first term on the left hand side of Equation 19 and Equation 20 on page 129 is the streaming operator. The second term on the left hand side of Equation 19 and Equation 20 is the collision or removal operator. Equation 20 is the Boltzmann Fokker-Planck transport equation, which is solved for the electron transport.

In Equation 20, the third term on the left represents the continuous slowing down (CSD) operator, which accounts for coulomb 'soft' electron collisions. The right hand side of Equation 19 and Equation 20 represent the scattering, production, and external source terms. The external source terms, q^γ and q^e, represent the photons and electrons output from the photon beam source model, including the primary source, the second source, and the electron contamination source.

The scattering and production sources are defined by:

Eq. 24

$$q^{\gamma\gamma}(\vec{r},E,\hat{\Omega}) = \int_0^\infty dE' \int_{4\pi} d\Omega' \sigma_s^{\gamma\gamma}(\vec{r},E' \to E, \hat{\Omega} \cdot \hat{\Omega}') \Psi^\gamma(\vec{r},E',\hat{\Omega}')$$

Eq. 25

$$q^{\gamma e}(\vec{r},E,\hat{\Omega}) = \int_0^\infty dE' \int_{4\pi} d\Omega' \sigma_s^{\gamma e}(\vec{r},E' \to E, \hat{\Omega} \cdot \hat{\Omega}') \Psi^\gamma(\vec{r},E',\hat{\Omega}')$$

Eq. 26

$$q^{ee}(\vec{r},E,\hat{\Omega}) = \int_0^\infty dE' \int_{4\pi} d\Omega' \sigma_s^{ee}(\vec{r},E' \to E, \hat{\Omega} \cdot \hat{\Omega}') \Psi^e(\vec{r},E',\hat{\Omega}')$$

where

$\sigma_s^{\gamma\gamma}$	=	Macroscopic photon-to-photon differential scattering cross section
$\sigma_s^{\gamma e}$	=	Macroscopic photon-to-electron differential production cross section
σ_s^{ee}	=	Macroscopic electron-to-electron differential scattering cross section

The basic assumptions used in Equation 19 and Equation 20 on page 129 are briefly summarized as follows. Both charged pair production secondary particles are assumed to be electrons instead of one electron and one positron. Also, the partial coupling technique is assumed, whereby photons can produce electrons, but electrons do not produce photons. Regarding the latter, the energy from photons produced by the electrons is accounted for, but assumed to be deposited locally.

These assumptions have only a minor effect on the energy deposition field, and are similar to those employed in clinical Monte Carlo codes. A primary assumption of Equation 20 on page 129 is that the Fokker-Planck operator (of which the CSD operator is the first order term), is used for coulomb, or "soft", interactions that result in small-energy losses. Catastrophic interactions that result in large energy losses are represented with the standard Boltzmann scattering.

To represent the anisotropic behavior of the differential scattering and production sources, the macroscopic differential scattering cross sections are expanded into Legendre polynomials, $P_l(\mu_0)$, where $\mu_0 = \hat{\Omega} \cdot \hat{\Omega}'$. This expansion allows the differential scattering or production cross section(s) to be expressed as:

Eq. 27

$$\sigma_s^{\gamma\gamma/\gamma e/ee}(\vec{r},E' \to E,\hat{\Omega} \cdot \hat{\Omega}') = \sum_{l=0}^{\infty} \frac{2l+1}{4\pi}\sigma_{s,l}^{\gamma\gamma/\gamma e/ee}(\vec{r},E' \to E)P_l(\mu_0)$$

where

$\sigma_{s,l}$ = Macroscopic differential scattering cross section for legendre moment l

Similarly, the angular fluence appearing in the scattering source is expanded into spherical harmonics moments:

Eq. 28

$$\Psi(\vec{r},E',\hat{\Omega}') = \sum_{l=0}^{\infty} \sum_{m=-l}^{l} \phi_{l,m}(\vec{r},E') Y_{l,m}(\hat{\Omega}')$$

where

$Y_{l,m}(\hat{\Omega})$ = Spherical harmonic functions

l,m = Angular indices

$\phi_{l,m}(\vec{r},E')$ = Spherical harmonics moments of the angular fluence, calculated as:

$$\int_{4\pi} d\Omega' Y^*_{l,m}(\hat{\Omega}')\Psi(\vec{r},\hat{\Omega}',E) ,$$

where * denotes the complex conjugate

The equations above are exact. Additionally, for purely isotropic scattering, $l = 0$ is also exact. However, Acuros XB sets a limit on the scattering order, $0 < l \leq 7$, and hence the number of spherical harmonic moments kept in the scattering/production source. Using the Legendre addition theorem, the scattering and production sources become:

Eq. 29

$$q^{\gamma\gamma/\gamma e/ee}(\vec{r},E,\hat{\Omega}) = \sum_{l=0}^{7} \sum_{m=-l}^{l} \int_0^{\infty} dE' \sigma_{s,l}^{\gamma\gamma/\gamma e/ee}(\vec{r},E' \to E)\phi_{l,m}(\vec{r},E') Y_{l,m}(\hat{\Omega})$$

Photon and Electron Sources

The external photon and electron sources, q^γ and q^e, are modeled as anisotropic point sources in Acuros XB. At each static beam phase space, a separate point source exists for each of the three sources of the photon beam source model. For the primary source, the anisotropy of q^γ is described through a 2D fluence grid, in which both the particle fluence and energy spectra are spatially variable. For the second source, the anisotropy of q^γ is described through a 3D fluence grid, and the energy spectra is spatially constant. For the electron contamination source, the anisotropy of q^e is described through a 3D fluence grid, and the energy spectra is spatially constant. All point sources are located at the target for the respective control static beam.

For a photon point source, $q^\gamma(E,\hat{\Omega})$ located at position, $\vec{r}_p$, Equation 19 and Equation 20 on page 129 become:

Eq. 30
$$\hat{\Omega} \cdot \vec{\nabla} \Psi^\gamma + \sigma_t{}^\gamma \Psi^\gamma = q^{\gamma\gamma} + q^\gamma(E,\hat{\Omega})\delta(\vec{r} - \vec{r}_p)$$

Eq. 31
$$\hat{\Omega} \cdot \vec{\nabla} \Psi^e + \sigma_t^e \Psi^e - \frac{\partial}{\partial E} S_R \Psi^e = q^{ee} + q^{\gamma e} + q^e$$

where

δ =   Dirac-delta function

The principle of linear superposition may be used to define the photon angular flux as the summation of uncollided and collided flux components,

Eq. 32
$$\Psi^\gamma \equiv \Psi_{unc}^\gamma + \Psi_{coll}^\gamma$$

where

Ψ_{unc}^γ =   Uncollided, or unscattered, photon angular flux. Refers to photons which have not yet interacted with the patient/phantom.

Ψ_{coll}^γ =   Collided, or scattered, photon angular flux. Refers to photons which were produced or scattered by a photon interaction in the patient/phantom.

Substituting Equation 32 on page 133 into Equation 30 and Equation 31 on page 133, and using linear superposition leads to the following system of transport equations:

Acuros External Beam Algorithm (Acuros XB) for Photons

Eq. 33

$$\hat{\Omega} \cdot \vec{\nabla} \Psi_{\text{unc}}^{\gamma} + \sigma_t^{\gamma} \Psi_{\text{unc}}^{\gamma} = q^{\gamma}(E,\hat{\Omega}) \delta(\vec{r} - \vec{r}_p)$$

Eq. 34

$$\hat{\Omega} \cdot \vec{\nabla} \Psi_{\text{coll}}^{\gamma} + \sigma_t^{\gamma} \Psi_{\text{coll}}^{\gamma} = q_{\text{coll}}^{\gamma\gamma} + q_{\text{unc}}^{\gamma\gamma}$$

Eq. 35

$$\hat{\Omega} \cdot \vec{\nabla} \Psi^e + \sigma_t^e \Psi^e - \frac{\partial}{\partial E} S_R \Psi^e = q^{ee} + q_{\text{coll}}^{\gamma e} + q_{\text{unc}}^{\gamma e} + q^e$$

where

$q_{\text{unc}}^{\gamma\gamma}$	=	First scattered photon source. Refers to photons which are created or scattered from the first photon interaction inside the patient/phantom.
$q_{\text{coll}}^{\gamma\gamma}$	=	Secondary scattered photon source. Refers to photons which are created or scattered from secondary photon interactions inside the patient/phantom.
$q_{\text{unc}}^{\gamma e}$	=	First scattered electron source. Refers to electrons which are created or scattered from the first photon interaction inside the patient/phantom.
$q_{\text{coll}}^{\gamma e}$	=	Secondary scattered electrons source. Refers to electrons which are created or scattered from secondary photon interactions inside the patient/phantom.

The solution to Equation 33 through Equation 35 on page 134 is identical to that of Equation 30 and Equation 31 on page 133. However, Equation 33 is decoupled from Equation 34 and Equation 35 and can be solved independently. Once the solution to Equation 33 is known, q_{unc}^{γ} and $q_{\text{unc}}^{\gamma e}$ are formulated and considered fixed sources in Equation 34 and Equation 35, which then may be solved within the patient/phantom geometry.

A property of Equation 33 is that $\Psi_{\text{unc}}^{\gamma}$ can be solved for analytically. Doing so provides the following expression for the uncollided photon angular flux from a point source:

Eq. 36

$$\psi_{\text{unc}}^{\gamma}\ (\vec{r}, E, \hat{\Omega}) = \delta(\hat{\Omega} - \hat{\Omega}_{\vec{r}, \vec{r}_p}) \frac{q^{\gamma}(E, \hat{\Omega})\, e^{-\tau(\vec{r}, \vec{r}_p)}}{4\pi \left| \vec{r} - \vec{r}_p \right|^2}$$

where

$\hat{\Omega}_{\vec{r}, \vec{r}_p}$ $=$ $\dfrac{\vec{r} - \vec{r}_p}{\left| \vec{r} - \vec{r}_p \right|}$, where $\vec{r}_p$ and $\vec{r}$ are the source and destination points of the ray trace, respectively.

$\tau(\vec{r}, \vec{r}_p)$ $=$ The optical distance (measured in mean-free-paths) between $\vec{r}$ and $\vec{r}_p$.

The electron contaminant source is modeled in a similar manner to the above, but with the inclusion of the CSD operator to account for charged particle interactions.

Acuros XB discretizes in space, angle, and energy to solve Equation 34 through Equation 36 on page 135. The discretization methods are summarized below.

Spatial Discretization

For spatial discretization, the computational volume domain, v, is subdivided into variable sized Cartesian elements, where material properties are assumed to be constant within each computational element. The computational grid in Acuros XB is spatially variable; the local element size is adapted to achieve a higher spatial resolution inside the beam, with reduced resolution in lower dose and lower gradient regions outside the beam penumbra.

Internally Acuros XB employs a finer resolution (equal to the user requested dose grid resolution h) to calculate the electron fluence inside the primary volume of interest (PVOI) and a coarser resolution (equal to 2xh) outside the PVOI. The PVOI is defined as the volume where the dose is estimated to be 10% or more of the maximum dose for static fields, or plans containing static fields, and 15% or more of the maximum dose for non-short arc fields, or plans containing non-short arc fields. A non-short arc field has more than 20 calculation directions and spans an arc of more than 10 degrees.

Commonly referred to as adaptive mesh refinement (AMR), the mesh is limited to refinement in factors of 2 (from one level to the next) in any direction, allowing for localized refinement to resolve areas of

sharp gradients. Equation 34 and Equation 35 on page 134, which solve for the collision components, are discretized using a linear discontinuous Galerkin finite-element method[22], providing a linear solution variation throughout each element, with discontinuities permitted across element faces.

The first scattered photon and first produced electron sources in Equation 36 are also represented as linear varying functions in each element, since these sources are used for the linear discontinuous discretization of Equation 34 and Equation 35 on page 134. To accurately integrate these first scattered sources, the analytic solution is computed at a density inside the primary beam and penumbras of at least 8 ray traces per output grid voxel.

Energy Discretization

Energy discretization is performed through the standard multigroup method[17], which is used in both the energy dependence of Equation 34 on page 134 and Equation 36 on page 135 and the Boltzmann scattering in Equation 35 on page 134. In energy, the energy derivative of the continuous slowing down (CSD) operator in Equation 35 is discretized using the linear discontinuous finite-element method[23]. The Acuros XB cross section library includes 25 photon energy groups and 49 electron energy groups, although not all groups are used for energies lower than 20 MV.

Angular Discretization

For spatially transporting the scattered particle field in the patient, the discrete ordinates method is used to discretize in angle[22]. The discrete ordinates method consists of requiring Equation 34 and Equation 35 on page 134 to hold for a fixed number of directions, $\hat{\Omega}_n$. These discrete directions are chosen from an angular quadrature set that also serves to compute the angular integrals in Equation 26 on page 131 for the generation of the scattering source.

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22. Lewis EE, Miller WF, "Computational methods of neutron transport", Wiley, New York, 1984.
23. Wareing TA, Morel JE, McGhee JM, "Coupled Electron-Photon Transport Methods on 3-D Unstructured Grids", Trans Am. Nucl. Soc., Washington D.C., Vol 83, 2000.

Square-Tchebyshev legendre quadrature sets are used and the quadrature order ranges from N=4 (32 discrete angles) to N=16 (512 discrete angles). The angular quadrature order varies both by particle type and energy. Higher energy particles have longer mean free paths, or ranges for electrons, and thus for each particle type, the angular quadrature order is increased with the particle energy.

A special mode is triggered in cases where a total volume of low density material (density below 0.12 g/cc) larger than approximately 250 cm^3 is present inside the body structure. When triggered, this mode will improve accuracy in large volumes of low density material. These conditions are typically only present in non-clinical heterogeneous phantom geometries.

Spatial Transport Cutoff

Acuros XB employs a spatial cutoff for electron energies below 200 keV, and for photon energies below 1 keV. When a particle passes below the cutoff energy, it is assumed to deposit all of its energy in the corresponding dose grid voxel.

Fluence to Dose Conversion

Once the electron angular fluence is solved for all energy groups, the dose in any output grid voxel, *i*, of the problem is obtained through the following:

Eq. 37

$$D_i = \int_0^\infty dE \int_{4\pi} d\hat{\Omega} \frac{\sigma_{ED}^e \ (\vec{r}, E)}{\rho(\vec{r})} \psi^e(\vec{r}, E, \hat{\Omega})$$

where

D_i	=	Dose in voxel *i*
σ_{ED}^e	=	Macroscopic electron energy deposition cross sections in units of MeV/cm.
ρ	=	Material density in g/cm^3

When dose to medium is calculated, σ_{ED}^e and ρ are based on the material properties of output grid voxel, *i*. When dose to water is calculated, σ_{ED}^e and ρ are based on water.

As described above, Acuros XB calculates the energy dependent electron fluence based on the material properties of the patient, regardless of whether dose to water or dose to medium is selected. When dose to water is selected, in non-water materials this is analogous to calculating the dose received by a volume of water which is small enough to not significantly perturb the energy dependent electron fluence. Due to the very short range of low energy electrons, this volume may be much smaller than either the output dose grid voxel size or detectors used to experimentally measure dose to water. This effect is most significant for non-biologic, high density materials such as aluminum, titanium, and steel. For biologic materials, the effect is most significant in bone. In such cases, when comparing Acuros XB to experimental measurements of dose to water, it is recommended to explicitly model a small water volume representing the detector in Acuros XB.

Both Acuros XB and Monte Carlo methods calculate dose to medium based on energy deposition, and produce very similar results. When calculating dose to water in non-water materials, Acuros XB and Monte Carlo methods employ different approaches. The approach employed by Acuros XB is described in the above. Monte Carlo methods directly calculate dose to medium, and generally employ stopping power ratios to convert dose to medium to dose to water[24].

The figure shows a comparison between energy deposition ratios (water/medium)[25] and collisional stopping power ratios (water/medium)[26] in different biologic materials as a function of electron energy. The energy deposition ratios (left in the figure) show the ratio of dose to water/dose to medium which would be calculated by Acuros XB, and the collisional stopping power ratios (right in the figure) show the ratio of dose to water/dose to medium which would generally be calculated by Monte Carlo methods.

24. JV Siebers, PJ Keall, AE Nahum, and R Mohan, "Converting absorbed dose to medium to absorbed dose to water for Monte Carlo based photon beam dose calculations", Phys. Med. Biol. 45 (2000) 983-995.

25. Lorence L, Morel J, and Valdez G, "Physics Guide to CEPXS: A Multigroup Coupled Electron-Photon Cross Section Generating Code," SAND89-1685, Sandia National Laboratory, 1989.

26. http://www.nist.gov/physlab/data/star/index.cfm
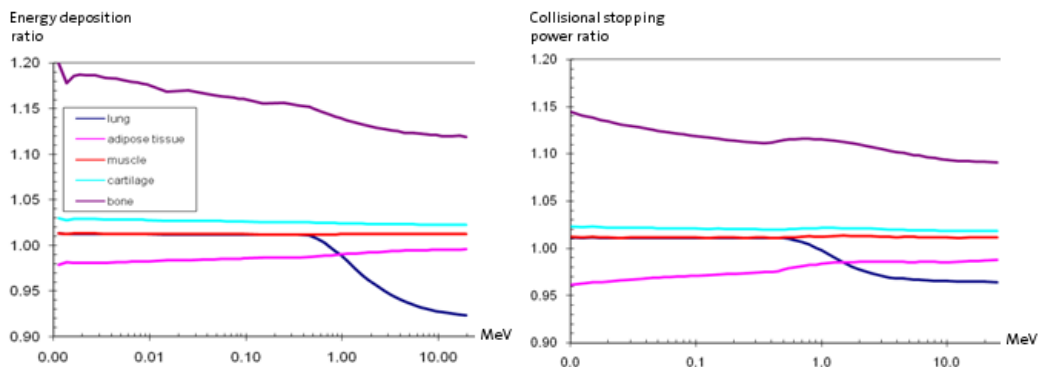
Figure 19 (left) Energy deposition ratios (water/medium) and (right) collisional stopping power ratios (water/medium), as a function of electron energy (MeV).

Material Properties

The fundamental data used by Acuros XB are macroscopic atomic cross sections. A macroscopic cross section is the probability that a particular interaction will occur per unit path length of particle travel, so it has units of cm^{-1}. Macroscopic cross sections are composed from two values: the microscopic cross section for a given interaction (generally given in barns/atom = 10^{-24} cm^2/atom and symbolized by $\tilde{\sigma}$) and the mass density of the material (ρ, given in g/cm^3). The expression for the macroscopic cross section, σ, is:

Eq. 38 $\qquad \sigma = \frac{N_\alpha \rho}{M} \tilde{\sigma}$

where

M	=	Mass of the atom in atomic mass units (AMU)
N_α	=	Avogadro's number

Acuros XB uses coupled photon-electron cross sections produced by CEPXS[27]. For photon interactions, CEPXS includes Compton scatter (also known as incoherent scatter), the photo-electric effect, and pair production. CEPXS does not account for Rayleigh scatter (also known as coherent scatter). Additionally, the energy from Bremsstrahlung

27. Lorence L, Morel J, and Valdez G, "Physics Guide to CEPXS: A Multigroup Coupled Electron-Photon Cross Section Generating Code," SAND89-1685, Sandia National Laboratory, 1989.

photons, produced by electron interactions inside the patient, is discarded. The effect of these assumptions is insignificant for dose distributions at energies typical in photon beam radiotherapy.

CT to Material Mapping

In order to perform a calculation, Acuros XB must know the macroscopic cross section in each element in its computational grid. Eclipse provides Acuros XB with a mass density and material type in each voxel of the image grid (see "General About Eclipse Algorithms" on page 22).

The Acuros XB algorithm stops the calculation if an HU value in the CT image is higher than or equal to the maximum HU value defined in the CT calibration curve. The volume spanned by CT image pixels whose mass density (derived either from the HU value in the image or assigned to a structure) exceeds the maximum mass density of the materials used in automatic conversion (3.0 g/cm^3) is calculated. If this volume is higher than a user defined maximum volume for automatic material assignment to high density artifacts, the calculation is prevented until a material is assigned via a structure. For smaller volumes, automatic conversion to a user defined material takes place. This is to prevent incorrect material assignment to a significant volume of a high density material.

For higher densities, extend the calibration curve so that it includes the highest density material you think of using. The highest density supported by Acuros XB is 8 g/cm^3, stainless steel. The CT calibration curve should be extended at least to a density of 8.1 g/cm^3 to cover all materials.

Any noise present in the CT image is transformed directly into a noise in the mass density map of the image. In the regions of the CT image where the mass density is very close to a minimum/maximum value of two materials (e.g., 1.075 g/cm^3, see Table 24) the discrete nature of the material assignment and the noise in the CT image may lead to a rapid alternation between two different material assignments. Depending on the strength of the noise and on the calculation grid size this effect may be seen in these regions as a slight noise in the dose distribution.

Overlapping Density Ranges in CT to Material Mapping

If the mass density ρ derived from the HU value is within the range of two materials A and B that are used in automatic CT to material conversion, a mixture of these two materials is assigned to the voxel. Assume that the minimum and maximum density of material A are $\rho_{min,A}$ and $\rho_{max,A}$, respectively, and those of material B are $\rho_{min,B}$ and $\rho_{max,B}$, and that $\rho_{max,A} > \rho_{min,B}$ and $\rho_{min,A} < \rho_{min,B}$. The overlapping range is from $\rho_{min,B}$ to $\rho_{max,A}$. The percentage of material A will be

$100\% \times \dfrac{\rho_{max,A} - \rho}{\rho_{max,A} - \rho_{min,B}}$. In other words, when materials A and B overlap,

there is a linear change from 100% material A to 100% material B.

Handling of Structures with Density and Material Assignments

Acuros XB resamples the CT image received from the Eclipse client in the following way: if the pixel size in each slice is smaller than the calculation grid size, the slices are used as is. Otherwise, they are resampled into the calculation grid. If the slice spacing is larger than the calculation grid size, extra slices are created so that the slice spacing of the new CT image is as close to the calculation grid size as possible. For more information on the calculation grid, see Chapter 3, Section "Calculation Options" on page 39.

During Acuros XB calculation, the average mass density and material is calculated in each voxel of the internal CT image grid. If the structure boundary divides a voxel so that only a part of the voxel belongs to the structure, the density of the voxel will be a weighted average of the density of the structure and the density that the voxel would have received otherwise (which may be derived from another overlapping structure or from the CT image). Similarly, the material of this boundary voxel will be a mixture of two materials with the percentages derived from the volume fractions into which the voxel is subdivided. However, note that each voxel material will be described as a mixture of at most two materials.

Supported Materials

The list of supported materials with associated density ranges is provided in the table.

Table 24 Material Mass Densities

Material	Density		
	Minimum (g/cm³)	Default (g/cm³)	Maximum (g/cm³)
Automatic CT to material conversion			
Air (STP)	0.0012	0.0012	0.0204
Lung (ICRP 1975)	0.0110	0.26	0.6242
Adipose Tissue (ICRP 1975)	0.5539	0.92	1.0010
Muscle, Skeletal (ICRP 1975)	0.9693	1.05	1.0931
Cartilage (ICRP 1975)	1.0556	1.10	1.60
Bone (ICRP1975)	1.10	1.85	3.00
Manual material assignment			
Aluminum	2.2750	2.70	3.56
Titanium Alloy	3.56	4.42	6.21
Stainless Steel	6.21	8.00	8.00
Water	0.0012	1.00	3.00
Wood	0.30	0.70	1.00
Cork	0.10	0.19	0.40
Polystyrene	0.59	1.05	1.0750
Epoxy		1.04	
PMMA		1.19	
Radel		1.30	
PEEK		1.31	
PVC		1.38	
Acetal		1.42	
PVDF		1.77	
PTFE		2.20	

Each Acuros XB algorithm version comes with a physical material table that lists the material densities used by the algorithm. RT Administration shows the material tables for different Acuros XB algorithm versions. For more information, refer to *RT Administration Reference Guide*.

In the following table, physical materials are defined in terms of atomic cross sections for Acuros XB, given the weight fractions, or chemical formula where applicable.

Table 25 Material Compositions

Material	Element	Weight Fraction
Air (STP)	C	0.000124
	N	0.755268
	O	0.231781
	Ar	0.012827
Lung (ICRP 1975)	H	0.101278
	C	0.102310
	N	0.028650
	O	0.757072
	Na	0.001840
	Mg	0.000730
	P	0.000800
	S	0.002250
	Cl	0.002660
	K	0.001940
	Ca	0.000090
	Fe	0.000370
	Zn	0.000010

Table 25 Material Compositions

Material	Element	Weight Fraction
Adipose Tissue (ICRP 1975)	H	0.119477
	C	0.637240
	N	0.007970
	O	0.232333
	Na	0.000500
	Mg	0.000020
	P	0.000160
	S	0.000730
	Cl	0.001190
	K	0.000320
	Ca	0.000020
	Fe	0.000020
	Zn	0.000020
Muscle, Skeletal (ICRP 1975)	H	0.100637
	C	0.107830
	N	0.027680
	O	0.754773
	Na	0.000750
	Mg	0.000190
	P	0.001800
	S	0.002410
	Cl	0.000790
	K	0.003020
	Ca	0.000030
	Fe	0.000040
	Zn	0.000050

Table 25 Material Compositions

Material	Element	Weight Fraction
Cartilage (ICRP 1975)	H	0.096
	C	0.099
	N	0.022
	O	0.744
	Na	0.005
	Mg	NA
	P	0.022
	S	0.009
	Cl	0.003
	K	NA
	Ca	NA
Bone (ICRP 1975)	H	0.047234
	C	0.14433
	N	0.04199
	O	0.446096
	Mg	0.0022
	P	0.10497
	S	0.00315
	Ca	0.20993
	Zn	0.0001
Aluminum	Al	1
Titanium alloy (Ti6Al4V)[a]	Ti	.90
	Al	.06
	V	.04

Table 25 Material Compositions

Material	Element	Weight Fraction
Stainless Steel	C	0.00080
	Si	0.01000
	P	0.00045
	Cr	0.19000
	Mn	0.02000
	Fe	0.68375
	Ni	0.09500
Water	H	0.111894
	O	0.888106
Wood and Cork	H	0.06216
	C	0.44445
	O	0.49339
Polystyrene	H	0.07742
	C	0.92258
All other plastics: Epoxy, PMMA, Radel, PEEK, PVC, Acetal, PVDF, PTFE	H	0.05011
	C	0.73282
	O	0.14461
	S	0.07246

a. Titanium alloys are commonly used in implants. Dose differences between pure Titanium and Titanium alloy are very small.

Output Dose Grid Control

The user can specify the geometric extents on which Acuros XB will output the 3D dose grid by using the Calculation Volume tool in Eclipse.

Regardless of the output grid size, Acuros XB will account for the effects of photon and electron transport throughout the full CT extents on the dose within the output dose grid. However, Acuros XB will reduce the spatial resolution external to the output dose grid to reduce the calculation time. For more information, see "Spatial Discretization" on page 135.

Through this feature, the user can minimize the Acuros XB dose calculation time by limiting the volume of interest for the dose calculation. For more information, see "Factors Affecting Run Time and Memory Consumption" on page 148.

Discretization Errors

As described earlier, in both Acuros XB and Monte Carlo a trade-off exists between computational speed and accuracy. In Monte Carlo, errors are generally stochastic, which are reduced when solutions are calculated to tighter statistical uncertainties. In Acuros XB, errors are deterministic and primarily result from the discretization resolution in space, angle, and energy.

Energy discretization errors are generally manifested as solution biases present over a large region. Angular discretization errors typically result in 'ray-effects', which are non-physical angular oscillations in the solution. These effects are most pronounced at far distances from localized sources in low density media. Lastly, due to the discontinuous nature of the DFEM spatial differencing used by Acuros XB, spatial discretization errors would typically be manifested by local solution over/under shooting, and caused by the requirement to fit a linear solution in each element while conserving particle balance. The energy, space, and angle discretization settings in Acuros XB are specified internally, and are not under direct user control.

Additional errors may also be present from the internally set convergence tolerances in Acuros XB. These tolerances control how tightly the inner iterations in Acuros XB are converged in energy group. These errors will generally be under 0.1% of the local dose in any element.

Factors Affecting Run Time and Memory Consumption

The factors influencing Acuros XB calculation times and memory consumption are different than those influencing pencil beam and Monte Carlo methods. Acuros XB is similar to Monte Carlo in the sense that calculation times are only weakly dependent on the number of fields.

However, memory consumption in Acuros XB is generally higher than that of other methods such as Monte Carlo. A principal reason for this is the large number of variables that Acuros XB has to solve. Although the output from Acuros XB is only a single dose value for each output voxel, to calculate this it is necessary for Acuros XB to solve for the full angular and energy dependence of the photon and electron fluences throughout the CT extents. The two dominant factors governing Acuros XB memory consumption and calculation time are the output grid voxel size and the volume of the radiation beams over the patient/phantom within the output grid extents.

Both memory consumption and calculation time are approximately inversely proportional to the output grid voxel volume. For example, an output grid voxel size of 1 mm will require approximately 8 times the memory and calculation time compared with 2 mm output grid voxels.

Memory consumption and calculation time are also roughly proportional to the total patient/phantom volume intersected by the beams, including associated penumbra regions. Acuros XB locally refines the calculation grid to resolve the solution field internal to the beams and penumbra in the patient/phantom. External to these regions, where the dose magnitude and gradients are low, the calculation grid is locally coarsened to reduce the computational effort.

The calculation grid is also coarsened in the air regions external to the patient/phantom. The net effect of this behavior is that in a majority of cases, except for small fields in large phantoms, most of the computational effort is dedicated to calculating the photon and electron fluences inside the beams.

Since the calculation grid is also coarsened external the output grid extents, even inside the beams, users can significantly reduce calculation time and memory consumption by decreasing the output grid extents encompassing the beams. Reducing the output grid size

will only have a significant effect when it also reduces the volume of the beams covering the patient/phantom within the output grid. In most cases, the total reduction in calculation time and memory consumption will be proportional to this decrease in volume.

To illustrate this, three calculations of a 10x10 cm^2 field oriented in the z-direction on a 40x40x40 cm^3 phantom are considered. In the first calculation, the output grid volume is equal to the phantom size, 40x40x40 cm^3. In the second calculation, the output grid volume is reduced by half in the depth-wise direction, to 40x40x20 cm^3. Including the effects of beam spreading with increasing distance from the source, the second calculation will generally require less than half the calculation time and memory consumption of the first calculation. In a third calculation, the output grid volume is changed to 20x20x40 cm^3. In this case, the third calculation will not reduce the phantom volume intersected by the beam, and therefore the calculation time or memory consumption will not significantly differ from that of the first calculation.

The calculation time and memory consumption are both only weakly dependent on the number of fields. Even in the range of most RapidArc calculations, 90 to 180 dose calculation directions per field, the dominant contributor to both calculation time and memory consumption is generally in calculating electron and photon transport in the patient/phantom, and not ray tracing of the primary, secondary, or electron contaminant sources into the patient/phantom. However, the ray tracing component is linearly dependent on the number of fields, and for RapidArc cases with increasing numbers of dose calculation directions, ray tracing will eventually become the dominant factor.

There is some dependence on the beam energy for both memory consumption and calculation times. With increasing beam energy, more energy groups are required to achieve an accurate solution, which requires a commensurate increase in both calculation time and memory consumption. As an example, a 20 MV calculation may require approximately 75% more CPU time than the same calculation with 4 MV beams.

Volume II   Other Dose Distribution Calculation Algorithms

Chapter 7   Cone Dose Calculation (CDC) Algorithm

Dose Calculation Model

The Cone Dose Calculation (CDC) algorithm is used in Eclipse Cone Planning to calculate the dose for stereotactic cone applicators used in stereotactic radiosurgery (SRS) treatments.

The CDC algorithm ignores bolus and any non-body structures. In Cone Planning, it is not possible to attach a bolus to an arc field or open a field that contains a bolus.

The CDC algorithm uses Tissue Maximum Ratios (TMR) and Off-Axis Ratios (OAR) to determine the dose at any point within the irradiated volume. This section describes the model with which the CDC algorithm calculates doses, and its limitations.

Outline of Dose Calculation

The dose, D, at any point, P, in the beam is determined as:

Eq. 39

$$D(r, d, SSD, S) = MU \times DR_{ref} \times OF_{TMR_{max}}(S) \times TMR(d,S) \times \left(\frac{SAD}{SSD + d}\right)^2 \times OAR(r,S)$$

where

r	=	Off-axis distance to point of interest
d	=	Depth to location of interest along central axis
SSD	=	Source-to-skin distance
S	=	Nominal diameter of conical collimator
$D(d,r,S)$	=	Dose at location of interest (point 'p' in Figure 20 on page 153).
MU	=	Monitor unit
DR_{ref}	=	Reference dose rate $= \left(\frac{D_{ref}}{MU_{ref}}\right)$, where D_{ref} is the absolute dose in water for the reference field size at the reference point at the calibration depth, expressed in Gray, and where MU_{ref} is the MU given to produce the reference dose for calibration (see Table 27 on page 159).

`OF(S)`	=	Output factor = $\left(\frac{D_S}{D_{ref}}\right)$, where D_S is the dose at a specific point on the central axis (at the isocenter) with depth, d, when conical collimator, S, is used, and where D_{ref} is the dose measured in the same spatial location and d, as D_S, using reference field size.
$OF_{TMR_{max}}(S)$	=	Output factor at $TMR_{max}(S)$, $OF(S) \times \frac{PDD(S, SSD, d_{max})}{PDD(S, SSD, d)} \times \left(\frac{SSD + d_{max}}{SAD}\right)^2$, where d is the depth used to measure `OF(S)`.
`TMR(d,S)`	=	Tissue-maximum ratio, $\left(\frac{D_d}{D_{d_{max}}}\right)$, where $D_{d_{max}}$ is the dose at a specific point on the central axis (at the isocenter), with maximum dose depth d_{max} of tissue equivalent material overlying the point, and where D_d is the dose at the same spatial point with an arbitrary depth, d, of overlying tissue equivalent material.
`SAD`	=	Source-axis distance.
`OAR(r,S)`	=	Off-axis ratio, $\left(\frac{D_r}{D_a}\right)$, where D_a is the dose on the central axis at depth, d, and D_r is the dose at an arbitrary off-axis distance, r, with the same central axis depth, d.

The parameters are illustrated in the figure.
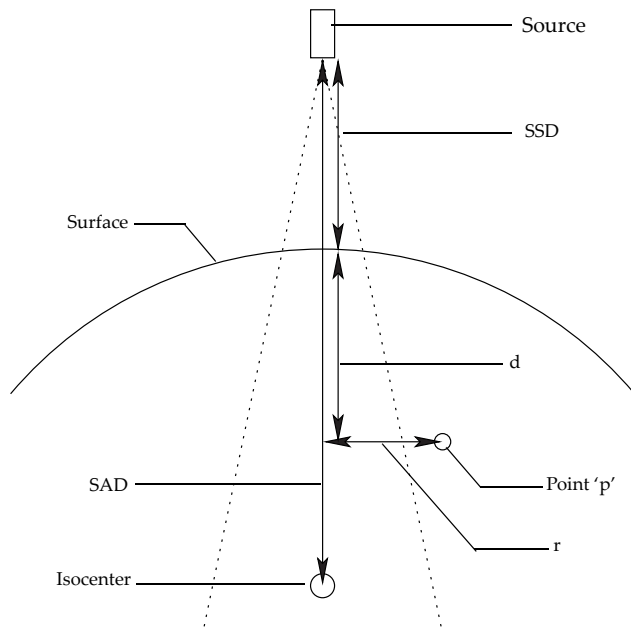
Figure 20   Cone Dose Calculation Geometry

Dose Matrix

When the dose calculation is initiated, dose is calculated for an array of points in two matrices. One of the matrices is coarse, with a point separation of 5.0 mm within the stereotactic space. The other matrix is fine, with a default point separation of 1.0 mm. The point separation of the fine matrix is configurable.

The size of the finer matrix depends on the size of the collimator at the isocenter plane. The distance of the matrix edge from the isocenter equals twice the diameter of the collimator plus an additional 5 mm margin.

Monitor Unit Calculation

The monitor units for a given field are calculated using the equation:

Eq. 40

$$\text{Monitor Units} = \frac{\text{Reference Dose}}{\text{Calibration Factor}}$$

where

Reference Dose $\quad = \quad \dfrac{\text{Repeat Factor} \times \text{Weight Factor}}{\text{TMR}_{\text{ave}}}$

Calibration Factor $\quad = \quad \text{OF}_{\text{TMR}_{\text{max}}}(S) \times \text{DR}_{\text{ref}}$

Repeat Factor $\times$ Weight Factor

$\quad = \quad$ Absolute dose contribution from an arc into the isocenter.

$\text{TMR}_{\text{ave}} \quad = \quad$ Average Tissue Maximum Ratio from the isocenter to the edge of the body contour.

Note that the arcs are given only relative weightings during the planning process, and their true relative dose weightings are not assigned until the time of dose prescription. The number of times the weights need to be multiplied to deliver the prescribed dose is indicated by the ratio of the dose at isocenter to the relative arc weight.

Limitations of the Dose Calculation Model

The dose calculation model has several limitations, described in this section.

Approximating Arc Beams as Static Beams

The CDC algorithm approximates arc dosimetry calculations as multiple static beams. To determine the average TMR for the arc, the system represents the arc as a set of a static beams at user-specified arc increments (between 1-10 degrees). The increments are specified using the Arc Angle Resolution setting in the Calculation tab in Eclipse Cone Planning. The system then averages the TMR from all of these beams

to determine an average for dosimetry calculations. The dose contribution for any particular arc is normalized to 1.0 at its isocenter and then multiplied by its weight.

Note: *The Dosimetry Report print-outs provide an average depth for each treatment arc. These are provided to enable an approximate hand calculation of monitor units. Monitor units calculated by hand using these average depths are not exact, but will be within approximately 2% of the correct values.*

Tissue Inhomogeneity

Tissue inhomogeneity is not taken into consideration, and all CT values are treated as having water equivalent densities once the entry point has been determined. All CT values before the entry point are treated as air. This is true also for beams entering through the base plate or any support structure. The entry point is the first point in the field central axis that hits the body structure. A base plate or a support structure should never be included in the body structure, as the air gap between the body structure and the base plate or support structure is treated as water.

This tissue inhomogeneity limitation is generally acceptable in the head, since most beam paths are through approximately water equivalent densities. For example, skull density is approximately 1.4 times that of water, and the skull thickness is approximately 0.75 cm. This means the equivalent thickness of the skull is $1.4 \times 0.75\,\mathrm{cm} = 1.05\,\mathrm{cm}$, resulting in a 0.3 cm error. For a 6MV beam, attenuation is approximately 4%/1 cm, resulting in a dose error of $0.3\,\mathrm{cm} \times \frac{4\%}{1\,\mathrm{cm}} = 1.2\%$.

Beam paths that traverse air cavities result in slightly higher errors, and you may want to alter beam entry points to avoid large path lengths through these cavities. For beams that enter or exit through cavities, you need to take into account that these areas are treated as having water equivalent densities.

Oblique Entry of Beams

The beam axis is assumed to always be normal to the patient contour, and no consideration is made for beam obliquity. Due to the small field sizes encountered in radiosurgery, this error is negligible.

Backscatter

The absence of backscatter near the cavities or where the beam exists the head is not taken into account. This results in the displayed dose near the surface being higher than the actual dose.

Off-Axis Ratio

The OAR is assumed to be independent of depth, and only dependent on the distance from radiation source. This assumption is valid since the collimators are small and span only the central area of the linear accelerator's broad beam.

Beam Energy Limits

The nominal energy defined for the treatment unit must be between 6MV and 10MV inclusive. During configuration the configuration program verifies that the nominal energy parameter (see Table 26 on page 158) is within these limits.

Valid Range of SSD and Depth

The valid range of SSD values is from 70.1 cm to 100 cm. The sum of SSD and depth of any calculation point must be less than 130 cm.

Configuration of the CDC Algorithm

The input of the Cone Dose Calculation configuration program consists of specific measured beam data and parameter values that are defined by the user. The parameters describe the measurement geometry and the physical characteristics of the beam.

The measured beam data files can be imported into Beam Configuration for the CDC configuration, or you can import existing FastPlan configuration data. For information on the configuration, see "Configuring CDC in Beam Configuration" on page 166.

This section describes the parameters and beam data measurements required for the configuration, the way the CDC configuration program works, and the configuration and measurement geometries.

It also provides step-by-step instructions for configuring the CDC in Beam Configuration, and describes how the configured CDC data can be evaluated.

Note: *When performing measurements and configuring the CDC, notice the following:*

- *The instructions for beam data measurements are recommendations only. Varian Medical Systems is not responsible for incorrect measurements or inaccurate configuration resulting from erroneous measurements.*

- *Clinical physicists responsible for the measurements must always use their own judgment in deciding the level of acceptable accuracy of the measurements in relation to the calculations, and find the compromises needed for each specific accelerator as far as measurements are concerned.*

- *It is important to configure the system so that it corresponds to the characteristics of the treatment machine.*

- *Periodically perform follow-up measurements and compare with the dosimetric beam data used for configuring the beam. If fluctuations are large and the configured beam data no longer represents the average beam delivered by the machine, reconfigure the beam data using the newer dosimetric beam data.*

- *Measure all dosimetric beam data in as stable conditions as possible.*

- *Perform all measurements as accurately as possible.*

- *Use the same file naming conventions in beam data measurements (input files) and in Beam Configuration (Therapy Unit name), and name the input files so that it is easy to match the beam data to the treatment unit during the configuration process.*

- *Due to the small fields used in stereotactic radiosurgery, partial volume effects are noticeable if large volume detectors are used.*

- *Although direct measurement of TMR is possible, it is fairly common practice to measure PDDs and then convert them to TMRs. It is very difficult to measure PDD reliably for very small fields. When PDDs are measured and then converted to TMRs, you need to ensure that the detector remains centered in the field at all depths. Measuring TMR directly is more reliable in these cases since the detector does not move during the measurement.*

- *Commission your beam configuration with high precision. Consider validating the calculation configuration following the guidelines set by IAEA[28]. If you notice anything unexpected in the configured data, trace*

the source of the error to a problem in the measured data, and correct the measured data. Do not proceed to patient treatments until the issues have been resolved.

For detailed information on using Beam Configuration, refer to the *Beam Configuration Reference Guide*. For information on how to select a calculation model for dose calculation in Eclipse Cone Planning, refer to *Cone Planning Online Help*.

Configuration Parameters

Beam Configuration uses measured beam data and a number of parameter values for calculating the configured beam data. Some the parameter values are read from RT Administration, and the rest are defined in Beam Configuration.

General Parameters

The CDC requires that the general treatment unit parameters (in the table) for importing measured beam data and for dose calculation are either read from RT Administration or defined in Beam Configuration. When configuring the CDC, verify that the parameters read from RT Administration are correct, and ensure that no required parameters are missing.

Table 26 General Parameters

Parameter	Description
Therapy unit name	Therapy unit name. Define this parameter in Beam Configuration.
Nominal energy	This parameter is read from RT Administration.
Radiation type	This must be "photon". This parameter is read from RT Administration.
Vendor	This parameter is read from RT Administration.
Source-to-axis distance expressed in cm	This parameter is read from RT Administration.

28. Commissioning and Quality Assurance of Computerized Planning Systems for Radiation Treatment of Cancer, Technical Reports Series No. 430 (IAEA).

Absolute Dose Calibration Parameters

The CDC requires the following absolute dose calibration parameters in Beam Configuration:

Table 27 Absolute Dose Calibration Parameters

Parameter	Description
Absolute dose reference field size [mm]	Size of the reference field used in configuration, expressed in millimeters. This should be the same size that was used to normalize the measured output factors (that is, the field size for which the output factor = 1.0).
Absolute dose calibration depth [mm]	Depth of the reference point used in configuration, expressed in millimeters.
Absolute dose calibration source-phantom distance	Distance between the source and the surface of the phantom (SPD) used during the absolute dose calibration, expressed in millimeters.
Reference dose at calibration depth [Gy]	Absolute dose in water for the reference field size at the reference point at the calibration depth, expressed in Gray.
Reference MU at calibration depth [MU]	MU given to produce the reference dose for calibration.

Required Beam Data Measurements

The CDC needs specific measured beam data for performing dose distribution calculations. All beam data must be measured under the same setup conditions.

For configuring the algorithm, the following measurements are required:

- Absolute Dosimetry for a reference field (for example, a 10 cm × 10 cm open field).
- Output Factors for all cones relative to absolute dosimetry reference field.
- Tissue Maximum Ratio for at least three cones (for example, 10 mm, 20 mm and 30 mm)
- Off-Axis Ratio for at least three cones (These may be measured with the same cones that were used to measure tissue-maximum ratio, but that is not necessary.)

Measurement Methods

There are minimum practical limits to the physical size of detectors used for beam measurements. The recommended detector systems are:

- *Diodes*—Choose a diode with a small active volume (a stereotactic diode) and with an energy response suitable for beam data acquisition.
- *Film*—Film has potentially the best spatial resolution. Note, however, that optical density does not respond to absorbed dose linearly and independently of the beam quality. Read the films with a high class digitizer, so that the spatial resolution of the film as well as the depth of optical density can be maintained.
- *Small Ionization Chambers*—Air filled ionization chambers are not recommended to be used for any measurements if the field size is smaller than four times the greatest dimension of the chamber. Ionization chambers are recommended for absolute dose measurements and for calibrating film and diode detectors in central axis beams that fulfill the field size criteria stated above.
- *Phantom*—Measure the beam data in tissue or water equivalent media.

Absolute Dosimetry Measurements

The absolute dose measurement of the reference field and the output factor measurements must be performed using the same phantom geometry. However, you can use any field size for absolute dosimetry measurements. For more information on the parameters, see "Absolute Dose Calibration Parameters" on page 159.

Output Factor Measurements

Note: *The jaw size defined in the treatment unit configuration must be used for all measurements, and the same jaw size should always be used for treatment. Using a different jaw size will cause the machine output to differ from the conditions defined in CDC configuration and could lead to higher or lower delivered dose. The jaw size should be between 4 and 5.6 cm inclusively.*

The Output Factor (OF) is the relative dose at reference geometry as a function of collimator size, normalized to unity for field size used in the absolute dose calibration (see "Absolute Dosimetry Measurements" on page 160). In other words, the output factor is a relative measurement against the dose calibration for the linear accelerator in use.[29]

The dose calculation algorithm uses the absolute dose calibration and the output factors for calculating monitor units (MU). An output factor is required for every circular collimator you use for radiosurgery.

If you import measurement data from FastPlan, the configuration program reads the output factors from the FastPlan configuration files. The dose calculation algorithm then uses the same reference geometry as FastPlan for calculating MU values. FastPlan assumes the machine is calibrated in such a way that 100 MU produces a dose of 1 Gy at the depth of maximum dose for the reference field.

Tissue Maximum Ratio Measurements

Tissue Maximum Ratio (TMR), in a water phantom irradiated by a photon beam, is the ratio of absorbed dose at any build-up depth along the beam axis to the dose at the same point with the surface of the phantom moved so that the build-up depth is at the depth of maximum absorbed dose. During measurement, the source-to-detector distance should be 100 cm with measurements taken with increasing build-up depth. TMR is a function of depth, beam quality, and collimator geometry.

Any collimator for which data are not entered has its data calculated by linear interpolation and extrapolation from the measured collimator data. While data should be measured for a representative

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29. Consider measuring the absolute dose and output factors in a geometrical setup that is as close to the treatment geometry as possible. For example, for a 6 MV beam: SSD = 95.0 cm and depth to point of interest = 5.0 cm.

set of collimators, the data entered for the minimum set of three collimators is sufficient for Beam Configuration to determine the TMR for all collimators.

Measure the TMR data using a resolution that is as accurate as possible. However, the recommended minimal data set should contain measured data in at most 0.5 cm increments from the surface to 1.0 cm past the point of dose maximum, and after that in at most 1.0 cm increments to define the exponential region to the 20.0 cm build-up depth. This data can be imported to Beam Configuration in w2CAD format.

Correct measurement of TMR is crucial for dose calculation accuracy. Therefore, consider validating the TMR data using at least two instruments which use different physical approaches.

Off-Axis Ratio Measurements

The off-axis ratio (OAR), in a water phantom irradiated by a photon beam, is the ratio of absorbed dose at any point to the absorbed dose on the beam axis at the same depth.

OAR data from at least one source-to-target distance (STD) are required. If more data are provided, these are used for averaging the input data for the fitting routine. Measure the OAR data at the depth of the dose maximum of a cone or deeper (typically, the dose maximum for a 6 MeV beam is at the depth of 1.5 cm) for at least three collimators. Sample the data at least every millimeter (that is, 1.0 mm spacing) regardless of the STD used and the collimator size.

CDC Configuration Program

The CDC configuration program adapts the measured beam data before generating the TMR and OAR configuration data from the adapted measured data.

Adaptation of Measurements in the Configuration

Before calculating the configured beam data, the CDC configuration program verifies the measured beam data and adapts the measured values if necessary. You can review the adapted and original measurements in the Beam Data workspace of Beam Configuration (see "Evaluating the Configured CDC Data" on page 170).

The CDC configuration program performs the following detections and adaptations:

- *Tissue-maximum ratios have negative values (for example, a few of the measurement points are in air)*: These values are removed.
- *Symmetric profiles are provided*: Only values with positive coordinates are used.
- *Tissue-maximum ratio curves or profiles drop to zero before the measurement ends*: These values are removed.
- *Tissue-maximum ratio curves normalized to some other value than 100% at maximum dose*: The curves are re-normalized to 100% at maximum dose.
- *Profiles normalized to some other value than 100% at the central axis*: The curves are re-normalized to 100% at the central axis.
- *Projected X-coordinate of the 50% value of the profile deviates more than 1 mm from the assumed field edge position at the distance of SAD=100cm*: An error message is shown.

Generating TMR Configuration Data from Adapted Measured Data

The CDC configuration program generates adapted TMR data, interpolates it linearly up to 10 mm past the maximum dose, and then fits the data to the expression in the equation. TMR values between the shallowest value entered and 0 mm are obtained by linear extrapolation from the two shallowest data points. TMR values are calculated as follows:

Eq. 41

$$\mathrm{TMR(d)} = A \times \exp(-\mu \times d) + h(d)$$

where

$h(d) =$ $B \times d^b \times \exp\left(-\left(\dfrac{d}{d_1}\right)^{10}\right),$ where $d_1 = 2 \times (d_{max} + 10\,mm)$

is a power law correction to the exponential function required to improve the continuity of the fitted function in the vicinity of d_{max}+10 mm.

d = Depth

d_{max} = Depth of dose maximum.

A, μ, B, b = Curve fitting parameters used in CDC configuration; μ can be considered as the linear attenuation coefficient for the given cone.

The parameters A and μ are obtained by fitting the exponential function to the adapted TMR data starting from the depth $d_{max} + 10\,mm$. Subtracting the resulting exponential curve from the adapted data results in a difference curve that is used for obtaining parameters B and b by fitting the power law function to that difference curve in the interval $d_{max}+10$ mm, d_1.

Any collimator for which data are not entered has its data calculated by power law interpolation and extrapolation from the measured collimator data. While data should be measured for a representative set of collimators, the data entered for the minimum set of three collimators is sufficient for Beam Configuration to determine the TMR for all collimators.

Generating OAR Configuration Data
from Adapted Measured Data

The CDC configuration program generates adapted OAR data and applies a curve fit algorithm using the following double exponential model:

Eq. 42

$$OAR(r) = \begin{cases} 0.5 + 0.5 \times \dfrac{f(r) - f(r0)}{f(0) - f(r0)} & (r \le r_0) \\[2mm] 0.5 \times \dfrac{g(r) - 1}{g(r0) - 1} & (r > r_0) \end{cases}$$

where

r	=	Distance from the central axis to the point of interest
r_0	=	Collimator radius corrected for source-to-target distance
f(r)	=	$(1 - \exp(\alpha_1 \times (r - r0))) \times (1 - \exp(\alpha_2 \times (r - 2 \times r0)))$
g(r)	=	$(1 - \exp(\beta_1 \times (r0 - r))) \times (1 - \exp(-\beta_2 \times r))$

where

$\alpha_1, \alpha_2, \beta_1, \beta_2$	Curve fitting parameters used in CDC configuration

Long tails of measured OAR curves are disregarded. Equation 42 on page 164 is fitted to the data points for which $r < r_{cut\ off}$, where $r_{cut\ off} = 0.75 \times r_0 + 0.5\,(cm)$. This approximates the spot where OAR has dropped below 1.5%.

Within measurable accuracy in the case of cone collimator fields, the shape of a rescaled OAR curve exhibits practically no dependence on the source-to-target distance (STD). Hence, for a given cone size, the OAR curves for all STDs can be obtained from one OAR curve by the following rescaling:

Eq. 43

$$OAR(r, STD_2) = OAR\left(\frac{STD_2}{STD_1} \times r, STD_1\right)$$

Before fitting Equation 42 on page 164 to measured OAR curves, all curves are rescaled according to Equation 43 on page 165 to one reference STD, STD_{ref}.

The resulting fitting parameters are interpolated by power law for all cone sizes. This gives OAR curves for each cone at STD_{ref}. The OAR for any other STD is obtained by using Equation 43 on page 165 again.

Data Generated in the Configuration

After the configuration is completed, the data items shown in the focus window include measured data and generated data.

The following measured data items are shown:

- Measured Output Factors
- Measured Tissue-Maximum Ratios
- Measured Off-Axis Ratios
- Absolute Dose Calibration Parameters
- FastPlan Import Files (This data item is present only when the CDC algorithm has been configured using FastPlan data.)

The CDC configuration program generates the following data:

- Processed Tissue-Maximum Ratios
- Processed Off-Axis Ratios
- Calculated Tissue-Maximum Ratios
- Calculated Off-Axis Ratios
- Gamma Errors for Tissue-Maximum Ratios
- Gamma Errors for Off-Axis Ratios
- Gamma Error Histogram

For information on using this data for evaluating the configured CDC data, see "Evaluating the Configured CDC Data" on page 170.

Configuring CDC in Beam Configuration

The CDC algorithm can be configured by importing new measured beam data into Eclipse or by using existing FastPlan configuration data (from FastPlan version 5.5.0 or later).

Note: *Before starting to configure the algorithm, you need to configure the cone applicators. For instructions, see "Configuring Cone Applicators in RT Administration" on page 172.*

Configuring the CDC by Importing New Measured Data

If you are configuring the CDC algorithm by importing new measured beam data, you need to import the Off-axis Ratio and Tissue-Maximum Ratio data in w2CAD format. For more information on the w2CAD format, see Appendix C on page 326. In addition, you need the absolute dose calibration and output factor data, both of which are added manually.

There are some requirements for the TMR and OAR data files containing the measured data. You need to verify the following in the TMR data file:

- The %TYPE parameter in the heading must be defined as TMR.
- If you have cone collimators with the diameter precision of 0.5 mm, make sure that the decimals are represented correctly in the file. That is, they must not be rounded up or down to the nearest full millimeter.

You need to verify the following in the OAR data file:

- The %TYPE parameter in the heading must be defined as OPP (Open Field Profile).
- You also need to make sure that the %SSD and depth (%DPTH) are defined for all measurements.

To Configure the CDC Using New Measured Data

1. Configure the cone applicators in RT Administration. For instructions, see "To Configure Cone Applicators in RT Administration" on page 172.

2. In Beam Configuration, go to the Beam Data workspace. For instructions on how to use the Beam Configuration, refer to the Eclipse online help system or *Beam Configuration Reference Guide*.

3. Add a new calculation model, beam data container and new beam data.

4. Verify the validity of the treatment unit parameters. For more information on the parameters, see "General Parameters" on page 158.

5. Add a new add-on of type *Cone set*.

6. In the Focus window, right-click the add-on and choose **Match and Assign Add-Ons**.

7. In the match and Assign Add-Ons dialog box, do the following:
   a. Select the beam data row of the cone set.
   b. Select the **In Use** check box.
   c. Under Automatic Match, click **All**.
   d. Click **Close**.

   Review the match to make sure that is valid.

8. In the Focus window, right-click an add-on and choose **Insert > New Absolute Dose Calibration Parameters**.

9. Type in the Absolute dose calibration parameters. For more information, see Table 27 on page 159.

10. In the Focus window, right-click the add-on and choose **Insert > Measured Output factors**.

11. Do the following:
    a. Type the cone sizes and corresponding output factor values in the Measured Output Factors table.
    b. Specify the output factor measurement source-to-phantom distance.
    c. Specify the output factor measurement depth.

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d. Specify the X and Y jaw positions (in mm) that were used during output factor measurement.

12. In the Focus window, right-click the add-on and choose **Import > Measured Tissue Maximum Ratios**.

13. In the **Look in** list box, navigate to the folder containing the files in w2CAD format to be imported and click **OK** to start the import.

    If you notice errors in the measured data, stop the import process. Trace the source of the error to a problem in the measured data, and correct the measured data before resuming the import procedure.

14. Specify the Tissue Maximum Ratio measurement source-to-detector distance.

15. Repeat step 12 and step 13 to import the Off-axis ratios.

16. Right-click the add-on in the focus window and choose **Calculate Beam Data**.

17. Verify the calculated data. For more information, see "Evaluating the Configured CDC Data" on page 170.

    Remember to save and approve your configured beam data. Validate the configured beam data in the Beam Data workspace. If you need to continue the configuration after validating the data, unapprove the data first. For instructions for approving, validating and unapproving beam data, refer to Beam Configuration Reference Guide.

Configuring the CDC by Importing Existing FastPlan Data

Note: *When configuring the CDC by importing existing FastPlan data, only FastPlan version 5.5.0 or later is supported.*

If you want to use existing FastPlan data to configure the CDC algorithm, you need to copy a set of files from the installed FastPlan system to a temporary directory on your computer. When configuring the system, you need to specify where this directory is located. All the files must be copied to the same directory. Note, that you cannot add or modify any data imported from FastPlan (for example, modify cone output factors or add an additional cone to the cone set) in Beam Configuration.

The files you need to copy are the OAR data file, the TMR data file, `.collimators` and `.hwconfig`. The exact names of the OAR and TMR files have been defined during the FastPlan configuration.

You should be able to find the files from the following locations in a FastPlan installation:

- The measured OAR and TMR data files are located in the `$SRSHOME/lib/data` directory. The exact location of this directory depends on how the `$SRSHOME` variable is set in your FastPlan installation. It can be, for example, `/home/linac/`.
- The files `.collimators` and `.hwconfig` are located in the `$SRSHOME/lib/` directory. Note, that these two files start with a full stop (.) which makes them hidden in the Linux operating system by default.

To Configure the CDC Using Existing FastPlan Data

1. Configure the cone applicators in RT Administration. For instructions, see "To Configure Cone Applicators in RT Administration" on page 172.

2. In Beam Configuration, go to the Beam Data workspace. For instructions on how to use the Beam Configuration, refer to the Eclipse online help system or *Beam Configuration Reference Guide*.

3. Add a new calculation model, beam data container and new beam data.

4. Verify that the treatment unit parameters match with the treatment unit you are now configuring. For more information on the parameters, see "General Parameters" on page 158.

5. Add a new add-on of type *Cone set*.

6. In the Focus window, right-click the add-on and choose **Match and Assign Add-Ons**.

7. In the match and Assign Add-Ons dialog box, do the following:
   a. Select the beam data row of the cone set.
   b. Select the **In Use** check box.
   c. Under Automatic Match, click **All**.
   d. Click **Close**.

   Review the match to make sure that is valid.

8. In the Focus window, right-click the add-on and choose **Insert > New FastPlan Import Files**.

   The FastPlan import files - Parameter View opens.

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9. In the first text box, type the path to the temporary directory where you placed the copied configuration files from FastPlan.

10. In the two file name text boxes below, type the names of the TMR and OAR files you copied from FastPlan to the temporary directory.

11. In the Focus window, right-click the add-on an choose **Calculate Beam Data**.

12. Verify the calculated data. For more information, see "Evaluating the Configured CDC Data" on page 170.

13. Check that the following values are set to *FastPlan default value*:

    ■ All values in Absolute Dose Parameters

    ■ Source-Phantom Distance and Detector Depth in output factor measurements.

    Do not change the imported FastPlan data.

    Remember to save and approve your configured beam data. Validate the configured beam data in the Beam Data workspace. If you need to continue the configuration after validating the data, unapprove the data first. For instructions for approving, validating and unapproving beam data, refer to Beam Configuration Reference Guide.

Evaluating the Configured CDC Data

You can evaluate the configured CDC data by reviewing the processed data or by evaluating Gamma error histograms and pointwise gamma errors. You can also create a plan with static fields, and use that for evaluating the configured data.

Evaluating the Adapted Data

The CDC configuration program adapts the measured beam data, for example, by removing unphysical values from the measured curves. The adapted data is called processed data, and it can be reviewed after the configuration program has completed in the Beam Data workspace. Each measured curve has a corresponding processed curve which is used in configuring the beam data. You can see each processed curve individually or through a Compare object displayed in the Focus window. The Compare object shows both curves in the same axis.

Evaluating Gamma Error Histograms

Using the fully configured Eclipse Cone Dose Calculation model, the gamma error[30] is calculated for each processed measurement curve by comparing it with adapted measurement points. For this purpose, the adapted points and calculated curves are superimposed to the same graph, in which the X-axis corresponds to position (mm) and the Y-axis to relative dose (%) as in the figure.
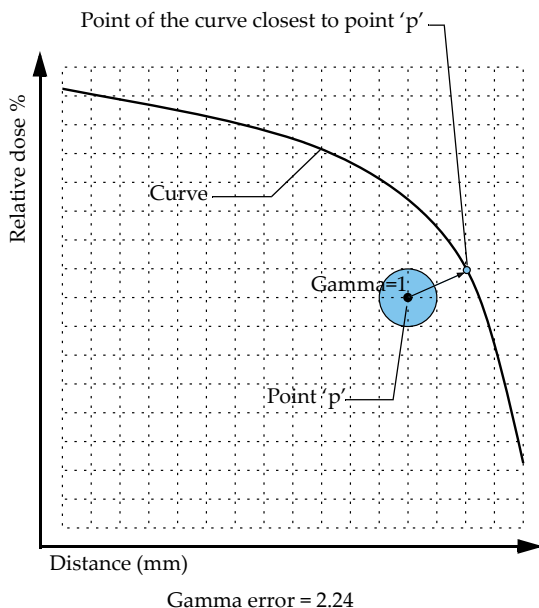

Figure 21 Definition of Pointwise Gamma Error

In the figure, the continuous line represents the calculated profile, the black dot indicates the adapted point 'p', and the blue dot indicates the point closest to point 'p' on the calculated curve.

The CDC configuration program calculates the gamma error for each processed measurement curve at each point by comparing the measured value with the calculated curve. These errors are shown at each point for each measured tissue-maximum ratio curve and profile.

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30. Daniel A. Low, William B. Harms, Sasa Mutic, and James A. Purdy, A technique for the quantitative evaluation of dose distributions. Med. Phys. 25 (5), 656–661 (1998).

The unit used for the relative dose difference is 1% and the unit of the distance is 1 mm. The resulting gamma error in the example in the figure is approximately 2.24.

The gamma error histograms for both TMR and OAR curves are calculated from the pointwise gamma errors.

Configuring Cone Applicators in RT Administration

You need to configure the cone applicators in RT Administration before you start to configure the CDC algorithm.

Note: *The field size defined on the applicator tab during the configuration is important, because it is used in dose calculation. Varian recommends the use of appropriate collimation to narrow the high-dose treatment field. Exceeding this limit will cause extra leakage outside the cone mount, which may result in excessive radiation dose to the patient. For all cones, the field size must be bigger than the diameter of the cone applicator, but it must not exceed 56 mm x 56 mm.*

To Configure Cone Applicators in RT Administration

1. In RT Administration, select the **Radiation & Imaging Devices** tab.

2. Select the treatment machine you are configuring.

3. Select the **Applicator** tab.

4. Click **New Applicator**.

5. On the **General** tab, do the following:
   a. In the **ID** field, type an ID for the cone applicator. The ID is shown in the Eclipse Cone Planning user interface, so it should state the size of the cone.
   b. In the **Name** field, type a name for the cone applicator. This can be identical with the ID.
   c. In the **Internal Code** field, type an integer you want to use as the internal code.
   d. If you are using PAVS and you want to print the bar code labels for the cones, select the **External Verification** check box.

6. Go to the Applicator tab in the Applicator Properties dialog.

7. Do the following:
    a. Make sure that the **Rectangular** check box is not selected.
    b. Select the **Stereotactic** check box.
    c. In the **Field Size** group box enter the cone diameter in centimeters in the **X** text box. The value must be between the defined operating limits. You can adjust the operating limits if necessary.
    d. Define the distance from the source to the head of the applicator.

8. Click the **Slots** tab, and assign a slot from the All Slots available list.

9. Click **OK**.

10. Repeat from step 4 to step 9 for the other cones.

11. Select the **Configured EMT** tab and do the following:
    a. In the **Configured EMT** group, select the Arc technique for the energy mode you want to use.
    b. When the **Add-on Validation for <nn>X / ARC** group is active, select the check boxes of the SRS cones you created to enable the add-on validation for them.
    c. To enable static cone fields, in the **Configured EMT** group, select the Static technique for the energy mode you want to use.
    d. When the **Add-on Validation for <nn>X / STATIC** group is active, select the check boxes of the SRS cones you created to enable the add-on validation for them.

    Repeat this step for all the energy modes you are going to use.

12. Select the Applicator tab and double-click the ID of the applicator you created.

13. Select the Applicator tab in the dialog box, and click **Configure Jaw Size**.

14. Type the jaw sizes for the cone for each energy you configured the cone for, and click **OK**.

    The jaw sizes you define must be the same you used for measuring the Output Factors.

15. Repeat from step 12 to step 14 for all cone applicators you are configuring. You can keep the Applicator Properties dialog box open, and click **Apply** to apply your changes when switching from one applicator to the next.

16. Click **OK** to close the Applicator properties dialog box.

Chapter 8   Electron Monte Carlo (eMC) Algorithm

About the Electron Monte Carlo (eMC) Algorithm

Note: *The eMC algorithm does not support the use of electron arc fields, although Eclipse External Beam Planning allows selecting the ARC field technique for an electron field.*

The electron Monte Carlo (eMC) algorithm is a fast implementation of the Monte Carlo method designed for the calculation of the dose distribution from high-energy electron beams. The eMC algorithm consists of two models:

- Transport model, Macro Monte Carlo (MMC) method[31] that transports electrons and calculates the dose deposited at each point.
- Initial Phase Space model (IPS) that describes the electrons and photons emerging from the treatment head of the linear accelerator.

Since the eMC uses material-specific properties during the particle transport and also when converting absorbed energy to dose, you will see the following text when a plan calculated with eMC is displayed on screen: "*Transport in Medium, Dose to Medium*".

The eMC algorithm does not take trays into account in dose calculation.

If a bolus is linked to a field, the eMC algorithm takes the bolus into account in dose calculation and the dose is visualized inside the bolus. All support structures, for example couches, are ignored. For other structures, only parts that are inside the body structure are taken into account.

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31. Neunschwander H, Mackie TR & Reckwerdt PJ: MMC—a high performance Monte Carlo code for electron beam treatment planning. Phys. Med. Biol. 1995 April; 40(4) 543–574.

Transport Model (MMC)

The transport model of the eMC algorithm is the Macro Monte Carlo (MMC) method, which is an implementation of the Local-to-Global Monte Carlo (LTG MC) method. Basically, the LTG-MC method is a two-step procedure:

1. Conventional MC simulations of electron transport are performed in a well-defined *local* geometry

   The result of these calculations is a library of probability distribution functions (PDFs) of particles emerging from the local geometry. These PDFs are calculated only once for a variety of clinically relevant materials and energies.

2. Absorber-specific MC calculation are performed in a *global* geometry

   Particles are transported through the absorber in macroscopic steps based on the PDFs generated in the local calculation.

Local Geometry Calculations

The MMC method uses spherical volume elements, referred to as *spheres* in this document, for the local calculations (see Figure 22 on page 178). The probability distribution functions (PDFs) were generated in extensive pre-calculations by employing the EGSnrc code system[32]. The pre-calculations simulated the transport of incident electrons of variable energies through macroscopic spheres of sizes and materials likely to be needed for actual MMC calculation. If more than one electron emerges from a sphere, the electron with the highest energy is called the primary electron. The other particles are called secondary particles (secondary electrons and Bremsstrahlung photons). All PDFs are stored in the `mmcDB.dat` file called the MMC database.

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32. The EGSnrc Code System: Monte Carlo Simulation of Electron and Photon Transport. I. Kawrakow and D.W.O. Rogers, Ionizing Radiation Standards, National Research Council of Canada, NRCC Report PIRS-701, April 19, 2002.

MMC Database

For primary electrons, the MMC database contains PDFs for the exit position α, the direction θ and the energy T_f of the emerging primary electrons. There is one PDF for each of these parameters for any combination of

- 5 different materials: air, lung phantom, water, lucite, and solid bone phantom (see Table 28 on page 177)
- 5 spheres of radii r equal to 0.5, 1.0, 1.5, 2.0, 3 mm, respectively
- 30 incident energy values T_i (0.2, 0.4, 0.6, 0.8, 1, 1.5, 2, 3, ... 24, 25 MeV)

For secondary particles (electrons and photons), only the average energy released to these particles per primary electron is stored as a function of the incident primary electron energy T_i in the MMC database. No position or direction parameters are stored for secondary particles.

The table lists the mass densities of the five preset materials.

Table 28 Mass Densities of Preset Materials

Material	Density [kg/dm³]
Air	0.0012
Lung phantom	0.30
Water	1.0
Lucite	1.19
Solid bone phantom	1.84

Example: If the average density within a sphere is 1.12, there is a 12/19 chance that the material is lucite, and a 7/19 chance that it is water.

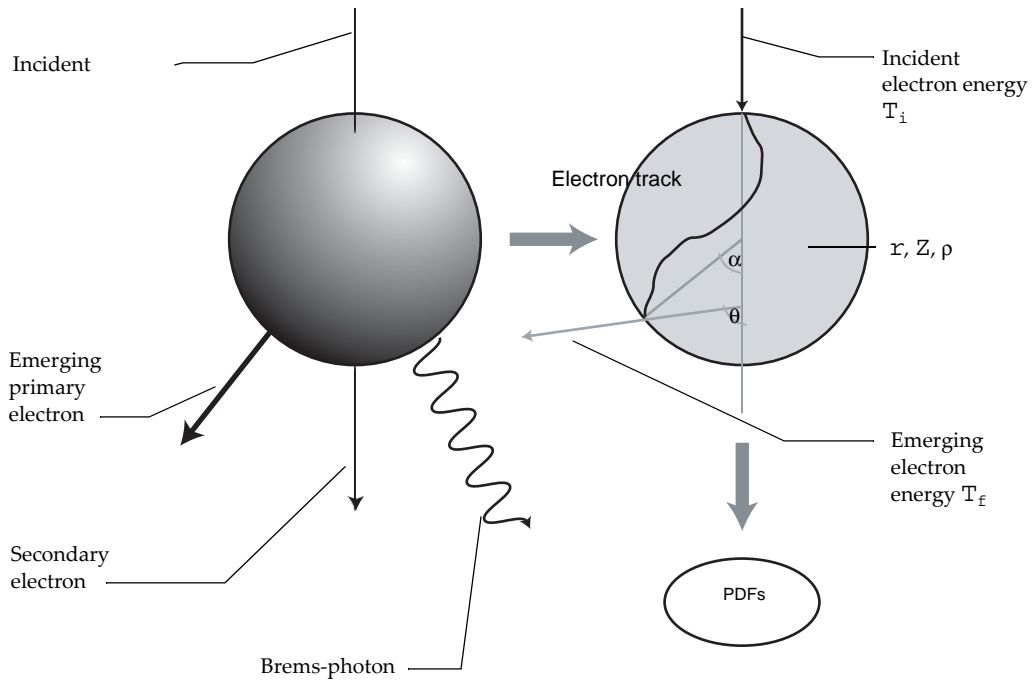The figure shows the local geometry used in the MMC algorithm.

Incident

Incident
electron energy
T_i

Electron track

α

r, Z, ρ

θ

Emerging
primary
electron

Emerging
electron
energy T_f

Secondary
electron

PDFs

Brems-photon

Figure 22   Local Geometry Used in MMC

Preprocessing the Absorber CT Volume

For the MMC sphere-by-sphere transport to work correctly, it is necessary to know, throughout the whole heterogeneous absorber volume, the size and mean density inside the spheres used for the transport steps. For a known sphere size, it is easy to determine the mean sphere density by averaging the density voxels of the absorber volume that are contained within the sphere. This determination of the mean sphere density could be done during preprocessing for each transport step. To avoid this time-consuming procedure, an algorithm was developed that allows the determination of sphere sizes and mean sphere densities at each position in the absorber by preprocessing the whole absorber CT volume prior to the MMC simulation.

The CT volume is first converted into a mass density volume with a user-defined high resolution (0.1–0.5 cm), applying appropriate CT-to-mass density conversion factors. The resulting density volume is then scanned for heterogeneity. To each voxel of the density-volume, a sphere index is assigned that corresponds to the maximal sphere

radius that can be used from the current voxel center without the corresponding sphere reaching into the other material. The process results in

- Small spheres assigned to voxels located near interfaces between materials
- Large spheres assigned to voxels at greater distances from material interfaces (see Figure 23 on page 180)

A voxel of the density volume is considered to be part of a heterogeneous volume if the density ratio of the voxel and its neighbors exceeds a limit (typically 1.5). If the densities in both voxels are below a threshold (typically 0.05 gcm^{-3}), the ratio is not evaluated. Entering a density threshold prevents noise in low-density data from being interpreted as heterogeneity. For densities and density ratios below the limits mentioned above, the MMC algorithm is capable of processing differences in the material without decreasing the step size.

The material assigned to each sphere depends on the average mass density within the sphere. If the average mass density of a sphere is exactly equal to the mass density of one of the preset materials, that preset material is selected for the sphere. If the mass density of a sphere is between two preset material values, the material is randomly selected from these two materials each time a particle enters the sphere. The probability for a material to be selected is proportional to the closeness of a sphere's average mass density to the mass density of the material. The mass densities of the preset materials are listed in Table 28 on page 177. If the mass density of a voxel exceeds the maximum mass density in the eMC database (currently 1.84), scattering may not be based on the correct material. However, the energy loss should be correct within first order.
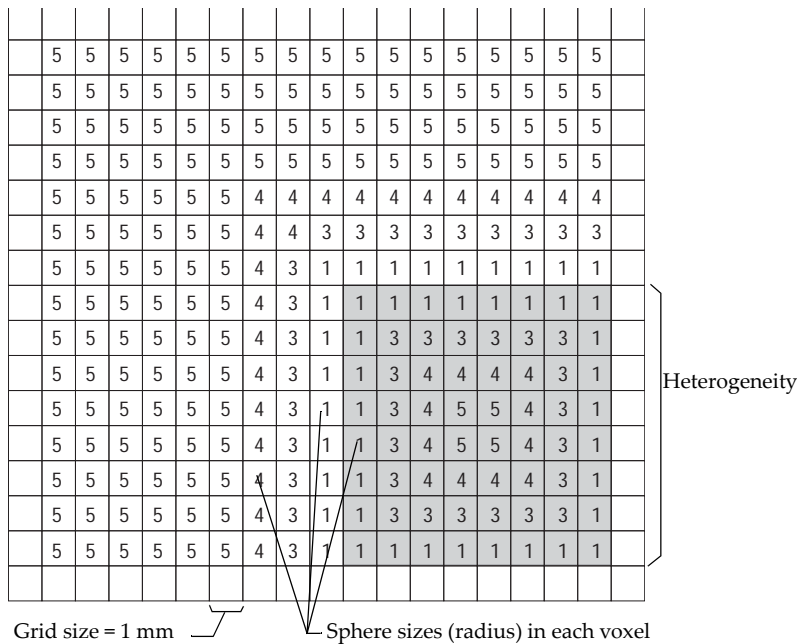
5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5
5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5
5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5
5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5
5	5	5	5	5	5	4	4	4	4	4	4	4	4	4	4	4
5	5	5	5	5	5	4	4	3	3	3	3	3	3	3	3	3
5	5	5	5	5	5	4	3	1	1	1	1	1	1	1	1	1
5	5	5	5	5	5	4	3	1	1	1	1	1	1	1	1	1
5	5	5	5	5	5	4	3	1	1	3	3	3	3	3	3	1
5	5	5	5	5	5	4	3	1	1	3	4	4	4	4	3	1
5	5	5	5	5	5	4	3	1	1	3	4	5	5	4	3	1
5	5	5	5	5	5	4	3	1	1	3	4	5	5	4	3	1
5	5	5	5	5	5	4	3	1	1	3	4	4	4	4	3	1
5	5	5	5	5	5	4	3	1	1	3	3	3	3	3	3	1
5	5	5	5	5	5	4	3	1	1	1	1	1	1	1	1	1

Heterogeneity

Grid size = 1 mm

Sphere sizes (radius) in each voxel

**Figure 23   Result of a Preprocessed CT Slice**

Primary Particle Transport and Energy Deposition

The scanning and averaging processes of the CT volume described in "Preprocessing the Absorber CT Volume" on page 178, reduces the determination of the appropriate sphere size and mean sphere density for an MMC step to a table lookup for the density voxel containing the current sphere center. The sphere center is placed at a distance from the current position of the primary electron in the direction of motion of the primary electron. This distance equals one radius of the maximum allowed sphere size of the previous step. The current position of the primary electron is the exit position on the previous sphere.

One feature of the adaptive step size algorithm is the ability to stop a particle at an interface between different materials (see D in the figure), and to restart the transport with a new sphere in the new material, preserving the particle's direction of motion. Stopping at interfaces is only necessary if the ratio of linear stopping powers in dose-volume voxels on both sides of the interface exceeds a limit (typically 1.5). For stopping power ratios below this limit, the MMC

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algorithm steps across material interfaces without stopping the particle at the interface.

The figure shows a schematic illustration of the primary particle transport algorithm.
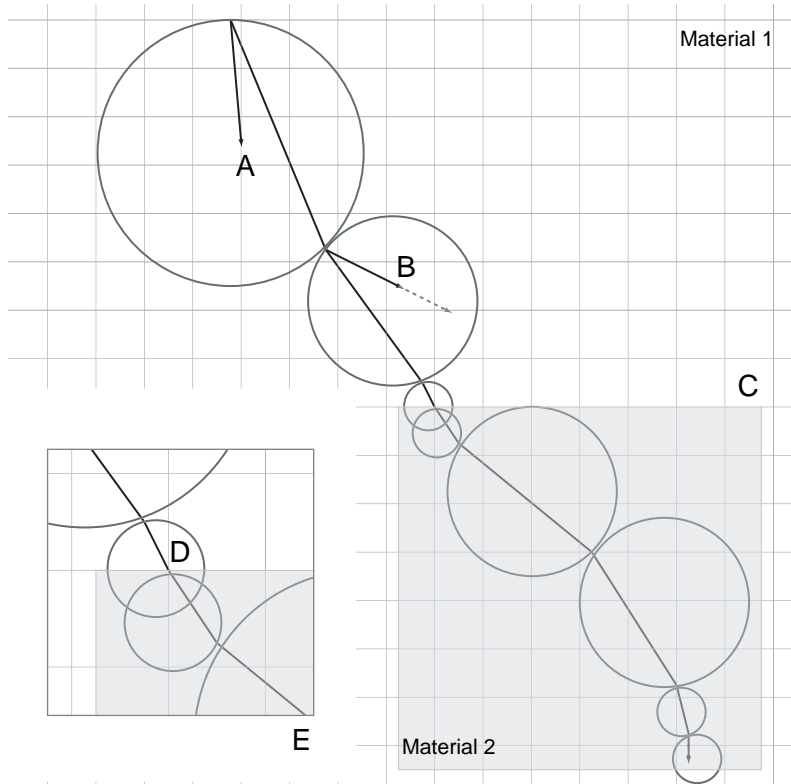
A. Electron direction and step size from previous sphere **B.** Step size reduction near boundary **C.** Heterogeneity **D.** Stop at interface **E.** Boundary crossing between materials

Figure 24   Primary Electron Transport

Primary photons travel along a straight trajectory until they interact with the medium and deposit their energy. The point where the interaction occurs is randomly selected. The energy deposition occurs along a straight line.

Primary energy is deposited along a straight line from the point where the primary electron enters the sphere to the point where it leaves. A ray trace between these two points is performed by a modified Siddon ray trace algorithm through the voxels of the dose volume. The energy T_{vox} deposited in each voxel along a ray is determined according to:

Eq. 44

$$T_{vox} = T_{dep} \frac{S_{vox} l_{vox}}{S_{kug} l_{dep}}$$

where

l_{vox}	=	Length of the ray segment inside the voxel
l_{dep}	=	Total length of the current transport step
T_{dep}	=	Primary electron energy to be deposited in the current step
S_{vox}	=	Linear stopping power of the voxel material
S_{kug}	=	Linear stopping power of the sphere that was used to look up the resulting electron parameters of the current transport step

As described above, the electron is stopped at a voxel boundary if the ratio of linear stopping powers between neighboring voxels along the ray trace direction is above a limit.

The amount of energy deposited in each voxel is calculated as:

Eq. 45

$$\Delta E_\gamma = \frac{1}{2} a_\gamma(\rho) \cdot b_\gamma(T_i) \cdot \rho \cdot 2\mathrm{MeVcm}^{-1} \cdot \Delta l \cdot \frac{T_\gamma}{T_\gamma^{spect}}$$

where

T_γ	=	Average amount of secondary photon energy to be deposited per primary electron[a]. Decreased continuously by ΔE_γ for each Bresenham step. Deposition stops if T_γ is zero.
T_γ^{spect}	=	Energy spectrum of photons leaving the sphere for incident energy T_i = 10 MeV. This spectrum depends loosely on the sphere size and is applied to other energies T_i and density values ρ by the scaling factors $a(\rho)$ and $b(T_i)$

---

a. T_γ is not the secondary photon energy. A secondary photon does not always emerge from the sphere. T_γ is the amount of secondary photon energy per primary incident electron corresponding to T_γ^{spect}.

Secondary Particle Transport and Energy Deposition

Figure 25 on page 185 shows the secondary particle transport and energy deposition algorithm. Since there is no information for the position and direction parameters of these particles available from the database, some simplifications have been made in secondary particle scattering and energy deposition.

Simplified scattering model

In air, secondary particles are modeled using a simple model that scatters them with a fixed angle with respect to the primary electron direction. Best results are obtained with a scattering angle of 20°.

Figure 25 on page 185 shows the start point of the randomly distributed secondary particle track (A) and the azimut f.

Simplified energy deposition

Energy deposition voxels are determined using a Bresenham algorithm. The path-length within one voxel has the constant value Δl = D/e, where D is the dose-grid pitch of the leading Bresenham coordinate and e is the direction cosine for this coordinate.

Deposition of secondary electron energy

Deposition of secondary electron energy starts at the distance d_1 from the entry point of the primary electron, with d_1 defined by:

Eq. 46 $d_1 = 2Rr_1$

where

R	=	Sphere radius
r_1	=	Random number 0–1

The amount of secondary electron energy deposited in each Bresenham voxel is calculated by:

Eq. 47

$$\Delta E_e = a_e(\rho) \cdot b_e(T_i) \cdot \rho \cdot 2\text{MeVcm}^{-1} \cdot \Delta l \cdot \frac{T_e}{T_e^{\text{spect}}}$$

where

T_e	=	Average amount of secondary electron energy to be deposited per primary electron[a]. T_e is decreased continuously by ΔE_e for each Bresenham step. Deposition stops if T_e is zero.
T_e^{spect}	=	Energy spectrum of secondary electrons leaving the sphere for incident energy T_i = 10 MeV. This spectrum depends loosely on the sphere size and is applied to other energies T_i and density values ρ by the scaling factors $a(\rho)$ and $b(T_i)$

a. T_e is not the secondary electron energy. There is not always a secondary electron coming out of the sphere. T_e is the amount of secondary electron energy per primary incident electron corresponding to T_e^{spect}. This procedure is a common variance reduction technique.

Energy deposition of Bremsstrahlung photons

Energy deposition of Bremsstrahlung photons starts at position $d_1 + d_2$ from the entry point of the primary electron with d_1 defined as Equation 46 on page 183 and d_2 defined on the basis of homogeneous water as in:

Eq. 48

$$d_2 = -a \times \log(r)$$

where

a	=	14.14 cm
r	=	Random number 0–1

The amount of energy deposited in each voxel is calculated as in Equation 45 on page 182:

Detailed physics

Simplified implementation

A. Primary electron B. Primary electron C. Secondary electron D. Brems photon E. Compton process F. Compton electron
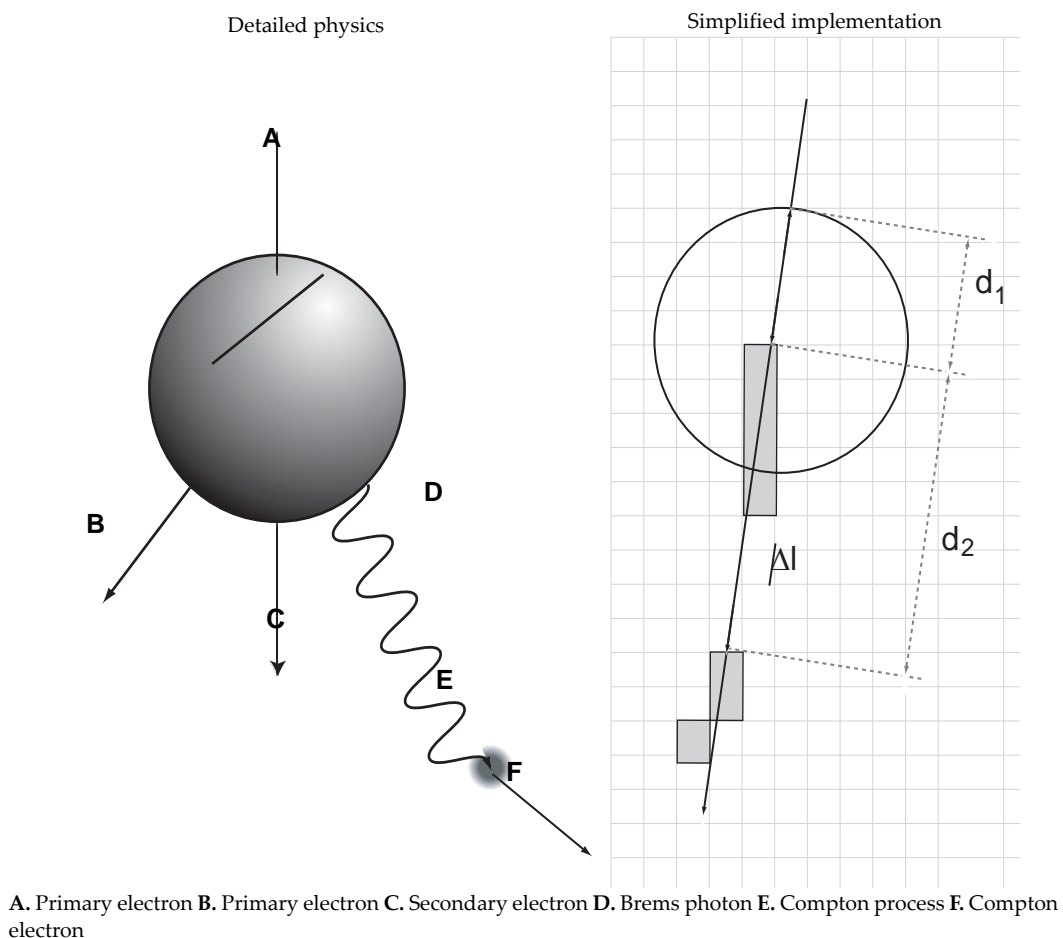
Figure 25   Secondary Particle Transport

Statistical Accuracy

The eMC defines the overall accuracy as the average statistical uncertainty in all voxels in the region of interest. The region of interest contains all voxels within the body contours with a dose larger than 50% of the maximum dose. The average statistical uncertainty S_{50} is calculated using formula:

Eq. 49

$$S_{50} = \frac{1}{N_{50}} \sum_{D_{ijk} > 50\% D_{max}} \frac{\Delta D_{ijk}}{D_{max}}$$

where

N_{50} = Number of voxels satisfying the condition $D_{ijk} > 50\% D_{max}$.

D_{ijk} = Dose at point (i, j, k)

D_{max} = Maximum dose

The simulation is divided into N_{batch} batches, each containing 10,000 particles. The minimum number of batches in simulation is 10. The statistical uncertainties ΔD_{ijk} were calculated using the following formula:

Eq. 50

$$\Delta D_{ijk}^2 = \frac{\langle D_{ijk}^2 \rangle - \langle D_{ijk} \rangle^2}{N_{batch} - 1}$$

where

$\langle D_{ijk} \rangle$ = Average dose

$\langle D_{ijk}^2 \rangle$ = Average dose squared

Dose Smoothing

The dose distributions from Monte Carlo simulations necessarily contain statistical noise due to the random nature of the simulation process. The final dose distribution can be smoothed to reduce the statistical noise. The use of statistical smoothing can also result in a more rapid convergence on a final solution, which will reduce the amount of time spent in the actual simulation of electron transport through the patient. The smoothing preserves meaningful structures and edges in the dose distribution, while smoothing out the noise.

The eMC algorithm supports two different dose smoothing methods, the Gaussian and the median smooth.

Gaussian Dose Smoothing

The Gaussian dose smoothing is a convolution smoothing method that uses a kernel representing the shape of a Gaussian (bell-shaped) curve.

Before the convolution, the Gaussian distribution is limited by truncating the kernel at the point of about three standard deviations from the mean. This is done to be able to restrict the convolution kernel to a practical size. After a suitable kernel size has been achieved, the Gaussian dose smoothing is performed using standard 3D convolution methods.

The degree of the Gaussian smoothing is determined by the standard deviation of the Gaussian (the Smoothing level calculation option, see "eMC Calculation Options" on page 188). The size of the deviation affects the size of the kernel required so that larger standard deviation Gaussians require larger convolution kernels.

The Gaussian smoothing produces a weighted average of each pixel's neighborhood, with the average weighted more towards the value of the central pixels.

Median Dose Smoothing

The Median dose smoothing determines the value of a pixel by examining the pixel values in its neighborhood on a slice and taking the median of these values. Each pixel and its neighbors are considered in turn. If a pixel is considered representative of its surroundings, it is replaced with the median of the pixel values in the neighborhood. The median is calculated by first sorting the pixel values into numerical order and then replacing the pixel with the middle value. If the neighborhood contains an even number of pixels, the average of the two middle pixel values is used. The Median smoothing is performed slice by slice.

The Median smoothing does not conserve the sum of the pixel values in the volume (the sum of the median values is not equal to the sum of the original values). If the window size is too large, this can lead to distortions in dose volume histograms. The eMC algorithm uses fairly small window sizes to minimize the error caused by distortions.

eMC Calculation Options

The following calculation options can be configured for calculation models based on the eMC algorithm in Beam Configuration:

- *Accuracy*—Average statistical uncertainty in the dose maximum region (see "Statistical Accuracy" on page 186). The average statistical uncertainty is based on reference calculations, which simulate a 10×10 field in a water phantom to the level of +-1% accuracy at the dose maximum. Increasing the accuracy from 2% to 1% also increases the required amount of particle histories to be simulated, and the time required for completing the simulations, four times.

  Possible values are 1, 2, 3, 5 and 8. Can be defined in External Beam Planning and Beam Configuration. This option is not used if the value of the *Maximum number of particle history* parameter is other than 0.

- *Accuracy Limit*—Limits the MU calculation from a dose with low accuracy. Can be defined in Beam Configuration.

- *Grid*—Defines the resolution of the dose calculation. Possible values: 0.1, 0.15, 0.20, 0.25 and 0.50 cm.

  Computer memory may run out when using small values for the grid size parameter. In this case, either increase the grid size option or reduce the calculation volume in External Beam Planning or Beam Configuration.

- *Random generator seed*—Defines the random number sequence used in the particle generator. Can be defined in External Beam Planning.

- *Maximum number of particle history*—Defines the accuracy of the calculation by the amount of particles processed. 0 value means that this option is not used; instead the Accuracy option is used.

  The eMC algorithm uses batches of particles in the simulation, each batch consisting of 10,000 particles. The value given for the *Maximum number of particle history* option is always rounded up to the nearest number divisible by 10,000. For instance, if the given

value is 10,001, eMC simulates two batches (equalling to 20,000 particles). The number of particles used in the simulation is reported in the dose calculation log.

If the requested accuracy goal from one calculation servant is higher than 8%, the batch size is reduced to 1000 particles. If the accuracy goal is higher than 15%, the batch size is further reduced to 100 particles. This may happen when the Monte Carlo field parallelization factor (defined in DCF settings) is larger than 1 and the value of the Accuracy parameter is high (5% or 8%). The accuracy goal for one servant is calculated as `Accuracy × sqrt(N)`, where N is the number of servants used in the calculation of one field.

- *Smoothing method*—Defines the method of dose distribution smoothing. Possible values are No smoothing, Gaussian and Median.
- *Smoothing levels*—Defines the strength of the dose smoothing. Possible values are Low, Medium and Strong. Smoothing changes the dose distribution, which then change the MU for the plan.

Initial Phase Space (IPS) Model

The IPS model is a multiple source model, adapted from the Rotterdam IPS model[33]. It contains several sub-sources:

- Main diverging beam (electrons and photons)
- Edge electron
- Transmission photons
- Second diverging beam (electrons and photons)

The model is based on precalculated data for a machine type, and configured using measured beam data.

Main diverging beam

The main diverging beam sub-source contains the electrons and photons emerging from the scattering foil. The distance of the focus is 10 cm below the nominal source, and the particles are sampled on a plane located 95 cm below the norminal source, inside the shape defined by the applicator or the insert.

33. Janssen JJ, Korevaar EW, van Battum LJ, Storchi PR & Huizenga H: A model to determine the initial phase space of a clinical electron beam from measured data. Phys. Med. Biol. 2001 Feb; 46(2): 269–286.
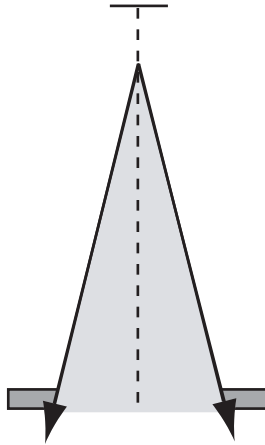
Figure 26   Main Diverging Beam

The directions of the photons and electrons are determined as follows:

- The direction of the photons is given by the sampled position on the plane and the Z-position of the focus (10 cm below the nominal target).
- The direction of the electrons is varied according to a Gaussian distribution with a sigma-theta that depends on the machine type and the nominal energy.

Edge electrons

The edge electrons sub-source is a line source along the opening of the applicator or the insert, containing scattered electrons.

Figure 27   Edge Electrons

There are two types of edge electrons:

- Electrons from the upper rim of the cutout, and produced by main electrons entering the cutout material on the upper plane.
- Electrons from the inner side of the cutout, and produced by main electrons entering the cutout material on the inner plane.

The edge electrons are sampled by use of precalculated scatter kernels.

Transmission photons

Transmission photons are sampled using pre-calculated kernels. They exit from the outer rim of the applicator and from the insert material.

Figure 28   Transmission Photons

The following three types of transmission photons are taken into account:

- Scattered photons produced by main electrons in the insert material, sampled by using a precalculated kernel.
- Main photons passing through the insert material without interaction. They have the same direction as the main photons but a different energy distribution.
- Scattered photons produced by main photons in the insert material, sampled by using a precalculated kernel.

Second diverging beam

The second diverging beam sub-source contains the electrons and photons from a virtual point source. The distance of the focus is 50 cm below the nominal target, and the particles are sampled on a plane 95 cm below the norminal source, inside the shape defined by the applicator or the insert. The direction of both electrons and photons is given by the sampled position on the plane and the Z-position of the focus (at 50 cm).
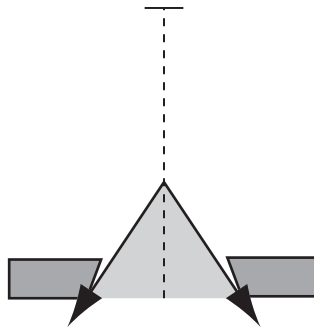
Figure 29   Second Diverging Beam

Machine Type Parameters in the IPS Model

The machine type parameters are used for creating precalculated data for the IPS model. The machine type parameters describe some of the physical properties of a treatment unit, and may vary between different treatment units. The properties of the machine type "Varian" are described in Table 29 on page 193.

Note: *Only Varian treatment units are currently supported by the IPS model.*

The following machine type parameters are used in the IPS model:

- Focus position of the main diverging beam
- Focus position of the second diverging beam
- Position of the lower end of the last applicator scraper
- Cutout (applicator or insert) material
- Cutout thickness
- List of possible energy modes
- List of possible applicators
- Energy modes defined by:
  - Nominal energy
  - $\sigma(\theta)$ for the main electrons
  - Energy spectrum of main photons
- Applicators defined by:
  - Dimensions of the cutout
  - Outer dimensions (used for transmission photons)

Precalculated Data Used for eMC Configuration

The IPS model contains the following precalculated data used for the configuration of the eMC calculation model:

- A set of 50 depth-dose curves for monoenergetic electrons calculated with MMC (0.5–25 MeV in 0.5 MeV steps), for all possible applicators and for two focus positions (10 cm and 50 cm).
- Depth-dose curves for edge electrons produced by monoenergetic target electrons for all possible energies and applicators.
- Depth-dose curves for transmission photons for all possible energy modes and applicators.
- Depth-dose curves for main photons calculated with MMC for all possible energy modes and all applicators.

Data that depends on the machine type parameters has to be calculated for every machine type.

Machine Type Varian

Currently only the data for one machine type (*Varian*) has been calculated.

Table 29 Parameters for Machine Type *Varian*

Parameter		Value
Focus position of main diverging beam		10 cm
Focus position of second diverging beam		50 cm
Lower end of the last applicator scraper		95 cm
Cutout (applicator or insert) material		Cerrobend
Cutout thickness		1.5 cm
List of possible energy modes		6e, 9e, 12e, 15e, 16e, 18e, 20e, 22e
List of possible applicators		6×6, 10×6, 10×10, 15×15, 20×20, 25×25
$\sigma(\theta)$ for the main electrons	6e	0.054
	9e	0.038
	12e	0.029
	15e	0.024
	16e	0.023
	18e	0.020
	20e	0.018
	22e	0.017
Energy spectra of main photons		From BEAM simulations

Table 29 Parameters for Machine Type *Varian*

Parameter		Value
Outer applicator dimensions		
	Inner edge	Outer edge
	6×6	8.5×8.5 cm
	10×6	12.52×8.5 cm
	10×10	12.52×12.52 cm
	15×15	16.0×16.0 cm
	20×20	22.4×22.4 cm
	25×25	27.4×27.4 cm

MU Calculation and Dose Normalization

The electron Monte Carlo (eMC) algorithm is configured using measured depth dose curves and profiles, to which pre-calculated data is fitted. In this process, it is determined how much energy a high-energy electron deposits in a water-like medium at the dose distribution maximum.

During dose calculation, the eMC algorithm tracks individual electrons through the patient geometry and calculates the energy deposited into each dose voxel along the electron path. The number of electrons tracked depends on the patient and field geometries, and the user-defined accuracy of the mean dose. After all the required electrons have been tracked, the energy deposited into each dose voxel is converted to dose (in Gy) by dividing it with the density and the volume of the voxel.

Due to the statistical and non-deterministic nature of Monte Carlo calculations, it should be noted that the resulting dose distribution contains noise. The relative magnitude of the noise depends on the statistical accuracy (see "Statistical Accuracy" on page 186) of the calculation: the better the accuracy, the lower the magnitude of the noise peaks. However, the maximum dose value is always an overestimate. The location of the dose maximum point may also be incorrect. Thus the dose maximum value should not be used alone to normalize the dose or evaluate the goodness of the distribution.

The absolute dose distribution is converted to relative units (percentage) and normalized. The dose calculated by the eMC is normalized to 100% at the dose maximum of the volume dose, if the No Plan Normalization method is used.

To calculate the Monitor-Units-per-Gray factor, the calculated dose distribution is smoothed with a Gaussian filter. Then, the dose maximum of the smoothed distribution and a calibration factor given in the configuration are used to determine the Monitor-Units-per-Gray factor.

Known Limitations of the eMC Algorithm

About the accuracy. The accuracy of the Transport (MMC) model and the Initial Phase-Space (IPS) model is typically 3% of the dose maximum. However, accuracy exceeding 3% has been observed for:

- Conditions where the measured open field dose with no applicator exceeds the dose measured with the applicator in place. For more information, see the Energy/Applicator measurements section below.
- 6 MeV dose in corners and with applicator openings 6 cm x 6 cm or smaller.
- Outer regions of the larger applicators such as 15 cm X 15 cm.
- Extended SSDs.
- Unusual body contour shapes, or presence of heterogeneities.
- Inconsistent measured beam data.

Energy/Applicator measurements. For the fitting process (configuration) to work properly, the absolute dose (in cGY/MU) of an applicator should be greater than or equal to the absolute dose of an open beam. Normally, this is the case, but there may be exceptions. For Varian C-series treatment units, in the case of a low energy (6 MeV) beam modified with a small applicator (6 x 6), the absolute dose value may be lower than or equal to that of an open beam. For Varian TrueBeam treatment units, the situation may occur for all applicator sizes for 6 MeV, and for the smallest applicator (6 x 6) for 9 MeV and 12 MeV. In these cases, the calibration process is slightly modified to better fit the precalculated data to the measured depth dose curves. This modification may decrease the accuracy of the MU calculation by

a factor of 1–2%. However, eMC can still produce acceptable results in this situation. Always verify with sufficient testing that the accuracy is within acceptable levels.

Dose in low density structures. It is possible that the dose calculated by the eMC shows an unexpected peak in low density structures, such as lungs. The effect is due to special conditions arising in the transport of secondary particles. Changing the seed value of random number generator in the calculation options is usually sufficient to remove the peak when one is encountered.

Cutout material thickness. Although the cutout material (block material) and thickness can be configured in RT Administration, and the transmission value for the cutout material in Beam Configuration, the eMC algorithm does not use these for dose calculation. Instead the algorithm uses the cutout parameters defined in the IPS model. If the cutout material and/or thickness in use differs from that defined in the IPS model, the calculated dose under the cutout may deviate slightly from the measured dose at the same point, especially when using high energies (18 MeV or higher).

Configuration of the eMC Algorithm

Note: *When configuring fluence delivery algorithms, notice the following:*

- *It is important to configure the system so that it corresponds to the characteristics of the treatment machine.*
- *Periodically perform follow-up measurements and compare with the dosimetric beam data used for configuring the beam. If fluctuations are large and the configured beam data no longer represents the average beam delivered by the machine, reconfigure the beam data using the newer dosimetric beam data.*
- *Measure all dosimetric beam data in as stable conditions as possible.*
- *Use the same file naming conventions in beam data measurements (input files) and in Beam Configuration (Therapy Unit name), and name the input files so that it is easy to match the beam data to the treatment unit during the configuration process.*

Beam Data Measurements for the eMC Algorithm

The configuration of the eMC algorithm requires beam data measurements for the full open field and energy/applicator combinations.

Open Field Measurements

The following full open-field measurements (without the applicator, with collimator jaws wide open) must be provided for each electron energy:

- Depth-dose curve in water at the Source-to-Phantom Distance (SPD) = 100 cm
- Absolute dose in water, expressed in [cGy/MU], at the calibration point on the depth dose curve (usually the d_{max} or a point close to it)
- Profile in air at 95 cm. Make sure that the measured profile covers the central axis (x = 0), that is, it is possible to interpolate a value from the curve at x = 0. The measurement must extend at least up to a distance, which corresponds to the corner of the largest applicator size (for example, up to 17.7 cm when the maximum applicator size is 25 cm x 25 cm).

Energy/Applicator Measurements

For each energy/applicator the following measurements must be provided:

- Relative depth-dose curve in water at SSD = 100 cm and absolute dose (in cGy/MU) at the calibration point on the depth dose curve (usually the d_{max} or a point close to it).

The first point of all depth dose curves must be at the depth of 0.5 mm or shallower.

The beam measurement data must be in the w2CAD format in order to transfer it to Beam Configuration (see Appendix C on page 326).

Note: *Notice the following regarding applicator measurements:*

- *The applicator size is read from the database to the General Parameters file. Verify that the value is correct.*
- *The field size is determined by the selected electron applicator. The electron applicator field size is entered in Beam Configuration. The jaw settings entered in Eclipse External Beam Planning have no effect on the calculated dose distribution.*

Treatment Unit Parameters

Specific parameters need to be defined for each treatment unit to be configured before importing measured beam data. Part of these parameters are read into Beam Configuration from RT Administration. When configuring the eMC algorithm, verify that the parameters read from RT Administration are correct, and add whatever parameters may be missing.

General treatment unit parameters

The eMC algorithm requires defining the following general treatment unit parameters for importing measured beam data and for dose calculation:

- Nominal energy (read from RT Administration).

  The nominal energy is interpreted as the energy of the incoming monoenergetic electron beam hitting the scattering foil. Its value determines the set of precalculated data fitted to measurements when configuring eMC algorithm. The fitting process can compensate for small deviations between the real electron beam energy and the eMC nominal energy.

- Therapy unit name (defined in Beam Configuration).

Model Parameter (Machine Type)

The model parameter required for importing the measured beam data and for dose calculation is read from the installed Data Type Specification file of the eMC algorithm. The model parameter defines the machine type.

Beam Data Created in the Configuration

During the configuration, the following calculated beam data is created in Beam Configuration.

Calculated Data for Open Beam

- Fitted Open Beam Depth Dose
    - Two curves—the *measured* depth dose curve and the *fitted* depth dose curve. The curves consist of value pairs of depths in [cm] and relative doses.
    - Chi2: Quality of fitting. Chi2 describes the difference between the original data set and the fitted curve. It is the sum of squared differences. Typically, for eMC Chi2 < 0.1. Note that small value of Chi2 does not automatically imply the high quality of the configured beam data.
- Primary Source Energy Spectrum
    - The curve consists of value pairs of energies in MeV and weights. The data contains the following read-only parameters:
        - Chi2: Quality of fitting
        - Electron weight: Weight of electron sources
        - Photon weight: Weight of photon sources

Calculated Data for Applicators

- Fitted Applicator Depth Dose
    - Two curves—the *measured* depth dose curve and the *fitted* depth dose curve. The curves consist of value pairs of depths in [cm] and relative doses.
    - Chi2: Quality of fitting. Chi2 describes the difference between the original data set and the fitted curve. It is the sum of squared differences. Typically, for eMC Chi2 < 0.1. Note that small value of Chi2 does not automatically imply the high quality of the configured beam data.

To Configure the eMC Algorithm in Eclipse

1. Configure the Calculation model (eMC). See *Beam Configuration Reference Guide* (Chapter 8, "Configuring Calculation Models").

2. In the Focus window, select the treatment unit and energy to be configured.

3. To insert new beam data, choose **Insert** > **New Beam Data**.

4. Define the name for the beam data (for example, eMC).

5. To import the depth dose curve for the open field, choose **File** > **Import > Depth Doses for Open Beam**.

   Note the format of the depth dose curve files (Appendix C on page 326 in this guide).

6. Select the depth dose curve from the lower left corner and define the values in the lower right window (Source-to-Phantom distance, calibration depth and dose at calibration depth).

7. To import the profile data for the open beam, choose **File** > **Import** > **Profile for Open Beam**.

8. Select the profile curve from the left lower corner and define the Source-to-Phantom distance in the right lower window.

9. To insert the applicators, choose **Insert** > **New Add-On**.

10. Enter the field size for the applicators in the Applicator Parameters window.

11. To match and assign the applicators against the database, choose **Beam Data** > **Match and Assign Add-ons**.

12. To import depth dose curves for the applicators, choose **File** > **Import** > **Depth Doses for Applicator**.

13. Select the depth dose curve from the lower left corner and define the values in the lower right window (Source-to-Phantom distance, calibration depth and dose at calibration depth).

14. To calculate beam data for the applicators, choose **Beam Data** > **Calculate Beam Data**).

15. In the Calculate Beam Data dialog box, select the desired configuration steps by selecting the corresponding check boxes.

If you are configuring several different applicators one at a time, and wish to keep the applicator-specific PDDs, it suffices to calculate open beam data only once, for instance, in connection with configuring the first applicator. Calculating the open beam data will override the existing PDDs of applicators configured earlier. To do this, make sure that you have the **Configure Applicator Data** *check box selected, and the* **Configure Open Beam and Applicator Data** *and the* **Configure Open Beam Data** *check boxes cleared.*

Remember to save and approve your configured beam data. Validate the configured beam data in the Beam Analysis workspace. If you need to continue the configuration after validating the data, unapprove the data first. For instructions for approving, validating and unapproving beam data, refer to Beam Configuration Reference Guide.

Volume III   Optimization Algorithms

Chapter 9   Dose Optimization Algorithms

General Information about Dose Optimization Algorithms

The dose optimization algorithms used in Eclipse are:

- Dose Volume Optimizer (DVO) algorithm—Determines the optimal field shape and intensity by iteratively conforming the dose distribution to the desired objectives until an optimum solution is reached.

- Plan Geometry Optimization (PGO) algorithm—Selects the beam angles based on user-defined dose-volume objectives. The PGO algorithm is based on the DVO algorithm and uses the same objectives.

- Progressive Resolution Optimizer (PRO) algorithm—Creates VMAT, or RapidArc, plans based on dose-volume objectives.

- Multi-Resolution Dose Calculation (MRDC) algorithm— Enables fast dose estimation inside the DVO, PGO and PRO to improve the optimization accuracy.

The table below is a summary of the features, objectives, parameters and their variants in the dose optimization algorithms. For details, see the sections after the table discussing the general features.

Table 30 A Summary of the General Features of Dose Optimization Algorithms

	DVO	PGO	PRO
Heterogeneity correction	Yes	No	Yes
Bolus	Yes	Yes	Yes
Support devices	Yes	No	Yes
DVH Objectives	Yes	Yes	Yes
Mean dose objective	No	No	Yes
Minimum dose	Min. Fluence	Min. Fluence	MU objective
Normal Tissue Objective	Static	Static	Interactive/ Automatic

Table 30 A Summary of the General Features of Dose Optimization Algorithms

	DVO	PGO	PRO
Restarting optimization	Yes (from fluence)	No	Yes
Intermediate dose calculation	Yes	No	Yes
Output	Fluence	Beam geometry	Leaf positions and MU/deg as a function of gantry angle
Geometric optimization	No	Local/global	Arc Geometry Tool
Dose calculation algorithm	MRDC	MRDC	MRDC with progressive dose calculation segments

Bolus and Patient Support Devices

Optimization algorithms take bolus and patient support devices (for example couch structures) into account. They interpret the assigned HU values and handle overlapping structures in the same way as in the dose calculation algorithm. However, because of how AAA and Acuros XB use heterogeneity correction in the full final dose calculation inside bolus and patient support devices, the heterogeneity correction must be turned on in the optimization algorithms. (For information on AAA and Acuros XB, see Chapter 4, "Photon Beam Source Model," on page 45.) If optimization is performed without the heterogeneity correction, the patient support devices are ignored (a warning is given in the calculation log), and bolus are treated as having the density of water.

Note: *The Plan Geometry Optimization (PGO) does not feature heterogeneity correction and does not take patient support devices into account.*

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Volume Representation

Volumes are represented by point clouds generated from user-defined segments. The sampling density of the point clouds is determined by the resolution and shape of the user-defined segments. Sub-volumes located close to the surface of the structures are represented more accurately, and the user-defined resolution is used inside the volume. If the Normal Tissue Objective (NTO) is used, additional points are used near target boundary to increase the accuracy.

For more information, see "Normal Tissue Objective" on page 208.

Both the representation accuracy of volumes and the total number of points affect the memory consumption and speed of the optimization algorithms. Using high numbers of points helps achieve higher accuracy in the volume representation, however, it will also increase memory consumption. Reducing the number of points will decrease memory consumption, but it may affect the accuracy of the volume representation adversely and compromise the quality of the DVH shown in the optimization. The optimization algorithms have the following restrictions related to the volume representation:

- *PRO algorithm:* Does not restrict the total number of points.
- *PGO algorithm:* Estimates the memory consumption at the beginning of the optimization. If the memory does not suffice for the optimization, an error message is issued, instructing the user to decrease either the number of points or initial fields in the plan.
- *DVO algorithm:* Does not restrict the total number of points.

Target Masking

The point set for the target is projected to the fluence matrix. Only rays within 0.5 cm from the closest projected point are allowed to have non-zero fluence values. Target masking includes the MLC geometry. This means that any leaf having any points within the 0.5 cm range includes all its rays to the field (in the Y-direction). The field sizes are automatically determined from the masking data.

In the PRO algorithm, target masking is used to limit the leaf positions, and it also takes into account the differences in the target projection forwards and backwards.

Dose Computation

A fast multi-resolution dose calculation is performed for each field during each optimization iteration. The dose calculation is based on multi-resolution 3D convolution of Monte-Carlo-generated point-spread function-kernels. For more information on the dose calculation, see "Multi-Resolution Dose Calculation (MRDC) Algorithm" on page 211.

Optimization Objectives

Dose-Volume Objectives

The optimization is based on dose-volume objectives (Upper and Lower objectives defined in the Optimization dialog box). Objectives are used to define the dose as follows:

- *Upper objective*—Is used to limit the dose in a given structure (for example, "no more than 20% of the structure may receive more than 25 Gy").
- *Lower objective*—Is used to define desired dose levels in target structures (for example, "at least 70% of the structure must receive at least 20 Gy").

The figure shows an example of an upper and a lower objective, plus a resulting DVH curve in the Optimization dialog box.
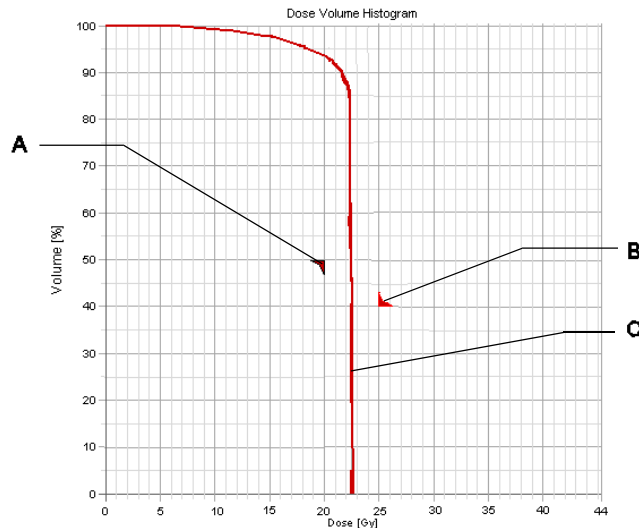
A. At least 50% of the structure must receive at least 20 Gy B. No more than 40% of the structure may receive more than 25 Gy C. Possible DVH curve resulting from the objectives

Figure 30   Upper and Lower Optimization Objectives

If the dose-volume objectives are exceeded, the points with the lowest dose among those that exceed the objectives are evaluated up to the defined portion of the volume with a weighted quadratic objective, and the value of this evaluation is added to the objective function.

The dose-volume objective of each point introduces discontinuities in the optimization space, and each additional objective may create thousands of new local minima. To overcome this, the DVO also has a more powerful dose-volume objective form, the spline dose-volume objective, that allows using very complex and expressive dose-volume objectives while creating fewer local minima.

Smoothing Objectives

The fluence needs to be smooth to enable leaf motion calculations with the LMC. Fluence smoothness is ensured by adding an objective that includes the difference between the neighboring fluence values (X smooth and Y smooth in the Optimization dialog box). This objective is linear up to the value of 3% of the maximum fluence value, where it saturates to a constant value. The saturation non-linearity allows for

large fluctuations in the fluence where required. The smoothing is performed in both X and Y-directions of the fluence, with different user-configurable weightings. Typically, it is more important to have a smoother fluence in the X-direction to ensure the minimal MU factor for the LMC.

Minimal Fluence Objective

An additional objective is provided for the definition of the required minimal fluence (Minimize dose defined in the Optimization dialog box). The minimal fluence objective works on per field basis. The optimization does not value extra fluence outside the target if no critical organs have been defined there. The minimal fluence objective allows for natural minimization of the fluence without introducing additional (or even artificial) critical organs.

MU Objective

The MU Objective can be used to control the number of MU that the PRO optimizer produces. Minimum and maximum values can be defined. An extra multiplier is applied to the total objective function value if the number of MU is not in the desired range. Strength value can be used to modify the strength of the effect. Because the value is a multiplier to total objective function value, the relative effect of the MU objective remains the same even when the priorities of the DVH objectives are changed.

Normal Tissue Objective

The Normal Tissue Objective is used for the part of the body which does not include the PTV to limit the dose level and prevent hot spots in healthy tissue. In addition, the Normal Tissue Objective can be used for obtaining a sharp dose gradient around the PTV.

Note: *With the PRO algorithm you can also use the automatic Normal Tissue objective. For more information, see "Automatic Normal Tissue Objective" on page 226.*

Normal Tissue Objective Shape

The shape of Normal Tissue Objective is controlled with the following parameters:

- Distance from PTV border (x_{start})
- Start dose (f_0)
- End dose (f_∞)
- Fall-off (k)

The shape of Normal Tissue Objective ($f(x)$) as a function of the distance from PTV border (l) is calculated as:

Eq. 51

$$f(x) = \begin{cases} f_0 e^{-k(x-x_{\text{start}})} + f_\infty(1 - e^{-k(x-x_{\text{start}})}), & x \geq x_{\text{start}} \\ f_0, & x < x_{\text{start}} \end{cases}$$

The figure shows a typical shape of the Normal Tissue Objective.
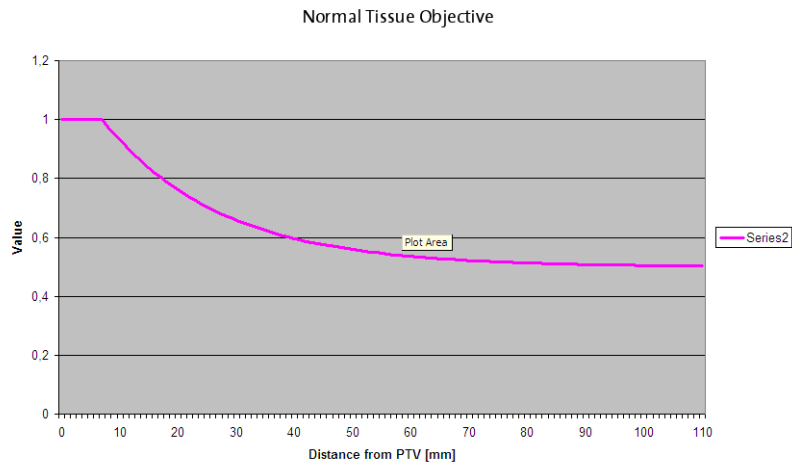
Figure 31   Example Shape of the Normal Tissue Objective

The shape of Normal Tissue Objective presented in the figure has been calculated with the following parameter values:

- x_{start} = 10 mm
- f_0 = 1.1
- f_∞ = 0.5
- k = 0.05

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Normalization of the Normal Tissue Objective is done as follows: level 1.0 (100%) corresponds to the lowest upper objective defined for the target. If no upper objective is defined, level 1.0 (100%) is 1.05 times the highest lower objective defined.

In addition to the parameters that control the shape of the Normal Tissue Objective, the importance of the Normal Tissue Objective in relation to the other optimization objectives is controlled with the Priority parameter. The Normal Tissue Objective is taken into use by defining a value for the Priority parameter. Then the Normal Tissue Objective values are calculated for all body points. If there are several PTVs, the Normal Tissue Objective value for a specific body point is the highest one of the Normal Tissue Objective values calculated at this point for all the PTVs. If the value of the Priority parameter is set to zero, the optimization does not use the Normal Tissue Objective.

Note: *Any structure with at least one lower objective is considered a PTV by the Normal Tissue Objective.*

Normal Tissue Objective Parameters

The table shows the Normal Tissue Objective parameters and their default values.

Table 31 Default Values for the Normal Tissue Objective

Parameter name	Range	Default	Use of Parameter
Distance from PTV border [cm]	-20–20	1.0	Determines the area where the Normal Tissue Objective value must be constant. Expressed in centimeters.
Start dose [%]	0–1000	105	Determines the relative dose level in the Normal Tissue Objective at the PTV border. Expressed in percentage.
End dose [%]	0–1000	60	Determines the relative dose level in the Normal Tissue Objective in the area furthest from the PTV border. Expressed in percentage.
Fall-off	0–100	0.05	Determines the steepness of the Normal Tissue Objective curve shape.
Priority	0–1000	0	Determines the relative importance of the Normal Tissue Objective. To use the Normal Tissue Objective in optimization, the Weight parameter must have a non-zero value.

Multi-Resolution Dose Calculation (MRDC) Algorithm

The Multi-Resolution Dose Calculation (MRDC) algorithm is used for fast dose estimation inside the DVO, PRO and PGO algorithms to improve the optimization accuracy, which can be seen as a good agreement between the optimization DVHs and the final DVHs. The high speed of the MRDC algorithm allows the optimization algorithms to perform full dose computation during each iteration.

The MRDC algorithm is based on the convolution superposition principle, and it uses 3D convolution scatter computation.

The scatter model is based on 3D superposition of point spread functions in the patient model. The point spread functions are built from Monte Carlo calculations.

Multi-resolution scatter computation calculates the scatter component using variable resolutions. Finer resolution is used close to the location of the primary interaction, while much lower resolution is used to compute the scatter component for larger distances (as far as 25 cm from the primary interaction). The convolution uses the divergence-corrected single kernel model in water-equivalent material.

Energy Spectrum

The energy spectra are based on the Monte Carlo calculations[34]. The nominal energy is used to select a spectrum from a set of precalculated data. The spectrum affects the primary component function and the point spread function. The primary component is corrected for inhomogeneities. This precalculated spectrum can be slightly optimized during the configuration of the DVO or PRO algorithm in Beam Configuration.

Intensity Profile

The intensity model of the primary component is radially symmetric around the central axis. The intensity profile is optimized from the measurement data. Diagonal profile measurements may improve the accuracy of MRDC for large field sizes.

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34. Mohan et al. Energy and angular distributions of photons from medical linear accelerators. Med. Phys. 12 (5), Sep/Oct 1985

Electron Contamination

The MRDC algorithm models the electrons created in air and the secondary collimators between the photon source and the body. Electron contamination is modeled as a depth-dependent intensity curve and a fluence-dependent spreading of contamination electrons, also extended outside the field area. The shape and the amplitude of the electron contamination curve are optimized during the configuration of the optimization algorithm.

Modeling of the Second Source

Radiation emerging outside the linac target (for instance, from the flattening filter) is modeled in the MRDC algorithm as a second photon source. The SSD of the second source, spreading of the second source photon fluence, effective photon energy, and the second source amplitude relative to the primary source are optimized during the configuration of the algorithm.

Dose Volume Optimizer (DVO) Algorithm

Eclipse IMRT is capable of creating highly conformal dose distributions by optimizing the beam intensity modulation from user-defined dose volume objectives. The algorithm used in Eclipse IMRT, Dose Volume Optimizer (DVO), determines the optimal field shape and intensity by iteratively conforming the dose distribution to the desired objectives until an optimum solution is reached.

The dose optimization algorithm performs the optimization as a minimization problem using simple gradient optimization with line minimization. Initially, all the fluences are zero, or, alternatively, the fluences from a previous optimization can be used as the initial guess. The optimization modifies these fluences in each iteration and calculates the dose from the fluences after each modification.

Once the doses at the points of the point clouds representing the patient volumes are evaluated, the objectives at the points and the derivatives of the point objectives can be calculated. The cost functionals are evaluated for each point in each volume. The derivatives of the costs at each point are back-projected to the fluences, forming the gradient.

The optimization uses the gradient search method. The gradient search is divided into two phases; gradient evaluation and line search. Gradient evaluation generates the gradient direction and the gradient length, and line search evaluates the objectives on a line segment along the gradient and finds the minimum along the line segment.

The DVO algorithm can use a calculated plan dose as an intermediate dose when optimizing a plan. The DVO algorithm calculates the difference between the intermediate dose and the first round optimization result and uses this difference to compensate the optimization result in the consequent iterations. If a new intermediate dose is calculated after the first optimization iteration, the difference is calculated again and it will be used to compensate subsequent iterations. Using an intermediate dose is particularly useful if the DVH calculated during optimization deviates from the DVH produced during dose calculation, for example when there is a lot of heterogeneity in the volume to be treated.

Plan Geometry Optimization (PGO) Algorithm

The Plan Geometry Optimization (PGO) algorithm enables the Eclipse Beam Angle Optimization, an integrated optimization option for the Eclipse treatment planning system, and is an essential component of effective intensity-modulated radiotherapy (IMRT). Beam Angle Optimization is an automated tool for selecting the suitable beam angles based on user-defined dose-volume objectives that speeds up the planning process for IMRT treatments. Beam Angle Optimization is performed with the PGO algorithm, which is based on the Eclipse DVO algorithm. Plan Geometry Optimization is designed to be run prior to Dose-Volume Optimization. The same DVH-based objectives can be used in both optimizations.

Plan Geometry Optimization Modes

The Plan Geometry Optimization (PGO) algorithm has the following operating modes:
- Global optimization mode
- Local optimization mode

Global Optimization Mode

Global optimization creates the new field geometry, which can be either coplanar or non-coplanar, depending on user-defined optimization parameters. The optimization starts from a set of uniformly distributed fields, and then narrows the number of fields down to a set that best fulfils the optimization objectives defined for the patient structures.

The global optimization mode starts with a large initial number of fields either in a 2D or 3D geometry. The PGO uses a fixed isocenter, which means that all fields in the initial field distribution share the same isocenter copied from the first field present in the plan before the PGO is started.

This is done by first optimizing a few fluences and removing fields individually in each iteration. The effect of this removal is evaluated by calculating the corresponding objective function value. The fields whose removal causes the smallest increase in the value of the objective function can be considered less important and are removed from the field geometry. The iterations are continued until the desired number of fields for the final plan has been reached. You can control the number of fields to be excluded after each iteration with a parameter value.

Initial Field Geometries

The way new fields are created depends on the selected global optimization mode. The optimization mode is defined with the Initial field distribution parameter. The global optimization mode can be one of the following:

- Coplanar (2D) field geometry—Creates equally spaced fields by increasing the gantry values. The couch angle is always zero (in IEC 61217 scale, which corresponds to 180 degrees in the Varian standard scale).
- Non-coplanar (3D) geometry—Creates fields by uniformly positioning them in three-dimensional space. The angle of each field to its closest neighbor is approximately the same for all fields. Opposing fields are avoided.

Note: *Fields that enter the patient through the end(s) of the CT stack are excluded by both the global and local optimization modes.*

The initial number of fields in both geometries is controlled with a parameter. The maximum initial number of fields is 400.

You can also specify a limit for the collimator angle between adjacent fields. If the limit is set to zero, the collimators are kept at zero angle. If the limit is set to 180 degrees, the direction of the MLC leaves coincides with the shortest dimension of the PTV in the BEV.

You can also control the offset for the gantry angles in the coplanar field geometry with the Coplanar offset angle parameter. This parameter does not affect the non-coplanar initial field distribution.

In the non-coplanar field geometry, you can enter a limit for the elevation angle of the fields from the coplanar plane. The fields in the initial field distribution do not have elevation angle values higher than the specified limit.

For a complete list of optimization parameters, see "Input Parameters for the PGO" on page 237.

Removing Forbidden Fields from the Initial Field Distribution

The initial field distribution may contain fields that cannot be used for dose calculations. Some fields might also be impossible to deliver due to the physical characteristics of the treatment unit (some gantry and/or couch rotations may not be feasible for the treatment unit). To perform plan geometry optimization only for valid fields, the following fields are excluded from the initial field distribution:

■ Fields intersecting the end(s) of the CT stack

   The field geometry in the initial field distribution is checked for fields entering the patient through the ends of the CT stack. If found, such fields are removed.

■ Fields with forbidden gantry/couch angle combinations

   The PGO reads the forbidden gantry/couch angle combinations from the `GantryCouchAngleCombinations.txt` file from the beam data directory root. If this file is not found in the PGO directory, it is created automatically. You can edit this file to include individual specifications for forbidden gantry/couch angle combinations.

The format of the `GantryCouchAngleCombinations.txt` file is the following:

```
[n]                 [m]
[t1]                          [t2]    ...    [tm]
[g1]                0/1       0/1     ...    0/1
[g2]                0/1       0/1     ...    0/1
...
[gn]                0/1       0/1     ...
```

where

n	=	Number of limits for gantry angle
m	=	Number of limits for couch angle
g1	=	First limit for gantry angles
gn	=	Last limit for gantry angles
t1	=	First limit for couch angles
tm	=	Last limit for couch angles
0	=	Forbidden gantry/couch angle combination
1	=	Allowed gantry/couch angle combination

The following shows an example of the `GantryCouchAngleCombinations.txt` file.

36			36										
	0	10	20	30	40	50	60	70	80	...	330	340	350
0	1	1	1	1	1	1	1	1	1	...	1	1	1
10	1	1	1	1	1	1	1	1	1	...	1	1	1
20	1	1	1	1	1	1	1	1	1	...	1	1	1
30	1	1	1	1	1	1	1	1	1	...	1	1	1
40	1	1	1	1	1	1	1	1	1	...	1	1	1
50	1	1	1	1	1	1	1	1	1	...	1	1	1
60	1	1	1	1	1	1	1	1	1	...	1	1	1
70	1	1	1	1	1	1	1	1	1	...	1	1	1
80	1	1	1	1	1	1	1	1	1	...	1	1	1
...	...	...	...	...	...	...	...	...	...	...	...	...	...
330	1	1	1	1	1	1	1	1	1	...	1	1	1
340	1	1	1	1	1	1	1	1	1	...	1	1	1
350	1	1	1	1	1	1	1	1	1	...	1	1	1

Figure 32   Example Forbidden Gantry/Couch Angle Combination File

In an automatically created gantry/couch angle combinations file, the limits for gantry and couch angles are specified with 10-degree intervals. Additional ranges for the limiting angles can be entered in, for example, MS Excel.

Note: *The number of specified gantry limits must be equal to* n, *and the number of specified couch limits equal to* m; *otherwise the PGO cannot read the gantry/couch angle combinations file.*

Final Number of Fields in the Plan

The final number of fields left in the treatment plan after the global optimization is controlled with the following parameters:

- *Minimum number of fields*—If this value equals the maximum number of fields, the specified number of fields is left in the final plan.
- *Maximum number of fields*—If this value exceeds the Minimum number of fields, the final field geometry has an optimal number of fields which belongs to the specified range.

The optimal number of fields is determined from the value of the objective function as follows: if the value of the objective function increases because of the removal of fields, the removal is canceled and the value of the field reduction rate is reduced to one half of the original value. Then the optimization iteration is re-calculated with the reduced field reduction rate. This is continued until the

- Decreased value of the objective function is obtained, and fields are removed according to the current field reduction rate, or
- Removal of the fields is canceled and the global optimization stops.

The effect of the number of fields on the objective function is adjusted with the field number objective (see Figure 33 on page 218).

Number of IMRT Iterations

The number of IMRT iterations run during one PGO iteration in the global optimization mode is controlled with a parameter value. It is recommended to use the minimum value of 3 for this parameter.

Field Reduction

The number of fields to be removed at the end of a global optimization iteration is controlled with the Field reduction rate (FRR) parameter. The number of fields to be removed is calculated as:

Eq. 52
$$n_{\text{removed}} = \text{FRR} \times (n_{\text{left}} - n_{\text{min}})$$

where

n_{removed}	=	number of fields to be removed
n_{left}	=	number of fields which are currently included in the plan
n_{min}	=	minimum number of fields to be left in the final plan

As a result, global optimization aims at leaving n_{min} fields in the plan.

Field Number Objective
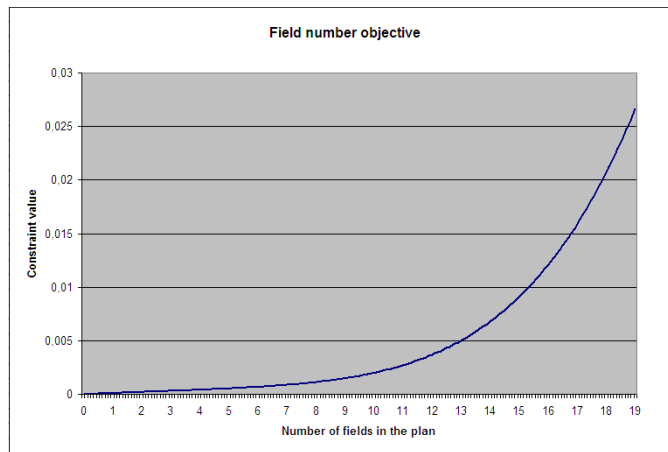
Figure 33   Shape of the Field Number Objective

With the Field number objective, the number of fields in the final plan is typically limited to fewer than 10 fields. The strength of the objective is adjusted with a weight parameter.

Lateral Inhibition

To prevent the PGO from removing all fields entering from a bad direction during the first global optimization iterations, the algorithm performs a lateral inhibition calculation. Lateral inhibition enhances

the values of the objective function close to removed fields. The inhibition gives increased objective function values to fields located close to removed fields, which results in retaining these fields in the plan. The calculation of the lateral inhibition is cumulated in the values of the objective function within one iteration. The effect of lateral inhibition is reset when the next iteration starts. The shape of the lateral inhibition function (LI) is a linear combination of cosine powers:

Eq. 53

$$LI = C \times (\cos^{2.5}\alpha + \cos^{18}\alpha) \times std$$

where

C   =   value of the weight parameter to control the strength of the lateral inhibition

α =   angle to the removed field

std   =   standard deviation of the field removal effects

The shape of the lateral inhibition function with std = 1 is shown in the figure.
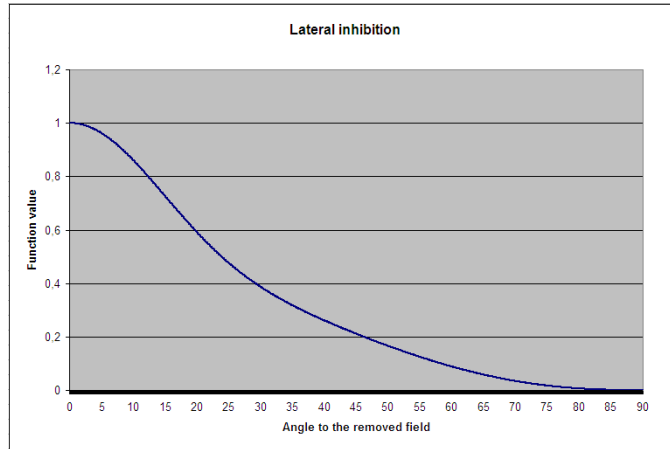
Figure 34   Shape of the Lateral Inhibition Function

The values of the objective function (OF) are then updated with the lateral inhibition as:

Eq. 54

$$OF_{new} = OF_{old} + LI$$

Thus, the importance of fields located close to a removed field is increased in relation to the remaining fields.

Proximity Effect

Sometimes the PGO results in plans containing fields located close to each other. In a final treatment plan, this is usually considered undesirable, because it can easily produce hot spots in normal tissue. To avoid closely located fields in the final treatment plan, the PGO performs a proximity effect calculation. The proximity effect is calculated similarly to the lateral inhibition, but in this case α is the angle to the closest field in the plan. The weight for the proximity effect calculation is adjusted with a parameter value. The amount of the proximity effect is then subtracted from the original values of the objective function to decrease the importance of fields located close to each other.

Minimum Field Separation Angle

Another mechanism of the PGO to exclude fields located close to each other is using a limiting value for the angle between fields in the final field configuration. The value for the limiting angle can be controlled by a parameter value.

Initial Field Removal Effects

The values of the field removal effects calculated during the first iteration are preserved for further use. These values contain information about the geometry of the patient, which is not included in the following iterations. The retained initial field removal effect values are included in the subsequent iterations by adding their weighted values into the current values of the objective function. The weight given to the initial field removal effects can be adjusted with a parameter value.

Local Optimization Mode

The local optimization continues from the result of the global optimization by fine-tuning parameters controlling the couch angles (for non-coplanar field geometry) and gantry angles (for both coplanar and non-coplanar field geometries). The collimator angles are also calculated if the limiting value for the collimator angle separation between adjacent fields is larger than zero. The local optimization does

not change the number of fields in the plan, but it can test any couch and gantry angle combinations to find the optimal geometry. The progress of the local optimization is shown with the objective function curve and the Number of iterations parameter.

The local optimization can be performed in two modes that are defined as a calculation option for optimization: the Downhill Simplex method and the Powell method[35]. In addition to the mode, the maximum number of local optimization iterations is controlled with a calculation option.

The information about the best field configuration found is stored throughout the local optimization to make it always available if the local optimization is interrupted.

The local optimization can also be run alone without first running the global optimization. This might be useful for testing purposes. However, the best beam angle optimization results are achieved by running both global and local optimizations.

Note: *The Simplex and the Powell methods require the objective function evaluations only, not the derivatives.*

Number of IMRT Iterations in Objective Function Evaluations

The number of fluence optimization iterations to be run within the local optimization iteration can be controlled with a parameter value.

Initialization Phase

Initialization Phase in the Simplex Algorithm. In the initialization phase of the Simplex algorithm, the corner points of the original simplex are generated. The number of the corner points is $N + 1$, where N is the number of parameters to be optimized, that is, the gantry angles in the 2D case, and the gantry and couch angles in the 3D case. The generation of each corner point requires a calculation of the objective function. The distance from each corner point to the starting point (the amount of change applied to each parameter in the construction phase of the simplex) is controlled by a parameter value. This value is common for gantry and couch angles.

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35. For information about the optimization methods, refer to *Numerical Recipes in C: The Art of Scientific Computing* (William H. Press, et al.)

Initialization Phase in the Powell Algorithm. The Powell algorithm calculates line minimizations along the specified search directions. The search directions are initialized with unit vectors. Thus, in the first Powell iteration, each parameter is optimized separately. The initial step size is controlled with the same parameter value as is used for the Simplex algorithm. The search space for each parameter is expanded until there is a minimum point found between the line end points.

Optimization Phase

Optimization Phase in the Simplex Algorithm. After the construction of the original Simplex, the corner points are modified according to the algorithm schema. New corner points are found in Simplex iterations. At the beginning of a Simplex iteration, the stopping criteria for the algorithm are checked. If none of the criteria are met, the algorithm continues by finding a new position for the worst corner point in the Simplex. If there is no improvement found in the value of the objective function, the Simplex stops.

Optimization Phase in the Powell Algorithm. After initializing the search directions with unit vectors, the Powell proceeds according to the algorithm schema by finding the conjugate search directions. The calculations performed during the line minimizations along the current search directions are called Powell iterations. At the beginning of a Powell iteration, the stopping criteria for the algorithm are checked first.

Additional Stopping Criteria

In addition to the conditions in the optimization phase, the local optimization uses three additional stopping criteria:

- Number of objective function calculations
- Convergence of the algorithm
- Invalid field parameters

Number of Objective Function Calculations. The maximum number of objective function calculations, that is, the number of local optimization iterations, can be used as a stopping criterion in the local optimization mode. This parameter is included in the list of input

parameters for the PGO. However, it is not recommended to define a low value for this parameter, because the algorithm may not have reached a minimum point if the execution is stopped too early.

Note: *In the Powell algorithm, the number of the calculated local optimization iterations is checked only at the beginning of a Powell iteration, not during the iteration. Therefore, the total number of local optimization iterations may exceed the given input parameter value.*

Convergence of the Algorithm. The convergence of the algorithm stopping criterion is used only for the Simplex algorithm.

The convergence of the algorithm is checked at the beginning of a Simplex iteration. If no significant changes are detected in the value of the objective function during recent iterations, the Simplex algorithm is stopped.

The evaluation of the convergence is controlled by the following parameter values:

- Number of Simplex iterations which is included in the evaluation.
- Limit value for the amount of change in the value of the objective function, which determines whether the optimization is continued.

These parameters are not PGO input parameters.

Invalid Field Parameters. Depending on the properties of the patient geometry and/or the definition of the valid gantry and couch angles, valid field parameters may not be found when generating new field directions in the local optimization. If valid field parameters cannot be found after a certain number of trials, the local optimization is stopped.

Progressive Resolution Optimizer (PRO) Algorithm

The Progressive Resolution Optimizer (PRO) algorithm creates VMAT (RapidArc) plans based on dose-volume objectives. VMAT fields use DMLC, variable dose rate and variable gantry speeds.

The PRO algorithm generates a sequence of control points which define MLC leaf positions and MU/deg as a function of gantry angle. MU/deg is encoded in DICOM and the Varian system database with the cumulative meterset weight, which defines the increase in MU between control points relative to the total MU in the field. This

information is transferred to the treatment machine as such, and the machine control system determines how dose rate and gantry speed will be modulated to deliver the plan. After dose is calculated, Eclipse shows estimated dose rate and gantry speed values in the Field Properties and MLC Properties pages. These values are estimates, and they are not part of the information sent to the treatment machine.

The PRO algorithm uses an objective function to optimize the plan and to evaluate its quality. The objective function is the sum of the dose-volume and other user-defined objectives.

Progressive Resolution

The initial conditions for the PRO algorithm are defined using control points to represent each VMAT field. The algorithm uses multi-resolution approach (first described in the research on volumetric modulated arc therapy[36]) to optimize the plan. This means that the dose is modeled using first a lower number of dose calculation segments that are distributed evenly in each field. The number of dose calculation segments increases when moving from one multi-resolution level to another.

The dose in a dose calculation segment is calculated from the combined fluence through the MLC apertures at the control points located within a certain sector of the arc. Leaf motion is modeled by interpolating leaf positions between the control points. Leaf tongues are modeled by modifying the MLC aperture outline to effectively account for the tongue-and-groove effect.

The angle resolution of the dose calculation segments gets more accurate as the optimization progresses, and in consequence, the dose also gets more accurate. The number of control points remains the same during the whole optimization.

At the beginning of the optimization, the initial MLC shapes are conformed to the targets and the initial dose rates are equal for all dose calculation segments. The MLC shapes and dose rates of the different control points in the VMAT field are optimized. During the initial phases of the optimization bigger adjustments are made in leaf sequencing. The size of these adjustments decreases as the optimization progresses through the levels.

36. Otto, K: Volumetric Modulated Arc Therapy: IMRT in a Single Arc, Medical Physics, Vol. 35, no. 1, 2008, 310–317

During the optimization, the algorithm proceeds through multi-resolution levels progressively increasing the accuracy of the dose calculation. At the first multi-resolution level, only a few dose calculation segments are used to model the dose, and each multi-resolution level contains progressively more dose calculation segments. The angle between the resulting dose calculation segments on the last multi-resolution level (4) will be approximately 2°-4°. The total number of dose calculation segments used depends on the span of the arc.

Inside each multi-resolution level there are several steps. Each step has its own internal calculation parameter set. The optimization allows some discontinuities in the delivery during early phases of the optimization, and decreases the size of the discontinuities stepwise as the optimization progresses. At the step borders, the delivery is forced to be within specified discontinuity levels. This may increase the objective function values when moving from one step to the next, and a peak in the objective function curve may be seen. The number of steps in different multi-resolution levels varies. Due to the nature of the optimization process, the PRO algorithm is not fully deterministic. Therefore successive optimizations with the same constraints may yield different results.

Dose Computation in the PRO Algorithm

A fast multi-resolution dose (MRDC) calculation is performed for each dose calculation segment. The MLC configuration and dose rate are converted into a fluence, which models the leakage caused by the rounded leaf ends, and the transmission (See Chapter 10, Section "Transmission and leakage" on page 250).

The dose calculation from the fluences is based on multi-resolution 3D convolution of Monte-Carlo-generated point-spread function kernels. For information on the dose calculation, see "Multi-Resolution Dose Calculation (MRDC) Algorithm" on page 211.

Avoidance Sectors

Avoidance sectors are ranges of gantry rotation with a zero delivered dose rate. You can define up to two avoidance sectors for each arc field in the optimization. The minimum length for an avoidance sector is 15

degrees. Similarly, the minimum length for the beam-on sector between two avoidance sectors, or between gantry start/stop angles and an avoidance sector is 15 degrees.

Avoidance sectors are supported only for Varian treatment units.

Automatic Normal Tissue Objective

The Automatic Normal Tissue objective uses a set of internal parameters, so the parameters in the Normal Tissue Objectives dialog box have no effect on it. The internal parameters depend on the distances of the high dose areas from the target, and they are adapted dynamically so that they are suitable for the patient anatomy and the objectives during the optimization. The Automatic Normal Tissue objective monitors the area within a certain distance around the target, and if there are doses that are exceptionally high considering the distance from the target, it tries to reduce the dose at the area using the user-defined priority value.
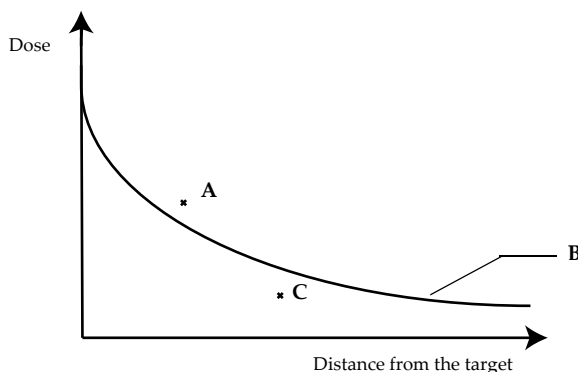
A. The dose at this point is above the accepted dose level, and therefore the optimization tries to reduce the dose in this area. **B.** Accepted dose level for this case. **C.** Points within this region are not affected.

Figure 35   Adjustment Criteria for Automatic Normal Tissue Objective

Mean Dose Objective

Mean dose objective is used to define the mean dose that should not be exceeded for a structure. It defines the mean dose in grays, but does not define any percentage of the structure that should not receive more than this dose. Mean dose objective is visualized in DVH during

optimization, and it can be adjusted interactively during optimization. You can add one mean dose objective per structure. Mean dose objective cannot be used to increase the dose to a structure.

Jaw Tracking

Jaw tracking dynamically moves the collimator jaws during beam-on to keep them as close to the target projection as possible. This reduces leakage between the MLC leaves. The initial user-defined collimator jaw positions for the plan are used as the maximum limit for the jaws. Jaw tracking does not move the collimator jaws outside this maximum limit.

Note: *Not all VMAT-capable Varian linear accelerators support jaw tracking. The option can be selected in VMAT Optimization dialog box only for plans to be delivered with a treatment machine that supports jaw tracking. Jaw tracking is automatically on for Elekta MLCi and MLCi2.*

Intermediate Dose

With the PRO algorithm you can optimize the plan, calculate the dose, and then use the calculated dose as an intermediate dose when continuing the optimization. This can be done manually by restarting the optimization and selecting "Use current plan dose as an intermediate dose for optimization" or automatically by selecting "Automatic intermediate dose" in the VMAT optimization dialog box when optimizing the first time. This is useful especially if the DVH calculated during arc optimization deviates from the DVH produced during dose calculation, for example when there is a lot of heterogeneity in the volume to be treated.

The optimization algorithm can adjust the leaf sequences based on the intermediate dose. It calculates the error between the first round optimization result and the dose calculation, and during the second optimization round, when the optimization is finalized, it compensates for the differences and tries to achieve a better agreement. The second optimization round starts at the last multi-resolution level (4).

Restarting Optimization

Optimization can be restarted from user-defined arc fields. The user-defined fields may be produced, for example, in a previous arc optimization, or it may be created manually.

Before restarting the optimization, the algorithm re-samples the arc treatment to suitable control point spacing. The optimization restarts from the last multi-resolution level that has the most accurate dose modeling. To allow bigger adjustments to the leaf sequence, the user should rewind the multi-resolution levels. This will allow more flexibility in changing the leaf sequence. However, the dose on the earlier multi-resolution levels, calculated with the MRDC algorithm, is less accurate.

If the arc field does not contain a DMLC, optimization is completely restarted from the first resolution level, and the DMLC is not taken into account in the optimization.

Calculation Options for the PRO Algorithm

The PRO algorithm has the following calculation options:

- *Inhomogeneity correction*—Defines whether tissue heterogeneity correction is applied during optimization.
- *Air cavity correction*—An additional parameter for fine-tuning inhomogeneity correction. This parameter has no effect if the Inhomogeneity correction parameter is set to *Off*. When the air cavity correction option is used, the dose in an air cavity is smaller than without this option. On the other hand, the target/any part of the target should not be contoured in air, as the target will not get enough dose.

System Configuration for Dose Optimization

Note: *When configuring dose optimization algorithms, notice the following:*

- *It is important to configure the system so that it corresponds to the characteristics of the treatment machine.*

- *Periodically perform follow-up measurements and compare with the dosimetric beam data used for configuring the beam. If fluctuations are large and the configured beam data no longer represents the average beam delivered by the machine, reconfigure the beam data using the newer dosimetric beam data.*

- *Measure all dosimetric beam data in as stable conditions as possible.*

- *Use the same file naming conventions in beam data measurements (input files) and in Beam Configuration (Therapy Unit name), and name the input files so that it is easy to match the beam data to the treatment unit during the configuration process.*

Beam Data Measurements for Dose Optimization

The configuration of the DVO, PRO and PGO algorithms requires the same basic measured beam data as the calculation algorithms used for the dose calculation.

The following basic measured beam data is required for the configuration of all three optimization algorithms:

- Open field profiles (OPP) for several field sizes at five depths. The minimum number of measured profiles required is three, but using five is recommended.

- Open field diagonal profile (DPR) for largest field size at five depths. It is possible to configure DVO, PRO and PGO algorithms without diagonal profiles. However, using diagonal profiles may improve the accuracy. It is recommended to use five measured diagonal profiles.

- Open field depth dose curves (OPD) for same field sizes as profiles

- Source-phantom distance (SPD) in cm

- Calculation grid size in cm. The calculation grid size used by MRDC dose calculation during optimization. For DVO and PGO, the calculation grid size is fixed to 0.25 cm. The default calculation grid size for PRO is 0.25 cm. When configuring PRO for Elekta Beam Modulator, the grid size of 0.20 cm must be used.

- Nominal energy (In MRDC, the nominal energy is a parameter related to the maximum energy in MV of the photon spectra. The configuration program further modifies the photon spectra together with other configuration parameters so that the calculated dose matches with the measurements.)
- Profile measurement depths in cm

Note: *The source-to-phantom distance (SPD) must be the same in the configuration of the dose calculation algorithm and the configuration of the DVO and PRO algorithms. The SPD value is defined in the General Parameters in Beam Configuration.*

The DVO, PRO and PGO have some special beam data configuration requirements:

- The maximum field sizes must be defined in the General Parameters (for instance, a 40×40 cm^2 field)
- Due to the characteristics of the optimization algorithm, the nominal energy (defined in the General Parameters) may not exceed 30 MV.

For a detailed description of the measured depth dose curves and the measured profile curve field sizes, see Chapter 4, Section "Configuration of Photon Beams" on page 55.

Based on the measured beam data, the configuration produces the Model Parameters for the MRDC and an indicator parameter (Maximum Error for Dose Estimation) for the successfulness of the configuration. The parameter is the maximum gamma index with the criteria of 1% for dose difference and 1 mm for the distance to agreement. (Typically, the value for a successful configuration should be smaller than 5. If the value is higher, the reason could lie in the measured beam data).

Model Parameters for the Progressive Resolution Optimizer (PRO)

The configuration of the PRO needs the definition of the following parameters in Beam Configuration:

Table 32 Absolute Dose Calibration Parameters for PRO

Parameter	Description
Absolute dose reference field size [mm]	Size of the reference field used in configuration, expressed in millimeters. Usually, this should be the same size that was used to normalize the measured output factor table (that is, the field size for which the output factor = 1.0).
Absolute dose calibration source-phantom distance	Distance between the source and the surface of the phantom (SPD) used in configuration, expressed in millimeters. (For an illustration of the geometry, see Figure 15 on page 103.)
Absolute dose calibration depth [mm]	Depth of the reference point used in configuration, expressed in millimeters. (For an illustration of the geometry, see Figure 15 on page 103.)
Reference dose at calibration depth [Gy]	Absolute dose in water for the reference field size at the reference point at the calibration depth, expressed in Gray.
Reference MU at calibration depth [MU]	MU given to produce the reference dose for calibration.

Configuration of the Dose-Volume Optimizer in Beam Configuration

You can configure the DVO algorithm based on:

- Previously configured beam data for a dose calculation algorithm (AAA/Acuros XB).
- Previously configured beam data for a photon optimization algorithm (PRO/DVO/PGO). For instructions on copying the beam data from another calculation model, refer to *Beam Configuration Reference Guide*.
- Basic measured beam data.

Note: *The recommended procedure is to first configure the PRO algorithm (if available), and then configure the DVO based on that. If the PRO algorithm is not available, it is recommended to configure the DVO based on a dose calculation algorithm (AAA/Acuros XB).*

This section only briefly covers the configuration of the DVO algorithm in Beam Configuration. For more details on using Beam Configuration, refer to *Beam Configuration Reference Guide*.

To Configure the DVO based on Configured AAA/Acuros XB

1. Verify that the dose calculation model you want to use (AAA/Acuros XB) is correctly configured in the system.

2. In the Scope window, select the optimization model to configure.

3. Choose **Insert > New Beam Data**.

4. Select the **Copy existing calculation model data to the optimization model** option.

5. Select the configured calculation model to use for the configuration of the new optimization model.

6. Click **OK**.

7. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. For more information on the grid size, see "Beam Data Measurements for Dose Optimization" on page 229.

8. In the Focus window, select the Open Field add-on and choose **Beam Data > Calculate Beam Data**.

9. If prompted to do so, select the beam data to be generated and then click OK to start the calculation.

To Configure the DVO based on Configured PRO/DVO/PGO

1. Go to Beam Configuration.

2. To add a calculation model for the DVO algorithm if not available, choose **Beam Data > Configure Calculation Models** and add the model.

3. In the Scope window, select the DVO calculation model and choose **Insert > New Beam Data**.

4. Define a therapy unit name for the calculation model and select the **Start with empty data** option.

5. Choose **File > Import > Eclipse Beam Data**, browse to the location of the appropriate beam data and import the data.

6. Match and assign the open field add-on.

7. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. For more information on the grid size, see "Beam Data Measurements for Dose Optimization" on page 229.

8. In the Focus window, select the Open Field add-on and choose **Beam Data > Calculate Beam Data**.

9. If the configuration was successful, approve the data.

To Configure the DVO based on Measured Beam Data

1. Go to Beam Configuration.

2. To add a calculation model for the DVO algorithm if not available, choose **Beam Data > Configure Calculation Models** and add the model.

3. In the Scope window, select the DVO calculation model and choose **Insert > New Beam Data**.

4. Define a therapy unit name for the calculation model and select the **Start with empty data** option.

5. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. For more information on the grid size, see "Beam Data Measurements for

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Dose Optimization" on page 229.

6. To add the open field add-on, choose **Insert > New Add-On**.

7. To import the beam data in the w2CAD format, go to the Focus window, select Open Field, choose **File > Import > Measured Diagonal Profiles**, **Measured Depth Doses**, or **Measured Profiles**, depending on the measurement type, and navigate to the location of your measured beam data files.

8. In the Focus window, select the Open Field add-on and choose **Beam Data > Calculate Beam Data**.

9. If the configuration was successful, approve the data.

Configuration of the Progressive Resolution Optimizer in Beam Configuration

You can configure the PRO algorithm based on:

■ Previously configured beam data for a dose calculation algorithm (AAA/Acuros XB).

■ Previously configured beam data for a photon optimization algorithm (PRO/DVO/PGO). For instructions on copying the beam data from another calculation model, refer to *Beam Configuration Reference Guide*.

■ Basic measured beam data.

Note: *The recommended procedure is to first configure the dose calculation algorithm (AAA/Acuros XB), and then configure the PRO based on that.*

This section only briefly covers the configuration of the PRO algorithm in Beam Configuration. For more details on using Beam Configuration, refer to *Beam Configuration Reference Guide*.

To Configure PRO based on Configured AAA/Acuros XB

1. Verify that the dose calculation model you want to use (AAA/Acuros XB) is correctly configured in the system.

2. In the Scope window, select the optimization model to configure.

3. Choose **Insert > New Beam Data**.

4. Select the **Copy existing calculation model data to the optimization model** option.

5. Select the configured calculation model to use for the configuration of the new optimization model.

6. Click **OK**.

7. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. For more information on the grid size, see "Beam Data Measurements for Dose Optimization" on page 229.

8. In the Focus window, select the Open Field add-on and choose **Beam Data > Calculate Beam Data**.

9. If prompted to do so, select the beam data to be generated and click **OK** to start the calculation.

To Configure the PRO based on Configured PRO/DVO/PGO

1. Go to Beam Configuration.

2. To add a calculation model for the PRO algorithm if not available, choose **Beam Data > Configure Calculation Models** and add the model.

3. In the Scope window, select the PRO calculation model and choose **Insert > New Beam Data**.

4. Define a therapy unit name for the calculation model and select the **Start with empty data** option.

5. Choose **File > Import > Eclipse Beam Data**, browse to the location of the appropriate beam data and import the data.

6. Match and assign the open field add-on.

7. In the Focus window, select Open Field, then choose **Insert > New Absolute Dose Calibration Parameters**, and type the same values to the parameters as are used in the AAA/Acuros XB configuration.

   The parameter values must be the same as in the AAA/Acuros XB configuration.

8. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. For more information on the grid size, see "Beam Data Measurements for Dose Optimization" on page 229.

9. In the Focus window, select the Open Field add-on and choose **Beam Data > Calculate Beam Data**.

10. If the configuration was successful, approve the data.

To Configure the PRO based on Measured Beam Data

1. Go to Beam Configuration.

2. To add a calculation model for the PRO algorithm if not available, choose **Beam Data > Configure Calculation Models** and add the model.

3. In the Scope window, select the PRO calculation model and choose **Insert > New Beam Data**.

4. Define a therapy unit name for the calculation model and select the **Start with empty data** option.

5. Absolute Dose Calibration Parameters default values are added.

6. Type the same values to the Absolute Dosimetry Calibration Parameters as are used in the AAA/Acuros XB configuration.

   The parameter values must be the same as in the AAA/Acuros XB configuration.

7. In the Focus window, select **Dose Calculation Parameters**, and select the calculation grid size in cm from drop down list. For more information on the grid size, see "Beam Data Measurements for Dose Optimization" on page 229.

8. To add the open field add-on, choose **Insert > New Add-On**.

9. To import the beam data in the w2CAD format, go to the Focus window, select Open Field, choose **File > Import > Measured Diagonal Profiles**, **Measured Depth Doses**, or **Measured Profiles**, depending on the measurement type, and navigate to the location of your measured beam data files.

10. In the Focus window, select the Open Field add-on and choose **Beam Data > Calculate Beam Data**.

11. If the configuration was successful, approve the data.

Configuring the PGO Algorithm

The appropriate way of creating a PGO calculation model is to have it use the same beam data as the DVO calculation model. This is defined in the Add Calculation Model dialog box in Beam Configuration (choose **Beam Data > Configure Calculation Models**). It is not possible to assign existing beam data from another model to the PGO in the Insert New Beam Data dialog box. For more information on Beam Configuration, refer to *Beam Configuration Reference Guide*.

Input Parameters for the PGO

The table lists the input parameters for the PGO algorithm used to control the execution. The table also includes information about the parameter types, their value ranges and default values (IEC 61217 for couch, gantry or collimator angles).

Table 33 Input Parameters for the PGO

Parameter name	Range (IEC 61217 for couch, gantry or collimator angles)	Default value (IEC 61217 for couch, gantry or collimator angles)	Use of Parameter
Initial field distribution	Coplanar, Non-coplanar, None	Coplanar	The initial coplanar (2D) and non-coplanar (3D) field geometries are created as described in "Initial Field Geometries" on page 214. Selecting None skips the global optimization and uses the active plan in Eclipse as input for local optimization.
Initial number of fields	2–400	71	Defines the initial number of fields to be created for the global optimization. However, the field geometry is checked before running the global optimization for fields that enter the patient through the end(s) of the CT stack (these fields are excluded). The number of fields left in the initial field distribution after the check may be lower than the number specified by this parameter.
Minimum number of fields	2–15	5	Defines the lower limit for the number of fields to be left in the plan after global optimization.
Maximum number of fields	2–15	9	Defines the upper limit for the number of fields to be left in the plan after global optimization.

Table 33 Input Parameters for the PGO (continued)

Parameter name	Range (IEC 61217 for couch, gantry or collimator angles)	Default value (IEC 61217 for couch, gantry or collimator angles)	Use of Parameter
Maximum collimator variation [deg]	0–180	0	Controls the variation of the collimator angle values between adjacent fields in the initial field distribution. ■ 0 = Leaves the collimators to zero angle (IEC 61217 scale, which corresponds to 180 degrees in the Varian Standard scale). ■ 180 degrees = The collimators are rotated between 270 degrees (that is, -90 degrees) and 90 degrees so that the direction of the MLC leaves coincides with the shortest dimension of the PTV in the BEV. This choice aims at the lowest possible number of carriage groups, and often also minimizes the exposure of healthy tissue. ■ > 180 degrees = The collimator angles stay within the specified limit. The movement direction of the leaves coincides with the shortest dimension of the PTV. *Individual machine limits for collimator angle rotation are not taken into account by the PGO. Constraining the collimator angle values to 270–90 degrees is considered sufficient for most linear accelerators.*
Coplanar offset angle [deg]	0–90	0	Adjusts the offset to the starting gantry angle (default = 0 degrees in IEC 61217, which corresponds to 180 degrees in the Varian Standard scale) for coplanar initial field distribution. Does not affect the non-coplanar initial field distribution.
Maximum elevation angle for non-coplanar fields [deg]	0–90	90	Controls the maximum elevation from the coplanar plane for non-coplanar initial field distribution.
Fluence iterations per global geometric iteration	1–20	3	Defines the number of fluence optimization iterations to be run in the global optimization.

Table 33 Input Parameters for the PGO (continued)

Parameter name	Range (IEC 61217 for couch, gantry or collimator angles)	Default value (IEC 61217 for couch, gantry or collimator angles)	Use of Parameter
Field reduction rate	0–1	0.5	Controls the number of fields to be removed from the plan during the global optimization. Increasing the value also increases the number of fields to be removed in each global geometry iteration, which makes the algorithm faster. However, it is not recommended to increase this value above 0.5.
Field number constraint weight	0–1	0.4	Controls the cost for leaving more fields in the final plan. For further details, see "Field Number Objective" on page 218.
First global iteration weight	0–1	0.1	For a description of the use of this parameter, see "Initial Field Removal Effects" on page 220.
Lateral inhibition weight	0–1	0.4	For a description of the use of this parameter, see "Lateral Inhibition" on page 218.
Proximity effect weight	0–1	0.4	For a description of the use of this parameter, see "Proximity Effect" on page 220.
Minimum field separation angle [deg]	0–90	10	Controls how close to each other the fields are allowed to stay in the final plan after the global optimization. The parameter also applies to the local optimization.
Local geometric optimization mode	Simplex, Powell, None	Simplex	Defines the mode for the local optimization. Selecting None skips the local optimization.
Fluence iterations per local geometric iteration	1–20	3	Defines the number of fluence optimization iterations in the local optimization.
Maximum number of local optimization iterations	0–500	40	Defines the upper limit for the number of objective function evaluations to be calculated in the local optimization and controls the execution time of the local optimization. For more details, see "Number of IMRT Iterations in Objective Function Evaluations" on page 221.

Table 33 Input Parameters for the PGO (continued)

Parameter name	Range (IEC 61217 for couch, gantry or collimator angles)	Default value (IEC 61217 for couch, gantry or collimator angles)	Use of Parameter
Initial step size in local optimization [deg]	1–180	10	Defines the initial distance between the original and the new field direction in the local optimization. Used by Simplex and Powell optimization.

Chapter 10   Fluence Delivery Modeling Algorithms

General Features of Fluence Delivery Modeling Algorithms

In Eclipse, the final dose calculation for all MLC fields is based on fluences. Moreover, some of the optimization algorithms give their results as fluences. Arbitrary fluence patterns and field apertures for arc fields can be produced on a treatment unit by means of DMLC. Fluence delivery modeling describes how the use of DMLC is modeled in various contexts and algorithms.

Features that are taken into account in all fluence delivery modeling algorithms include leaf transmission, dosimetric leaf gap, and tongue-and-groove modeling. They are used in the final fluence calculation for all fields that contain an MLC, such as static MLC fields, IMRT fields and all arc fields. These features are also taken into account in the PRO algorithm.

Fluences needed by the final dose calculation are calculated as part of the dose calculation. This differs somewhat from version 10.0 or earlier dose calculation algorithms where the actual fluence of IMRT was calculated in LMC algorithm and delivered to dose calculation algorithm by client. The visible difference is that when the final dose is calculated using new dose calculation algorithms, the actual fluence of IMRT fields can be visualized after dose calculation, not immediately after LMC calculation that performs the leaf sequencing only.

Note: *Because of the change in actual fluence handling, version 11.0 or later dose calculation algorithms require the use of version 11.0 or later of the LMC algorithms. The previous dose calculation algorithms work only with previous LMC algorithms (version 10.0 or earlier).*

Transmission in Fluence Delivery Modeling Algorithms

The MLC leaves do not block the radiation completely, but transmit a small amount of radiation directly through the leaves. The amount of the transmission can be configured for a given treatment unit and

energy in Beam Configuration (for more information on using Beam Configuration, refer to *Beam Configuration Reference Guide*). The configured transmission factor is used in all fluence calculations, including the internal fluence calculation of Leaf Motion Calculators (LMC) and final fluence calculation for static MLC, DMLC and arc fields. Transmission factor is defined also for block materials and the transmission factor for physical jaws is 0. In order to minimize the effects of the transmitted radiation, LMCs also compensate for the transmission while generating a leaf sequence. For more information on measuring the leaf transmission factor, see "Measuring the Leaf Transmission Factor" on page 267.

Dosimetric Leaf Gap in Fluence Delivery Modeling Algorithms

To achieve better off-axis dosimetric characteristics, the ends of the MLC leaves are rounded in some MLC devices. Because of the rounded shape, some radiation passes between the leaves even through completely closed leaf pairs (see the figure). This phenomenon is called the *rounded leaf end transmission*.

The fluence delivery algorithms deal with the rounded leaf end transmission by means of the *dosimetric leaf gap* configuration parameter. The algorithms model the shape of the leaf edges as sharp (as opposed to rounded) and take the rounded leaf transmission into account by shifting the leaf tip positions in the actual fluence calculation. Leaf tips are shifted by pulling each of them back by half the value of the dosimetric leaf gap parameter so that the gap between a fully closed leaf pair equals the dosimetric leaf gap parameter. The dosimetric leaf gap parameter can be defined in Beam Configuration for each treatment unit and energy (for instructions, see "Configuration of the MLC Parameters" on page 266). The spot size parameter affects effectively the penumbra shape as described in Chapter 4, Section "Tuning of the effective spot size parameters" on page 58.
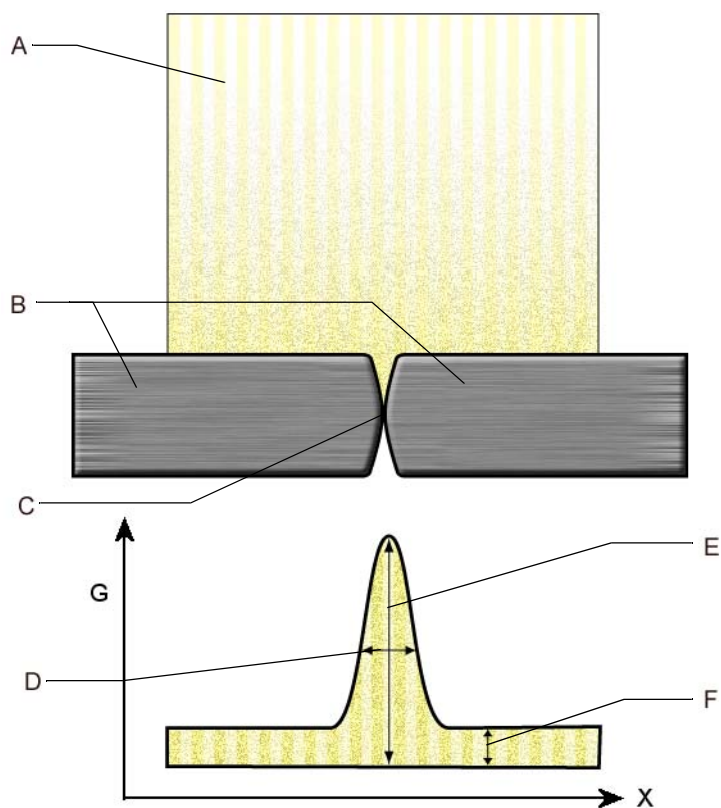
A. Radiation Beam **B.** MLC leaf **C.** Rounded leaf ends **D.** Value of dosimetric leaf gap **E.** Dose transmitted through closed, rounded MLC leaf ends **F.** Dose transmitted through MLC leaves **G.** Dose

Figure 36   Rounded Leaf End Transmission

Tongue-and-Groove Modeling
in Fluence Delivery Modeling Algorithms

To minimize the inter-leaf leakage, some MLC device models have a tongue-and-groove design.
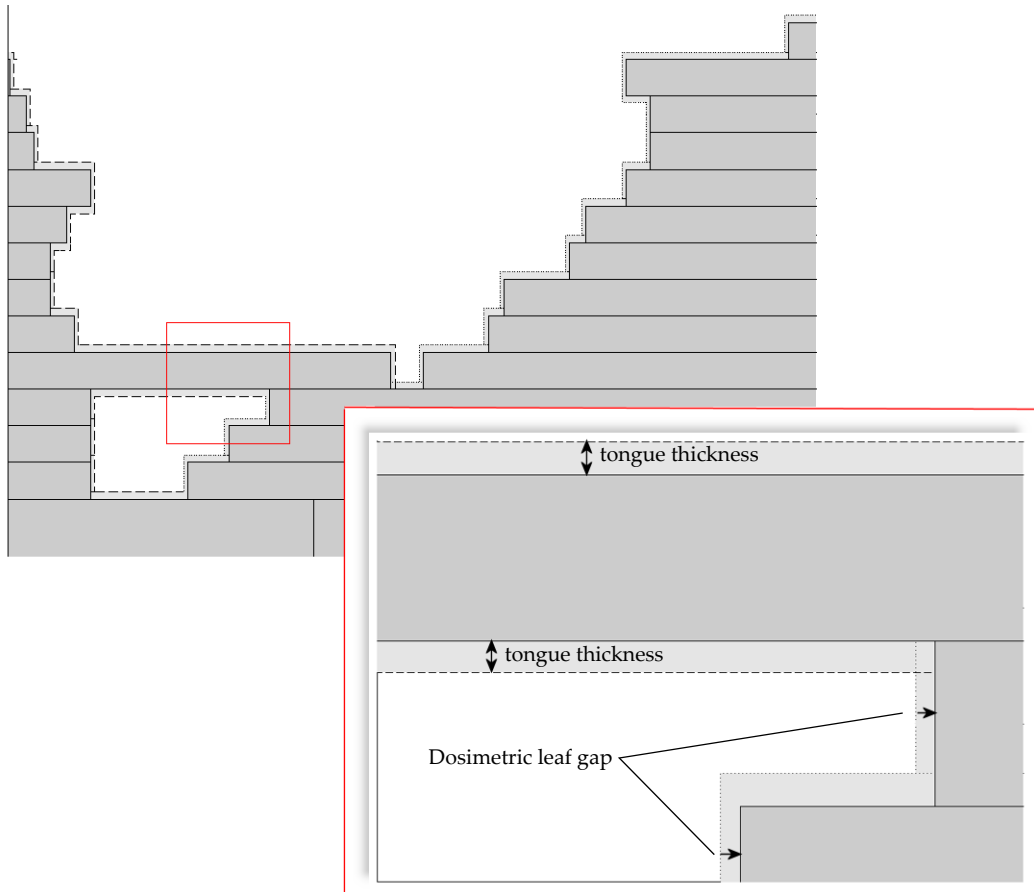
Figure 37   Tongue-and-Groove Design

An exposed tongue in a field modifies the delivered fluence by blocking some of the additional radiation. The amount of blocking is proportional to the ratio between the tongue and leaf widths. (The groove also modifies the fluence, but that effect is smaller and is not modeled in the algorithms.) This is called the tongue-and-groove effect.

The tongue-and-groove effect is modeled in the fluence delivery algorithms by extending the leaf projections in the direction perpendicular to the leaf motion with an approximate extension parameter (see the above figure), which is slightly smaller than the real tongue width. This parameter is not user-configurable, and it depends on the MLC model and algorithm version.

The tongue-and-groove effect is taken into account in all fluences used in dose calculation and is visible in the actual fluence shown for IMRT fields. The effect is more significant in DMLC and arc treatments than static MLC delivery techniques.

Leaf Motion Calculator (LMC)

The Leaf Motion Calculator (LMC) program calculates the DMLC leaf motion patterns required to deliver the dose defined by the optimal fluence[37]. Because of physical and mechanical characteristics of the DMLC device, the produced DMLC leaf motion patterns can deliver an actual fluence that only approximates the desired optimal fluence.

The LMC supports two delivery techniques for the dose dynamic delivery of an IMRT treatment

- Sliding Window (SW) technique (Varian and BrainLab MLC devices)
- Multiple Static Segments (MSS) technique (Varian, BrainLab, Siemens and Elekta MLC devices)

The leaf motion patterns for the MSS technique used in Siemens and Elekta MLCs are calculated using an advanced optimization method that takes into account the interdigitation limitations of the MLC device, while the leaf motion patterns for both the sliding window and MSS techniques used in Varian MLCs are calculated using a more direct algorithm.

This section describes how the leaf sequencing is done in these two techniques and how the MU factors are generated for the calculation of the dose distribution and MU in Eclipse.

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37. For another discussion on the topic, refer to Spirou SV & Chui CS: *Generation of Arbitrary Intensity Profiles by Dynamic Jaws or Multileaf Collimators*. Med. Phys. 1994, Jul; 21 (7): 1031–41

Sliding Window Method

The Sliding Window method is one of three commonly used DMLC intensity modulation methods, in addition to the Multiple Static Segments and Close-In methods.

The main idea of the Sliding Window method is to sweep MLC leaf pairs of varying aperture sizes and speed over a field during the beam-on. To achieve clinically applicable results, the following objectives must be respected:

- The beam-on time must be short to speed up the treatment and to avoid extra dose resulting from transmission and leakage.

- Because of the rounded leaf end transmission ("Dosimetric Leaf Gap in Fluence Delivery Modeling Algorithms" on page 242) and the minimum leaf gap, leaf pairs exposing the target to a low dose start behind the main collimators. This minimizes the additional dose for leaf pairs that give a very small total dose.

- The rounded leaf end transmission is configured as the *dosimetric leaf gap* parameter in the Beam Configuration. For information about this and the *minimum leaf gap* configuration parameter, see "System Configuration for Fluence Delivery Modeling" on page 258.

- The physical characteristics of the MLC device must be respected. This requires techniques for handling multiple carriage groups needed for larger fields, and leaf movement objectives. The maximum leaf speed and the minimum leaf gap must be respected.

Implementations of the Sliding Window method for field widths under the Effective Leaf Out of Carriage Distance (ELOC)[38] use the following strategy:

- Start of delivery (see the figure): Leaf pairs are at the left border of the target. Leaf pairs exposing the target to a normal or large amount of radiation are open and inside the target. Leaf pairs

---

38. Leaf out of Carriage Distance (LOC, leaf span). The maximum FX distance of adjacent MLC leaves. Also the maximum width of a subfield for the conventional sliding window method.

Effective Leaf out of Carriage Distance (ELOC). Same as LOC, but the leaf parking and the collimator FX margin distances are reduced from it. Defines the field size crossover point between a single carriage group and double carriage group treatments.

giving a very low dose remain behind the left collimator for some time at the beginning of the treatment. These leaf pairs start moving at the maximum speed once it is safe to include them in the treatment. This minimizes leaf gap effects.

- End of delivery: All leaf pairs are at the right edge of the target (see the figure).

- At least one leaf of a pair always moves at the maximum speed to minimize the delivery time. Because of the requirements for the beginning and the end of the delivery presented above, and the differences in the complexity of the image planes, the maximum speed is individual for each leaf pair.

Fluence to be delivered

First segment: Leaf pairs parked at the left border of the target

Last segment: Leaf pairs parked at the right edge of the target
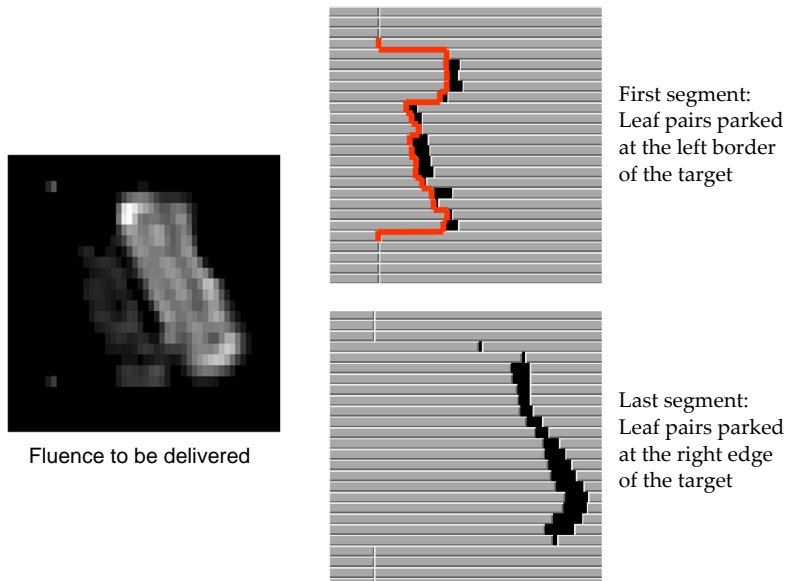
Figure 38   First and Last Segment Delivering a Fluence

Example Sliding Window Case

Input data

Consider the example of a 5×3 fluence matrix (three leaf pairs) in the table.

Table 34 Simple Fluence Matrix

Slice 0	0	0.5	1	0.6	0.8
Slice 1	0.2	0.5	0.7	0.5	0.2
Slice 2	0	0	0.4	0.6	0.3

Between the given points, the profile is considered linear. The individual slices are plotted in the figure. There are two local maxima in slice 0, while in slice 1 and 2 there is only one each.
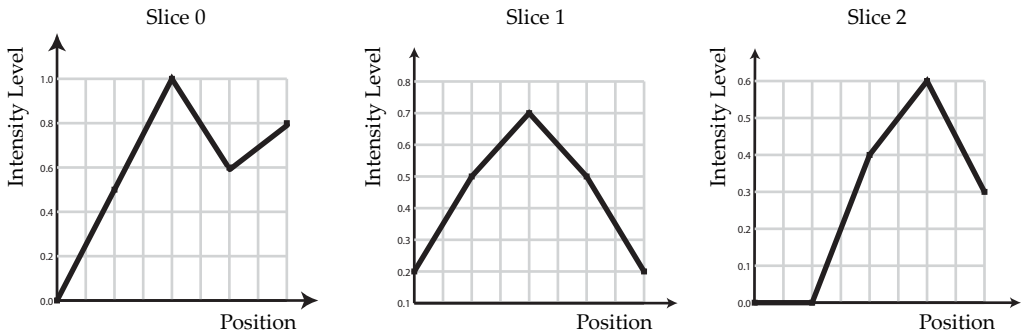
Figure 39   Plotted Intensity Profiles (Distributions) for Each Slice

Max leaf speed

The complexity Σ of a slice in terms of the Sliding Window method is given by the number and intensity deltas of incrementing segments.

Slice 0: $\Sigma = 0.5 + 0.5 + 0.2 = 1.2$

Slice 1: $\Sigma = 0.2 + 0.3 + 0.2 = 0.7$

Slice 2: $\Sigma = 0.4 + 0.2 = 0.6$

Slice 0 is the most complex slice, which gets the absolute (physical) maximum leaf speed as the maximum speed. Assuming a field width of 10 cm, a physical max. leaf speed of 2 cm/s, a dose rate of 600 MU/min (= 10 MU/s) and a desired output max. of 200 MU (at intensity 1), it takes 10.0/2 = 5 s to sweep the field at the physical maximum speed, during which 50 MU or 1/4th of the output maximum will be delivered. The beam-on time, measured in intensity T, is thus 1.2 + 0.25 = 1.45 (the total machine output is 290 MU).

The leaf motion plan for slice 0 is shown in the figure.
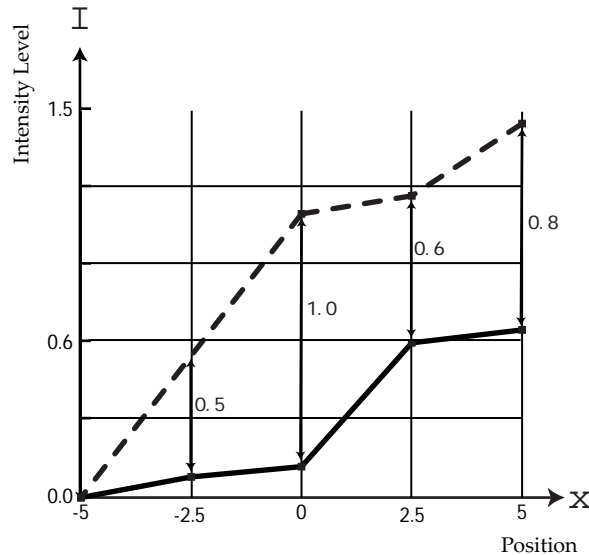
Figure 40   Leaf Motions for Slice 0

The width of the sliding window (the horizontal distance between the two trajectories) is thus, for instance, 0 cm at intensity level 0, approximately 4.7 cm at level 0.6, approximately 5 cm at level 1.1, and 0 cm again at level 1.45.

For all other slices, the leaf pairs are also closed at the right edge of the field at 1.45 (290 MU), so accordingly, their maximum speeds decrease.

For small fields with a width below ELOC, the other slices could be delivered with the same maximum speed, the leaf pair could stop closed at the right edge under a collimator jaw. However, this approach is not universal for all fields.

Transmission and leakage

If the above motion plan is put on the treatment unit, the profile delivered would not be the desired one, but the desired profile plus a certain amount of transmitted or leaked radiation at every point. Let I_x be the desired intensity at position x (x = -5.0, -2.5, 0, 2.5, 5 cm in this example) and $\alpha = 0.025$ an estimated weighted average of leakage and transmission factors. What would be delivered at every point would then be $I' = I_x + \alpha(T - I_x)$, which is considerably different to the initial data from Table 34 on page 248.

Table 35 Desired Intensity + Transmission and Leakage

Slice 0	0.04	0.52	1.01	0.62	0.81
Slice 1	0.23	0.52	0.72	0.52	0.23
Slice 2	0.04	0.04	0.43	0.62	0.33

The above figures are not only realistic, they also show that the significance of the unwanted extra radiation grows when the desired intensity decreases. This effect can, however, be corrected to some extent by solving the above equation for I_x, replacing every intensity point with $I^{new}_x = (1-\alpha)^{-1}(I_x - \alpha T)$ and feeding the new matrix to the algorithm. Negative values are clamped to zeros in the corrected intensity file.

Large-Field DMLC

With modulated fields wider than the Effective Leaf Out of Carriage Distance (ELOC), the carriages cannot move while the beam is on. In this case, the original field is split into subfields which are narrower than the ELOC and perform a Sliding Window algorithm for each subfield separately. Because it is practically impossible to connect sharp edges of subfields accurately, the subfields are given an overlapping area. When the beam is turned off for a carriage shift, all leaf pairs are required to form a window inside the overlapping area. An optimization strategy has been implemented to find out

- How many subfields are required
- Where the field must be split

Consider a leaf plan similar to Table 34 on page 248, but with a field width of 16 cm. One choice for the overlapping area for one slice would then be as shown in the figure. T_{off} would be the beam-on time intensity equivalent at which the beam is turned off for the carriage displacement. At that time, for this very slice, the window width is inside the physical carriage limits. Carriage groups would be from -8.0 cm to +4.5 cm and -4.2 cm to +8.0 cm, thus conforming to the ELOC, at maximum 14.5 cm. To reduce the sensitivity to uncertainties in patient and MLC leaf positioning, the window width should be as large as possible.

The field wider than the ELOC is split into two or three subfields, each smaller than the ELOC. The split to three fields is performed at fixed locations so that the maximum jaw over carriage distance is not exceeded. The two-field split minimizes the sum of the T-factors by selecting the crossfade position and width.

The additional leakage due to the collimator X-margins is modeled and reduced from the optimal fluences. Once the actual fluence is calculated for the first field, the actual fluence is subtracted from the initial optimal fluence, resulting in a new optimal fluence for the next carriage group.
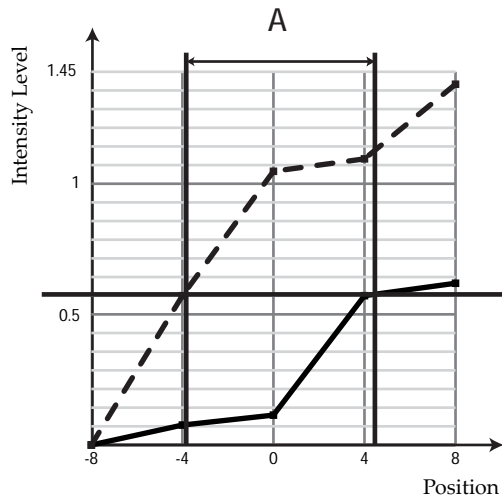
A. Overlapping area

Figure 41 Overlapping Area

The algorithm must ensure that the overlapping area is correctly chosen for all slices at the same time.

Calculation of the Actual Fluence

When calculating the final dose distribution of a modulated treatment, the clinician wants to know as accurately as possible which dose will be delivered to the patient. If the final dose calculation is based on a fluence map generated from simplified physics and delivery models incorporated in the DVO, the calculated dose distribution may significantly differ from a distribution obtained through measurements. To be able to see the actual fluence, you need to calculate the dose after running the LMC.

Calculation of MUFactor

In the LMC, the beam-on time equivalent in intensity, MUFactor, is given as:

Eq. 55

$$\texttt{MUFactor} = w \cdot s_{\min} + c$$

$$c = \max_j\{\Sigma_j\}$$

where

Σ_j	=	sum of positive intensity deltas in slice j
$c = \max_j\{\Sigma_j\}$	=	maximum of these sums for all slices, complexity constant for a certain fluence matrix, depending on (relative) intensity values of the matrix only.
w	=	width of the field in cm, constant for a given matrix as well
$s_{\min}$	=	minimal slope for a leaf trajectory in cm^{-1}, depending on leaf speed, dose rate and MU maximum of the field as follows:

$$s_{min} = R/(60 \cdot D \cdot v)$$

where
R = dose rate in MU/min
D = field maximum in MU
v = maximum leaf speed in cm/s

LMC is required to know R, D and v to achieve correct results.

Although the MLC controller can adjust the dose rate (R), the exact `MUFactor` value must be known for transmission correction. It depends on s_{min} which is a ratio of R, D and v. If the correct transmission correction is to be achieved, at least this ratio must be the same for the leaf motion calculation and the delivery of the calculated plan. Once a leaf plan has been calculated, the `MUFactor` is implicitly contained in it.

If, for instance, upon delivery, D is changed by specifying a different number of total monitor units O, (D = O/MUFactor), the MLC controller will adjust the machine parameters, and the dose distribution will be correct, but the delivery will not be optimal anymore in terms of minimal beam-on time.

Calculation of MUfactor for Smart LMC

The MUFactors for Smart LMC are calculated from the actual fluence as:

Eq. 56

$$ \text{MUFactor} = \frac{1}{\max_{\{j,i\}}(f(i,j))} $$

where

f(i, j) = A cell in the opening ratio matrix of the leaf sequence calculated from the final leaf sequence using the same pixel size as in optimal fluence. The highest value is taken from a matrix that describes the relative transmission compared to the total transmission of open field ($0 \le f(i,j) \le 1$).

Multiple Static Segments Method

As an alternative to the Sliding Window method, the LMC also supports the Multiple Static Segments (MSS) method.

MSS Method for Varian MLC Devices

The MSS method is embedded in exactly the same framework as the Sliding Window method, that is, it uses the same input data and produces the same types of output data. MSS modulation may also be combined with portal imaging. The MSS and Sliding Window use the same physics model for the MLC.

In the MSS method, the smallest entity making up the fluence profile is a static MLC shape. The MSS field consists of several static MLC shapes.

Overview of the Algorithm

The Sliding Window algorithm is first applied to the fluence. The leaf trajectories are sampled to a smaller number of segments. The number of segments to be sampled is `MU Factor × IntensityLevels`. For example, with an intensity spacing of 10 and an MU Factor of 1.6, there are 16 static MLC shapes in the MSS field.

These shapes are fine-tuned after this process by iteratively adjusting a "working fluence". This process takes into account the transmission effects.

Calculation of MUFactor

The MUFactor is calculated similarly to the Sliding Window method. However, in the MUfactor calculation, leaf speed is assumed to be infinite, because the beam is never on during leaf movement. This leads to a simpler equation, where the MUFactor is directly obtained from the complexity constant:

Eq. 57

$$\text{MUFactor} = c$$

where

Σ_j	=	sum of positive intensity deltas in slice j
$c = \max_j\{\Sigma_j\}$	=	maximum of these sums for all slices, complexity constant for a certain fluence matrix, depending on (relative) intensity values of the matrix only.

The MUFactor is iteratively modified using the "working fluence" optimization to compensate for the leaf transmission.

MSS Method in Smart LMC

The optimization method used in the MSS method of Smart LMC to minimize fluence discrepancies is not based on the Sliding Window method. Instead, the optimal set of apertures is obtained by iteratively correcting leaf positions and segment weights to minimize the difference between actual and optimal fluence. The optimization starts from an initial estimate formed using the Close-In method. The

optimization prevents the creation of single apertures that are very small in size, but does not explicitly eliminate segments solely because of their small weight.

MSS Method for Siemens and Elekta MLC Devices

The MSS method for Siemens and Elekta machines uses an optimization method to minimize fluence discrepancies. This method is able to observe restrictions set by the MLC hardware, for example, the interdigitation constraint that apply to certain MLCs. The number of iterations is user-defined, and the progress of the objective function may be monitored during the calculation. The optimization method is also capable of processing uneven MU per aperture, which provides better results, but is slower than the traditional MSS leaf motion calculation algorithm used for Varian's multi-leaf collimators.

MLC devices with a leaf span shorter than the full field width can also be used. In such cases, all apertures in the final MLC sequence will be narrower than the leaf span.

Jaw Tracking Capability of Smart LMC

Smart LMC can generate leaf sequences during which the jaws are moving, or, in other words, jaw position changes while the beam is on. If the Jaw Tracking option is chosen, the jaws are set at each control point to bound the MLC aperture without using any jaw setbacks. The jaw position and speed limits are taken into account. Since the maximum speed of jaws is typically slightly slower than the maximum speed of leaves, in some cases it is possible that jaws do not always follow the MLC aperture. Leaf tail exposure is nevertheless taken into account.

If the Jaw Tracking option is used together with the Fixed Field Borders option, the jaw positions are still set dynamically at each control point, but the user defined jaw positions are considered as a bounding box for the possible jaw positions.

MU Calculation in the LMC

The MU to dose calibration factor `MUGy(x,y)` is defined as the number of monitor units required to get 1 Gy on the field central axis at the 10 cm depth for a rectangular field with a $X \times Y$ cm^2 collimator opening in a water equivalent medium, SSD being the same as during

the beam profile measurements (SPD). Specifically, the value of MUGy for a 10 × 10 cm^2 field, `MUGy(10,10)`, serves as an absolute fluence calibration point for the MU calculation system in IMRT planning. In addition to the reference level provided by `MUGy(10,10)`, it must be possible to compute the patient scatter and collimator backscatter for absolute dosimetry.

The collimator back-scatter factor `CBSF(x,y)` is calculated from MU table by removing the phantom scatter part `PSF(x,y)` from the measurements of different openings. The `CBSF(x,y)` is a function of the x and y openings as in:

Eq. 58

$$\mathtt{CBSF}(x,y) \ = \ \frac{1}{\mathtt{PSF}_{10\ cm}(x,y)} \times \frac{\mathtt{MUGy(10,10)}}{\mathtt{MUGy}(x,y)}$$

where `PSF`$_{10cm}$`(x,y)` is the phantom scatter at 10 cm depth, normalized to 1.0 for 10 × 10 cm field.

Note: *The above equation is used for defining the collimator back-scatter factor* `CBSF` *in the case of the Pencil Beam Convolution (PBC) algorithm only. If you are using the Anisotropic Analytical Algorithm (AAA) or Acuros XB for dose calculation, the calculation of the* `CBSF` *is slightly different. For more information, see Chapter 3, "Implementation of AAA and Acuros XB in Eclipse," on page 30, Equation 1 on page 31.*

In addition to the collimator back-scatter factor and `MUGy(10,10)`, the MU value is affected by the plan normalization and the dose prescription percentage. A normalization factor `NF` is calculated according to:

Eq. 59

$$\mathtt{NF} \ = \ \left(\frac{D_{\mathtt{total}}}{N_{\mathtt{fraction}}}\right)\left(\frac{\mathtt{Plan}_{\mathtt{NORM\%}}}{100}\right)\left(\frac{100}{D_{\mathtt{Presc\%}}}\right)$$

Inside the DVO, the phantom scatter factor is calculated using the 3D convolution algorithm, and is not separately modeled.

Finally, the total monitor units `MU`$_{\mathtt{total}}$ are calculated in accordance with the following equation. The fluence used in patient treatment provides two values for the optimization; the maximum value of the optimal fluence `OF`$_{\mathtt{max}}$, and the intensity modulation factor `MUFactor` that depends on the shape of the fluence, which are multiplied in the total number of MU:

Eq. 60

$$MU_{\text{Total}} = \frac{\text{MUGy}(10,10) \times NF \times \text{MUFactor} \times OF_{\text{max}}}{\text{CBSF}(x,y)}$$

Example

When the plan normalization is set to 100%, the dose prescription percentage to 100%, and the fraction dose is set to 1.0, and there is a unit fluence of size 10×10, that is, when all elements are set to value 1.0, the obtained dose should be 1.0 Gy in the measurement geometry, when the field MU contribution is `MUGy(10,10)`.

MUtotal Calculation in Smart LMC

Since Smart LMC can handle moving jaw positions, the monitor units cannot be calculated directly using Equation 60 on page 257, which assumes that CBSF is the same for all control points. Instead the MU_{total} is given by:

Eq. 61

$$MU_{\text{total}} = \frac{\text{MUGy}(10,10) \times \text{NF} \times \text{MUFactor} \times OF_{\text{max}}}{\text{CBSF}_{\text{eff}}}$$

where

$$\text{CBSF}_{\text{eff}} = \frac{1}{\text{sum}_{\{i\}}\left(\dfrac{w_i}{\text{CBSF}(x_i,y_i)}\right)}$$

where

$\text{sum}_{\{i\}}$	=	Sum is taken over all control points, `i`.
x_i, y_i	=	The opening at control point `i`.
w_i	=	Non-cumulative meterset weight of individual control points.

Fluence Normalization

The fluence normalization is such that constant $10 \times 10 \text{ cm}^2$ fluence with value 1.0 provides the measured dose at 10 cm depth with the specified SPD for semi-infinite water phantom for the given amount of MU. The SPD for the normalization geometry is the same that is used in the configuration of the treatment unit. The normalization is based on superposition, that is, a $20 \times 20 \text{ cm}^2$ field with a constant fluence of

1.0 leads to roughly 1.1 times the dose (+10% of the dose) at the depth of 10 cm, while a 5×5 cm^2 field gives only around 0.9. The dose values are obtained by multiplying the values by NF (Equation 59 on page 256).

The fluence values do not compensate for the CBSF effect. CBSF is only compensated for in the MU calculation.

Arc Fields in Fluence Delivery

The arc fields are modeled as a sum of individual sub-fields with a static gantry angle. Each of these sub-fields represents a range of gantry angles in arc field. The leaf positions and dose rate within the angular range are interpolated and the average fluence is calculated. This average fluence is then assumed to be delivered from the static gantry angle for each contributing sub-field. The dose for the whole arc field is the sum of the doses of the static gantry angle sub-fields.

System Configuration for Fluence Delivery Modeling

Note: *When configuring fluence delivery algorithms, notice the following:*

- *It is important to configure the system so that it corresponds to the characteristics of the treatment machine.*
- *Periodically perform follow-up measurements and compare with the dosimetric beam data used for configuring the beam. If fluctuations are large and the configured beam data no longer represents the average beam delivered by the machine, reconfigure the beam data using the newer dosimetric beam data.*
- *Measure all dosimetric beam data in as stable conditions as possible.*
- *Use the same file naming conventions in beam data measurements (input files) and in Beam Configuration (Therapy Unit name), and name the input files so that it is easy to match the beam data to the treatment unit during the configuration process.*

Configuration of the LMC

Configuration of the Default LMC Technique

The LMC supports two fluence delivery techniques:

- Sliding Window (SW) technique (Varian and BrainLab MLC devices)
- Multiple Static Segments (MSS) technique (Varian, BrainLab, Siemens and Elekta MLC devices)

The default technique to be used can be defined in Default LMC tab of the Task Configuration dialog box. The delivery technique selection is clinic-wide, and making changes in it affects all treatment units using the same MLC model.

Note: *Versions 11.0 or later of the AAA and Acuros XB dose calculation algorithms require versions 11.0 or later of the LMCs.*

To Configure the Default LMC Technique

1. Choose **Tools > Task Configuration**.

2. Select the **Default LMC** tab.

3. To select the LMC algorithm version you want to configure, click the cell in the Algorithm Name And Version column and select the algorithm version from the drop-down list that opens.

4. Do one of the following:
   - *If you selected MSS Leaf Motion Calculator in the previous step:* Click **OK** to close the Task Configuration dialog box, or continue by configuring the MSS delivery mode (see "Configuration of Multiple Static Segments Mode" on page 262).
   - *If you selected Varian Leaf Motion Calculator or Smart LMC:* Continue from step 5 below.

5. Click **Edit**.

6. In the left pane, select **LMCV calculation options**, or **Smart LMC options** (only for treatment machines with Jaw Tracking available).

7. In the default delivery method drop-down list, select the default technique (**Sliding window**, **Multiple Static Segments** or **None**).

8. Click **OK**.

   Continue by configuring the sliding window mode (see "Configuration of Sliding Window Mode" on page 260).

   The delivery technique selection is clinic-wide, and making changes in it affects all treatment units using the same MLC model.

Configuration of Sliding Window Mode

The Sliding Window technique uses DMLC to produce complex intensity-modulated dose distributions to the target volume. In Eclipse, the linear motion of the DMLC is divided into field segments. The more segments that are used in the treatment, the closer the actual dose distribution will be to the dose distribution produced with the pre-calculated optimal fluence.

The Sliding Window segment data is transferred from Eclipse to the treatment unit via the Integrated Treatment. For complex fluences, this may be a time-consuming process. Moreover, older treatment units cannot deal with a multitude of segments. Slower hardware and network connections may also slow down the process in complex treatments.

To avoid unnecessary delays, Eclipse allows you to limit the number of Sliding Window segments. Using fewer segments, however, can affect the quality of the treatment, so modifying the number of sliding window segments always entails trade-offs between the speed and quality of the treatment.

You can define the number of Sliding Window segments by

- Letting Eclipse choose the necessary number of segments up to the defined maximum level (*Normal* mode). The number of Sliding Window segments is determined dynamically per subfield, based on the intensity levels and the field complexity (MU factor, see "Calculation of MUFactor" on page 252). To ensure the quality of all treatments, Eclipse uses an internal constant minimum number of segments (64).

- Defining a constant number of segments (*Fixed* mode).

The following value ranges and default values are used in the Sliding Window mode:

- *Intensity levels:* from 30 up to the maximum number of control points; default = 70.

- *Maximum number of control points* (per subfield): range: 64-320; default = 166.

- The defined Maximum number of control points value is first multiplied by the number of subfields and then divided optimally between carriage groups based on subfield complexity (defined by the MU factor, see "Calculation of MUFactor" on page 252). The resulting number of segments per subfield is always relative to the MU factor per subfield.

- In large fields, the MLC type (a parameter selected for MLC devices in RT Administration) also affects the resulting number of segments. If the MLC device has limitations in treating multiple segments, the result may clearly differ from the defined Maximum number of segments value. If this is the case, it is shown in the Calculation tab of the Planning Field Properties dialog box after calculating the DMLC leaf motion patterns.

Note: *When doing changes in the Sliding Window parameters, notice the following:*

- *The Sliding Window parameters are clinic-wide, and making changes in them affects all treatment units using the same MLC model.*

- *Using the Normal mode with the default settings is recommended for best results.*

- *Modifications in the segment parameters only affect the fluences that have not yet been calculated.*

- *You can also modify the Sliding Window options in External Beam Planning, when you start the leaf motion calculation (for details, see Treatment Planning for External Beam - Eclipse Reference Guide).*

To Configure the Sliding Window Mode

1. Choose **Tools > Task Configuration**.

2. Select the **Default LMC** tab.

3. To select the LMC algorithm version you want to configure, click the cell in the Algorithm Name And Version column and select the algorithm version from the drop-down list that opens.

4. Click **Edit**.

5. In the left pane, select LMCV calculation options.

6. In the **Default delivery method** drop-down list, choose **Sliding Window (SW)**.

7. Select **Sliding window options** in the left pane, and select the desired mode from the **Mode** drop-down list.

   ■ To allow Eclipse to define the number of Sliding Window segments dynamically:
      ■ In the Mode drop-down list, choose **Normal**.
      ■ Select **Normal mode options** in the left pane, and define the desired number of intensity levels and maximum number of control points in the text boxes.
   ■ To use a constant number of Sliding Window segments:
      ■ In the Mode drop-down list, choose **Fixed**.
      ■ Select **Fixed mode options** in the left pane, and define the number of segments.

8. Click **OK**.

   The Sliding Window parameters are clinic-wide, and making changes in them affects all treatment units using the same MLC model.

Configuration of Multiple Static Segments Mode

The Multiple Static Segments technique always needs to have the desired number of intensity levels (Varian Leaf Motion Calculator) or static segments (MSS Leaf Motion Calculator, Smart LMC) defined. The detailed significance of this parameter depends on the selected LMC algorithm:

■ When Varian Leaf Motion Calculator is used (Varian MLC or BrainLab), the final number of segments of each field is multiplication of the optimal fluence complexity (MU Factor), the requested number of intensity levels, and the number of carriage groups in the field.

■ When MSS Leaf Motion Calculator is used (Siemens, Elekta), the total number of segments is redistributed between the fields based on their complexity: a more complex field gets a larger suggested value. These suggested values can be changed in the MSS Leaf

Motion Calculator (LMSMSS) Delivery Options dialog box to further control the LMC calculation (for details, see *Treatment Planning for External Beam - Eclipse Reference Guide*).

■ When Smart LMC is used, the final number of segments of each field is the multiplication of the requested number of segments, and the number of carriage groups in the field.

In all cases, the final number of static segment can vary a little from the requested one.

To Configure the Multiple Static Segments Mode

1. Choose **Tools > Task Configuration**.

2. Select the **Default LMC** tab.

3. To select the LMC algorithm version you want to configure, click the cell in the **Algorithm Name And Version** column and choose the algorithm version from the drop-down list that opens.

4. Click **Edit**.

5. Do one of the following:
   - ■ For Varian Leaf Motion Calculator:
     - ■ In the Default delivery method drop-down list, choose **Multiple Static Segments (MSS)**.
     - ■ Specify the default number of intensity levels in the text box.
   - ■ For MSS Leaf Motion Calculator, specify the default number of static segments in the text box.

6. Click **OK**.

   The Multiple Static Segments parameters are clinic-wide, and making changes in them affects all treatment units using the same MLC model.

Configuration of Sliding Window Mode and Multiple Static Segments Mode for Smart LMC

The Sliding Window mode for Smart LMC is similar to the fixed mode in LMCV (see "Configuration of Sliding Window Mode" on page 260). That is, you define a constant number of Sliding Window segments.

The following value ranges and default values are used in the Sliding Window mode for Smart LMC:

- *Number of control points*: range: 64-500; default = 166.
- The defined Number of control points value is divided between carriage groups. When multiple carriage groups are used, the total number of control points might differ slightly from the defined number. This happens, for example, if the defined number cannot be divided evenly between the subfields or if additional control points are needed because of carriage position changes.

  If the Maximum Number of Control Points defined for the treatment machine in RT Administration (in Radiation & Imaging Devices > MLC > MLC Configuration Properties > MLC tab) is smaller than the number of control points set for the LMC, the value from RT Administration overrides the LMC setting.
- *Default jaw tracking*: On / Off. If jaw tracking is set to *Off*, jaws are not moving while beam is on.

The Multiple Static Segments mode for Smart LMC is handled in the same way as sliding window, except that the number of static control points means the control points required to produce the desired number of static segments.

To Configure the Sliding Window Mode for Smart LMC

1. Choose **Tools > Task Configuration**.

2. Select the **Default LMC** tab.

3. To select the LMC algorithm version you want to configure, click the cell in the **Algorithm Name And Version** column and choose the algorithm version from the drop-down list that opens.

4. Click **Edit**.

5. In the left pane, select **Smart LMC options**.

6. In the **Default delivery method** drop-down list, choose **Sliding Window (SW)**.

7. Select **Sliding window options** in the left pane, and do the following:
   - Define the number of control points in the text box.
   - Select whether to use jaw tracking in the **Default jaw tracking** drop-down list.

8. Click **OK**.

   The Sliding Window parameters for Smart LMC are clinic-wide, and making changes in them affects all treatment units using the same MLC model.

To Configure the Multiple Static Segments Mode for Smart LMC

1. Choose **Tools > Task Configuration**.

2. Select the **Default LMC** tab.

3. To select the LMC algorithm version you want to configure, click the cell in the **Algorithm Name And Version** column and choose the algorithm version from the drop-down list that opens.

4. Click **Edit**.

5. In the left pane, select Smart LMC calculation options.

6. In the Default delivery method drop-down list, choose **Multiple Static Segments (MSS)**.

7. Select **MSS options** in the left pane, and do the following:
   - Define the number of control points in the **Number of static control points** text box.
   - Select whether to use jaw tracking in the **Default jaw tracking** drop-down list.

8. Click **OK**.

   The Multiple Static Segments parameters for Smart LMC are clinic-wide, and making changes in them affects all treatment units using the same MLC model.

Configuration of the MLC Parameters

To have the dose calculation, PRO algorithm and LMC work correctly, the MLC parameters must be correctly defined in RT Administration or Beam Configuration, with particular attention paid to the following:

- *Minimum dose dynamic leaf gap* (RT Administration)—Defines the minimum gap to be maintained at all times between moving DMLC leaves during the treatment. The recommended values are 0.05–0.10 cm.

- *Maximum number of control points* (RT Administration)—If the Maximum Number of Control Points defined for the treatment machine in RT Administration (in Radiation & Imaging Devices > MLC > MLC Configuration Properties > MLC tab) is smaller than the number of control points set for the LMC, the value from RT Administration overrides the LMC setting.

- *Dose dynamic leaf tolerance* (RT Administration)—Defines the allowed inaccuracy in the DMLC leaf motions. The default of 0.2 allows for some slack in the moving leaves.

- *Dosimetric leaf gap* (Beam Configuration)—Accounts for dose transmission through the rounded MLC leaves. The exact value of the parameter depends on the MLC device and the energy spectrum of the accelerator. (For details, see "Dosimetric Leaf Gap in Fluence Delivery Modeling Algorithms" on page 242.) The dosimetric leaf gap needs to be measured for each MLC and rechecked as part of treatment machine QA, especially when MLC calibration is performed.

  The dosimetric leaf gap includes the contribution from the penumbra region. The shape of the penumbra is affected by the Spot size parameter as described in Chapter 4, Section "Tuning of the effective spot size parameters" on page 58.

- *MLC transmission factor* (RT Administration and Beam Configuration, refer to *Beam Configuration Reference Guide*)—Beam Configuration considers MLCs to be add-ons of a treatment unit. To define the MLC transmission factor, you first define the material used for each MLC in RT Administration. You then go to Beam Configuration, match the MLC of the beam data with the MLC of the treatment unit for each MLC configured in RT Administration, and define the transmission factor for the MLC in Beam Configuration.

To Configure Dosimetric Leaf Gap

1. In RT Administration, create the add-on material for the MLC to be used for DMLC treatments.

2. Assign beam energies for the MLC material.

3. Define the material for the MLC device and the dosimetric leaf gap to the dosimetric data of the MLC material.

   For instructions, see *RT Administration Reference Guide*.

Measuring the Leaf Transmission Factor

In order to get the dose of an IMRT field to match the measurements, the MLC leaf transmission factor (LTF) and Dosimetric Leaf Gap (DLG) should be calibrated. The leaf transmission factor can be estimated as the ratio of the measured dose in an open field and the measured dose when using the same field size with all MLC leaves closed behind the jaws. The leaf transmission factor is an effective parameter that describes the average transmission and it does not take into account local variations in leaf width or in the energy spectrum of the beam.

Since the effective leaf transmission depends slightly on the field size and measurement depth, the measurement geometry should be similar to clinically relevant geometries. In Y direction the field should be wide enough so that the different types of leaves in the MLC are exposed. For example, for Millennium 120 MLC this means full and half leaves. For Varian HD-120 MLC the recommended field size is 10 cm x 15 cm (X, Y), and for Millennium 120 MLC the recommended field size is 10 cm x 20 cm (X, Y). In all cases symmetric jaw positions should be used. Measurements should be done in a homogeneous phantom at 10-15 cm depth at isocenter plane (SSD 85-90 cm; the measurement depth must be deeper than d_{max}). A separate measurement should be done for both leaf banks.

The figure shows the measurement setup for leaf bank A of HD-120 MLC using the recommended field size of 10 cm x 15 cm. Except the first leaf pair, all leaves are closed at 9 cm off the central axis behind the X1 jaw (position: -9 cm). The first leaf pair is positioned at 6 cm off the central axis to the opposite direction, just behind the X2 jaw (position: +6 cm). Note that the positions are chosen so that the maximum leaf span is just reached. The purpose of the first leaf pair

position is to force the carriage box of bank A behind the X2 jaw. It should also be verified that the first leaf pair is completely behind the Y1 jaw.
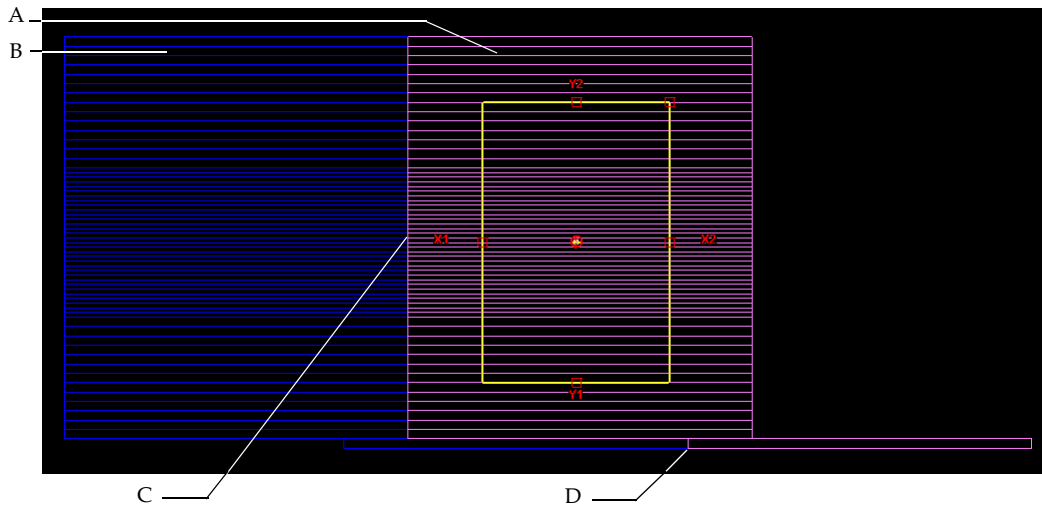
A. Leaf Bank A **B.** Leaf Bank B **C.** Leaves closed behind X1 jaw at 9 cm from the central axis.
D. First leaf pair forces the carriage box of Bank A completely behind the X2 jaw.

Figure 42   Leaf Positions in Static Field for Measuring Leaf Transmission for Varian HD-120 MLC

The exact measurement procedure depends on the measuring devices used. The leaf transmission measurement can be performed using a large variety of measurement devices, such as ion chamber, film or portal imager. It is very important that the measurements are done in several positions and the average of the values are used. This ensures that leaf transmission factor contains effects from inter leaf leakage and takes into account small variations in leaf thickness. The measurement should be repeated for the leaf bank B by using a mirrored image of the leaf positions described above.

To Measure the Leaf Transmission Factor

1. Measure the transmission for leaf bank A using the leaf positions described in Figure 42 on page 268.

2. Measure the transmission for leaf bank B using a mirrored image of the leaf positions described above.

3. Do the measurements for an open field.

4. For each of the measurements above, calculate an average over a spatially representative area. The averaging needs to be done in the same way for all three measurements.

5. Calculate the total average of bank A + bank B transmission.

6. Compare total average of bank A + bank B with the average of the open field.

To Measure Dosimetric Leaf Gap

You can measure the dosimetric leaf gap (DLG) with a series of DMLC setups using the procedure described by LoSasso et al.[39] and Arnfield et al[40].

1. Measure leaf transmission factor as described in "To Measure the Leaf Transmission Factor" on page 268.

2. Measure the dose of sweeping gap DMLC motion with various gap widths (for example, 0.5, 0.7, 1.0, 2.0, 5.0 mm).

3. Subtract the contribution from leaf transmission from the sweeping gap measurements.

4. Plot the corrected sweeping gap measurements against nominal gap width and fit a regression line to the measurement points.

5. Obtain the dosimetric leaf gap by extrapolating the regression line to zero measurement and reading the corresponding gap width. The extrapolated gap width should be negative and DLG is the absolute value of it (see Figure 7 in LoSasso et al.).

Note: *When producing the DMLC motion files for various gap widths, make sure to split the leaf motion to several control points so that leaves do not move more than 1 cm between any two consecutive control points. This is necessary because the leaf position correction (to take into account how the rounded leaf tip cuts the beam) is applied only in the control point locations.*

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39. T. LoSasso, C.-S. Chui, and C. C. Ling, "Physical and dosimetric aspects of a multi-leaf collimation system used in the dynamic mode for implementing intensity modulated radiotherapy." Med. Phys. 25, 1919-1927 (1998).

40. M. R: Arnfield, J. V. Siebers, J. O. Kim, Q. Wu, P. J. Keal, and R. Mohan, "A method for determining multileaf collimator transmission and scatter for dynamic intensity modulated radiotherapy." Med. Phys. 27, 2231-2241 (2000).

Chapter 11   Portal Dose Calculation (PDC)

About PDC (Portal Dose Calculation)

PDC (Portal Dose Calculation) is used to calculate portal dose images for fields containing fluences as part of pre-treatment verification for IMRT planning. The pre-treatment verification is performed by using a portal imager in order to compare the accuracy of the planned fluence produced by the treatment planning system with the fluence delivered by the DMLC motions. This comparison is done in the absolute mode of Portal Dosimetry. Since the fluence cannot be measured directly, and since the detector response is sensitive to photon energy, PDC enables comparing the planned fluence to the delivered fluence measurement.

PDC can also be used for VMAT and conformal arc fields. For these fields Eclipse calculates the planned fluence by summing up the individual aperture fluences from the control points of the field. The dynamic dose rate is taken into account in the summing, and the fluence accumulated between control points is also accounted for. The PDIP algorithm calculates the predicted image based on this sum fluence in the same way as for IMRT fields. The configuration of the PDIP algorithm must be done with IMRT fields, but once done, it is valid also for arc fields.

Note: *When actual fluence is mentioned in this chapter, it also refers to the summed-up fluences of the individual aperture fluences for arc fields.*

Workflow for Dosimetry for IMRT and VMAT Plans Using PDC

Portal Dosimetry is used to acquire images of the fluence, while Eclipse is used to compute a corresponding dose picture. Both images can be viewed and quantitatively compared in Portal Dosimetry.

The following figure describes the process of using calculated and measured portal images for the verification of IMRT and VMAT plans.
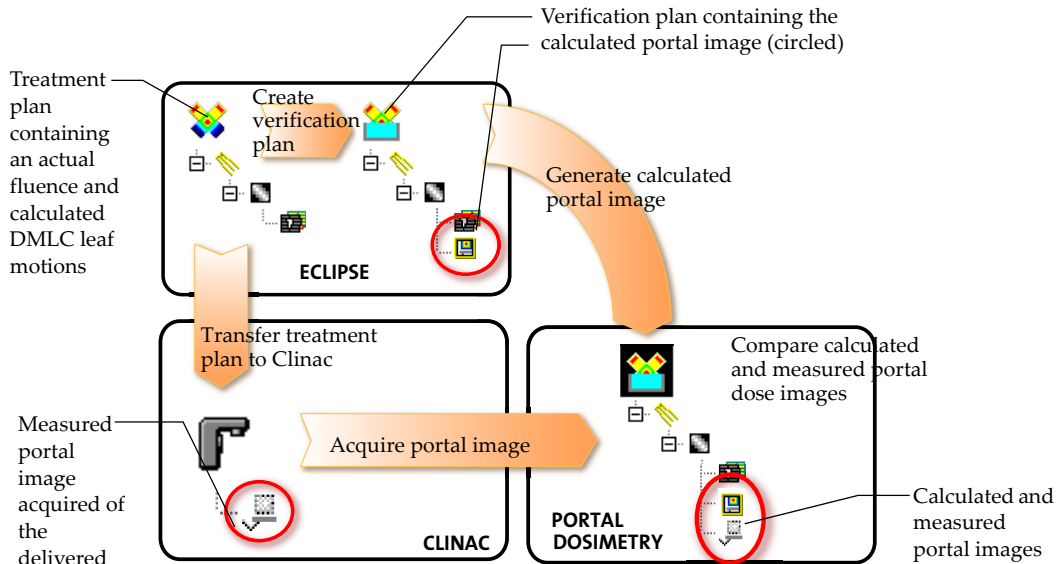
Figure 43   Verification of Plans Using Calculated and Measured Portal Images

The following table describes the process of using calculated and measured portal images for the verification of IMRT and VMAT plans.

Table 36 Dosimetry Workflow Using PDC

Step	Application/Module
Create an IMRT or a VMAT plan	
Create the plan and optimize the dose.	Eclipse External Beam Planning
Create a verification plan of the optimized IMRT or VMAT plan.	Eclipse External Beam Planning
Create more fractions for the plan.	Eclipse External Beam Planning
Planning approve the verification plan.	Eclipse External Beam Planning
Prepare the plan for treatment	
Verify the plan and calculated portal image.	Plan Parameters
Update reference point limits, if needed.	Reference Points
Schedule the plan and set the method for acquiring the image for each field in the plan (integrated image).	Scheduling
Treatment Approve the plan.	Treatment Preparation
Deliver the dose at the treatment unit	
Create an appointment for the Clinac.	
Deliver the verification dose at the Clinac.	Clinac
Evaluate the dosimetry in Portal Dosimetry	
Review the calculated and delivered images next to each other.	Portal Dosimetry
Align the images to correct for small inaccuracies in the imager position calibration.	Portal Dosimetry
Compare the images using different analysis tools.	Portal Dosimetry

PDC Algorithm

PDC is determined at the detector plate of the portal imager ignoring the couch or the patient. PDC produces an image in terms of CU (CU = calibrated unit). PDC always takes the measurement source-to-detector distance (SDD) into account. The image resolution is then projected to the source-to-axis distance (SAD), and correct collimator rotation is applied.

Note: *Although PDC and portal dose measurements can be performed at any SDD, the optimum accuracy is achieved when working at a single SDD, namely at the distance used for the detector calibration. It is recommended to perform calibration, configuration, and PortalVision acquisition at a fixed distance, as close to the isocenter as possible (SDD = 100 cm for Exact Arm, SDD = 105 cm for the R-arm in the Clinical mode). The IAS2 can exhibit significant saturation effects for the higher dose rate modes at the closest SDD. The precise onset of saturation depends on the local machine calibration (MU/Gy in reference conditions), but as a general guideline it is not recommended to exceed a dose rate of 400 MU/min at SDD = 100 cm.*

PDC calculates the portal dose image by convolving the fluence with Gaussian kernels as:

Eq. 62

$$P = f' \times k \cdot \left(\frac{\text{SAD}}{\text{SDD}}\right)^2 \frac{\text{OF}(\text{fs}_x, \text{fs}_y)}{\text{PSF}(\text{fs}_x, \text{fs}_y)}$$

where

P	=	Calculated portal dose image in terms of CU
f'	=	Input fluence corrected by the intensity profile and scaled by detector distance
x	=	Convolution operator
k	=	Portal imager dose kernel
SDD	=	Source-to-detector distance of the portal image measurement
SAD	=	Source-to-axis distance of the treatment unit
fs_x	=	Field size at the SAD in the FX-direction
fs_y	=	Field size at the SAD in the FY-direction
$\text{PSF}(\text{fs}_x, \text{fs}_y)$	=	Phantom scatter factor for field size fs_x, fs_y defined at SAD
$\text{OF}(\text{fs}_x, \text{fs}_y)$	=	Output factor for field size fs_x, fs_y defined at SAD and normalized to a 10×10 cm field

Parameters for PDC

PDC uses input data from the PDC configuration performed in Beam Configuration, and from the verification plan created in External Beam Planning. The following input data is taken from the PDC configuration:

- Output factors for the selected energy/mode (measured on the central axis for each field size)
- Kernels for the selected energy/mode
- Intensity profile describing the fluence off-axis dependence
- SAD (configured treatment machine's SAD, which is copied to Beam Configuration)

The following input data is taken from the verification plan:

- Actual fluence and the corresponding MU factor
- Source-to-detector distance (SDD) of the portal image during measurement (best results are achieved at a distance close to the isocenter)
- Collimator rotation (may differ from the actual collimator rotation)

Correction with Intensity Profile and MU Factor

The open field fluence output of a radiation device is typically not uniform across the field. PDC compensates for the non-uniformity of the open beam fluence by modifying each pixel as:

Eq. 63

$$f'(x,y) = \frac{f(x,y)\,v(r_{x,y})}{MU_{factor}\,OF_{max}}$$

where

f'	=	Corrected actual fluence
f	=	Actual fluence from the planning system (dose picture)
x,y	=	Coordinates of a point in the beam
v(r)	=	Radially symmetrical intensity value
$r_{x,y}$	=	Radial distance from the beam axis
MU_{factor}	=	MU factor from the dose calculation, used to scale the fluence
OF_{max}	=	Maximum value of the optimal fluence, used to scale the fluence

Phantom Scatter Factor

The phantom scatter factor is calculated by constructing a flat intensity image for a rectangular field where the intensity is defined as 1.0 within the field and equal to 0.0 outside the field. Then the fluence is convolved with the kernel. The value of the center pixel is used as the PSF value. This calculation is done at the SAD.

Calculation of Configured Beam Data for PDC

The configured beam data (the kernel) is calculated for the PDC model by performing deconvolution with the Tikhonov regularization. A special test fluence is used to ensure the accuracy of the kernels (see "About the Test Fluence" on page 284). The kernel derived from measurement is radially symmetrical, and it consists of a sum of Gaussians of different amplitudes a_i and sizes σ_i:

Eq. 64

$$k(r) = \sum_i a_i \frac{1}{\sqrt{2\pi}\sigma_i} e^{-r^2/2\sigma_i^2}$$

where r   =   distance from origin

The number of kernel components (Gaussian components) is set to 10 in the configuration.

The following input data is used in Beam Configuration for calculating the kernels for PDC:

- Output factors for the chosen energy/mode (measured dose on central axis for each field size). Measure the output factors for a sparse grid of points, and Beam Configuration interpolates the remaining values.
- Intensity profile describing the off-axis behavior of the fluence. The format of the intensity profile is a one-dimensional circularly symmetric curve. The value at center should be 1.0; the scaling at the isocenter.
- Actual fluence and the corresponding MU factor for the test plan
- Portal images of the test plan
- MU amount used to produce the image
- Collimator rotation
- SAD
- Monitor unit (MU) value corresponding to 100 calibrated units (CU) at SDD = SAD; usually 100 MU

The PDC algorithm requires the measurement of the acquired portal dose image at a user-specified distance. To compute a correction factor for the SDD, it is recommended to acquire a second portal dose image at a different SDD. The first image should be acquired preferably at the default SDD for portal dose acquisition (mostly SDD = 100 cm). The second image acquired at a different SDD is not mandatory but allows for better kernel configuration when measurements are going to be performed at multiple SDDs.

Accuracy of PDC

As a general guideline, after careful alignment, a gamma evaluation of PDC and measurement should be within the acceptance criteria for > 95% of the portal image when using 4%, 4 mm gamma analysis criteria.

In cases where the field size defined by jaws is much larger than the aperture defined by an MLC, the difference between the predicted and measured values can exceed 4%. This can be compensated by rescaling the Output Factors table in PDC beam data.

System Configuration Required for IMRT, VMAT and SRS Dosimetry

To be able to use IMRT and VMAT dosimetry, and SRS dosimetry, and have the PDC algorithm function correctly, you need to configure the system correctly. Either follow the system-specific configuration procedure described in this section, or use a preconfigured set of calibration files (Portal Dosimetry pre-configuration (PDPC) package).

The Portal Dosimetry pre-configuration package consists of

- Pre-configured beam data for the "Portal Dose Image Prediction" calculation model.
- A two dimensional beam profile correction file to be imported during "Dosimetry Calibration" on the 4DITC workstation.
- A set of verification plans ensuring the proper installation of the package.

The PDPC package supports various machine types, beam energies and source-imager distances. Beside a simplified calibration procedure, it provides an optimal beam profile correction along with a

backscatter correction for MV imagers mounted on exact arms. The Portal Dosimetry pre-configuration package is available on my.varian.com.

The system-specific configuration procedure takes you through calibrating the device you are using, performing beam data measurements, importing a test plan, configuring the system, and verifying that the configuration was successful and will produce expected results.

Note: *When configuring fluence delivery algorithms, notice the following:*

- *It is important to configure the system so that it corresponds to the characteristics of the treatment machine.*
- *Periodically perform follow-up measurements and compare with the dosimetric beam data used for configuring the beam. If fluctuations are large and the configured beam data no longer represents the average beam delivered by the machine, reconfigure the beam data using the newer dosimetric beam data.*
- *Measure all dosimetric beam data in as stable conditions as possible.*
- *Use the same file naming conventions in beam data measurements (input files) and in Beam Configuration (Therapy Unit name), and name the input files so that it is easy to match the beam data to the treatment unit during the configuration process.*

Workflow for Configuring the System for PDC

The overall calibration and configuration procedure is the following:

Step	See page	Application/Module
Calibrate the aS detector		
Calibrate the aS detector in the absolute mode.	279	PortalVision, AM Maintenance
Create and measure a test plan		
To ensure correct visualization of the collimator rotation, create an artificial image for each treatment field.	284	Plan Parameters
Create the calibration test plan using the test fluence for deriving the kernels.	285	Eclipse External Beam Planning Plan Parameters
Measure the calibration test plan.	287	4DITC or PortalVision Treatment Acquisition
Measure the output factors		
Create a dummy patient for storing the output factor measurements.	289	Plan Parameters
Measure the output factors.	291	4DITC or PortalVision Treatment Acquisition
Configure the PDC algorithm		
Configure the algorithm parameters for PDC.	293	Beam Configuration
Verify the PDC configuration		
Verify the configuration of PDC by creating a verification plan and an artificial image for the fields.	298	Eclipse External Beam Planning Plan Parameters
Compare the predicted and measured doses.	299	Portal Dosimetry

Calibrating the Detector for Dosimetric Acquisition

The calibration of the aS detector enables PortalVision to create a dosimetric image from the grayscale image acquired by the aS detector. Doing the calibration in absolute mode means that the dosimetric image created in PortalVision will be in CU, which is the unit used in the calculated portal dose images produced by PDC.

To be able to account for the changes in the behavior of the aS detector over time, the calibration is done in reference to a 10 x 10 cm^2 field by fixing the amount of pixel counts in this reference field to correspond to, for instance, 1 CU. This calibration value must match the PDC Dose Rate Table calibration.

To complete the calibration of the aS detector for PDC, you must first calibrate the detector for dosimetric acquisition in the *IMRT scanning mode*, and then calibrate the detector for the *absolute mode*.

Note: *In the calibration of the aS detector, notice the following:*

- *It is recommended to calibrate, configure and acquire the calibration image at a fixed distance, as close to the isocenter as possible (for example, SDD = 100 cm for ExactArm, SDD = 105 cm for the R-arm in the Clinical mode).*

- *In the Portal Dosimetry Calibration mode, the IAS2 takes longer to get ready for data acquisition than in the Normal (Dosimetric) Acquisition mode. Wait for 10 to 15 seconds after pressing Start before starting the beam-on in calibration.*

Calibration of the aS detector for PDC is performed using the

- *AM Maintenance* application if the imager is connected to the *4DITC*, or the

- *PortalVision* application running in a *PortalVision workstation* in the case of a stand-alone installation.

For more details on using these applications, refer to the user documentation for each application or the online help system[41].

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41. For more details on the aS detector characteristics and the PDC algorithm, refer to Van Esch A, Depuydt T, Huyskens DP: *The use of an aSi-based EPID for routine absolute dosimetric pre-treatment verification of dynamic IMRT fields.* Radiother. Oncol. 2004 May; 71(2): 223–34.

Calibrating the Detector in the IMRT Scanning Mode

Before the dosimetric calibration, perform initial dark field (no radiation) and flood field (full signal) calibration. Calibration datasets for IMRT read out mode are stored independently of datasets for normal imaging modes. The calibration needs to be performed using Service Monitor.

To Calibrate the Detector in the IMRT Scanning Mode

1. In the treatment room, align the arm of the PV imager with the beam central axis, for example, SDD = 105 cm (Vrt = -5.0, Lng = 0, Lat = 0). The arm will retain this position throughout the entire calibration procedure.

2. Close the Treatment application.

3. Open the MLC Workstation application and put the MLC to the Park mode.

4. Open the AM Maintenance application.
   - If you use PortalVision in the Standalone mode, open the PortalVision application and select the Maintenance workspace.

5. Choose **Maintenance > Service monitor**.

6. Select tab Treatment Acquisition Modes and choose energy and dose rate.

7. To perform the dark field (no radiation values) and flood field (maximum values) calibration, let the system acquire at least 50 frames and then stop the acquisition.

8. Click **Save Calibration Set/Update Calibration Set** to store data into IAS2/IAS3 unit.

9. Repeat the calibration for all other acquisition modes used for portal dosimetry.

   The maximum field size for the flood field calibration at SDD = 105 cm is X = 38 cm, Y = 28.5 cm (0° collimator rotation)

10. To finish the calibration, click **Close**.

Calibrating the Detector in the Absolute Mode

Before starting the aS detector calibration, prepare a w2CAD file for the calibration so that it contains the measured diagonal profile for a large field size at the d_{max} (measured in water) and no other curves. If you have configured the PBC algorithm in Eclipse and used equidistant measurements for the PBC open field diagonal profile, no new measurement is required. You can use the PBC open field diagonal profile for the calibration of the detector. However, you may need to edit the w2CAD file in a text editor and remove all other curves except the diagonal profile. If the previous measurements for the diagonal profile have not been equidistant, you need to re-measure the profile using equidistant measurement points (for instructions, see Chapter 7, Section "Measuring open diagonal profile" on page 157 in this guide).

Note: *Notice the following when preparing the w2CAD file for the detector calibration:*

- *The file must not contain any other curves.*
- *The curve has to start at the (0;0;depth) location (at the central axis) and ascend to a positive value.*
- *The position data points along the curve may change only at one axis.*
- *The measurement points along the diagonal profile must be equidistant.*

To Calibrate the Detector for the Absolute Mode

1. Choose **Maintenance > Dosimetry Calibration**.

2. Select each energy and dose rate to be calibrated for dosimetric use and click **OK**.

3. Select **Dose normalization** and **Beam Profile Correction**, and define, for example, IDU Vrt = -0cm (for SDD = 100 cm).

4. Navigate to the folder where you have the w2CAD files (either those used for the *PBC algorithm configuration* or those created for this calibration) and select the diagonal profile file for each energy.

5. Perform the absolute calibration:
   a. Start Clinac in the Service Mode.
   b. Set up the parameters for the calibration field (*field size = 10 × 10 cm, 100 MU, selected dose rate*).

6. *IMPORTANT: In case of the IAS2, click **Start** and wait for at least 15 seconds after the message "Acquisition ready" is displayed. Then switch the beam on and irradiate the calibration field. In case of the IAS3, no additional waiting time is required.*

7. Define the measured dose as follows:

   In principle, the calibration value can be chosen by the user as long as the imager calibration value corresponds to the calibration defined in the PDC configuration. However, to avoid discrepancies in this correspondence, it is recommended to set the calibration of the detector to a value of 1 CU for 100 MU delivered with a 10×10 cm^2 field at SDD = 100 cm. When performing the actual calibration procedure at a different SDD, for example, SDD = 105 cm, you have to apply the inverse square law correction to correct for this small difference in distance: $\left(\frac{100}{105}\right)^2 = 0.907$ CU

   The small Dose Measurement window is sometimes hidden behind the larger Dose Normalization window. If the Dose Measurement window does not appear after Beam Off, and the application seems to "freeze", move the Dose Normalization window to see the Dose Measurement window.

8. Click **OK**.

9. Repeat the above for each beam energy and dose rate.

10. Save all data.

11. Exit the AM Maintenance application.

Note: *To undo the dosimetry calibration, you can delete the existing calibration files from the hard disk of the Treatment Console workstation or the PortalVision workstation. The calibration files are located in the following folders, depending on the installation:*

- *Integrated ARIA Treatment console:*
  `...\Oncology\Treatment\AM\config\AM\do.`
- *Standalone PortalVision installation:*
  `...\RV71\Vision\config\pv\do.`

Calibrating the Detector in the SRS Mode

Before the dosimetric calibration, perform initial dark field (no radiation) and flood field (full signal) calibration.

To Calibrate the Detector in the SRS Mode

1. In Service Mode on the Clinac, set the mode to SRS Fixed to set the energy to 6X and the dose rate to 1000MU/Min.

2. Open the MLC Workstation application and put the MLC to the Park mode.

3. Open the AM Maintenance application.
   - If you use PortalVision in the Standalone mode, open the PortalVision application and select the Maintenance workspace.

4. Choose **Maintenance > Service monitor**.

5. To perform the dark field (no radiation values) calibration, let the system acquire at least 60 frames and then stop the acquisition. After each dark field acquisition, click **Save Calibration Set/Update Calibration Set** to store data into IAS2/IAS3 unit.

6. Set the imager SDD to 140 cm.

7. Set the field size to X = 28.5 cm and Y = 21.5 cm. You need to override the **Coll** interlock to allow treatment with this field size.

8. To perform the flood field (maximum values) calibration, let the system acquire at least 30 frames and then stop the acquisition. After each flood field acquisition, click **Save Calibration Set/Update Calibration Set** to store data into IAS2/IAS3 unit.

9. To finish the calibration, click **Close**.

10. Choose **Maintenance > Dosimetry Calibration**.

11. Select the acquisition mode for 6X, 1000 MU/Min, SRS-Integrated and click **OK**.

12. Select **Dose normalization** and **Beam Profile Correction**, and define IDU Vrt = -40cm (for SDD = 140 cm).

13. Navigate to the folder where you have the w2CAD files (either those used for the *PBC algorithm configuration* or those created for this calibration) and select the diagonal profile file for each energy.

14. Perform the absolute calibration:
    a. Start Clinac in the Service Mode.
    b. Set up the parameters for the calibration field (*field size = 10 × 10 cm, 100 MU, selected dose rate*).

15. *IMPORTANT: In case of the IAS2, click **Start** and wait for at least 15 seconds after the message "Acquisition ready" is displayed. Then switch the beam on and irradiate the calibration field. In case of the IAS3, no additional waiting time is required.*

16. In the Dose Measurement dialog box, keep the SDD at 140 cm and set the measured dose value to 51.0. This is the measured dose value when the inverse square of $\left(\frac{100}{140}\right)^2$ is applied.

    The small Dose Measurement window is sometimes hidden behind the larger Dose Normalization window. If the Dose Measurement window does not appear after Beam Off, and the application seems to "freeze", move the Dose Normalization window to see the Dose Measurement window.

17. Click **OK**.

18. Save all data.

19. Exit the AM Maintenance application.

20. Continue by following the steps in "To Create the Calibration Test Plan in Eclipse" on page 285 and "To Measure the Calibration Test Plan" on page 287.

Creating a Test Plan for Deriving the Kernels

The kernels are derived from the actual fluence contained in a test plan, which ensures optimum quality of the kernel creation.

Creating a test plan with the test fluence requires using *Eclipse External Beam Planning, Plan Parameters, ARIA Treatment Acquisition* and *Portal Dosimetry*. For details on how to use these applications, refer to the user documentation for each application or the online help system.

About the Test Fluence

The test fluence is an optimal fluence specially designed for the configuration and verification of PDC. It is easy to verify the configuration and test images because of the specific characteristics of the test fluence.

The installation of the PDC algorithm copies the test fluence to the calculation server directory `\\<Server name>\dcf$\client\PreconfiguredBeamData\Portal Dose Image Prediction <version>\PDIP-configuration.optimal_fluence`. Import the test fluence into a PDC test plan (see "Creating a Test Plan for Deriving the Kernels" on page 284) for use in the configuration of the algorithm. The format of the fluence is the same as in `dcm2ascii` with additional field size parameters.

The test fluence is pyramid-shaped and contains multiple rectangular slabs. The fluence consists of a port of 120×250 mm (or 120×220 mm for the HDMLC) with 5 rectangular slabs of the intensity of 1.0 and fluence of 0.0 outside the slabs (see the figure).
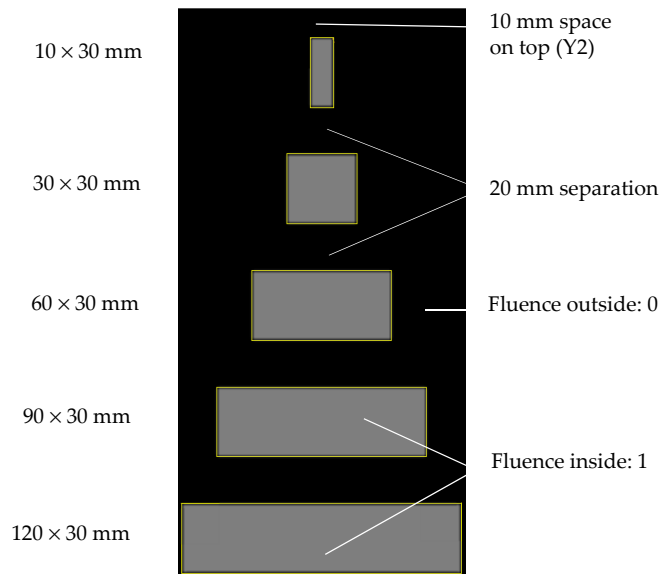
Figure 44 Test Fluence

To Create the Calibration Test Plan in Eclipse

1. Go to External Beam Planning.

2. Open any test phantom patient. Make sure that you include a structure set.

   The structure set only enables creating the test plan. It is not used for the dose distribution calculation. Therefore, any available structure set (patient or phantom) can be used for creating the test plan.

3. For each beam energy, create a new plan containing one field. For SRS, select 6X-SRS energy for the field.

4. In the Field Properties dialog box, select the General tab, and define the following values:
   - Treatment time
   - Tolerance table

5. Select the Geometry tab, and define the following:
   - Collimator Rotation: 90°
   - Couch rotation (if needed)
   - Field X: 12 cm
   - Y1: -13 cm
   - Y2: 12 cm (IEC 61217).

   For the HDMLC, set Field X to 12 cm and Y to 22 cm.

   For SRS, set Field X to 12 cm and Y to 15 cm.

6. To import the configuration optimal fluence, in the Focus window, right-click the field and then select **Import Optimal Fluence**.

7. In the Import Optimal Fluence dialog box, navigate to `\\<ServerName>\DCF$\client\PreconfiguredBeamData\ Portal Dose Image Prediction <version>\`, and select the `PDIP-configuration.optimal_fluence` file for the Standard and Millenium MLC (80 and 120) or the `HDMLC-PDIP-configuration.optimal_fluence` file for the HDMLC, and then click **Open**.

8. *For SRS:*
   - *SRS:* Open Fluence Editor and erase the fluence outside the Y jaw settings (3 middle bars will stay).

9. In the Info Window, select the Dose Prescription tab and define the following dose prescription for the configuration plan: 2 fractions, 1.0 Gy/Fraction.

10. Calculate the dose distribution for the current plane. Make sure that the calculation grid size is 2.5 mm.

11. In the Leaf Motion Calculator dialog box, select the appropriate LMC and click **OK**.

12. In the Varian Leaf Motion Calculator (LMCV) Delivery Options dialog box, set the delivery method to **Sliding window**, select **Fixed Jaw** and click **OK**.

    The dose distribution is calculated only to obtain the actual fluence. The spatial dose distribution itself does not play a role. Therefore, it suffices to calculate the dose to a single plane.

    The Dosimetric Leaf Gap and MLC Leaf Transmission parameters significantly affect the value calculated by the LMC. Make sure that these parameters have the correct values.

13. To save the calibration test plan, choose **File > Save All**.

14. To planning approve the verification plan, in the Context window, right-click the plan and then choose **Plan Approval > Planning Approved.**

    The Plan Validation dialog box shows warnings and errors. You can ignore warnings and click **OK**. If there are errors, the plan cannot be approved.

15. In the Authorization for Status Change dialog box, type in your user name and password.

16. Go to the **Plan Scheduling** workspace.

17. Select the plan and click **Schedule**.

18. Display the field (by expanding the plan) and select the scheduled fractions by painting them with the mouse.

19. To add portal imaging to all fields in the plan, click **Add imaging** and choose the acquisition mode set option for portal dosimetry (for example, Integrated Image).

20. Approve the plan for treatment.

21. Save your work.

    Continue by measuring the calibration test plan by delivering the calculated fluences at the 4DITC.

To Measure the Calibration Test Plan

1. Schedule the calibration test patient for treatment in Time Planner.

2. Start the Treatment application and log in.

3. Align the PV imager with the beam CAX to the selected SDD (for instance, for SDD = 105 cm, use: Vrt = -5.0, Lng = 0, Lat = 0).

4. On the 4DTC console, click **Open Patient**, and then in the Today's Schedule dialog box, select the calibration patient and then click **OK**.

5. Select the calibration plan and click **Mode Up**.

6. Mode up the treatment unit and deliver the test field.

   If Advanced imaging (OBI) is installed on the delivery system, make sure that the OBI application is opened.

7. Repeat steps 1–6 with the PV imager at the extended SDD (for example, for SDD = 145 cm, use Vrt = -45.0, Lng = 0, Lat = 0).

   Acquiring and using a second image at the extended SDD is optional.

8. Go to **Portal Dosimetry** and open the calibration test patient.

9. Select the plan. Make sure that you select the correct one.

10. In the Field tab, right-click the first acquired image and choose **Export to Text File**.

11. Navigate to a save location that is accessible throughout the network, define the file name and save the text file.

12. *Optional:* To export the second acquired image, repeat steps 9–11.

Measuring the Output Factors

Beam Configuration uses output factors for calculating the kernels for PDC. For other input for the configuration, see "Calculation of Configured Beam Data for PDC" on page 275. The output factors are measured for the selected energy or mode, and they consist of the measured dose on central axis tabulated for each (fs_X, fs_Y) pair.

Note: *Calibrate the detector before doing output factor measurements to have dosimetry images available in CU.*

Doing the output factor measurements requires using *Plan Parameters*, *ARIA Treatment Acquisition* and *Portal Dosimetry*. For details on using these applications, refer to the user documentation for each application or the online help system.

**To Create a Test Patient for Storing
the Output Factor Measurements**

1. Using the **Quicklinks** menu, go to **Plan Parameters**.

2. Choose **Tools > Task Configuration** and select the **Advanced feature set** check box.

3. Restart the Plan Parameters workspace to activate the setting.

4. In the Patient Explorer, create a new test patient.

   Name your test patient so that it is easily recognizable. For instance, use naming such as: Last Name: "Output factors", First Name: "PDC", ID: "PDC001".

5. Insert a new course and then insert a new plan.

6. Go to the **General** tab of the Plan Properties dialog box and select the patient orientation from the **Patient Position** drop-down list.

7. Go to the **Dose** tab of the Plan Properties dialog box and set **Number of Fractions** to 5 and **Prescribed Dose/Fraction** to 100 cGy.

8. Insert one new treatment field. Remember to also define the tolerance table.

9. To save your work, choose **File > Save All**.

10. If necessary, to show the Context Window, choose **Window > Context Window**.

11. In the Context Window, right-click the test plan and then choose **Copy Plan**.

12. To create a verification plan out of the test plan, in the Context Window, right-click the course of the calibration test plan and then choose **Paste > Plan as Verification Plan**.

    Perform the remaining steps using the verification plan. After successfully completing and saving the verification plan, you can delete the original treatment plan.

13. Edit the Plan Properties, and change the Plan ID to "Y03" to indicate a plan where all FY sizes are 3 cm. Click **OK**.

14. In the Viewing Pane, do the following:
    - Change the **Field ID**.
    - Define the **MU** value (from 50 to 100 MU).
    - Define the **Treatment Time**.
    - Set the imager position.
    - Change the **Field X** (FX) and **Field Y** (FY) values.

    This procedure assumes source to imager position of 0 (SID = 100 cm). For SID > 100 cm, scale the field sizes accordingly to cover only the active part of the DU. This may be necessary for R-Arm.

15. To create one field for each FX size to be measured, copy and paste the initial field as many times as is necessary to create the desired number of fields.

    For example, use field sizes such as 3×3 cm^2, 5×3 cm^2, 10×3 cm^2, 15×3 cm^2, 20×3 cm^2, 28×3 cm^2, and 38×3 cm^2. For the recommended field sizes, see the table below.

Table 37 Recommended Field Sizes for Output Factor Measurements

		Width (FX)						
		S[a]	5	10	15	20	28	38
Height (FY)	S[a]	$S \times S$	$S \times 5$	$S \times 10$	$S \times 15$	$S \times 20$	$S \times 28$	$S \times 38$
	5	$5 \times S$	5×5	5×10	5×15	5×20	5×28	5×38
	10	$10 \times S$	10×5	10×10	10×15	10×20	10×28	10×38
	15	$15 \times S$	15×5	15×10	15×15	15×20	15×28	15×38
	20	$20 \times S$	20×5	20×10	20×15	20×20	20×28	20×38
	28	$28 \times S$	28×5	28×10	28×15	28×20	28×28	28×38
	38	$38 \times S$	38×5	38×10	38×15	38×20	38×28	38×38[b]

a. S = smallest field size

b. For 40 x 40imager only.

16. To create a set of the fields with the same FY size (for example, 3×3 cm^2 to 38×3 cm^2), edit the **Field ID** and **Field X** value of each field.

17. Copy and paste the verification plan to the same course.

18. Increment the ID of the new plan to indicate the next FY size (for example, change the ID from "Y03" to "Y05").

19. Increment the **Field Y** value for all the fields in the new plan.

20. Repeat steps 17–19 for other FY sizes to be created.

21. *For the 40 x 30 imager only:* In the plan for FY = 38, delete the 38 × 38 field and change the collimator rotation of the remaining fields to 90°.

22. To save your work, choose **File > Save All**.

23. Go to the **Plan Scheduling** workspace.

24. In the Plan Scheduling Pane, click **Schedule** for the all the verification plans.

25. Highlight all the scheduled fractions for all the plans with the mouse, right-click and choose **Add Imaging > Integrated Image**.

26. To save your work, choose **File > Save All**.

27. Go to the **Reference Points** workspace.

28. Select the reference point for a plan, and add planned dose and dose limits if required.

29. If necessary, to show the Context Window, choose **Window > Context Window**.

30. To planning approve all plans, in the Context Window, right-click each plan and then choose **Plan Approval > Planning Approved**.

31. To treatment approve all plans, in the Context Window, right-click each plan and then choose **Plan Approval > Treatment Approved**.

32. To save your work, choose **File > Save All**.

33. Open Time Planner and create an appointment for the test patient.

To Measure the Output Factors

Note: *Calibrate the imager first! Make sure that all acquisition technique parameters are set correctly. Perform Dark and Flood Field calibration for the energy/dose rate combination to be used. Perform the dosimetry calibration of the imager.*

Note: *When performing and recording the output factor measurements using a 40 x 30 imager, notice that with a collimator rotation of 0°, you can only measure field sizes up to 38 cm in the FX direction and 28 cm in the FY direction. To measure the output factors for field size of 38 cm in the FY direction, the collimator rotation needs to be 90° and the field sizes in FX*

direction set to values ≤28 cm. For more information, see "To Create a Test
Patient for Storing the Output Factor Measurements" on page 289.

1. In Treatment Delivery, deliver all planned fields and acquire the Integrated Images.

2. Open Portal Dosimetry.

3. Open the test patient created for storing the output factors.

4. From the Plan drop-down list, select the plan for the first field size (the field with the smallest Y-size).

5. In the Field display, select the first acquired image to be evaluated (the field with the smallest X-size).

6. Choose **Tools > Output Factor tool**.

7. Define **Averaged Area** and then click **Get Dose at Isocenter**.

8. Select the acquired image for the field with the next larger X-size, and click **Get Dose at Isocenter**.

9. Repeat step 8 for all the fields in the plan, proceeding in the order of increasing the FX size, for example, from 3×3 cm^2, 5×3 cm^2, 10×3 cm^2 and so on, to 38×3 cm^2.

10. Repeat steps 7–9 to measure output factors for all the plans, opening the plans in order of increasing FY size.

11. Click **Copy to Clipboard**. The values are comma-delimited as required by the MUTAB format used for the output factors.

12. Paste the copied result into a blank text document, such as the one shown here:
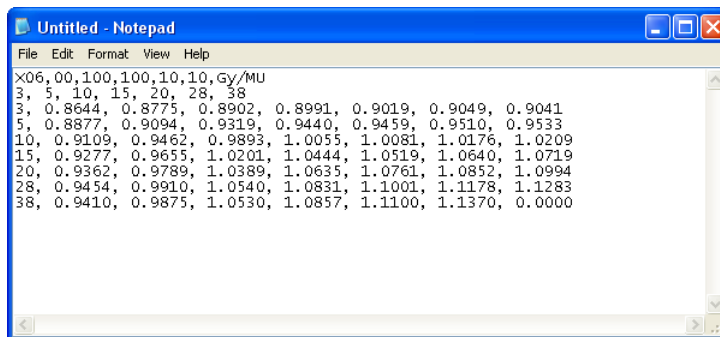
13. Save the text document.

Note: *Clinical physicists responsible for the measurements must always use their own judgement in deciding the level of acceptable accuracy of the measurements in relation to the calculations, and find the compromises needed for each specific accelerator as far as measurements are concerned.*

Configuring the PDC Algorithm

Configuring the PDC algorithm requires using Beam Configuration. For more details, refer to *Beam Configuration Reference Guide* or the online help system.

The purpose of the configuration of the PDC algorithm in Beam Configuration is to have the kernels calculated for the PDC model. For more information on how the calculation is done, see "Calculation of Configured Beam Data for PDC" on page 275.

Kernel Data in Beam Configuration

The calculation results are shown in Beam Configuration as a kernel curve and numerical data about the kernel. The figure shows an example of a calculated kernel.
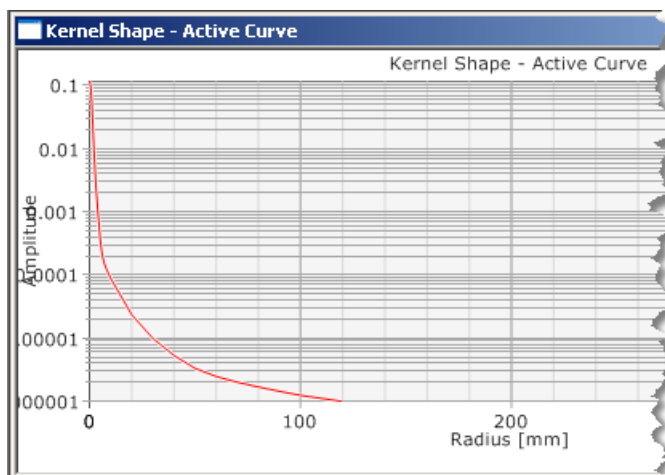
Figure 45   Example Kernel Curve [$k(r)$**]**

The shape of the kernel curve should be steeply descending, with all values close to 0 (zero), with no negative values, and free of oscillations.

If you compare the data with Equation 64 on page 275, the Kernel Shape curve shows the $k(r)$ part of the equation, whereas the two columns in the Kernel Shape table show the σ_i (left column) and a_i (right column) parts. The individual Gaussians have no physical meaning, and small negative values of a_i can occur. It is only the summed kernel that reflects the response of the portal imager.

To Configure the PDC Algorithm

1. Make sure that the PDC calculation model is activated (choose **Beam Data** > **Configure Calculation Models**). The name of the calculation model is "Portal Dose Image Prediction" in Beam Configuration.

2. In the Context window, select the PDC calculation model.

3. To insert new beam data
    a. In the Focus window, select the PDC model and choose **Insert > New Beam Data**.
    b. Select **Start with empty data** and define the data set name.

4. Insert the open field add-on.
    a. In the Focus window, select the PDC model and choose **Insert > New Add-on**.
    b. Select **Open Field** and click **OK**.

5. In the Focus window, select PDIP Parameters, and type value 100.0 to the **Calibration MU** parameter.

6. To define the portal image parameters, go to the Focus window, select Portal Image Parameters and type the following values to the parameters:

Number of Portal Images	Number of dosimetric images (2) acquired of the calibration test plan
Image 1 - Import Portal Image File From Path	File path and file name of the file containing the first dosimetric image (as exported after acquisition). To navigate to the file, choose **Beam Data > Parameter Values > Browse File Path to Parameter Value**.
Image 1 - Rotation	90.0 degrees
Image 1 - Mu	MU used for the dosimetric image acquisition

7. Repeat step 6 for the second dosimetric image.

8. Save all changes.

9. Import the intensity profile from the configured Pencil Beam Convolution (PBC) or Anisotropic Analytical Algorithm (AAA) calculation model:

    a. In the Focus window, select the open field add-on and choose **Insert > New Intensity Profile**.

    b. In the Scope window, click the PBC or the AAA object.
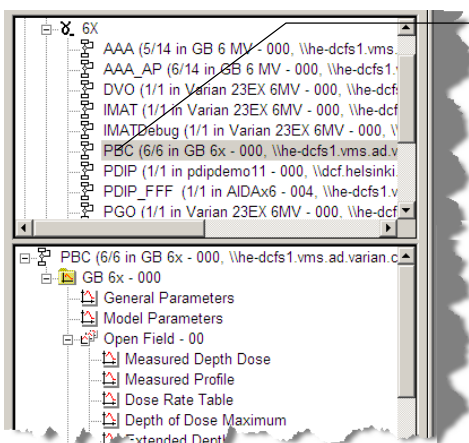
To display the Intensity Profile object of the PBC or the AAA model, click the PBC or the AAA object in the Scope window.

c.   In the Focus window, click the Intensity Profile under Open Field.

To display the intensity profiles configured for the PBC or the AAA model, click the Intensity Profile object in the Focus window.
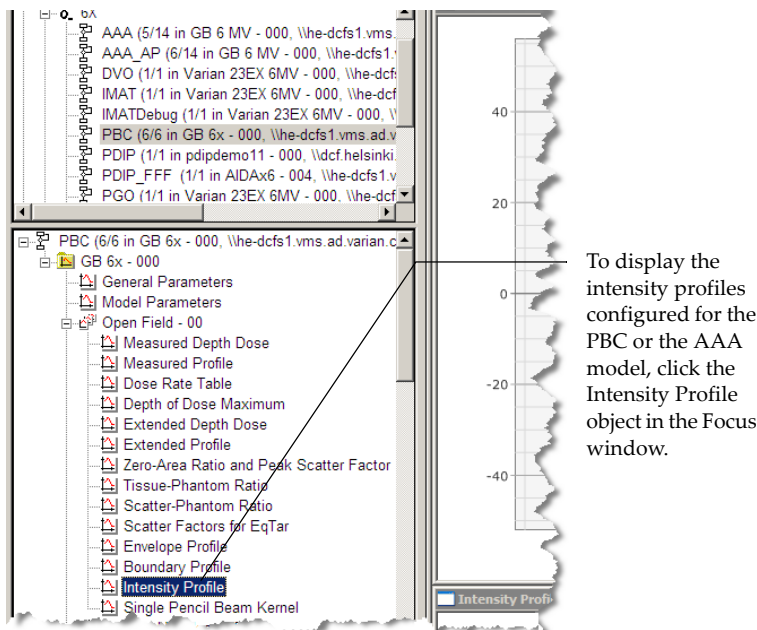
d.   In the Object window, click the thumbnail of the intensity profile at the d_{max} or a depth as close to the d_{max} as possible and then choose **Edit > Copy Curve**.

In the Object window, click the icon of the intensity profile at d_{max}.
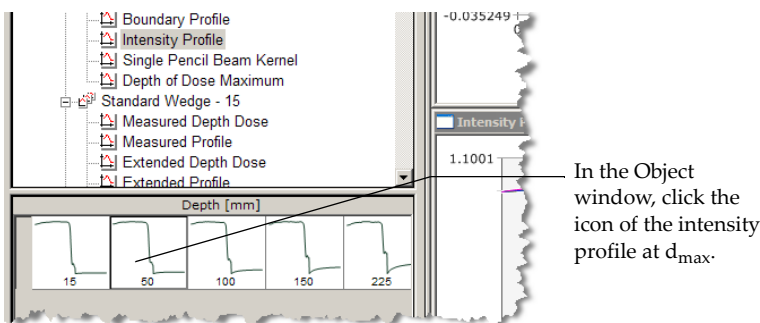
e. In the Scope window, click the PDC model.

To display the PDC model, click the PDC object in the Scope window.
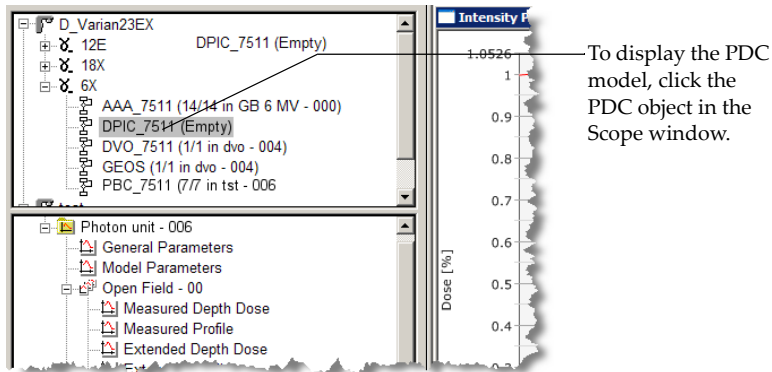
f. In the Focus window, click the empty Intensity Profile created in step 9A and then choose **Edit > Paste Curve**.

g. Define the **Distance From Source** parameter for the intensity profile. The distance is defined as `target - profile distance`.

10. Import the actual fluence from the test plan to the configuration data:

a. In the Focus window, select the Open Field add-on created in step 4.

b. Choose **File > Import > Actual Fluence from Database**.

c. In the Patient Explorer, navigate to the test plan that contains the test fluence (created in "Creating a Test Plan for Deriving the Kernels" on page 284), select the fluence and click **OK**.

The actual fluence data object appears in the Focus window.

11. Define the output factors:

a. Choose **Import > Output Factors**.

b. To complete the values in the output factor table, choose **Beam Data > Interpolate missing values**.

12. To calibrate the Output Factors Table, right-click Output Factors, choose **Calibrate Dose Rates** and type the calibration value in the New Output Factor box. The value should correspond to that used in the calibration of absolute dose values (see "Calibrating the Detector for Dosimetric Acquisition" on page 279). The calibration value in the Output Factors table assumes SDD = 100 cm. If the

recommended calibration values were used for the absolute calibration of the portal imager, the output factors should be normalized to the $10 \times 10 \text{ cm}^2$ field, that is, $OF(10,10) \cong 1$.

13. Choose **File > Save All**.

14. To generate the calculated beam data, go to the Focus window, select Open Field and choose **Beam Data > Calculate Beam Data**.

   The calculated kernel curve and kernel data are displayed. For more information about this data, see "Kernel Data in Beam Configuration" on page 293.

15. In the Focus window, select the therapy unit (object under the PDC model) and choose **Beam Data > Approve**.

Note: *The intensity profile can also be defined as follows:*

- *Define the intensity profile curve values manually using the Curve Editor. You need a profile measurement at the SAD and at a shallow depth for this.*

- *Record the intensity profile to a w2CAD file and import it. Make sure that the value of the TYPE attribute in the w2CAD file is* IntensityProfile.

Note: *The output factors can also be defined as follows:*

- *Record the output measurements to a w2CAD file and import it.*

- *Record the output measurements to a spreadsheet file, such as an Excel file, and copy/paste the values to the output factor table.*

Verifying Portal Dose Prediction Configuration

Verifying the PDC configuration can be performed either by using the verification plans in the Portal Dosimetry pre-configuration package, or by using *Eclipse External Beam Planning* and *Portal Dosimetry*. For details on how to use these applications, refer to the user documentation for each application or the online help system.

To Verify the Configuration of PDC

1. Go to External Beam Planning.

2. Open your calibration test plan and verify that the MU value in the Field Properties correspond with that used for measuring the image.

3. Create a verification plan.
   - Choose **Planning > Create Verification Plan**. Select a course to which the verification plan will be stored or create a new one.
   - Select the **Portal Dose Prediction** option.
   - Define the SDD at which one of the dosimetric test images was acquired.
   - Clear all field geometry changes check boxes.
   - Select a tolerance table with large tolerance levels on the treatment couch.

   Eclipse calculates the predicted dosimetric portal image.

   The calculated dosimetric portal image is not displayed in the image views. The predicted portal dose image icon appears in the Focus window under the field in the verification plan.

4. Approve the created verification plan:
   - Choose **Edit > Plan Approval > Planning Approved**.
   - Select the **Calculate treatment times for treatment fields** check box and define a multiplication factor.

5. Use the **Quicklinks** menu to go to the **Plan Parameters** workspace.

6. Open the verification plan.

7. Right-click the target field and choose **Add field image**.

8. Browse to select the portal dose image acquired for the original calibration test plan.

9. To save your work, choose **File > Save all**.

   Continue to Portal Dosimetry to compare the predicted and measured doses.

To Compare the Predicted and Measured Doses

1. Open Portal Dosimetry.

2. To align the acquired and predicted images to correct for small inaccuracies in the imager positioning, select the measured portal dose and then select the **Alignment** tab.

3. Move the image with the arrow keys until the line profiles show good positional alignment, or click **Auto Align**.

   Inaccuracies in the imager position calibration exceeding 3 mm in any direction can cause sub-optimal kernel calculation during the configuration of the PDC. If considerable adjustment (> 3 mm) is necessary to align the acquire test image with its prediction, it is recommended to redo the imager position calibration and acquire a new image for the configuration.

4. To accept the new image coordinates, click **Set Aligned**.

5. Select the **Evaluation** tab.

6. Click **Options** and define the values of the evaluation options as follows:
   - Dose Tolerance: 4%.
   - DTA: 4 mm.
   - Area Gamma: < 1.0 > 99%.

7. Click **OK**.

8. Click **Perform Analysis** to apply the criteria to the images.

   Gamma Evaluation should produce a near-blank image where gamma < 1 for 99% of the field for criteria of 4%, 4 mm. Since the default evaluation takes the entire detector plate into account, the results may be affected by an occasional error caused by stray pixels outside the range. If necessary, use the ROI (region of interest) settings to focus on the irradiated area. Additionally, misalignment of the images may also affect the evaluation; misalignment below ~2 mm should result in an acceptable evaluation.

Volume IV   Miscellaneous Algorithms

Algorithms for Automatic Segmentation

Miscellaneous Algorithms

Flood Fill

The flood fill algorithm iteratively fills a smoothly connected volume with similar reference image values. A goodness value is calculated for all the voxels connected to but not included in the volume at hand. The goodness value is defined as a sum of image similarity value and a smoothness value. If the sum is below a user-defined threshold, the voxel is attached to the volume.

k-NN Extension of Segments

The k-Nearest Neighbor (k-NN) algorithm is a classical classification algorithm. In Eclipse segmentation it is used to classify voxels into those belonging or not belonging to a segment. The algorithm extends the segment from source plane to the destination plane.

Points close to the segment to be continued on the source plane are mapped to a six-dimensional feature space. The features of interest are spatial coordinates on the plane, the image value, the smoothed image value and image value gradients. Before being mapped to the feature space, the components are transformed by calculating a weighted sum of a normalized feature value and an equalized feature value after a sigmoidal transformation. For each point in the destination area of interest (points close to the source segment), a set of closest points in the feature space are searched. These points use a weighted voting method to decide whether a point belongs to the segment or not.

Automatic Segmentation Tools

Spine Segmentation

Automatic spine segmentation is based on the k-NN algorithm. The segmentation starts from a user-defined seed. The seed is then extended in the positive and negative Z-direction of the volume. Extending is performed on a plane-to-plane basis. Extending stops at a plane where no continuity is found.

Lung Segmentation

Automatic lung segmentation first finds a slice with most air inside the body structure in two connected areas. A flood fill algorithm is then used to fill the lungs, starting from points inside the two largest connected areas. The volume that can be filled is limited by the Volume of Interest (VOI) and the body structure.

Brain Segmentation

Brain segmentation is started by finding and selecting bones resembling the skull on planes inside the body structure using area and momentum criteria. A flood fill algorithm with weaker filling parameters is used to fill most of the brain. Planes that are too far from planes containing skull-like bones are cleared. The produced volume is then dilated and used as a constraining volume for a more powerful flood fill.

Eye Segmentation

Eye segmentation consists of two phases. In the first phase, a point inside each eye is found, and in the second phase, the eye segment is generated around these points.

The *first phase* is initiated by calculating an eyeness map. A point in the map describes how much the local neighborhood of a given point resembles a neighborhood of a point where eyes are likely to appear. The following information is used to estimate the local eyeness value:

- Distance from the point to the body outline
- Distance from the point to the skull-like bone
- Distance from the point to the maxillary sinus-like volume
- Distance from the point to air
- Distance from the point to the symmetry axis in the image planes

Skull-like bones are found as described in "Brain Segmentation" on page 303. The maxillary sinus-like volume is generated by searching air pockets inside the body that fulfill the area requirements.

After the eyeness volume has been generated, two connected areas with the highest integrated eyeness values are selected. Within these volumes, the eyeness-weighted center points are calculated. These points are then used in the second phase.

In the *second phase*, the flood fill algorithm starts from the most probable eye locations found in the first phase. First, weaker filling parameters are used to produce a rough segment containing the interior of an eye. The rough eye segment is then used to estimate the volume and center point of the eye. A stronger flood fill is then started from the estimated center point. This second fill is constrained by a ball-shaped Volume of Interest (VOI), which is centered to the estimated center point of the eye and has a slightly larger volume than the rough eye segment.

Bone Segmentation

Bones are segmented by selecting points with a CT value typical of bone structures. Very small bone segments (smaller than 50 mm^3) are removed.

MRI Body Search Algorithm

The body search algorithm for MR images uses an adapted watershed transformation algorithm. The algorithm operates on a slice-by-slice basis.

The principle of the algorithm is that the MR image is considered as a topographic surface where the pixel intensity constitutes elevation. A rising water level is simulated by repeatedly flooding the surface of the image with varying threshold levels. The flooding is initiated from slice local minima. In each iteration, the area above the water level is considered the body segment. As the water level rises, the algorithm evaluates its progress and determines the appropriate level which denotes the final body segment. The decision is based on predefined knowledge of the expected results, such as the expected size of the body contour, results from the segmentation of previous slices, and the expected progression of the algorithm close to the body contour.

To reduce possible noise, the algorithm operates on a gaussian smoothed copy of the MR image. The current Window/Level parameters defined by the user are applied to the working copy prior to smoothing.

Algorithm for Stereotactic Radiosurgery (SRS) Localization

The Stereotactic Radiosurgery (SRS) localization algorithm is used in the *Eclipse SRS Localization* module for determining the position of the localizer box in the patient CT image and, based on this, for creating a stereotactic 3D image for use in stereotactic treatment planning. (For information on using the Eclipse SRS Localization module, refer to *Treatment Planning for External Beam - Eclipse Reference Guide*.)

The stereotactic 3D image created by the Eclipse SRS Localization module is aligned with the SRS coordinate system, which is determined by the localizer box. Because the localizer system uses one coordinate system (SRS coordinate system) and the CT image uses a different coordinate system, translations and rotations are needed in the alignment. The SRS Localization algorithm determines the required coordinate transformations (shifts and rotations).

The SRS Localization algorithm identifies the localizer box in the CT image in the following steps:

1. Detection of rod positions—The algorithm automatically finds the localizer rod positions in the CT image.

2. Automatic identification of the localizer model—The algorithm automatically identifies the localizer model based on the detected rod positions.

3. CT slice localization—The algorithm determines the position and orientation of individual CT slices in the SRS coordinate system.

4. Validation of slice localization—The algorithm validates the detected slice positions and orientations in the SRS coordinate system.

5. Creation of the stereotactic 3D image—The algorithm creates the stereotactic 3D image, which is aligned with the SRS coordinate system.

Detection of Rod Positions in the CT Slices

The SRS localization algorithm first automatically detects the rod positions in the CT slices. It identifies contiguous regions consisting of pixels with an image intensity value greater than or equal to a user-specified detection threshold. These regions are then modeled as circles by determining the smallest circle that completely encloses the corresponding pixel region. The centers of these circles are candidates for the rod center points.

Identification of the Localizer Model

After detecting the rod positions, the SRS Localization algorithm automatically recognizes the localizer model based on the rod positions. The algorithm first forms continuous cylinders using the circles found in the previous step, by stacking circles that overlap from slice to slice. Only circles with radii between 0.5–7 mm are considered. The resulting cylinders are compared with the vertical rods found in the geometrical description of the localizer models. The geometrical descriptions are predefined in the configuration of the planning system and are not user-definable. The first geometrical description that is an adequate match is used to define the detected localizer box. If none of the geometrical descriptions match closely enough, the localizer model remains undefined.

CT Slice Localization

CT slice localization determines the position and orientation of the individual slices in the input CT image in relation to the stereotactic coordinate system, which is defined by the localizer. This can be performed for each slice only when all rod positions have been defined on the slice (automatically or manually).

The figure shows how the slice localization is performed.
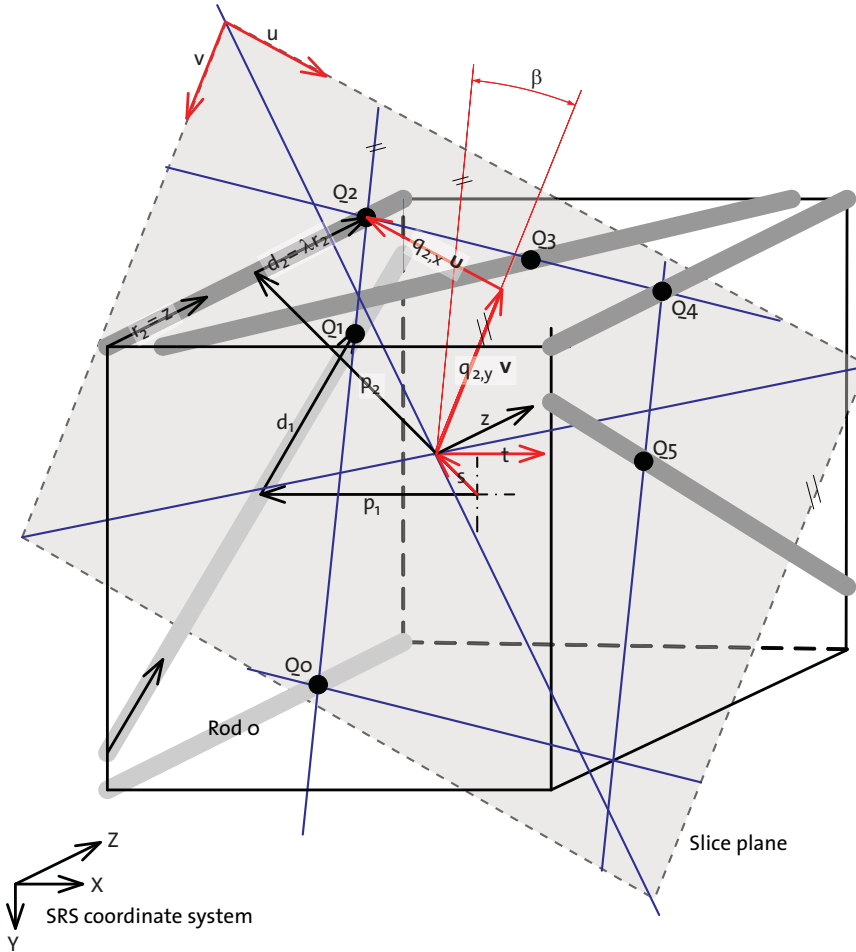
Figure 46   Localization of an Image Slice Intersecting a Localizer Box (VMS Model)

In the figure, the position and orientation of a CT slice are described by a translation s of the CT slice center point in relation to the localizer center (stereotactic origin), the direction of the CT slice normal vector t (tilt vector) and an angle β (spin angle) of rotation about that normal vector. The tilt angle is the angle between the Z-axis and the normal vector. The intersection points of the CT slice and the localizer rods are described in the SRS system as points on the localizer rods and as points on the slice plane. On the slice plane, these points are described using planar coordinates ($q_{i,x}$ and $q_{i,y}$) and normalized row and column vectors u and v.

The slice plane position and orientation in the SRS coordinate system can thus be obtained by solving a system of linear equations or a linear least squares fit, depending on the number of known rod intersection points.

Validation of Localization

After the slice localization is completed, the average spin angles and tilt directions are calculated from the values obtained from the individual slices. Furthermore, a linear fit of the detected slice center positions is made. Then the algorithm excludes slices with spin, tilt and center position values deviating from the average by more than a configurable amount, slices with detected position outside the localizer box, and re-calculates the average values. The average values are used to produce the final output.

The algorithm does not allow creation of the stereotactic 3D image if one of the following criteria applies:

- Less than 70% of the range defined by the lowermost and uppermost localized slice overlaps with the localizer box range.
- Average spin or tilt angle is greater than 30 degrees.

In addition to the above criteria, the algorithm also checks that not more than 10% of the slices contain localization errors and that the average spin or tilt angle is below 5 degrees. If these criteria are not met, a warning message is shown, but the algorithm still allows the creation of a stereotactic 3D image in the next step.

Creation of Stereotactic Volume

The stereotactic volume is a 3D image created from all input slices and aligned with the stereotactic coordinate system using the average rotations. The stereotactic volume pixels are shifted in the X, Y and Z-direction using a slice-specific translation value (obtained from a linear fit calculation through the detected rod positions), and the center of the localizer box is set at X = 0, Y = 0, Z = 0. Finally, the stereotactic volume is placed to a position where the stereotactic origin is at X = 0, Y = 0, Z = 0 in the patient space.

The stereotactic origin for the VMS and BRW localizer models is conventionally at the center of the localizer box and the head ring (in the X and Y-directions), and at 80 mm cranial of the head ring upper edge.

Volume Interpolation Algorithm

Eclipse models structures using shape-based interpolation in segmentation tools, volume calculation, 3D visualization and dose volume histogram calculation. Shape-based interpolation is obtained by tri-linear interpolation of a stack of 2D distance transforms of transaxial shapes.

The shape-based interpolation model is able to reproduce structures (shapes with curvature) that closely correspond to anatomical shapes. However, in the case of geometrical structures, such as boxes, the model rounds the ends of the box, which affects the calculated volume of the structure. As an example, Eclipse approximates the volume of a box with dimensions 4 cm × 4 cm × 3 cm to 40 cm^3 instead of the exactly calculated volume of 48 cm^3. The volume of a sphere is, however, reproduced more accurately.

The figure describes the shape-based interpretation of structure volumes.

1) Shape-based interpolation

2) Shape interpolation, sphere
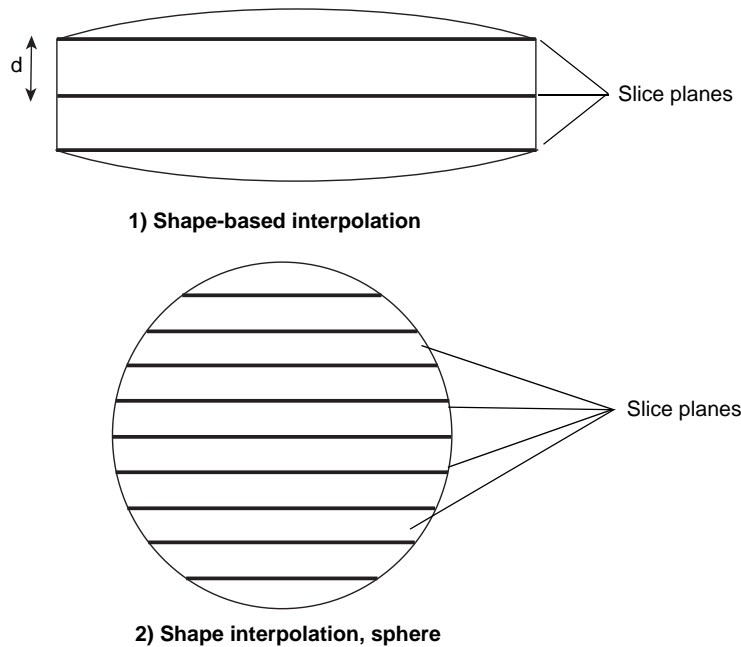
Figure 47   Shape-Based Interpretation of Structure Volumes

In the figure, *1)* shows how the shape-based interpolation model treats the outermost planes in a box-like structure; *2)* shows how the system interpolates and extrapolates a spherical shape, reproducing the curvature between the planes accurately.

Distance Transform

The shape-based interpolation algorithm is based on a *distance transform*[42]. This interpolation method linearly interpolates the shape of the structure between image planes, and smooths the structure boundaries. The distance transform is calculated for the structure boundary on each image plane. The minimum distance of each voxel from the structure boundary on the current plane is calculated and stored in the voxel. The interpolation algorithm marks the distances with negative values inside and positive values outside the structure. The structure boundary is formed by points that have values near zero (zero-crossing values). After the distance calculation, the distance

42. Herman GT & Zheng J, Bucholtz CA (1992) Shape-based interpolation. IEEE; Computer Graphics and Applications 12: 69–79.

values are used for the linear interpolation that approximates a continuous model of the structure. To determine the distance of a point from the structure boundary, the distance value of the point is calculated by interpolating the value from the nearest two image planes. The interpolation is always performed tri-linearly, that is, linearly in the directions of the three coordinate axes.

Surface Modeling

The surface model that is used for visualizing structures three-dimensionally is a triangle mesh. The position of the surface of a structure is located at the zero-crossing of the linearly interpolated distance transform.

Volume Calculation

The volume calculation to determine the total volume of a structure is also based on the distance values. The total volume is calculated by integrating the volume for which the interpolated distance values are negative.

DVH Calculation

The DVH is formed by binning the dose values inside the volume of the specified structure. The shape-based interpolation method is used to determine the structure shape. First, the distance transform of the structure is resampled over the dose matrix. Then the software uses the distance transform values to determine which dose values fall inside the structure. The dose values inside the structure are used to compute the DVH by linearly interpolating between neighboring dose voxels.

A dose-volume histogram is calculated in dose matrix coordinates. In Eclipse, the grid of a structure does not necessarily match the grid of the dose matrix exactly, leading to small differences in the volume calculation. The differences may be larger if the dose matrix and the structure grids have different orientations or Z-positions. In normal use, Eclipse creates dose matrices that have a co-aligned grid structure, leading to minor resampling errors. However, imported DICOM data may have dose and structure data in different orientations and Z-positions, leading to more significant levels of resampling inaccuracies. Also, miniscule structures may have a higher relative

level of resampling inaccuracy. The DVH algorithm in Eclipse reports the resampling accuracy by comparing structure volumes before and after resampling.

Verification of the Effective Depth

The effective depth value is used for manually verifying the MU calculation. The effective depth, the PSSD (reference point SSD) and the depth of the reference point are printed to the treatment report under the reference point information of each field in an external plan. These values are calculated to take into account any bolus that may be present. For information on treatment reports, see *Treatment Planning for External Beam - Eclipse Reference Guide*.

Calculation of the Effective Depth

The effective depth is calculated along the fanline from the source to the reference point, starting from the body outline:

Eq. 65

$$d_{eff} = \int_0^{Depth} \rho_e^-(l)dl$$

where

Depth $\quad = \quad$ Depth of reference point from the surface along the fanline

$\rho_e^-(l) \quad = \quad$ Electron density at depth l along the fanline

The algorithm only considers areas that are inside either the bolus or the Body structure.
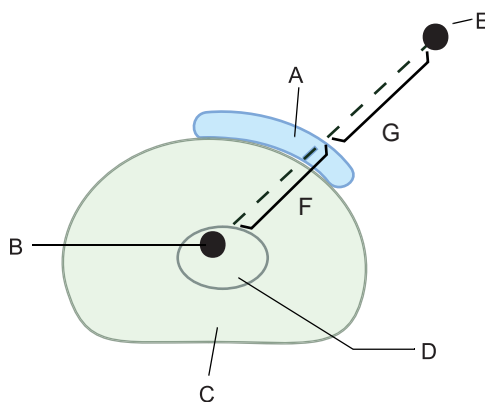
A. Bolus structure **B.** Reference point **C.** Body structure **D.** Structure inside the Body structure
E. Source. F. PSSD G. Depth

Figure 48   Effective Depth Calculation

First, the fanline line from the source to the reference point is
calculated. Then the algorithm calculates the intersection of the fanline
with each bolus and the Body structure, and the path lengths inside
them. The length of the path inside the bolus is multiplied by the
electron density. If the Body structure has a CT value assigned to it, the
CT value is used in the calculation of the fanline inside the Body
structure, otherwise CT value integration along the fanline path is
used. If other structures that the fanline intersects have CT values
assigned to them, the CT values are used in the calculation of the
fanline inside the structures, otherwise, CT value integration is used.
The PSSD is calculated by comparing the distances along the reference
point's fanline from the source with the intersection points of the Body
and bolus structures. The shortest distance is returned as the PSSD.

Dose Data of Large DMLC Fields

Large planning fields with multiple MLC carriage groups are divided
into subfields, each containing one MLC carriage group. The dose
contribution of each original planning field is divided into subfield
dose contributions, which sum up to the field dose contribution of the
original field. The MU are calculated in the same way.

The MU for the subfields are calculated as follows:

Eq. 66

$$MU_{\text{sub}} = \frac{\text{CMW}_{\text{last}} - \text{CMW}_{\text{first}}}{\text{FCMW}} \cdot MU_{\text{total}}$$

where

CMW_{last}	=	Cumulative meter set weight at the last control point of the subfield
$\text{CMW}_{\text{first}}$	=	Cumulative meter set weight at the first control point of the subfield
FCMW	=	Final cumulative meter set weight of the field
MU_{total}	=	Total MU of the field

The subfield dose contributions to reference points are calculated as follows:

Eq. 67

$$FDC_{\text{sub}} = \frac{\text{CMW}_{\text{last}} - \text{CMW}_{\text{first}}}{\text{FCMW}} \cdot FDC_{\text{total}}$$

where

CMW_{last}	=	Cumulative meter set weight at the last control point of the subfield
$\text{CMW}_{\text{first}}$	=	Cumulative meter set weight at the first control point of the subfield
FCMW	=	Final cumulative meter set weight of the field
$\text{FDC}_{\text{total}}$	=	Total dose contribution of the field to the reference point

Fit-and-Shield Algorithm

The Fit-and-Shield algorithm is implemented in the Eclipse Fit-and-Shield optimization tool, which positions MLC leaves around the target structure to expose the target while covering critical organs. The Fit-and-Shield optimization is mainly designed for modified hollow-out planning, which is a treatment technique employing conformal arc fields, but it can also be used for static fields and static arc fields. The tool creates the necessary number of fields or conformal arc fields and automatically determines the MLC leaf positions in each arc field segment. (For more information about using the Fit-and-Shield tool, refer to *Treatment Planning for External Beam - Eclipse Reference Guide*.)

The Fit-and-Shield algorithm is divided into the following parts:

- *Calculation of the field geometry*—The field geometry is considered by the Fit-and-Shield algorithm as a binary optimal fluence from each BEV projection along the field. The binary fluence is constructed by first projecting the target, which may be partially or completely cleared by the projections of the critical organs, depending on the direction of the projection.

- *Estimation of number of arc fields*—The number of arc fields required is determined from the maximum sum of the positive differences along the leaf trajectory (for each fluence and leaf pair). The maximum number of arc fields can also be manually defined. Each segment is assigned to its specific arc, and then the segments are optimized to match the motion limits of the DMLC with a minimal difference between the optimal and actual fluences. The Fit-and-Shield algorithm calculates the DMLC motions for one or more arc fields, attempting to match the target projection using the DMLC.

- Calculation of DMLC leaf positions—The Leaf Motion Calculator (see "Leaf Motion Calculator (LMC)" on page 245) is used to construct the arc field segments, formed by the DMLC leaf apertures. To make the DMLC leaf apertures feasible for the MLC device, the LMC applies machine-specific limitations to each MLC segment.

Approximated Minimum Distance Estimation in the Arc Geometry Tool

The Arc Geometry Tool shows approximated distances from the treatment unit head model to the couch model and to the patient model.The treatment unit head for Varian machines is modeled as a cylinder with the diameter of 80 cm. For Elekta treatment units, the diameter is 72 cm. The bottom of the cylinder for Varian machines is at 60 cm from the source level. For Elekta treatment units, the value is 58 cm. The whole cylinder is taken into account when measuring the distances, so the distances are also approximated from the edge of the cylinder, and not only along the central axis.

Treatment Unit Head to Patient Distance

The treatment unit head model to patient model distance estimation uses the contoured Body structure, and it approximates the shortest distance from the cylindrical treatment unit head model to the Body structure.

Note: *If part of the body is not contoured, it is not taken into account when approximating the distances.*

Treatment Unit Head to Couch Distance

The treatment unit head to couch algorithm approximates the shortest distance from the cylindrical treatment unit head model to the edge of the couch model.

The algorithm places a 53 cm wide default couch under the Body. The smallest possible box is fitted around the Body, and the couch is positioned under this box symmetrically in lateral direction.

All couch structures, and patient support and fixation structures, in the image are taken into account. If the image has not been enlarged when the couch was added (in other words, the widest part of the couch extends all the way to the image edge on both sides), a default width of 53 cm is used. If the widest couch structure does not extend out of the image on both sides, then just the visible width of the couch in the image is used.

In both cases, the thickness of the couch used in calculations is 3 cm. The length of the couch is not modeled; in other words, it is infinite. If couch rotation exceeds 15 degrees, distance calculation is disabled.

Irregular Surface Compensation Algorithm

The irregular surface compensation algorithm constructs an irregularly shaped surface. The intensity of each beamlet is modulated to achieve a uniform dose on this irregular compensation surface. The surface is calculated from the penetration depths of the fanline rays, which are traced through the patient. The compensation surface automatically includes the effects of beam divergence. Patient

geometry is considered in determining the compensation surface, but heterogeneity is accounted for in the field fluence calculation, not in determining the compensation surface.

The irregular surface compensation calculation is performed with the Dose Volume Optimizer (DVO) algorithm, which uses the gradient method (see Chapter 9, Section "Progressive Resolution Optimizer (PRO) Algorithm" on page 223). The algorithm checks the penumbra area to keep the difference in the fluence between the margin area and areas nearer to the fluence center under 20%. The volumetric dose calculation within the optimization is performed with the MRDC model (see Chapter 9, Section "Multi-Resolution Dose Calculation (MRDC) Algorithm" on page 211).

Volume Construction for Irregular Surface Compensation

The irregular compensation surface is constructed from the surfaces of the Body structure within the field aperture. First, the front and back Body surfaces are calculated using the depth buffering technique. The compensation surface is then interpolated from the Body surfaces, using a user-specified interpolation factor.

To reduce the effect of border compensation caused by high fluence at field edges, three compensation surfaces are constructed:

- Border surface—Includes points that are closer than from 5 mm (low energies) to 7.5 mm (high energies) from the field edge. To avoid overshoots at the edges due to scatter compensation, the border surface is allowed to receive 80% to 100% of the prescribed dose.
- Corner surface—To avoid overshoots at the edges of the fluence due to scatter compensation, the corner surface is allowed to receive 62% to 100% of the prescribed dose.
- Center surface—The center surface is allowed to receive 100% of the prescribed dose.

Isocenter Spacing in Cone Planning

When a stereotactic cone plan includes multiple isocenters, Cone Planning checks the spacing between all isocenters. If an isocenter is too close to another isocenter, a warning message is shown. The check is based on a predefined chart of optimal distances between isocenters defined for each collimator size (see the table).

The warning message is shown when a change that affects the isocenter location or cone sizes is made. The warning threshold between any two isocenters can be seen in the Isocenter Spacing tool. The Isocenter Spacing tool also allows the distance between isocenters to be set to a suggested value derived from the collimator spacing chart.

Table 38 Chart of Optimal Distances Between Isocenters

cone/mm	5	8	10	12	14	16	18	20	22	24	26	28	30	35	40	45	50
5	3.80	5.90	7.20	7.90	9.20	10.10	11.40	12.70	13.60	14.90	15.90	16.90	17.70	20.70	23.40	26.20	28.90
8		7.50	8.50	9.30	10.70	11.70	13.20	14.50	15.40	16.60	17.60	18.70	19.50	22.20	25.30	28.10	30.70
10			9.00	10.40	11.80	12.80	14.80	16.00	16.80	18.00	18.60	20.20	20.80	23.00	26.70	29.50	32.10
12				10.80	12.60	13.80	15.40	16.60	17.40	18.60	19.40	20.80	21.80	24.20	27.50	30.40	33.00
14					13.80	15.00	16.40	17.60	18.80	20.00	21.40	22.00	22.80	25.40	28.70	31.50	34.30
16						16.00	17.20	18.60	19.60	21.00	22.00	23.00	23.80	26.60	29.60	32.40	35.20
18							18.20	19.60	21.00	22.00	23.00	24.00	25.00	27.80	30.40	33.20	36.00
20								21.00	21.60	22.80	24.00	25.00	26.00	29.00	31.30	34.10	36.70
22									22.60	23.60	25.00	26.00	27.00	30.20	32.40	35.20	37.80
24										24.60	26.00	27.00	28.00	31.40	33.40	36.10	38.70
26											27.00	28.00	29.00	32.60	34.70	37.30	39.90
28												29.00	30.00	33.80	35.60	38.40	41.00
30													31.00	35.00	36.80	39.60	42.40
35														36.40	40.20	43.00	45.70
40															42.20	44.90	47.60
45																47.70	50.30
50																	53.20

The chart is used as follows:

- If the distance between any two isocenters is smaller than the value in the chart + 0.7 mm, the hotspot warning is shown.
- The Auto spacing in the isocenter spacing tool sets the distance between isocenters to the value in the chart + 1.2 mm.
- If there are cones of different sizes at one isocenter, (for example, 1 x 10 mm cone and 4 x 12 mm cones) the value of the largest cone (in this example, the 12 mm cone) is used.
- If there are cones the sizes of which are not included in the chart, the closest available value is used (for example, 17.5 mm is rounded up to 18 mm). If the cone size falls exactly between two values in the chart, the higher value is used (for example, for a 15 mm cone the value for a 16 mm cone would be used).

Volume V   Appendices

Appendix A   Abbreviations

BSF	Back Scatter Factor
CSSD	Central Axis Source-to-Skin Distance. Distance from the radiation source to the surface of the skin along the field central axis.
d_{max}	Depth of the field dose maximum at the central axis.
Dmax	Dose maximum
EDW	Enhanced Dynamic Wedge field accessory.
EqTAR	Equivalent TAR inhomogeneity correction method.
GPB	Generalized Pencil Beam algorithm for electron calculations.
ICRU	International Commission on Radiation Units and Measurements.
MLC	Multileaf Collimator field accessory.
MU	Monitor Unit.
NACP	Nordic Association of Clinical Physics.
PDD	Percentual Depth Dose. Absorbed dose at a specified depth expressed as a percentage of the absorbed dose at a reference depth on the central field axis.
PSF	Peak Scatter Factor. Ratio of the measured dose in water-equivalent phantom at the depth of the d_{max} in air and the dose to the same point, defined for a given source-detector distance and field size.
SAD	Source-to-Axis Distance. Distance between the radiation source and the isocenter of the treatment unit. All field sizes are defined at the SAD.
SAR	Scatter-air ratio. Ratio of the scattered dose at a specified point in the phantom to the dose at the same point in free space.
SDD	Source-to-Detector Distance

SFED	Source-Field Entry Point Distance.
SID	Source-to-Imager Distance
SMR	Scatter-maximum ratio. Ratio of the scattered dose at a specified point in the phantom to the effective primary dose at the same point at the reference depth of the maximum dose. Special case of SAR, where the reference point is different.
SPB	Single Pencil Beam algorithm for photon calculations.
SPD	Source-to-Phantom Distance. Distance between the radiation source and the surface of the water phantom. Used in beam data measurements.
SSD	Source-to-Skin Distance. Distance between the radiation source and the surface of the patient's skin. Used in beam data configuration and treatment planning.
STT	Segmented Treatment Data Table. Describes the treatment unit movements during a segmented treatment field.
TAR	Tissue-Air Ratio. Ratio of the absorbed dose at a given point in the phantom to the absorbed dose at the same point in free space.
TMR	Tissue-Maximum Ratio. Ratio of the absorbed dose at a point in the phantom to the same point when it is at the d_{max}. Special case of the TPR, where the reference depth is the d_{max}.
TPR	Tissue-Phantom Ratio. Ratio of the absorbed dose at a point in the phantom to the absorbed dose at the reference depth.
w2CAD	Waterphantom-CadPlan file format for water phantom data. Used to transfer the measured beam data from water phantom devices.

Appendix B   Definition of Field Geometry

The figure shows the definitions of the field dimensions as seen from the Beam's Eye View. The gantry is at the top if the collimator angle is 0°.
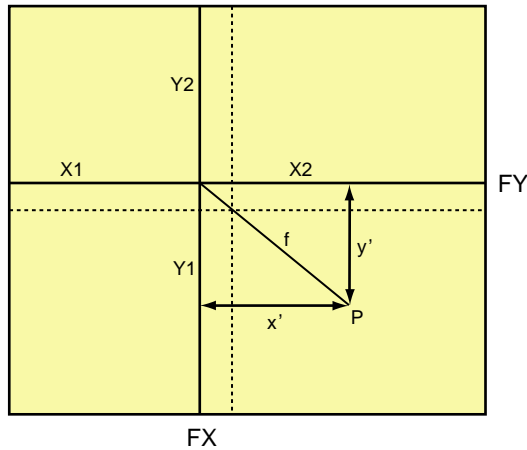
$$x' = \frac{SAD}{CSSD + d_1} \bullet x_1 \qquad \text{and} \qquad y' = \left[\frac{SAD}{CSSD + d_1} \right] \bullet y_1$$

Figure 49   Field Size and Grid Point Geometry at SAD Level from BEV

The following figure shows the definitions of the distances used in calculations of depth dose and oblique corrections.
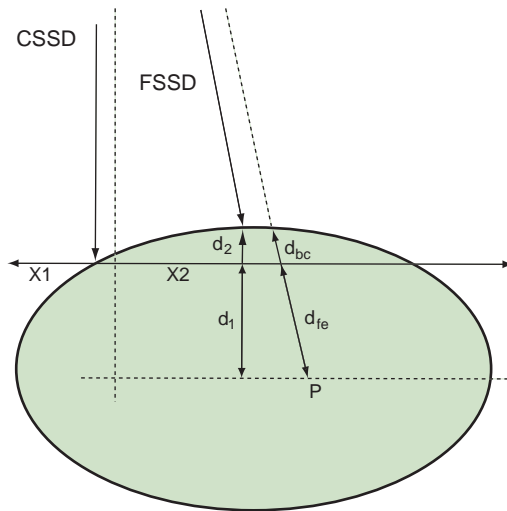
Figure 50 Distances Used in Depth Dose Calculations and Oblique Corrections

Table 39 Variables in Field Geometry Definitions

Variable	Meaning
CSSD	Central axis Source-to-Skin Distance.
d_1	Shortest distance between parallel planes, perpendicular to the field central axis, intersecting the grid point and the point where the field central axis intersects the body contour.
d_2	Shortest distance between the plane perpendicular to the field central axis, intersecting the grid point and the point where the fanline from the grid point to the focus intersects the body contour.
d_{bc}	Distance between the grid point and the body contour, measured along the fanline from the grid point to the focus.
d_{fe}	Distance between the grid point and the plane perpendicular to the field central axis where the central axis intersects the body contour, measured along the fanline.
FSSD	Fanline Source-to-Skin Distance.
FX	Symmetrical lateral field size, defined at the SAD.

Table 39 Variables in Field Geometry Definitions

Variable	Meaning
FY	Symmetrical longitudinal field size, defined at the SAD.
SAD	Source-to-Axis Distance.
SPD	Source-to-Phantom distance.
SSD	Source-to-Skin distance.
x	Distance of the grid point from the field central axis in the field lateral direction, defined at grid point level.
X1	Lateral field size on the left side of the field, defined at the SAD.
X2	Lateral field size on the right side of the field, defined at the SAD.
y	Distance of the grid point from the field central axis in the field longitudinal direction, defined at grid point level.
Y1	Longitudinal field size on the lower side of the field, defined at the SAD.
Y2	Longitudinal field size on the upper side of the field, defined at the SAD.
z	Axis parallel to the central axis.

Appendix C   File Formats for Measured Beam Data

w2CAD File Format

The w2CAD (waterphantom-CadPlan) file format is used to transfer the measured beam data from various water phantom devices. Beam data measurements must be saved into ASCII files that can be read in any text editor. For examples of w2CAD table formats, see Appendix D on page 337.

Note: *Keep all open field depth dose curves and profiles in one file, and the depth dose curves and profiles for each wedge in a separate file. The diagonal profiles and wedge longitudinal profiles can be saved in separate files or in the same files with the depth dose curves and profiles, respectively. Do not include any other type of data in these files.*

Store depth dose curves starting from the water surface. Store all profiles in the same order, either from left to right or right to left.

Initial Characters and Separation Between Measurements

The initial characters and the delimiter tags between measurements are the same in the w2CAD files for all algorithms.

Table 40   Meaning of Initial Characters in w2CAD Files

Text	Meaning
$	Separation between measurements
#	Comment text[a]
%	Header line
<xyz>	Measurement data, points x, y, z

a. Comment text can be placed anywhere in the file.

Text	Meaning
`$STOM:`	Start of one measurement
`$ENOM:`	End of one measurement
`$ENOF:`	End of the file
`$NUMS XXX:`	Number of measurements in this file (not necessary)

w2CAD Files for the AAA and the Acuros XB Algorithms

The w2CAD files contain several measurements (one curve represents one measurement). Each measurement consists of a header and data information.

Table 42 Header lines

Text	Meaning
`%DATE DD-MM-YYYY:`	Date of the measurement
`%VERSION XX:`	Version of W2CAD file format The current version number is 02. In the previous w2CAD file format, a version number was not used.
`%DETY XXX:`	Detector type ■ `CHA` = Ionization chamber ■ `DIO` = semiconductor detector ■ `DIA` = Diamond
`%BMTY XXX:`	Beam type ■ `PHO` = High energy photons (MV energies)

Table 42 Header lines

Text	Meaning
`%TYPE XXX:`	Measurement type ■ `OPD` = Open field depth dose curve ■ `OPP` = Open field profile ■ `WDD` = Wedge depth dose curve ■ `WDD_SSD80` = Wedge depth dose curve, SSD 80 cm (AAA and Acuros XB only) ■ `WDD_SSD120` = Wedge depth dose curve, SSD 120 cm (AAA and Acuros XB only) ■ `WDP` = Wedge profile ■ `WLP` = Wedge longitudinal profile ■ `DPR` = Diagonal profile
`%WDGL XX:`	Wedge name (2 characters, wedged fields only)
`%WDGD X:`	Wedge direction (wedged fields only) ■ `L` = Thin edge left (negative in X-direction as in IEC 61217) ■ `R` = Thin edge right (positive in X-direction as in IEC 61217)
`%AXIS X:`	Measurement axis ■ `X, Y` = Horizontal Axes ■ `Z` = Vertical Axis (the depth axis) ■ `D` = Diagonal Axis `%AXIS` must be D, when both the X and Y horizontal axis values are given for the diagonal profile. `%AXIS` can be X or Y if only one horizontal axis is used to store the point distance from the origin. `%AXIS Z` defines the measurement axis with the other measurement types.
`%PNTS NNN:`	Number of points
`%STEP XXX:`	Point separation in 1/10 mm
`%SSD  XXXX:`	SSD in mm
`%FLSZ XXX*XXX:`	Field size in mm Each value consists of three characters. For measurements under 100 mm, type 0 in front of the value, or use spaces in front of and after the asterisk (`*`), for instance, `%FLSZ 010*010` or `%FLSZ 10 * 10`.
`%DPTH XXX:`	Measurement depth in mm (only profiles)

The measurement data is in the format

```
<SXXX.X SYYY.Y SZZZ.Z SDDD.D>
```

where

S	=	Sign (+/-)
XXX.X	=	X-coordinate in mm
YYY.Y	=	Y-coordinate in mm
ZZZ.Z	=	Z-coordinate in mm
DDD.D	=	Dose values in %

Example of a file with one depth dose curve and one profile made from 10×10 cm open field measurement:

Table 43 Example w2CAD File

```
$NUMS 002
$STOM
#
#CLINAC 2 6 MV PHOTONS
#FIELD SIZE 10x10 cm
#
%DATE 12-12-1997
%DETY CHA
%BMTY PHO
%TYPE OPD
%AXIS Z
%PNTS 051
%STEP 050
%SSD  1000
%FLSZ 100*100
#
<+000.0 +000.0 +000.0 +030.0>
<+000.0 +000.0 +005.0 +076.0>
<+000.0 +000.0 +010.0 +093.4>
<+000.0 +000.0 +015.0 +098.7>
<+000.0 +000.0 +020.0 +100.0>
<+000.0 +000.0 +020.0 +099.2>
.
.
.
<+000.0 +000.0 +245.0 +034.4>
<+000.0 +000.0 +250.0 +033.7>
$ENOM
$STOM
#
#CLINAC 2 6 MV PHOTONS
#FIELD SIZE 10x10 cm
#
%DATE 12-12-1997
%DETY CHA
%BMTY PHO
%TYPE OPP
%AXIS X
%PNTS 037
%STEP 025
%SSD  1000
%FLSZ 100*100
%DPTH 050
#
<-090.0 +000.0 +050.0 +002.4>
<-087.5 +000.0 +050.0 +002.6>
<-085.0 +000.0 +050.0 +002.8>
<-082.5 +000.0 +050.0 +003.0>
<-080.0 +000.0 +050.0 +003.4>
<-077.5 +000.0 +050.0 +003.8>
<-075.0 +000.0 +050.0 +005.3>
<-072.5 +000.0 +050.0 +012.6>
<-070.0 +000.0 +050.0 +061.5>
<-067.5 +000.0 +050.0 +094.9>
<-065.0 +000.0 +050.0 +098.3>
.
.
.
<+087.5 +000.0 +050.0 +002.9>
<+090.0 +000.0 +050.0 +002.5>
$ENOM
$ENOF
```

w2CAD Files for the CDC Algorithm

The w2CAD files for the Cone Dose Calculation (CDC) algorithm contain several measurements (one curve represents one measurement). Each measurement consists of a header and data information.

Table 44 Header lines

Text	Meaning
`%DATE DD-MM-YYYY:`	Date of the measurement
`%VERSION XX:`	Version of W2CAD file format The current version number is 02. In the previous w2CAD file format, a version number was not used.
`%DETY XXX:`	Detector type ■ `CHA` = Ionization chamber ■ `DIO` = semiconductor detector ■ `DIA` = Diamond
`%BMTY XXX:`	Beam type ■ `PHO` = High energy photons (MV energies)
`%TYPE XXX:`	Measurement type ■ `TMR`= Tissue Maximum Ratio ■ `OPP` = Off-axis Ratio. The same tag is used for Open field profile and Off-axis ratio in the w2CAD files.
`%AXIS X:`	Measurement axis ■ `X` or `Y` = Horizontal Axes ■ `Z` = Vertical Axis (the depth axis)
`%PNTS NNN:`	Number of points (optional).
`%FLSZ X.X*X.X:`	Field size in mm For cone sizes containing decimals, use decimal points. For instance, when measuring with a 7.5 mm cone, type the filed size as `%FLSZ 7.5*7.5`.
`%DPTH XXX:`	Measurement depth in mm (only profiles)

The measurement data is in the format

```
<SXXX.X SYYY.Y SZZZ.Z SDDD.D>
```

where

S	=	Sign (+/-)
XXX.X	=	X-coordinate in mm
YYY.Y	=	Y-coordinate in mm
ZZZ.Z	=	Z-coordinate in mm
DDD.D	=	Dose values in %

Example of a file with one depth dose curve and one profile made from 7.5×7.5 mm cone field measurement:

Table 45 Example w2CAD File

```
$NUMS 002
$STOM
#CLINAC 2 6 MV PHOTONS
#FIELD SIZE 0.75 cm CONE
#
%DATE 12-12-2008
%VERSION 02
%DETY CHA
%BMTY PHO
%TYPE TMR
%AXIS Z
%PNTS 076
%FLSZ 7.5*7.5
<+000.0 +000.0 +000.0 +040.6>
<+000.0 +000.0 +002.5 +065.7>
<+000.0 +000.0 +005.0 +090.5>
<+000.0 +000.0 +007.5 +098.3>
<+000.0 +000.0 +010.0 +100.0>
.
.
.
<+000.0 +000.0 +164.9 +041.8>
<+000.0 +000.0 +167.4 +041.3>
<+000.0 +000.0 +169.9 +040.8>
$ENOM
$STOM
#CLINAC 2 6 MV PHOTONS
#FIELD SIZE 0.75 cm CONE
#
%DATE 12-12-2008
%DETY DIO
%BMTY PHO
%TYPE OPP
%AXIS X
%PNTS 053
%STEP 005
%SSD  0900
%FLSZ 7.5*7.5
%DPTH 100
<+000.0 +000.0 +100.0 +100.0>
<+000.5 +000.0 +100.0 +099.1>
<+001.0 +000.0 +100.0 +097.5>
<+001.5 +000.0 +100.0 +094.8>
<+002.0 +000.0 +100.0 +090.4>
<+002.5 +000.0 +100.0 +082.2>
<+003.0 +000.0 +100.0 +070.5>
<+003.5 +000.0 +100.0 +055.1>
.
.
.
<+009.5 +000.0 +100.0 +001.6>
<+010.0 +000.0 +100.0 +001.4>
<+010.5 +000.0 +100.0 +001.2>
<+011.0 +000.0 +100.0 +001.1>
<+011.5 +000.0 +100.0 +001.0>
$ENOM
$ENOF
```

w2CAD Files for the eMC Algorithm and IPS Model

To import and configure the eMC algorithm correctly, the Beam Configuration task requires parameters to specify the data in the w2CAD files. These parameters include mandatory and optional parameters. The optional parameters can also be entered afterwards in the Beam Configuration task.

Note: *To ensure successful configuration, the data must start from depth = 0.0 cm.*

Table 46 Mandatory Parameters

Text	Meaning	
`%VERSION 02`	w2cad file format version, must be `02`	
`%BMTY ELE`	Beam type, must be `ELE` (= electron)	
`%TYPE xxx`	The measurement type parameter must be one of the following:	
	`xxx = MeasuredDepthDosesForOpenBeam`	Depth dose curve without applicator
	`xxx = MeasuredProfileForOpenBeam`	Open beam profile
	`xxx = MeasuredDepthDosesForApplicator`	Depth dose curve with applicator
`%ID Open`	Curve identifier	Used only for open type data

Table 47 Optional Parameters

Text	Meaning
`%SPD x.x`	Source-Phantom Distance in [cm] for all curves
`%CalibrationDepth x.x`	Depth of the calibration point in [cm] for depth dose curves
`%CalibrationFactor x.x`	Absolute dose in [cGy/MU] at the calibration point for depth dose curves

Table 48 Example

```
$NUMS 003
$STOM
#
# Clinac 2100CD 12 MeV w/o applicator
# DDM IN AIR AT SPD 95 cm
# DATE: 2-Jun-2002
#
%VERSION 02
%BMTY ELE
%TYPE MeasuredDepthDosesForOpenBeam
%ID Open
%SPD 100.0
%CalibrationDepth 3.05
%CalibrationFactor 0.944
#
<+000.0 +000.0 +000.0 +076.41>
<+000.0 +000.0 +003.0 +081.46>
<+000.0 +000.0 +006.0 +083.73>
<+000.0 +000.0 +009.0 +086.46>
.
.
.
<+000.0 +000.0 +095.0 +001.94>
$ENOM
$STOM
#
# Clinac 2100CD 12MeV
# X PROFILE IN AIR SSD 95 cm
# DATE: 26-Jun-2002
#
%VERSION 02
%BMTY ELE
%TYPE MeasuredProfileForOpenBeam
%ID Open
%SPD 95.0
#
<-210.0 +000.0 +000.0 +040.83>
<-200.0 +000.0 +000.0 +052.85>
<-190.0 +000.0 +000.0 +061.38>
<-180.0 +000.0 +000.0 +068.70>
<-170.0 +000.0 +000.0 +073.47>
.
.
.
<+210.0 +000.0 +000.0 +034.99>
$ENOM
$STOM
#
# Clinac 2100CD 12 MeV
# Depth-Dose SPD 100 cm
# DATE: 2-Jun-2002
#
%VERSION 02
%BMTY ELE
%FLSZ 100*100
%TYPE MeasuredDepthDosesForApplicator
%SPD  100.0
%CalibrationDepth 3.05
%CalibrationFactor 1.067
#
<+000.0 +000.0 +000.0 +080.68>
<+000.0 +000.0 +003.3 +083.30>
<+000.0 +000.0 +007.0 +085.71>
<+000.0 +000.0 +010.0 +088.14>
<+000.0 +000.0 +014.0 +090.22>
.
.
.
<+000.0 +000.0 +120.0 +001.43>
$ENOM
$ENOF
```

Compensator Attenuation Curve Data File Format

A user-defined compensator attenuation curve data can be imported in Beam Configuration in a separate file. You need to manually create the file for the import. To enable Beam Configuration to read the file, it must use a specified file format.

The file must be a text file that consists of two columns separated by a space. The first column is for the energy (in MeV), the second column is for the mass attenuation coefficient μ/ρ (in cm^2/g).

The following shows an example of a compensator attenuation curve data file.

Table 49 Example of Compensator Attenuation Curve Data File Format

1.00E-02	2.22E+02
1.50E-02	7.67E+01
2.00E-02	3.50E+01
3.00E-02	1.13E+01
4.00E-02	5.06E+00
5.00E-02	2.72E+00
6.00E-02	1.65E+00
8.00E-02	7.90E-01
1.00E-01	4.73E-01
1.50E-01	2.26E-01
2.00E-01	1.58E-01
3.00E-01	1.13E-01
4.00E-01	9.46E-02
5.00E-01	8.39E-02
6.00E-01	7.65E-02
8.00E-01	6.62E-02
1.00E+00	5.92E-02
1.25E+00	5.27E-02
1.50E+00	4.81E-02
2.00E+00	4.22E-02
3.00E+00	3.61E-02
4.00E+00	3.33E-02
5.00E+00	3.19E-02
6.00E+00	3.13E-02
8.00E+00	3.10E-02
1.00E+01	3.13E-02
1.50E+01	3.28E-02
2.00E+01	3.45E-02

Appendix D   Table Input Formats

Output Factor Table Format for AAA and Acuros XB

An output factor table, required by the configuration program for photon beams, can be imported into Beam Configuration in a separate measurement file. To enable Beam Configuration to read the file, it must use a specified file format.

The output factor table file consists of a header section and a data section. The table describes the format to be used in the header section.

Table 50 Output Factor Table Format

Text	Meaning
`%VERSION XX`	Version number.
`%DATE DD-MM-YYYY`	Date of measurement.
`%BMTY PHO`	Beam Type. Only `PHO` is supported.
`%TYPE nnn`	Type of the output factor table. Elekta Beam Modulator treatment unit: `BMOutputFactorTable` Other treatment units: `OutputFactorTable`
`%SourcePhantomDistance nnn`	Source to phantom distance used for the measurements, expressed in millimeters.
`%DetectorDepth nnn`	Detector depth, expressed in millimeters.
`#`	Line containing a comment. These lines are not mandatory, and they can be inserted anywhere in the file.

The output factor measurement data is recorded to the Data section of the file. The Data section must use the following format:

- *First line*—X field sizes (in accordance with IEC 61217 and expressed in centimeters) for the table, each value separated by a comma: X1, X2, X3,,,Xn.

- *Following lines*—Output factor values for all field sizes in cm, organized to lines by the Y field sizes. Each line starts with the Y field size, and then lists the output factor values for the X field sizes (specified in the first line). The values are separated by a comma.

The following shows an example of a Beam Modulator Output Factor Table file:

Table 51 Example Output Factor Table File

```
#
# Example Output factor table for Beam Modulator
#
%VERSION 03
%DATE 27-08-2010
%BMTY PHO
%TYPE BMOutputFactorTable
%SourcePhantomDistance 1000
%DetectorDepth 50
# Data
2.4, 3.2, 4, 5.6, 8, 10.4, 12, 16, 21
2.4, 0.810, 0.824, 0.833, 0.845, 0.857, 0.862, 0.865, 0.868, 0.872
3.2, 0.832, 0.844, 0.860, 0.870, 0.883, 0.899, 0.894, 0.900, 0.904
4.0, 0.836, 0.854, 0.872, 0.890, 0.904, 0.913, 0.921, 0.926, 0.929
5.6, 0.854, 0.872, 0.886, 0.910, 0.935, 0.948, 0.950, 0.967, 0.967
8.0, 0.860, 0.887, 0.905, 0.936, 0.967, 0.977, 0.986, 1.004, 1.015
10.4, 0.862, 0.893, 0.918, 0.948, 0.980, 1.000, 1.005, 1.023, 1.040
12.0, 0.865, 0.896, 0.918, 0.951, 0.990, 1.012, 1.016, 1.034, 1.047
16.0, 0.870, 0.905, 0.924, 0.964, 0.996, 1.020, 1.030, 1.051, 1.066
```

Beam Configuration can still read the CSV based (CadPlan) output factor table format. However, the new format explicitly shows the measurement geometry and includes fractional field sizes.

Absolute Point Doses File Format for AAA and Acuros XB

The absolute point doses required for the configuration of the AAA and Acuros XB for Elekta Beam Modulator can be imported into Beam Configuration in a separate measurement file. You need to manually create the file for the import. For each measured field, the absolute point doses table indicates the asymmetrical jaw positions, the

detector position and the measured point dose at the detector. To enable Beam Configuration to read the file, it must use a specified file format.

The file consists of a header section and a data section. The table describes the format to be used in the header section.

Table 52 AAA and Acuros XB Absolute Point Doses File Format, Header Section

Text	Meaning
`%VERSION XX`	Version number. The current version number is 01.
`%DATE DD-MM-YY`	Date of measurement
`%BMTY PHO`	Beam Type. Only PHO is supported.
`%TYPE PointDoseTableIEC`	Must be PointDoseTableIEC
`%SourcePhantomDistance nnn`	Source to phantom distance used for the measurements in mm.
`#`	Line containing a comment. These lines are not mandatory, and they can be inserted anywhere in the file.

The measurement data must be recorded in the Data section of the absolute point doses file. The Data section must use the following format:

Table 53 AAA and Acuros XB Absolute Point Doses File Format, Data Section

Text	Meaning
`X1[mm], X2[mm], Y1[mm], Y2[mm], X[mm], Y[mm], Z[mm], Dose[cGY/MU]`	
	First line in the Data section. The first line in the data section identifies the column header for the subsequent data point lines. It must follow this format. The measurement values must be separated with a comma.
`R<n>`	Identifier of each measurement. `<n>` is the measurement number.
`X1[mm]`	Position of the X1 jaw, expressed in millimeters and in accordance with IEC 61217.
`X2[mm]`	Position of the X2 jaw, expressed in millimeters and in accordance with IEC 61217.

Table 53 AAA and Acuros XB Absolute Point Doses File Format, Data Section

Text	Meaning
Y1 [mm]	Position of the Y1 jaw, expressed in millimeters and in accordance with IEC 61217.
Y2 [mm]	Position of the Y2 jaw, expressed in millimeters and in accordance with IEC 61217.
X [mm]	X-coordinate of the measurement point (detector position) taken from the intersection of the CAX and the phantom surface, expressed in millimeters and in accordance with IEC 61217.
Y [mm]	Y-coordinate of the measurement point (detector position) taken from the intersection of the CAX and the phantom surface, expressed in millimeters and in accordance with IEC 61217.
Z [mm]	Z-coordinate of the measurement point (detector position) taken from the intersection of the CAX and the phantom surface, increasing depth from the phantom surface to floor, expressed in millimeters.
Dose [cGY/MU]	Measured point dose at the detector, expressed in cGy/MU.

The following shows an example of an Absolute Point Doses Beam Data file.

Table 54 Example Absolute Point Doses Beam Data File

```
#
# Example of PointDoseTableIEC file
#
%VERSION 01
%DATE 12-02-10
%BMTY PHO
%TYPE PointDoseTableIEC
%SourcePhantomDistance 950
# Data
  ,X1[mm], X2[mm], Y1[mm], Y2[mm], X[mm], Y[mm], Z[mm], Dose[cGY/MU]
R1, -20, 20, -20,  20,  0,  0, 50, 0.881
R2, -20, 20,  40,  80,  0, 60, 50, 0.900
R3,  65, 105, -20, 20,  85, 0, 50, 0.912
R4,  20, 60,  20,  60, 40, 40, 50, 0.904
R5,  65, 105, 40,  80,  85, 60, 50, 0.923
R6, -52, 52, -52,  52,  0,  0, 50, 0.951
R7, -52,  52, -24, 80, 0,  28, 50, 0.966
R8,  1, 105, -52, 52, 53, 0, 50, 0.966
R9,  1, 105, -24, 80, 53, 28, 50, 0.971
```

Appendix E   Beam Data Measurement Forms

Table 55 Open Field PDDs[a]

Field	Field Size										
	Smallest	4	6	8	10	12	15	20	25	30	35	Largest
Open											

a. Measured in the surface–30 cm range

Table 56 Wedged Field PDDs[a]

Field	Field Size									
	Smallest	4	6	8	10	12	15	20	Largest square	Largest rectangular
Wedge 1										
Wedge 2										
Wedge 3										
Wedge 4										

a. Measured for all hard and motorized wedges in the surface–30 cm range

Table 57 Open Field Profiles at 5 Depths

Depth	Field Size										
	Smallest	4	6	8	10	12	15	20	25	30	35	Largest
1. d_{max_10}											
2.											
3.											
4.											
5.											

Table 58 Wedged Field Profiles at 5 Depths

Wedge 1										
	Field Size									
Depth	Smallest	4	6	8	10	12	15	20	Largest square	Largest rectangular
1. d_{max_10}										
2.										
3.										
4.										
5.										
Wedge 2										
	Field Size									
Depth	Smallest	4	6	8	10	12	15	20	Largest	Largest rectangular
1. d_{max_10}										
2.										
3.										
4.										
5.										
Wedge 3										
	Field Size									
Depth	Smallest	4	6	8	10	12	15	20	Largest	Largest rectangular
1. d_{max_10}										
2.										
3.										
4.										
5.										
Wedge 4										
	Field Size									
Depth	Smallest	4	6	8	10	12	15	20	Largest	Largest rectangular

Table 58 Wedged Field Profiles at 5 Depths

1. d_{max_10}									
2.									
3.									
4.									
5.									

Table 59 Open Diagonal Profiles[a]

	Field Size
Depth	Largest
1. d_{max_10}	
2	
3	
4	
5	

a. Measured at 5 Depths

Table 60 Wedge Longitudinal Profile[a]

Field	Largest measured field size (AAA and Acuros XB)
Wedge 1	
Wedge 2	
Wedge 3	
Wedge 4	
Wedge 5	

a. Measured at 1 depth for all hard and motorized wedges

Table 61 Block and MLC Transmission Factors[a]

	Results	$R_{tray + block}$	R_{tray}
Material			
1			
2			

Table 61 Block and MLC Transmission Factors[a]

	Results	$R_{tray + block}$	R_{tray}
3			
4			
5			

a. Measure R_{tray} and $R_{tray + block}$ in water for each block material using a small field

Table 62 Shadow Tray Factors[a]

	Results	R_{open}	R_{tray}
Tray Model			
1			
2			
3			
4			
5			

a. Measure R_{tray} and R_{open} in water for each shadow tray model using a mid-range field size

Table 63 Open Field Output Factors

Field Size, Height (FY)	Field Size, Width (FX)											
	Smallest	4	6	8	10	12	15	20	25	30	35	Largest
Smallest												
4												
6												
8												
10												
12												
15												
20												
25												
30												
35												
Largest												

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Table 64 Wedged Field Output Factors[a]

Wedge 1												
	Field Size, Width (FX)											
Field Size, Height (FY)	Smallest	4	6	8	10	12	15	20	25	30	35	Largest
Smallest												
4												
6												
8												
10												
12												
15												
20												
Largest												
Wedge 2												
	Field Size, Width (FX)											
Field Size, Height (FY)	Smallest	4	6	8	10	12	15	20	25	30	35	Largest
Smallest												
4												
6												
8												
10												
12												
15												
20												
Largest												

Table 64 Wedged Field Output Factors[a]

Wedge 3												
	Field Size, Width (FX)											
Field Size, Height (FY)	Smallest	4	6	8	10	12	15	20	25	30	35	Largest
Smallest												
4												
6												
8												
10												
12												
15												
20												
Largest												
Wedge 4												
	Field Size, Width (FX)											
Field Size, Height (FY)	Smallest	4	6	8	10	12	15	20	25	30	35	Largest
Smallest												
4												
6												
8												
10												
12												
15												
20												
Largest												

a. Measure for all hard and motorized wedges

Table 65 Treatment Unit Parameters and Limits

General Parameters				
Source axis distance				
Source phantom distance				
Collimator skin distance				
No. of wedges and wedge codes	Code 1	Code 2	Code 3	Code 4
Gantry Parameters				
Angle of minimum rotation				
Direction of the increase	Clockwise/Counterclockwise			
Start angle in CW direction				
Stop angle in CW direction				
Collimator Parameters				
Angle of minimum rotation				
Direction of the increase	Clockwise/Counterclockwise			
Start angle in CW direction				
Stop angle in CW direction				
	FX		FY	
Field edge, X direction				
Field edge, Y direction				
	X1/Y1		X2/Y2	
Jaw labels, X direction				
Jaw labels, Y direction				
	Up	Down	Left	Right
Wedge direction labels				
Allowed wedge directions	Up/down/left/right			
Field Size	**X Direction**		**Y Direction**	
Minimum open field size				
Maximum open field size				
Minimum field size wedge 1				
Maximum field size wedge 1				
Minimum field size wedge 2				
Maximum field size wedge 2				
Minimum field size wedge 3				
Maximum field size wedge 3				
Minimum field size wedge 4				
Maximum field size wedge 4				

Table 65 Treatment Unit Parameters and Limits

Couch Parameters		
Angle of minimum rotation		
Direction of the increase	Clockwise/Counterclockwise	
Start angle in CW direction		
Stop angle in CW direction		
(Couch height at isocenter)		
(Couch height at lowest)		
(Couch height at position)		
Multileaf Collimator Parameters		
(MLC model)	Internal/External	
Leaf direction	X/Y	
Number of leaves		
Leaf width at SAD		
Minimum opening		
Maximum opening		
	X_1/Y_1	X_2/Y_2
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Maximum overtravel X_1/Y_1		
Maximum leaf span		
Maximum leaf tolerance		

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