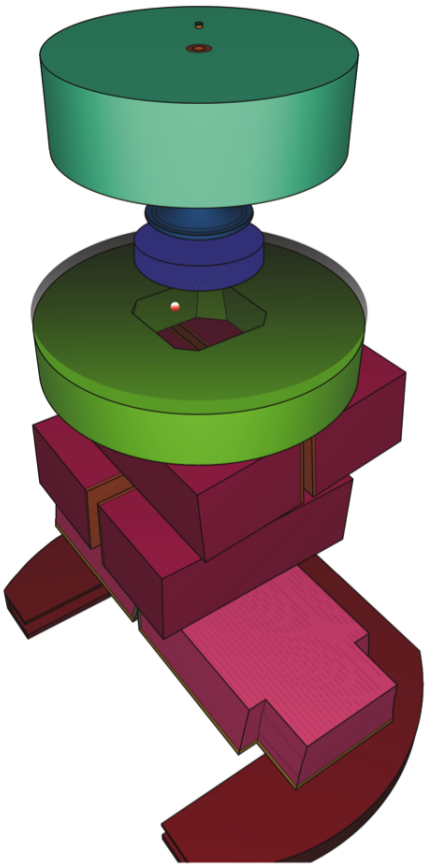
PRIMO
User's Manual



Brualla · Rodriguez · Sempau

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PRIMO USER'S MANUAL
SOFTWARE VERSION 0.1.5.1300

WWW.PRIMOPROJECT.NET

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Typeset by the authors with the LaTeX Documentation System. The *Legrand Orange Book* template downloaded from `http://www.LaTeXTemplates.com` was used to write this manual.

24th April 2015

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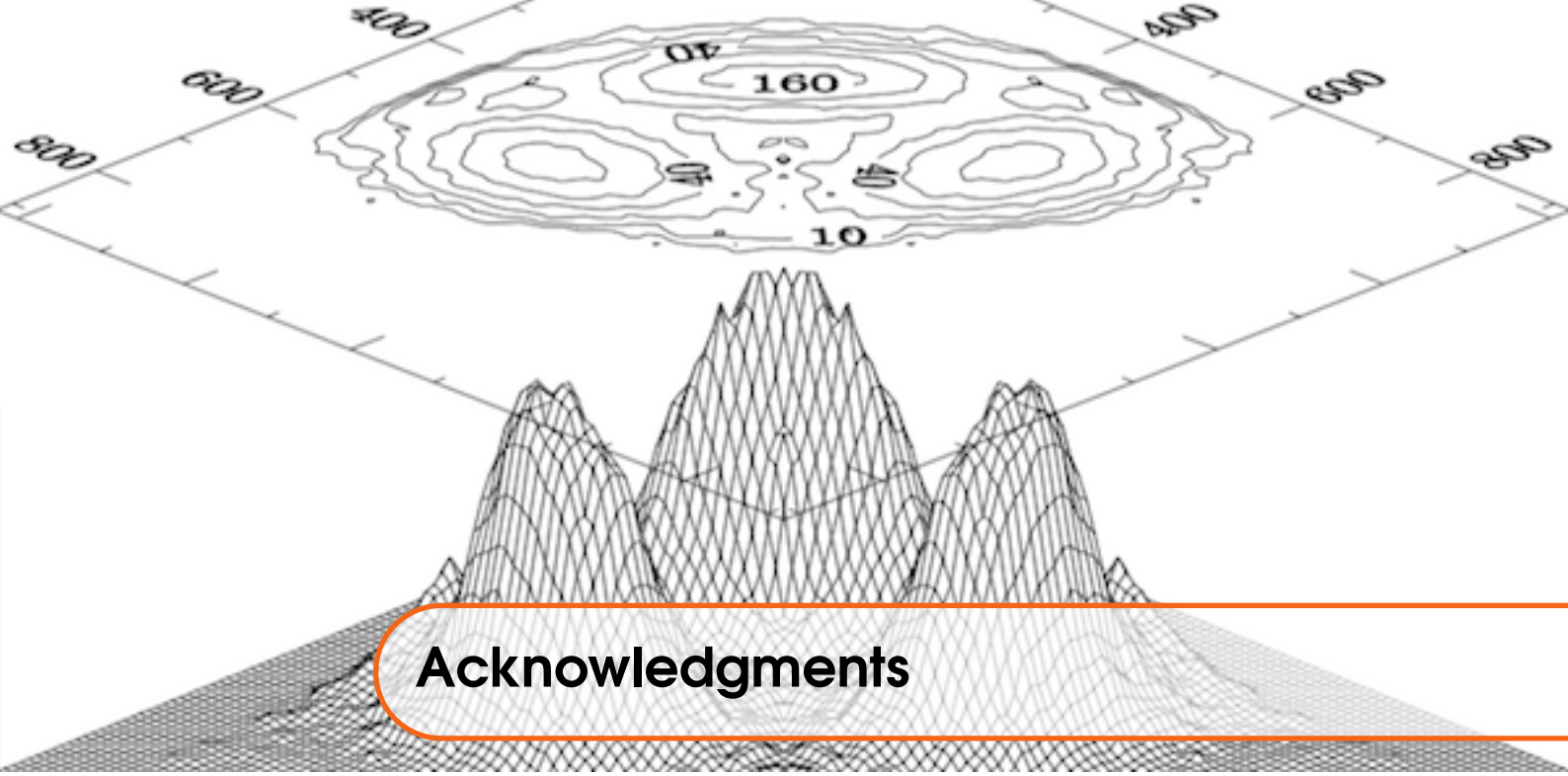

Acknowledgments

PRIMO is the result of many years of work. In that time several persons and organizations have provided us with their help and support. We are thankful to all of them. In particular, we are grateful to Wolfgang Sauerwein (Universitätsklinikum Essen, Germany) for his continued support and efforts that have contributed to make feasible the distribution of PRIMO. Luca Cozzi, Antonella Fogliata and Francesca Belosi (Istituto Oncologico della Svizzera Italiana, Switzerland) have put in a tremendous amount of work in beta-testing the code. Josep Pujal (Universitat Politècnica de Catalunya, Spain) and Michael Nieporte (Universitätsklinikum Essen, Germany) have taken the burden of all matters related to setting up computer clusters and information technology.

The Monte Carlo engine of PRIMO is PENELOPE. We express our gratitude to Francesc Salvat and José María Fernández-Varea (Universitat de Barcelona, Spain) not only for their work as PENELOPE authors, but also for the long-lasting close and rewarding collaboration that has allowed us to learn from their experience.

For validating the coded geometries we have had recourse to experimental data provided by the following persons: Luca Cozzi and Antonella Fogliata (Istituto Oncologico della Svizzera Italiana, Switzerland), Nuria Escobar-Corral (Universitätsklinikum Aachen, Germany), Andrea Flühs (Universitätsklinikum Essen, Germany), Dietmar Georg and Gabriele Kragl (Medizinische Universität Wien, Austria), Núria Jornet (Hospital de la Santa Creu i Sant Pau, Spain), Ricardo Palanco-Zamora (Karolinska Universitetssjukhuset, Sweden) and Klemens Zink (Universitätsklinikum Giessen und Marburg, Germany). We are appreciative of their help.

We gratefully acknowledge Varian Medical Systems International AG (Zug, Switzerland) and Elekta Limited (Crawley, United Kingdom) for authorizing the distribution of the encoded geometry files related to their respective linac models.

We thank the Deutsche Forschungsgemeinschaft (project BR 4043/3-1, Germany) and the Ministerio de Economía y Competitividad (project FIS2012-38480, Spain) for financial support.

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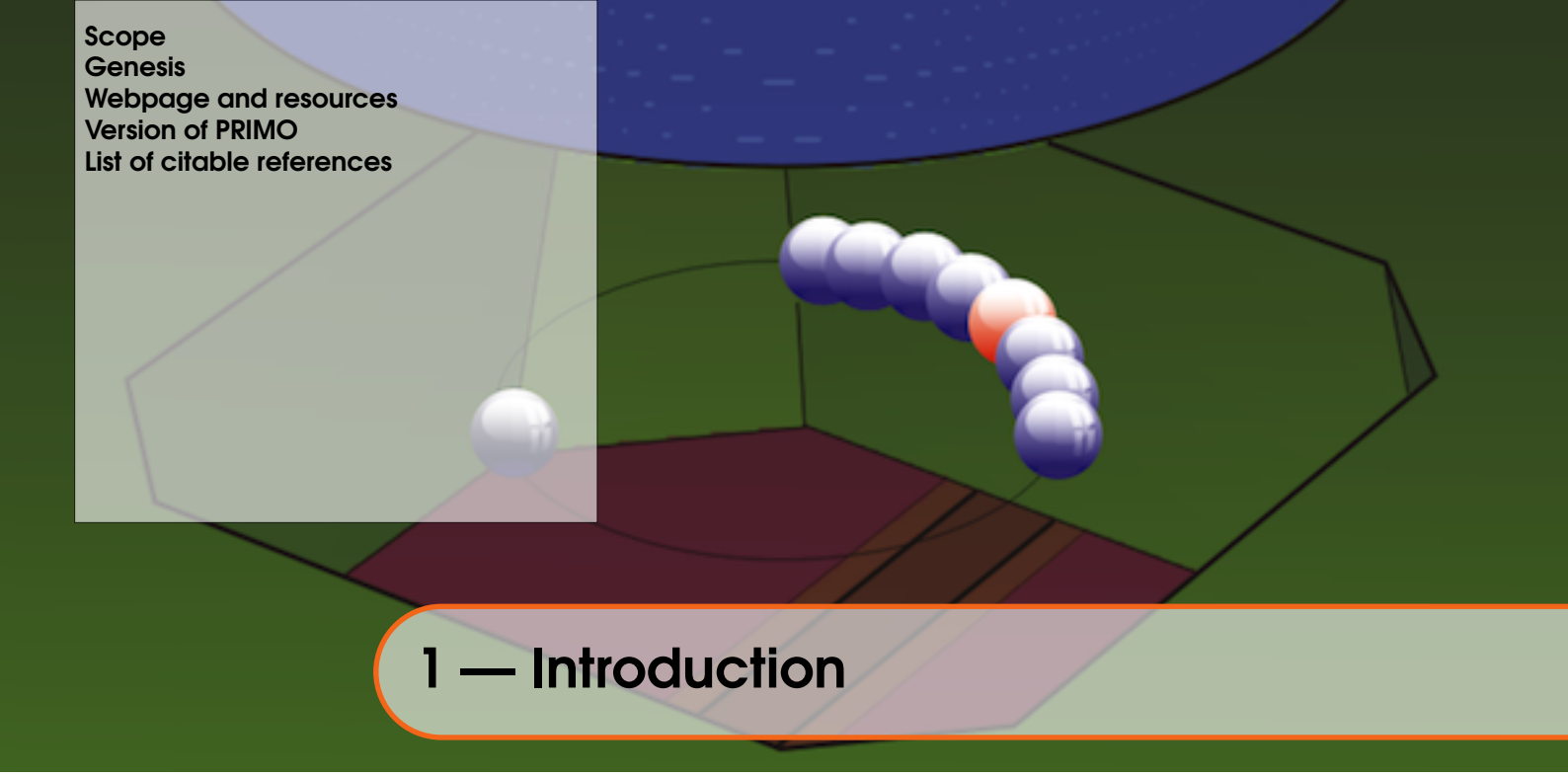

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1 — Introduction

The accurate Monte Carlo simulation of a linac requires a detailed description of its geometry and the application of variance-reduction techniques [JNR98]. The interpretation of linac blueprints and the coding of the geometry into the Monte Carlo system can be a tedious and error-prone task. The introduction of variance-reduction techniques, in turn, may require the modification of the computer code and this can involve a substantial programming effort by the end user [Bru12; Rey+07; SV13; SL08].

PRIMO is a program based on the codes PENELOPE 2011 [Bar+95; SFS11; Sem+97], PENEASY [SBB11], PENEASYLINAC [SBB11] and a graphical user interface that encompasses all these components in a single user-friendly environment. PENELOPE is a set of subroutines for the Monte Carlo simulation of coupled electron and photon transport. PENEASY is a general-purpose main program for PENELOPE that includes several source models, tallies, variance-reduction techniques and the possibility of combining quadric and voxelized geometries. PENEASYLINAC is a complementary tool that generates the input files required for the simulation of most Varian[1] and Elekta[2] linacs with PENELOPE/PENEASY. The Graphical Layer for the Automation of the Simulation System (GLASS) is a graphical user interface that allows users to define the configuration of the simulated machine, that is, irradiation mode, beam nominal energy, jaw positions, position of every leaf of the multileaf collimator (photon mode) or type of electron applicator (electron mode). All the other parameters, those of the simulation and of the applied variance-reduction techniques, are automatically selected by the system without user intervention. PRIMO incorporates graphical and numerical tools for the analysis of phase-space files and absorbed dose distributions tallied during the simulations. PRIMO can also import and simulate phase-space files written by other codes in the International Atomic Energy Agency (IAEA) binary format [Cap+06]. Dose distributions can be tallied in phantoms or computerized tomographies of patients.

In a nutshell, PRIMO is an automated, self-contained, fully Monte Carlo-based linac simulator and dose calculator with a user-friendly graphical interface.

[1] Varian Medical Systems Inc., California, USA
[2] Elekta AB, Sweden

1.1 Scope

PRIMO facilitates the Monte Carlo simulation with PENELOPE of most Varian and Elekta linacs and the estimation of the dose distribution in water phantoms and computerized tomographies. Knowledge of the Monte Carlo method, of programming, of the peculiarities of PENELOPE and of the physics of radiation transport is not necessary in order to set up, run and analyze the simulation of a linac and the subsequent dose distribution. Users of other Monte Carlo codes can also benefit from PRIMO thanks to the possibility of importing and simulating external phase-space files written in the IAEA format.

Owing to a number of specifically developed variance-reduction techniques [BSP09; BS10; RSB12; SBB11] PRIMO simulates linac geometries efficiently. Users with a multiple-core computer can reduce simulation time by automatically distributing the simulation among the available computing cores. Also, the code is capable of computing a dose distribution produced by a multiple-field irradiation. Most cases can be simulated in the time frame of one to three hours using an 8-core computer, obtaining a dose distribution within clinical requirements.

PRIMO performs the full Monte Carlo simulation of radiation transport from the primary electron source of a linac downstream to estimate the absorbed dose in a phantom or computerized tomography. This process uses the PENELOPE code as the computation engine. Therefore, PRIMO is based on one of the most accurate general-purpose Monte Carlo codes available [Fad+08; Fad+09; SF09; Sem+03].

Although PRIMO is mainly conceived as research software, it finds multiple applications in the daily clinical practice. For example, it can be used as an independent quality assurance tool. However, it must be stressed that PRIMO is not medical software and it does not have any certification or warranty. Please refer to the disclaimer and copyright statements for further details.

1.2 Genesis

Due to its layered software structure, PRIMO inherits important characteristics from the codes that constitute it. The components of PRIMO benefit from having been coded by a reduced number of developers. Additionally, these same components have been available for many years to a large number of users who have extensively tested them. PENELOPE, developed by F. Salvat, J.M. Fernández-Varea and J. Sempau, was first released in 1996. PENEASY, whose main author is J. Sempau, was first released in 2004. L. Brualla, the author of PENEASYLINAC, published its first version in 2009. The authors of PRIMO, L. Brualla, M. Rodriguez and J. Sempau, started to work on the GLASS that integrates all the aforementioned codes into PRIMO in 2010. The layered structure of PRIMO and the fact that all codes contained within are written by only five researchers facilitates the maintenance tasks and the development of new features.

1.3 Webpage and resources

Notice 1.1 PRIMO is free software. However, PRIMO is not open-source and reverse-engineering on any distributed or generated file from PRIMO is expressly forbidden. Please refer to the disclaimer and copyright statements for further details. ■

Notice 1.2 PRIMO can be downloaded from the PRIMO project webpage `http://www.primoproject.net`. It is forbidden to redistribute copies of PRIMO. ■

The sources of information about PRIMO are the following:

User's manual The document you are reading now. This manual is in its early stage. Future versions of the manual will include details on the models implemented. Currently, it only describes how to operate PRIMO at the user's level. Furthermore, the manual does not include any information on how to interpret results or about the intricacies of Monte Carlo simulation.

The PENELOPE 2011 **manual** Help on matters related to the Monte Carlo simulation might be found in the PENELOPE 2011 manual. Users can obtain a copy of the PENELOPE 2011 distribution by contacting the Nuclear Energy Agency (`http://www.oecd-nea.org/`).

The PENEASY **documentation** Since PENEASY is the main program steering the PENELOPE simulation, problems related to the Monte Carlo simulation might also be solved with the help of the documentation included in the PENEASY code available at `http://inte.upc.es/downloads`.

1.4 Version of PRIMO

PRIMO is still considered beta-software. Current version is 0.1.5.1300. The first, second, third and fourth number of the version are the major version, minor version, release and build numbers, respectively. New releases will be made available through the PRIMO project webpage.

1.5 List of citable references

If PRIMO is used for research conducting to publications the following bibliographical reference should be cited:

- Rodriguez M, Sempau J, Brualla L. PRIMO: A graphical environment for the Monte Carlo simulation of Varian and Elekta linacs. *Strahlenther Onkol* DOI 10.1007/s00066-013-0415-1. Available online at `http://link.springer.com/article/10.1007/s00066-013-0415-1`.
  Main PRIMO reference

The following references can also be useful:

- Sempau J, Badal A, Brualla L. A PENELOPE-based system for the automated Monte Carlo simulation of clinacs and voxelized geometries—application to far-from-axis fields. *Med Phys* 2011;38:5887–5895.
  Main PENEASYLINAC and PENEASY reference

- Salvat F, Fernández-Varea JM, Sempau J. PENELOPE 2011—A code system for Monte Carlo simulation of electron and photon transport. OECD Nuclear Energy Agency, Issy-les-Moulineaux.
  PENELOPE manual

- Sempau J, Acosta E, Baró J, Fernández-Varea JM, Salvat F. An algorithm for Monte Carlo simulation of coupled electron-photon transport. *Nucl Instrum Meth B* 1997;132:377–390.
  PENELOPE reference

- Baró J, Sempau J, Fernández-Varea JM, Salvat F. PENELOPE: an algorithm for Monte Carlo simulation of the penetration and energy loss of electrons and positrons in matter. *Nucl Instrum Meth B* 1995;100:31–46.
  PENELOPE reference

- Brualla L, Salvat F, Palanco-Zamora R. Efficient Monte Carlo simulation of multi-leaf collimators using geometry-related variance-reduction techniques. *Phys Med Biol* 2009;54:4131–4149.
  Movable-skins variance-reduction technique

- Brualla L, Sauerwein W. On the efficiency of azimuthal and rotational splitting for Monte Carlo simulation of clinical linear accelerators. *Rad Phys Chem* 2010;79:929–932.
  Rotational splitting variance-reduction technique

- Rodriguez M, Sempau J, Brualla L. A combined approach of variance-reduction techniques for the efficient Monte Carlo simulation of linacs. *Phys Med Biol* 2012;57:3013–3024.
  Splitting roulette variance-reduction technique

- Brualla L. Simulation of medical linear accelerators with PENELOPE. On *Radiation damage in biomolecular systems*. Eds. García Gómez-Tejedor G, Fuss MC. Springer, 2012.
  General introduction to the subject

2 — Installation

2.1 Tested hardware and software

We have tested and successfully run the code in the following hardware and software configurations:

- Computer with Intel 64 bits processor
- Windows 64 bits[1] operating system[2]
- Administrator rights
- Recommended 1 GB RAM per computing core. For example, a computer with 2 CPUs each with 4 computing cores requires about 8 GB RAM.[3]
- The hard drive must be either local or accessible through a high speed connection (at least 6 GB/s).
- PRIMO occupies less than 100 MB of disk space. Owing to the fact that large files might be generated during execution a minimum of 100 GB of free disk space is recommended for a normal usage of the software.
- Minimum screen resolution 1280×960 pixels. The default font size in Windows (smaller size) should be used for this minimum resolution.

2.2 Whence to obtain PRIMO

1. Visit the webpage `http://www.primoproject.net`.
2. Enter the section 'Download' and enter your name, email address and affiliation. You will receive an email with a link for downloading the software. PRIMO is distributed as a Windows installer `msi` file.
3. With the same link sent for downloading PRIMO it is possible to download already simulated examples. Each example is distributed as a compressed `zip` file.

[1] PRIMO has been successfully tested on Windows XP, Windows 7, Windows 8/8.1, Windows Server 2008 and Windows Server 2012. The classical view of the Windows desktop does not permit to see the full graphical quality of the program's icons.

[2] PRIMO may give problems on virtual machines (Parallels, VirtualBox, VMWare, etc.) and it does not run on Windows emulators (Wine, CrossOver, etc.)

[3] This 1 GB RAM rule also applies to logical computing cores in case of using hyper-threading. However, use of hyper-threading is not recommended.

2.3 How to install/uninstall PRIMO

2.3.1 Installer `msi` file

1. Execute the `msi` file.
2. The installation program will guide you through the installation process. The default installation folder is `c:\PRIMO` but it can be changed during the installation process.

> **Warning 2.1** Errors during simulation execution could occur when PRIMO is installed in the `Program Files` folder of a server computer running Windows Server 2012. In that case it is advisable to select a different installation folder, such as `c:\PRIMO`.

2.3.2 Unistall

Use the Windows Start Menu –> Control Panel –> Programs and Features to uninstall any version of PRIMO that was installed from an `msi` file.

> **Warning 2.2** Uninstall any previous version before installing a new one.

2.4 How to install the examples

1. Create a directory called `PRIMOexamples` under `c:\`.
2. Unpack the downloaded files inside the just created directory `c:\PRIMOexamples`. The unpacked files will each one create a directory called `Example`*mn*, with *mn* a two digits number.

2.5 List of examples

Example01 Photon reference field from a Varian Clinac 2100 C/D. Nominal energy 6 MV. Field size 10×10 cm^2. Tallied results: phase-space files and dose distribution.

Example02 Electron reference field from an Elekta SL15. Nominal energy 15 MeV. Electron applicator 20×20 cm^2. Tallied results: phase-space file and dose distribution.

Example03 Photon reference field from a TrueBeam STx. Nominal energy 6 MV (free flattening filter). Field size 40×40 cm^2. Tallied result: dose distribution.

Example04 Brain irradiation with two fields from a Varian Clinac 2100 C/D conformed with a MLC 120 High Definition. Nominal energy 6 MV. Tallied results: phase-space files and dose distribution.

Please notice the following remark:

Examples 01, 02 and 03 contain subdirectories named `Experiment` where experimental data files are stored for comparison with simulated results.

3 — Linac and absorbed dose simulation

Medical linear accelerators (linacs) are routinely used in radiotherapy units for the treatment of cancer. The purpose of all linacs is the same: to accelerate electrons through resonant cavities to energies on the order of a few MeV. The beam leaving the accelerating structure has a relatively narrow energy distribution with a diameter of about 1 mm. In general, Monte Carlo simulations start from that position in the linac head, assuming as primary electron source a beam with given spatial and energy distributions. Particles are then transported downstream the linac head. Therefore, from a Monte Carlo simulation point of view, the relevant constructive elements of the linac are those found downstream of the primary electron source.

3.1 Linac simulation

Some linacs operate only with electron beams (*e.g.*, Siemens Mevatron ME), others with photon beams (*e.g.*, Varian Clinac 600 C/D), while others can operate either with electron or photon beams (*e.g.*, Varian Clinac 2100 C/D). Those irradiating with electron beams usually include some thin material layers downstream of the primary electron source, called scattering foils, whose purpose is to spread the beam and hence to cover a large field. Linacs irradiating with photon beams have a thick material target, usually made of tungsten, in the beam path. This target produces photons by bremsstrahlung emission. In many cases a flattening filter is placed at the position of the scattering foils in order to homogenize the photon energy flux. From the primary electron source downstream to this position in the linac head all modeled linacs in PRIMO exhibit cylindrical symmetry. This segment of the linac head is referred to as the upper part. Next to the upper part a series of collimating structures are found whose purpose is to conform the beam to the required field shape. When a linac operates in photon mode, these structures consist of one or two sets of jaws and possibly a multileaf collimator. In the case of a linac operating in electron mode, an electron applicator is added below the multileaf collimator position. The constructive elements found downstream of the upper part are collectively called lower part of the linac, which does not exhibit cylindrical symmetry. Figure 3.1 shows four images of the constructive elements of the Varian Clinac 2100 C/D and Elekta MLCi operating in photon and electron modes. These images are actual representations of some of the simulated geometries in PRIMO.

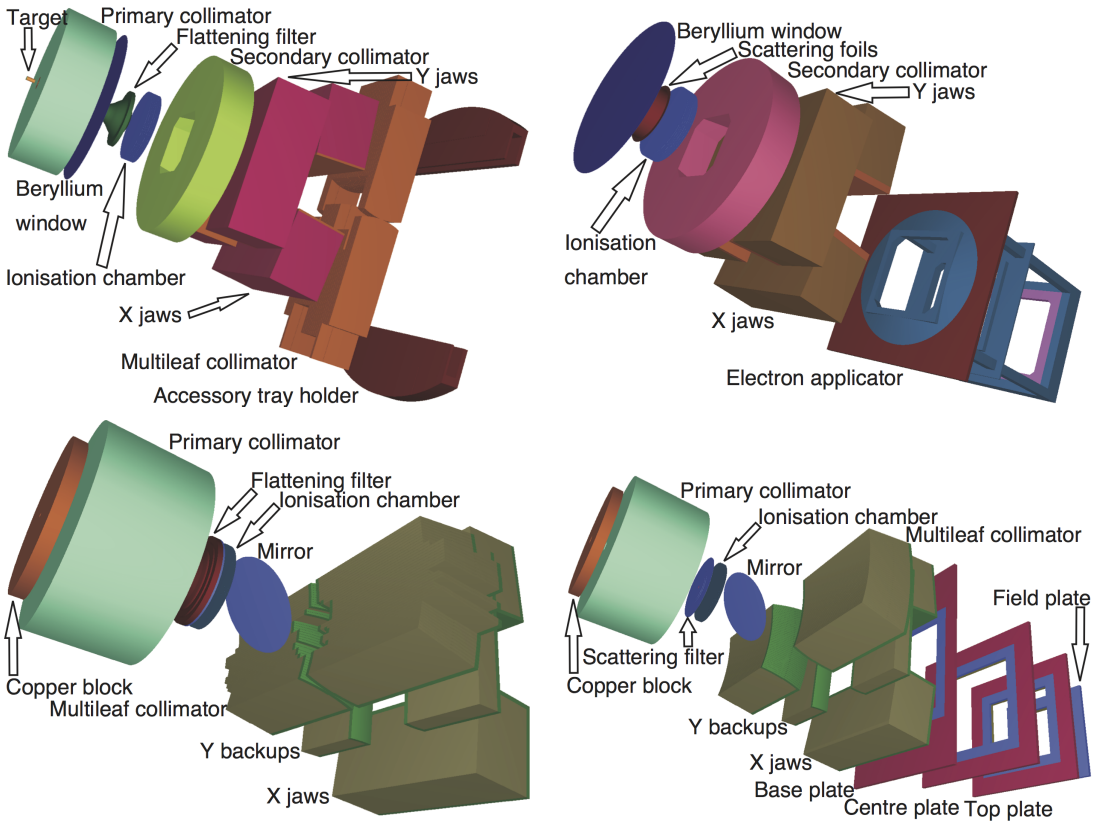


Figure 3.1: Varian Clinac 2100 C/D operating in photon mode at 18 MV (upper left) and electron mode at 6 MeV (upper right), Elekta MLCi operating in photon mode at 10 MV (lower left) and electron mode at 4 MeV (lower right). These images are the actual simulated geometries in PRIMO.

3.2 Absorbed dose simulation

After the lower part of the linac, the beam enters the region relevant for dosimetry purposes. The absorbed dose can be tallied either in a binned water phantom or in a voxelized structure. PRIMO can import RT-STRUCT files allowing for the simulation in voxelized phantoms generated in treatment planning systems by delineating structures. DICOM files containing computerized tomography images can also be imported and the dose tallied therein.

PRIMO reports dose in units of eV/g per primary particle. These units are equivalent to Gy/(mA s), whence the dose in Gy can be calculated knowing the current intensity at the target in mA and the irradiation time in s. When comparing with experimental profiles relative dosimetry is assumed.

3.3 Histories and particles

When a primary electron enters the modeled geometry, upstream of the upper part of the linac, an electromagnetic shower is simulated. It may occur that the primary electron is absorbed or escapes the geometry without further consequences, or it may happen that the primary electron produces secondary particles, namely, electrons, photons or positrons. In turn, these secondary particles may produce another generation of particles, and so on. The primary particle and all its descendants are simulated until all of them have been either absorbed or escaped the geometry. When this occurs one *history* has been completed. Therefore, the number of simulated particles and the number of simulated histories, in general, do not coincide. All the quantities reported in PRIMO are expressed in units per history, *e. g.*, the dose is expressed in units eV/g per history.

3.4 Phase-space files

When simulating radiation transport with the Monte Carlo method it is possible to define a surface, usually a plane, at any location in the geometry. Particles traversing this plane are stopped and their state (*i.e.*, energy, position, direction of flight, etc.) recorded on a file called phase-space file. When a phase-space file is 'sufficiently rich', that is, it contains a 'large number' of particles, it is possible to neglect the geometry upstream of the phase-space surface, and to consider the phase-space file as the radiation source for subsequent Monte Carlo simulations. The expressions 'sufficiently rich' and 'large number' refer to statistical properties of the phase-space file whose description is beyond the scope of this manual [Sem+01].

3.5 Statistical uncertainty

A straightforward approach to evaluate if a simulation has run long enough or if a phase-space file is sufficiently rich is by means of the statistical uncertainty estimator of the absorbed dose. PRIMO reports the average statistical uncertainty of all voxels (from computerized tomographies) or bins (from water phantoms) accumulating more than 50% of the maximum absorbed dose. All uncertainties reported by PRIMO are given at 2 standard deviations.

Statistical uncertainties obtained from PRIMO are correctly estimated provided the simulation has been wholly done inside PRIMO, that is, from the primary electron source to the patient or phantom. This is because PENELOPE keeps track, even in phase-space files, of the history to which each particle belongs. Not all general-purpose Monte Carlo codes keep such record. It is impossible to correctly estimate the statistical uncertainty when PRIMO uses phase-space files generated with codes that do not keep this record. Instead, PRIMO gives an approximation to the statistical uncertainty whose accuracy cannot be evaluated.

3.6 Variance-reduction techniques

The simulation of radiation transport through the linac head and the patient (or phantom) geometry is a very intensive computational task. A direct approach to the problem using analogue simulation with PENELOPE—'analogue' meaning that radiation interactions with matter are modeled as closely to reality as possible—would require of the order of several months of CPU processing for typical voxel sizes and statistical uncertainties [SBB11].

To reduce this unaffordable amount of computing time the so-called variance-reduction techniques can be used. They rely on the idea that a given probability distribution (of depositing a certain energy in a voxel, for instance) can be arbitrarily altered if the corresponding variable of interest (energy deposited, in our example) is also changed appropriately so as to keep its mean value unbiased. If the new probability distribution is chosen wisely, the statistical uncertainty Δ achieved in a given amount t of computation time can be substantially reduced. Or, equivalently, a given uncertainty Δ can be achieved in considerably less computing time.

A convenient measure of the efficacy of a certain variance-reduction technique is given by the simulation efficiency ε, defined as

$$\varepsilon = \frac{1}{\Delta^2 t}. \tag{3.1}$$

In PRIMO Δ (of the absorbed dose distribution) is computed as twice the average standard statistical uncertainty, expressed as a percentage of the mean dose. Notice that this definition renders the dimensions of ε equal to those of t^{-1}. Thus, for a given simulation, the quantity

$$t_{1\%} = \frac{1}{\varepsilon} \tag{3.2}$$

represents the simulation time that would be required to achieve an average relative uncertainty (at two sigma) of 1%.

3.7 Simulation segments

PRIMO allows to tally a phase-space file at the downstream end of the upper part of the linac. This part is called segment 1 (s1). Similarly, a phase-space file can be tallied at the downstream end of the lower part of the linac. This region is called segment 2 (s2). The part of the simulation dedicated to the dose estimation is called segment 3 (s3).

Segments must, obviously, be simulated in sequential order, that is $\mathrm{s1}, \mathrm{s2}, \mathrm{s3}$. However, they can be grouped according to the user's requirements. They can be simulated individually as $(\mathrm{s1}, \mathrm{s2}, \mathrm{s3})$; or grouped in a single simulation as $(\mathrm{s1} + \mathrm{s2} + \mathrm{s3})$; or in smaller groups simulating s1 first and then s2 and s3 together $(\mathrm{s1}, \mathrm{s2} + \mathrm{s3})$; $(\mathrm{s1} + \mathrm{s2}, \mathrm{s3})$ is also possible.

> **Warning 3.1** Combined quadric-voxelized geometries are not currently supported. Consequently, segments corresponding to the linac head (s1 and s2) cannot be grouped with the segment s3 if the dose is calculated in a CT.

A simulation can either tally a phase-space file or a dose distribution. Therefore, if simulating for example $(\mathrm{s1} + \mathrm{s2} + \mathrm{s3})$ a dose distribution will be tallied. Simulation of $(\mathrm{s1} + \mathrm{s2})$ and then a subsequent simulation of s3 will produce a phase-space file at the downstream end of the lower segment during the first simulation and a dose distribution during the simulation of s3.

The phase-space file obtained with the simulation of s1 depends on the primary beam parameters and the number of histories simulated. Once the primary beam parameters of a linac

have been tuned for a given nominal energy to reproduce experimental data from that linac, it is desirable to run, once and for all, a long simulation of s1 that can be re-used in subsequent simulations of the rest of the linac. This approach conduces to a substantial saving in simulation time, particularly in the case of photon beams.

Linacs operating in electron mode have one additional segment, namely, (s1, s2, s2e, s3). s1 and s3 correspond to the segments previously described. Segment s2 simulates the movable collimators (*i.e.*, the jaws) and the uppermost two scrapers of the electron applicator, tallying a phase-space file at the downstream end of the middle scraper. Segment s2e simulates the lowermost scraper and tallies a phase-space file at its downstream end. If the electron field is standard, as conformed by the electron applicator, then s2 and s2e should be simulated together. However, if the user is interested in adding a customized collimator at the lowermost scraper it is necessary to simulate only up to s2. In that case, segment s2e with the customized collimator must be simulated with an external program, such as, PENELOPE. The current version of PRIMO does not allow for the simulation of customized electron collimators.

When importing external phase-space files, PRIMO assumes that they have been tallied at the downstream end of s1. After importing the phase-space file, s1 will appear as already simulated and the user will be given the possibility of either simulating (s2 + s3) or (s2, s3).

Except under special conditions, the most common approach to simulate the linac and the subsequent dose distribution is (s1, s2, s3).

4 — PRIMO usage

This chapter is the core of the manual, covering how to operate PRIMO. The graphical interface is designed to reduce the user's effort to accomplish the steps of *simulation setup*, *execution* and *analysis of results*. Any interface element can be associated to one of these three main categories.

4.1 Simulation setup

Immediately after launching PRIMO in the simulation setup environment the user can either start a new simulation project or open an already simulated one (figure 4.1).

4.1.1 New project

When the *New project* button is clicked the New Project window (figure 4.2) appears. The following elements are available in that window:

- Project ID: Mandatory field in which the name of the project is entered. A maximum of 15 characters is allowed. The name cannot contain spaces or other characters that are usually not accepted for file names.
- Project name: Optional field in which a succinct explanation about the characteristics of the project may be given.
- *Browse*: By default PRIMO will save the new project in the installation directory. Nevertheless, it is possible to save the new project in any other logical drive and directory. The *Browse* button allows to decide in which drive and directory the project will be saved. A logical drive mounted on a remote disk can be used. However, the recommended communication speed must be at least 6 GB/s. Once a project has been saved in a given directory it cannot be moved to any other location.
- Linac model: This drop-down menu allows to choose the desired linac model to be simulated. Please refer to table 4.1 in order to decide which model corresponds to the

Figure 4.1: Main task bar of the simulation setup environment. First two buttons from left to right are *New project* and *Open project*.

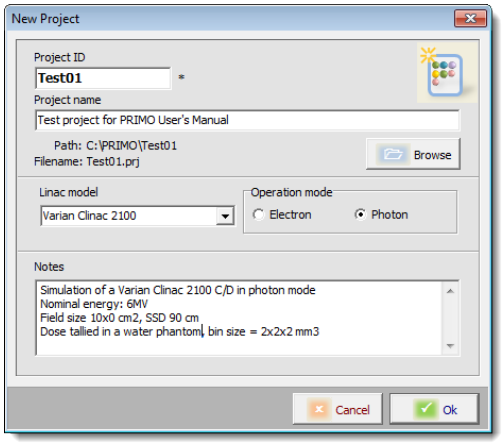


Figure 4.2: New project window.

PRIMO	commercial
Elekta SL	SL series
Elekta MLCi	SLi Plus, Axesse, Affinity, Synergy, Precise
Varian Clinac 600C	Clinac 600 C
Varian Clinac 600CD	Clinac 600 C/D
Varian Unique	Unique
Varian Clinac 2100	Clinac C series, TrueBeam (sect. 5.3)
Varian Clinac 2300	Clinac 2300 C/D
FakeBeam	TrueBeam 6- and 10-FFF beams

Table 4.1: The column 'PRIMO' indicates the name given to the available linacs in the program. The column 'commercial' indicates the different commercial names that the same linac in PRIMO might have. FakeBeam is an experimentally based geometry of TrueBeam developed in-house.

desired linac.

- Operation mode: These radio buttons allow to decide whether the linac will irradiate either in electron or photon mode.
- Notes: This field can be used for text notes.

Warning 4.1 Elekta linacs have been recently coded into PRIMO. Therefore, they have not been neither extensively tested, nor fine tuned. It is recommended that users willing to simulate Elekta linacs dedicate some effort in fine tuning the primary beam parameters.

Warning 4.2 The only multileaf collimator model in PRIMO that has been experimentally validated is the Varian MLC 52.

Simulation setup tab

After clicking the *Ok* button in the New Project window, the program presents the window corresponding to the Simulation Setup tab selected (figure 4.3).

The screen of the Simulation Setup tab is divided in two areas, namely, the Simulation Segments and the Segment setup. A logical tree containing the objects of the project appears

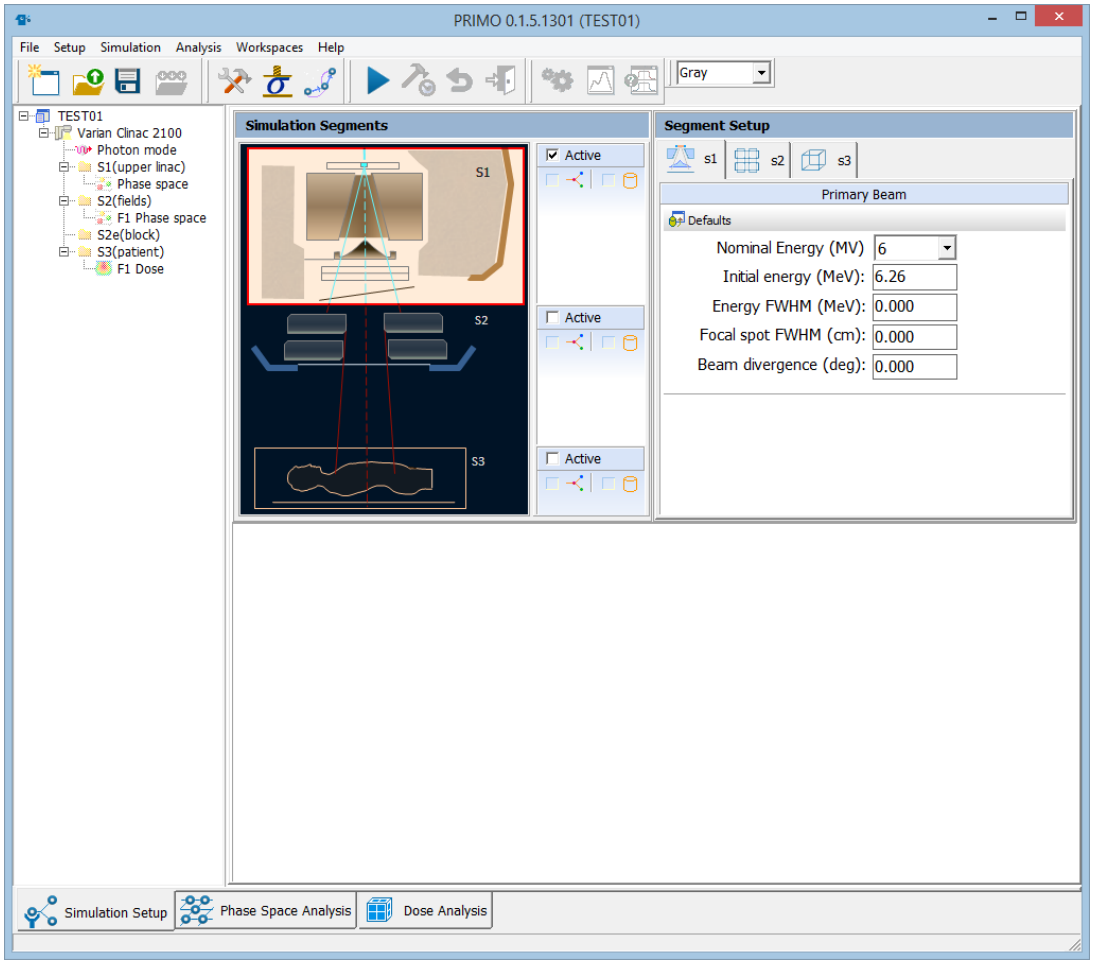


Figure 4.3: Simulation Setup tab.

always at the left in the main screen.

Simulation Segments

The Simulation Segments area indicates in a schematic view of a linac the segments (see section 3.7) that will be or have been simulated. Segments that are required to be simulated must be checked in their corresponding Active checkbox. When a segment is selected for simulation the corresponding area of the linac is highlighted in the schematic view. Once a segment has been simulated a check mark appears next to the three-particle interaction symbol of the corresponding segment. If that segment has produced a tally (phase-space file or dose distribution) a check mark appears next to the hard drive symbol (a cylinder).

4.1.2 Beam, field and dose tally configuration

The Segment Setup area allows users to configure each segment of the simulation.

> **Notice 4.1** When the configuration of s2 and s3 is known beforehand, it is recommended to configure segments s1, s2 and s3 (see section 3.7) at the very beginning of the simulation project, even if only segment s1 will be simulated (*e. g.*, variance-reduction techniques applied at s1 could be related to the field size selected in s2). ■

Beam parameters (s1)

The nominal beam energy is chosen in the drop-down menu in tab s1. For each nominal energy a set of recommended initial beam parameters is suggested. These parameters are: the initial electron energy, the energy full width at half maximum (FWHM), the FWHM of the focal spot size and the beam divergence. A Gaussian distribution for the energy and for the radial distribution is assumed. Beam divergence is implemented such that the angular divergence is for each point emitting from the source plane.

Default beam parameters have been tuned, in the case of Varian linacs, to reproduce experimental results from the corresponding linac and energy. In the case of Elekta linacs the beam parameters have not been tuned yet. In all cases the user can modify the values.

Field conformation (s2)

The field to be simulated in s2 is defined by selecting the tab s2 (figure 4.4). It is possible to simulate multiple fields. To simulate more than one field the *Add new field* button must be clicked. There is also a button for deleting a selected field. The *Edit selected field* button opens the corresponding screen (figure 4.5) which allows to define the field size and position, as well as gantry, collimator and couch angles, and isocenter position. Multileaf collimators or electron applicators can be selected in this screen. The field Phase space plane informs the distance of the phase-space plane of s2 from the primary source. This distance cannot be changed by the user, it is fixed such that the phase-space plane is near to the exit of the linac head, although it varies with the linac model, operation mode and accessories selected (*e. g.*, it is 70.0 cm for a Varian Clinac 2100 in photon mode).

In electron mode, the field apperture as defined by the jaws is automatically set according to the default specified by the manufacturer for the beam energy and electron applicator selected. However, the user is able to reposition the jaws conveniently.

When the patient model in s3 is a CT (see Dose tallying (s3)), each field in a multi-field project can have a different isocenter position. By default all fields are grouped (the option *Group all* is checked) such that they all have a unique isocenter position. To change the isocenter position for a field, uncheck the option *Group all* and change manually the isocenter position in the *Field Edit window*. To assign a unique isocenter position to all fields, select the field that

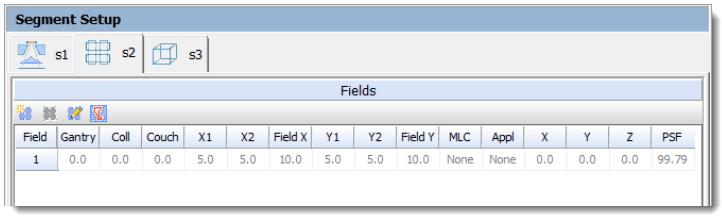


Figure 4.4: Field definition window. s2 tab.

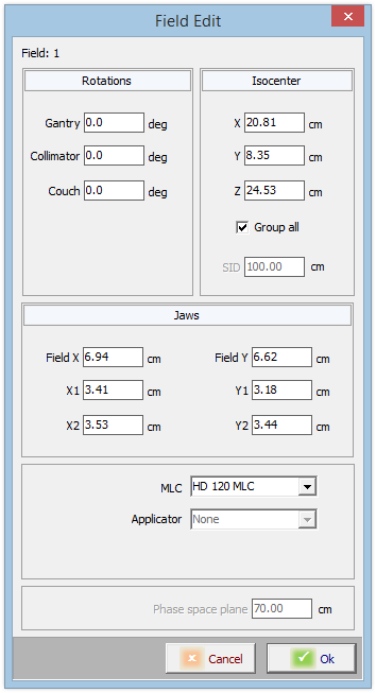


Figure 4.5: Edit selected field. s2 tab.

will be used as the reference, open the *Field Edit window* and check the option *Group all*. The position of the isocenter for the selected field will be assigned to all fields.

R The linac source-to-isocenter distance is a constant (100 cm) and it is specified in the field *SID*. Extended SSDs are only allowed in simulations of a water phantom.

The *Field Edit BEV* button opens an interactive window that facilitates the setup of the fields (figure 4.6). This allows to set the field parameters from a beam eye view (BEV) perspective in which the position of the jaws, the isocenter and the multileaf collimator (MLC) are represented superimposed to the Digitally Reconstructed Radiograph (DRR) of the CT volume. Delineated or imported structures can also (optionally) appear projected on the image. The position of the isocenter, as well as the projection of the radiation fields, are also represented on the CT/phantom slices corresponding to the isocenter position. The position of the jaws and the isocenter can be changed by dragging the corresponding symbols in the image. In the same way, the MLC leaves can be selected and dragged to move them to a particular position. While dragging, the corresponding position values are automatically updated. The tool bar at the bottom of the image allows to manually edit the selected field, to refresh the DRR, to zoom in and out the image and

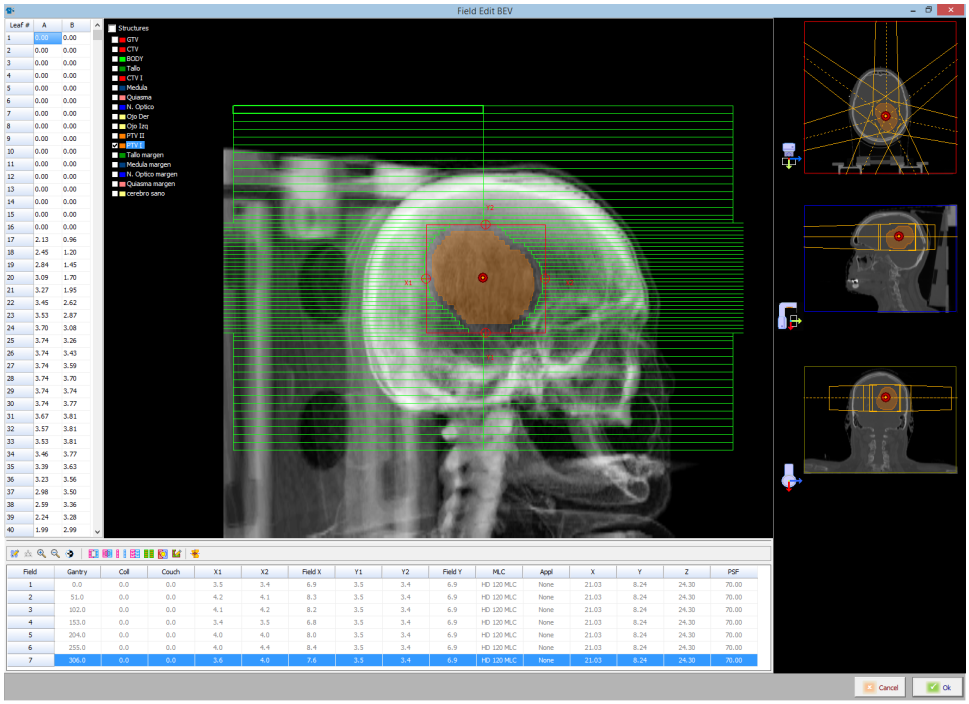


Figure 4.6: Field Edit BEV dialog.

to invert the color lookup table. It also includes functions to visualize and position the MLC. Several contiguous MLC leaves can be selected and displaced together. To select a range of leaves, left click on the first leaf and press shift + left click on the last leaf. The position of the leaves selected can be changed by dragging them or by specifying the new position numerically with the keyboard. This is available by pressing the *Edit selected leaves* button in the toolbar.

Two targeting functions are implemented to facilitate the field positioning, namely, the MLC can be fitted to a structure contour and the isocenter position can be situated at the centroid of a structure. Those functions are available by pressing the buttons *Fit to structure* and *Adjust isocenter to target*, respectively. A dialog appears in each case to select the target structure and a margin out of the structure contour in the case of fitting the MLC.

Notice 4.2 The *Field Edit BEV* window can be resized/maximized conveniently. ■

Dose tallying (s3)

There are two geometry models (patient models) available for dose calculation that can be chosen in segment s3 setup, namely, an homogeneous water phantom and a computerized tomographic volume. The water phantom is selected by default. To change the model, a CT volume (formatted as a set of DICOM images) must be imported or a slab phantom can be created. A slab phantom is treated in PRIMO as a CT volume. The current dimensions of the phantom or the CT volume are shown in the s3 tab (figure 4.7).

Water phantom

To change the dimensions of the water phantom, click the button *Edit phantom dimensions*. In the appearing Phantom Setup dialog window (figure 4.8) it is possible to set the source-to-phantom-surface distance, the phantom size and the bin size along the three coordinate axes. It is also possible to define a measurement depth along the phantom central axis in order to calculate

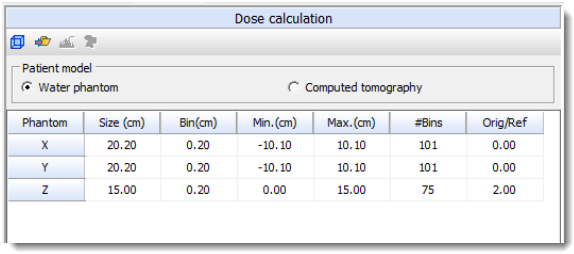


Figure 4.7: Dose calculation. s3 tab.

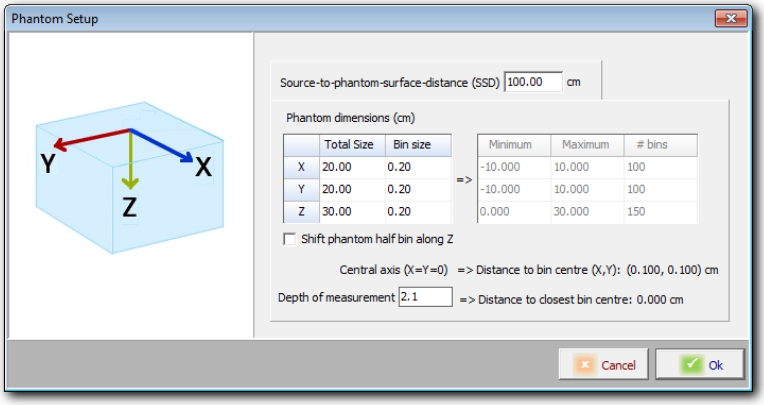


Figure 4.8: Phantom Setup dialog.

the distance from that depth to the center of the closest bin in the z-axis direction, according to the phantom and bin dimensions chosen. This is useful if one needs to ensure that a particular depth along the central axis coincides exactly with the center of a bin. In this case the calculated distance should be equal to 0.0 in the three axes. There is also the option Shift phantom half bin along Z that produces a displacement of the bins deeper into the water such that the surface of the phantom (the interface air-water) lies at a distance of one bin of the center of the first layer of bins in the z-axis direction.

The coordinate systems used in phantom simulations and CT volume simulations are shown in figure 4.9. The default isocenter is set at the center of the upstream surface of the phantom. Only one field can be created at gantry angle 0 degrees and the source-to-phantom-surface-distance should be defined in the s3 segment setup. Observe that for an water phantom, the *Field Edit BEV* dialog is useful only to set the field size and the MLC leaves positions.

R If the dose is calculated in a water phantom only one field is allowed and it is placed centered at the linac CAX at a given SSD. The gantry, collimator and table angles are fixed at $0, 0, 0$, respectively for the field.

Notice 4.3 — Maximum number of bins. The maximum number of bins ($\text{nbin}_x \times \text{nbin}_y \times \text{nbin}_z$) allowed in a phantom simulation is 10^7. ■

R When simulating the whole linac and a water phantom, consider to separate the segments s1 and s2 (involving the radiation transport through the linac geometry) from the segment s3 (involving the phantom geometry only) as it is more efficient than simulating the three

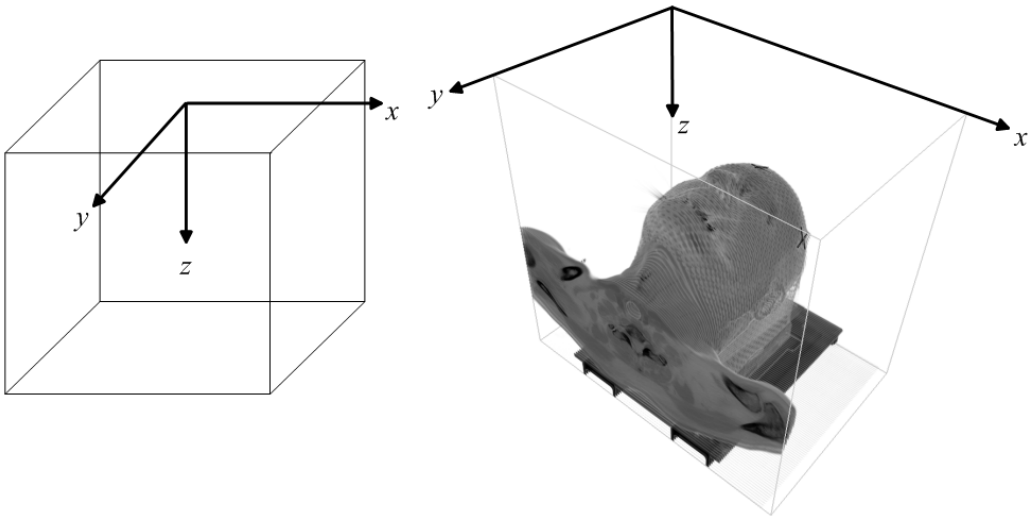


Figure 4.9: Coordinate system of the phantom and the CT volume used to setup the dose tally.

segments together. In the current version, separation of the segment s3 simulation is mandatory when the patient model is a CT volume.

CT scan

To change the patient model from the default water phantom to a CT volume select the *Import a CT volume* option on s3. In the appearing standard File Open window from the operating system select a set of files containing each a CT slice. All slices must belong to the same study. Files must conform with the Digital Imaging and COmmunications in Medicine (DICOM-CT) format. The DICOM Image Import dialog (figure 4.10) will process the DICOM files to check for errors or inconsistencies and will build the tomographic volume. The set of images imported and some relevant data are presented on the screen. Once the button *Import* is pressed, the images are imported into the project and each slice is converted to a size of 256×256 pixels.

Warning 4.3 Any segmentation done on the CT volume and any previously imported or delineated structure will be permanently deleted if the patient model is changed to a water phantom or another CT is imported.

The origin of the coordinate system is set in the CT volume at its upper left behind corner, as represented in figure 4.9. The isocenter is by default placed at the center of coordinates, *i. e.*, at position (0,0,0). When the project is created, one default 10×10 cm^2 field is created with gantry angle equal $0\,^\circ$, centered at the position of the default isocenter. It must be noted that in this situation only half the CT is represented in the DRR. To change the isocenter to the desired position there are three forms: (1) manually; (2) by dragging it over the DRR image or (3) by positioning it at the centroid of an structure. For the field created by default, option (2) will only modify the x and y coordinates. To change the third coordinate with this procedure, a new field can be created with gantry angle at $90\,^\circ$ and used to displace the isocenter over the DRR. This "auxiliary" field can be erased after positioning the isocenter.

The imported CT volume is used to generate a voxelized simulation geometry. This geometry consists of a set of material and mass density value pairs. There is one pair per voxel in the

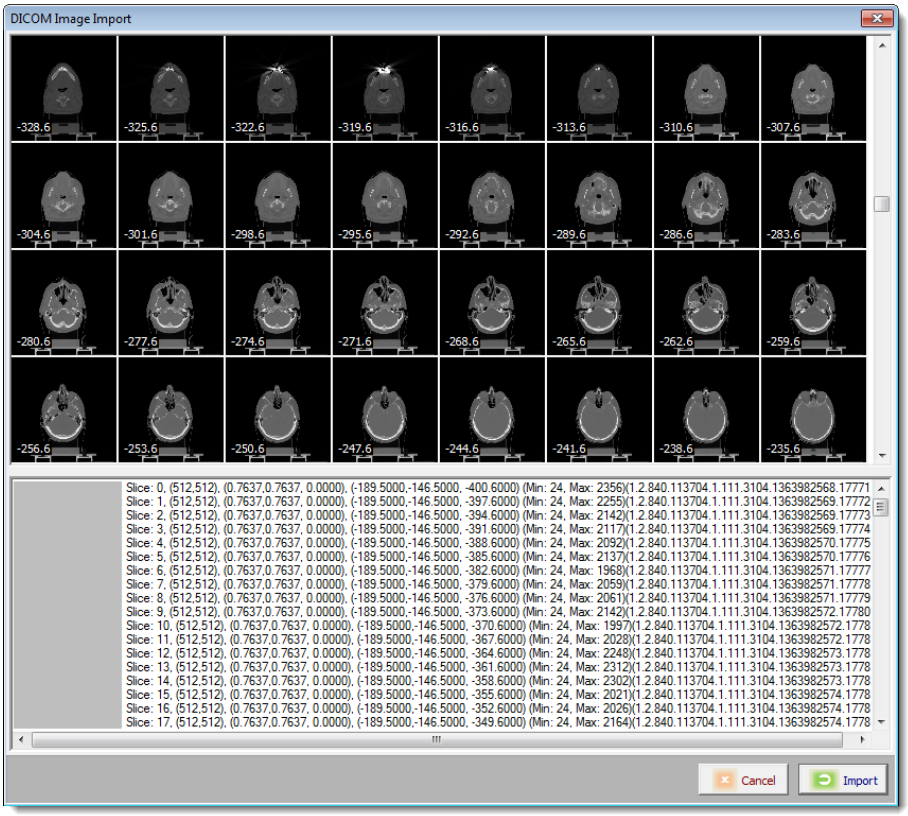


Figure 4.10: DICOM Image Import dialog. The gray scale is mapped into each image Hounsfield number range.

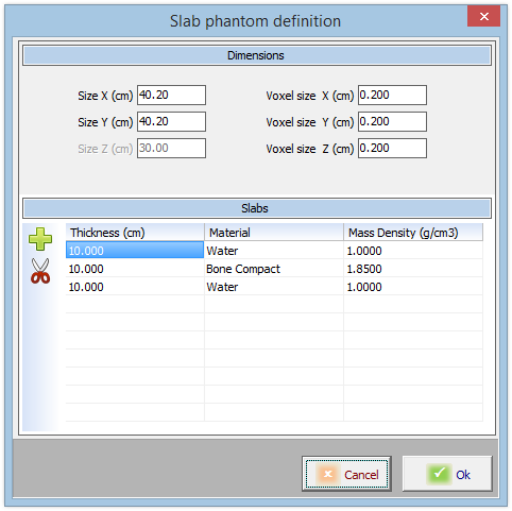


Figure 4.11: The *Slab phantom definition* dialog.

tomographic volume. The option Calculate density and materials in the s3 tab displays the CT Volume Segmentation dialog that allows to create the voxelized geometry (figure 4.12).

Slab phantom

In the case of the patient being a slab phantom, there is not need to import the phantom from a DICOM-CT file. A phantom of slabs can be created using the function *Construct a slab phantom* in segment s3 setup. The *Slab phantom definition* dialog allows to establish the dimensions and the voxel size of the phantom and to add/delete slabs with a material composition selected from a list (Figure 4.11). The slabs are created with a default thickness of 10 cm but this value is editable. A maximum of 10 slabs can be included in the phantom. A slab must contain an integer number of voxels, consequently the voxel size along z and the slabs thicknesses must be adjusted accordingly. The phantom is created as a CT volume, so all the functions associated to the management of a CT patient model apply to the phantom. There is no need to use the function *Calculate densities and materials* for a phantom of slabs. When the phantom is created the isocenter is automatically positioned at the center of the upstream surface of the phantom (SSD=100 cm) for all the fields. The user can, as in the case of a CT patient, reposition the isocenter and change other parameters of the fields in the *Field Edit BEV* window.

Note that once the *Slab phantom definition* dialog is closed and the slab phantom is created as a CT scan it cannot be further changed.

Warning 4.4 The dimensions and voxel size of the slab phantom must be such that the total number of voxels does not surpass 10^7. Dimensions are limited to a maximum of 50 cm along x and y. Additionally, two different materials with the same mass density cannot be included in the phantom.

4.1.3 Material and density assignment

The volume segmentation is done by assigning a material to a CT number interval. Up to 10 materials, chosen from a list of more than 40, can be assigned to a CT volume. The list of assigned materials, and their corresponding CT number interval, appears under the title Materials

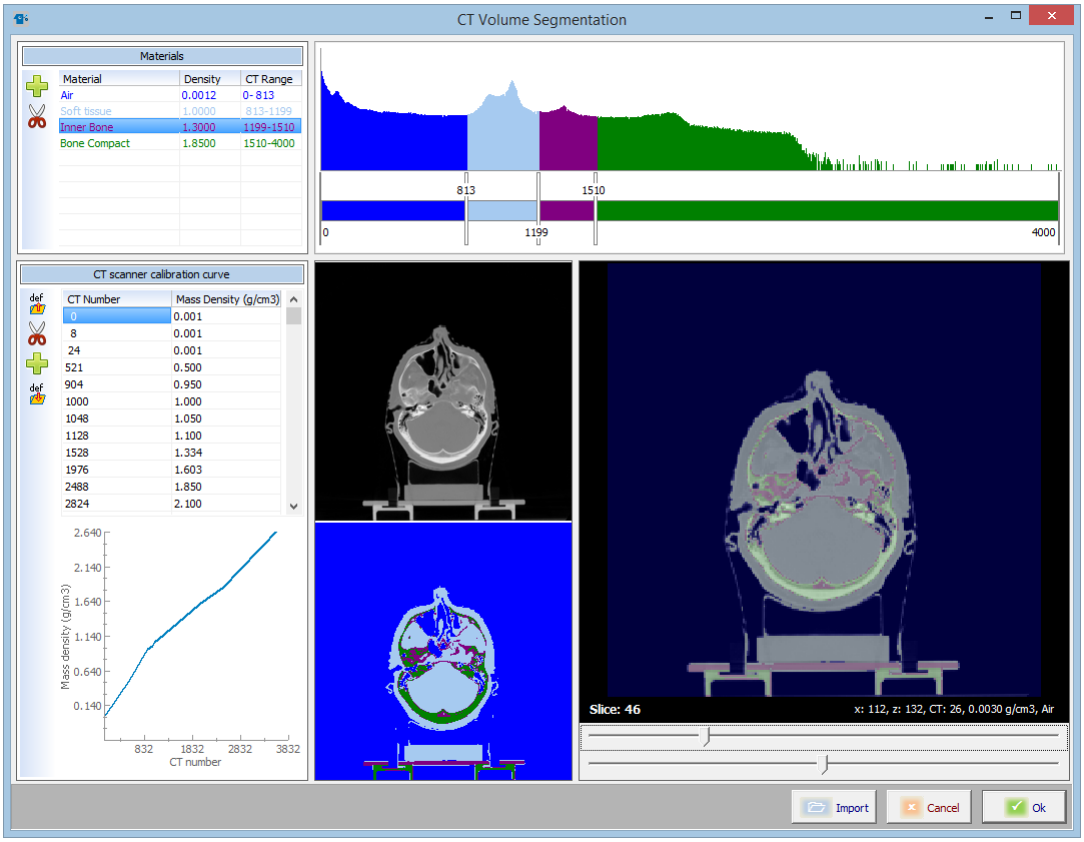


Figure 4.12: CT Volume Segmentation dialog. Generation of voxelized geometries.

on the left top corner of the dialog. Each material/interval is differentiated with color. The buttons on the left allow to remove and add materials to the list. Changing a CT number interval for a material is performed by dragging the sliders along the CT number histogram.

Notice 4.4 — Working with the Hounsfield numbers histogram. As the mouse is moved over the histogram, the corresponding CT number is displayed. Right clicking at the histogram will move the slider situated on the left side of the mouse pointer to the clicking position in the histogram. Left clicking at the histogram will move the slider situated on the right side of the mouse pointer position. ■

The CT scanner calibration curve is used for assigning mass densities to CT numbers. A default curve is provided, but it is possible to edit the default curve to create a custom one. In the CT scanner calibration curve sheet, it is possible to select a cell and change its value. It is also possible to add or delete entries. The plot updates automatically according to the changes made in the cells. The *Save the curve as default* button allows to save the edited curve as the default one.

Warning 4.5 Once a mass density versus CT number calibration curve is saved as default, the original default curve supplied with PRIMO is lost.

The image displayed at the right bottom corner of the CT Volume Segmentation dialog is a blended image of densities and materials. Densities are mapped to a gray scale and materials to

a discrete color scale. Moving the slider at the bottom of the image to the left will foreground the densities in the image and moving it to the right will foreground the materials. The lower slider allows to change the displayed CT slice, this can also be done by scrolling with the mouse wheel. Clicking the *Ok* button will save the current segmentation and will create the voxelized geometry. A segmentation created in another project can be imported into the current one by clicking the *Import* button.

Notice 4.5 Moving the mouse over the blended image produces a display (at the bottom of the image) of the coordinates, CT number, mass density and material of the image pixel under the mouse pointer. ■

4.1.4 Contouring

A set of structures can be created from drawing its contours on the CT volume. Contours can also be imported provided they are formatted as the DICOM-RT STRUCT standard. Press the Delineate structures button in the s3 tab to open the contouring dialog (figure 4.13). In the Contouring dialog menu bar, click the button *Create* to create a new structure. A dialog (figure 4.13) appears querying for the ID and color that will identify the structure. To draw a structure contour, first select a structure in the list, and then press the button *Draw*. To delineate the contour do the following:

- Select the reference image by moving the sliders in the three dimensions.
- Create the first point of the contour by clicking the left mouse button on the image.
- To create a continuous contour, move the mouse along the path of the contour while keeping the left mouse button pressed.
- To create a discrete (point to point) contour, click the left mouse button at the points. The contour is formed by connecting the points with lines.
- To delete a point, click the right button of the mouse.
- To close the contour, approximate the mouse pointer to the first point, a small circle appears, then click inside the circle and the contour will be closed.

Contours can be drawn on selected image planes. Missing contours will be created by clicking the *Interpolate* button.

Zoom In/Out the CT volume by pressing the *Zoom the Image* button. Drag the mouse over the image in the left-up/right-down direction to zoom in/out the CT volume. The point where the three planes intersect is taken as the center of the zoomed region, which can be changed by panning the image with the *Pan* button.

Import structures

Structures created externally can be imported by selecting the button *Import a structure set*. In the standard File Open dialog select the file containing the structure set. The file must be formatted as a DICOM-RT STRUCT object and the structures must belong to the same study of the imported CT volume. The DICOM-RT STRUCT Import dialog (figure 4.15) shows a graphic representation of the contours on each image plane and a list of structures and their attributes. Uncheck the box under the column *Import* to exclude a structure. In case a Hounsfield number is associated to a structure the CT volume can be modified by assigning that number to all the voxels inside the structure. To accomplish this, check the box under the column Mod. CT. Finally, press the button *Import* to start importing the selected structures into the PRIMO project.

Warning 4.6 The Hounsfield numbers of the CT volume regions changed when importing structures with the *Mod.CT* option checked are lost.

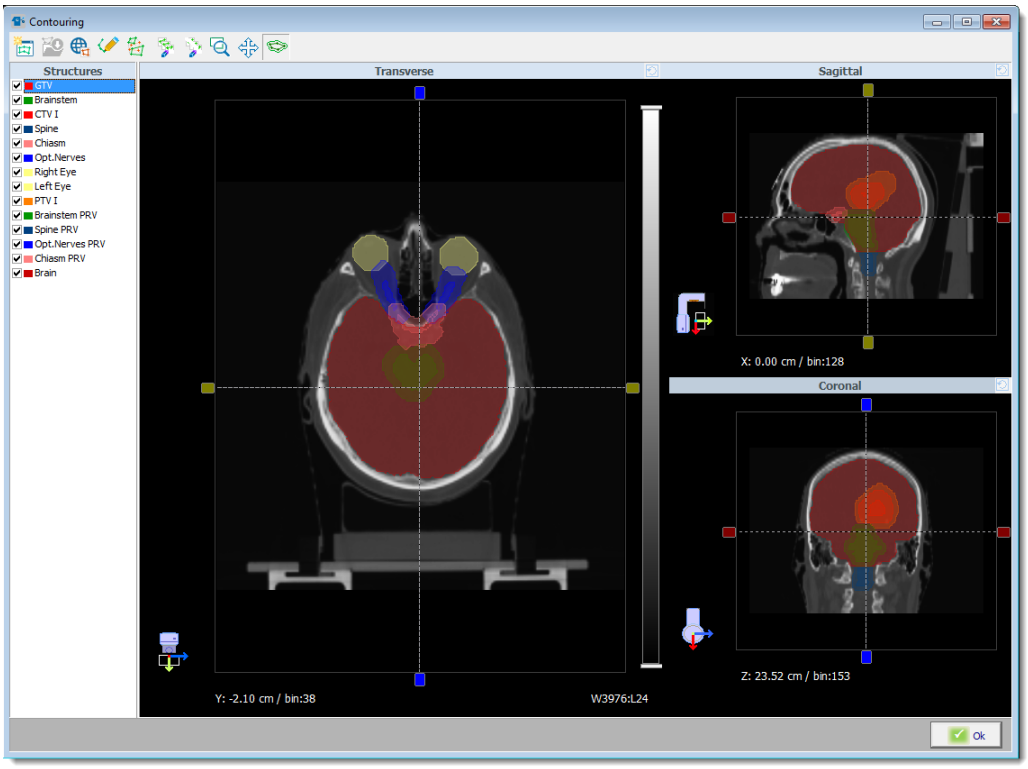


Figure 4.13: Contouring dialog. Creation of structures.

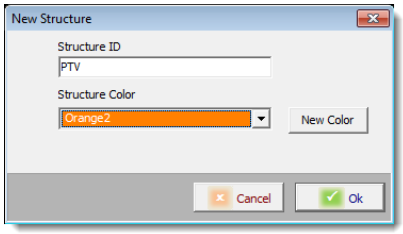


Figure 4.14: New structure dialog.

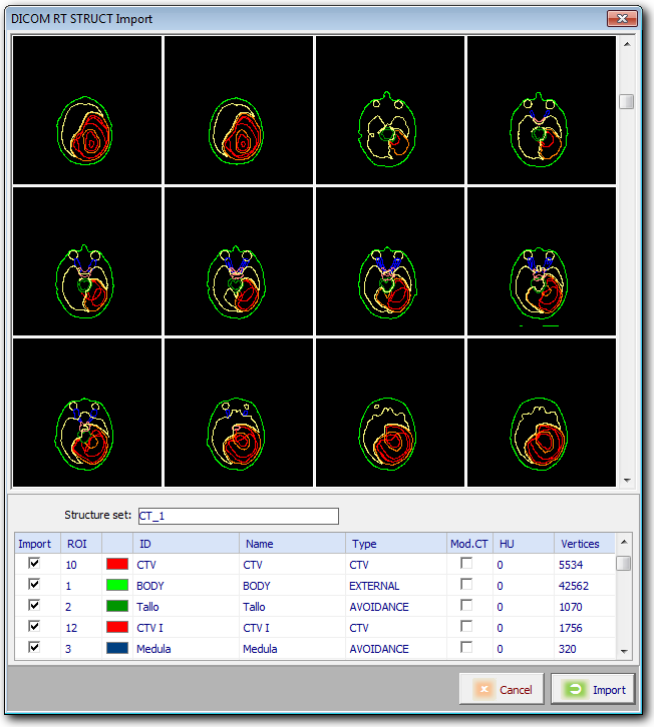


Figure 4.15: Import DICOM-RT STRUCT dialog.

4.1.5 Simulation configuration

To have access to the parameters that govern the simulation execution, select *Configure simulation options* in the main menu or main tool bar. The Simulation configuration dialog (figure 4.16) allows to set the seeds of the random number generator, the stop conditions of the simulation, the frequency of reporting partial simulation results, and the number of CPU cores used. New seeds can be entered manually or automatically generated by clicking on the small dice in the dialog. In the latter case seeds are generated with a separation of 10^{15} calls to the pseudo-random number generator [BS06; SFS11].

R If both stopping conditions, time and number of histories simulated are set, the first fulfilled condition will end the simulation.

Warning 4.7 Setting more simulation processes than available CPU cores slows down the simulation. The minimum amount of Random Access Memory (RAM) required for a simulation is about 0.5 GB per process.

4.1.6 Transport parameters

PENELOPE requires to define a set of simulation parameters which determine the trade-off between speed and accuracy. Refer to the PENELOPE 2011 manual [SFS11] for detailed information about the transport parameters. PRIMO provides default values for this set. Nevertheless, users can modify the default set by editing the table found under the option *Configure transport parameters* in the main menu and the main tool bar. It is advisable to carefully read the PENELOPE 2011 manual before attempting any change in this table, which can be edited by checking

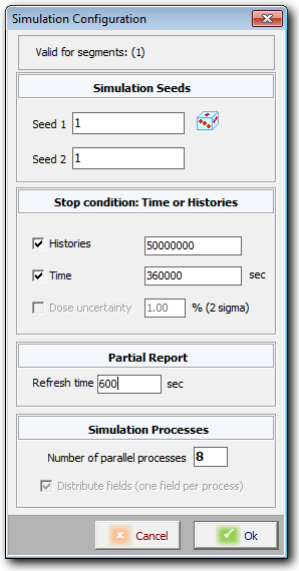


Figure 4.16: Configure simulation options dialog.

the Enable Editing box of the dialog (figure 4.17). The works of Brualla and co-workers [BSP09], Sempau and Andreo [SA06] contain some advices on how to set the transport parameters. The button Load default values will restore the default set of transport parameters.

> **Warning 4.8** Modification of the transport parameters table should only be attempted by experienced users.

4.1.7 Variance reduction

Several variance-reduction techniques are available under the main toolbar function *Configure variance reduction*. These techniques include forcing of bresstrahlung interactions in the linac target, simple splitting in the water phantom or the CT, and two splitting techniques developed by the authors of the code, the rotational splitting [BS10] and splitting roulette [RSB12]. Additionally, moveable-skins [BSP09] are used in the jaws, the primary collimator and the MLCs. An appropriate skin thickness is automatically selected by the code for each component and nominal energy.

A suitable combination of interaction forcing in the target and splitting in the patient can in some cases improve the efficiency considerably, the appropriate combination of forcing and splitting factors depends on the energy and the field size and it is currently under study. As a general rule it is recommended to keep the forcing factor relatively small (*e. g.*,in the vicinity of 16), because large forcing factors increase considerably the simulation time and counterbalance the effect that reducing the variance has on the simulation efficiency.

The methods that, so far, have proven to be the most efficient are rotational splitting and splitting roulette, combined with a simple splitting in the dose tallying region. As a general rule, splitting roulette is more efficient than rotational splitting at low energies, so it is the recommended method for beams with energies under 15 MV.

Most of the parameters of these two techniques are configured such that to obtain the optimal efficiency. One of the few setting let to the user is that of defining the size of the splitting region, a circular region located at a plane upstream the jaws, and that is used, although playing a different

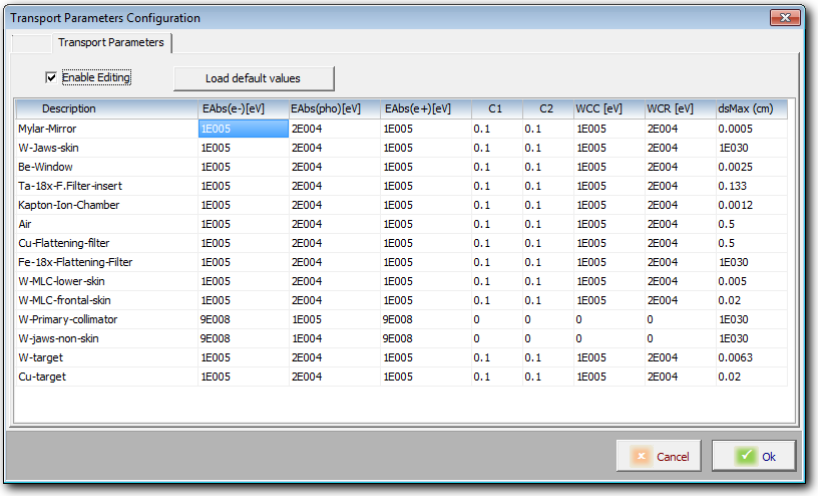


Figure 4.17: Configure transport parameters dialog.

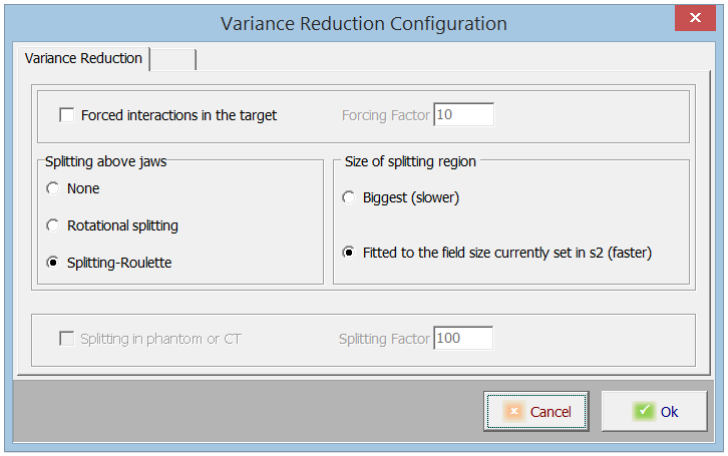


Figure 4.18: Variance reduction configuration dialog.

role, in both techniques. Particles flying in the direction of this region are considered in the splitting roulette technique with high probability of contributing to the dose. Rotation splitting is done only to particles crossing the plane of the splitting region inside its limits. In both cases, particles crossing the plane of the splitting region out of its limits are removed from simulation. Consequently, the diameter of the splitting region must be set larger than the diagonal size of the field as defined by the jaws (assuming the field is symmetrical with respect to the CAX).

On one side, smaller splitting regions are more efficient. On the other side, arbitrarily removing from simulation particles that otherwise would contribute to the dose biases the results. The optimal situation for a given field is to adjust the size of the splitting region to be slightly larger than the field size. This is done using the option *Fitted to the field size currently set in s2*. However, this criterion can conducts to errors if a PSF is tallied at segment s1 to be used as the source of particles in simulations of s2 and s3 with variable field sizes. There could be cases in which the region irradiated by the field is not completely covered by the splitting region used to tally the PSF. To avoid biasing the dose in these cases, the CROI size must be set with respect to the maximum possible field size (40×40 cm^2) using the option *Biggest*.

When rotational splitting is selected at s1 while an off-axis field is configured at s2, PRIMO automatically applies the fan splitting technique. This variance-reduction technique has been developed for improving simulation efficiency of off-axis fields [SBB11].

Warning 4.9 When employing splitting roulette or rotational splitting to tally a phase-space file at segment s1, it is safer to select the option *Size of splitting region* as the *Biggest* to avoid biasing the simulation of fields larger than the splitting region. Select *Fitted to the field size currently set in s2* only when there is certainty that the largest field that will be simulated with the source PSF is the one currently set in the segment s2 configuration.

Notice 4.6 — Adequate variance-reduction parameters. The following variance-reduction parameters are a reasonable first choice when attempting a given simulation. For nominal energies below 15 MV (photon mode) it is recommended to use splitting roulette for s1. For nominal energies above 15 MV rotational splitting is usually more efficient. Regarding simulation of s3, a splitting factor of 100 usually works fine. It is advisable to check the estimated time after launching the simulation of s3. If the estimated time with a splitting factor of 100 is exceedingly long then reset the simulation, modify the splitting factor for s3 and launch it again. For an explanation on simple splitting at s3 see section 5.1.1. ■

4.1.8 Importing external phase-space files

Phase-space files produced with PRIMO or other simulation codes can be imported provided they are saved in the IAEA format [Cap+06]. Phase-space files can be imported in the s1 segment only. Importing a phase-space file is a process similar to producing it by simulation. Previously to importing, a new project must be created and the selected linac must be the same as the one simulated to produce the phase space (with the exception of TrueBeam, see below). Also, the `s1` tab segment configuration must be set with the same parameters of the initial beam that were used to create the phase-space file, or an approximation to them. The segment `s1` checkbox must be active and the project must be saved. To import the phase-space file, select the option *Import a phase space* in the main menu or main tool bar. In the standard File Open dialog select one or several phase space header files (`*.IAEAheader`). The Phase space import dialog (figure 4.19) shows the progress of the importing process. After imported, the phase-space file is incorporated into the project as if it were the result of simulating the s1 segment.

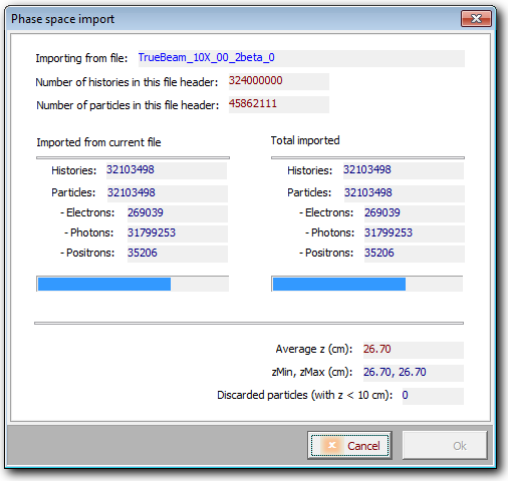


Figure 4.19: Phase space import dialog.

To import a TrueBeam phase-space file, create a project for a Varian Clinac 2100 linac, then set the `s1` tab parameters to match those used to simulate the phase-space file (see the Example 03).

Warning 4.10 When importing an external phase space separated in several files, in the File Open dialog select all the header files belonging to the phase space.

4.1.9 Duplicating a project

The option Save As in the main menu allows to create a copy of the project, including all the imported data and the simulation results. The Save As dialog is the same as the New Project dialog with the exception that the option to select the linac is blocked. Enter a new project ID (different to that of the original project) and path and, optionally, a new name and comments. The copy process could take a considerable amount of time, depending on the size of the project files, especially of the phase-space files. No progress dialog will appear.

4.2 Execution

Once the simulation setup is finished and saved the *Run* button in the main window can be clicked and the simulation starts running. The main window disappears and *in lieu* the execution window is presented (figure 4.20).

The execution window reports the progress of the processes requested for the simulation during the setup process. A maximum of 120 processes can be unleashed simultaneously.

The toolbar of the execution window contains 4 buttons as shown in figure 4.21. From left to right these buttons are

- *Run simulation*: this button is not operative during simulation.
- *Change simulation parameters in flight*: allows to change simulation parameters during runtime (section 4.2.1). The button becomes active after all cores have initialized their respective simulations and one minute of simulation time has elapsed for all of them.
- *Reset simulation*: This button allows to reset the simulation, that is, to return to the simulation setup **losing all computed results**.

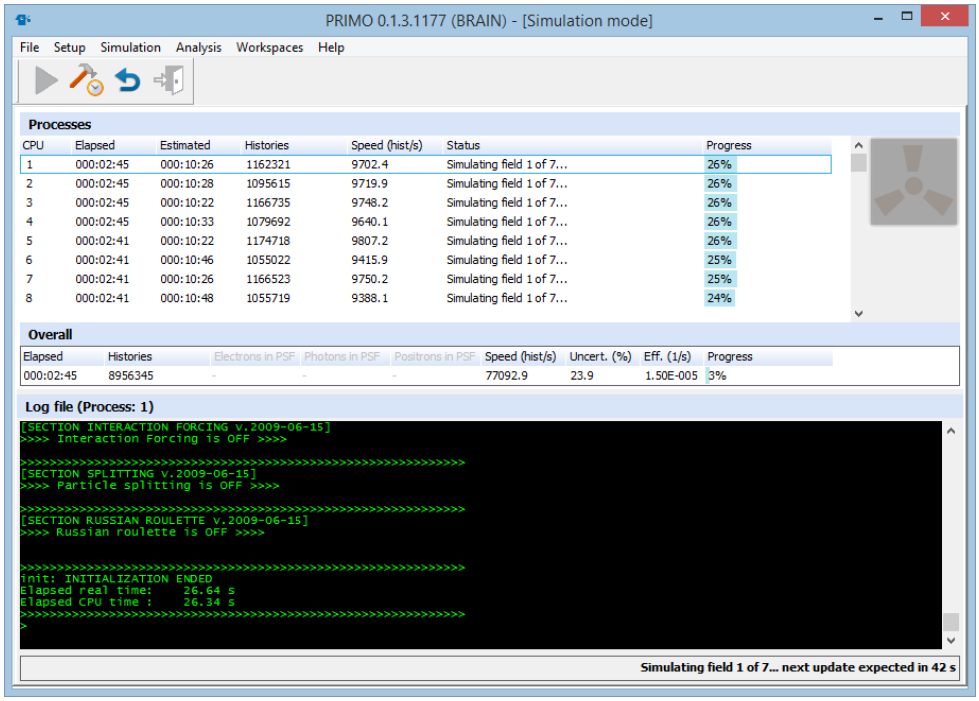


Figure 4.20: Execution window.

Figure 4.21: Taskbar of the execution window.

- *Exit simulation mode*: This button becomes active only once all cores have completed their jobs (for all fields) and all the computed results from all cores have been integrated. It allows to exit the simulation mode and resumes the main PRIMO screen.

Warning 4.11 If the Reset button is clicked while executing a simulation, all tallied results will be lost. PRIMO will return to the state prior to launching the simulation.

The execution window is divided in two panels. The upper panel presents the status of each running process and the overall status. It includes the time elapsed since the process started to execute, the estimated time of execution, the number of histories simulated, the speed in histories/second and the percentage of execution. The integrated results of the simulation shown in the overall status are the statistical combination of the results obtained in all simulation cores. In the case of a dose distribution is being tallied, the overall window shows the average statistical uncertainty of the dose σ which is calculated as,

$$\sigma = \sqrt{\frac{1}{N^2}\sum_{k=1}^{P}(\sigma_k n_k)^2}, \tag{4.1}$$

where n_k is the number of histories simulated by the *k-th* process, P is the number of processes, N is the total of histories simulated ($N = \sum n_k$) and σ_k is the average statistical uncertainty of the dose distribution tallied by the *k-th* process calculated as,

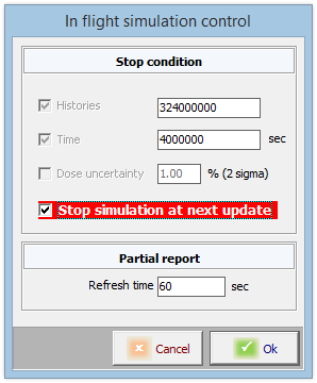


Figure 4.22: In flight simulation control window.

$$\sigma_k = 2.0 \times \sqrt{\frac{1}{\eta}\sum_{j=1}^{\eta}\sigma_{kj}^2}, \tag{4.2}$$

where η is the number of bins in the dose distribution with a dose larger than half the maximum dose ($d_j \geq d_{max}/2$) and the sum is done for those j bins satisfying the condition. σ_{kj} is the statistical uncertainty of the dose in the j-*th* bin for the k-*th* process.

In the case a phase space is being tallied the overall window shows the current number of particles tallied in the phase space. The information appearing in the upper panel is refreshed every update interval as it has been specified in the simulation setup. The lower panel (green characters on a black background) shows the log file corresponding to process selected in the upper panel. The log file is generated during execution and contains the simulation input parameters and the output of PENEASYLINAC and PENEASY generated during their execution. An explanation of the PENEASY output can be found in its documentation (section 1.3). Simulation of several fields is done sequentially.

4.2.1 Changing parameters at runtime

Through this dialog it is possible to modify the total simulation time requested, the number of simulated histories and the update interval. Additionally, it is possible to stop the simulation while keeping the already simulated results. The changes take effect at the end of the update interval. For example, if the update interval was set in the setup section as 600 seconds, and the Stop simulation at next update checkbox is marked, the simulation will continue running until the next update interval is reached, in at most 600 seconds. Then simulated results will be collected and presented to the user. This way of stopping the simulation is notoriously different from using the *Reset* button. If the *Reset* button is clicked the simulation stops immediately and all results are lost.

Warning 4.12 In a multi-field simulation it is not possible to change the stop conditions (by number of histories or time) in flight. In the same manner, once the simulation of the first field has finished, the simulation cannot be stopped by pressing *Stop simulation at next update*, otherwise the relative weights of the fields (in simulated histories per field) would be altered.

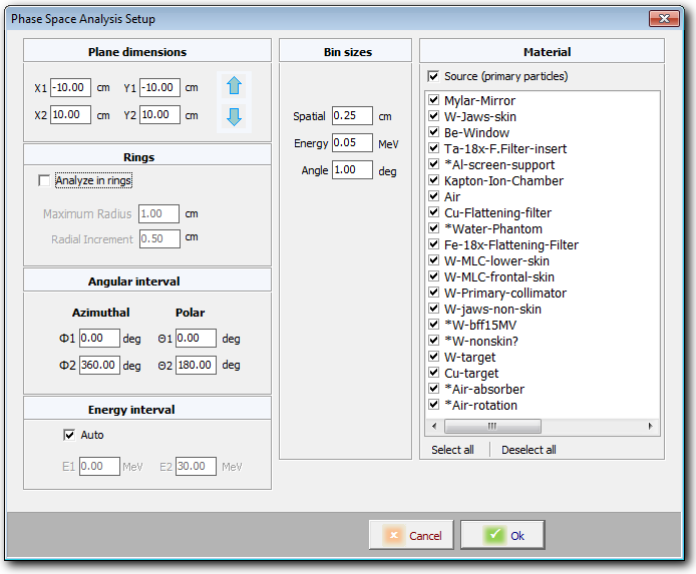


Figure 4.23: Phase space analysis setup dialog.

4.3 Analysis of results

There are two main categories of results that can be tallied with PRIMO, namely, phase-space files and dose distributions. Each of these categories has a dedicated tab in the main screen, which are named Phase Space Analysis and Dose Analysis.

4.3.1 Phase-space file analysis

Once the simulation of a phase-space file has been completed, or a phase-space file has been imported, a check mark will appear next to the corresponding hard drive symbol in the Simulation Segments panel. Also the simulated phase-space file will appear in full color in the objects tree instead of being grayed-out.

In order to analyze a given phase-space file, select the Phase Space Analysis tab in the lower part of the main PRIMO window, drag the colored phase-space icon from the objects tree and drop it into the main blank area of the analysis window. Alternatively, right click on the phase-space icon and select the option *Analyze* in the appearing pop-up menu. The Phase Space Analysis setup dialog (figure 4.23) contains several options for filtering the phase space and setting the probability distribution intervals.

Only particles from a rectangular region of the phase-space plane are included in the analysis. This region is determined by the values entered in x1, x2, y1 and y2. It is possible to select the intervals and bin sizes of the angular and energy probability distributions. If the phase-space file has been tallied with PRIMO, then it is also possible to filter the particles by the material where they were produced. This feature has no effect on imported phase-space files tallied with other Monte Carlo codes.

If the option Analysis in rings is checked, then the analysis is performed by subdividing the whole phase space plane into concentric rings centered at the central axis. The number of rings is determined by the values of the maximum radius and the radial increment set in the dialog.

Warning 4.13 There is a maximum number of bins for the probability distributions cal-

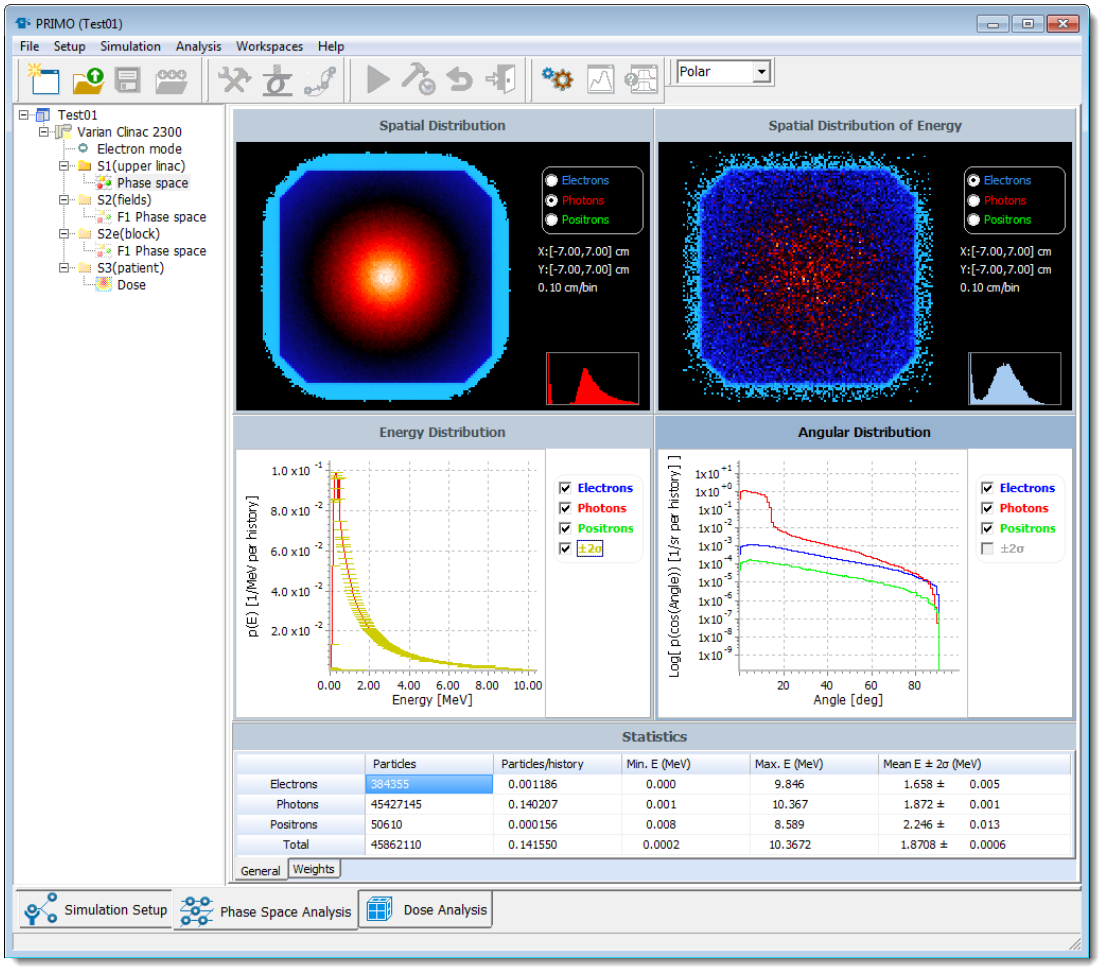


Figure 4.24: Phase space analysis window.

culated in a phase-space analysis. The maximum number of bins allowed for the angular, energy and spatial distributions are 1.8×10^2, 5×10^3 and 10^6, respectively.

Once the analysis parameters are defined, the particles in the phase-space file are read, filtered and the probability distributions calculated. Figure 4.24 shows the analysis window. The images in the upper part are the 2D spatial probability distributions of the particles (left) in units of [cm^{-2} per history] and the energy (right) in units of [MeV cm^{-2} per history] in the rectangular region of the phase space set in the configuration. Distributions are separated by kind of particle. Click the radio-button at right hand side of the image to select the desired distribution. Change the color lookup table by using the drop-down list in the main tool bar. To extract horizontal and vertical profiles of the 2D distribution, select the option *Make a profile* in the main menu or main tool bar (figure 4.25). In the Profile of the spatial distribution dialog, drag the horizontal and vertical lines over the image to update the profiles.

The 1D probability distributions of the energy and angle are also separated by kind of particle. In this case, the distributions can be included in, or removed from, the graph by checking or unchecking the box at the right hand side of the plot. The statistical uncertainty ($\pm 2\sigma$) of the distribution can also be plotted by checking the corresponding box.

Some additional tools can be found by right clicking on the title bar of a probability distribution graph. A pop-up menu appears with the following options:

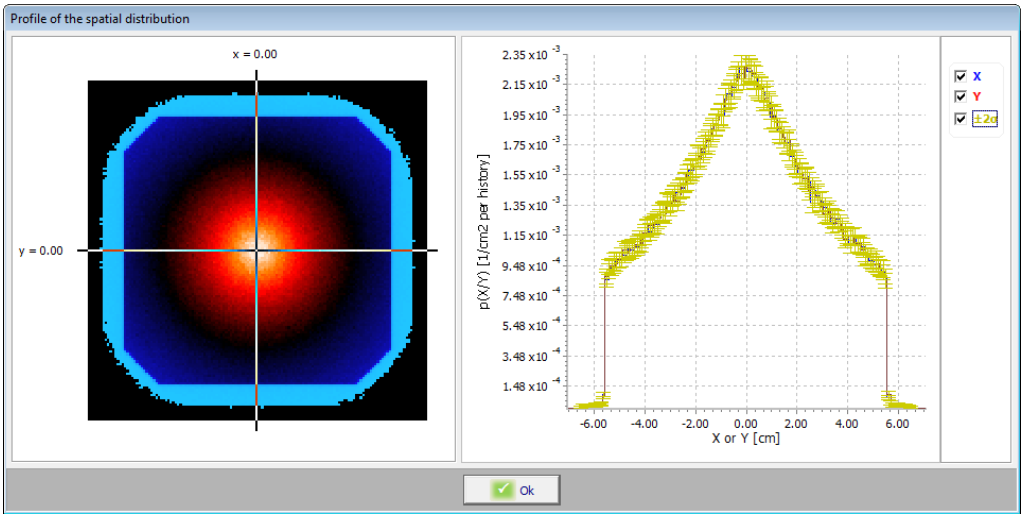


Figure 4.25: Profile of the spatial distribution dialog.

- *Maximize*: Maximize the graph to the whole analysis window.
- *Restore*: Restore a maximized window to its normal size.
- *Copy to clipboard*: Copy the graph to the clipboard as an image.
- *Logarithmic scale*: Show the graph (1D distributions) in a semilogarithmic scale.
- *Normalize to cosine*: Angular distributions are normalized to $\cos\theta$, where θ is the particle polar angle. This is the normalization by default of the angular distribution.
- *Show as surface*: A 2D distribution is shown as a surface.
- *Save as text*: The (1D or 2D) distribution is presented as a text file that can be saved.

Some statistical data of the phase space (classified per kind of particle) are shown in the table at the bottom of the analysis window. These include the total number of particles in the phase space, the number of particles per history, and the mean energy. Statistical weights are shown in a separated (Weights) tab.

In an analysis performed in rings, separated 1D probability distributions and statistical data are calculated for each ring, i.e. by including only the particles located inside the ring. In this case, a tool bar appears on top of the statistics table containing buttons to change the ring whose results are presented in the analysis window. Also the rings are shown superimposed to the 2D spatial distributions (figure 4.26).

4.3.2 Dose analysis

Once the simulation of a dose distribution has been completed, a check mark will appear next to the corresponding hard drive symbol in the Simulation Segments panel. Also the dose icon in the objects tree will appear in full color.

In order to analyze the dose distribution, select the Dose Analysis tab in the lower part of the main PRIMO window, drag the colored dose icon from the objects tree and drop it into the main blank area of the analysis window. Alternatively, right click the dose icon and select the option *Analyze* in the appearing pop-up menu. The 3D dose distribution is shown superimposed to the phantom or CT slices in the transversal, sagittal and coronal planes (figure 4.28). The whole dose volume can be navigated by changing the planes. To change a plane, drag its sliders to the desired position. The planes can also be changed with the mouse wheel. Each plane is identified with a different color and the sliders are of the color of the plane that it represents.

The planes *xz*, *yz* and *xy* are the transversal, sagittal and coronal planes, respectively. Dose

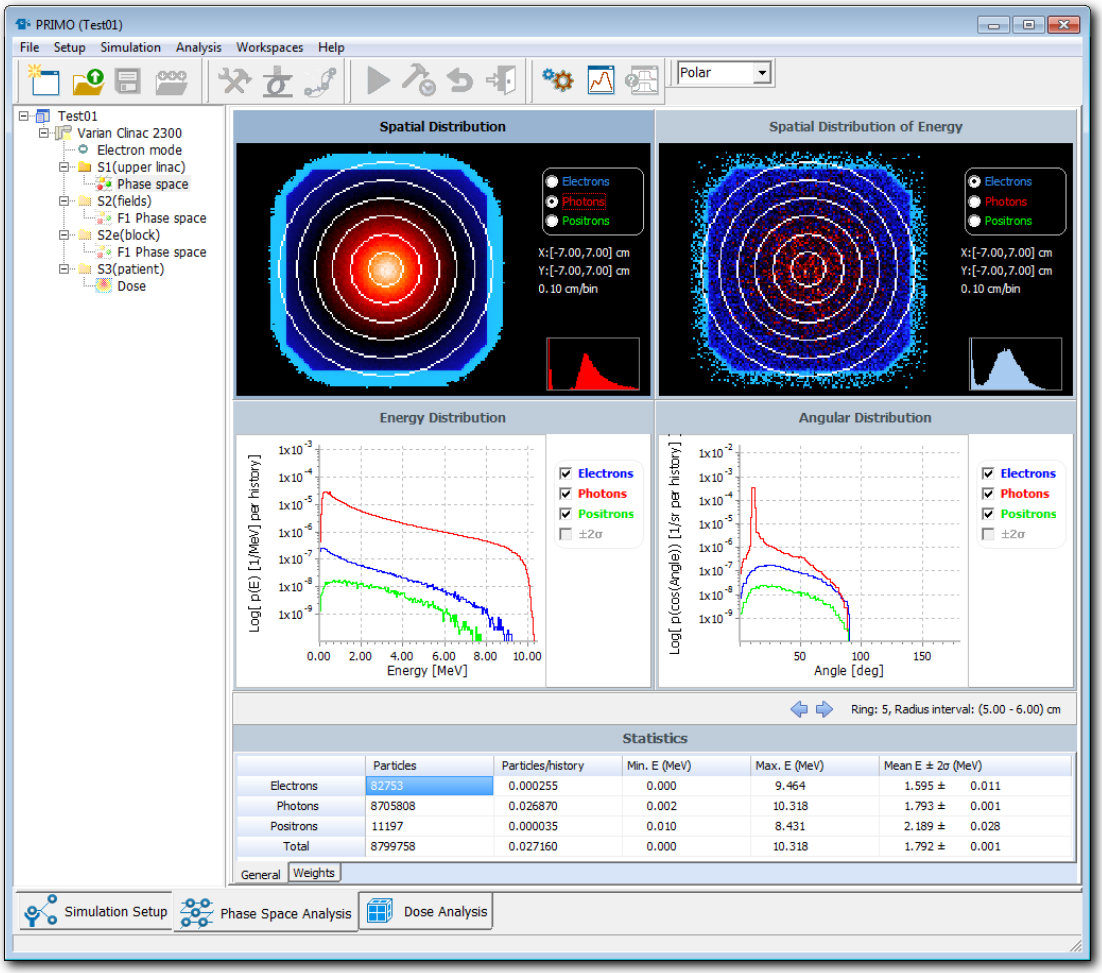


Figure 4.26: Phase space analysis window showing the results of an analysis made in rings. The tool bar on top of the Statistics table allows to navigate the results of the ringed regions.

profiles can be taken along the x, y and z directions (figure 4.28). In case the dose distribution is calculated in a CT volume dose profiles do not appear by default. Instead dose-volume histograms (DVH) for all structures are created or imported. In case no structure was created the DVH of the whole CT volume is shown. To show dose profiles select the option *Toggle profiles and DVHs* in the pop-up menu that appears by right clicking on the title bar of the window. Other options are:

- *Maximize*: To maximize the selected window to the whole analysis window.
- *Restore*: To restore a maximized window to its normal size.
- *Show dose as color wash*: To toggle between visualizing the dose as a color map (default) or as isodose curves.
- *Interpolate planes*: When the option is active the visualization algorithm uses an interpolation to show the dose distribution, the Hounsfield numbers and the structures according to the window size.
- *Zoom*: To activate the zoom in/out function. To zoom in/out, drag the mouse over the image in the left-up/right-down direction. The point where the three planes intersect is taken as the center of the region zoomed.
- *Restore original size*: To restore a zoomed image to its original size.
- *Inspect dose*: To inspect the dose values in the dose distribution (see Inspecting the dose distribution section below).
- *Saves curves as text*: To save the dose profiles or DVHs in text files. In dose profiles, the coordinates of the point set by default are those of the center of the bin. It can be changed to be the coordinates of the low end of the bin by checking the box Save the coordinates of the low end of the bin in the Save curves as text dialog.
- *Pan*:To move the zoomed region.
- *Move planes to the origin*: To position the sliders (intersect the three dose planes) at the origin of coordinates.
- *Move planes to dose maximum*: To position the sliders (intersect the three dose planes) at the point of maximum dose.
- *Toggle profiles and DVHs*: To toggle between visualizing dose profiles or DVHs.
- *Differential DVHs*: To calculate differential DVHs instead of cumulative DVHs (default option).
- *Copy to clipboard*: To copy the dose plane or graph to the clipboard as a bitmap.
- *Change field weight*: To change the relative weight of the fields (see next section).

4.3.3 Changing the relative field weight

Weight factors can be assigned to fields. This is done post simulation. In a multi-field simulation, a separate dose distribution is generated per field and are integrated to form the total dose distribution for analysis and visualization. Weight factors are applied to the partial dose and its uncertainty in each bin during integration. The total dose d_i in a bin i is calculated as,

$$d_i = \frac{1}{N} \sum_{f=1}^{F} d_{if} n_f w_f, \tag{4.3}$$

where N is the total of histories simulated, n_f is the total of histories simulated for the field f, F is the number of fields and w_f is the weight factor for the field f. The uncertainty σ_i of the dose in the bin is evaluated as,

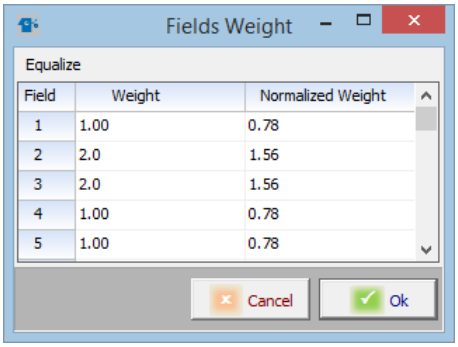


Figure 4.27: The *Fields weight* dialog.

$$\sigma_i = \sqrt{\frac{1}{N^2}\sum_{f=1}^{F}(\sigma_{if} n_f w_f)^2}, \tag{4.4}$$

where σ_{if} is the uncertainty of the dose in the bin i for the field f. Weight factors w_f are normalized such that,

$$\frac{1}{F}\sum_{f=1}^{F} w_f = 1. \tag{4.5}$$

The dose distribution is loaded from disk and integrated every time the weight factors are changed. To change the field weights, select the option *Change field weight* in the pop-up menu that appears by right clicking on any title bar of the dose analysis window. The dialog represented in figure 4.27 will appear. The option *Equalize* makes all the weights equal. Weight factors set by the user are normalized to satisfy equation 4.5. Normalized values are shown in the dialog.

4.3.4 Inspecting the dose distribution

The option Inspect dose in the pop-up menu (that appears by right-clicking on the title bars of the windows) of the dose analysis windows is useful to know the absolute value of the dose (in units of eV g^{-1} per history) at any point of the dose distribution. In the Inspect dose dialog (figure 4.29), define the point of inspection by entering its coordinates in the fields x, y and z. The dose ($\pm 2\sigma$) is displayed at the bottom. The buttons at left hand side allow to inspect the dose at predefined positions, namely, the point of maximum dose, the center of coordinates of the dose distribution and the point of intersection of the three orthogonal planes. The button *Move the planes at this point* displaces the planes to the position given by the values in the fields x, y and z.

> **Notice 4.7** To locate the point of maximum dose in a 3D dose distribution, in the Inspect dose dialog, first select the 3D dose maximum option and then Move planes to this point. ■

4.3.5 Comparing to experimental data

A calculated spatial dose distribution can be compared to measurements of lateral, diagonal or depth dose curves. This can be done by selecting the option Compare with experimental data in the main menu or main tool bar. In the standard Open File dialog, select a text file containing

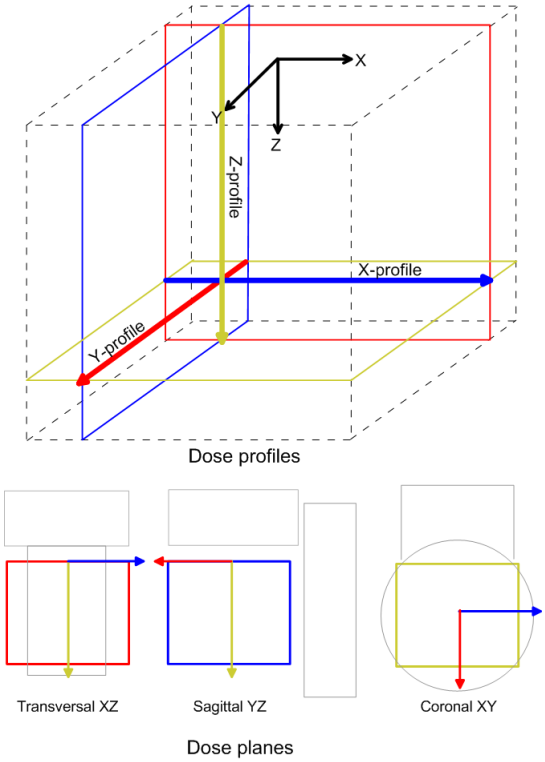


Figure 4.28: Planes of the 3D dose distribution and how the dose profiles are read.

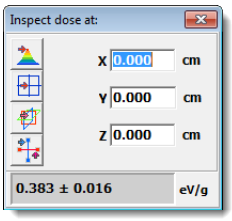


Figure 4.29: Inspect dose dialog.

the experimental data. The file must be formatted as specified in figure 4.30. It must be a plain text file consisting of a list of four data values per line, namely, the three coordinates (x, y, z) of the measurement point and the dose. The coordinates of the measurement point must be specified in the same reference system as those of the simulation of the water phantom (refer to section 4.1.2) and in units of cm whereas dose units are relative. Measurement points are not required to be equally spaced. In case they are not equally spaced, the minimum distance between two consecutive measurements is taken as reference and the experimental curve is linearly interpolated so as to obtain a uniform grid of coordinates. The simulated curve is obtained on the same uniform grid of the experimental curve by using tri-linear interpolation. The normalization values for the dose curves can be chosen in a drop-down menu among either the dose at the central axis (default for lateral profiles), or the maximum dose (default for depth-dose curves), or the dose at an arbitrary point. Additionally, the curves can be normalized to the ratio of the integral under the experimental curve to the integral of the simulated curve *Integral ratio*. The integral is taken in the region beyond $d_{\mathrm{e}}^{\max}$.

Notice 4.8 The Normalization drop-down box offers the possibility of not normalizing the dose curves. This option is suitable in case both data sets are in the same units. For example, in the case the 'experimental' dose curve was obtained by exporting a dose distribution as a text file previously simulated in PRIMO (see Example 01: 'Comparison with another simulation'). ■

The Dose curve comparison dialog (figure 4.31) presents the comparison including the graph of the experimental, calculated and difference curves, a number of parameters calculated from the curves and the gamma analysis (section 4.3.6). Comparisons can be evaluated at an arbitrary point by entering its value in the field Evaluate at or by clicking on the graph area. In both cases a vertical yellow bar (curve cursor) is positioned at that point. This point can also be used as the point of normalization by selecting At current cursor position in the Normalization drop-down box and then pressing the *Apply* button below.

The difference curve is calculated for a position p as:

$$\Delta d(p) = 100\frac{d_{\mathrm{e}}(p) - d_{\mathrm{c}}(p)}{d_{\mathrm{e}}^{\max}}, \tag{4.6}$$

where $d_e(p)$ and $d_c(p)$ are doses at the position p of the experimental and calculated curves, respectively, and $d_{\mathrm{e}}^{\max}$ is the maximum dose of the experimental curve.

The following parameters are reported for each curve:

- *Position of maximum*: The position of maximum dose.
- *Dose at 10 cm depth*: The value of the dose at 10 cm depth (only for depth-dose curves).
- *Dose at 20 cm depth*: The value of the dose at 20 cm depth (only for depth-dose curves).
- *Practical range*: The practical range (valid only for depth-dose curves produced from electron beams) is calculated by performing a linear fit of a segment of the curve defined around the depth of maximum dose gradient and reporting the value where the fitted line intersects the abscissa.
- *Range at 50% of the dose*: The depth at which the dose falls to 50% of its maximum value (valid for depth-dose curves).
- *Left off-axis distance at 50% of dose*: In lateral or diagonal dose profiles, this is the distance from the central axis to the point at which the dose falls to 50% of its maximum value, measured in the direction of the negative x or y coordinate.
- *Right off-axis distance at 50% of dose*: In lateral or diagonal dose profiles, this is the distance from the central axis to the point at which the dose falls to 50% of its maximum

```
# ------------------------------------------------
# Example: Experimental data file format
# This exemplifies the format of the text
# file used to import lateral and diagonal
# profiles or depth dose curves into PRIMO.
#
# Rules:
# - The file must be a plain text file
#   (ASCII or ANSI encoding).
# - Lines (like this one) begining with the
#   symbol '#' are considered comments. Any
#   other line is considered as data.
# - Comment lines can be inserted anywhere
#   in the file.
# - Coordinates are expected in units of cm.
# - Dose units are irrelevant (as the
#   comparison is relative).
# - Special characters (such as tabs) must
#   not appear in the data lines.
# - Data must be arranged in columns separated
#   by space characters.
# - The order of columns is this:
#   X[spaces]Y[spaces]Z[spaces]Dose
#
# - All columns are mandatory
# - Coordinate values must be listed in
#   sequencial order (ascending or descending).
# ------------------------------------------------
# Data
# X(cm)  Y(cm)  Z(cm)         Dose
  0.0    0.0    0.000        1.3178E+00
  0.0    0.0    0.300        1.3405E+00
  0.0    0.0    0.600        1.3721E+00
  0.0    0.0    0.900        1.3878E+00
  0.0    0.0    1.200        1.3981E+00
  0.0    0.0    1.500        1.4091E+00
  0.0    0.0    1.800        1.4140E+00
  0.0    0.0    2.100        1.4171E+00
  0.0    0.0    2.400        1.4196E+00
```

Figure 4.30: Example of text file used to import experimental data for dose comparisons. Format specifications are explained in the file header.

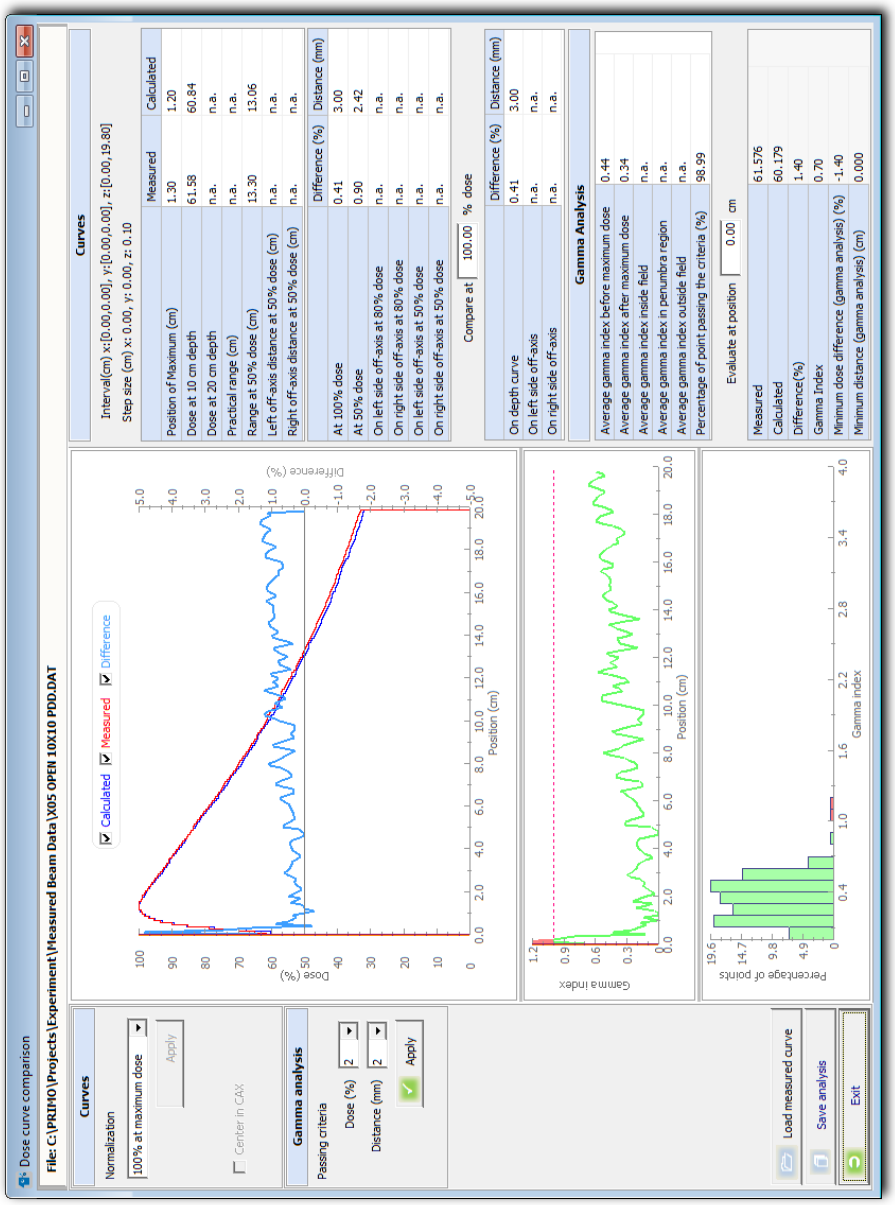


Figure 4.31: The Dose curve comparison dialog. Results from a comparison of an experimental depth-dose curve with a calculated dose distribution. The acceptance criteria for the gamma analysis are set at 2% and 2 mm, for the dose and the distance-to-agreement, respectively.

value, measured in the direction of the positive x or y coordinate.

Parameters relative to both curves are the following:

- *The difference at 100% dose*: The relative difference of the dose at the position of d_e^{max}.
- *The difference at 50% dose*: The relative difference of the dose at the position of $0.5d_e^{max}$.
- *The distance at 100% dose*: The distance (in mm) between the points of maximum dose.
- *The distance at 50% dose*: The distance (in mm) between the points of 50% of the maximum dose.
- *The difference on the left side off-axis at 80% dose*: The relative difference of the dose at the position of $d = 0.8d_e^{max}$, taken in the negative direction of x.
- *The difference on the right side off-axis at 80% dose*: The relative difference of the dose at the position of $d = 0.8d_e^{max}$, taken in the positive direction of x.
- *The distance on the left side off-axis at 80% dose*: The distance (in mm) between the points of 80% dose, taken in the negative direction of x.
- *The distance on the right side off-axis at 80% dose*: The distance (in mm) between the points of 80% dose, taken in the positive direction of x.
- *The difference on the left side off-axis at 50% dose*: The relative difference of the dose at the position of $d = 0.5d_e^{max}$, taken in the negative direction of x.
- *The difference on the right side off-axis at 50% dose*: The relative difference of the dose at the position of $d = 0.5d_e^{max}$, taken in the positive direction of x.
- *The distance on the left side off-axis at 50% dose*: The distance (in mm) between the points of 50% dose, taken in the negative direction of x.
- *The distance on the right side off-axis at 50% dose*: The distance (in mm) between the points of 50% dose, taken in the positive direction of x.

The relative difference of the dose and the distance between points of the two curves can also be evaluated at an arbitrary percentage of the experimental maximum dose by entering it in the Compare at field.

R The option Save analysis creates a text file containing all the results of the analysis.

The option Center in CAX produces a shift of the experimental profile such that the distance from the central axis to the points of 50% dose in both, the negative and positive directions of the x or y axis, are the same. The shift is applied to the experimental curve and then the simulated curve is extracted again from the 3D dose distribution.

4.3.6 Dose comparison by gamma analysis

The gamma analysis [Low+98] is a method that combines the dose-difference criterion and the distance-to-agreement criterion to compare two distributions. The Dose curve comparison dialog performs the gamma analysis of the experimental curve and the simulated 3D dose distribution. The dose difference is evaluated by exploring the dose distribution in the vicinity of the experimental points. For a given experimental point p and the dose at that point $d_e(p)$ the gamma index, Γ, is evaluated as

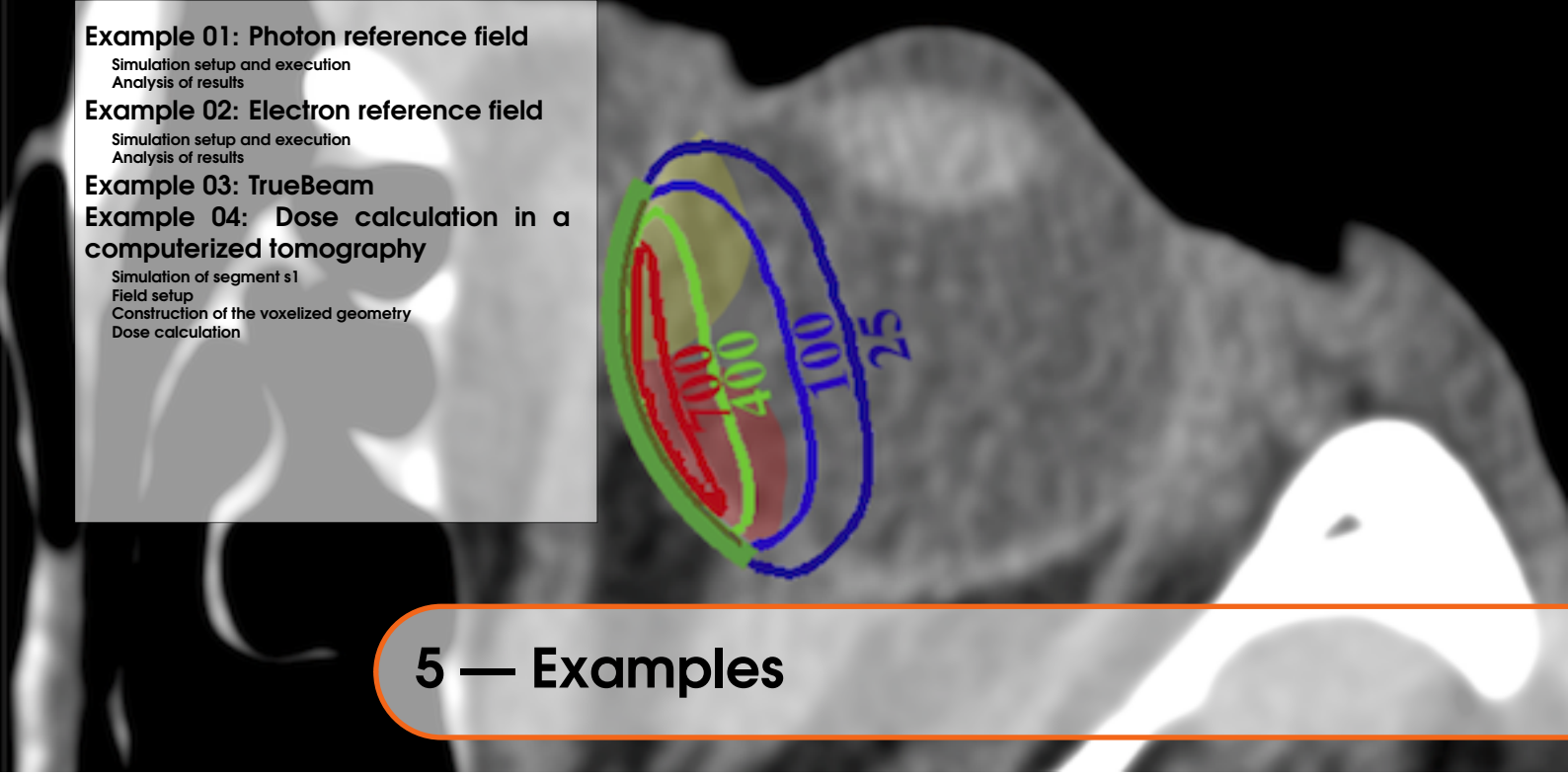
$$\Gamma = \min \left\{ \sqrt{\left(\frac{\Delta d_i}{\Delta D}\right)^2 + \left(\frac{\Delta s_i}{\Delta S}\right)^2} \right\}, \tag{4.7}$$

where ΔD and ΔS are arbitrary constants known as the acceptance criteria for the dose difference and for the distance-to-agreement, respectively. The term Δd_i is the difference between $d_e(p)$ and the simulated dose at a certain point p_i. The term Δs_i is the distance between p and p_i. The minimum of the expression in curly braces is evaluated for the set of points $\{p_i\}$. This

set contains the points in the vicinity of p that extends up to a distance of $5\Delta S$ (or a maximum of 1.5 cm). The resolution in each spatial direction is enhanced to one fifth of the bin size by tri-linear interpolation of the simulated dose distribution.

The values of *Dose difference (gamma analysis)* and *Distance (gamma analysis)* reported in the Dose curve comparison dialog represent the values of the terms Δd_i and Δs_i, respectively, where the minimum in equation 4.7 is reached.

Notice 4.9 PRIMO assumes that the imported data for a comparison is the reference data set. Consequently, data from the active simulation is the evaluated data set. Notice that the gamma test is not symmetric with respect to the reference and the evaluated data sets. ■



5 — Examples

The examples presented in this chapter are intended to be followed in sequential order. The first example is presented very detailedly, while the following examples only show details on the aspects not previously discussed.

R The files with the results of executing the examples presented in this chapter can be downloaded from `http://www.primoproject.net`. The downloaded files are to be uncompressed in the directory `c:\PRIMOexamples`. The file size of each compressed example is the following:

- `Example01.zip` 971 MB
- `Example02.zip` 11 MB
- `Example03.zip` 82 MB
- `Example04.zip` 836 MB

5.1 Example 01: Photon reference field

This example covers the simulation of all segments of a linac in the sequence s1, s2, s3 (section 3.7) to tally intermediate phase-space files and the dose distribution in a water phantom. The configuration chosen for this example is the following:

Linac Varian Clinac 2100 C/D
Mode Photon
Nominal energy 6 MV
Field size 10×10 cm^2
MLC None
Dose tallying Water phantom
SSD 95 cm
Bin size $0.2 \times 0.2 \times 0.2$ cm^3
Dose tallying volume $16.2 \times 16.2 \times 31.0$ cm^3

R Unless it is explicitly stated all default values have been used.

5.1.1 Simulation setup and execution

After launching PRIMO click the *New Project* button and select the linac model and operation mode in the corresponding window (figure 5.1).

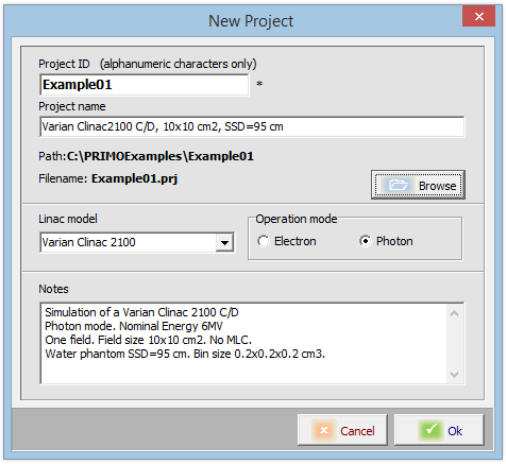


Figure 5.1: New Project window. Notice the linac model and operation mode chosen.

For this simulation project a phase-space file will be tallied at s1. After clicking the configuration button, the Simulation Configuration window is presented (figure 5.2). The simulation time is set to 10 hours (36,000 seconds). This time can be reduced to a few minutes if the aim is to test the functionalities of PRIMO without seeking a low statistical uncertainty.

For simulations of segment s1 of linacs operating in photon mode it is advisable to use either rotational splitting or splitting-roulette. For energies below about 15 MV splitting-roulette is more efficient than rotational splitting. The splitting-roulette technique will be applied to a 10×10 cm^2 field, therefore the phase-space file produced can only be used for simulations of this field size. Smaller field sizes can also be simulated with the phase-space file tallied with this example provided they are located within the illuminated area of a centered 10×10 cm^2 field. For a phase-space file to be used on any field size the Biggest option, which is slower to simulate, must be chosen (figure 5.3). Access to the variance-reduction options is done by clicking the corresponding button on the main PRIMO window. The default beam parameters given in panel Segment Setup, tab s1 are used for this simulation. In tab s2 the default field, a centered 10×10 cm^2 field size is also left unmodified.

Notice 5.1 Since the phase-space file generated at s1 occupies about 5 GB of disk space it is not distributed with the example. ■

Finally, the characteristics of the water phantom where the dose will be tallied are also defined at this step by clicking tab s3. The binned region is defined as a parallelepiped of $16.20 \times 16.20 \times 31.00$ cm^3 with bin size equal to $0.2 \times 0.2 \times 0.2$ cm^3. Notice that the center of a column, along the z-direction, of bins is located along the central axis of the beam (figure 5.4). It must be stressed that the binned region defines the size of the calculation grid, not the size of the water phantom. The size of the water phantom is always chosen much larger than the field size.

Once the project is saved the simulation can be launched by pressing the *Run* button (figure 5.5).

After the run has finalized the *Exit* button becomes active. Click it to return to the main PRIMO window. Mark the checkbox for s2 and click the *Configuration* button to proceed with the next segment (figure 5.6). Notice that we now choose the number of histories as the stopping condition since we are interested in using all particles tallied in the phase-space file computed during the simulation of s1. The number of histories appearing in the Histories field correspond

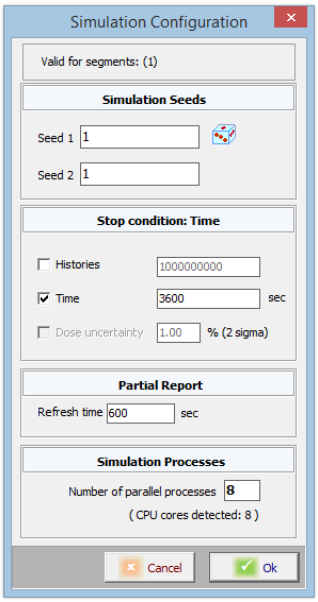


Figure 5.2: Simulation Configuration window. Notice that the only stoppping condition is the simulation time. The update interval is set to 600 seconds. Eight simulation cores are chosen.

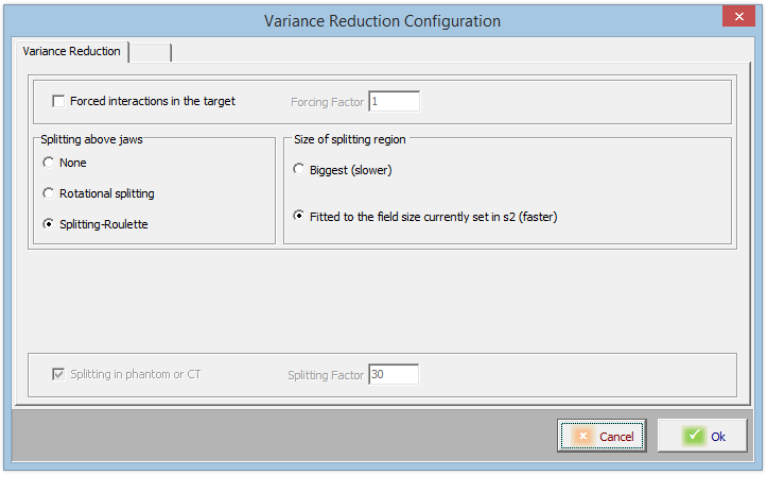


Figure 5.3: Variance reduction configuration window. Splitting-roulette fitted to the field size is chosen.

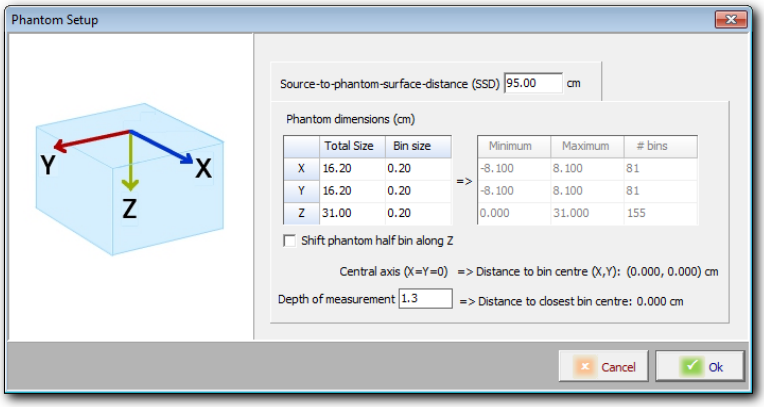


Figure 5.4: Patient Model window, Phantom tab. SSD is set to 95 cm.

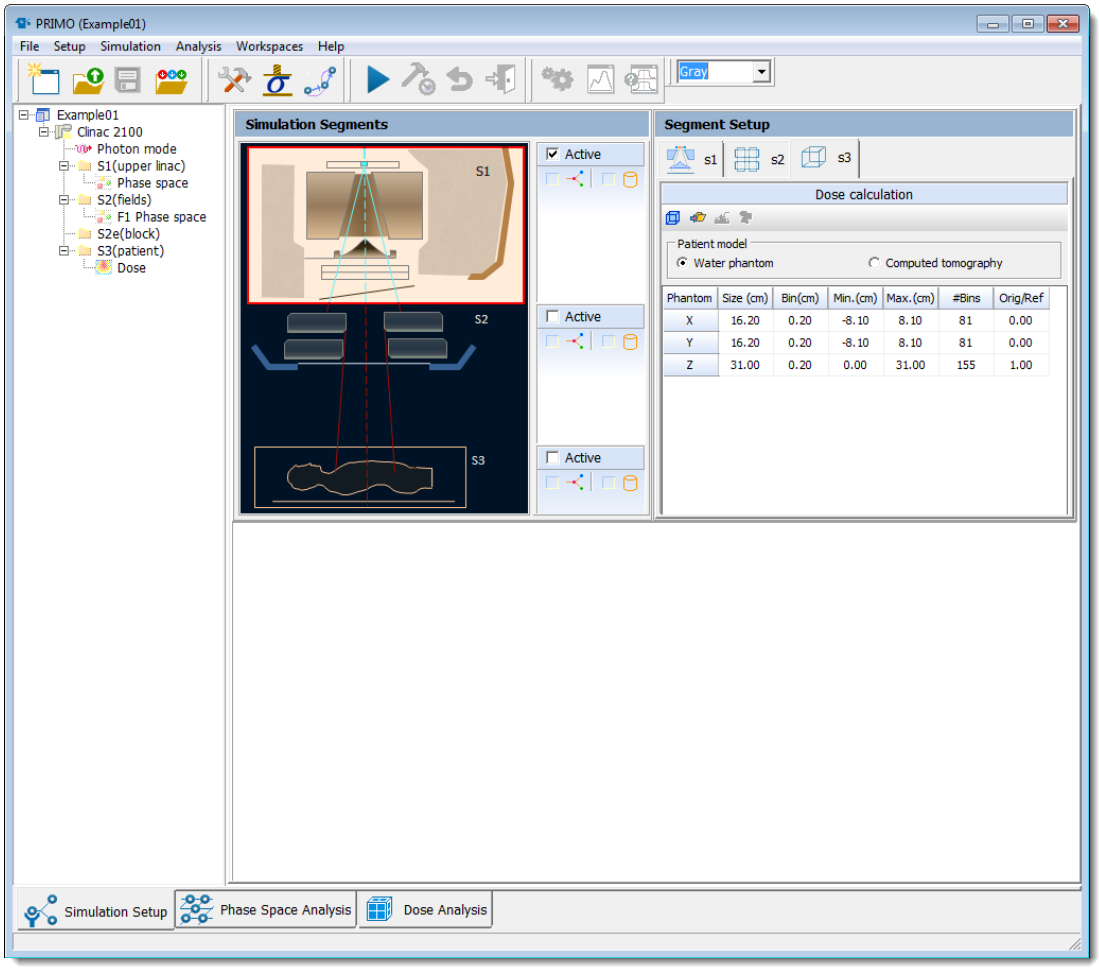


Figure 5.5: Main PRIMO window just before launching the simulation of s1.

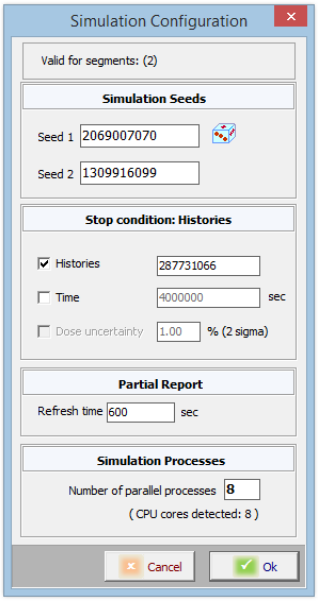


Figure 5.6: Simulation Configuration window prepared for simulating s2.

to the number of histories simulated in s1. The seeds of the random number generator should not be changed, since they are the latest seeds used in the previous segment. In that way it is guaranteed that the sequence of pseudo-random numbers of s2 does not overlap with that used during the simulation of s1. Notice that it is not necessary that all segments use the same number of computing cores.

No user-selectable variance-reduction techniques are available for s2. They are automatically chosen and adjusted by PRIMO. After saving the project the simulation can be launched (figure 5.7).

Once the simulation of s2 is completed the procedure to resume the main PRIMO window is the same described above. To reduce the statistical uncertainty in the estimation of the absorbed dose distribution we apply particle splitting to the phase-space file tallied at the downstream end of s2. By clicking the button for variance reduction the corresponding window is shown (figure 5.8). For this case a splitting factor of 200 is entered. The adequate value of the splitting factor can be found by trial and error. A simple method to estimate an appropriate value of the splitting factor is the following:

1. Simulate s3 using a splitting factor equal to 1.
2. Let us call Δ the obtained average statistical uncertainty as reported by PRIMO.
3. Define $n = \Delta/\delta$, where δ is the desired statistical uncertainty.
4. Let us call f the ceiling of n^2, that is, $f = \lceil n^2 \rceil$. Then f is the splitting factor required for the simulation of s3.
5. Re-run s3 using the recently calculated splitting factor f.

However, bear in mind that:

- The simulation of s3 with a splitting factor f will last on average a time ft, where t is the time that it took to simulate s3 with a splitting factor of 1 (assuming all the other conditions equal).
- It is possible that despite using the splitting factor f the desired statistical uncertainty is not reached. If this happens it is because the tallied phase-space file is not large enough to attain the requested uncertainty under the given simulation conditions. Possible solutions

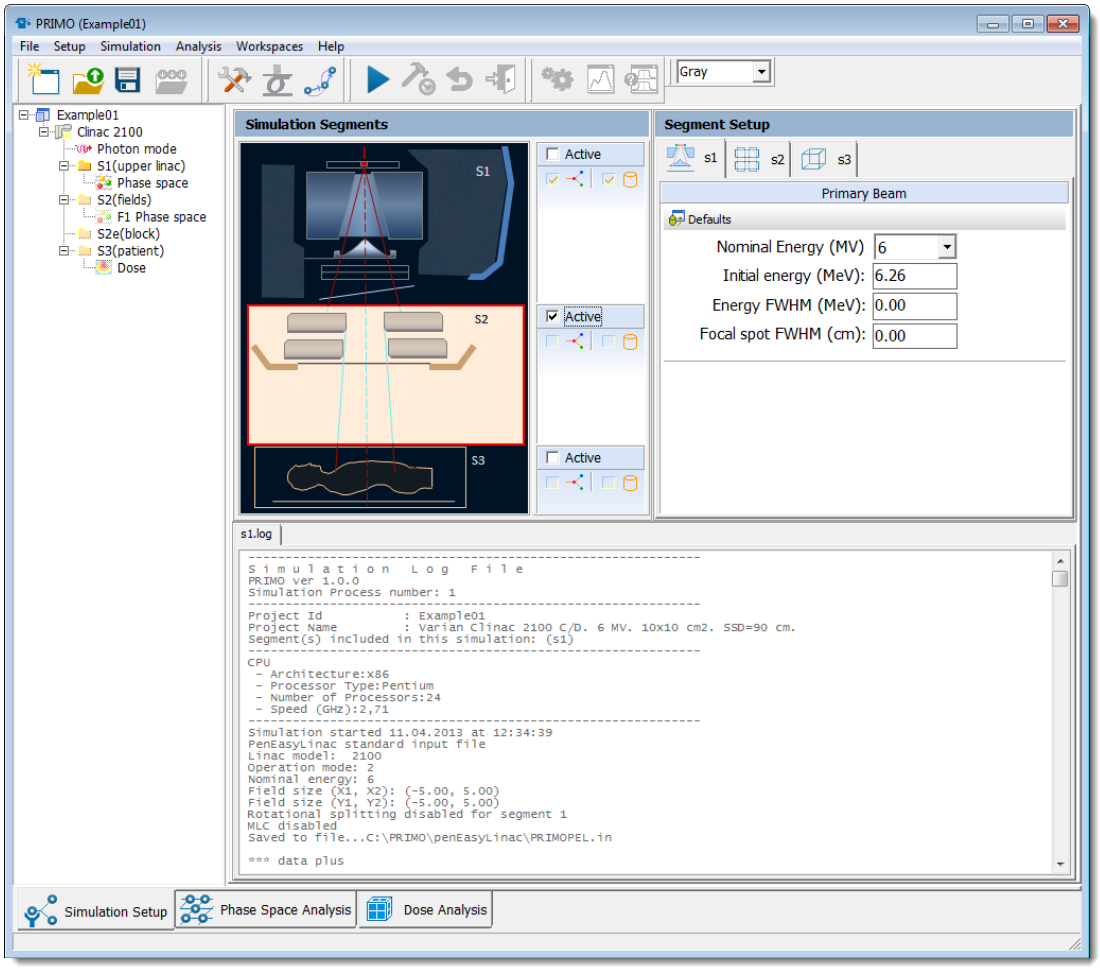


Figure 5.7: Main PRIMO window just before launching the simulation of s2.

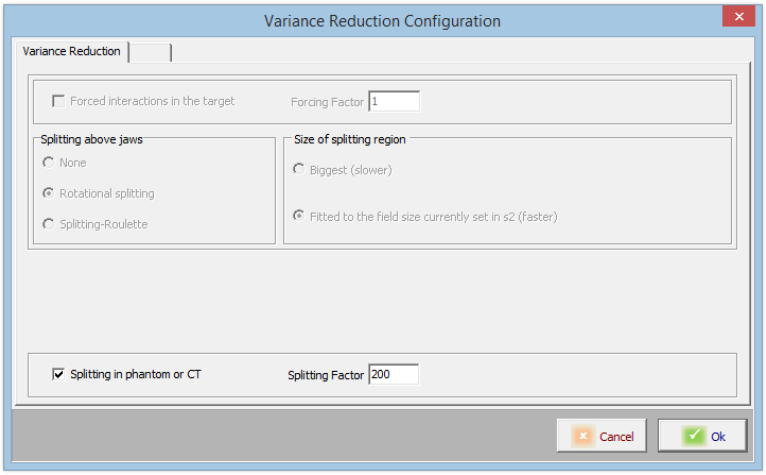


Figure 5.8: Variance reduction for s3.

to this problem are to tally a larger phase-space file or to make the simulation conditions at s3 less demanding (*e.g.*, use a larger bin size).

Notice 5.2 All statistical uncertainties reported by PRIMO are given to 2 standard deviations ($\pm 2\sigma$ rule). ■

After saving the project the simulation of s3 can be launched (figure 5.9).

Once the simulation of s3 is completed PRIMO will return to its main window by clicking the open door button, as usual.

5.1.2 Analysis of results

In this section the data analysis screens are depicted. In this example the analysis is shown at the very end of the simulation of all segments for clarity reasons. However, the analysis of the results produced at each segment can be done immediately after the simulation of the segment has been completed.

For analyzing the phase-space files tallied at s1 and s2 the Phase Space Analysis tab is clicked in the main PRIMO window and the desired phase-space file is dragged from the logical tree and dropped in the empty area to its right (figures 5.10 and 5.12).

On each of the graphical panels in the Phase Space Analysis tab it is possible to right click the figure and further options are offered to the user. Below the graphical panels two tabs give statistical information about the analyzed phase-space file, including data about the statistical weight of tallied particles.

By clicking the plot button in the main PRIMO window it is possible to plot profiles of the spatial distribution of particles in the phase-space file (figure 5.11). The drop-down menu in the upper part of the main PRIMO window, which by default shows *Gray*, allows to change the color scale used for showing maps. A *Rainbow* scale better reveals the spatial extend of the phase-space file.

Simulation details from the phase-space files can be viewed by right-clicking the phase-space file icon in the logical tree and then left-clicking the *Properties* button.

The dose distribution can be analyzed by selecting the Dose Analysis tab and then dragging the dose icon from the logical tree and dropping it in the blank area. After reading the tallied spatial dose distribution dose maps in the transverse, sagittal and coronal planes are shown.

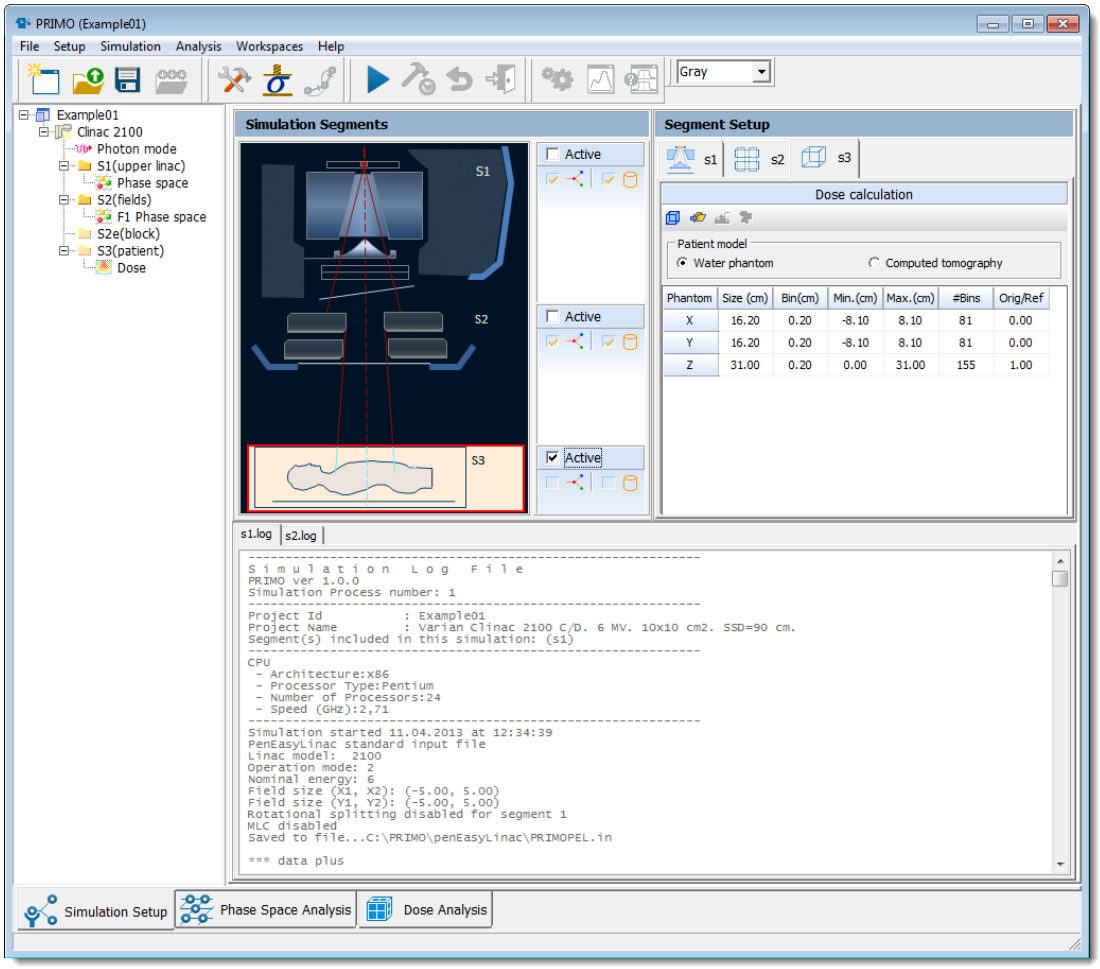


Figure 5.9: Main PRIMO screen just before launching the simulation of s3. Segments s1 and s2 appear as simulated and both with a phase-space file tallied.

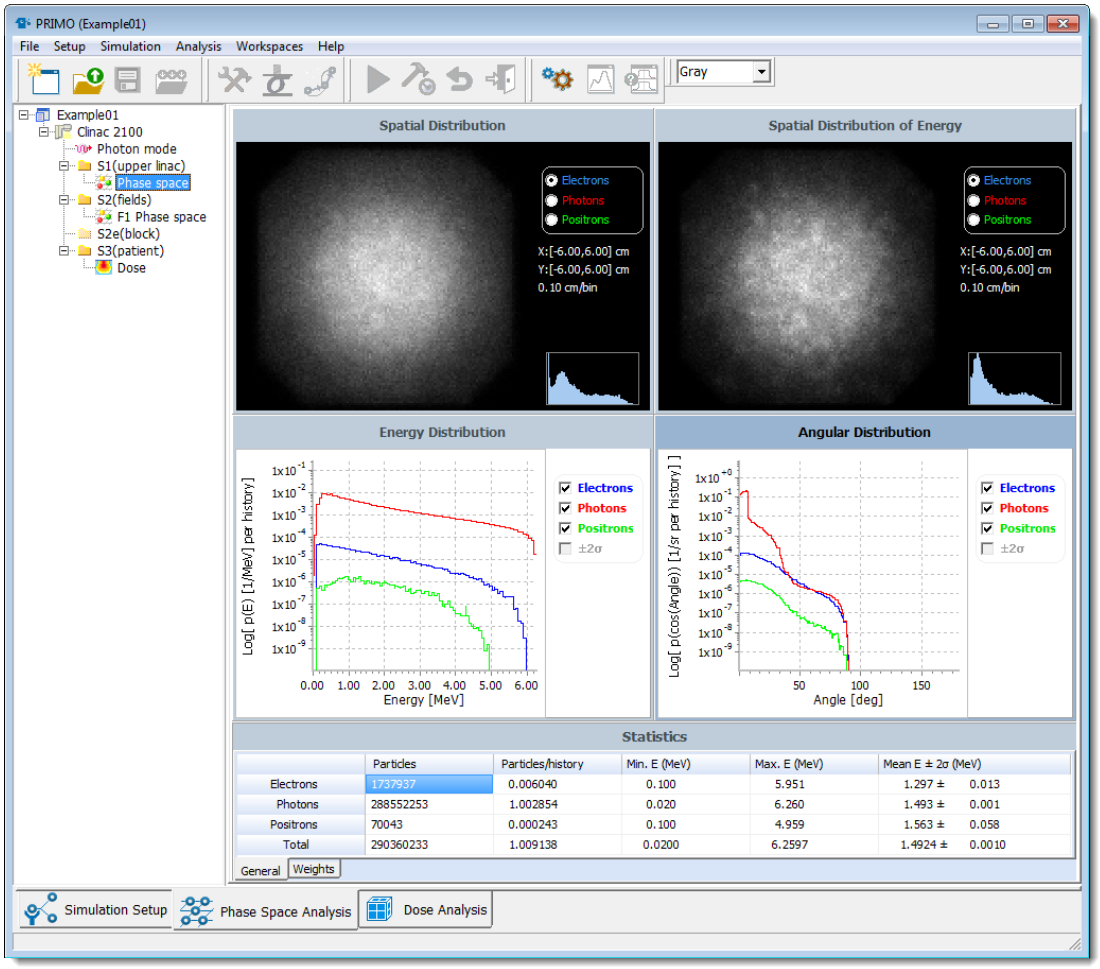


Figure 5.10: Analysis of the phase-space file produced at the downstream end of s1. For this figure the spatial and energy distribution maps show the electron contamination. The energy and angular distribution plots are depicted in semi-log scale (option available by right clicking on the figure).

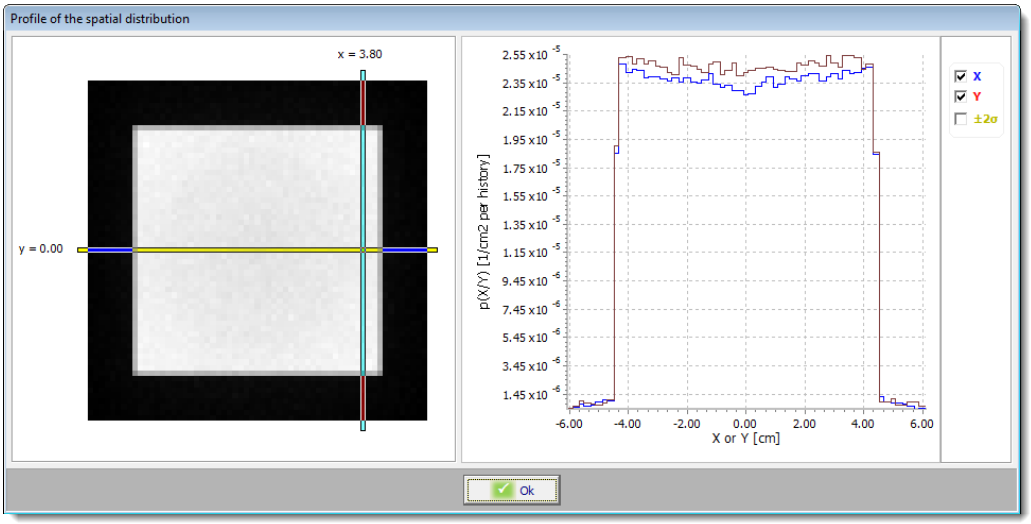


Figure 5.11: Profiles of the spatial distribution of photons in the phase-space file obtained with the simulation of s2.

Additionally, dose distributions along x, y and z are plotted. The position of these variables used for the profiles can be modified by dragging the handles on each of the aforementioned dose maps.

In the Dose Analysis window it is also possible to right click over any of the four graphical panels in order to obtain menus with further options. For example, it is possible to change the view of the dose maps from color wash to isodoses (figures 5.13 and 5.14).

Comparison with experiment

For the simulation of s1 the default primary beam parameters were used, that is, a monoenergetic pencil beam electron source of 6.26 MeV. PRIMO has built-in analysis tools for comparing experimental dose profiles with the simulated spatial dose distribution. An experimental percentage depth dose and a lateral profile measured on a Varian Clinac iX are found inside the directory `Experiment` distributed with the file `Example01.zip`. To load these profiles into PRIMO for comparison purposes click the *Compare* button on the main window. It must be stressed that the primary beam parameters of the simulation have not been tuned for the particular linac used for measuring the experimental data. The reason for this is twofold. First, we are interested in assessing how PRIMO shows the discrepancies between the two datasets. Secondly, we show how the default beam parameters are a reasonable choice for most linacs. In this case, almost 90% and more than 95% of the analyzed data points exhibited a gamma index (section 4.3.6) smaller than 1 with a passing criterion of 1%–1 mm in the depth dose and lateral profile curves, respectively (figures 5.15 and 5.16).

For importing the experimental data the button for dose curve comparison in the main PRIMO window is clicked while this window is showing the simulated dose maps. Then the experimental percentage dose distribution located in the directory

`c:\PRIMOexamples\Example01\Experiment` is loaded (figure 5.15).

Similarly, the same procedure is followed for loading the experimental lateral profile (figure 5.16).

It is possible to export most of the plotted curves as text files. The exported text files can be used with software for data analysis, publication quality plotting, etc. All exported data files

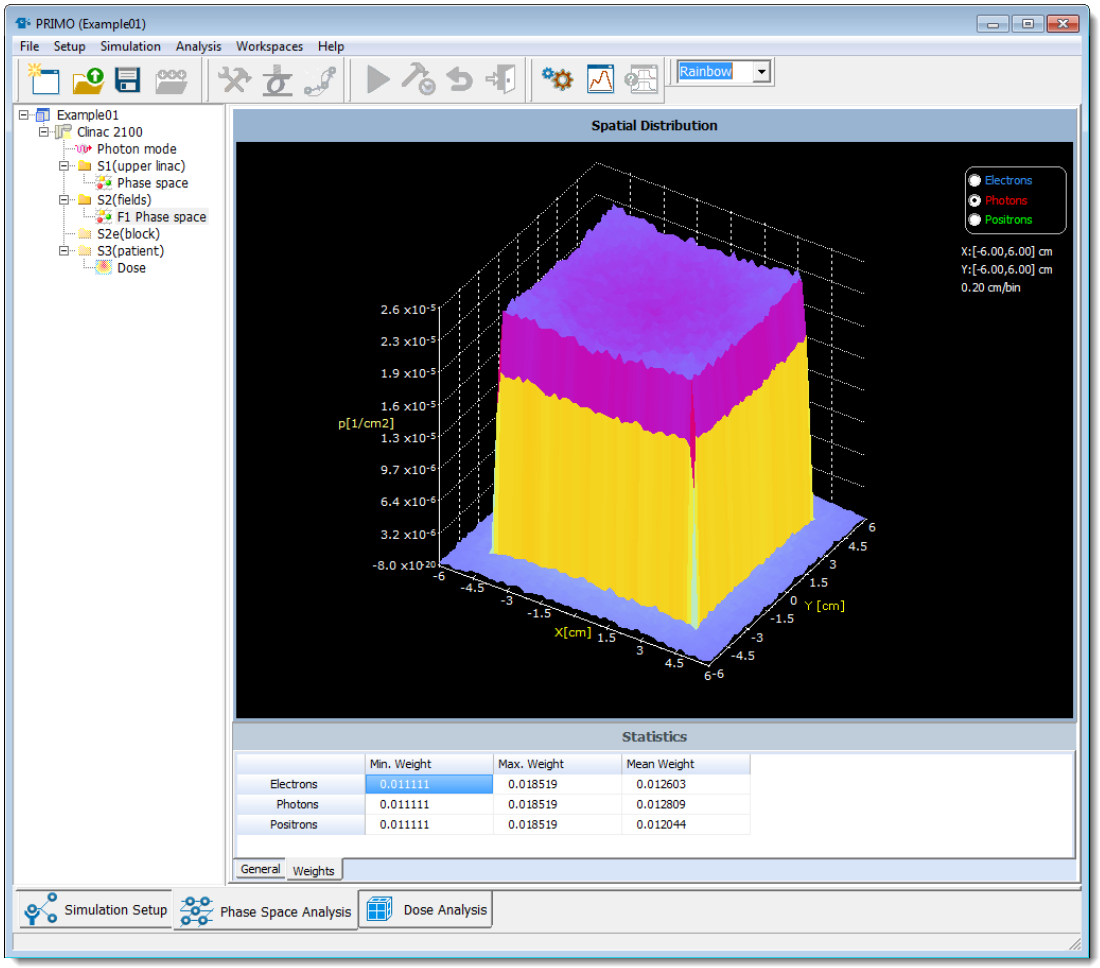


Figure 5.12: Analysis of the phase-space file produced at the downstream end of s2. For this figure the spatial distribution map is shown as a surface. The panel containing the surface plot has been maximized. The figure can be rotated on the screen using the mouse (left button pressed).

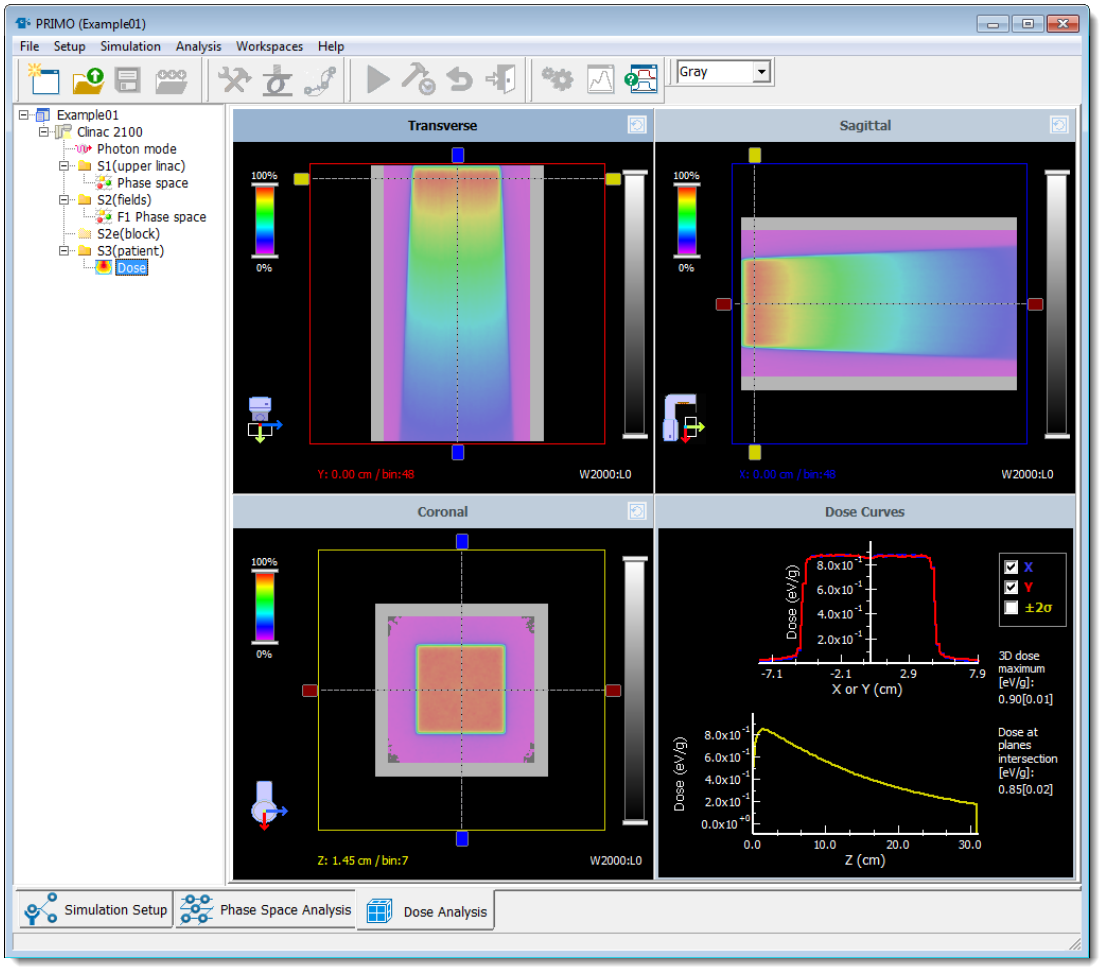


Figure 5.13: Dose maps shown with color wash.

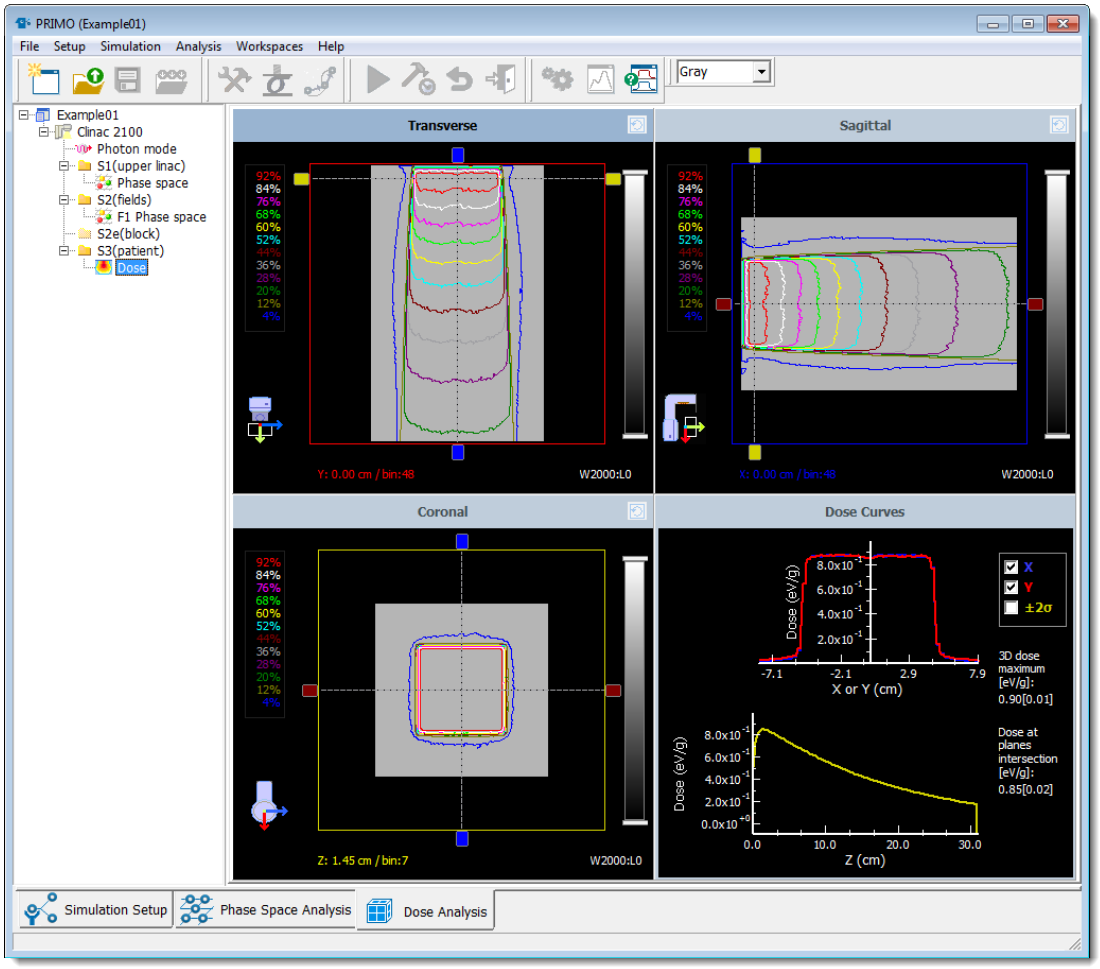


Figure 5.14: Dose maps shown with isodose curves. This option is accessible through the menu obtained by right clicking on any of the three dose maps.

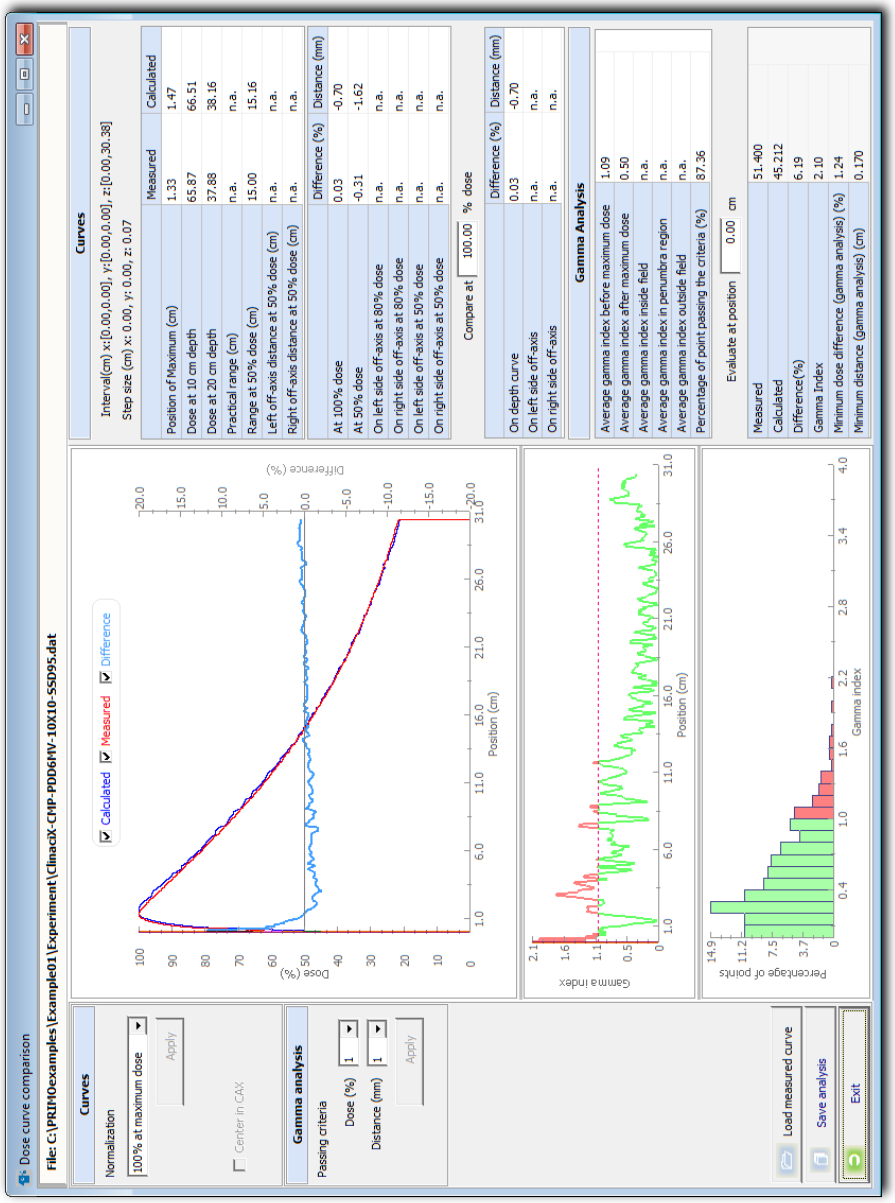


Figure 5.15: Comparison of experimental and simulated percentage depth doses.

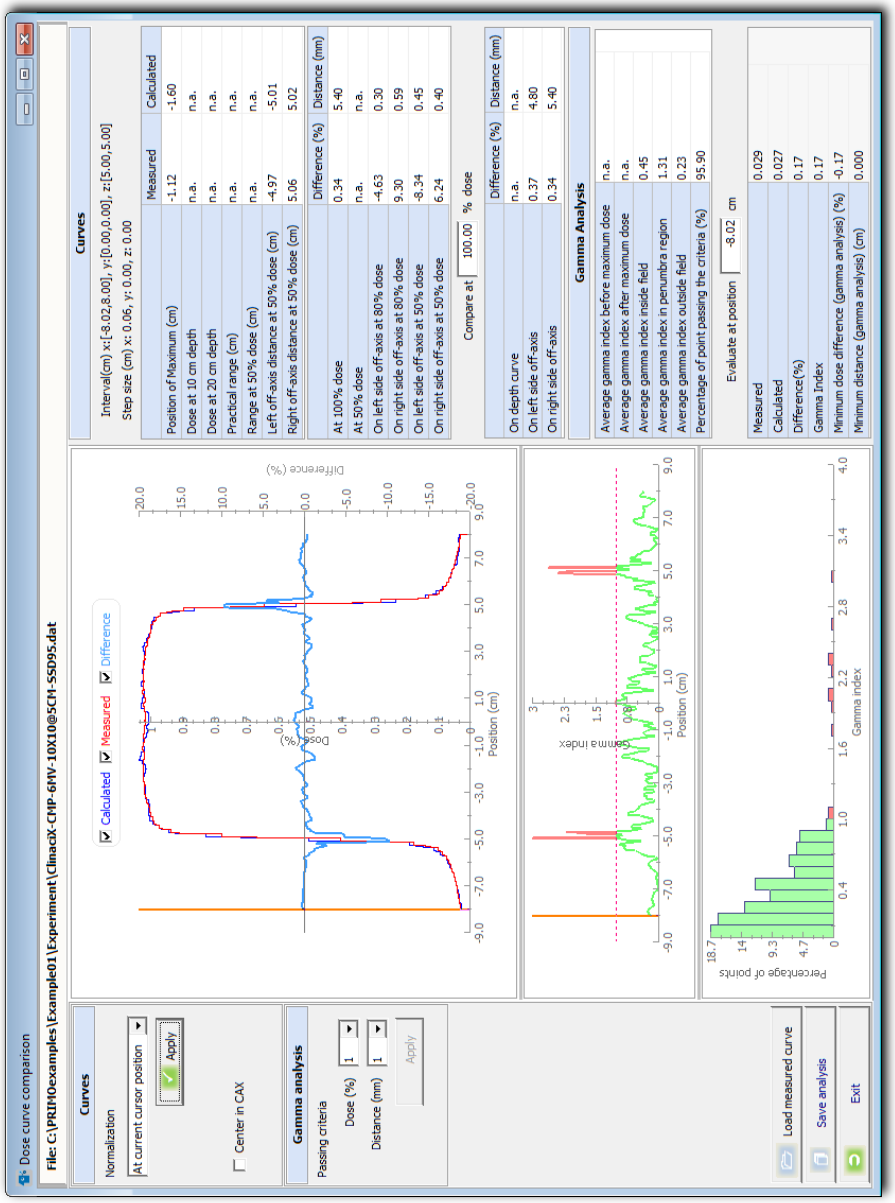


Figure 5.16: Comparison of experimental and simulated lateral profiles.

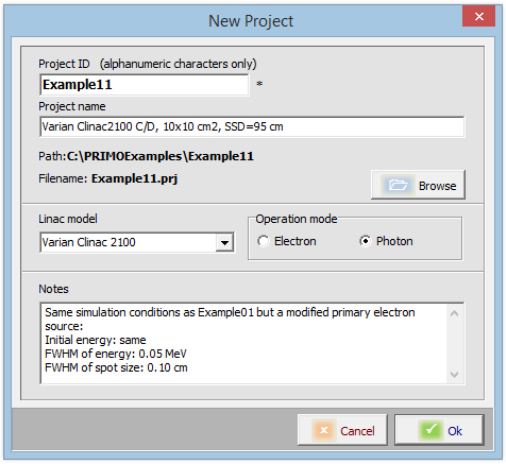


Figure 5.17: New Project window for the simulation with new primary source parameters.

follow the syntax of the Gnuplot program[1].

R The names assigned to exported data files must have the extension `.dat` if these files are to be later read by PRIMO.

Comparison with another simulation

It is possible to compare dose profiles from two simulations. In order to do so the desired profiles must be exported from one simulation as data files. Then these exported profiles will be read by another simulation as *experimental* data.

To exemplify this feature another simulation of the same linac under the same conditions was run and named Example011. The only difference between Example01 and Example011 is that the latter has a primary electron source defined with a Gaussian distribution of the energy and a finite focal spot size (figures 5.17 and 5.18).

The simulation process followed for Example011 is the same that has been already described. Once the dose distribution has been tallied and it is being inspected, it is necessary to right click over the dose profiles shown in the lower-right panel of the Dose Analysis tab (figure 5.19). It is possible to save the depth dose curve and the lateral profiles along x and y (figure 5.20). The exported files must have the `.dat` extension.

When this step is completed the simulation Example01 is opened again using the *Open* button in the main PRIMO window.

R The Example011 files are not distributed in the PRIMO project website. However, the exported profiles can be found in the directory `Experiment` under the names of `Simulated-PDD.dat`, `Simulated-LatX.dat` and `Simulated-LatY.dat`.

The final step is to import the simulated data as it has been done for the experimental data in section 5.1.2 (figures 5.21 and 5.22).

Notice 5.3 PRIMO assumes that the imported data for a comparison is the reference data set. Consequently, data from the active simulation is the evaluated data set. Notice that the gamma test is not symmetric with respect to the reference and the evaluated data sets. ■

[1] `http://www.gnuplot.info`

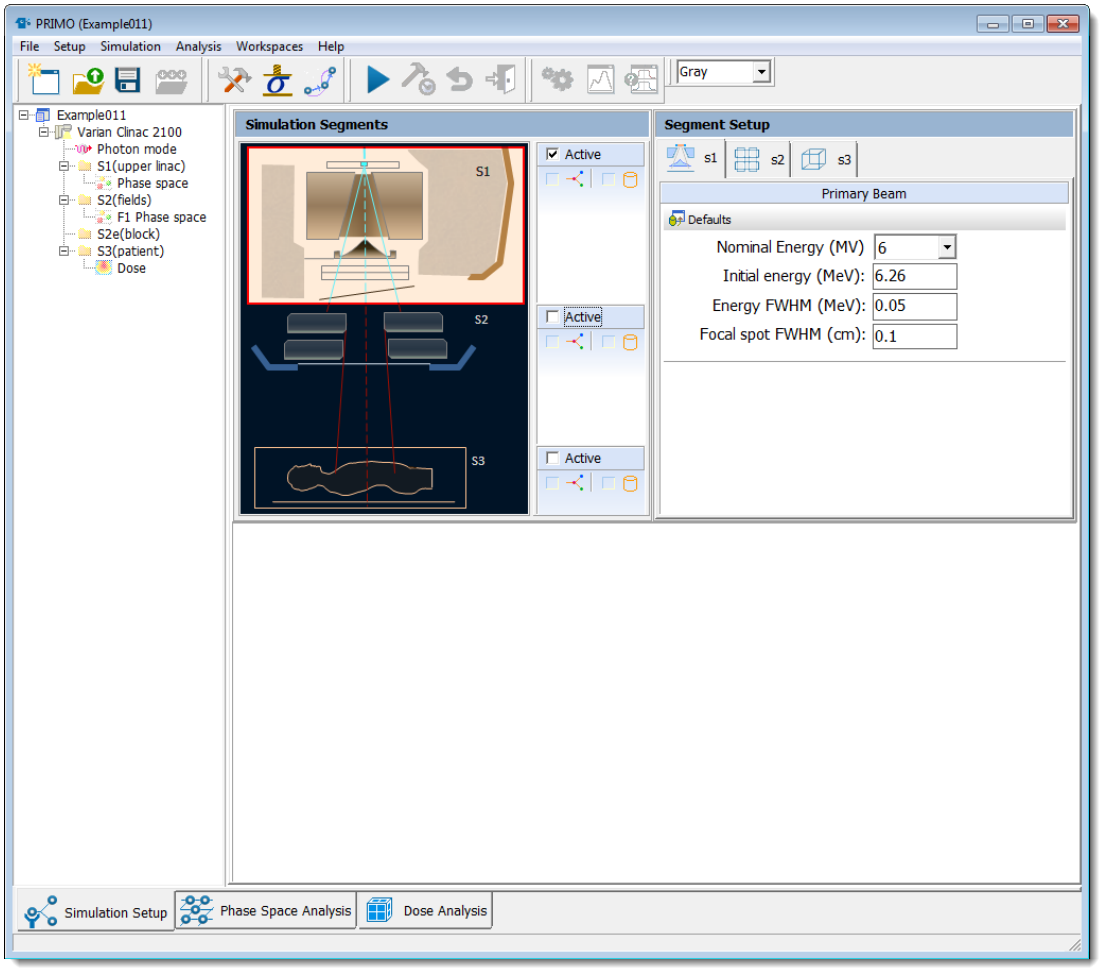


Figure 5.18: Main PRIMO screen before launching the simulation of s1 with the new primary source parameters.

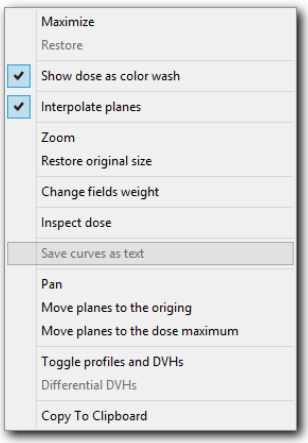


Figure 5.19: Menu obtained when the dose profiles are right-clicked. The mouse pointer is showing the option to save curves as text files.

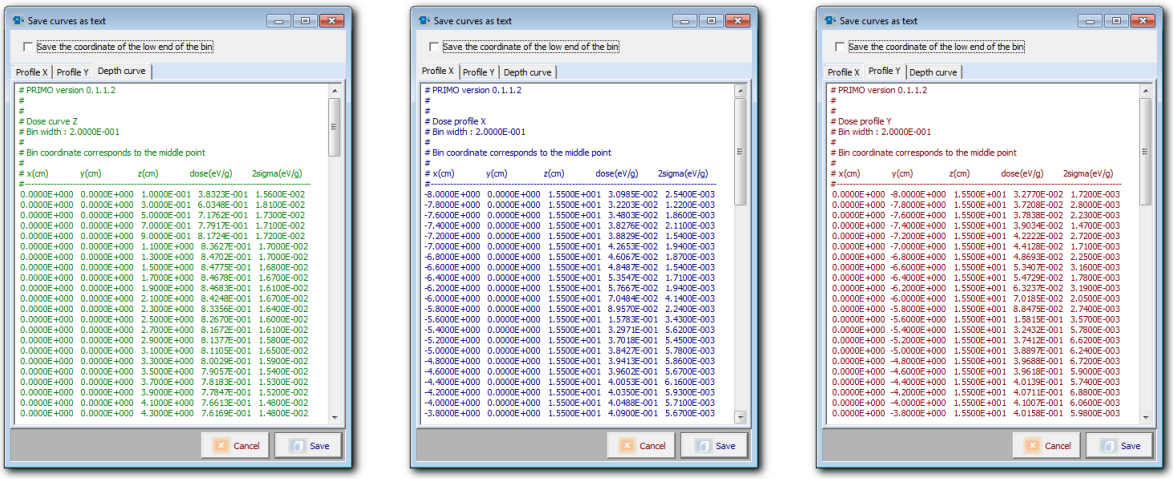


Figure 5.20: Screens showing how to export dose profiles as text files.

5.2 Example 02: Electron reference field

This example covers the simulation of an Elekta SL15 linac in electron mode. The nominal energy is 15 MeV and the field is conformed by the 20×20 cm^2 electron applicator.

Simulation of s1 in any linac operating in electron mode is usually very fast. It is so fast that sometimes it does not pay off tallying a phase-space file for that segment. Instead, it could be more efficient to simulate the whole linac at once. Whether or not is more convenient to simulate each segment separately is something to be decided by the user depending on the particular problem under consideration.

In this example we shall simulate the linac in a single simulation step and in a second step we shall tally the absorbed dose in a water phantom. Thus, the simulation will be performed in the form $(\mathrm{s1} + \mathrm{s2} + \mathrm{s2e}, \mathrm{s3})$ (section 3.7).

Notice 5.4 In order to reduce the file size of `Example02.zip` the phase-space file of this example is not included among the distributed files. ■

5.2.1 Simulation setup and execution

The simulation conditions entered in the simulation setup screens are the following:

Linac Elekta SL15 (in PRIMO Elekta SL)
Mode Electron
Nominal energy 15 MeV
Initial energy 15.10 MeV
Energy FWHM 0.8 MeV
Focal spot size FWHM 0.7 cm
Field size 20×20 cm^2 electron applicator
SSD 95 cm
Bin size $0.2 \times 0.2 \times 0.2$ cm^3
Dose tallying volume $26.2 \times 26.2 \times 12.0$ cm^3 (water phantom)
Stop condition Time, 25,200 seconds[2]
Refresh time 600 seconds

[2]This example has been simulated for a long time for the purpose of this manual. Users can obtain clinically acceptable uncertainties in a fraction of this time.

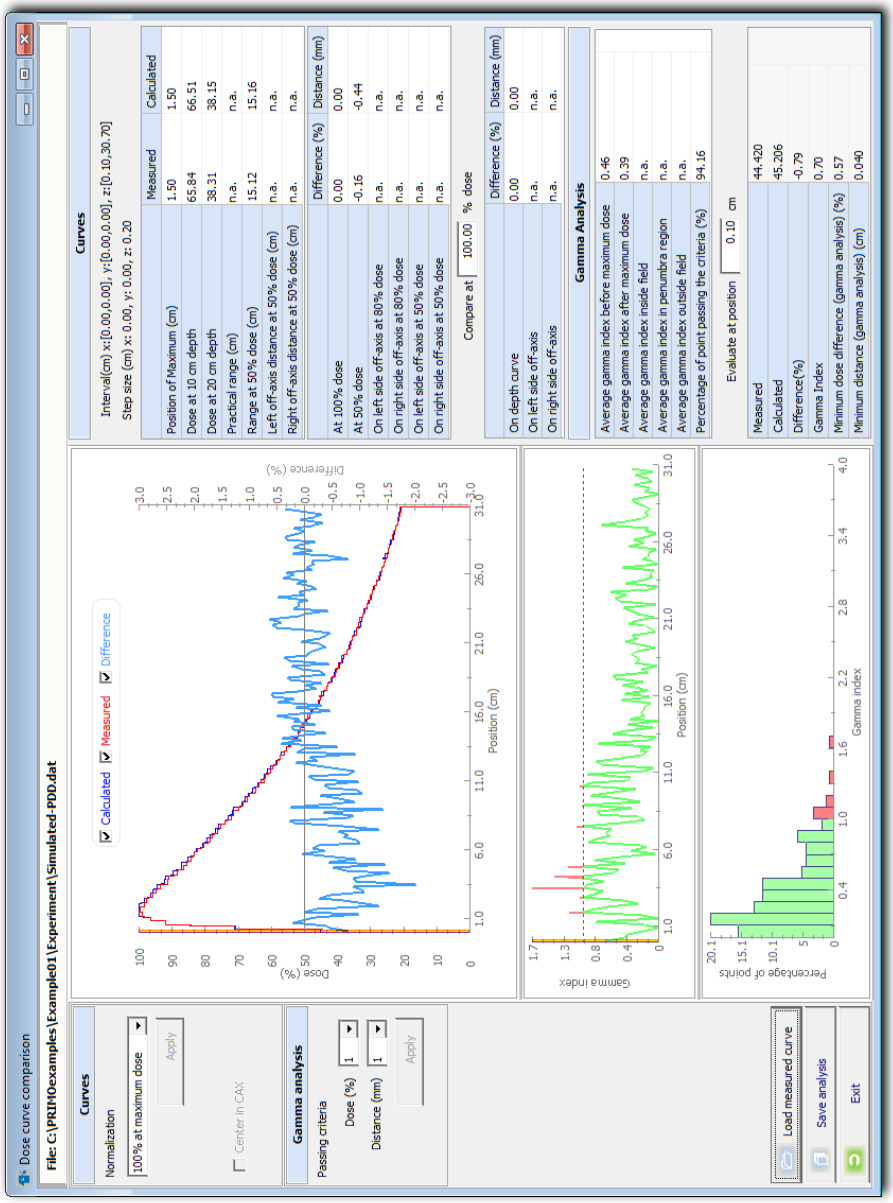


Figure 5.21: Depth dose profile comparison between simulations Example011 and Example01.

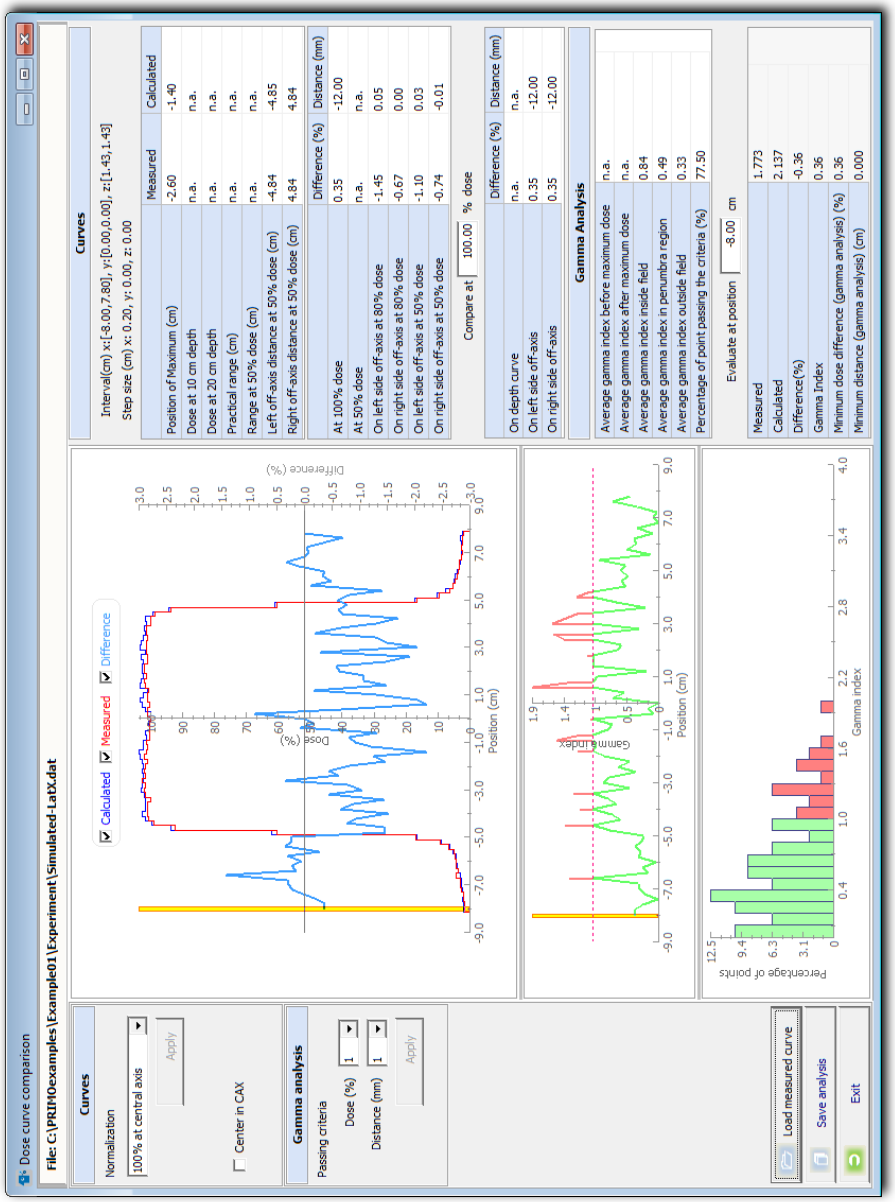


Figure 5.22: Lateral dose profile along x. Comparison between simulations Example011 and Example01.

Number of parallel processes 12 cores[3]
Variance reduction for s3 Splitting with factor 25

R In order to obtain a tallying binned region with a column of bins centered with respect to the central beam axis choose an arbitrary bin size in each direction and set the total size of the binned region as the bin size times an arbitrary odd number. In this example the binned region size is 26.2×26.2 cm^2 and the bin size 0.2×0.2 cm^2.

R There are no user-selectable variance-reduction techniques for segments s1, s2, s2e in electron mode.

Notice 5.5 The maximum number of bins in a water phantom is 10^7. ■

Varian and Elekta linacs do not use the jaws in the same way when irradiating in electron mode with an electron applicator. Varian linacs have preset positions of the jaws for every combination of applicator size and nominal energy. These preset positions, far apart from the beam path, are used in the simulation. Elekta linacs use the jaws to modify the beam. The field conformed by the jaws is similar to the field conformed by the electron applicator. The position of each jaw for every combination of applicator size and nominal energy is adjusted while commissioning the linac, since small changes in the positions of the jaws have an effect in the dose distribution. For that reason, PRIMO allows jaws to be moved when using electron mode with an applicator. The program suggests for each combination of applicator size and nominal energy a reasonable position that must be further adjusted in order to match the dose distribution of the simulated Elekta linac.

Notice 5.6 Jaw positions for Elekta linacs in electron mode must be adjusted by the user for each combination of applicator size and nominal energy in order to match experimental dose profiles. ■

The following positions of the jaws were used in the simulation:
X1 11.7 cm
X2 11.7 cm
Y1 13.0 cm
Y2 13.0 cm

Notice that the field defined by these values is not square.

The Elekta recommendation for SSD when measuring dose profiles in electron mode is 95 cm[4]. However, the lowermost surface of all Elekta applicators is also at 95 cm from the primary source. In order to avoid contact of the water with the electron applicator the experimental measurements are performed at a SSD slightly larger. For the same reason, the phase-space file tallied at the downstream end of s2e is positioned at $z = 95.1$ cm. The minimum distance allowed between the phase-space file and the surface of the water phantom is 0.1 cm. Consequently, the minimum value that can be entered for SSD is 95.2 cm.

Notice 5.7 Due to geometrical constrains the minimum distance allowed in PRIMO between a phase-space file and the surface of a water phantom is 0.1 cm. ■

[3] Users running this example by their own should adapt the number of processors so as to not exceed the maximum number of processing cores available in their computer.

[4] For further information see section 2.2.3.1 of "Elekta Digital Linear Accelerator. Custormer Acceptance Tests", 1024313 01, Elekta Limited, UK, March 2012

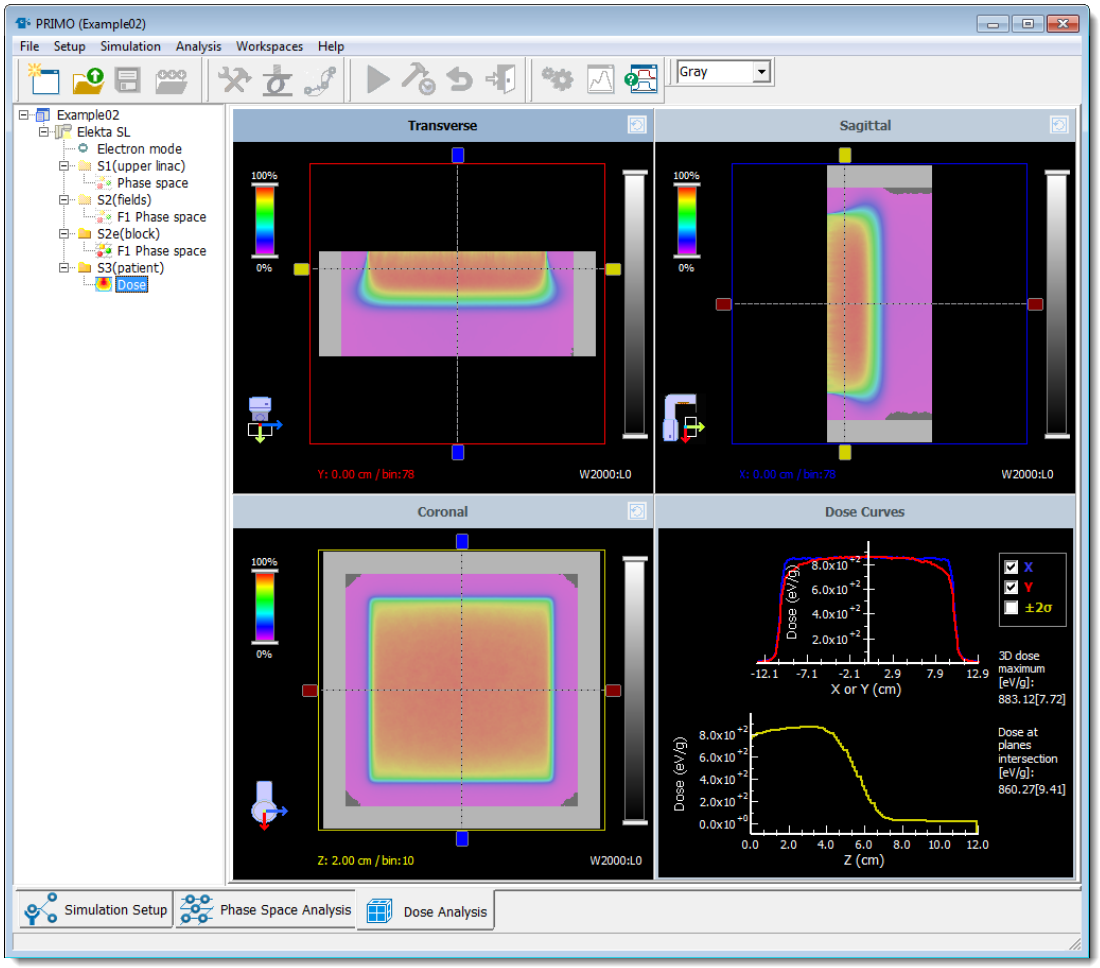


Figure 5.23: Dose maps and dose profiles obtained for the simulation of an Elekta SL15 operating in electron mode. The nominal energy is 15 MeV. The electron applicator size is 20×20 cm^2.

5.2.2 Analysis of results

The analysis procedure is the same as described for the previous example. Figure 5.23 shows the dose maps and the dose profiles obtained. It can be seen that the x and y lateral profiles are slightly different due to the different aperture of the corresponding jaws.

5.3 Example 03: TrueBeam

This example presents the simulation of a Varian TrueBeam linac operating in free flattening filter mode at 6 MV. The geometrical details of the TrueBeam linac corresponding to the s1 region are undisclosed by the vendor. Instead, Varian gives access to TrueBeam owners to a set of phase-space files tallied at the downstream end of s1. These phase-space files are recorded according to the IAEA format and, therefore, PRIMO can read them and simulate the radiation transport downstream. Since the phase-space files are proprietary confidential information from Varian Medical Systems they are not distributed in the example. The example only includes the absorbed dose distribution tallied in a water phantom obtained from the simulation of the aforementioned phase-space files.

The scope of this example is to illustrate the steps for simulating a TrueBeam linac using

external phase-space files. These steps are the same in case of simulating any other external phase-space file written in IAEA format.

Notice 5.8 Users willing to simulate this example by their own must have access to the TrueBeam phase-space files distributed by Varian. ■

R After unzipping the `Example03.zip` file inside `c:\PRIMOexamples`, the project files will be found in `c:\PRIMOexamples\Example03\TB6FFF40\`.

For the simulation of TrueBeam it is necessary to start a new project choosing the Clinac 2100 C/D in photon mode as the linac to be simulated. The nominal energy chosen must be either 6 or 10 MV, depending on the nominal energy of the phase-space file.

R To simulate a TrueBeam a Varian Clinac 2100 C/D must be chosen.

It is recommended to set the conditions for s2 and s3 before actually starting the simulation. For this example the simulation parameters were set to:
Linac TrueBeam (in PRIMO Varian Clinac 2100 C/D)
Mode Photon
Nominal energy 6 MV
Field size 40×40 cm^2 electron applicator
SSD 100 cm
Bin size $0.2 \times 0.2 \times 0.2$ cm^3
Dose tallying volume $46.2 \times 46.2 \times 31.0$ cm^3
Stop condition 10^9 umber of histories [5]
Refresh time 600 seconds
Number of parallel processes 12[6]
Variance reduction for s3 Splitting with factor 25

Only `s1` must be checked as active. After saving the project, the button *Import PSF* becomes active. After clicking this button a browser window will appear. The phase space of TrueBeam is distributed in several files. The user can choose to simulate as many files as desired. For this example all files were selected.

Notice 5.9 Only phase-space files tallied at the downstream end of s1 can be imported. ■

Once the phase-space files have been imported, the program shows s1 as if it had been simulated in PRIMO. The simulation of the rest of the segments proceeds as usual. Figure 5.24 shows the dose map obtained.

Warning 5.1 The phase-space files distributed by Varian for the simulation of TrueBeam linacs do not contain a field called the incremental shower number for each tallied particle. Therefore, the uncertainties estimated by PRIMO are only an approximation whose accuracy is unknown (section 3.5).

In this example we use a diagonal lateral profile to compare the simulated dose distribution with the experimental data. In the Dose Analysis tab click the *Compare* button to import the dose profile stored in the `Experiment` directory within the example. PRIMO identifies, by means

[5] This arbitrarily large number guarantees that all histories of the distributed phase-space file at s1 are used.
[6] Users running this example by their own should adapt the number of processors for not exceeding the maximum number of processing cores available in their computer.

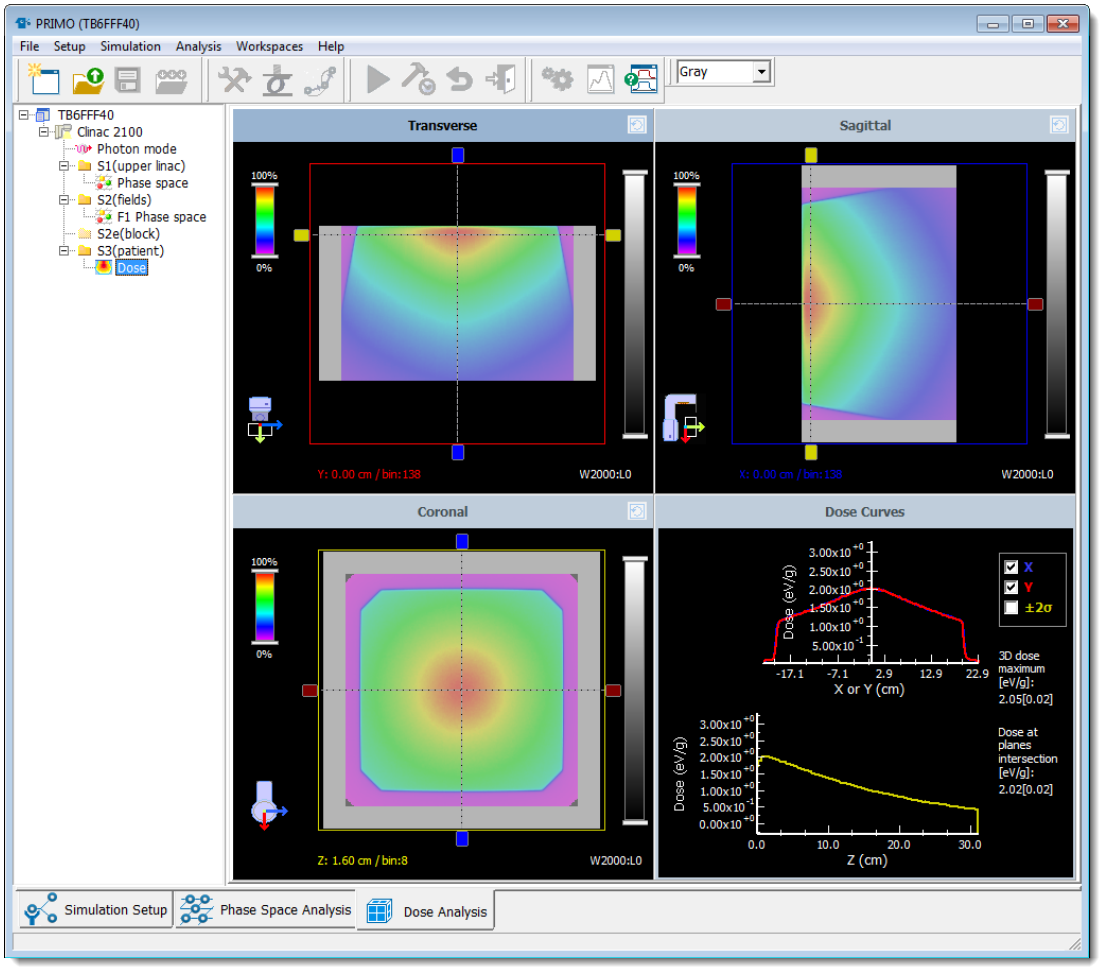


Figure 5.24: Dose maps and dose profiles obtained for the simulation of a TrueBeam linac operating in free flattening filter mode at 6 MeV. The field size is 40×40 cm^2.

of the point coordinates, that the data correspond to a diagonal and performs the comparison (figure 5.25).

> **Warning 5.2** Phase-space files have been removed from the distributed data in this example. Although PRIMO shows the phase-space file icons in the logical tree as available, do not try to analyze them since dragging them into the Phase Space Analysis tab will produce an error.

PRIMO can compare simulated data with experimental diagonal profiles.

5.4 Example 04: Dose calculation in a computerized tomography

In this example the creation of a typical radiotheraphy plan for the irradiation of the whole brain with two parallel-opposed fields is described. Since the CT study of the patient and the delineated structures are not distributed with the example, users will not be able to repeat the steps related to data import. Also, the phase-space file of the segment s1 is not included in the files of this example, so, although it appears in the *Project Tree* as active, dragging it to the phase-space analysis window will produce an error message.

5.4.1 Simulation of segment s1

The segment s1 was simulated to create a phase-space file with the following conditions:
Linac Varian Clinac 2300
Mode Photon
Nominal energy 6 MV
Stop condition Histories
Number of histories 500,000,000
Variance reduction method Rotational splitting[7]

5.4.2 Field setup

Prior to field setup it is necessary to import the CT volume. This is done in the setup tab s3, selecting the option *Import a CT volume*. The next step is to create the structures. In this case, the structures were delineated in the Eclipse Treatment Planning System (Varian Medical Systems), saved in a DICOM file and imported into PRIMO.

Two fields were added using the option *Add new field* and configured using the option *BEV Edit*. The isocenter and jaws positions were set according to the shape of the PTV (in this case the whole brain). The configuration of the fields is shown in figure 5.26.

The segment s2 was simulated to produce two phase spaces (one per field). All particles in the source phase space were simulated (approximately 3.1×10^8). The result of the analysis of the phase-space file of field 1 is shown in figure 5.27.

5.4.3 Construction of the voxelized geometry

The voxelized geometry is created by associating a material and a mass density to each voxel in the CT volume. This is done in the s3 tab with the option Calculate densities and materials. Four materials were considered for this example, namely, air, soft tissue, inner bone and compact bone. The default CT scanner calibration curve was used (figure 5.28).

[7] Although it had been more efficient for this energy to use splitting-roulette, rotational splitting was chosen to show that is also a suitable variance-reduction technique.

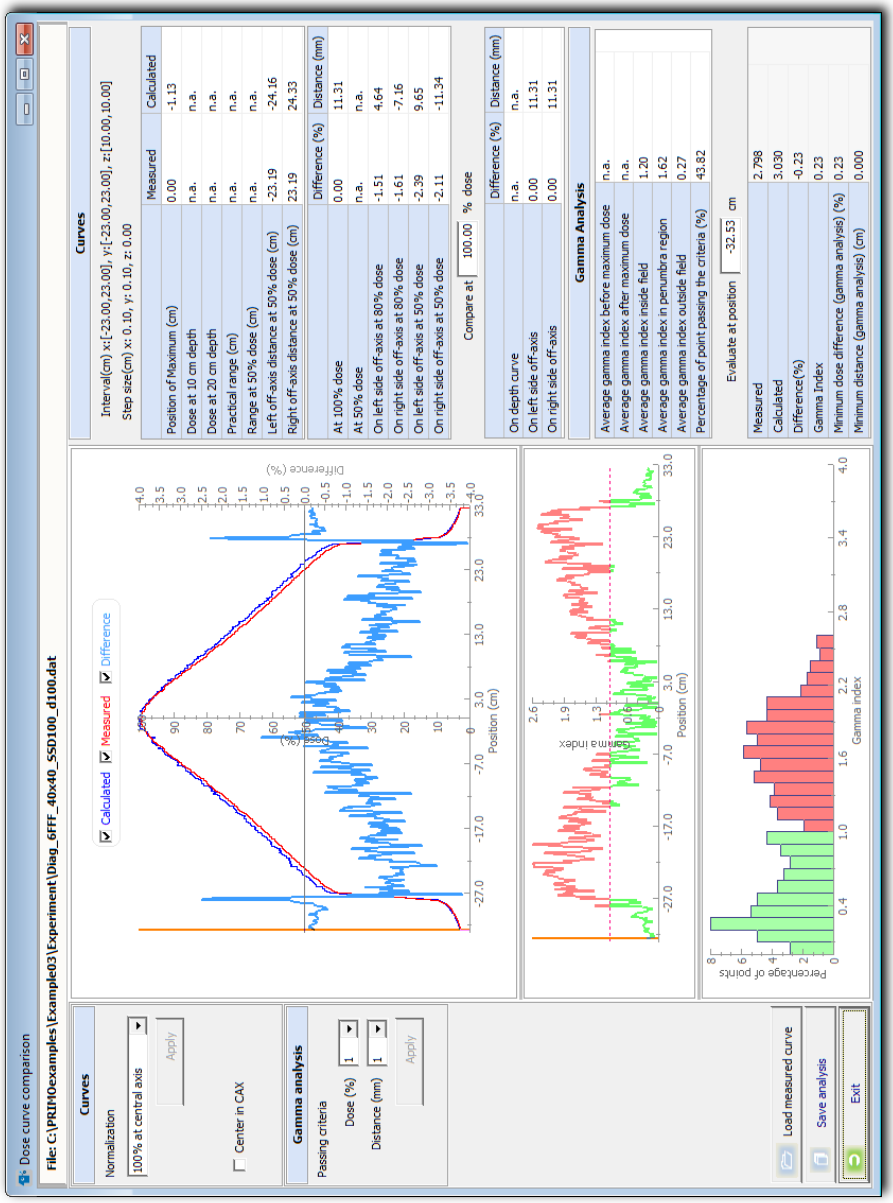


Figure 5.25: Comparison of the experimental and simulated data through a diagonal lateral profile.

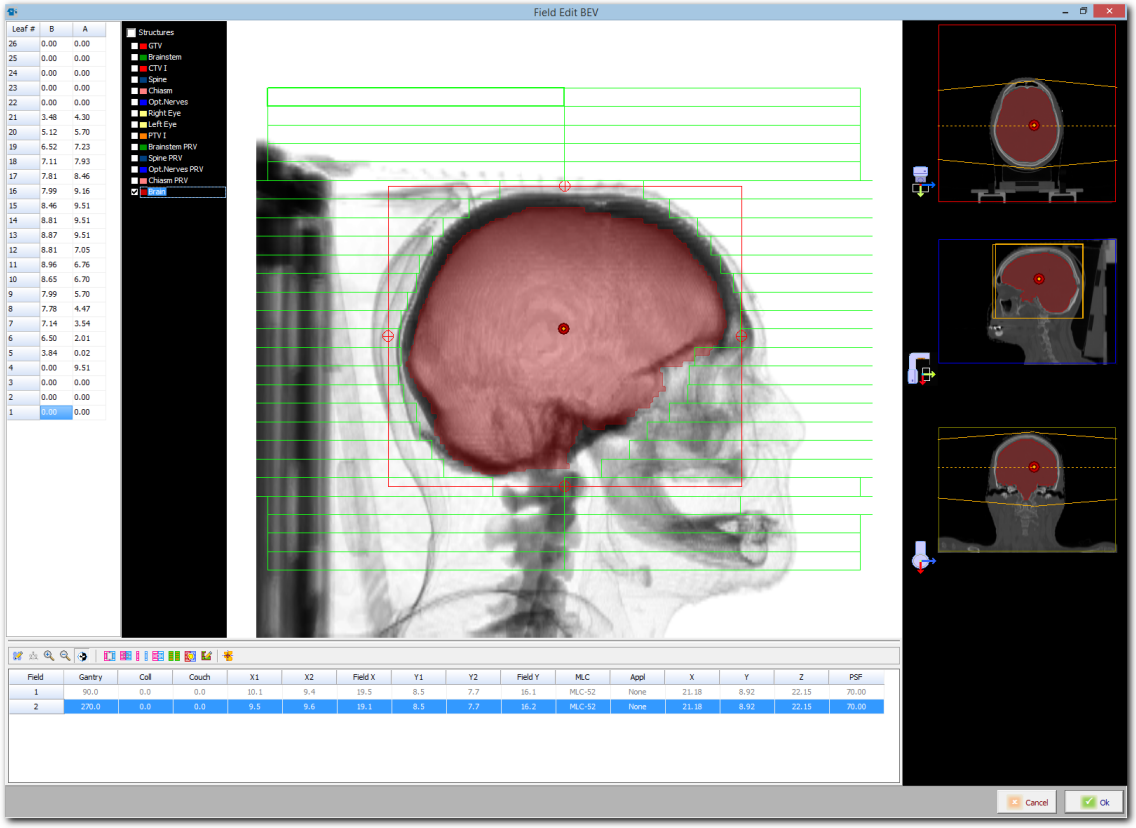


Figure 5.26: Parameters of the two parallel-opposed fields as seen in the BEV Edit dialog.

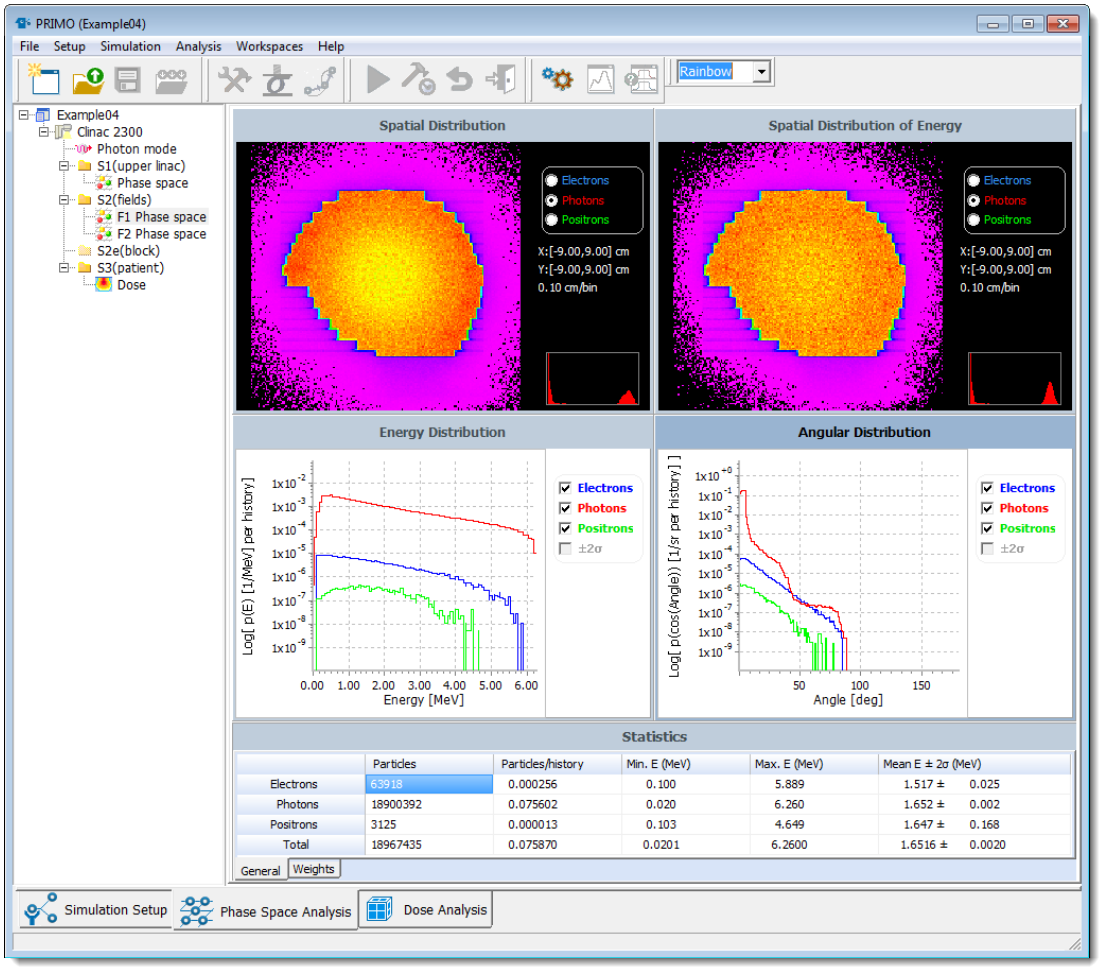


Figure 5.27: Analysis of the phase space created on the simulation of field 1.

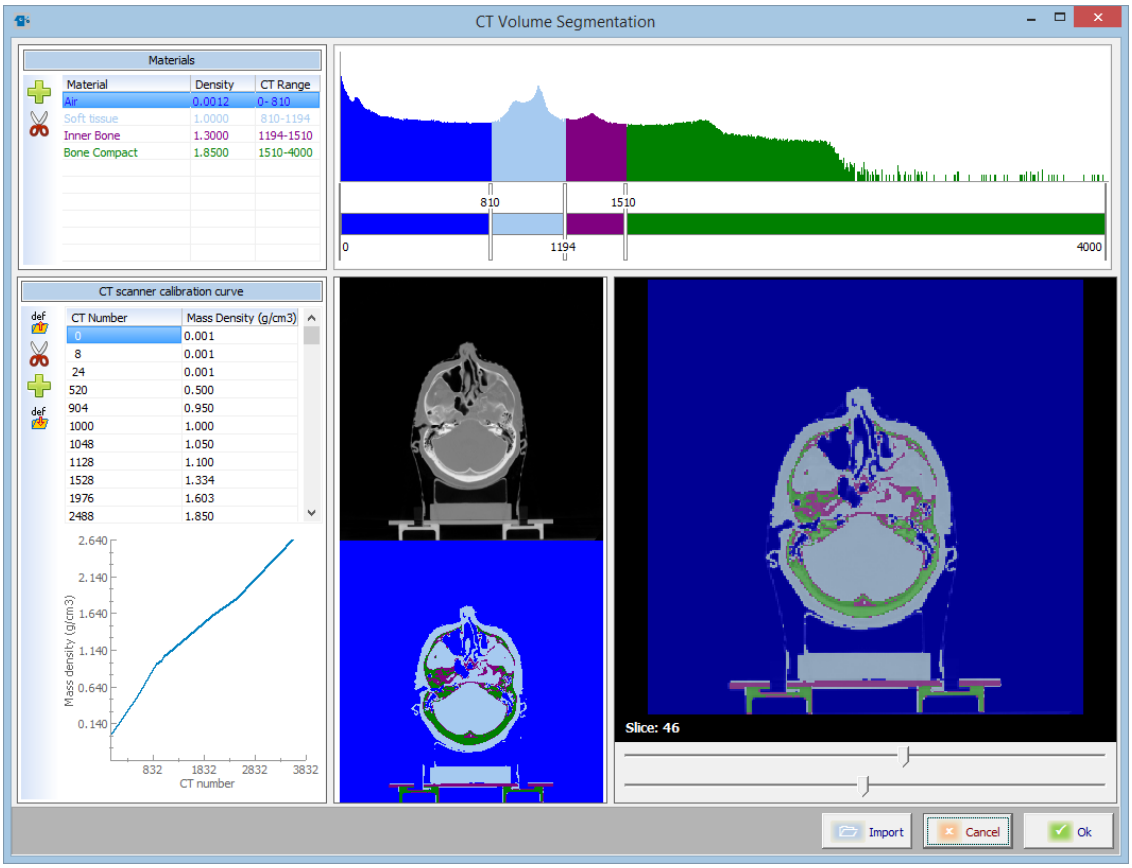


Figure 5.28: Construction of the voxelized geometry. Materials and densities used are shown.

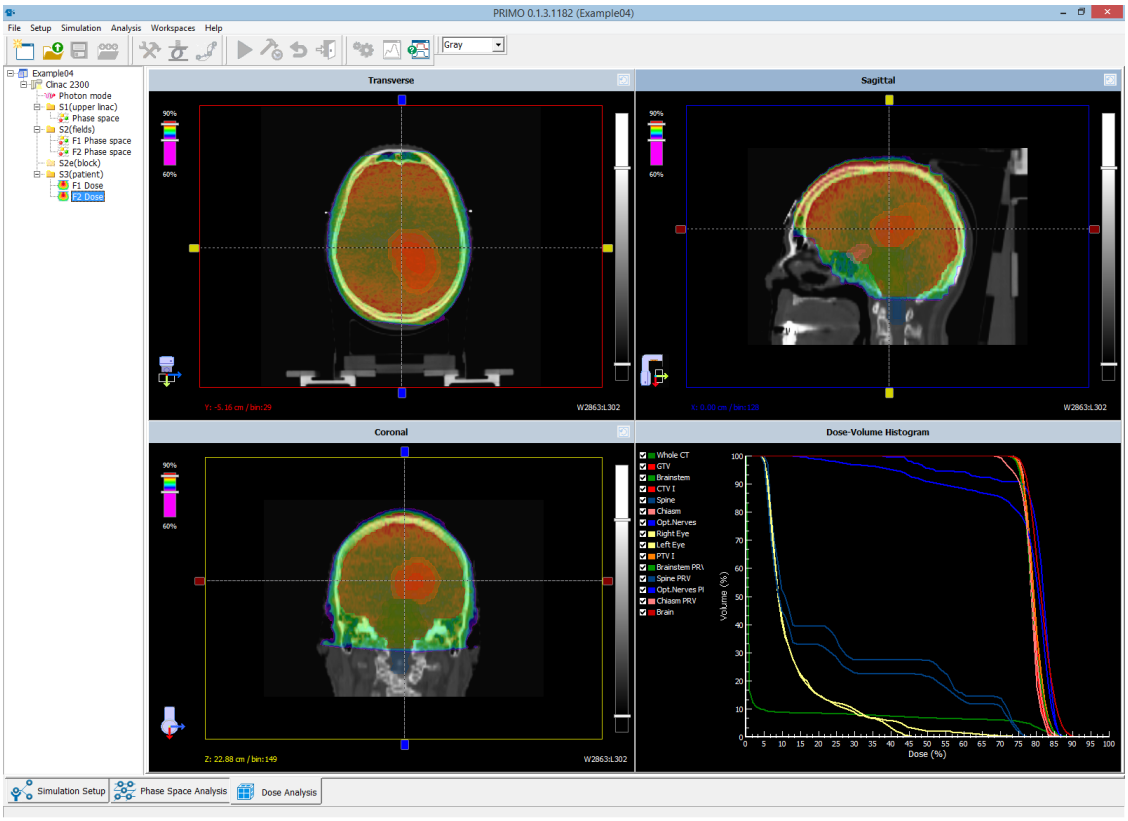
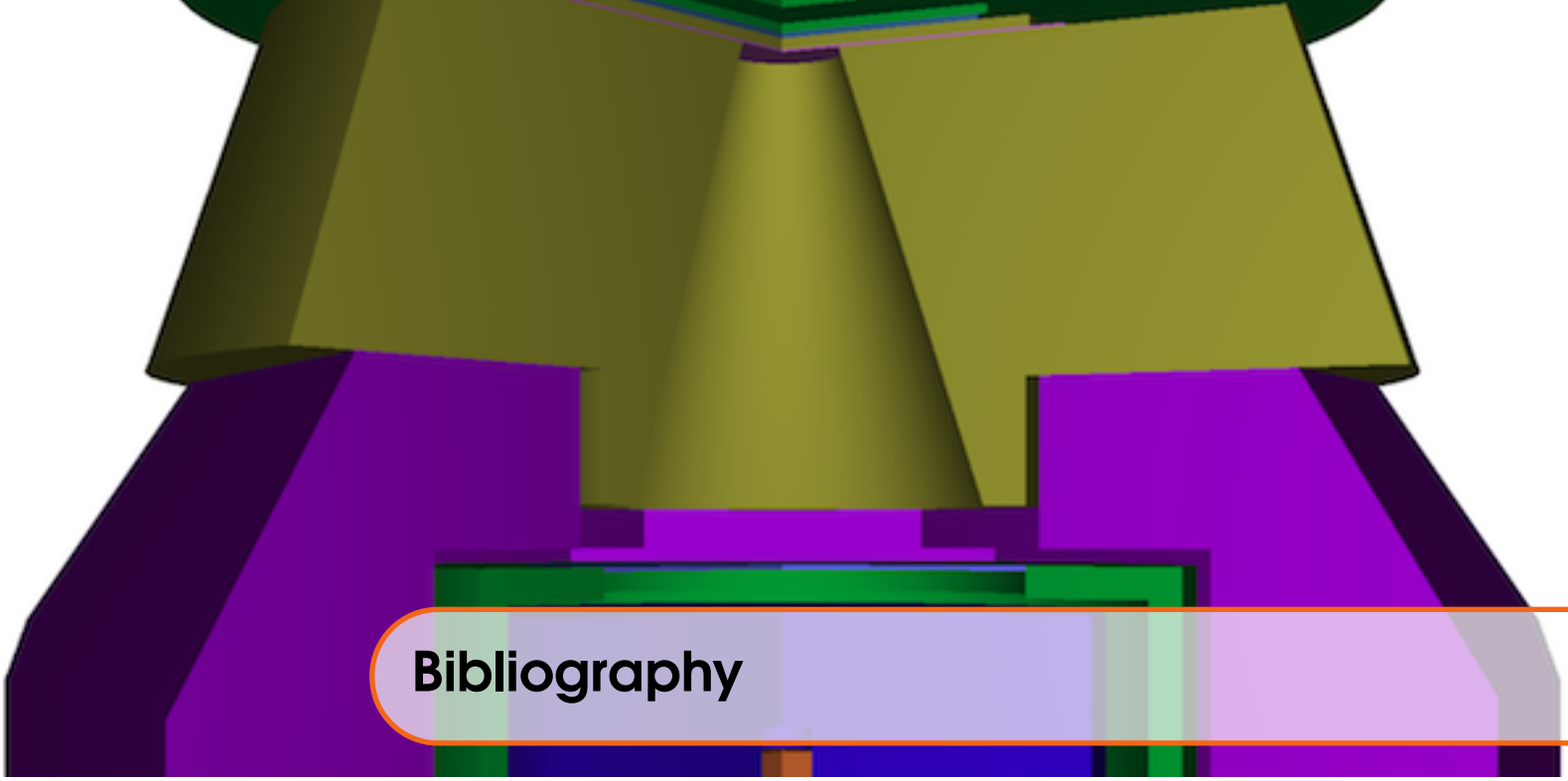


Figure 5.29: Dose distribution in the CT volume.

5.4.4 Dose calculation

For the simulation of segment s3, splitting with a factor of 30 was used. The stopping condition of the simulation was determined by the relative uncertainty of the dose, which was set at 4% (2σ). The dose distribution and the DVHs are shown in figure 5.29.



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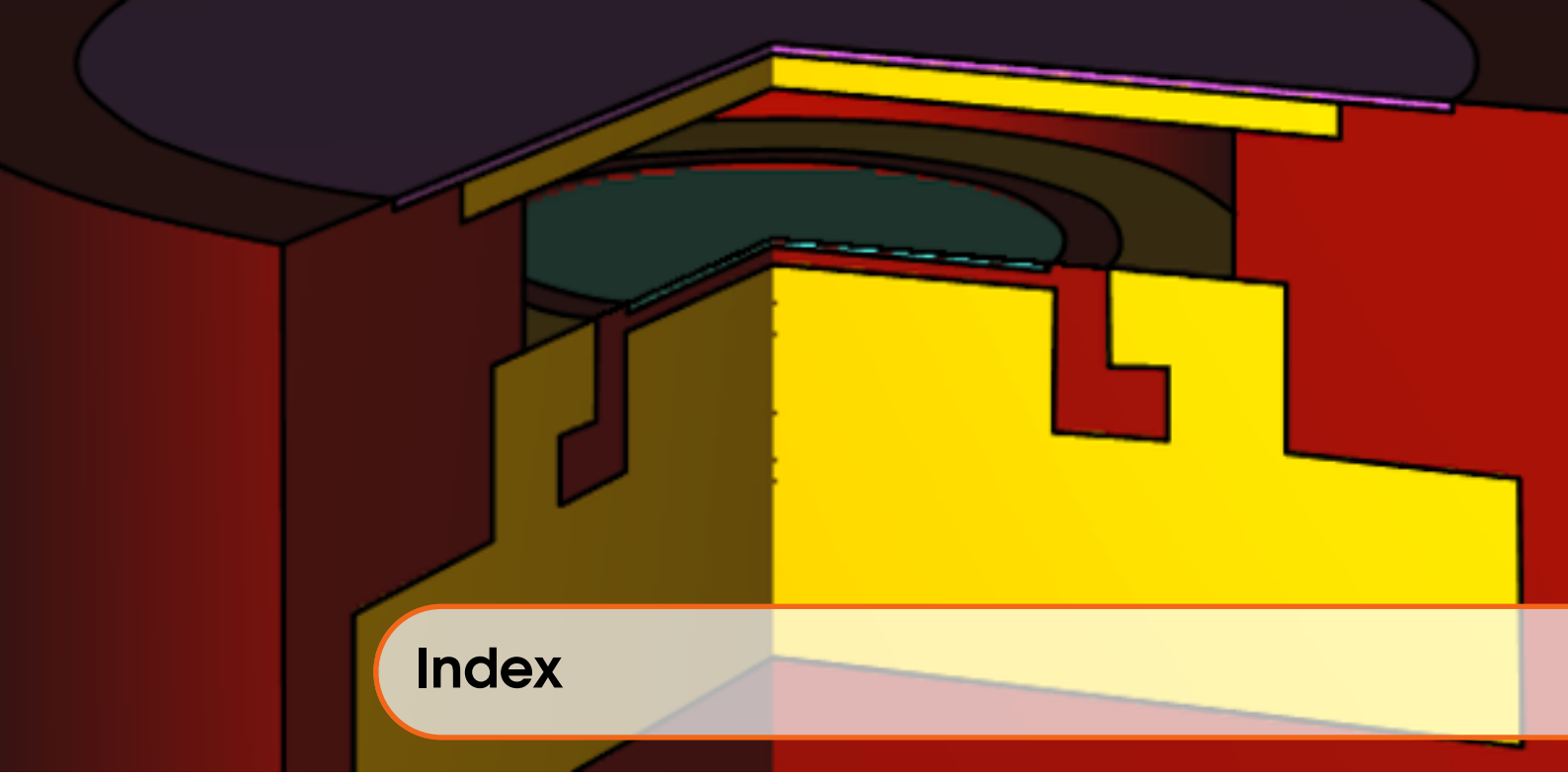

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