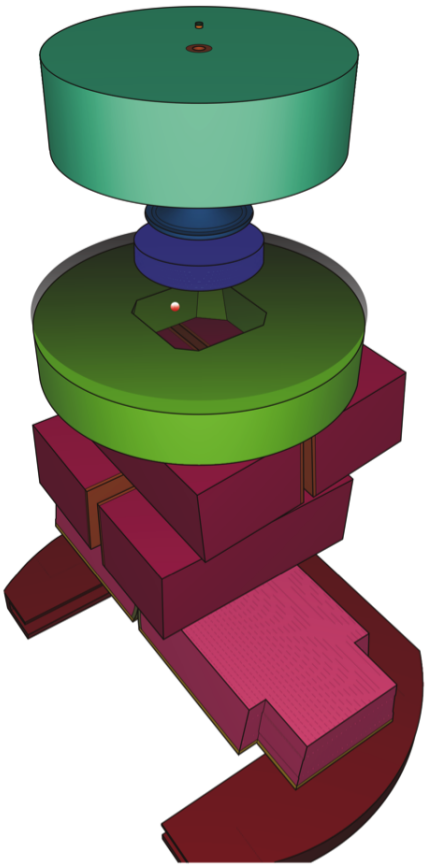
PRIMO
User's Manual



Brualla · Rodriguez · Sempau

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PRIMO USER'S MANUAL
SOFTWARE VERSION 0.3.1.1770

WWW.PRIMOPROJECT.NET

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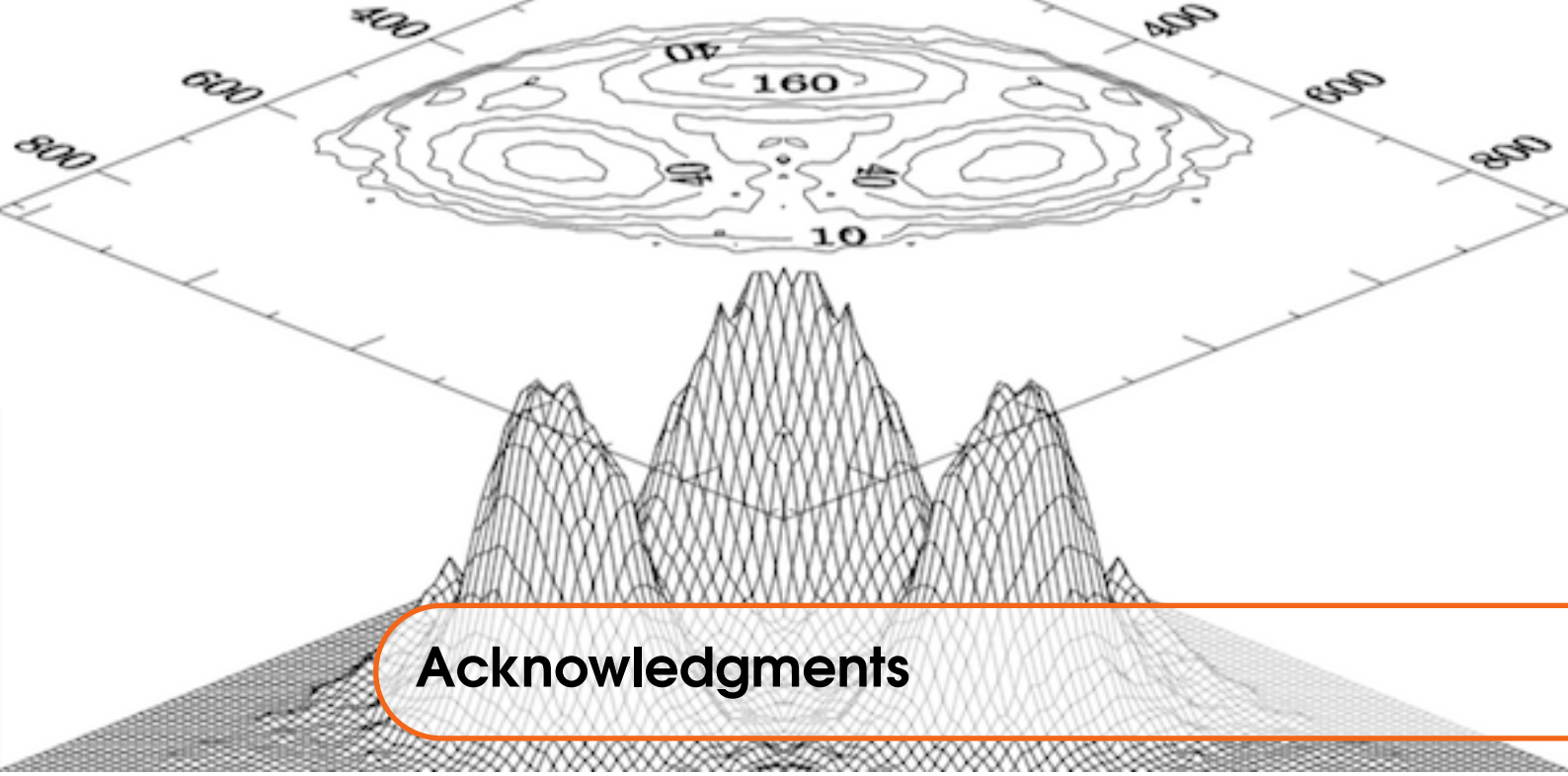

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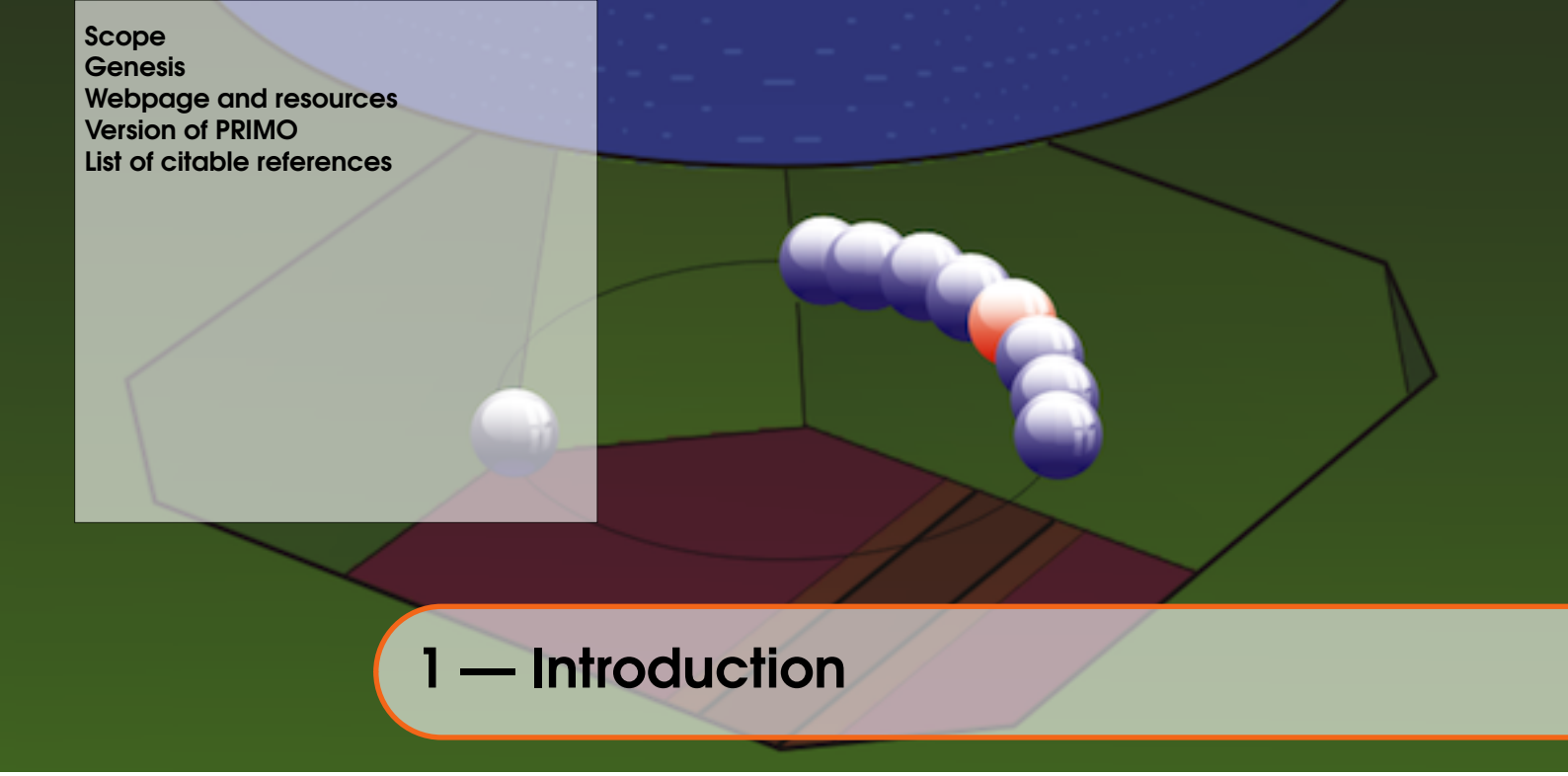


1 — Introduction

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], Dose Planning Method (DPM) [SWB00], 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. DPM is a program for fast Monte Carlo simulation of coupled electron and photon transport. 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 some 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]. Additionally there is the option to perform fast Monte Carlo transport in the patient-dependent part of the linac and in the computrized tomography using the fast Monte Carlo code DPM [Rod+19].

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. DPM was developed by J. Sempau and collaborators in 1999. 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 0.3.1.1770. 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

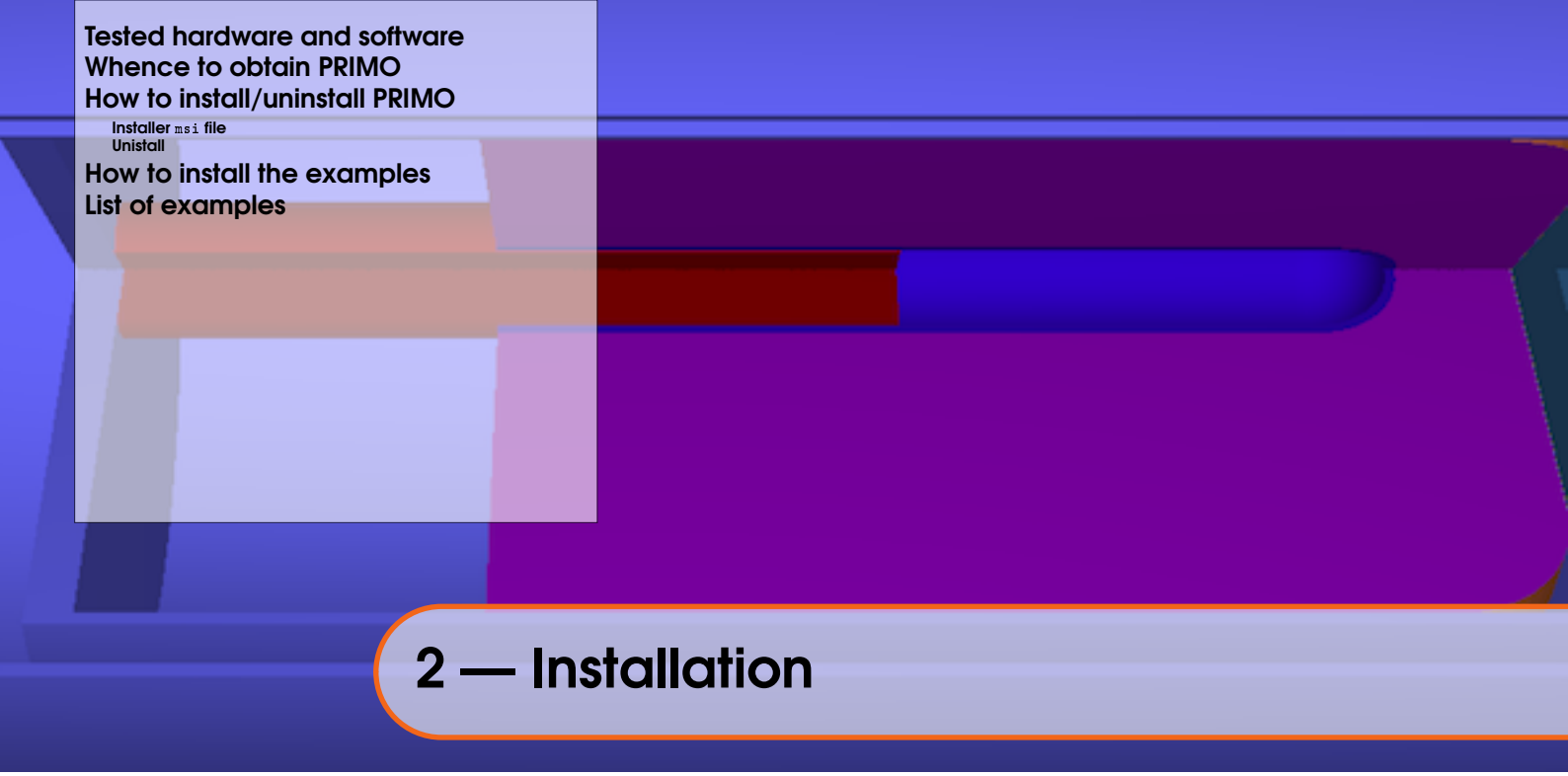
- Brualla L, Salvat F, Palanco-Zamora R. Efficient Monte Carlo simulation of multi-leaf collimators using geometry-related variance-reduction techniques. *Phys Med Biol* 2009;54:4131–4149.
  Movable-skins variance-reduction technique

- 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

Tested hardware and software
Whence to obtain PRIMO
How to install/uninstall PRIMO
Installer msi file
Unistall
How to install the examples
List of examples



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 IA32 [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.
- A graphic card supporting OpenGL 4.0 or above.
- Minimum screen resolution 1280×960 pixels. The default font size in Windows (smaller size) should be used for this minimum resolution.
- In order to take full advantage of PRIMO graphic output when PRIMO is run remotely using Windows Remote Desktop Connection Manager (RDC), the server machine must run Windows Server 2016 and should have installed a GPU card such that it enables OpenGL 4.0 or above support on RDC. We have tested an NVIDIA Quadro K620 successfully.

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

[1] PRIMO has been successfully tested on Windows 7, Windows 8/8.1, Windows 10 and Windows Server 2016. 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.

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.

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

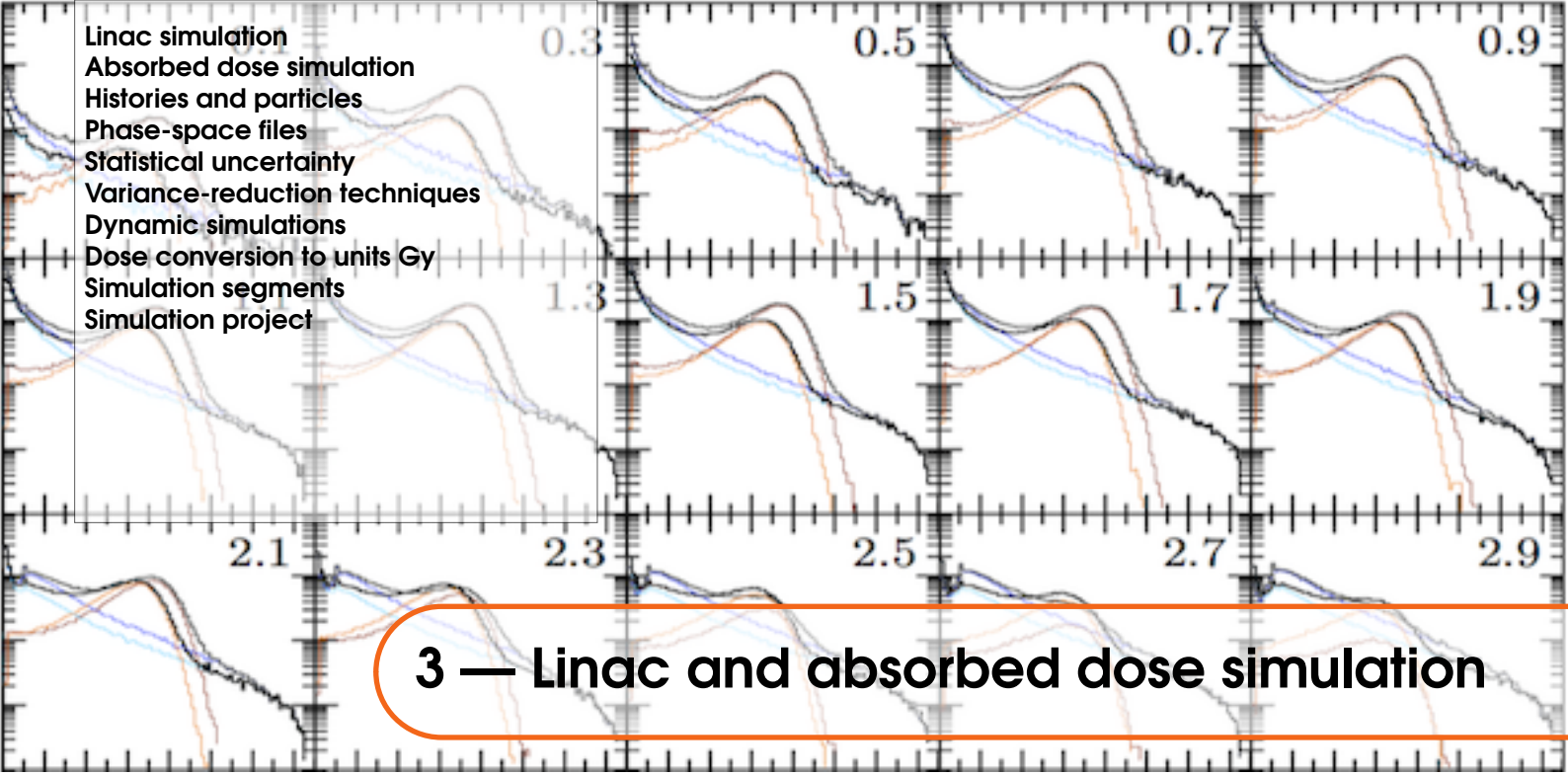
1. Create a directory called `PRIMOexamples` under `c:\`.
2. Unpack the downloaded files inside the just created directory `c:\PRIMOexamples`. The unpacked files will each one create a directory called `Example`*mn*, with *mn* a two digits number.

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 simulated using penEasy.

Example02 Same as example 01 but the dose distribution is estimated using Dose Planing Method. A comparison with the dose distribution estimated in Example 01 is made.

Example03 Clinical test case. Irradiation of brain PTVs using a VMAT plan for a Varian Clinac 2100 C/D modulated with a MLC 120. Nominal energy 6 MV. Tallied results: dose distribution. A comparison is made with a dose distribution imported from a Treatment Planning System.



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 medical 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 (it is also called the patient-dependent 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.

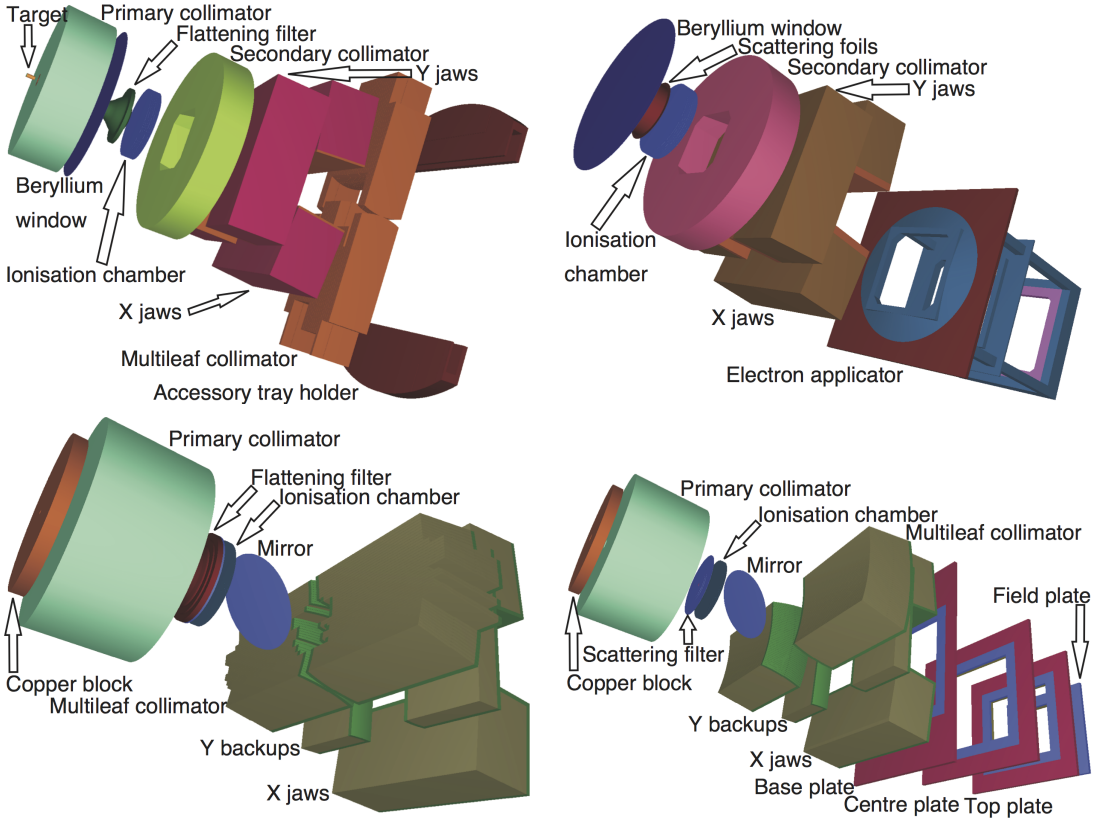


Figure 3.1: Varian Clinac 2100 C/D operating in photon mode at 18 MV (upper left) and electron mode at 6 MeV (upper right), Elekta MLCi operating in photon mode at 10 MV (lower left) and electron mode at 4 MeV (lower right). These images are the actual simulated geometries in PRIMO.

3.2 Absorbed dose simulation

Downstream 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) 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 unfordable 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 Dynamic simulations

Dynamic simulations are those in which the patient-dependent part of the linac geometry changes during simulation. Along this manual we refer to a control point as the moment in simulation time in which the radiation transport stops and the geometry changes. Subsequently, the geometry remains static and the radiation transport is active until the next control point or the end of simulation is reached. A single static field is considered a particular case of dynamic geometry with one control point at the start of simulation. The number of histories to be simulated for a control point n_p is calculated as,

$$n_p = \frac{N w_p}{\sum_{p=1}^{P} w_p}, \tag{3.3}$$

where N is the total number of histories, w_p is the weight of the control point and P is the total number of control points. Both penEasy and DPM, the two simulation engines implemented in PRIMO, can manage simulations with dynamic geometries.

3.8 Dose conversion to units Gy

In order to convert a dose distribution from units eV/g to units Gy it is necessary to perform a dose calibration. The dose must be measured in reference conditions using an appropriate

detector (e.g., ion-chamber). Also a Monte Carlo simulation must be performed in the same reference conditions and the dose in the central bin at the reference depth must be taken. The dose conversion factor for a given treatment plan is calculated as,

$$f = f_r \frac{D_m^{ref} MU}{D_{mc}^{ref} MU^{ref}}, \tag{3.4}$$

where f_r is the number of fractions of the plan, D_m^{ref} is the dose measured in reference conditions, D_{mc}^{ref} is the dose estimated by a Monte Carlo simulation in reference conditions, MU^{ref} are the reference MUs (used to obtain the measured reference dose) and MU are the MUs of the treatment plan.

When the purpose of converting the dose to units Gy is comparing a dose distribution estimated with PRIMO with the dose calculated with a treatment planning system it should be taken into account that the beam used for the Monte Carlo simulation to determine the reference dose should be representative of the beam used to measure the reference dose and to calculate the dose in the TPS. That is, a beam matching process must be performed previous to calibration. Commonly, beam matching is performed through an iterative process in which the beam is defined by a set of initial parameters and the dose distribution estimated in water for that beam is compared to the measured dose. The process is repeated by changing the initial beam parameters until a match between the estimated and measured dose is achieved.

3.9 Simulation segments

PRIMO allows to tally a phase-space file at the downstream end of the upper part of the linac. This part of the linac is identified in PRIMO as segment 1 (s1). Similarly, a phase-space file can be tallied at the downstream end of the region corresponding to the patient-dependent part of the linac which is identified as segment 2 (s2). The geometric region corresponding to the patient or phantom, in which the absorbed dose is estimated is called segment 3 (s3).

Segments must, obviously, be simulated in sequential order, that is $s1, s2, s3$. However, they can be grouped according to the user's requirements. They can be simulated individually as $(s1, s2, s3)$; or grouped in a single simulation as $(s1 + s2 + s3)$; or in smaller groups simulating s1 first and then s2 and s3 together $(s1, s2 + s3)$; $(s1 + s2, s3)$ is also possible. Restrictions described in warnings 3.1 and 3.3 apply.

> **Warning 3.1** The Dose Planing Method (DPM) engine can only simulate the combined segments s1 and s2.

A simulation can either tally a phase-space file or a dose distribution. Therefore, if simulating for example $(s1 + s2 + s3)$ a dose distribution will be tallied. Simulation of $(s1 + s2)$ 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.

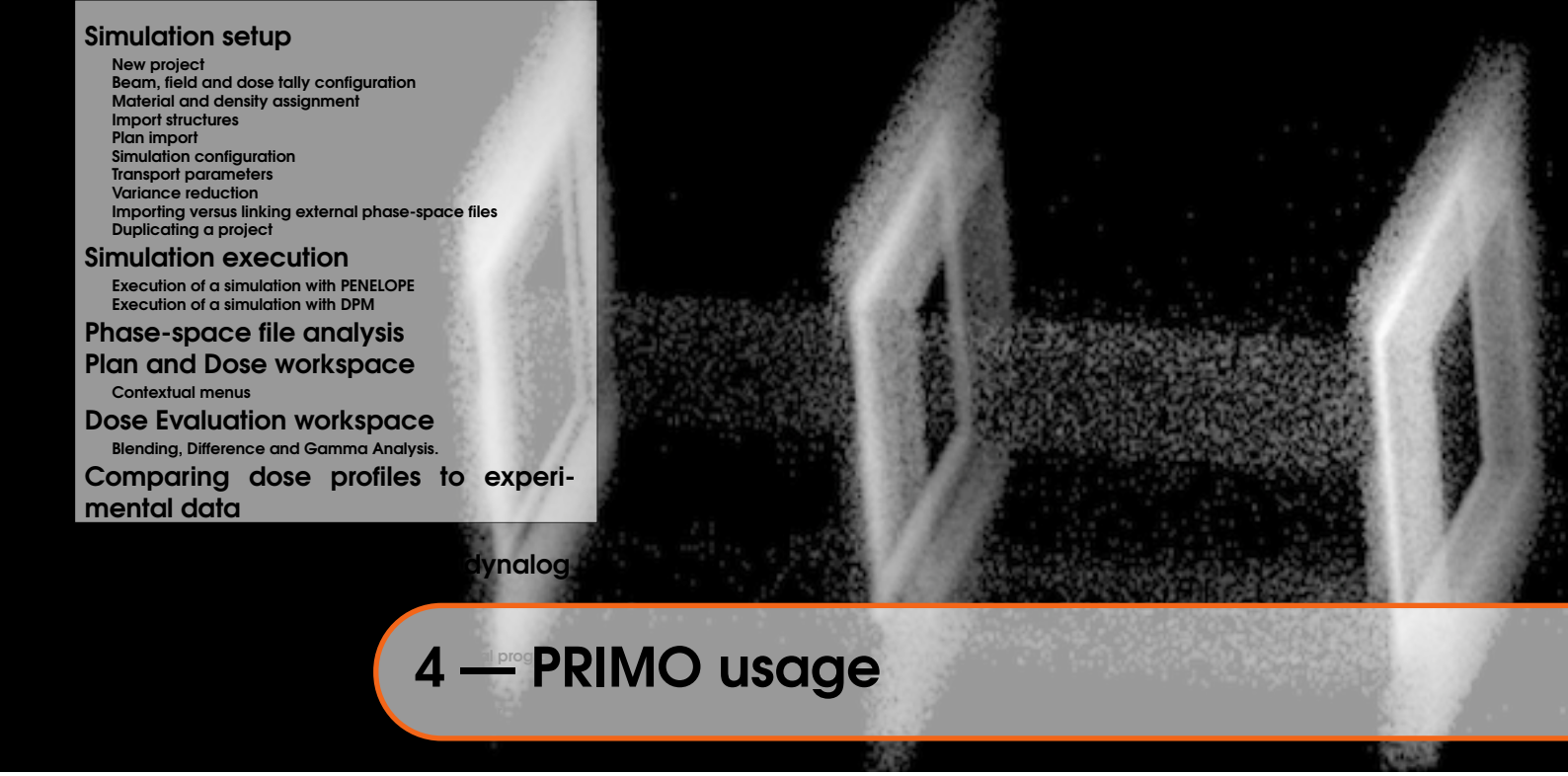
Warning 3.2 The current version of PRIMO does not allow for the simulation of customized electron collimators.

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

Warning 3.3 In projects with more than one radiation field a phase space cannot be tallied at segment s2 because the gantry, collimator and table angles are not saved in the phase space. That is, the position of the particle is not completely defined. The same applies to the case of a plan with only one static field but in which any of those angles are different of zero.

3.10 Simulation project

A simulation project is the collection of all the simulation data. These data must include, one particular linac model and beam, a set of radiation fields, a model of the patient and a simulation configuration data. Additionally it may include, a set of contours defining structures (regions) in the patient, the tallied (or imported) phase-space files and a dose distribution.



4 — PRIMO usage

This chapter is the core of the manual, covering how to operate PRIMO. All the program functions are grouped in four blocks or workspaces. These are:

- Simulation Setup. In this workspace the user defines the simulation segments and all their associated parameters as well as other related simulation variables.
- Plan and Dose. This workspace is used to visualize a geometrical model of the patient, the dose distribution and the treatment fields.
- Dose Evaluation. This workspace is designed to compare two dose distributions, the one that has been tallied in the project and an external dose distribution.
- Phase Space Analysis. This workspace allows the analysis of phase-space files tallied with PRIMO or imported from external files.

In the rest of this chapter the complete operation of PRIMO is depicted by describing the details of the interaction with each one of its workspaces.

4.1 Simulation setup

This is the workspace that appears when PRIMO is first launched. The whole simulation project can be managed from this workspace. So, after launching PRIMO and previous to any other operation the user must create a new simulation project or load an existing one. Figure 4.1 depicts the Simulation setup workspace.

4.1.1 New project

A new project is created by clicking in the New Project button. The basic elements that define the new project are set in the window in (figure 4.39). They are:

- 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 operating system current 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

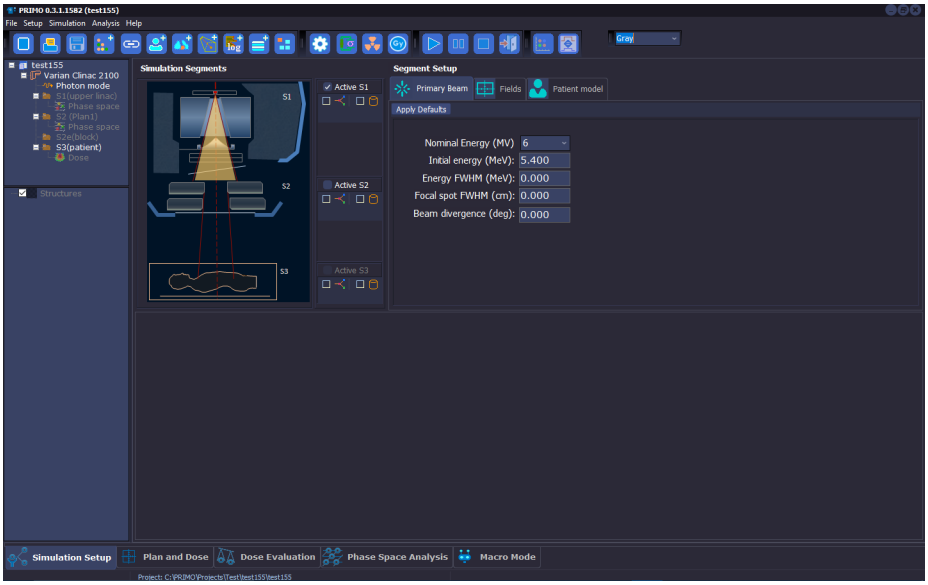


Figure 4.1: The simulation setup workspace. The segment s1 has been selected and appears illuminated. The tree at left shows (above) the project and its relevant tallied data.

PRIMO	Commercial
Varian Clinac 600C	Clinac 600 C
Varian Clinac 600CD	Clinac 600 C/D
Varian Unique	Unique
Varian Clinac 2100	Clinac C series, TrueBeam (sect. **??**)
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.

will be saved. A logical drive mounted on a remote disk can be used. However, the recommended communication speed is 6 GB/s or more. Once a project has been saved in a given directory it cannot be moved to any other location but a copy can be made in a different path.

- 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 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.

In addition to the parameters set in the New Project window, the created project will contain (created by default) the following elements:

- A default set of values for the parameters that define the electron beam impinging on the target according to the linac and beam selected in the New Project window.

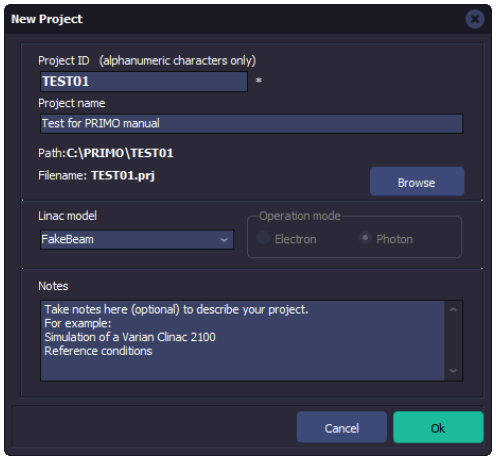


Figure 4.2: New project window.

- A CT volume defining an homogeneous water phantom of size $40.25 \times 40.25 \times 40.0$ cm^3 and bin size $0.5 \times 0.5 \times 0.5$ cm^3.
- A 10.0×10.0 cm^2 field with the isocenter located at $(0,0,0)$, *i. e.*, centered at the phantom surface and with the gantry, collimator and table set at angle 0 deg.
- A default Monte Carlo simulation geometry for the water phantom.
- A default configuration for the simulation parameters, *i. e.*, the random number generator seeds, the simulation engine, the simulation stop conditions, the default variance-reduction techniques, the number of computer cores used to simulate, etc.

Notice 4.1 Given that default data is created with the project, the user can start a segment s1 simulation right away after creating the project. ■

Simulation Segments

Simulation segments are selected by simply checking the Active checkboxes at the right side of the linac image (figure 4.1). There is a Simulation Setup tab associated to each simulation segment. They are depicted in figure 4.40. Most of the parameters for simulations with open fields can be completely set by the options contained in these tabs with the exception of the patient model (imported CT or slab phantom) which is set by selecting functions enclosed in the main menu bar.

Notice 4.2 The Patient model tab is only informative. The patient model is actually changed by importing DICOM CT files or by creating a slab phantom. All these functions are available in the main menu bar. ■

Once a segment has been simulated a check mark appears next to the three-particle interaction icon 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 icon (a cylinder) as an indication that the tally is saved as a part of the project data. Also, the icon of the tally will illuminate in the project tree (see figure 4.1).

Notice 4.3 When the configuration of s2 and s3 is known beforehand, it is recommended

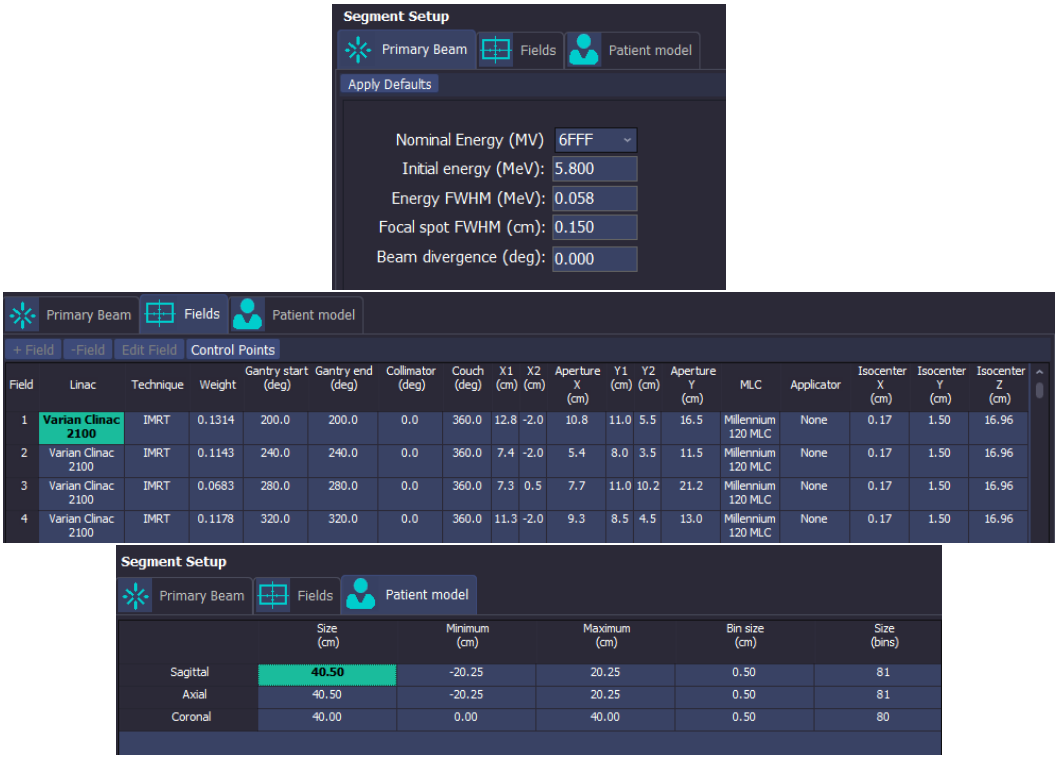


Figure 4.3: Simulation Setup tabs.

to configure segments s1, s2 and s3 (see section 3.9) at the very beginning of the simulation project, even if only segment s1 will be simulated (*e. g.*, a parameter associated to the splitting-roulette and rotational splitting variance-reduction techniques applied at s1 is related to the field size selected in s2). ■

4.1.2 Beam, field and dose tally configuration

Beam parameters (s1)

Primary Beam

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 (figure 4.4). When a value higher than zero is set for the FWHM a Gaussian distribution for the energy or the radial distribution is assumed. Beam divergence is implemented such that the angular divergence is for each point emitting from the source plane.

Notice 4.4 Default beam parameters have been tuned to reproduce experimental results from the corresponding linac and energy. ■

Field configuration (s2)

Fields

Fields are configured by selecting the tab s2 (figure 4.5). New fields are added by clicking the +Field button. The selected field is deleted by clicking the -Field button. The Edit Field button

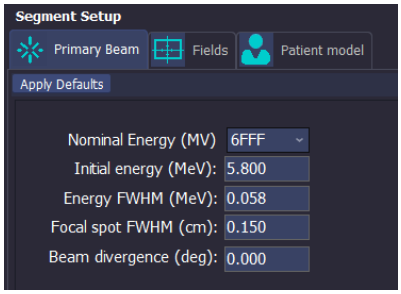
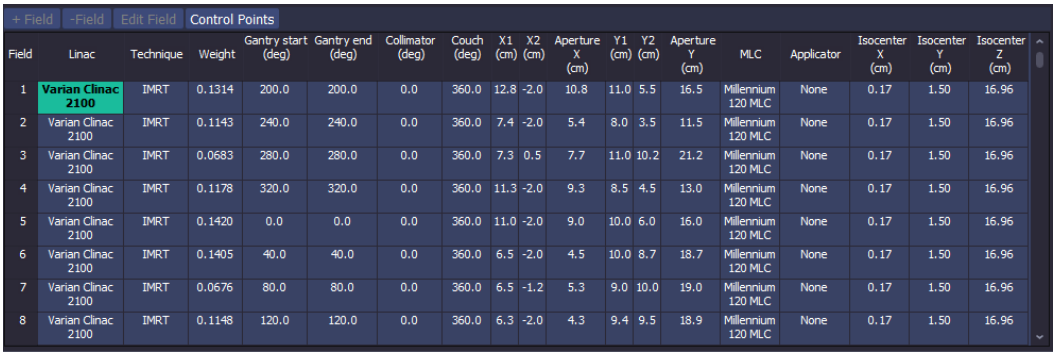


Figure 4.4: Simulation Setup tab of segment s1.



Field	Linac	Technique	Weight	Gantry start (deg)	Gantry end (deg)	Collimator (deg)	Couch (deg)	X1 (cm)	X2 (cm)	Aperture X (cm)	Y1 (cm)	Y2 (cm)	Aperture Y (cm)	MLC	Applicator	Isocenter X (cm)	Isocenter Y (cm)	Isocenter Z (cm)
1	**Varian Clinac 2100**	IMRT	0.1314	200.0	200.0	0.0	360.0	12.8	-2.0	10.8	11.0	5.5	16.5	Millennium 120 MLC	None	0.17	1.50	16.96
2	Varian Clinac 2100	IMRT	0.1143	240.0	240.0	0.0	360.0	7.4	-2.0	5.4	8.0	3.5	11.5	Millennium 120 MLC	None	0.17	1.50	16.96
3	Varian Clinac 2100	IMRT	0.0683	280.0	280.0	0.0	360.0	7.3	0.5	7.7	11.0	10.2	21.2	Millennium 120 MLC	None	0.17	1.50	16.96
4	Varian Clinac 2100	IMRT	0.1178	320.0	320.0	0.0	360.0	11.3	-2.0	9.3	8.5	4.5	13.0	Millennium 120 MLC	None	0.17	1.50	16.96
5	Varian Clinac 2100	IMRT	0.1420	0.0	0.0	0.0	360.0	11.0	-2.0	9.0	10.0	6.0	16.0	Millennium 120 MLC	None	0.17	1.50	16.96
6	Varian Clinac 2100	IMRT	0.1405	40.0	40.0	0.0	360.0	6.5	-2.0	4.5	10.0	8.7	18.7	Millennium 120 MLC	None	0.17	1.50	16.96
7	Varian Clinac 2100	IMRT	0.0676	80.0	80.0	0.0	360.0	6.5	-1.2	5.3	9.0	10.0	19.0	Millennium 120 MLC	None	0.17	1.50	16.96
8	Varian Clinac 2100	IMRT	0.1148	120.0	120.0	0.0	360.0	6.3	-2.0	4.3	9.4	9.5	18.9	Millennium 120 MLC	None	0.17	1.50	16.96

Figure 4.5: Simulation Setup tab of segment s2 (Field definition).

opens the dialog of the figure 4.6 which allows to define the field size and position, as well as gantry, collimator and couch angles, and the isocenter position in the patient. Multileaf collimators or electron applicators can be selected in this screen. The position of the leaves of the multileaf collimator can be imported from a text file. The format of this file is depicted in figure 4.7. Pressing the Control Points button opens a dialog in which some parameters of the control points are depicted, that is, the jaws aperture, the gantry angle and the weight. The parameters of the control points are not editable (see section 3.7). In case of static fields (with only one control point) this button always appears as disabled.

In electron mode, the field aperture 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.

Dose tallying (s3)

The patient model is always defined by a CT volume. Even for the default phantom or when a slab phantom is created, a CT volume is also created to represent the phantom. The Simulation Setup tab of s3 displays the most relevant parameters of the CT volume, *i. e.*, the volume dimensions, the bin size and the number of bins (or voxels) in each spatial direction. The patient CT can be changed by selecting the Import a CT or Create a slab phantom options of the Main menu bar. A simulation (voxelized) geometry must be generated from the CT volume previous to the simulation of segment s3. Details on how the voxelized geometry is generated can be found on section 4.1.3.

Figure 4.6: Field edit dialog.

```
# PRIMO
# This is an example of the file format used to import the position of
# the MLC leaves in PRIMO.
#
# Rules:
#
# - The file must be a plain text file (ASCII or ANSI encoding).
# - Lines beggining with the symbol '#' (like this one) are considered
#   comments instead of data
# - Comment lines can be inserted anywhere in the file
# - A leaf position is assumed to be in cm and defined at 100 cm from
#   the linac source (at the isocenter).
# - Special characters (such as TABs) MUST NOT be present in the text
# - Data must be arranged in columns separated by spaces.
# - The order of columns is:
#     leaf number <space> position (bank A) <space> position (bank B)
# - All the columns are mandatory
# - The number of leaves listed must correspond to the number of leaves
#   of the MLC model selected in PRIMO.
#
0  -6  6
1  -6  6
2  -6  6
3  -6  6
4  -6  6
5  -6  6
6  -6  6
```

Figure 4.7: Format of the text file containing MLC leaves positions.

Notice 4.5 — Maximum number of voxels. The maximum number of voxels allowed by the PENELOPE engine in a s3 simulation is 10^8. In simulations with the DPM engine the number of voxels is only limited by the amount of memory assigned by the operating system (OS) to the program. In a Microsoft Windows IA32 environment it is a maximum of 4 GB. ■

CT scan import

The patient can be defined either from an imported CT volume or from a internally created slab phantom. To import a CT scan select the Import a CT option in the main menu. In the appearing standard File Open dialog select all the files of CT slices that form the CT volume. 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 4.8) 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 shown in the dialog.

In the DICOM Image Import dialog there is the option to change the CT slice size to 256×256 bins. The option is set by default in the Reduce the original slice size check box. Unchecking the check box produces the importing of the slices in its original size. The slice shrinking or enlargement is done by linear interpolation, as a consequence the spatial resolution of the image is reduced or increased accordingly.

There is also the option to automatically generate a default voxelized geometry for simulation immediately after importing the CT volume. This option is set by default in the Create the default simulation geometry check box. Uncheking the check box produces that no voxelized geometry is generated by default and the user must expressly generated it previous to simulate the s3 segment. Details on how the default voxelized geometry is generated are given on section 4.1.3. The coordinate system used in PRIMO for the patient representation is depicted in figure 4.9.

Warning 4.1 Importing a CT volume implies that any previously imported structures and the current dose distribution are deleted permanently. Also, the plan is reset to the default (one field) as described in section 4.1.1

Slab phantom

In the case of the patient model being a slab phantom, there is not need to import the phantom from a DICOM-CT file. A phantom composed of slabs of variable materials can be directly created using the function Create a slab phantom in the main menu. 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 4.10). 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. There is no need to recreate the voxelized geometry for a slab phantom but one can use the function Calculate densities and materials in order to check the assignment of materials and densities are the expected for the slabs in the phantom. When the phantom is created the isocenter is automatically positioned at the center of the upstream surface of the phantom. However, notice that the warning 4.1 also applies for the creation of a slab phantom.

R Note that once the Slab phantom definition dialog is closed and the slab phantom is created as a CT scan it cannot be further edited. Any change in the phantom definition requires the creation of a new phantom from scratch.

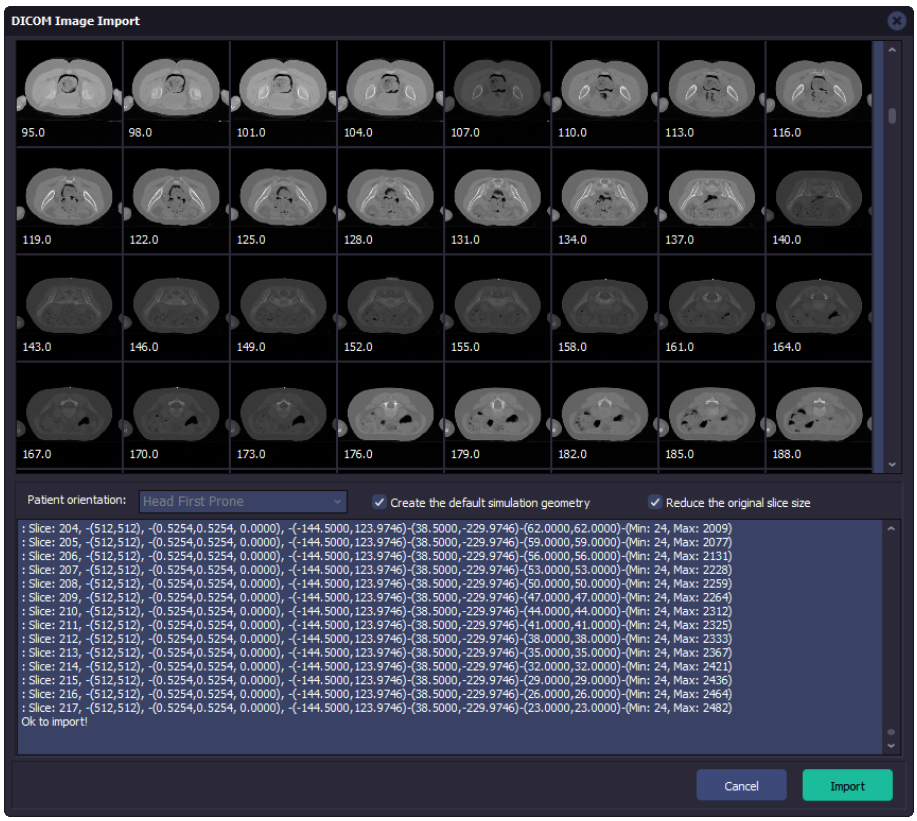


Figure 4.8: DICOM Image Import dialog. The gray scale is mapped into each image Hounsfield number range.

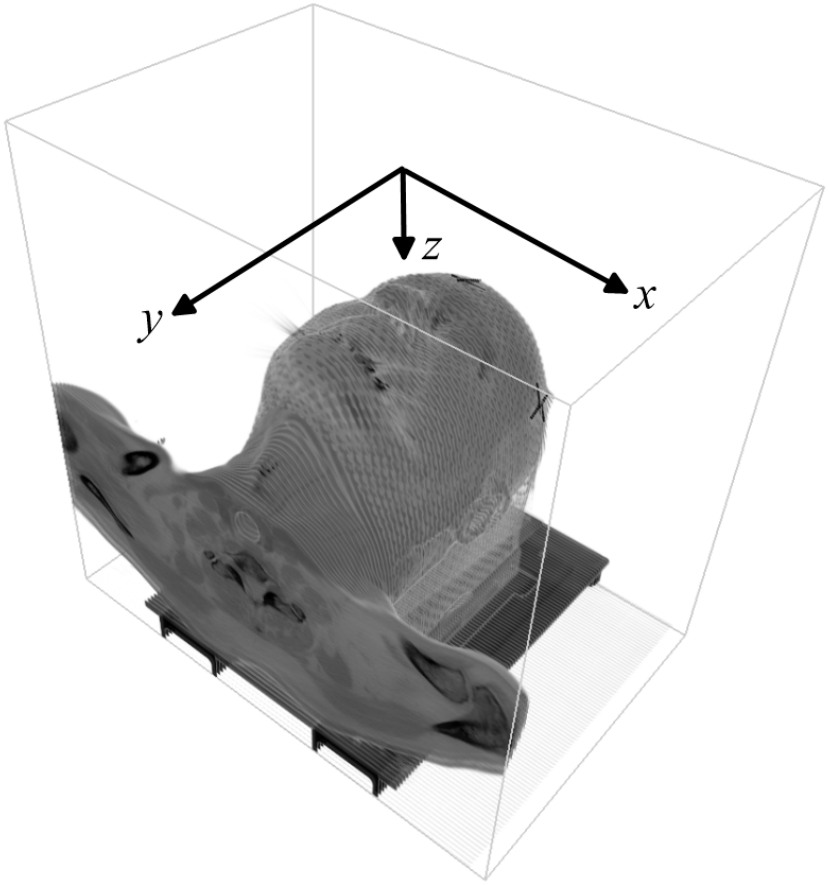


Figure 4.9: Coordinate system used in PRIMO for the patient. Assuming that the array of voxels of the CT forms a parallelepiped whose upper side is facing the linac gantry at angle 0, the center of coordinates is set, on the x- and y-axes at the center of the parallelepiped and on the z-axis at its top side. The patient represented in the figure is in the head-first supine (HFS) position.

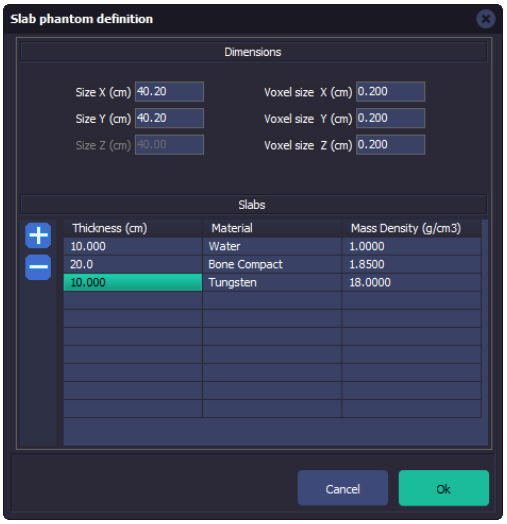


Figure 4.10: The Slab phantom definition dialog.

Warning 4.2 In case of the slab phantom being simulated with penEasy, its dimensions and voxel size must be such that the total number of voxels does not surpass 10^8. There is not such limitation for simulations with DPM. Dimensions are limited to a maximum of $60 \times 60 \times 60$ cm^3. Additionally, two different materials with the same mass density cannot be included in the phantom.

4.1.3 Material and density assignment

A voxelized simulation geometry must always be generated previous to any simulation. This geometry consists of a set of material and mass density value pairs. There is one pair per voxel in the tomographic volume. The option Create the voxelized geometry in the main menu is the way to access the CT Volume Segmentation dialog (see figure 4.11) which aids to create the voxelized geometry .

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 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 4.6 — 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

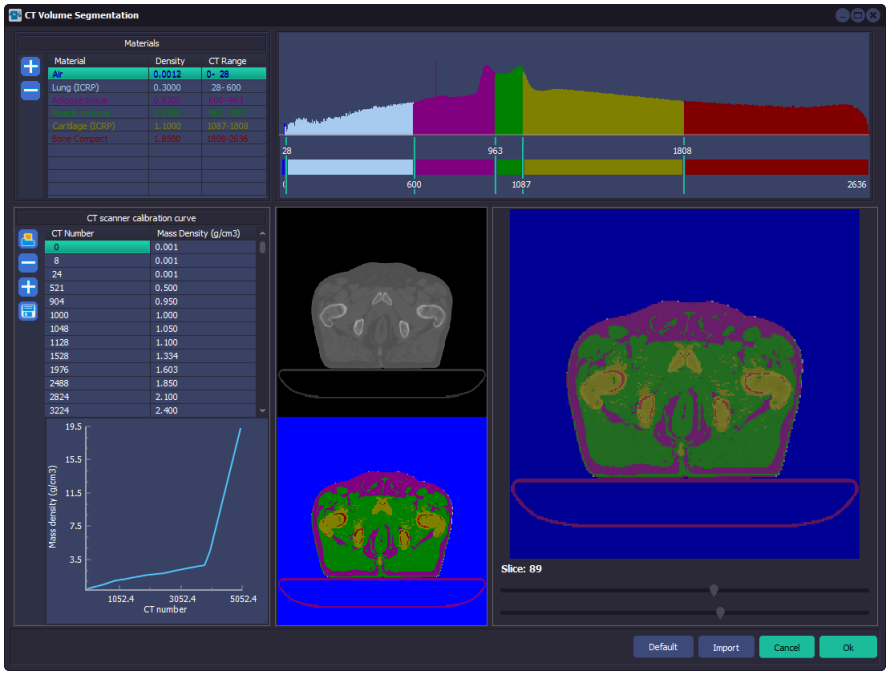


Figure 4.11: CT Volume Segmentation dialog aids on the definition of voxelized geometries.

also possible to add or delete entries. The plot updates automatically according to the changes made in the cells. The CT Save the curve as default button allows to save the edited curve as the default one.

> **Warning 4.3** 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. A segmentation created in another project can be imported into the current one by clicking the Import button.

The option Default allows to create a voxelized geometry by selecting a default set of six materials, namely, air, lung ICRP, adipose tissue, muscle skeletal, cartilage and compact bone. These materials are assigned to the voxels according to their density and the CT calibration curve. The whole range of CT numbers is divided into six intervals, the center of each interval determined by the mass density of the default material and the lower and higher limits determined by taking the mean density between intervals, except for the air for which an arbitrary narrow interval is set.

When the Ok button is clicked a segmentation file describing the materials, intervals and the calibration curve is saved and the voxelized geometry is created. The segmentation file can be used to apply exactly the same material and density assignment in other project by selecting the option Import in the CT volume segmentation dialog.

Notice 4.7 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 Import structures

Structures created externally can be imported by selecting the main menu option Import structures. In the standard File Open dialog select the file containing the structure set. The file must be formatted as a DICOM-RT STRUCT object. The DICOM-RT STRUCT Import dialog (figure 4.12) shows a graphic representation of the contours on each image plane and a list of structures and their attributes. Uncheck the box in the column Import to exclude a structure.

In the Identify body contour list box, select the structure which is the body contour. If there is a structure with ID = 'BODY' then it is chosen by default but this selection can be changed. For the chosen body contour there is the option to set to air all voxels outside the structure by checking the check box Set to air any CT voxels outside body contour. The air HU is taken from the PRIMO default CT calibration curve. This is useful to exclude from simulation devices present in the CT simulation but not in the patient treatment.

The region defined by a given contour can be filled in the CT volume with the structure associated HU. When the Modify CT box is checked for a structure, all the voxels of the CT inside the contour are changed to have the value of the contour associated HU (0 is water). This option allows to account for boluses and support structures (bed) in the Monte Carlo simulation. Notice that filling the CT with the HU of a bolus or a support structure is the only way to transfer it to the voxelized geometry used in simulation (see section 4.1.3). Figure 4.11 shows a support structure that has been included in the voxelized geometry.

Finally, press the button Import to start importing the selected structures into the PRIMO project.

Notice 4.8 Filling with air the CT region outside the body contour is applied first. Then, the structures selected with the Modify CT option are filled with its associated HU. This guarantee that those structures located outside the body contour, *e. g.*, the bed, are not filled with air. ■

4.1.5 Plan import

PRIMO has not support to create complex treatment plans, particularly, those that involve an inverse planning optimization process. Treatment plans can be imported from a DICOM PLAN archive. To import a plan select either the function Import a RT plan in the main menu or Plan import in the Plan and Dose workspace (see section 4.4). In the File Open dialog select the DICOM formatted file containing the RT PLAN. The Import DICOM-RT PLAN dialog will present a dynamic representation of the jaws and the MLC positions and a list of the data found in the archive. For the MLC representation a default MLC model is assumed. However, the right MLC model can be selected from a list of the supported MLC models associated to the treatment machine declared in the archive. When any of the isocenter positions declared in the file is out the spatial range of the CT, the isocenter position of each field is set at the center of coordinates in the PRIMO coordinate system (see figure 4.9). The number of control points in the DICOM file can be increased by a given integer factor. This allows to increase the time resolution of dynamic plans. The new control point parameters are calculated by linear interpolating the MLC leaves positions and the dose fraction.

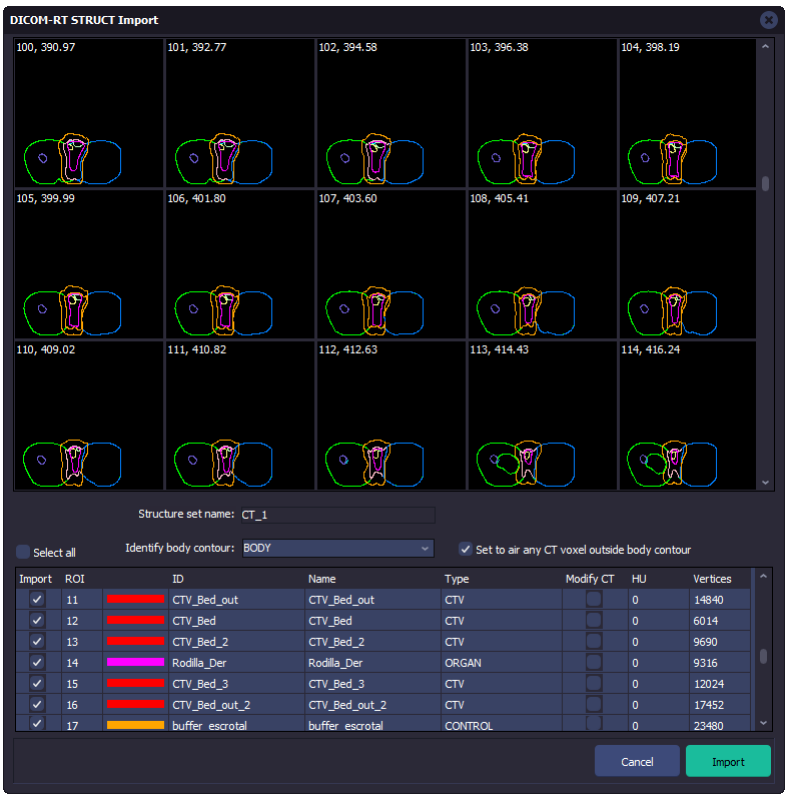


Figure 4.12: Import DICOM-RT STRUCT dialog.

Figure 4.13: Import DICOM-RT PLAN dialog.

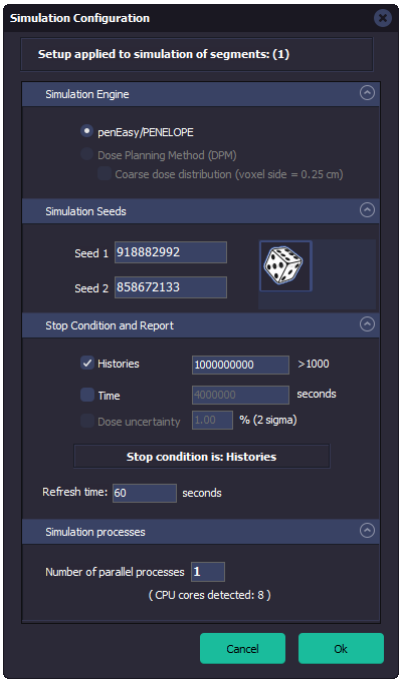


Figure 4.14: Configure simulation options dialog.

4.1.6 Simulation configuration

To gain 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 4.14) allows to set the simulation engine, 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 generated by clicking on the small dice in the dialog. Every time the dice button is pressed a new pair of seeds for a new sequence with a period of 10^{15} is generated [BS06; SFS11].

R If both stopping conditions, time and number of histories simulated are set, the first fulfilled condition will end the simulation. DPM can only stop by completing a number of histories simulated.

Warning 4.4 Setting more penEasy simulation processes than available CPU cores slows down the simulation and could crash the system. The minimum amount of Random Access Memory (RAM) required for a simulation with penEasy is about 0.5 GB per process. Segment s1 can only be simulated with penEasy.

Notice 4.9 DPM always uses all the available cores in the computer. ■

For simulations with DPM there is the option of incrementing the size of the voxel to speed up the simulations when the check box Coarse dose distribution is checked. When this option is active the voxel size is arbitrarily set to $(0.25\ \text{cm})^3$. The CT volume is contracted using an algorithm that calculates the HU of a voxel as the average of the HU of the neighbor voxels

weighted by the fraction of the voxel involved in the average. The voxelized geometry for the contracted CT volume is generated in the flight before simulation. At the end of simulation, the dose distribution (and the distribution of dose uncertainties) are expanded by linear interpolation to match the original voxel size.

Warning 4.5 The option Coarse dose distribution is not applied when the voxel size is larger than $(0.25\ \text{cm})^3$.

Warning 4.6 The option Coarse dose distribution must be used with caution because it can lead to a lost of resolution of the dose distribution beyond desirable, *e. g.*, in plans with small fields or small PTVs.

4.1.7 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. The simulation parameters table can be edited by checking the Enable Editing box of the dialog (figure 4.15). However, it is advisable to carefully read the PENELOPE 2011 manual before attempting to change the default table. 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 4.7 Modification of the transport parameters table should only be attempted by users with experience in Monte Carlo radiation transport.

Notice 4.10 The transport parameters table has not significance when simulating with DPM which uses the same transport parameters for all the materials in the geometry with absorption energies of 50 keV and 200 keV for photons and electrons, respectively. ■

4.1.8 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 linac 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

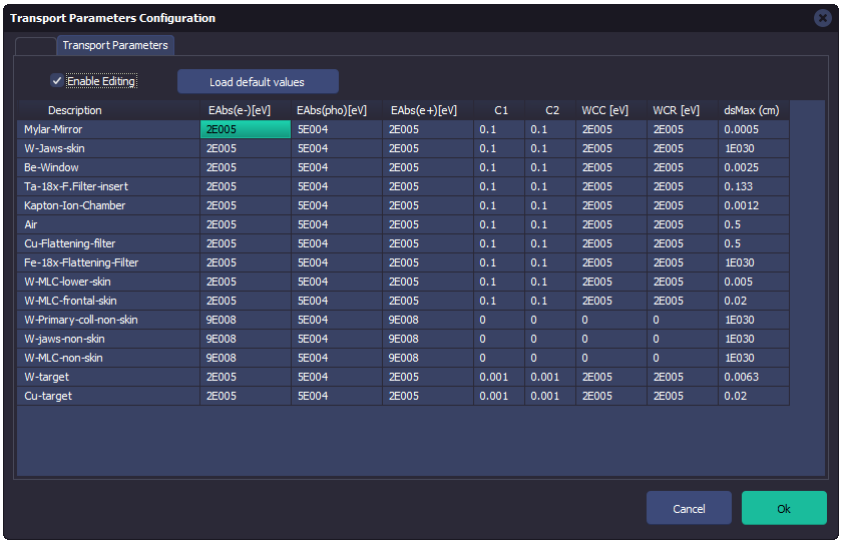


Figure 4.15: Configure transport parameters dialog.

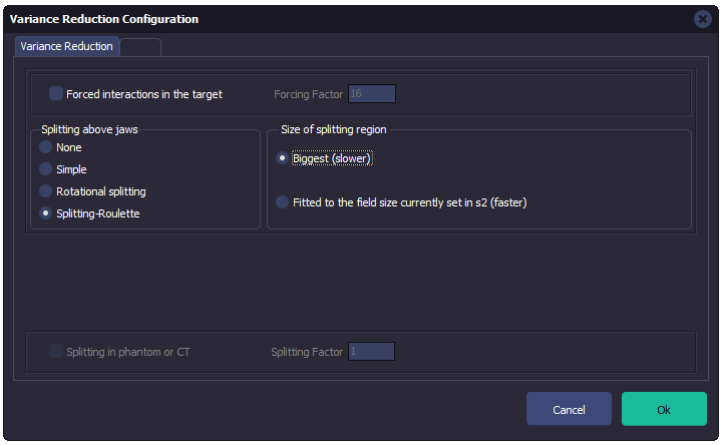


Figure 4.16: Variance reduction configuration dialog.

the effect that reducing the variance has on the simulation efficiency.

The methods that, so far, have proven to be the most efficient among those implemented in PRIMO, 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 which is used -although playing a different 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 radius of the splitting region 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 4.8 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 4.11 — 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 for PENELOPE and 300 for DPM 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 5.1.2. ■

Notice 4.12 — Variance-reduction techniques in DPM. Two variance-reduction techniques are used in simulations with DPM. Moveable-skins (applied in the jaws and the MLCs) and simple splitting in the voxelized geometry. The former is applied by default and is not configurable by the user. ■

4.1.9 Importing versus linking 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 check box 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 4.17) 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.

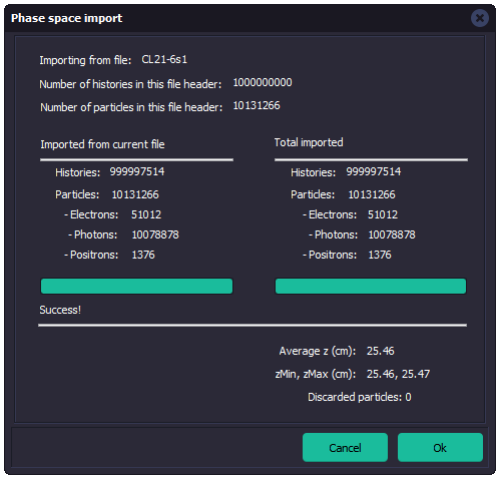


Figure 4.17: Phase space import dialog.

Warning 4.9 Importing a phase space file that has been not tallied upstream the jaws conducts to unexpected errors.

R 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.

Linking a phase-space file is similar to import it except that the file is not copied to the project folder. It remains in its original location and its path is added to the project data. A phase-space file is linked by selecting the option Link a phase space in the main menu.

Notice 4.13 Linking a PSF (instead of importing it) is an efficient way to reuse it in many simulation projects. ■

Warning 4.11 A PSF that has been split into several parts cannot be fully linked to a project. In order to link a split PSF it must be necessary first to joint the parts by importing those in a project using the Import a phase space option.

Warning 4.12 Removing a PSF from its location will produce an error in any simulation project to which that PSF has been linked.

4.1.10 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

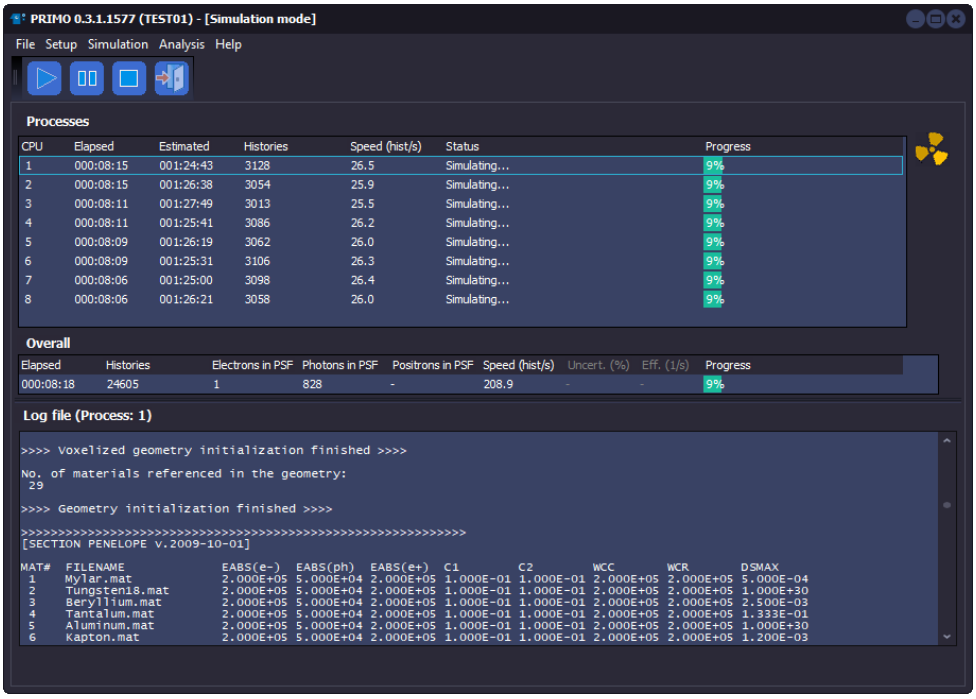


Figure 4.18: Simulation window for PENELOPE. The upper part shows a list of running CPU processes. Below the log file of the process selected in the list.

(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 bar will appear.

4.2 Simulation execution

Once the simulation setup is finished and saved, press the Run button in the main window to start running the simulation. If the active simulation engine is PENELOPE the main window disappears and *in lieu* the simulation window is presented (figure 4.18). When DPM is the active simulation engine the simulation window appears on top of the main window (figure 4.21).

4.2.1 Execution of a simulation with PENELOPE

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

The toolbar of the simulation window contains 4 buttons as shown in figure 4.19. From left to right these buttons are

- Run simulation: this button is not active 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 partial results**.
- 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.

Figure 4.19: Taskbar of the simulation window for PENELOPE.

Warning 4.13 When the simulation is reset by clicking the Reset button, all partially tallied results are lost. PRIMO will return to the state prior to launching the simulation.

The simulation window for PENELOPE is divided into two panels. The upper panel presents progress data of each running process and the overall progress data. 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 data 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,

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

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 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).

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.

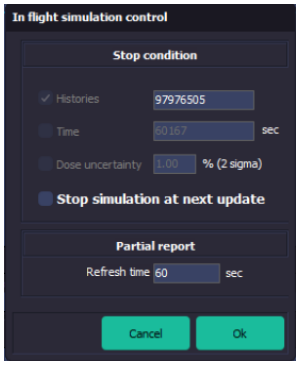


Figure 4.20: In flight simulation control window.

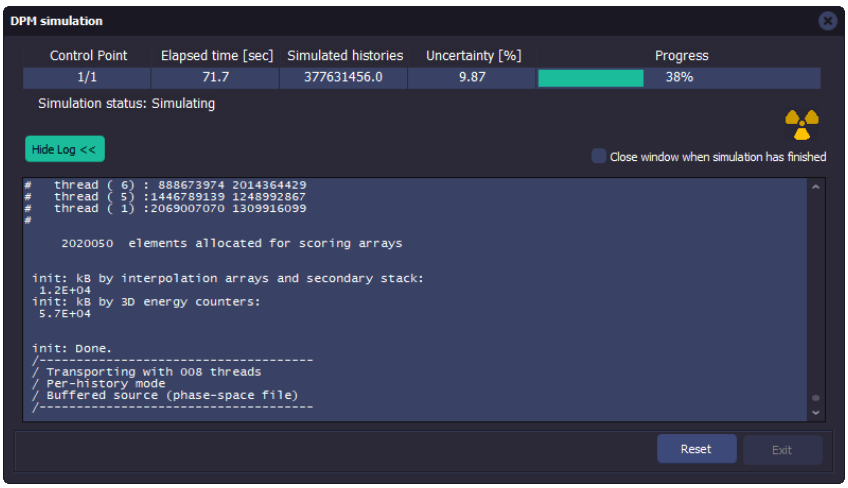


Figure 4.21: Simulation window for DPM.

4.2.2 Execution of a simulation with DPM

penEasy is a sequential (not parallel) program. In order to optimize simulations with penEasy, multiple instances of the program are executed simultaneously and they are controlled by PRIMO. Input data has to be split before initiating the simulation and output data has to be integrated at the end. On the contrary, DPM is a true parallel program. It has been coded to that effect. So, only one instance of DPM is running during simulation and PRIMO has not control on the parallel tasks execution. For that reason the simulation window cannot present the current status of each task. Another aspects that makes the difference between the DPM and PENELOPE execution windows is the fact that usually DPM performs quite faster than PENELOPE and there is not need to hide the main window during simulation as in the case of PENELOPE.

The DPM execution window displays the current control point being processed, the elapsed time since the simulation started, the number of histories simulated, the statistical uncertainty (calculated by equation 4.2) and the progress bar. A log file can be displayed/hidden at the bottom of the window by pressing the button Show/Hide log. When the check box Close window when simulation has finished is checked, the execution window is automatically closed at the end of simulation, otherwise the user has to close the window by pressing the Exit button. Pressing the Reset button during the execution has the effect of closing the simulation execution and returning PRIMO to the state previous to starting the simulation. Consequently, all partial results are lost.

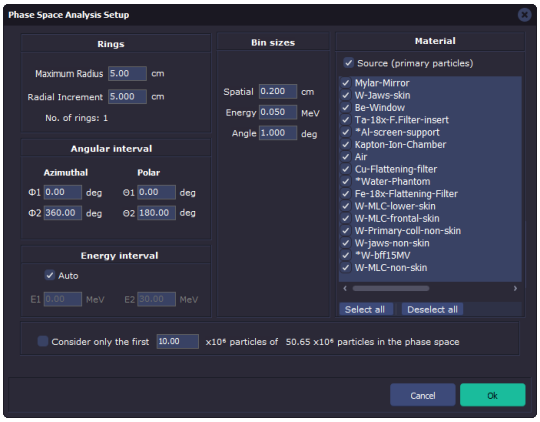


Figure 4.22: Phase space analysis setup dialog.

However, the user is prompted for confirmation.

Notice 4.14 For parallel execution DPM creates the maximum number of tasks available in the operating system. ■

4.3 Phase-space file analysis

Phase Space 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 illuminated 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 4.22) contains several options for filtering the phase space and setting the probability distribution intervals.

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. 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.

Warning 4.14 There is a maximum number of bins for the probability distributions calculated 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 4.23 shows the analysis window. The images in the upper part are the 2D spatial probability distributions of the particles in units of [cm^{-2} per history] or the probability distribution of energy in units of [MeV cm^{-2} per history] depending on what is selected on the menu panel at right. Distributions are separated by the kind

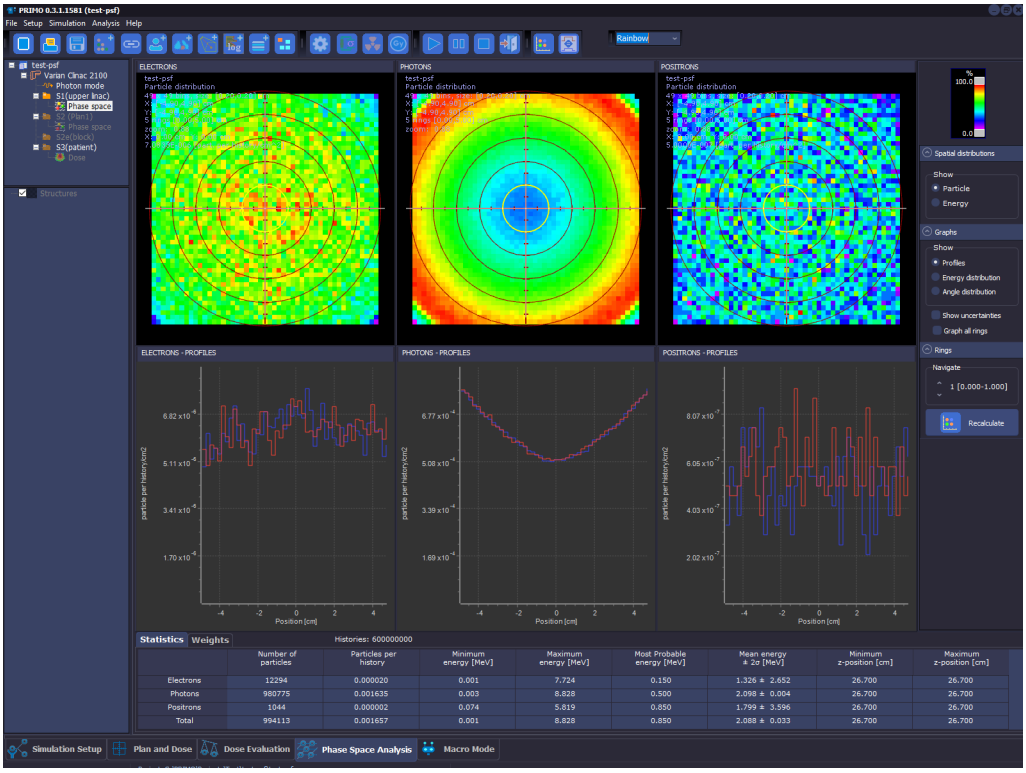


Figure 4.23: Phase space analysis window.

of particle. By default the horizontal and vertical profiles of the 2D distribution in the graph panels below each 2D distribution. To explore the 2D distributions click on the 2D distribution. To display the energy or spatial distribution graphs select the corresponding option on the menu panel at right. The statistical uncertainty ($\pm 2\sigma$) of the distribution can be plotted by checking the corresponding box on the menu.

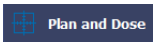
Some additional tools can be found by right clicking on the panels. A pop-up menu appears with the following options:

- Maximize: Maximize the panel to the whole analysis window.
- Restore: Restore a maximized window to its normal size.
- Logarithmic scale: Show the graph (1D distributions) in a semilogarithmic scale.
- Save as text: To save the distributions in a text file.

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.

Separated probability distributions and statistical data are calculated for each ring, i.e. by including only the particles located inside the ring. To navigate the rings use the option in the menu panel.

4.4 Plan and Dose workspace



This workspace is useful to explore the treatment fields and the simulated dose distributions. Its components are shown in figure 4.24. These are:

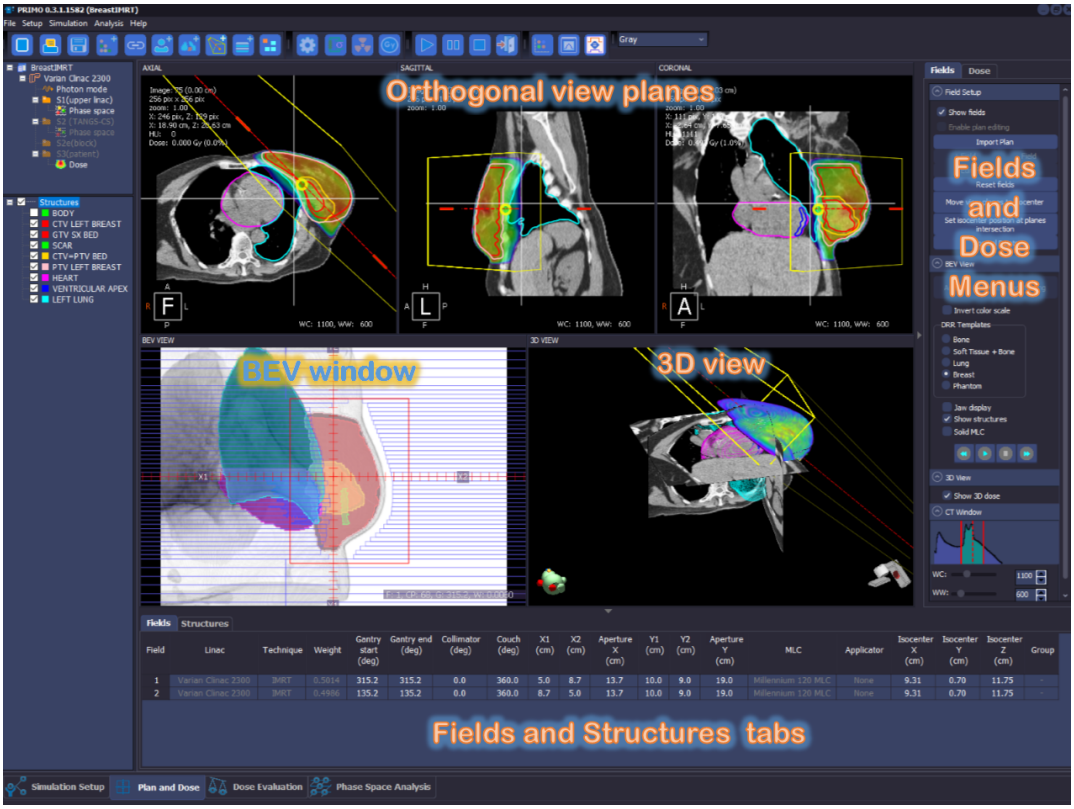


Figure 4.24: Plan and Dose workspace. Its component windows are identified in the figure.

- Orthogonal view planes: Display the fields, contours and the dose (if any) superimposed to the CT slices. Click on the image to change the view plane. The planes intercept at the clicking point. Rotating the mouse wheel allows to navigate the focused view through the direction normal to the plane. Right click to display a contextual pop-up menu. Figure 4.25 depicts the patient orientation indicator that is shown at the bottom-left of each view.

  > **Warning 4.15** When any of the parameters that were used to estimate the dose distribution is changed (including the CT segmentation), the warning message "Invalid dose!" appears on the orthogonal view planes.

- Beam Eye View (BEV): Displays the Digitally-Reconstructed Radiograph (DRR) created for the field selected on the Fields tab . The DRR is a 2D projection of the CT volume taken from the point of view of an observer situated in the linac target and looking in the direction of the field. The jaws, MLC and contours are also projected on the DRR. In dynamic fields, the movement of the MLC leaves and the jaws (*e. g.*, jaw tracking) can be visualized in cine mode on the BEV view by pressing the Play button in the Fields menu. The range of the CT numbers considered in creating the DRR can be chosen from a set of predefined templates in the Fields menu. Click with the right button of the mouse to display a contextual pop-up menu. One of the functions included in the contextual menu (Show DVHs/profiles) hides the BEV view and in its place, shows a view of the dose profiles or the dose-volume histograms (DVHs)(see figure 4.26).
- Dose profiles and DVH view: When a dose distribution has been estimated, the BEV view can be switched to a view showing dose profiles or DVHs by selecting the function Show

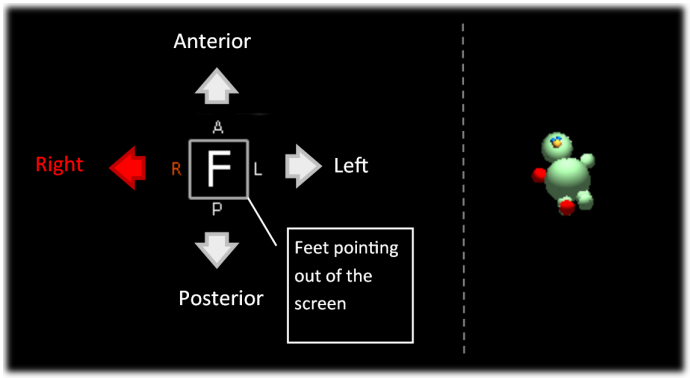


Figure 4.25: Plan and Dose workspace. Patient orientation indicators of the orthogonal view planes (left) and of the 3D view (right). Note that the right of the patient is always drawn in red.

Figure 4.26: Plan and Dose workspace. The BEV view is switched to the profiles and DVHs view. The list box in the window caption allows to select the curve (among the profiles and DVHs) that is visualized in the window.

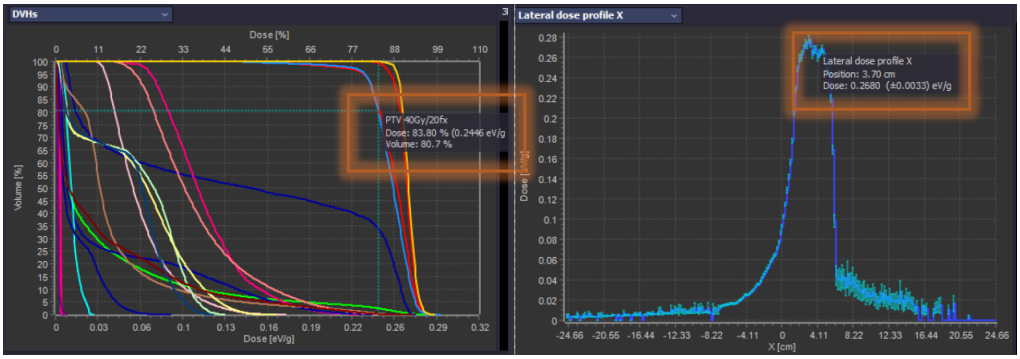


Figure 4.27: Plan and Dose workspace. Clicking on a dose profile or a DVH produces that the data of the curve is presented on a small box. To remove the box from screen click on any location outside the box.

DHVs/profiles) in the contextual menu that appears when the right mouse button is clicked on the BEV view. This is illustrated in figure 4.26. The Dose profiles and DVH view presents dose profiles taken along the axial, sagittal and coronal directions of the current orthogonal planes selected in the views. To select a dose profile for visualization in the view use the list box in the window caption bar. The same way, this list box allows to select the DVHs for visualization. Click on a point of the profile curve to retrieve the data of the point. Also click on a DVH to retrieve its data as it is shown in figure 4.27.

- 3D view: Displays the fields, the selected structures, the current CT slices and the dose in a 3D scene of the patient. Drag with the left button of the mouse to rotate in the azimuthal and polar angles. Click with the right button of the mouse to display a contextual pop-up menu. The patient position is represented by the little man at bottom-left and the linac gantry position for the current field is represented by the linac at bottom-right.
- Fields tab: Displays the field parameters. Most of these parameters are editable except for dynamic fields (fields with more than one control point).
- Structures tab. Displays the list of structures and its parameters including the structure volume, its minimum, maximum and average dose in percentage of the maximum dose (of the whole distribution) and in absolute units (either eV/g per history or Gy).
- Fields menu: The function grouped in this menu are the following (see figure 4.28):
  - Show fields: Toggles between showing or not the fields on all the views.
  - Enable plan editing: Toggles between enabling and disabling field editing. Dynamic fields (with more than one control point) are not editable. For those plans only the position of the isocenter can be modified.
  - Plan import: Imports a plan from a DICOM RT PLAN formatted file (see section 4.1.5).
  - +Field, -Field: (+) Inserts a new field, (-) deletes the selected field. Enabled only when Enable plan editing is checked (see section 4.1.2).
  - Edit Field parameters: Opens a dialog to edit the field parameters as it is described in section 4.1.2.
  - Reset fields: Deletes all the fields and creates a default, 10×10 cm^2 field with the isocenter set at $(0,0,0)$ cm (see figure 4.9). This operation is not reversible. A warning message is issued.
  - Move view planes to isocenter: Sets the intersection point of the view planes to the isocenter position.
  - Set isocenter position at planes intersection: Changes the position of the isocenter

to the current view planes intersection point. In complex IMRT plans the position of the isocenter can be changed using this function. This operation is not reversible, therefore, the previous position of the isocenter is lost. A warning message is issued.

- Control Points: Opens a window that shows information about the control points in the plan (see section 4.1.2).
- Activate isocenter repositioning: Activates a mode that allows to reposition the isocenter in the BEV image. Once activated, the field aperture representation can be dragged over the DRR image to reposition the isocenter in the plane of the DRR.
- DRR templates: Selects a predefined template to create the DRR. A template assigns weight factors to ranges of CT numbers ($CTnumber = HU + 1000$). These weight factors are applied to enhance or suppress the visualization of given tissues in the DRR according to its density (*e. g.*, the Bone template produces a DRR showing the bones by excluding from the DRR all those tissues with a CT number less than 1160).
- Jaw display: Toggles between showing and hiding the jaws visualization on the BEV view.
- Show structures: Toggles between showing and hiding the selected structures on the BEV view.
- Solid MLC: Toggles between showing a transparent MLC leaf and showing a semi-transparent leaf visualization on the BEV view.
- Cine mode controls: one step backward, play, stop, step forward: Controls the dynamic representation (cine mode) of the MLC leaves and the jaws on the BEV view.
- Show 3D dose: Toggles between showing or not the dose distribution in the 3D view.
- CT Window: Controls the CT-number window used to assign the color scale to the CT slices displayed in the orthogonal views. The window is defined by a window center (WC) and a window width (WW). Click on the histogram to place the window center at the clicked position. Move the sliders to modify the WC and the WW. They can also be changed by using the spin editors. Click with the right button to pop up a menu with predefined windows.

  R In the PRIMO convention the HUs are added to a value of 1000, thus a CT number of 1000 corresponds to water.

- Dose menu: The function grouped in this menu are the following (see figure 4.28):
  - Show dose: Toggles between showing or not the dose distribution on all the views.
  - Show dose scale: Toggles between showing or not the color scale for the dose. When the dose is displayed as isodose curves the isodose levels can be edited by right clicking on the scale.
  - Dose inspection: Reports the minimum and maximum dose and the dose at the intersection point of the orthogonal planes. When the buttons Min. dose or Max. dose are pressed, the intersection point of the orthogonal planes is set at the point of minimum or maximum dose, respectively. Enter a value for the Sagittal, Axial and Coronal edit boxes and press Apply to move the planes intersection to that point and to obtain the value of the dose at that point. Also, when the orthogonal planes are changed their intersection point is reported in these edit boxes. Notice that the dose is reported together with the value of its statistical uncertainty ($\pm 2\sigma$) expressed in absolute and in relative units.
  - Denoise dose: Performs a denoising of the dose distribution using the IRON algorithm [FN03]. Notice the number of denoising applied on the dose distribution

Figure 4.28: Plan and Dose workspace. Fields menu (left) and Dose menu (right).

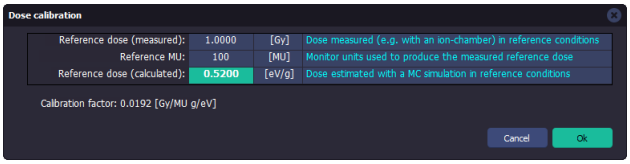


Figure 4.29: Dose calibration dialog.

appears in parentheses at the side of the button.

- Toggle isodose/color wash: Toggles between visualizing the dose as isodose lines or as a color wash map.
- Dose in Gy: Convert the dose from eV/g to Gy. A dose calibration must exist for the project. The Monitor Units in the edit box are the total MU for the plan read from the DICOM file and cannot be edited. The number of fractions are also read from the DICOM file but can be changed by the user. Refer to section 3.8 for an overview of the dose calibration process. A dose conversion factor for a project is introduced by selecting the option Set a dose conversion factor in the main menu and editing the values of the reference doses and monitor units in the Dose calibration dialog (see figure 4.29).
- Null dose voxels with uncertainty higher than: When applied it sets to zero all the dose voxels whose uncertainty (in relative units) is higher than the value set in the edit box. The dose distribution is not permanently modified. Notice the maximum, average and minimum uncertainty in the dose distribution is reported.
- Reload the dose: Reloads the (unaltered) dose from disk. Any denoising or dose

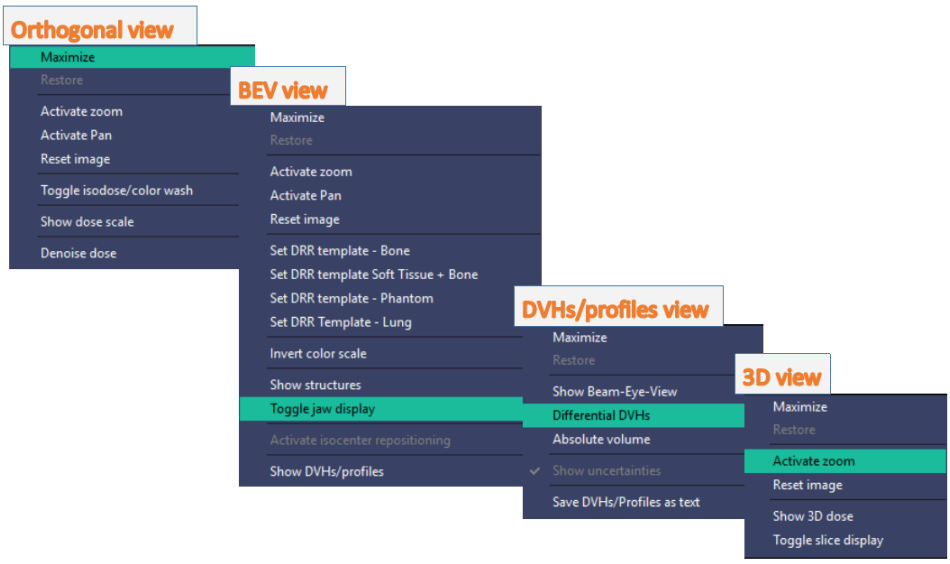


Figure 4.30: Plan and Dose workspace. Contextual menus.

conversion operation previously done on the dose distribution is lost.

- Export the dose to a text file: Exports the whole dose distribution to a text file. The format of the file is such that it can be directly plotted with the GNUPLOT program.
- Differential DVHs: Toggles between presenting the Dose-Volume Histograms in differential or cumulative mode.
- Absolute volume: Toggles between presenting the structure volume in absolute or relative units in the DVHs.
- Show uncertainties: Toggles between showing or not the uncertainties in the dose profiles.

4.4.1 Contextual menus

Right clicking on any of the view of the Plan and Dose workspace displays a contextual menu. These contextual menus offers, in most of the cases, a shortcut to the functions grouped in the Fields and Dose menus. Figure 4.30 illustrate the contextual menus associated to the views.

The functions contained in these menus that were not described in the previous section are:

- Maximize: Maximizes the selected view window.
- Restore: Restores the maximized window to its normal size.
- Activate zoom: Activate zooming in/out the view. The cursor changes indicating that the zoom function is active. Drag with the mouse over the view in the diagonal direction up to zoom in and down to zoom out.
- Activate Pan: Activate panning the view. The cursor changes indicating that the pan function is active. Drag with the mouse in the desired direction to shift the image.
- Reset image: Restores any zoomed or shifted image to its regular size and position in the view.
- Save dose plane as text: Exports the current dose plane (the one represented in the panel selected) to a text file. Two options are provided; a text file in a PRIMO format –such that it can be directly plotted with the GNUPLOT program– and the OmniPro ImRT (IBA dosimetry GmbH, Schwarzenbruck, Germany) ASCII format.

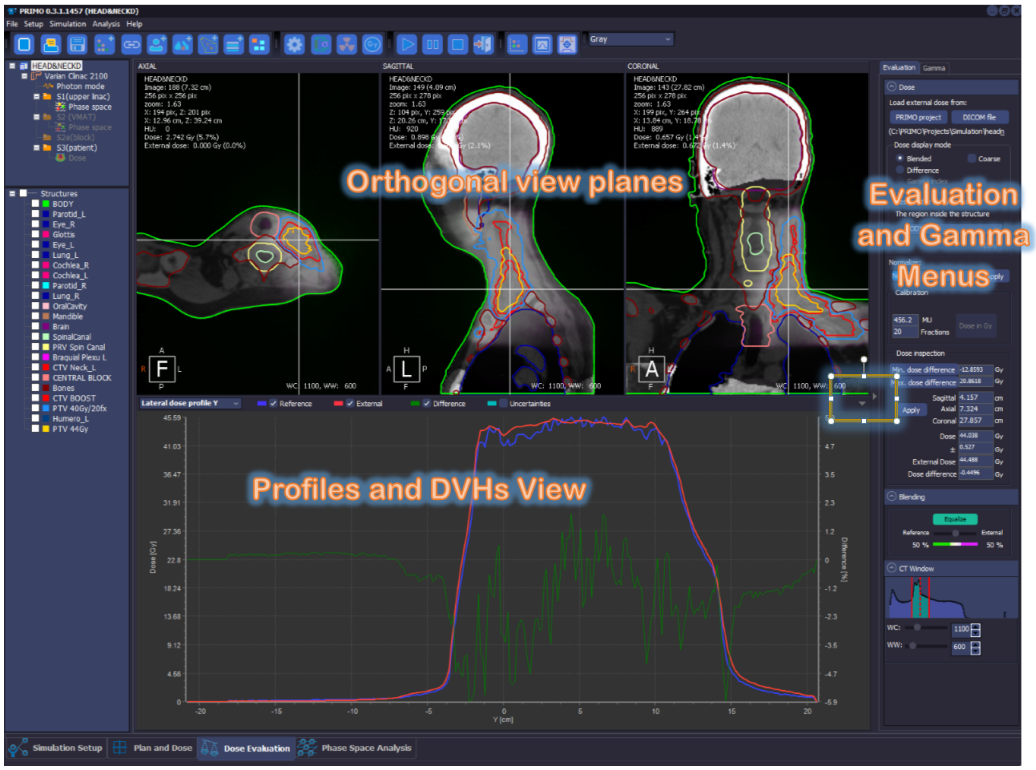


Figure 4.31: Dose Evaluation workspace. Blending two dose distributions. The window components are identified in the figure. Click on the small sliding buttons enclosed in the box to hide the Profiles and DVHs view and the Evaluation and Gamma menus

4.5 Dose Evaluation workspace

Dose Evaluation

Dose Evaluation workspace provides an environment to compare two dose distributions, the one estimated in the project which is referred to as *Reference* and an external dose distribution which is identified as *External*. The external dose distribution can be either a dose estimated by other PRIMO project or a dose distribution imported in DICOM RTDOSE format. Restrictions apply for the former, that is, the size of the dose matrix and its spatial resolution must match exactly those of the *Reference* dose. Contrarily, these restrictions do not apply for the latter because in this case the *External* dose distribution is suitably interpolated to match the size and spatial resolution of the *Reference* dose distribution.

4.5.1 Blending, Difference and Gamma Analysis.

There are three ways to compare the *External* with the *Reference* dose distribution, these are dose blending, dose difference and gamma analysis. Blending is a visual comparison tool that shows a blended image of the two dose distributions in each orthogonal view plane. Regions where the *Reference* dose is predominant appear in shades of green and regions where the *External* dose is predominant appear in shades of magenta. Regions of similar dose appear on gray. The relative weight of each dose distribution considered in forming the blended image can be regulated. Figure 4.31 illustrates the blending of two dose distributions.

Calculating the difference dose distribution, *i. e.*, *Reference*−*External* is another form of comparison available. In this case the difference-dose planes are presented in a red-blue color

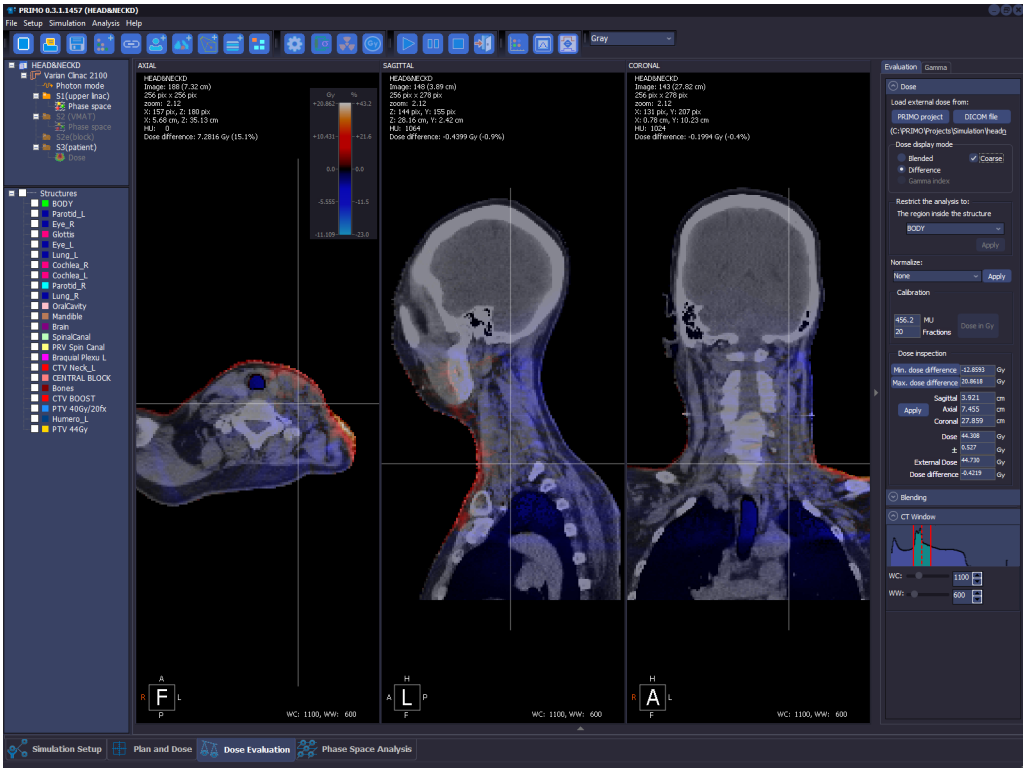


Figure 4.32: Dose Evaluation workspace. Showing the difference of two dose distributions.

scale such that positive differences appear in shades of red and negative differences in shades of blue. Figure 4.32 illustrates the difference analysis.

Both dose distributions can also be compared by performing a gamma analysis [Low+98] (see also section 4.6.1). Gamma analysis is performed for the whole *Reference* dose distribution (*i. e.*, it is a 3D-3D analysis) and the search for criteria compliance is performed in the *External* dose distribution. However, a gamma index is not strictly calculated for every dose point, instead a flag indicating whether or not the point passes the criteria is produced. Notice that it is a faster approach because the search in the vicinity of the dose point can be ended as soon as the fulfillment of the criteria is found. Also because the farthest searching distance (from the analyzed dose point) is restricted by the DTA criteria. The spatial resolution of the analysis is always set one fifth the spatial resolution of the dose distribution in each spatial direction. Trilinear interpolation is used to determine the dose in the search.

The default analysis is global. That is, the dose difference is calculated as a percentage of the maximum dose in the reference dose distribution. However, the analysis can be set as local, in which case the dose difference is calculated as a percentage of the reference dose in the voxel analyzed. Visually, the result of the analysis is presented as an image in which the voxels passing the criteria are represented in blue and those that don't are represented in red. The analysis is not only performed for the structured selected, but also for each PTV and OAR. Numerical results are presented as the Gamma Pass Rate (GPR) which represents the percentage of points of the region fulfilling the criteria. Figure 4.33 illustrates the gamma analysis.

Gamma analysis is complemented by the comparison of DVHs using the Percentage of Agreement (PA). Given DVH_1 and DVH_2, the PA is defined as

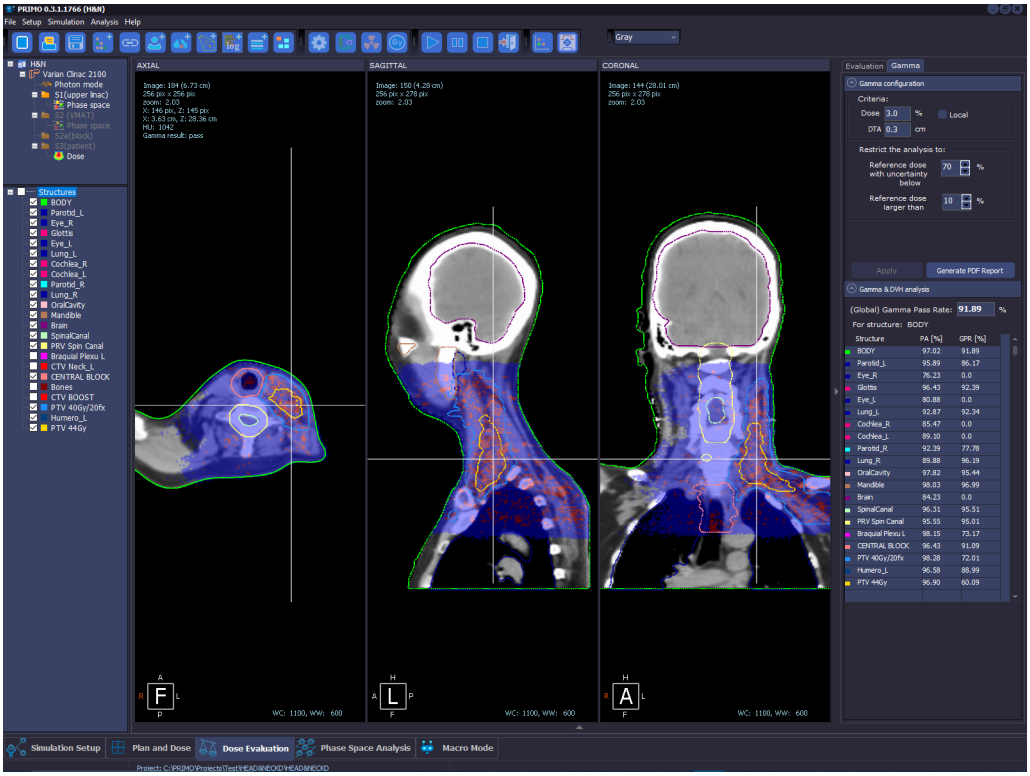


Figure 4.33: Dose Evaluation workspace. Gamma analysis. Pixels in red and blue correspond to voxels that fail and pass the analysis, respectively. Pixels not shown in the image correspond to voxels that were not included in the analysis either because the reference dose is below the dose threshold selected for the analysis or the voxel is out the region selected for the analysis.

$$\mathtt{PA} = 100\left[1 - \frac{\delta_A}{\mathtt{max}(A_1, A_2)}\right], \tag{4.3}$$

where δ_A is the absolute value of the difference area under DVH_1 and DVH_2, and where the areas under these histograms are named A_1 and A_2, respectively.

A PDF report with the results of the extended gamma analysis and DVH percentage agreement can be created by pressing the Create PDF report button. The report is saved in the project path with the name `<projectname>-dose_report.pdf`. An example is shown in figure 4.34.

Additionally to the three forms of comparison described above there is also the comparison of the dose profiles and DVHs of both distributions. The profiles are presented by default in the Profiles and DVHs View as seen in figure 4.31. The method to toggle among the dose profiles and DVHs is the same as described in section 4.4. That is, by choosing the desired curve in the list box located in the view caption bar. In this case the *Reference* profile, the *External* profile and the dose difference profile are displayed. The check boxes on the window caption allow to hide/show a profile or the visualization of the uncertainties. By clicking on a point of the profile makes that point to be the intersection of the orthogonal view planes. The dose data corresponding to the point selected is visualized on the Evaluation menu.

The functions enclosed on the Evaluation menu are (see figure 4.35):

- Load external dose from:. Select PRIMO project to load the *External* dose distribution from a PRIMO project. In the standard File Open dialog select the *.ppj project file (not the

Dose evaluation report

Created with the PRIMO system ver: 0.3.1.1582

Reference project ID: H&N

External project ID or file: RD.Wong.dcm

*Average dose standard uncertainty (%): 5.34

*Computed for all the voxels with a dose above Dmax/2 and the conditions of dose threshold and uncertainty limit specified below

Results of gamma analysis:

Dose difference criterion (%): 3.00 (Global)

DTA criterion (cm): 0.30

Dose threshold (%): 10.00

Dose uncertainty upper limit (%): 70.00

Region: BODY (EXTERNAL)

Points analyzed : 677334

Points passing : 622386

% Points passing : 91.89

Dose-Volume Histograms:

Structure	PA [%]	GPR [%]	Difference [%] D95%	D50%	D5%	D0%
BODY	97.02	91.89	-173.20	-8.12	-1.16	13.03
Parotid_L	95.89	86.17	-21.22	-5.85	3.27	9.17
Eye_R	76.23		-595.71	19.03	21.50	50.00
Glottis	96.43	92.39	-4.12	0.71	4.75	10.82
Eye_L	80.88		-629.03	-7.24	10.78	46.67
Lung_L	92.87	92.34	-2005.69	-29.21	-1.41	4.76
Cochlea_R	85.47		-33.70	-11.01	23.62	33.33
Cochlea_L	89.10		-19.11	-11.87	11.62	27.27
Parotid_R	92.39	77.78	-19.32	-9.76	3.30	24.14
Lung_R	89.88	96.19	-2429.32	-6.31	-2.81	7.59
OralCavity	97.82	95.44	-5.14	-0.72	3.69	30.26
Mandible	98.03	96.99	-2.30	-1.57	1.08	13.85
Brain	84.23		-90.62	-90.62	-16.26	20.00
SpinalCanal	96.31	95.51	-15.42	-4.47	-0.45	10.00
PRV Spin Canal	95.55	95.01	-19.70	-5.31	-1.84	11.35
Braquial Plexu L	98.15	73.17	-2.85	-0.87	3.86	13.03
CENTRAL BLOCK	96.43	91.09	-11.77	-0.73	2.87	9.69
PTV 40Gy/20fx	98.28	72.01	-4.02	-0.09	4.37	13.03
Humero_L	96.58	88.99	-4.60	-4.36	-2.18	8.41
PTV 44Gy	96.90	60.09	-6.74	-0.10	5.97	12.68

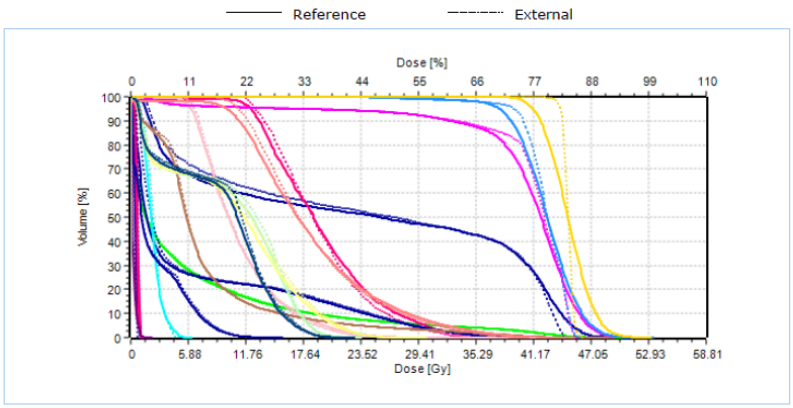


Figure 4.34: Example of a extended gamma analysis results PDF report.

dose distribution file). Select DICOM file to load the dose from a DICOM RTDOSE file. In the File Open dialog select the DICOM formatted file. In this case the dose is imported with the aid of a dialog as the one shown in figure 4.36. Select Import in the dialog to load the *External* dose and start the comparison.

> **Warning 4.16** The *External* dose distribution selected from a PRIMO project must have the same dimensions and spatial resolution of the *Reference* dose distribution.

- Dose display mode. Select Blended to make effective the comparison by blending. Select Difference to make effective the comparison by dose difference. Notice that Gamma is only an indicator because gamma analysis is controlled in the Gamma menu. Select Coarse to toggle between presenting the CT and the analysis resulting color map interpolated or not.
- Restrict the analysis to the region inside the structure: By default, the analyses are performed for the whole dose distribution. Select a region in the list box to restrict the analysis, *i. e.*, the dose difference or gamma analysis, to the voxels inside the selected region. The dose profiles are also recreated only for the voxels inside the region selected. Press the button Apply to make effective the restriction of the current analysis to the selected region.
- Normalize: By default the dose comparison is made in absolute units, either eV/g per history or Gy. That is, no normalization is applied to any of both dose distributions. This function allows to normalize the dose distributions to the common maximum or to the dose value in the voxel at the intersection point of the orthogonal view planes. These options are selected from the list box. When a normalization is done, the comparison of both distributions is presented in relative units.

> **Warning 4.17** When a normalization is made the dose is expressed in relative units. If the default option Normalize: None is selected again the analysis is still considered as relative. In order to make the comparison in absolute dose units the external dose must be reloaded.

- Dose in Gy: Convert the *Reference* dose from eV/g to Gy. A dose calibration must exist for the project. The Monitor Units in the edit box are the total MU for the plan read from the DICOM file and cannot be edited. The number of fractions are also read from the DICOM file but can be changed by the user. Refer to section 3.8 for an overview of the dose calibration process.
- Dose inspection: Reports the minimum and maximum dose difference. By pressing the Min. dose difference and Max. dose difference buttons the intersection of the orthogonal view planes goes to the voxel of minimum and maximum dose difference, respectively. It also reports the *Reference* and *External* doses and the dose difference at the intersection point. By entering the position of a given voxel in the Axial, Sagittal and Coronal edit boxes, the dose at the voxel is reported. Pressing the Apply button moves the orthogonal view planes to intersect at that voxel.
- Blending: Controls the relative intensity of the *Reference* and *External* doses in the blending map. Move the slider to change the relative intensity. The button Equalize returns the relative intensity to 50/50%.
- CT Window: Controls the CT-number window used to assign the color scale to the CT slices displayed in the orthogonal views. The window is defined by a window center (WC) and a window width (WW). Notice that in the PRIMO convention the HUs are added to a value of 1000, thus a CT number of 1000 corresponds to water. Click on the histogram to place the window center at the clicked position. Move the sliders to modify the WC and the WW. They can also be changed by using the spin editors. Click with the right button

Figure 4.35: Dose Evaluation workspace. Evaluation and Gamma menus.

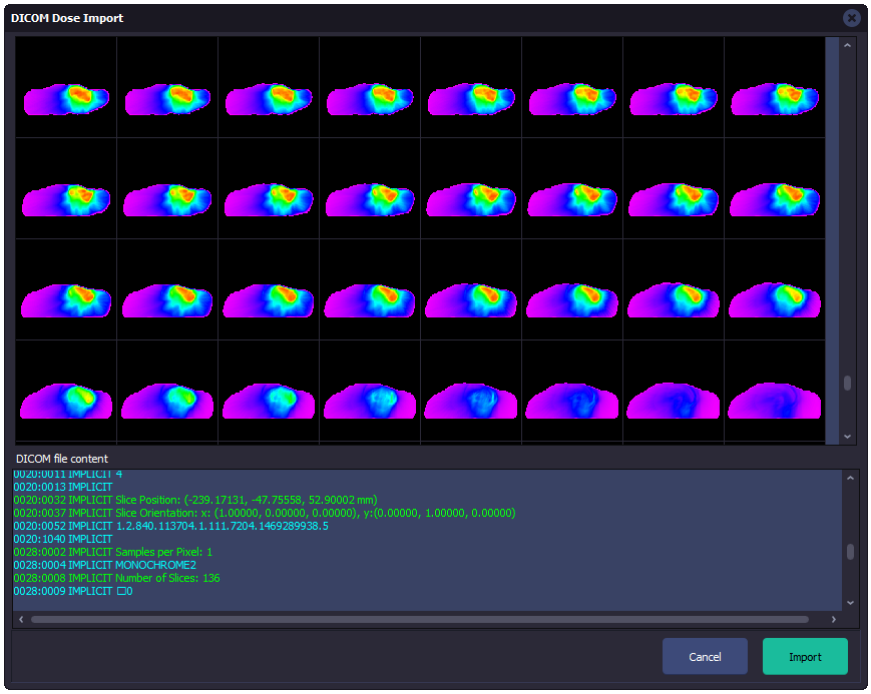


Figure 4.36: Dose Evaluation workspace. Importing an *External* dose distribution from a DICOM RTDOSE file.

to pop up a menu with predefined windows.

4.6 Comparing dose profiles 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 the experimental data. The file must be formatted as specified in figure 4.37. 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_e^{max}.

Notice 4.15 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,

```
# ---------------------------------------------
# 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 4.37: Example of text file used to import experimental data for dose comparisons. Format specifications are explained in the file header.

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 4.38) 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 4.6.1). 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:

$$\Delta d(p) = 100\frac{d_{\mathrm{e}}(p) - d_{\mathrm{c}}(p)}{d_{\mathrm{e}}^{\max}}, \tag{4.4}$$

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.

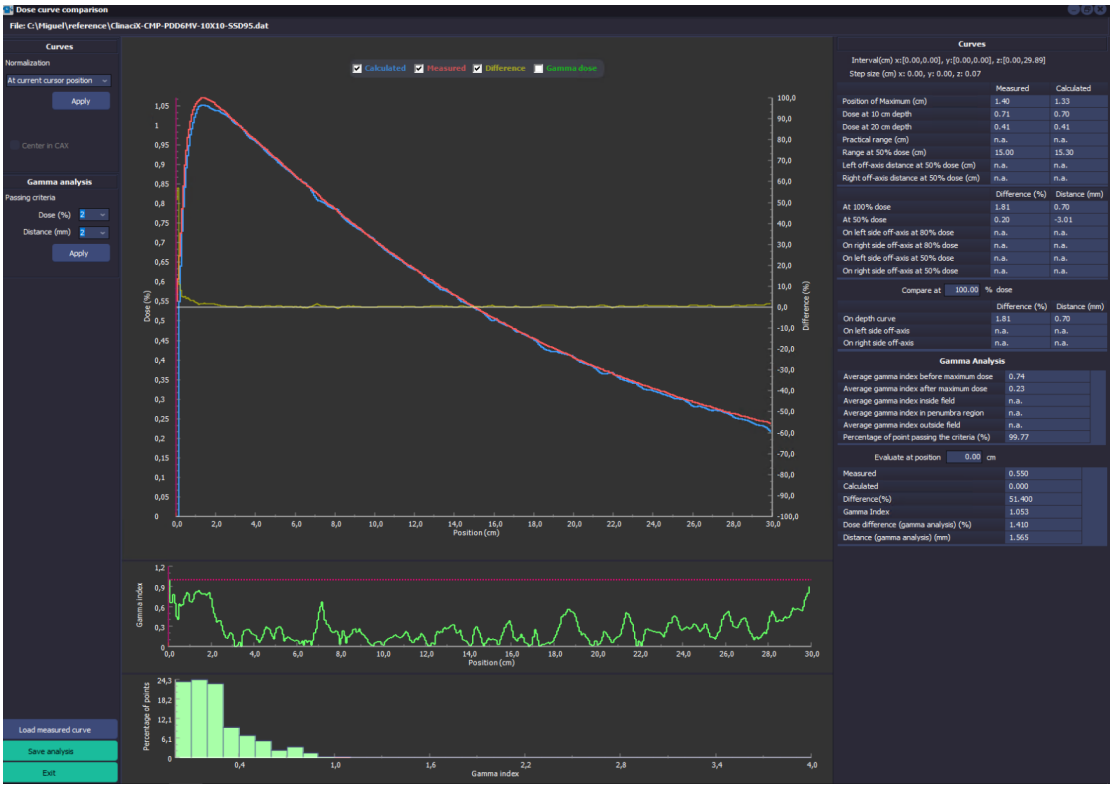


Figure 4.38: The Dose curve comparison dialog. Results from a comparison of an experimental depth-dose curve with a calculated dose distribution. The acceptance criteria for the gamma analysis are set at 2% and 2 mm, for the dose and the distance-to-agreement, respectively.

- *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 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.

4.6.1 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

$$\Gamma = \min \left\{ \sqrt{\left(\frac{\Delta d_i}{\Delta D}\right)^2 + \left(\frac{\Delta s_i}{\Delta S}\right)^2} \right\}, \tag{4.5}$$

where ΔD and ΔS are arbitrary constants known as the acceptance criteria for the dose difference and for the distance-to-agreement (DTA), 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 4.5 is reached.

Notice 4.16 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. ■

4.7 Reconstructing a plan from dynalog files

A dynalog file describes the dynamics of the MLC during the patient treatment. A dynalogs file is created for each bank of the MLC. The first letter in the file name identifies the bank (A or B). Each record in the file is taken every 50 ms by the linac MLC controller. In a Varian TrueBeam machine it is taken every 20 ms. The record contains the current and expected positions of each MLC leaf, the beam status (ON/OFF), the beam hold-off signal status, the fraction of the total dose delivered, the position of the jaws and the angles of rotation of the gantry and the collimator, among others. Together all those parameters can be used to evaluate the magnitude of errors in the MLC positioning during the treatment and their repercussion on the dose delivered to the patient.

In PRIMO there is a function that reconstructs a treatment plan from the data contained in the dynalogs files. The purpose of this function is to produce a plan that could be used to estimate the actual dose delivered to the patient during the treatment [RB19].

There are two parameters, necessary to reconstruct the plan, not stored in the dynalog files namely, the couch rotation and the position of the isocenter. During reconstruction, that data is extracted from the original plan imported from the DICOM data. Therefore, if a comparison with the original plan will be carried out in the patient's geometry, the original plan should be imported in the project previous to import the dynalog files. However, in the case it is not, the couch rotation angle is set to zero and the isocenter position is also set to coordinates $(0,0,0)$ in the reconstructed plan. After the plan is reconstructed, the position of the isocenter can be changed using the options available in PRIMO. This mechanism opens the option to compare the original plan or the plan reconstructed from the expected MLC positions with the plan reconstructed from the actual MLC positions in an arbitrary patient (e.g, a phantom).

Three methods of reconstruction are available. These are:

1. Uniform reconstruction (UR): Reconstructing by uniformly sampling the records in the dynalog files, that is, by taking records at a given time interval. This interval can be freely chosen, with a minimum value of 50 ms, in which case all records are considered.

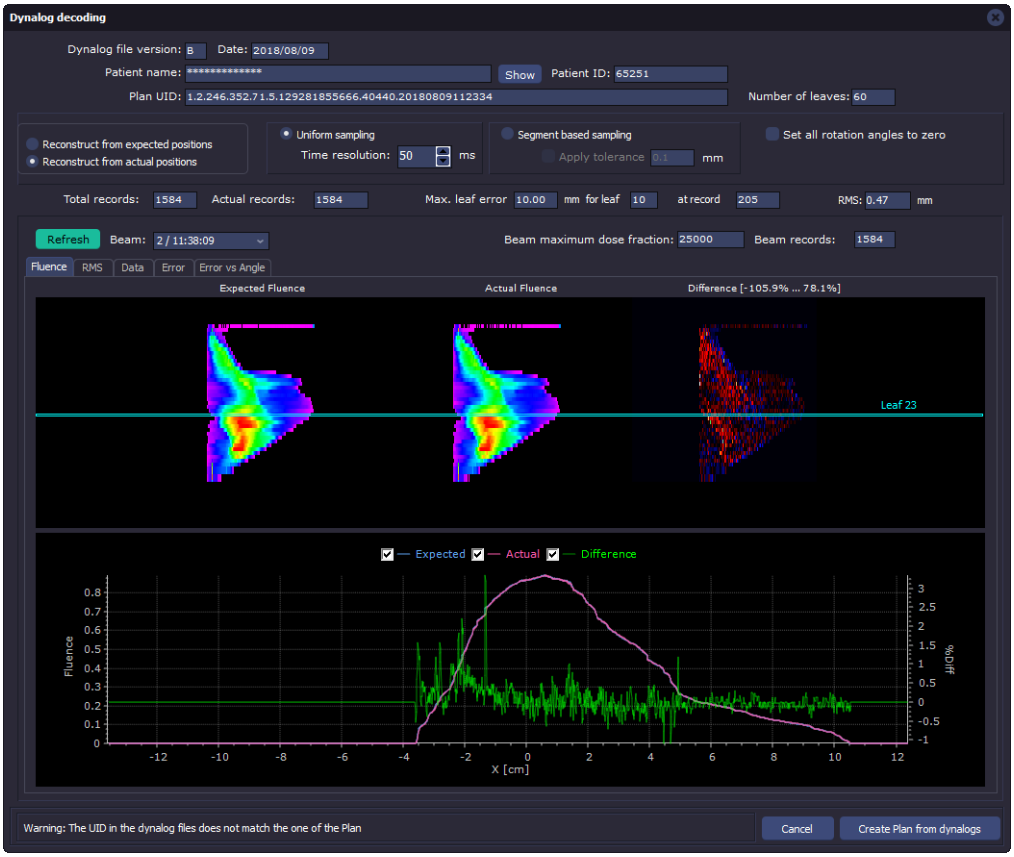


Figure 4.39: Dynalog decoding window.

2. Per-segment-reconstruction (PSR): The segment number stored in the dynalog files is used to sample only those records in which a change of segment occurs. This reconstruction method renders the same number of control points as the original plan.
3. Per-segment-reconstruction with error detection (PSR-ED): The reconstruction is made by including the records in which a change of segment occurs, in addition to all other records where at least one leaf is found having a position error above a given tolerance. The tolerance can be freely chosen starting from zero, in which case all records are considered. When the selected tolerance equals to or exceeds the maximum leaf error in the dynalog file, this reconstruction becomes equivalent to the PSR.

Dynalog files are imported by selecting the option Reconstruct the plan from dynalog files in the main menu. In the standard Open dialog select all the dynalog files corresponding to one treatment session. Notice that there is two dynalog file per treatment field, one per MLC carriage. The Dynalog decoding window is shown in figure 4.39. The upper panel in this window shows the general information of the patient, the unique identifier of the treatment plan and the dynalog file version. Only version B is supported. The name of the patient is hidden by default, but it can be displayed by pressing the Show button. The configurable elements of the Dynalog decoding window are:

- Set rotation angles to zero. If checked, all the rotation angles of the gantry, the collimator and the table are set to zero in the reconstructed plan.
- Reconstruct from expected positions. If checked, the plan is reconstructed from the expected leaf positions instead of actual leaf positions and the reconstruction is made by uniformly sampling the dynalog files.

- Uniform sampling. Activate uniform reconstruction. The time resolution of uniform sampling can be defined in the Time resolution edit box. The minimum value of time resolution that can be set is that producing a number of control points in the reconstruction that does not exceed the maximum allowed (3000). The maximum value of time resolution is 1s.
- Segment based sampling. Activate per-segment reconstruction. If the Apply tolerance is checked, the error detection option is activated. The value in the edit box establishes the tolerance value in mm.

The Total records and Actual records data informs the total number of records in the dynalogs and the total number of records (and hence of control points) considered in the reconstruction, respectively. Also, the maximum error found in any leaf, the record and leaf number where it was detected and the overall root mean square error (RMS) are reported.

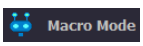
The lower panel contains a tab panel that allows to perform an analysis of the data included in the reconstruction. Those tabs are:

- Fluence: A comparison of the actual and expected planar fluence. The actual fluence is produced by the actual positions of the MLC whereas the expected fluence is produced by the expected positions. To calculate the fluence, all the rotation angles (gantry, collimator and couch) are set to zero. The fluence difference is calculated as $expected - actual$ and is expressed in percentage of the maximum expected fluence. The graph shows the comparison of the actual and expected fluence profiles for a given leaf that can be selected by clicking with the mouse on the images. This is shown in figure 4.39.
- RMS: Presents a histogram of the root mean square error (RMS) of each leaf. Histograms are separated by MLC carriage. The RMS for a leaf l is calculated as

$$\mathrm{RMS}_l = \sqrt{\frac{\sum_{i=1}^{N} (x_{l,i}^e - x_{l,i}^a)^2}{N}}, \tag{4.6}$$

  where N is the total number of records in the beam and $x_{l,i}^e$ and $x_{l,i}^a$ are the expected and actual position of the leaf l in the record i, respectively.
- Data: Shows all the data stored in the dynalogs.
- Error: Shows the distribution of the leaf error. The distribution is calculated as the number of positions with a given error. The error is considered as the absolute difference between the expected and the actual position.
- Error vs Angle: Shows a graph of the total error per gantry rotation angle. The total error is the sum of all the differences of the same sign for a given gantry angle. Therefore, two values of the total error are calculated per angle, representing the sum of positive and negative errors.

4.8 Macro mode



Macro mode is a way to automatize the execution of multiple functions, thus minimizing the user intervention. In macro mode it is possible to define a logical sequence of commands (the macro program) which are interpreted and executed by the macro interpreter to accomplish a given task.

Macro mode is located at the Macro mode workspace. The workspace is composed by three windows, the Macro editor, the Macro interpreter output and the Macro command output. The Macro editor is intended to edit the macro program. However, the macro program is a plain text file and could be written or modified with any text editor. Figure 4.40 shows the Macro mode workspace.

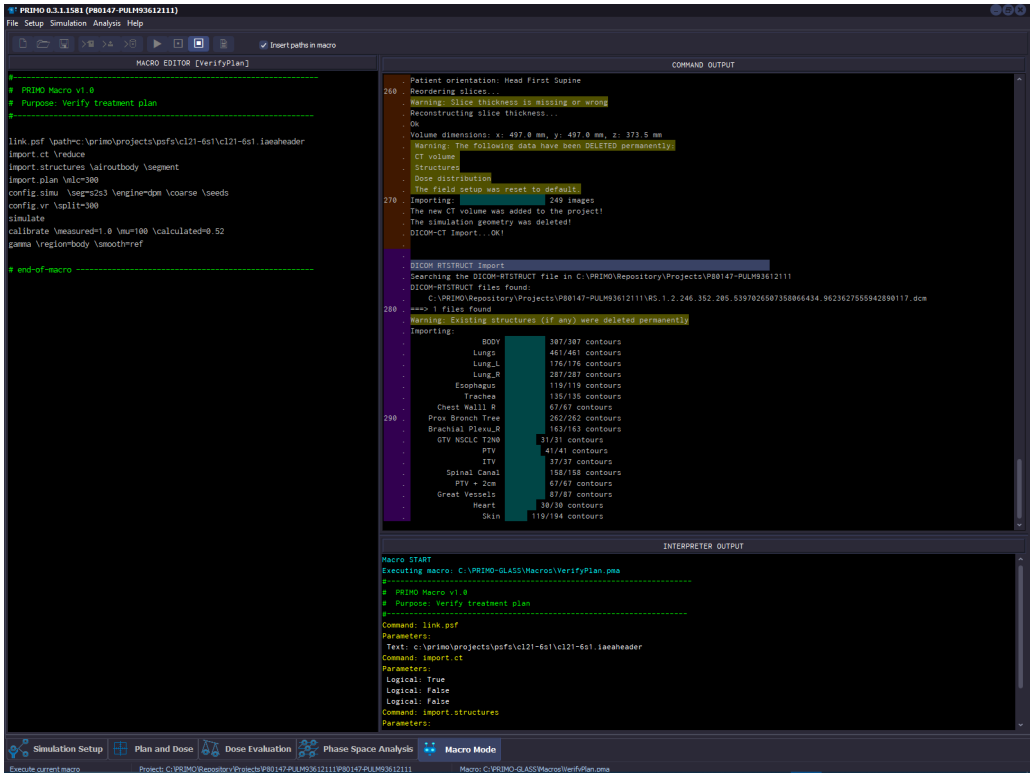


Figure 4.40: Macro mode workspace.

The functions grouped in the main menu are the following:

- Create a new macro: Initializes the macro mode. All the windows are cleared and the macro file name is reset to "default.pma" (pma stands for PRIMO macro).
- Open a macro: Loads a macro program from a text file.
- Save the current macro: Saves the macro program to a text file.
- Run set.primo.repository command: Executes a `set.primo.repository` command to define the path to the PRIMO repository. It is equivalent to command `set.primo.repository` executed from a macro program but, in this case, the path is obtained from a Browse for Folder dialog. If the check box Insert paths in macro is active the command with the selected path is inserted in the macro editor at the current cursor position. The PRIMO repository is the folder of a PRIMO project containing a dose distribution which can be compared with the one in the current project.
- Run set.dicom.repository: Executes a `set.dicom.repository` command to define the path to the DICOM repository. It is equivalent to command `set.dicom.repository` executed from a macro program but, in this case, the path is obtained from a Browse for Folder dialog. If the check box Insert paths in macro is active the command with the selected path is inserted in the macro editor at the current cursor position. The DICOM repository is a folder containing DICOM files related to the current project.
- Run link.psf command: Executes a `link.psf` command to define the path to a phase space file used as source of particles in the current project. It is equivalent to command `link.psf` executed from a macro program but, in this case, the path is obtained from a Browse for Folder dialog. If the check box Insert paths in macro is active the command with the selected path is inserted in the macro editor at the current cursor position.
- Execute current macro: Executes the macro defined in the macro editor.

- Stop PENELOPE execution: Stops the simulation with PENELOPE. Although the simulation with PENELOPE is stopped the tallies are not lost.
- Stop macro execution: Aborts the execution of the macro. The result data expected from any unfinished command as, for instance, a simulation, is lost. The user is not requested for confirmation.
- Command reference: Outputs the command reference text in the Macro command output editor. It is equivalent to command `?`.

4.8.1 PRIMO execution in macro mode from an external program

PRIMO can be executed in macro mode from an external program. The execution syntax is:

```
primo project macro
```

where `project` is the full path –including the file name and extension– of a PRIMO project `.ppj` file and `macro` is the full path –including the file name and extension– of a PRIMO macro `.pma` file. If the parameters are valid PRIMO will be executed, the project will be loaded and the macro executed.
Example:

```
primo c:\PRIMO\MyProject\MyProject.ppj c:\PRIMO\Macros\TheMacro.pma
```

When the caller application is Windows directly (*e. g.*, the Windows command line), PRIMO will run normally, otherwise it will run minimized in the taskbar.

Warning 4.18 Both parameters `project` and `macro` are mandatory, if any is absent, PRIMO will just run but no project will be loaded or macro executed. The macro file must exists and contain a valid macro program, otherwise and error will be issued and PRIMO will halt.

The project specified in the `project` parameter could not exist, in that case a new default project will be created at the specified path with the following parameters:

Linac Varian Clinac 2100 C/D
Mode Photon
Nominal energy 6 MV
Initial energy 5.4 MV
Energy FWHM 0 MeV
Focal spot FWHM 0 cm
Beam divergence 0 degrees
No variance reduction
Simulation engine penEasy
Stop condition 1.0×10^9 histories
Field size 10×10 cm^2
MLC None
Dose tallying Water phantom
Isocenter position $0, 0, 0$ cm (at CAX and at the phantom surface)
Bin size $0.5 \times 0.5 \times 0.5$ cm^3
Dose tallying volume $40.5 \times 40.5 \times 40.0$ cm^3

These parameters can all be adjusted properly by using `config`–like and other macro commands (see next sections).

4.8.2 PRIMO data exchange file

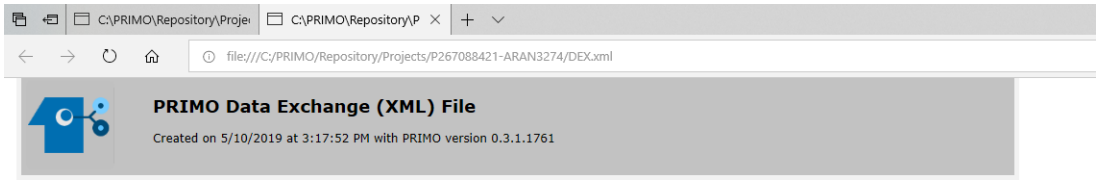
The use of the `extended` option of the `gamma` command in macro mode will activate the creation of a XML file named as DEX.xml (DataEXchange) in the project directory. The file contains the results of the analysis in XML format. The file also has an associated XSL code for its readable visualization in an internet browser or XML editor (see figure 4.41). An example listing is following:

```
<PRIMODataExchangeFile>
    <Prefix>
        <ProjectName>c:\primo\ref\ref.ppj</ProjectName>
        <exProjectName>c:\primo\ext\ext.ppj</exProjectName>
        <MacroName>plan_verify.pma</MacroName>
        <creation_date>01/12/2018</creation_date>
        <creation_time>09:25:12 AM</creation_time>
        <primo_version>0.3.1.1581</primo_version>
        <Status>4</Status>
        <ErrorMsg></ErrorMsg>
    </Prefix>
    <Table>
        <data_type>PEX_GAMMA</data_type>
        <region_id>body</region_id>
        <region_type>EXTERNAL</region_type>
        <dose_mode>DM_GLOBAL</dose_mode>
        <setting-0>3.000</setting-0>
        <setting-1>0.300</setting-1>
        <setting-2>1.000</setting-2>
        <setting-3>70.000</setting-3>
        <setting-4>0.000</setting-4>
        <result-0>293580.000</result-0>
        <result-1>122327.000</result-1>
        <result-2>98.667</result-2>
        <result-3>0.000</result-3>
        <result-4>0.000</result-4>
    </Table>
    <Table>
        <data_type>PEX_PA</data_type>
        <region_id>BODY</region_id>
        <region_type>EXTERNAL</region_type>
        <dose_mode>DM_GLOBAL</dose_mode>
        <setting-0>0.000</setting-0>
        <setting-1>0.000</setting-1>
        <setting-2>0.000</setting-2>
        <setting-3>0.000</setting-3>
        <setting-4>0.000</setting-4>
        <result-0>97.017</result-0>
        <result-1>0.000</result-1>
        <result-2>0.000</result-2>
        <result-3>0.000</result-3>
        <result-4>0.000</result-4>
     </Table>
</PRIMODataExchangeFile>
```

Meaning of the XML tags is depicted in table 4.2.

Tag	Meaning
<PRIMODataExchangeFile>	Marks the start and end of the file
<Prefix>	The file prefix data. Contains general data on the analysis
<ProjectName>	The path and file name of the reference project ppj in the comparison
<exProjectName>	The path and file name of the external project ppj file in the comparison
<MacroName>	Name of the macro program that executed the analysis
<creation_date>	Date of the XML file creation
<creation_time>	Time of the XML file creation
<primo_version>	The PRIMO version used for the analysis
<Status>	The exit status of the macro program that executed the processing. Possible values are: -3: timed out -2: aborted by user -1: unknown $+0$: waiting or unknown $+1$: processing pending $+2$: copied and pending $+3$: ongoing processing $+4$: finished successfully.
<ErrorMsg>	An error message, if any; otherwise empty.
<Table>	Marks a block of results. There is two <Table> blocks per structure, one for reporting the results of gamma analysis and the other reporting the PA.
<data_type>	The kind of result reported in the table. Possible values are: PEX_GAMMA and PEX_PA, for gamma analysis and PA, respectively.
<region_id>	The region id as imported from the DICOM file.
<region_type>	The region type as imported from the DICOM file.
<dose_mode>	Possible values: DM_GLOBAL and DM_LOCAL, for global and local analysis, respectively. It is meaningful only for gamma analysis.
<setting-0>	Setup parameter 0. For gamma analysis it is the dose difference criterion in %. Not used for PA.
<setting-1>	Setup parameter 1. For gamma analysis it is the DTA criterion in cm. Not used for PA.
<setting-2>	Setup parameter 2. For gamma analysis it is the dose threshold in %. Not used for PA.
<setting-3>	Setup parameter 3. For gamma analysis it is the dose uncertainty upper limit in %. Not used for PA.
<result-0>	Result value 0. For gamma analysis it is the number of points (dose voxels) analyzed; for a PA analysis it is the PA value in %.
<result-1>	Result value 1. For gamma analysis it is the number of points passing the criteria. Not used for PA.
<result-2>	Result value 2. For gamma analysis it is the gamma pass rate in %. Not used for PA.
<result-3>	Result value 3. Not used, set to 0.
<result-4>	Result value 4. Not used, set to 0.

Table 4.2: Tag meaning in the PRIMO data exchange XML file.



Reference Project: C:\PRIMO\Repository\Projects\P267088421-ARAN3274\P267088421-ARAN3274
External Project: C:\PRIMO\Repository\Projects\P267088421-ARAN3274\RD.1.2.246.352.71.7.129281855666.63100.20180907115342.dcm
Processing Macro: C:\PRIMO\Repository\Macros\VerifyPlan_test.pma

Result type	Region id	Region type	Dose mode	Setting(0)	Setting(1)	Setting(2)	Setting(3)	Setting(4)	Result(0)	Result(1)	Result(2)	Result(3)	Result(4)
PEX_GAMMA	body	Unknown	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	713838.000	361075.000	50.582	0.000	0.000
PEX_GAMMA	BODY	EXTERNAL	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	713838.000	361075.000	50.582	0.000	0.000
PEX_GAMMA	Brain	AVOIDANCE	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	451497.000	202884.000	44.936	0.000	0.000
PEX_GAMMA	Brainstem1	ORGAN	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	5477.000	5477.000	100.000	0.000	0.000
PEX_GAMMA	Eye_R	AVOIDANCE	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	83.000	83.000	100.000	0.000	0.000
PEX_GAMMA	Eye_L	AVOIDANCE	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	22.000	22.000	100.000	0.000	0.000
PEX_GAMMA	Lent_R1	ORGAN	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	1.000	1.000	100.000	0.000	0.000
PEX_GAMMA	Opit_N_R	ORGAN	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	9.000	9.000	100.000	0.000	0.000
PEX_GAMMA	Optic_N_L	ORGAN	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	7.000	7.000	100.000	0.000	0.000
PEX_GAMMA	Chiasm	ORGAN	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	90.000	90.000	100.000	0.000	0.000
PEX_GAMMA	Hippo_R	ORGAN	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	1138.000	976.000	85.764	0.000	0.000
PEX_GAMMA	Hippo_L	ORGAN	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	993.000	993.000	100.000	0.000	0.000
PEX_GAMMA	PTV_24.75Gy	PTV	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	7629.000	0.000	0.000	0.000	0.000
PEX_GAMMA	PTV_20Gy	PTV	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	57051.000	639.000	1.120	0.000	0.000
PEX_GAMMA	Brain_out_ptv	AVOIDANCE	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	365493.000	197053.000	53.914	0.000	0.000
PEX_GAMMA	PTV_total	PTV	DM_GLOBAL	3.000	0.300	1.000	70.000	0.000	64680.000	639.000	0.988	0.000	0.000
PEX_PA	BODY	EXTERNAL	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	67.233	0.000	0.000	0.000	0.000
PEX_PA	Brain	AVOIDANCE	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	68.010	0.000	0.000	0.000	0.000
PEX_PA	Brainstem1	ORGAN	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	78.763	0.000	0.000	0.000	0.000
PEX_PA	Eye_R	AVOIDANCE	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	46.483	0.000	0.000	0.000	0.000
PEX_PA	Eye_L	AVOIDANCE	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	49.091	0.000	0.000	0.000	0.000
PEX_PA	Lent_R1	ORGAN	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	46.610	0.000	0.000	0.000	0.000
PEX_PA	Opit_N_R	ORGAN	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	37.683	0.000	0.000	0.000	0.000
PEX_PA	Optic_N_L	ORGAN	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	38.556	0.000	0.000	0.000	0.000
PEX_PA	Chiasm	ORGAN	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	55.034	0.000	0.000	0.000	0.000
PEX_PA	Hippo_R	ORGAN	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	75.904	0.000	0.000	0.000	0.000
PEX_PA	Hippo_L	ORGAN	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	87.304	0.000	0.000	0.000	0.000
PEX_PA	PTV_24.75Gy	PTV	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	65.750	0.000	0.000	0.000	0.000
PEX_PA	PTV_20Gy	PTV	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	65.823	0.000	0.000	0.000	0.000
PEX_PA	Brain_out_ptv	AVOIDANCE	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	69.364	0.000	0.000	0.000	0.000
PEX_PA	PTV_total	PTV	DM_GLOBAL	0.000	0.000	0.000	0.000	0.000	65.813	0.000	0.000	0.000	0.000

Figure 4.41: A PRIMO data exchange file DEX.xml loaded in a Web browser.

4.8.3 Macro mode rules

Command syntax:

```
<command name> <parameter> <parameter> ...
```

Rules:

- At least one space character must be placed separating the command and the parameters.
- Comment lines must start with a # character. The whole line starting with this character is ignored by the macro interpreter.
- A comment line can be placed anywhere in the macro program.
- Empty lines are ignored by the command interpreter.
- Unrecognized commands or syntax errors provoke the macro execution abortion.
- Syntax is not case sensitive.
- Command parameters start with the \ character.
- Command parameters must be separated by, at least, one space character.
- Parameter values are specified in this manual as either <text>,<integer>,<float>. It means that a text, integer value or floating point value must be specified, respectively. The <> characters must be not included in the parameter value.
- The order of the parameters is not relevant.
- A command and all its parameters must be in the same line of text.
- Units must be never included in a parameter value.

4.8.4 Macro commands reference. In alphabetical order

`add.field`

Adds a new field. The new field parameters are copied from the last field defined in the linac. That is, if for instance a third field is being added it will be identical to field 2. Use the `\config.field` command to change the field parameters.

- Parameters:
  None.

Example:

```
add.field
```

`calibrate`

Establishes a factor to convert the dose from units eV/g to units Gy.

- Parameters:
  `\measured=<float>`
  Measured dose (in Gy/MU) in reference conditions. Default is `\measured=1.0`.
  `\mu=<float>`
  Monitor units used to obtain the measured reference dose. Default is `\mu=100.0`.
  `\calculated=<float>`
  The dose (in eV/g per history) estimated by a Monte Carlo simulation in reference conditions. This parameter is mandatory, there is not default.

Example:

```
calibrate \calculated=0.781
```

`config.beam`

Configures the initial parameters of the beam.

- Parameters:
  `\nominal=<integer>`
  The index of the nominal energy. See the command `list`. The default is `\nominal=1`.
  `\energy=<float>`
  The initial energy in MeV. If not specified the default value for the selected nominal energy is taken.
  `\efwhm=<float>`
  The full-width-at-half-maximum of the normal distribution of the initial energy (in MeV). If not specified the default value for the selected nominal energy is taken.
  `\focal=<float>`
  The radius of the beam focal spot. If not specified the default value for the selected nominal energy is taken.
  `\div=<float>`: The beam divergence in degrees. If not specified the default value for the selected nominal energy is taken.

Example:

```
config.beam \nominal=1 \energy=6.2 \focal=0.1
```

`config.field`

Configures a field.

- Parameters:
  `\field=<integer>`
  The number of the field to be removed. Fields are numbered starting from 1. Trying to configure a field of an IMRT plan will also produce an error. Default is `\field=1`.
  `\rotations=<float,float,float>`
  The rotation angles (in degrees) of the gantry, collimator and table. If this parameters is not specified, rotations remain unchanged.
  `\jaws=<float,float,float,float>`
  The jaws aperture. The order is x_1, x_2, y_1, y_2. If this parameter is not specified the jaws aperture remains unchanged.
  `\iso=<float,float,float>`
  The position x, y, z of the isocenter. If this parameter is not specified the isocenter remains unchanged. The isocenter position is changed not only for the field being configured but for all fields in the plan.
  `\mlc=<integer>`
  The code of the MLC to be linked to the field. If not specified a MLC is not linked to the field. To see the available MLC codes use the `list` command. The MLC is changed not only for the field being configured but for all fields in the plan.
  `\eappl=<integer>`
  The code of the electron applicator to be linked to the field. If not specified an electron applicator is not attached to the field. To see the available codes use the `list` command.

Example:

```
config.field \field=1 \rotations=180,0,0 \iso=0,0,5.0
```

`config.linac`

This command changes the linac model and linac operating mode of the project. This command resets all the project data (including the patient model) to default. Also, all simulation results are deleted. Therefore, this command must be used with extreme caution.

- Parameters:

  `\linac=<integer>`
  The linac model code. Default is `\linac=6` which corresponds to a Varian Clinac 2100 C/D. To see the available linac codes use the `list` command.
  `\mode=<integer>`
  The linac operation mode. Accepted values are `\mode=1` and `\mode=2` which corresponds to electron and photon modes, respectively.

Example:

```
config.linac \linac=5 \mode=2
```

`config.simu`

Configures the simulation parameters.

- Parameters:

  `\seg=<text>`
  Defines the segment to be configured. Default is `\seg=s1`. Accepted values are: `s1`, `s2`, `s3`, `s1s2`, `s1s2s3`, `s2s3`
  `\engine=<text>`
  Defines the simulation engine. Default is `\engine=penelope`. Accepted values are: `penelope`, `dpm`
  `\coarse`
  If specified and the selected engine is DPM, coarse simulation is set.
  `\seeds`
  If specified a new sequence of the random number generator is generated.
  `\time=<float>`
  Set the stop condition to be the simulation time in seconds. Default stop condition is by number of histories. This option is only valid when the simulation engine selected is PENELOPE.
  `\histories=<float>`
  Set the stop condition to be the number of histories.
  `\sigma=<float>`
  Set the stop condition to be the uncertainty (in %). This option is only valid when the simulation engine is PENELOPE and the tally is the dose distribution.
  When no stop condition is specified, the stop by number of histories condition is set and the number of histories is taken from the default for the segment to be simulated (10^9 for segment s1 or the total number of histories in the source phase space for other segments).
  `\refresh=<float>`
  Set the output refresh time in seconds. Default is `\refresh=60`. This option is only valid when the simulation engine is PENELOPE.
  `\cpus=<integer>`
  Set the number of processes used in simulations with PENELOPE. Default is `\cpus=1`. This parameter is not used in simulations with DPM.

Example:
```
config.simu \seg=s1 \engine=penelope \time=3600 \histories=10000000 \cpus=8
```

`config.vr`

Configures the variance-reduction techniques.

- Parameters:

  `\force=<integer>`
  Activates interaction forcing in the linac target. The parameter value is the forcing factor.
  `\rotational`
  Activates rotational splitting (with the option 'fitted') in the simulation of segment s1.
  `\rotationalfull`
  Activates rotational splitting (with the option 'biggest') in the simulation of segment s1.
  `\roulette`
  Activates splitting roulette (with the option 'fitted') in the simulation of segment s1.
  `\roulettefull`
  Activates splitting roulette (with the option 'biggest') in the simulation of segment s1.
  `\split=<integer>`
  Activates simple splitting in phantom or CT in the simulation of segment s3. The parameter value is the splitting factor.

Example:
```
config.vr \split=300
```

`gamma`

Performs a comparison by gamma analysis of the project dose distribution with an external dose distribution.

- Parameters:

  `\primo`
  The external dose is expected to be primo formatted and will be search for in the PRIMO repository. Default is `\dpm`.
  `\deltadose=<float>`
  The dose difference criterion in percentage. Default is 3.0%
  `\dta=<float>`: The distance-to-agreement criterion in centimeters. Default is 0.3 cm.
  `\threshold=<float>`
  The dose threshold in percentage. Only dose values greater than this threshold will be considered in agamma analysis. Default is 10% of the maximum reference dose.
  `\unc=<float>`
  The uncertainty lower limit in percentage. All those voxels of the reference dose distribution with uncertainty larger than the specified value will be not included in gamma analysis. Default is 100%.
  `\region=<text>`

The ID of a structure. Only those voxels inside this region will be considered in the analysis. Typically `\region=body`, nevertheless by default the analysis is performed in the whole dose distribution.

`\ref=<text>`

Sets the reference dose. By default the reference dose is the project dose. Set this parameters to `\ref=external` to force the reference dose to be the imported dose.

`\smooth=<text>`

Smooths the dose distribution previous to gamma analysis. Possible values are: `ref` to smooth the reference dose when it is the Monte Carlo estimated dose of the project; `both` to smooth both dose distributions, the internal and external provided they both are Monte Carlo estimated dose distributions. The dose imported in DICOM format is never smoothed. If the parameter `\ref=external` is employed, using `\smooth=ref` will have no effect whatsoever. In this case use `\smooth=both` to smooth the non-reference project dose distribution.

`\extended`

Extends the gamma analysis to all the structures identified as PTVs and OARs. It also extends the analysis to DHVs comparison by PA calculation. This option produces the creation of a XML file containing the analysis results. See section 4.8.2.

`\report`

Creates a PDF report with the results of the analysis as described in section 4.5.1.

`\local`

Activates local analysis. The dose difference is compared with the specified percentage of the local reference dose. By default the analysis is global, that is, the dose difference is compared with the specified percentage of the global maximum dose.

Example:

```
gamma \deltadose=2.0 \dta=0.2 \region=body \ref=external
```

`get.env`

Outputs the paths of the DICOM and PRIMO repositories.

- Parameters:

  None

Example:

```
get.env
```

`import.ct`

Imports DICOM-CT files.

- Requirements:
  - The CT files are searched for in the DICOM repository with the search mask `CT*.dcm`
- Parameters:

  `\reduce`

  If specified, this parameter force to reduce the size of the CT volume. Otherwise the CT volume is imported in its original size.

  `\segment`

  If specified, this parameter force to create the simulation geometry by segmenting the CT volume after import. Otherwise the simulation geometry is not created.

Example:
`import.ct \reduce \segment`

`import.dynalogs`

Reconstructs the plan from the dynalog files. See section 4.7.

- Requirements:
  - The dynalog files are searched for in the DICOM repository with the search mask `*.dlg`
- Parameters:

  `\uniform`
  Forces to uniform sampling.
  `\timeres=<float>`
  Defines the time resolution in milliseconds for sampling. Default value is `\timeres=500`.
  `\tolerance=<float>`
  Defines the tolerance in mm for non-uniform sampling. Default value is `\tolerance=0.1`.
  `\resetangles`
  If specified the gantry, collimator and couch angles are set to 0 degrees.
  `\fromexpected`
  If specified the reconstruction is made from the expected MLC leaves positions instead of the actual positions.

Example:
`import.dynalogs \tolerance=0.2 \resetangles`

`import.plan`

Imports a DICOM-RTPLAN file.

- Requirements:
  - The RTPLAN file is searched for in the DICOM repository with the search mask `RP*.dcm`
- Parameters:

  `\mlc=<code>`
  Define the code of the MLC that will be selected for the plan. If not specified, the Varian 120 Millenium MLC (`\mlc=300`) is selected. To see the valid mlc codes for the linac model of the project use the `\list` command.

Example:
`import.plan \mlc=300`

`import.structures`

Imports a DICOM-RTSTRUCT file. The region defined by all those structures with an associated HU or physical density is filled in the CT.

- Requirements:
  - The RTSTRUCT file is searched for in the DICOM repository with the search mask `RS*.dcm`
- Parameters:

`\airoutbody`
If specified the CT is filled with air in the region outside the body contour. The structure defined by the body contour is selected automatically.
`\fillbody`
If specified the CT is filled with the HU of the region inside the body contour. The structure defined by the body contour is selected automatically. This option is useful when importing phantoms created from contours.
`\segment`
If specified, this parameter force to create the simulation geometry by segmenting the CT volume after importing the structures. Otherwise the simulation geometry is not created.

Example:
```
import.structures \airoutbody \segment
```

`new.project`

Creates a new project. The path of the new project is assumed to be the PRIMO repository. See command `set.primo.repository`.

- Parameters:
  `\id=<text>`
  The project ID. The project ID must not contain space or special characters and must have a maximum of 11 characters. This parameter is mandatory, its omission will produce an error and the macro abortion.
  `\linac=<integer>`
  The linac model code. Default is `\linac=6` which corresponds to a Varian Clinac 2100 C/D. To see the available linac codes use the `list` command.
  `\mode=<integer>`
  The linac operation mode. Accepted values are `\mode=1` and `\mode=2` which corresponds to electron and photon modes, respectively.

Example:
```
new.project \id=myproject \linac=6 \mode=2
```

`link.psf`

Links a PSF to the project.

- Requirements:
  - The specified path must contain a valid IAEA-formatted phase-space file (*i. e.*, both the header and data files).
- Parameters:
  `\path=<text>`
  The path (including the file name) to a PSF header.

Example:
```
link.psf \path=c:\PSF\MyPhaseSpace.IAEAheader
```

`list`

Lists the available energies, mlc models, electron applicators and materials available for the linac model associated to the project.

- Parameters:
  `\linacs`
  Lists the supported linac models and their codes.
  `\energies`
  Lists the available nominal energies for the project linac in the current operation mode (photon or electron).
  `\mlcs`
  Lists the available mlc models for the project linac.
  `\eapplicators`
  Lists the available electron applicators for the project linac.
  `\materials`
  Lists the materials that can be used for CT segmentation of slab phantom creation.

  When no parameter is specified all the lists are output.

Example:
`list`

`pause`

Disables the macro interpreter. Any command received after a call to `pause` is ignored by the macro interpreter. It is used in conjunction with command `resume`.

- Parameters:
  none

Example:
`pause`

`phantom`

Creates a slab phantom

- Parameters:
  `\dim=<float,float>`
  The phantom dimensions (in cm) in the *x* and *y* axes. Default is `\dim=40.25,40.25`
  `\bin=<float,float,float>`
  The bin size (in cm) in the *x*, *y* and *z* axes. Default is `\bin=0.5,0.5,0.5`
  `\mats=<text,text,text,text,...>`
  A list of (maximum 10) slabs materials. The names must correspond exactly to the names in the material table of PRIMO without space characters. Example, the material appearing in the PRIMO table as `MixD Wax` would be used in this command as `\mats=mixdwax`. This parameter is mandatory, there is not default. The materials will appear in the order given in the parameter list, starting from the surface of the phantom. Use the command `\list` to obtain a list of the available materials.
  `\thicks=<float,float,float,float,...>`
  A list of slabs thickness. There must be one thickness per material listed in the parameter `\mats=`

Example:

```
phantom \dim=20.2,20.2 \bin=0.2,0.2,0.2 \mats=water \thicks=20.0
```

`remove.field`

Removes a field.

- Parameters:
  `\field=<integer>`
  The number of the field to be removed. Fields are numbered starting from 1. Trying to remove a field from a plan with only one field will produce an error. Trying to remove a field from an IMRT plan will also produce an error.

Example:

```
remove.field \field=1
```

`resume`

Enables the macro interpreter. It is used in conjunction with command `pause`.

- Parameters:
  none

Example:

```
resume
```

`save.dose.plane`

Saves a dose plane as a text file. Two formats are available: a PRIMO formatted text (default file extension .dat) and OmniPro I'mRT ASCII (default file extension .opg). The file is saved in the project folder with the name '<direction>-dose-plane-(<plane*100>)' and extension 'opg' or 'dat'.

- Requirements:
  - The project must contain a simulated dose distribution.
- Parameters:
  `\dir=<integer>`
  The plane direction 0: axial; 1: sagittal; 2: coronal. Default is \dir=2.
  `\plane=<float>`
  The plane position (in cm) in the selected direction.
  `\smooth`
  Request that the dose distribution is smoothed previous to saving the dose plane.
  `\Gy`
  Requests that the dose distribution is converted to units Gy previous to saving the dose plane. If \format=opg is selected and \Gy is not specified, the dose is normalized to 100% the maximum dose in the selected plane and saved in relative units.

Example:

```
save.dose.plane \plane=0.0 \dir=2 \format=opg \smooth \Gy
```

The dose distribution is smoothed, converted to units Gy and the plane at position 0.0 in the coronal direction is saved in a file named as coronal-dose-plane-(0).opg.

`set.dicom.repository`

Defines a path to be the repository of DICOM files. All the import commands will look in this repository to retrieve DICOM files.

- Requirements:
  - The name of the CT files deposited in the folder must start with the CT letters.
  - The name of the RT-PLAN files deposited in the folder must start with the RP letters.
  - The name of the RT-STRUCT files deposited in the folder must start with the RS letters.
  - The name of the RT-DOSE files deposited in the folder must start with the RD letters.
  - All DICOM files must have the .dcm extension.
- Parameters:
  `\path=<text>`
  The DICOM repository path.

Example:

```
set.dicom.repository \path=C:\PRIMO\DICOM
```

`set.primo.repository`

Defines a path to be the repository of a PRIMO project file. If a PRIMO dose distribution is imported for gamma analysis it is expected to be in this repository.

- Requirements:
  - The folder must contain a valid PRIMO project and a dose distribution in PRIMO format.
- Parameters:
  `\path=<text>`
  The PRIMO repository path.

Example:

```
set.primo.repository \path=C:\PRIMO\Project
```

`simulate`

Starts the simulation execution using the defined engine.

- Parameters:
  None.

Example:

```
simulate
```

`stop`

Stops macro execution.

- Parameters:
  None

Example:

```
stop
```

`trace.out`

This command produces the replication of macro execution output to a rich text format file. The file name is defined as, `macroname-output-startdate@starttime.rtf`

- Parameters:

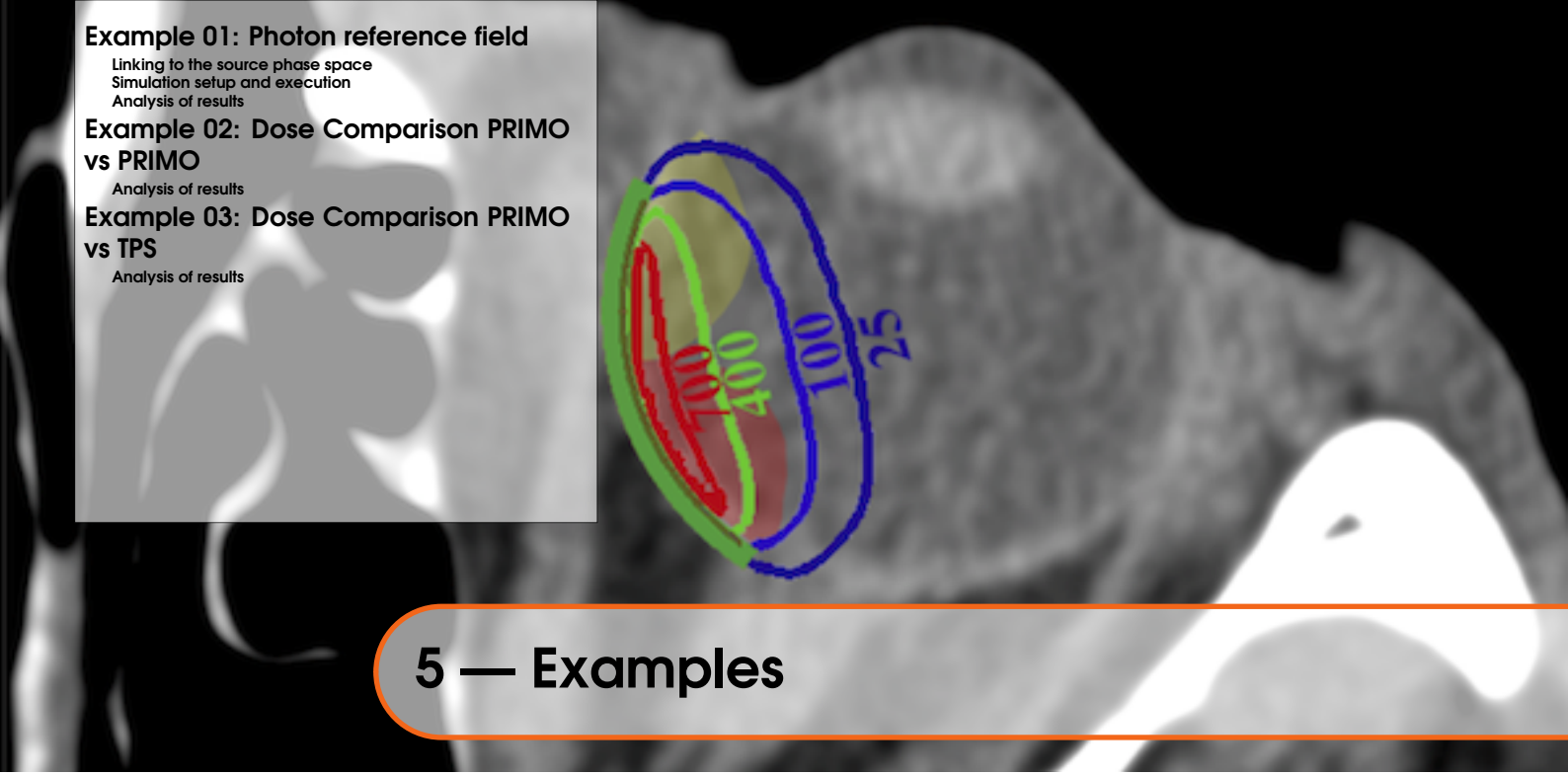
  `\off`

  Deactivates the trace.out state –which is active by default when the macro starts–. After a call to `trace.out \off`, the state can be reactivated by executing `trace.out` without parameters.

Example:

`trace.out`

Example 01: Photon reference field
Linking to the source phase space
Simulation setup and execution
Analysis of results
Example 02: Dose Comparison PRIMO vs PRIMO
Analysis of results
Example 03: Dose Comparison PRIMO vs TPS
Analysis of results



5 — Examples

This chapter presents basic project examples aimed at introducing the user on the practical use of PRIMO. The steps that were followed to produce the tallies included in the examples are described detailedly and they are supposed to be followed by the user. However, all the example files contain the complete project data including the tallies. Therefore, the user can optionally just to review and analyze the tallied results of the downloaded project. It will be indicated in each case how to skip the configuration and simulation steps and to proceed directly to the inspection of the results.

The examples presented in this chapter are intended to be explored in sequential order. Therefore, the first example is presented very detailedly, while the following examples only show details on the aspects not previously discussed. Furthermore, it is mandatory that the first example, Example 01, is installed to execute the other two because the phase space included in Example 01 is used as the source of particle for simulations in all three.

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` 248 MB
- `Example02.zip` 14 MB
- `Example03.zip` 156 MB

5.1 Example 01: Photon reference field

This example covers the simulation of linac segments s2 and s3 (section 3.9) to tally a dose distribution in a water phantom for a open photon field.

For this simulation project a phase-space file has been tallied at s1. The phase-space file is distributed with the example and its simulation is not included in the steps of the example. The main reason for this decision is practical, the simulation to create this phase space without using any variance reduction technique takes about 15 days in a 32 cores workstation. Variance reduction techniques were not used in order to generate a phase space with a latent variance low enough to produce dose distributions with reasonable uncertainties (for the purpose of the examples) and at the same time a phase space file with a reasonable small size (of about 0.5 Gb). However, the conditions used to produce the phase space were the following:

Linac Varian Clinac 2100 C/D
Mode Photon
Nominal energy 6 MV
Initial energy 5.4 MV
Energy FWHM 0 MeV
Focal spot FWHM 0 cm
Beam divergence 0 degrees
No variance reduction
Simulation engine penEasy
Stop condition 1.0×10^9 histories

The rest of the configuration chosen for this example is the following:

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 $16.2 \times 16.2 \times 30.0$ cm^3

R Unless it is explicitly stated default values are used in the configuration of the example projects.

Notice 5.1 Go to section 5.1.3 for analysis and review of the results of this example. ■

5.1.1 Linking to the source phase space

Despite the phase space tallied at segment s1 should be part of the project, we are going to link it to the project as if it were an external phase space. The purpose of this is to emphasize the idea that a s1 phase space has to be created only once for a given beam and subsequently used to estimate the dose for that beam in any project. To link the phase space to the project select the segment s1 for simulation. If there is a dose estimated for the project, PRIMO will issue a warning (indicating that the existing tallies of subsequent segments will be deleted) and a request for validation. Validate and save the project. Select the option Link to a phase space in the main menu. The phase-space file is located in the folder `c:\PRIMOexamples\PhaseSpace`. In the standard File Open dialog select the header file `ExamplesPSF`.

5.1.2 Simulation setup and execution

The default symmetric field of size 10×10 cm^2 is left unmodified except for the SSD which must be changed to be 95 cm. To accomplish that, select the option Edit Field on the s2 tab and set the isocenter position at $(0, 0, 5)$ cm as it is shown in figure 5.1

The default water phantom is not used in this case. Therefore, the characteristics of the water phantom where the dose will be tallied must be defined. Define a new phantom by selecting the option Create slab phantom (button in the main menu). In the Slab phantom definition dialog set the phantom dimensions to 16.20 cm and 16.20 cm in the x and y axis, respectively, with bin size equal to $0.2 \times 0.2 \times 0.2$ cm^3 and insert a layer of water of 31.00 cm (see figure 5.2 and section 4.1.2).

Active the check boxes for the simulation of s2 and s3 and click the Configuration button to proceed with the configuration of simulation for the active segments (figure 5.3). Notice that we now choose the number of histories as the stopping condition since we are interested in using all the particles tallied in the phase-space file. The number of histories appearing in the

Figure 5.1: Field edit dialog. Changing th SSD to 95 cm. Notice that to set a SSD of 95 cm the isocenter must be located at 5 cm below the phantom surface.

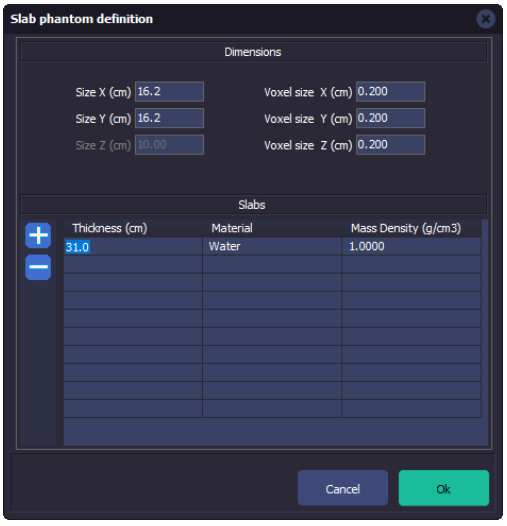


Figure 5.2: Slab phantom definition dialog. Creation of the patient model as a slab phantom.

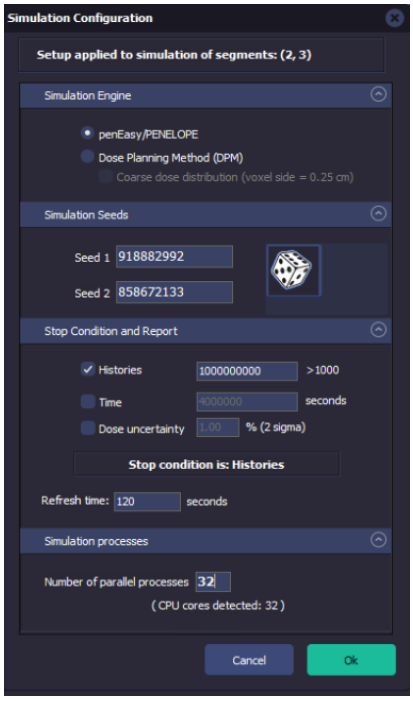


Figure 5.3: Simulation Configuration window prepared for simulating s2.

Histories field correspond to the number of histories simulated in s1. The seeds of the random number generator should be changed, for that press the dice button to generate a new sequence of pseudo-random numbers. In that way it is guaranteed that the sequence of pseudo-random numbers of s2s3 does not overlap with that used during the simulation of s1. Select penEasy as the simulation engine and set the number of processors according to the computer used.

To reduce the statistical uncertainty in the estimation of the absorbed dose distribution we apply splitting to the particles entering the phantom. Select the option Configure variance reduction in the main menu. Set the Splitting in phantom or CT check box and type a value of 300 for the splitting number as shown in figure 5.4. 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 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).

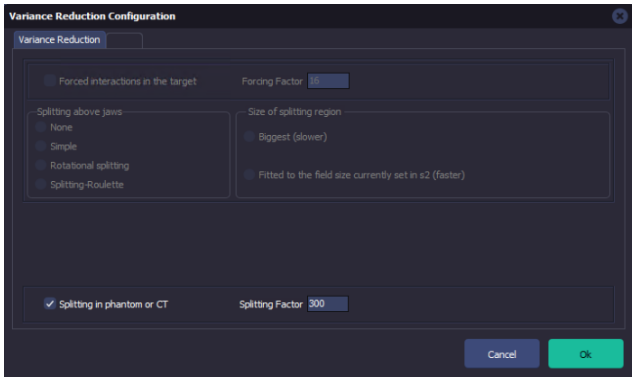


Figure 5.4: Variance reduction for simulation of segment s3.

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

Select Play to start the simulation. It takes about $760s$ in a 32 cores workstation to complete the simulation. Once the simulation of segments s2 and s3 is completed (see figure 5.5) press the Exit button and PRIMO will return to its main window.

5.1.3 Analysis of results

In this section the data produced in the simulations of the example 01 is reviewed and analyzed.

Phase space analysis

Despite the phase space used as a source of particles for simulation of segments s2 and s3 was not simulated in the example it will be reviewed here. For analyzing the phase-space select the Phase Space Analysis workspace and drag the phase space icon from the logical tree and dropped in the empty area to its right (figures 5.6 and **??**). Another way to send the phase space to analysis is by right clicking on the phase space icon in the logical tree and selection the option Analyze in the appearing pop-up menu.

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.

Dose analysis

The dose distribution estimated in the simulation of segments s2 and s3 can be reviewed by selecting the Plan and Dose workspace (figures 5.7 and 5.8). See section 4.4 for a detailed description of the options in this workspace.

Comparison with experiment

The simulation of segment s1 that tallied the phase space used as a source of particles of this example used the default primary beam parameters, that is, a monoenergetic pencil beam electron source of 5.4 MeV. PRIMO has built-in analysis tools for comparing experimental dose profiles with the simulated 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 with experimental data button on the main window. The experimental percentage dose distribution is located in the directory `c:\PRIMOexamples\Example01\Experiment`. It must be stressed that the primary beam parameters of the simulation have not been tuned for

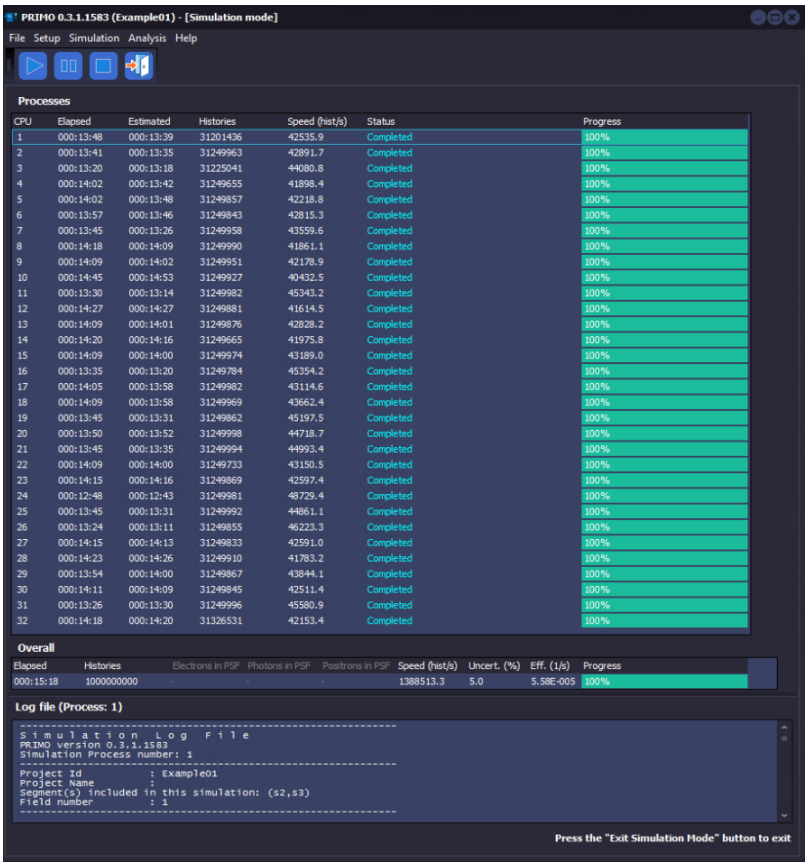


Figure 5.5: Simulation of Example 01 has finalized.

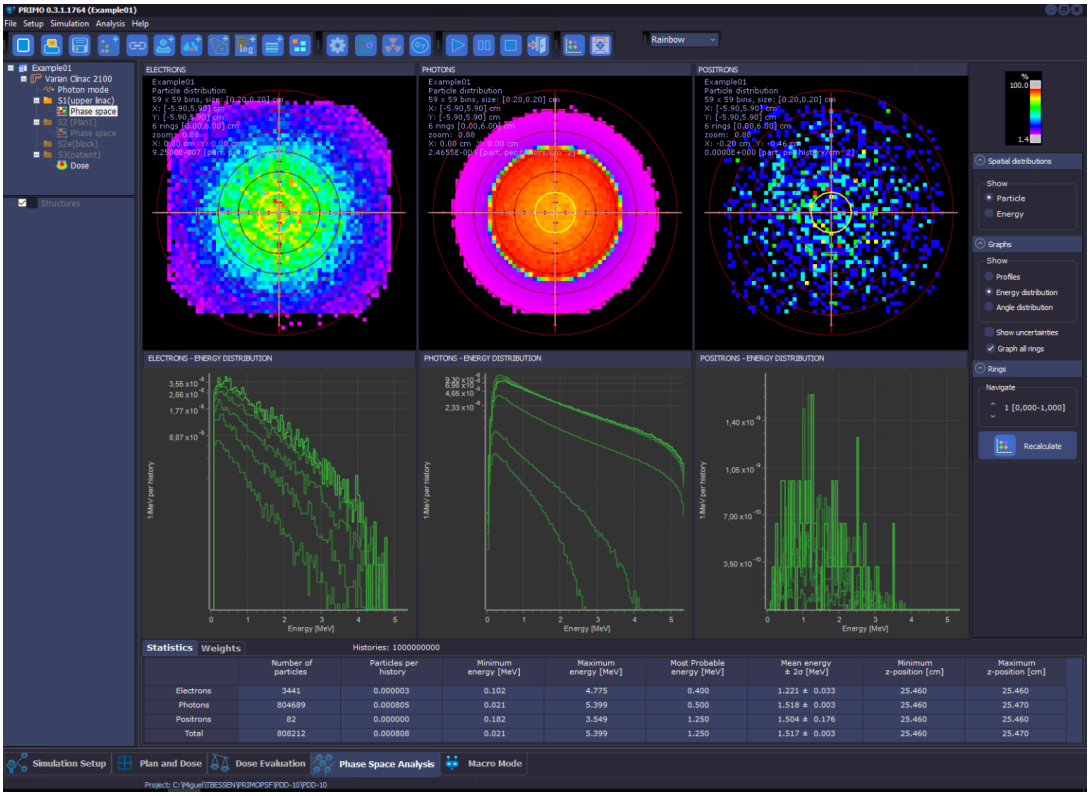


Figure 5.6: Analysis of the phase-space file linked to segment s1. Six rings were selected with 1 cm radial increment. Notice the circular area in the phase space plane irradiated by the source has been truncated by applying splitting-roulette with the option Fitted to the field size. The energy distributions are plotted in a semi-log scale (except for protons).

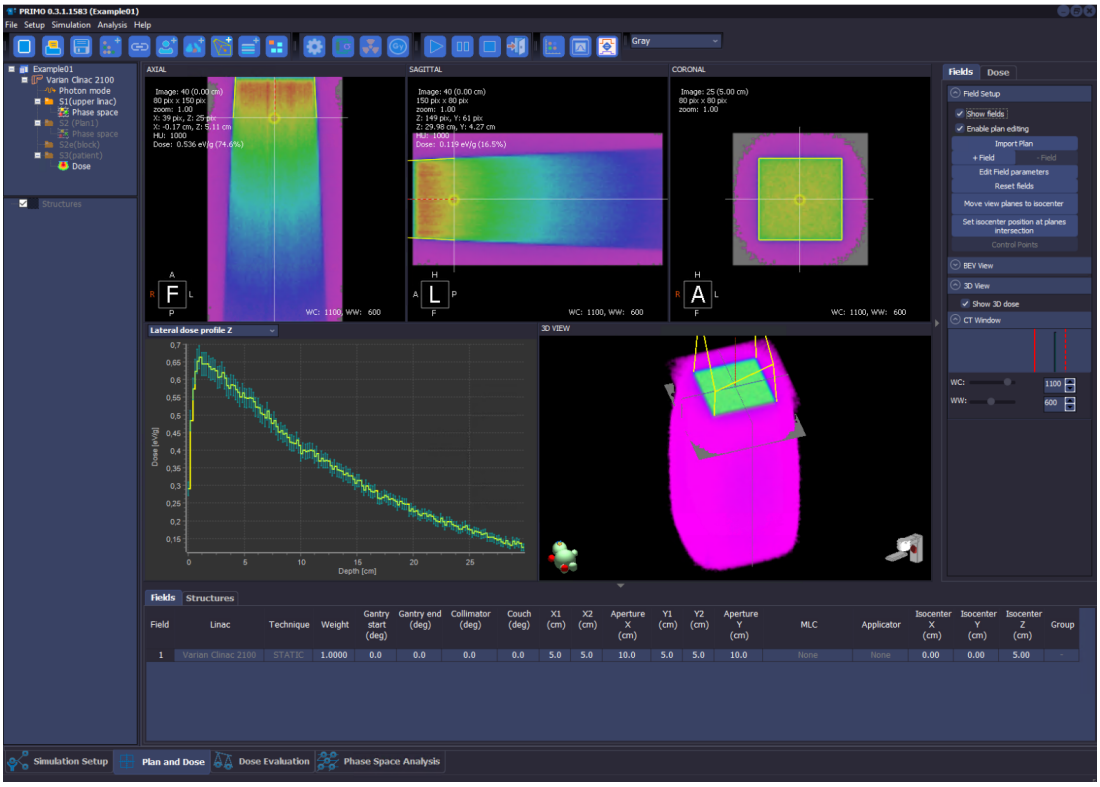


Figure 5.7: Plan and Dose workspace showing the dose distribution estimated for the simulation of segments s2 and s3. Dose is shown as a color wash map.

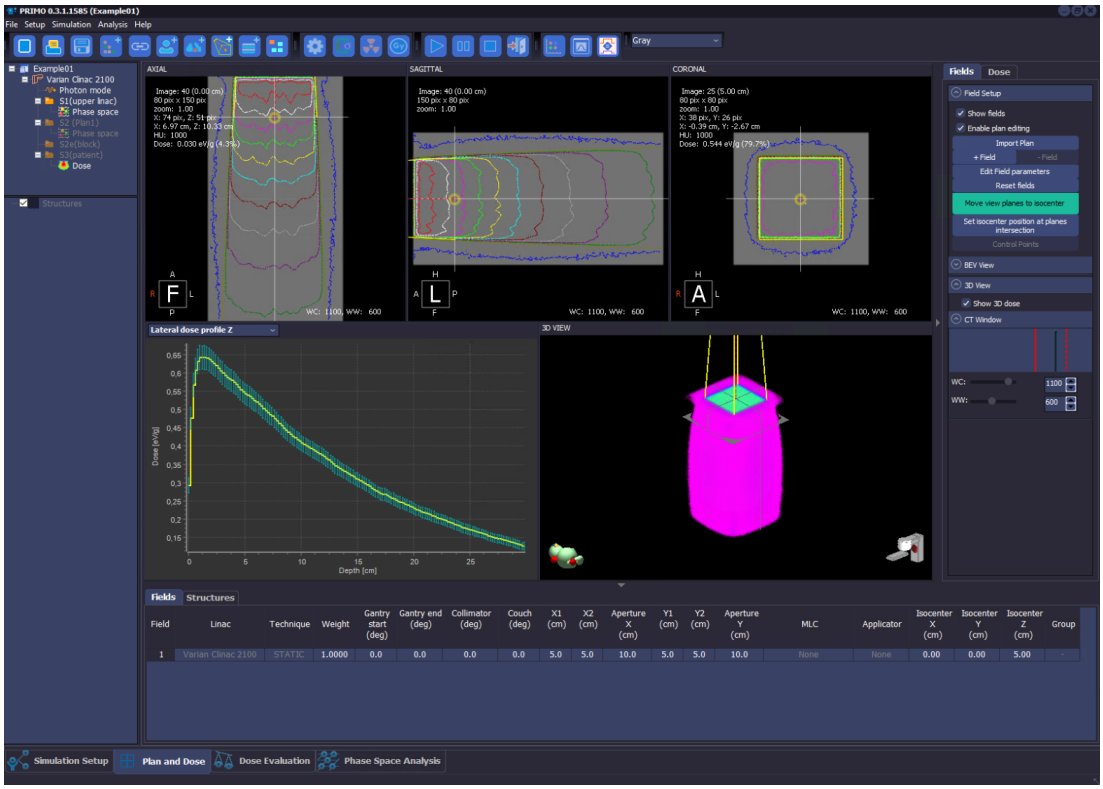


Figure 5.8: Plan and Dose workspace showing the dose distribution estimated for the simulation of segments s2 and s3. Dose is shown as isodose curves after applying denoising.

Figure 5.9: Comparison of experimental and simulated percentage depth doses.

the particular linac used for measuring the experimental data. The reason for this is that we are interested in assessing how PRIMO shows the discrepancies between the two datasets (figures 5.9 and 5.10).

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 follow the syntax of the Gnuplot program[1].

5.2 Example 02: Dose Comparison PRIMO vs PRIMO

In this example we are going to explore the comparison of two dose distributions estimated with PRIMO. Both estimated in the same conditions but using different simulation engines. In Example 01 we addressed the dose estimation in a reference photon field using PENELOPE as the simulation engine. In this example we will estimate the dose for the same field (and any other condition) but using DPM as the simulation engine.

Notice 5.3 Go to section 5.2.1 for analysis and review of the results of this example. ■

Configuration for Example 02 is basically the same as Example 01. So, project Example 02 is basically a duplicate of project Example 01. Notice that this project could have been created as a copy of the Example 01 project thus avoiding to follow all the steps to create a new project and configure it. For making a copy of the Example 01 project use the option Save As in the main menu. In the Project Save As dialog type the ID of the copy project *e. g.*, `Example02a`, press

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

Figure 5.10: Comparison of experimental and simulated lateral profiles.

Browse to change the default destination folder. Notice that there cannot be two projects with the same ID in the same folder.

Mark the check box for s2 and s3 to active these segments for simulation. The only one parameter that must be configured in Example 02 is the simulation engine. In this case, if the project was created as a copy of Example 01 we should select the Configuration button in the main menu and set the check box Dose Planning method to select DPM as the simulation engine (see figure 5.12). Select Play to start the simulation. It takes about 140 s to complete the simulation with DPM as it is seen in figure 5.13. So, the first comparison that can be made is that DPM is about 5.4$\times$ faster than penEasy in this simulation.

5.2.1 Analysis of results

To compare the dose distributions of Example 01 and Example 02, select the Dose evaluation workspace and the option Load external dose from: PRIMO project. In the File Open dialog select the project file `Example01.ppj`.

5.3 Example 03: Dose Comparison PRIMO vs TPS

In this example we are going to explore the comparison of two dose distributions but in this case a dose distribution estimated with PRIMO using DPM as the simulation engine versus a dose distribution exported from a treatment planning system as a DICOM RT DOSE file.

> **Notice 5.4** Go to section 5.3.1 for analysis and review of the results of this example. ■

First step is to link the source phase space to the project. For this, proceed as in example

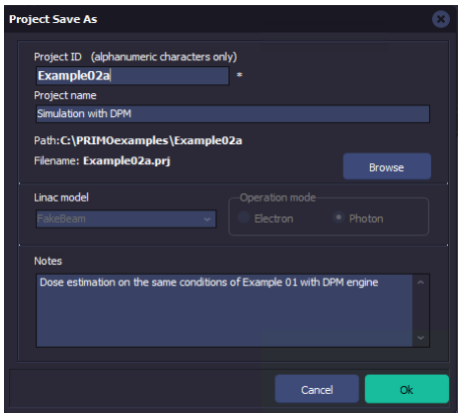


Figure 5.11: Making a copy of the Example 01 to create Example 02 (ID: Example02a).

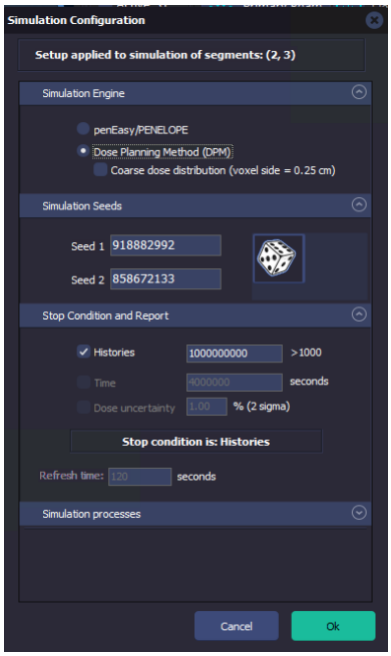


Figure 5.12: Configuring the simulation engine as DPM.

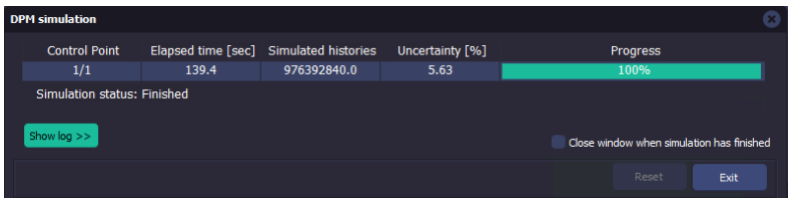


Figure 5.13: The simulation of Example 02 has finished.

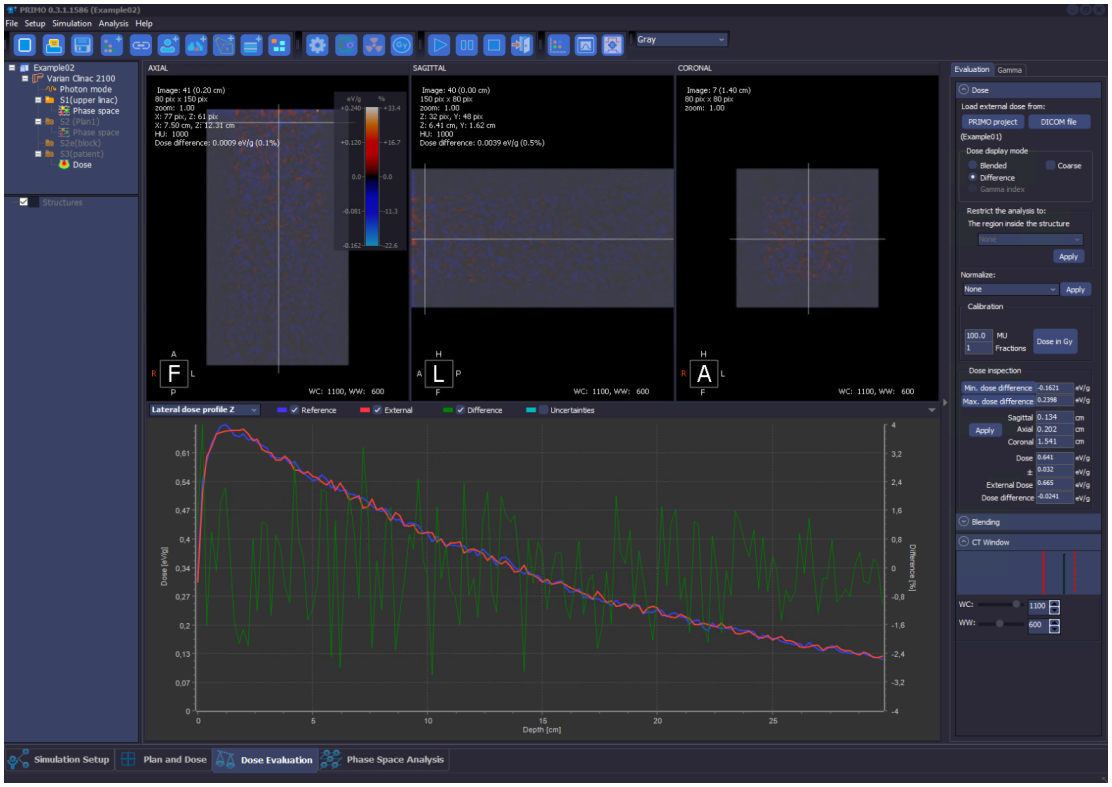


Figure 5.14: Comparison of the dose distribution of Example 02 (DPM) and Example 01 (PENELOPE). The difference dose is shown.

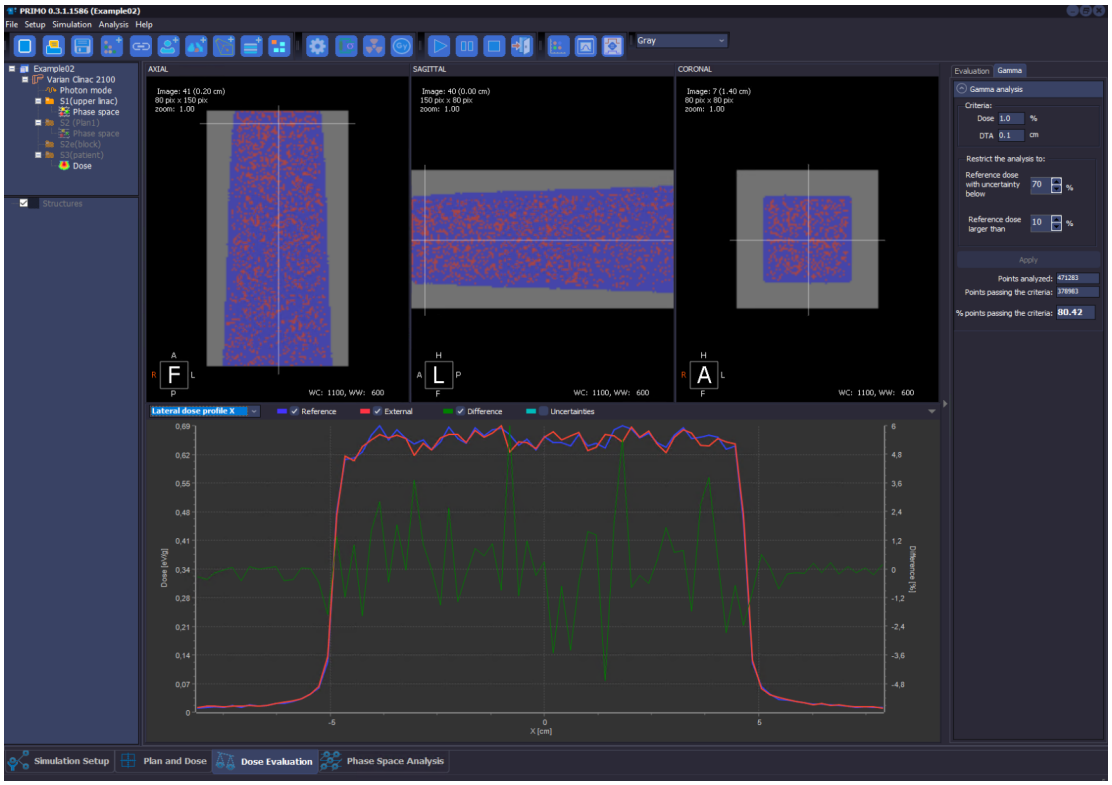


Figure 5.15: Comparison of the dose distribution of Example 02 (DPM) and Example 01 (PENELOPE). The gamma analysis with criteria of 1%, 1 *mm* is shown. Notice that the criteria is too demanding given the level of uncertainty of the dose distribution (average uncertainty of about 5%). Only 80% of the dose voxels pass the criteria.

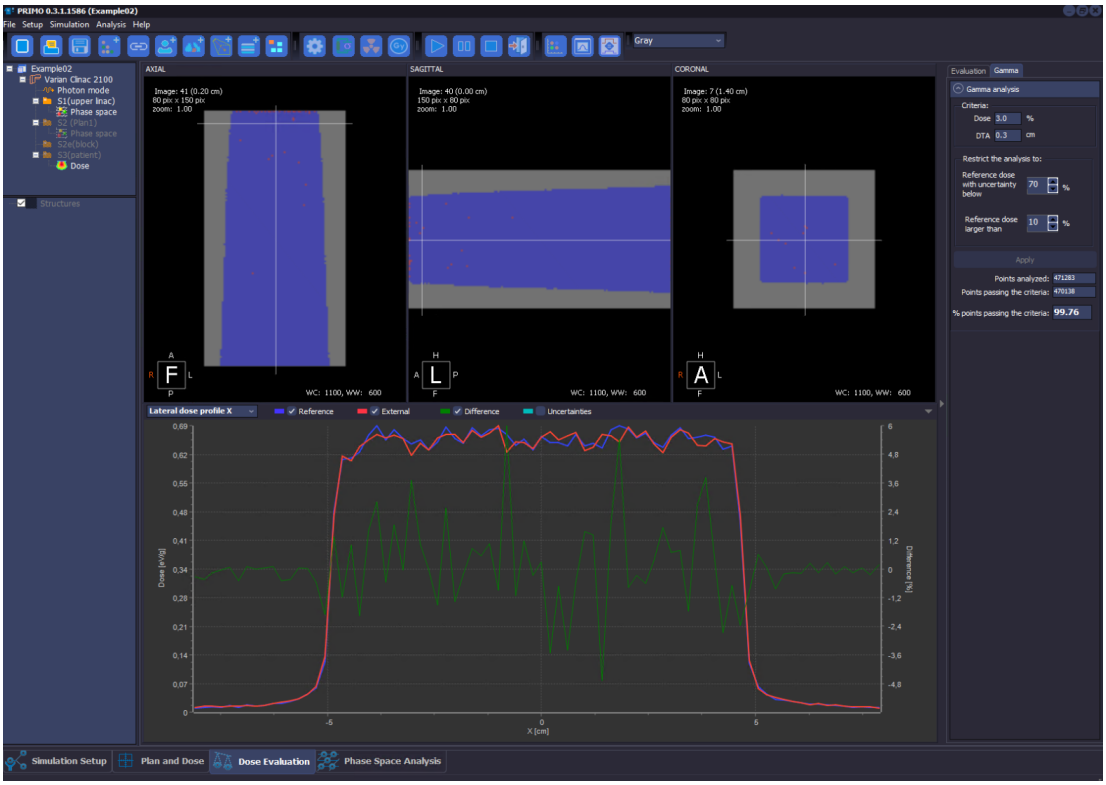


Figure 5.16: Comparison of the dose distribution of Example 02 (DPM) and Example 01 (PENELOPE). The gamma analysis with criteria of 3%, 3*mm* is shown. Notice that when the criteria is relaxed the number of dose voxels passing the criteria increases considerably (99.8%).

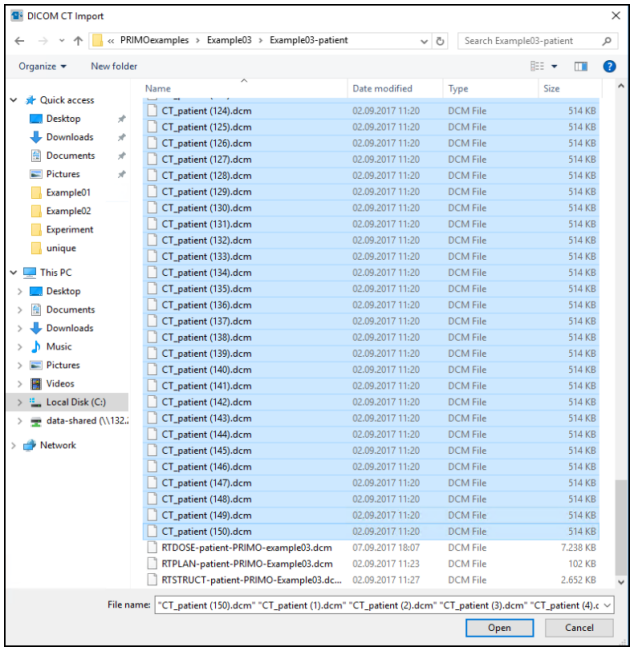


Figure 5.17: Example 03. Selecting the CT files to import.

01, section 5.1.1. Next step is to import the patient data, that is the CT, structures and the plan. To import the CT data select the option Import a CT . In the File Open dialog go to the `c:\PRIMOexamples\Example03\Example03-patient` folder and select all the files with the name `CT_patient(XXX).dcm` as it is shown in figure 5.17. In the DICOM image import dialog uncheck the Create the default simulation geometry check box as it is shown in figure 5.18.

To import the structures select the option Import structures . In the Open dialog, select the file `RTSTRUCT-patient-PRIMO-Example03.dcm`. In the DICOM-RT STRUCT Import dialog check the Set to air any CT voxel outside body contour as shown in figure 5.19. As the CT has been modified, PRIMO will ask to recreate the simulation geometry, Reply Yes to the request (see figure 5.20).

Finally, to import the treatment plan select the option Import plan in the main tool bar. In the File Open dialog select the file `RTPLAN-patient-PRIMO-Example03.dcm`. Reply Yes to the request of saving the project. To review the plan select the Plan and Dose tab. The screen should look very similar to the one in figure 5.21. To setup the simulation, go back to the Simulation setup workspace and select segments s2 and s3 for simulation, then select the Configure simulation option in the main menu. Set DPM as the simulation engine and the check box Coarse dose distribution. Press the dice button to change the random number generator sequence. Select the Configure variance reduction and set splitting with factor 300. Start the simulation by pressing the button. The simulation of the 177 control points takes about 6 min in a 32 cores CPU with an average statistical uncertainty of $\sim 6\%$.

In order to express the simulated dose in units Gy we will establish a dose calibration factor for the project. To accomplish this, select the option Set a dose conversion factor in the main menu and set a value of 1.0, 100 and 0.520 for the measured reference dose, reference monitor units and the Monte Carlo reference dose, respectively in the Dose calibration dialog as in figure 4.29. Figure 5.22 shows the simulated dose distribution in the Plan and Dose tab. Notice that the dose has been converted to units Gy using the previously defined dose conversion factor.

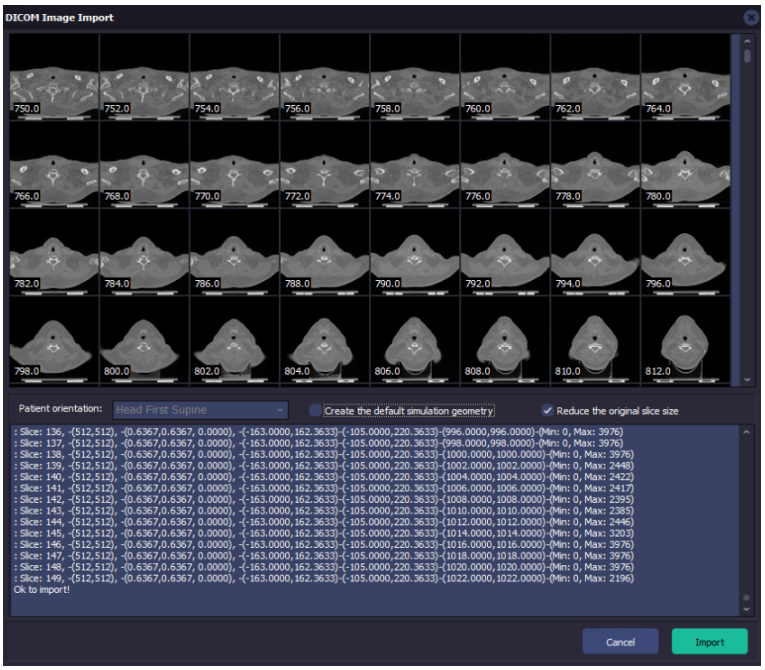


Figure 5.18: Example 03. DICOM image import. Uncheck the Create the default simulation geometry check box.

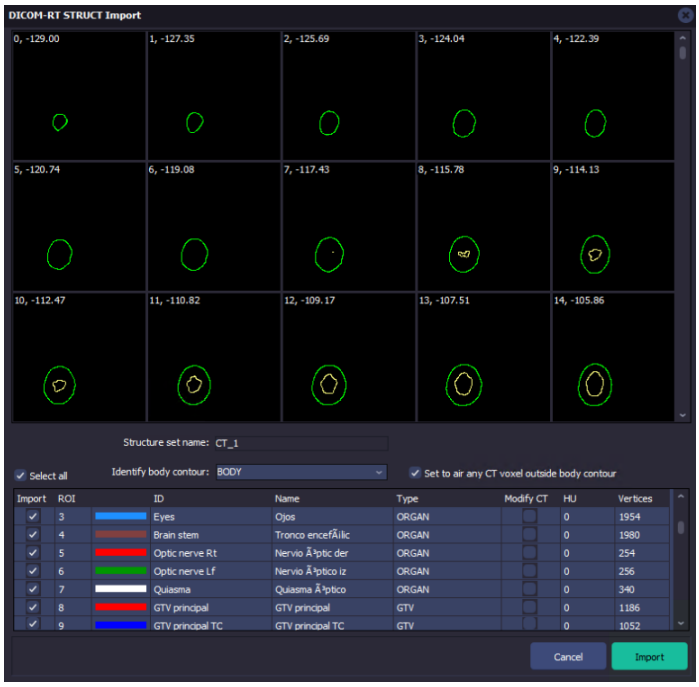


Figure 5.19: Example 03. DICOM RT STRUCT import. Check the Set to air any CT voxel outside body contour check box.

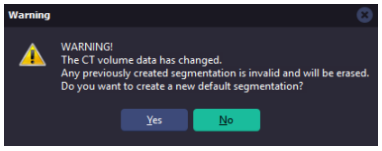


Figure 5.20: Example 03. Answer Yes to the request of recreating the simulation geometry.

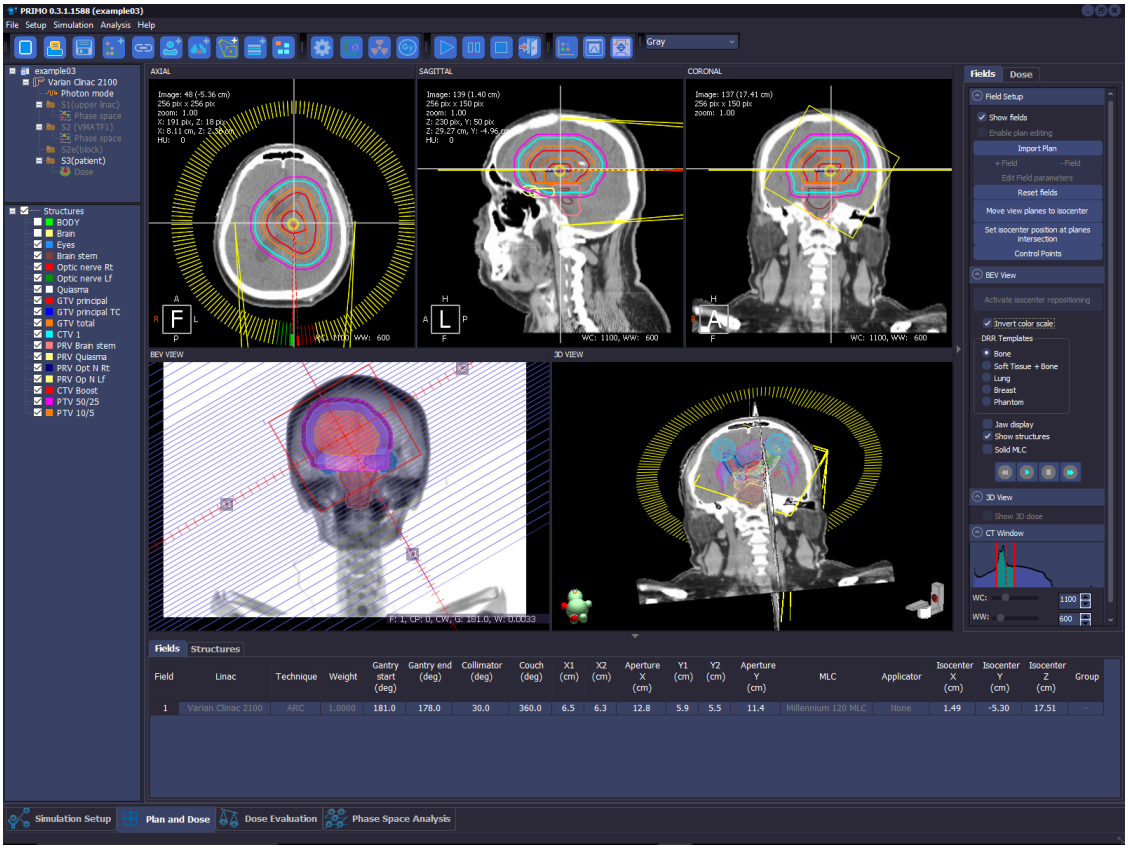


Figure 5.21: Example 03. Review of the imported CT, plan and structures.

5.3.1 Analysis of results

In order to compare the simulated dose to the dose calculated by a Treatment Planning system go to the Dose Evaluation tab and select the option Import from: DICOM file. In the File Open dialog select the file `RTDOSE-patient-PRIMO-Example03.dcm`. Press the Import button in the DICOM dose import dialog and reply Yes to the request for converting the dose to units Gy. Back in the Dose Evaluation tab explore the dose profiles, DVHs and select the option Restrict the analysis to: BODY and perform a gamma analysis. The results must be similar to those illustrated in figure 5.23.

Figure 5.22: Example 03. Review of the dose distribution. The dose has been converted to units Gy.

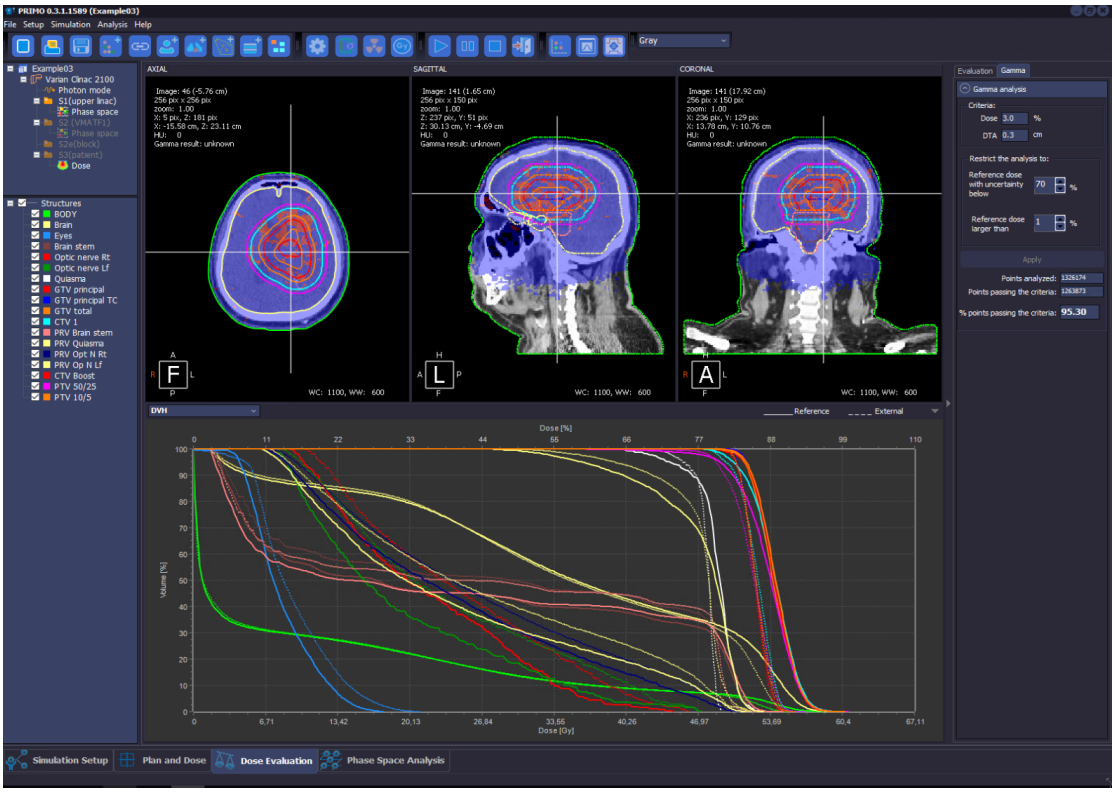
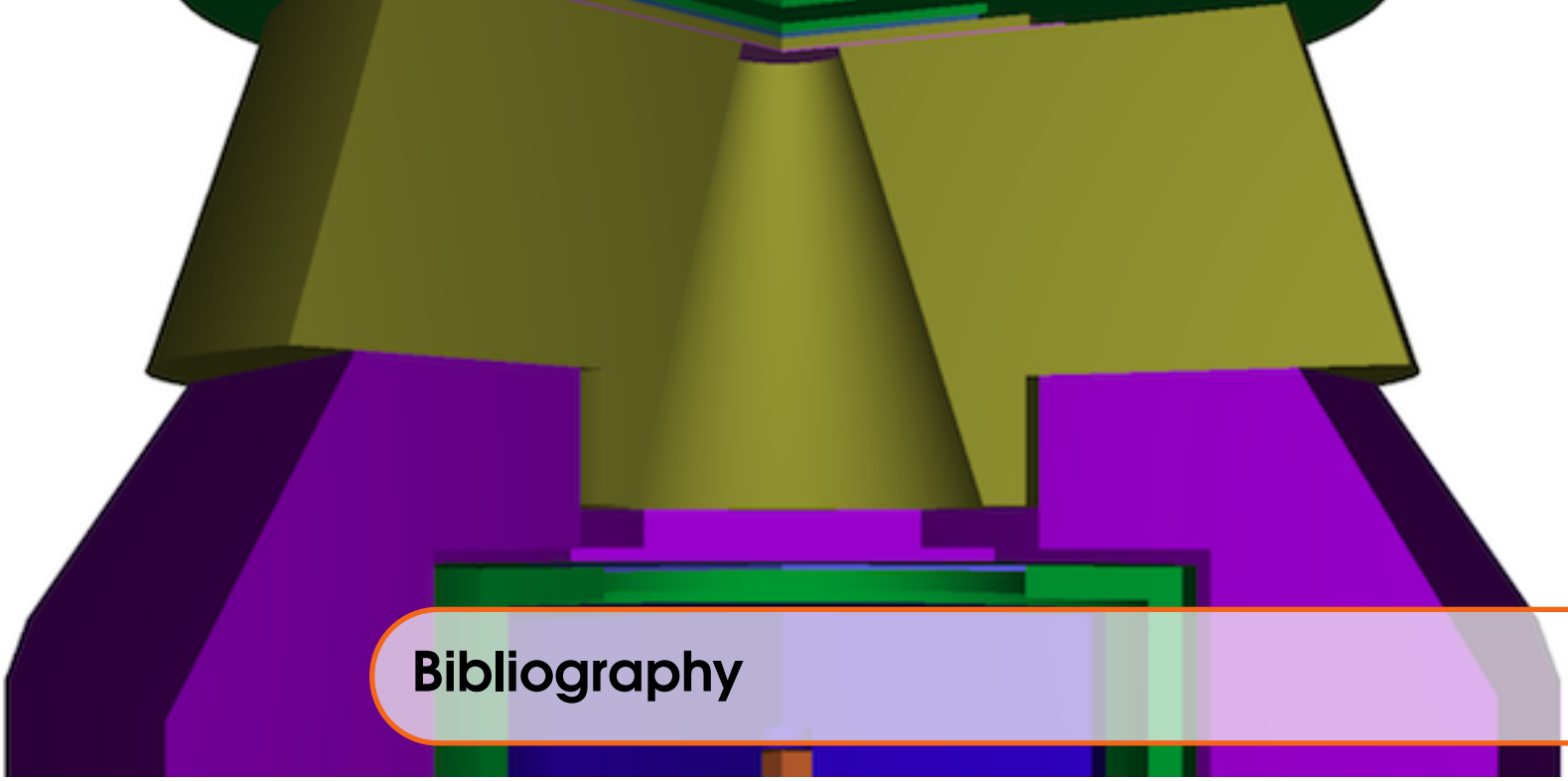


Figure 5.23: Example 03. Results of gamma analysis restricted to the BODY structure.



Bibliography

Books

[Bru12] L Brualla. *Simulation of medical linear accelerators with* PENELOPE. Edited by G García Gómez-Tejedor and MC Fuss. Springer, 2012, pages 313–325 (cited on page 11).

[Cap+06] R Capote et al. *Phase-Space Database for External Beam Radiotherapy*. Volume INDC (NDS)-0484. INDC International Nuclear Data Committee. Vienna: International Atomic Energy Agency, Jan. 2006 (cited on pages 11, 39).

[JNR98] MT Jenkins, WR Nelson, and A Rindi, editors. *Monte Carlo Transport of Electrons and Photons*. City: Plenum Press, Jan. 1998 (cited on page 11).

[SFS11] F Salvat, JM Fernández-Varea, and J Sempau. PENELOPE 2011—*A code system for Monte Carlo simulation of electron and photon transport*. Issy-les-Moulineaux: OECD Nuclear Energy Agency, 2011 (cited on pages 11, 36, 37).

[SV13] J Seco and F Verhaegen, editors. *Monte Carlo Techniques in Radiation Therapy*. 1st edition. Taylor & Francis, Mar. 2013 (cited on page 11).

Articles

[BS06] A Badal and J Sempau. "A package of Linux scripts for the parallelization of Monte Carlo simulations". In: *Comput Phys Commun* 175 (2006), pages 440–450 (cited on page 36).

[Bar+95] J Baró et al. " PENELOPE: an algorithm for Monte Carlo simulation of the penetration and energy loss of electrons and positrons in matter". In: *Nucl Instrum Meth B* 100 (1995), pages 31–46 (cited on page 11).

[BSP09] L Brualla, F Salvat, and R Palanco-Zamora. "Efficient Monte Carlo simulation of multileaf collimators using geometry-related variance-reduction techniques". In: *Phys Med Biol* 54 (2009), pages 4131–4149 (cited on pages 12, 37).

[BS10] L Brualla and W Sauerwein. "On the efficiency of azimuthal and rotational splitting for Monte Carlo simulation of clinical linear accelerators". In: *Radiat Phys Chem* 79 (2010), pages 929–932 (cited on pages 12, 37).

[Fad+08] B A Faddegon et al. “Benchmarking of Monte Carlo simulation of bremsstrahlung from thick targets at radiotherapy energies”. In: *Med Phys* 35 (2008), pages 4308–4317 (cited on page 12).

[Fad+09] B A Faddegon et al. “The accuracy of EGSnrc, Geant4 and PENELOPE Monte Carlo systems for the simulation of electron scatter in external beam radiotherapy”. In: *Phys Med Biol* 54 (2009), pages 6151–6163 (cited on page 12).

[FN03] Matthias Fippel and Fridtjof Nüsslin. “Smoothing Monte Carlo calculated dose distributions by iterative reduction of noise.” In: *Phys. Med. Biol.* 48.10 (2003), pages 1289–1304 (cited on page 49).

[Low+98] D Low et al. “A technique for the quantitative evaluation of dose distributions”. In: *Med Phys* 25 (1998), pages 656–661 (cited on pages 53, 61).

[Rey+07] N Reynaert et al. “Monte Carlo treatment planning for photon and electron beams”. In: *Radiat Phys Chem* 76 (2007), pages 643–686 (cited on page 11).

[RB19] M Rodriguez and L Brualla. “Treatment verification using Varian’s dynalog files in the Monte Carlo system PRIMO”. In: *Radiat Oncol* 14 (2019), page 67 (cited on page 62).

[RSB12] M Rodriguez, J Sempau, and L Brualla. “A combined approach of variance-reduction techniques for the efficient Monte Carlo simulation of linacs”. In: *Phys Med Biol* 57 (2012), pages 3013–3024 (cited on pages 12, 37).

[Rod+19] M Rodriguez et al. “DPM as a radiation transport engine for PRIMO”. In: *Radiat Oncol* 13 (2019), page 256 (cited on page 12).

[SF09] F Salvat and J M Fernández-Varea. “Overview of physical interaction models for photon and electron transport used in Monte Carlo codes”. In: *Metrologia* 46 (2009), S112–S138 (cited on page 12).

[SA06] J Sempau and P Andreo. “Configuration of the electron transport algorithm of PENELOPE to simulate ion chambers”. In: *Phys Med Biol* 51 (2006), pages 3533–3548 (cited on page 37).

[SBB11] J Sempau, A Badal, and L Brualla. “A PENELOPE-based system for the automated Monte Carlo simulation of clinacs and voxelized geometries—application to far-from-axis fields”. In: *Med Phys* 38 (2011), pages 5887–5895 (cited on pages 11, 12, 20, 39).

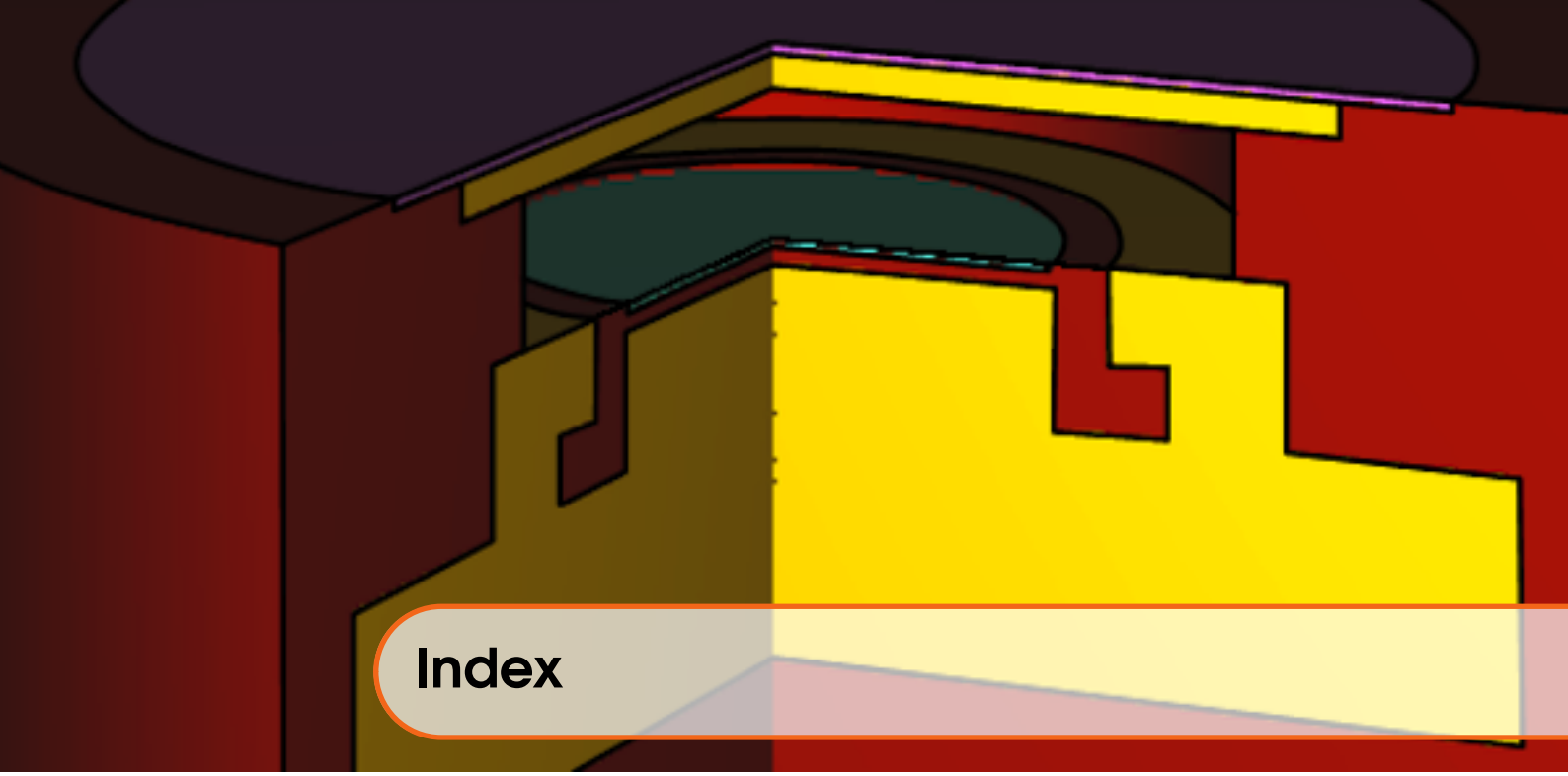
[SWB00] J Sempau, S J Wilderman, and A F Bielajew. “DPM, a fast, accurate Monte Carlo code optimized for photon and electron radiotherapy treatment planning dose calculations”. In: *Phys Med Biol* 45 (2000), pages 2263–2291 (cited on page 11).

[Sem+97] J Sempau et al. “An algorithm for Monte Carlo simulation of coupled electron-photon transport”. In: *Nucl Instrum Meth B* 132 (1997), pages 377–390 (cited on page 11).

[Sem+01] J Sempau et al. “Monte Carlo simulation of electrons beams from an accelerator head using PENELOPE”. In: *Phys Med Biol* 46 (2001), pages 1163–1186 (cited on page 19).

[Sem+03] J Sempau et al. “Experimental benchmarks of the Monte Carlo code PENELOPE”. In: *Nucl Instrum Meth B* 207 (2003), pages 107–123 (cited on page 12).

[SL08] E Spezi and G Lewis. “An overview of Monte Carlo treatment planning for radiotherapy”. In: *Radiat Prot Dosim* 131 (2008), pages 123–129 (cited on page 11).



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