Linac modeling with PENELOPE

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MEDIZINISCHE FAKULTÄT
DER UNIVERSITÄT DUISBURG-ESSEN

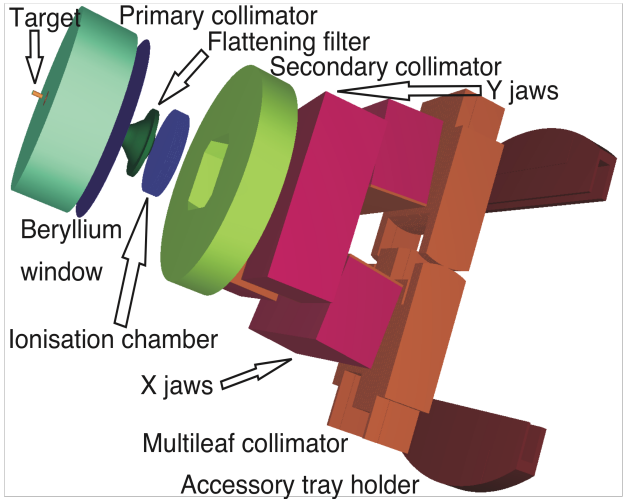
Universitätsklinikum Essen

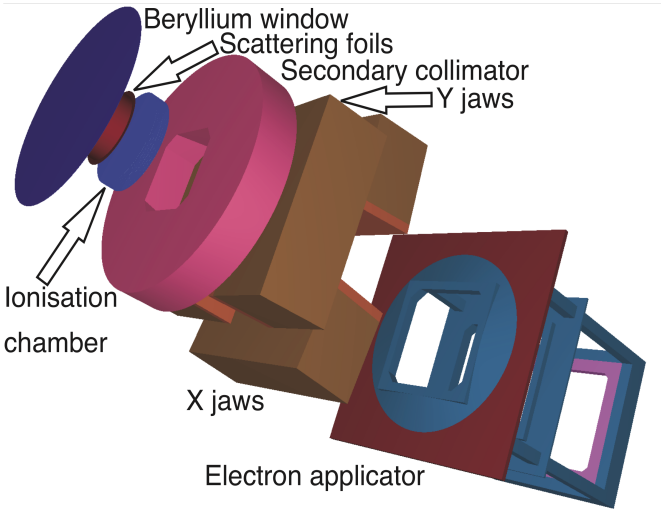
Description of a simulated linac

Photon mode

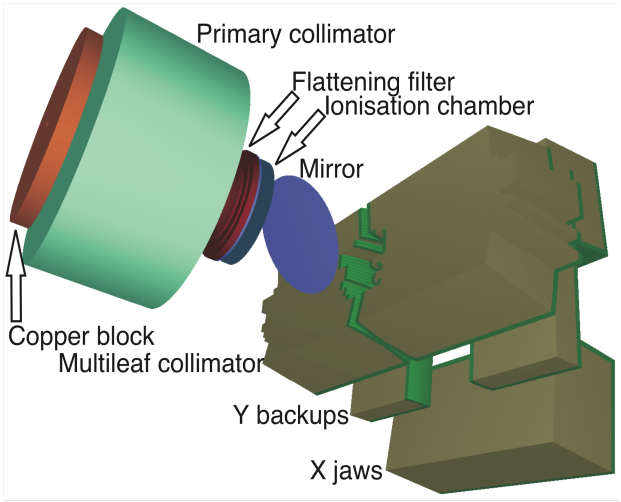
Electron mode

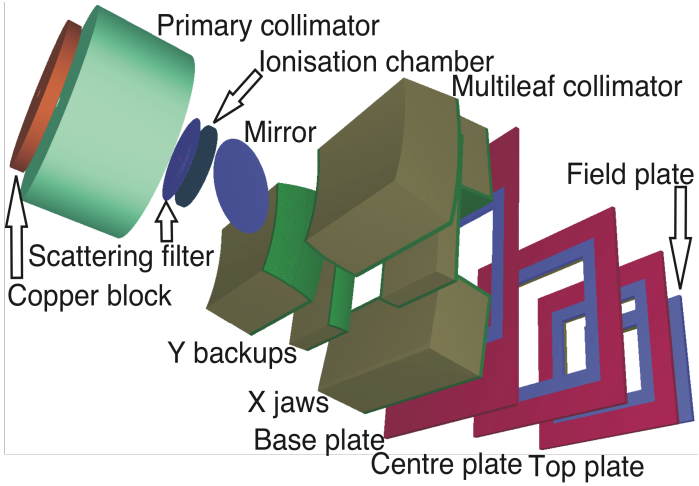
Varian





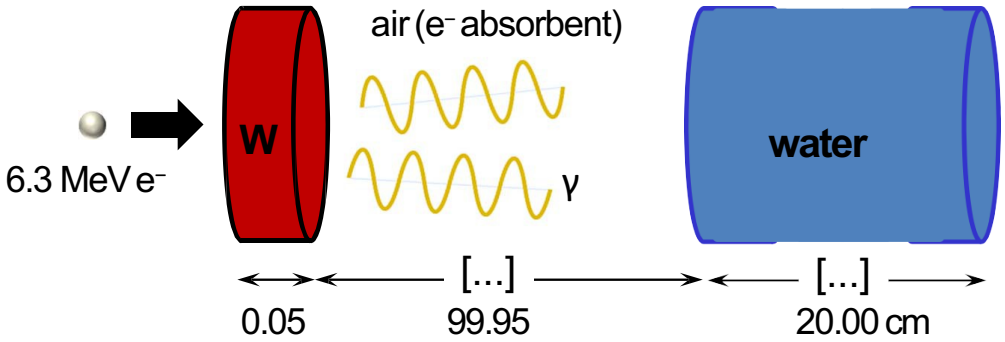
Elekta





Target simulation

Test: simulation setup

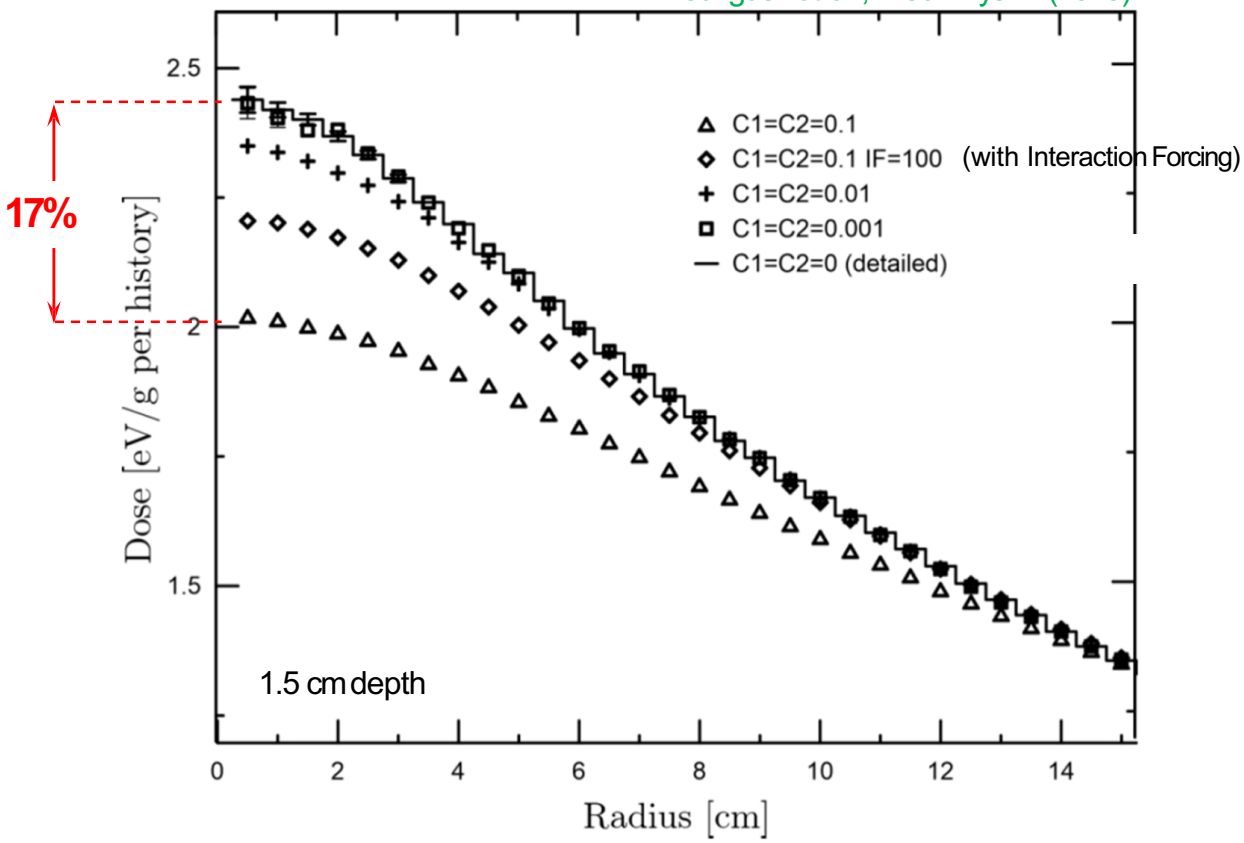


- The radial dose distribution in water is studied as a function of the *C* parameter in tungsten.
- Standard parameter values are used for the other materials.

Target simulation

Test: results

M Rodríguez *et al.*, Med Phys 42 (2015)



Technical Note: Study of the electron transport parameters used in PENELOPE for the Monte Carlo simulation of Linac targets

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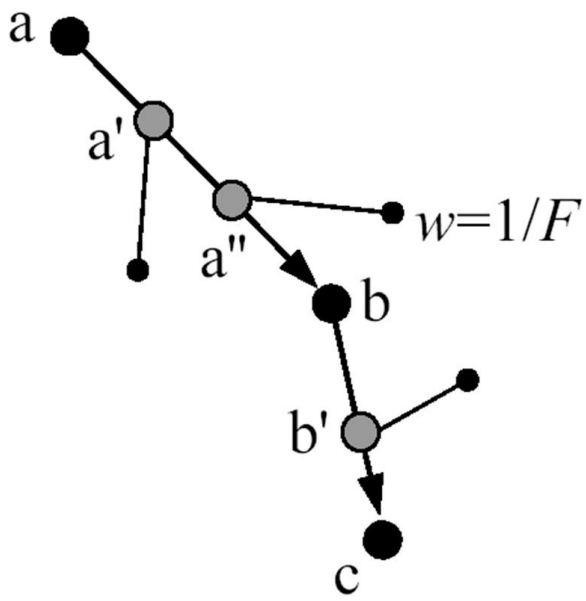
2877 Med. Phys. 42 (6), June 2015 0094-2405/2015/42(6)/2877/5/$30.00

Target simulation

Why does interaction forcing (IF) partially correct for too long steps?

- IF is applied in the target to increase bremsstrahlung production.
- This increases the efficiency, reducing the CPU time for a given uncert.

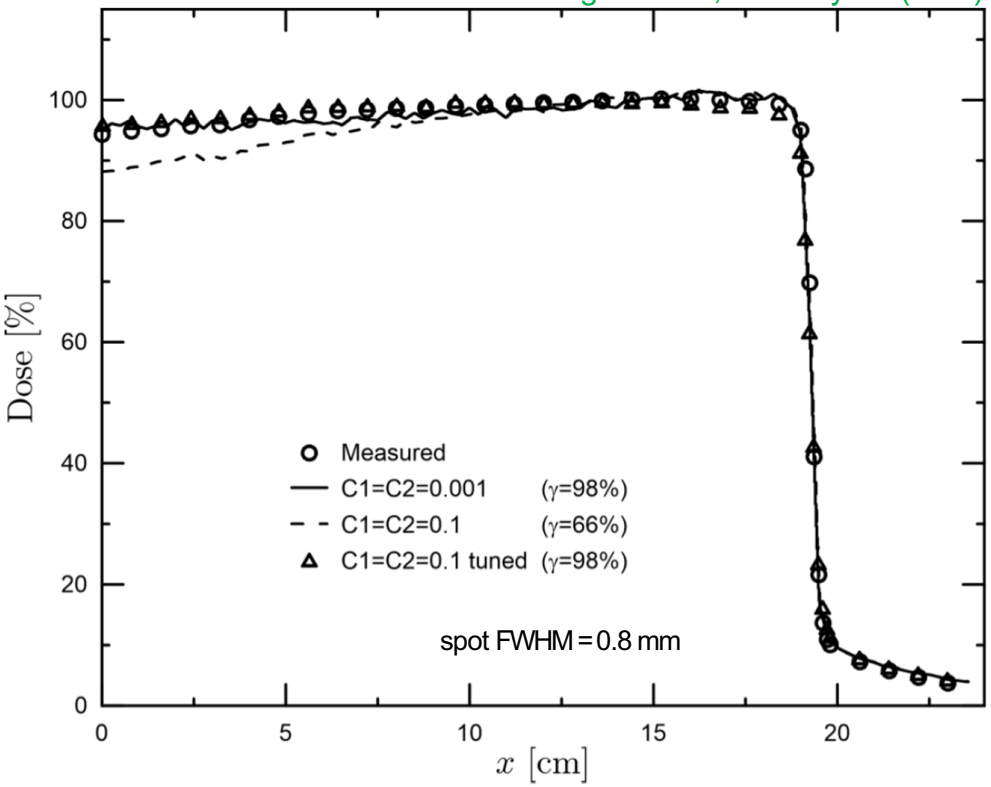


IF masks the effect of inappropriate transport parameters.

Target simulation

Varian Clinac 2100, 6 MV

M Rodríguez *et al.*, Med Phys 42 (2015)



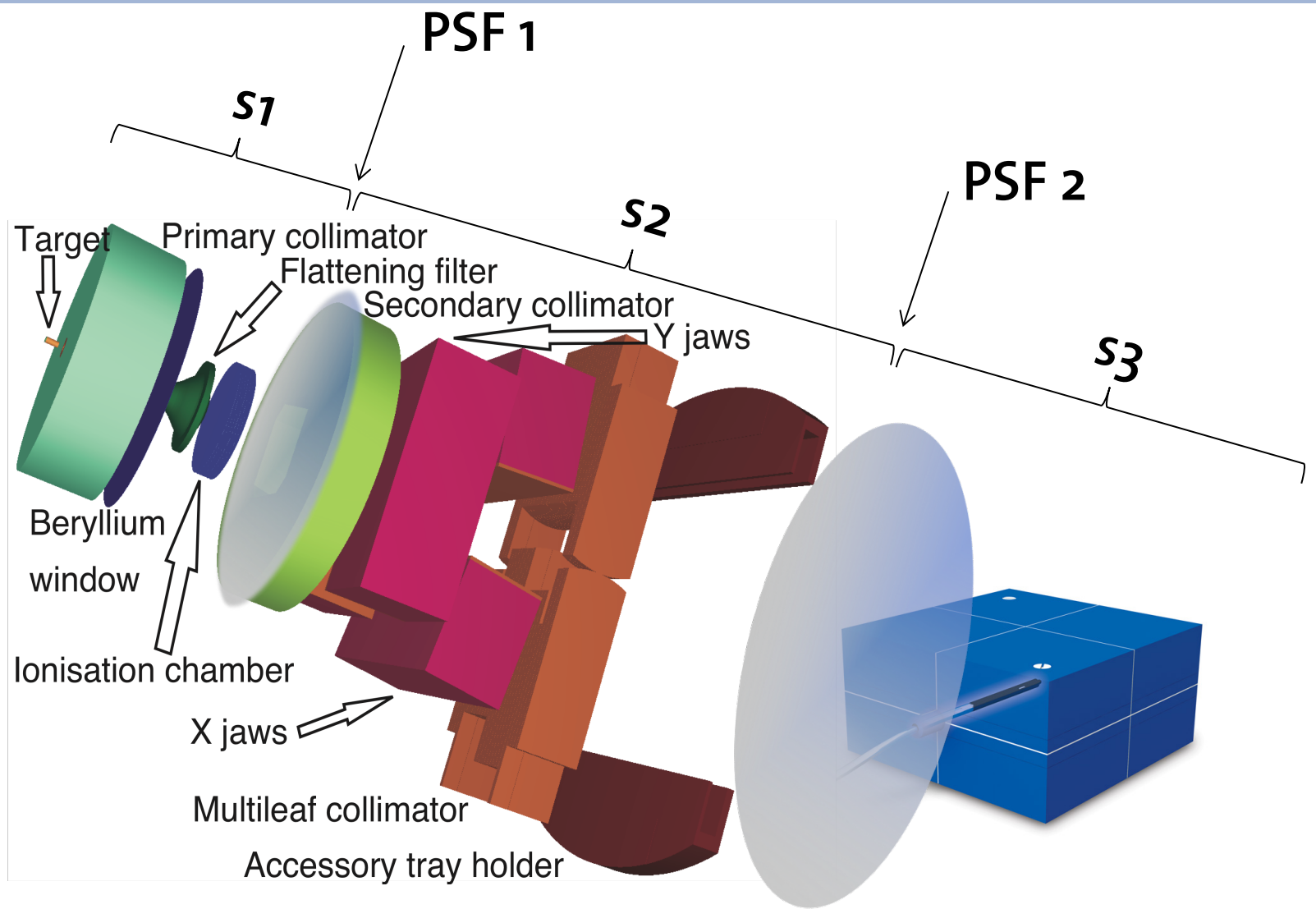
Tuning of initial beam parameters may mask the artifact too.

Target simulation

Are other MC codes affected too?

- All general-purpose MC codes rely on the condensed history technique to transport high energy electrons.
- Different codes use different multiple scattering theories and transport mechanics.
- All the approaches involve approximations of variable accuracy. In general, longer steps reduce the accuracy.
- Therefore, all codes may also exhibit similar artifacts. **Long steps should not be used without a previous thorough investigation.**

Phase-space file (PSF)



How does a PSF look like?

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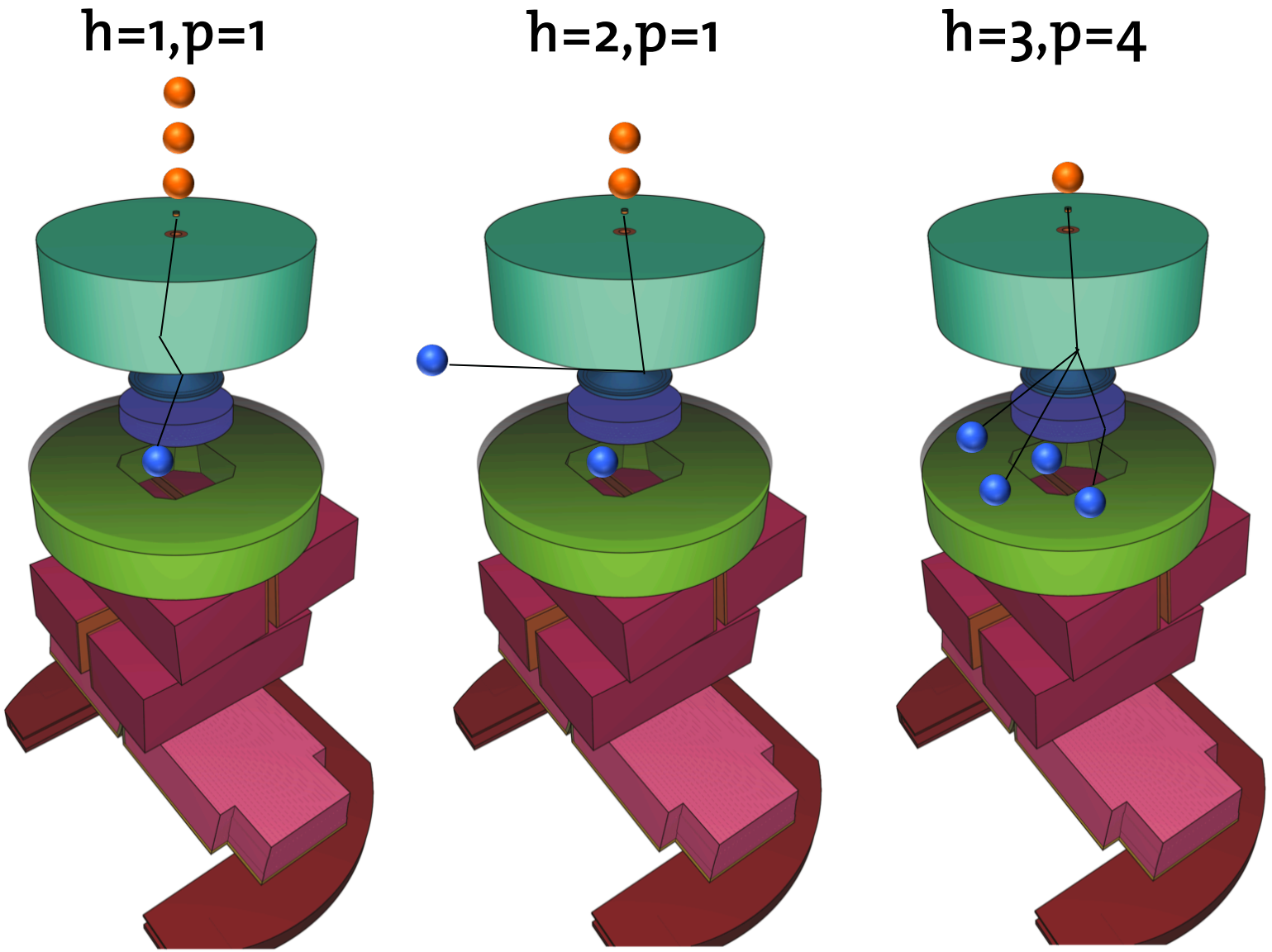
```

Key concepts: history versus particle



Incremental shower number

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```
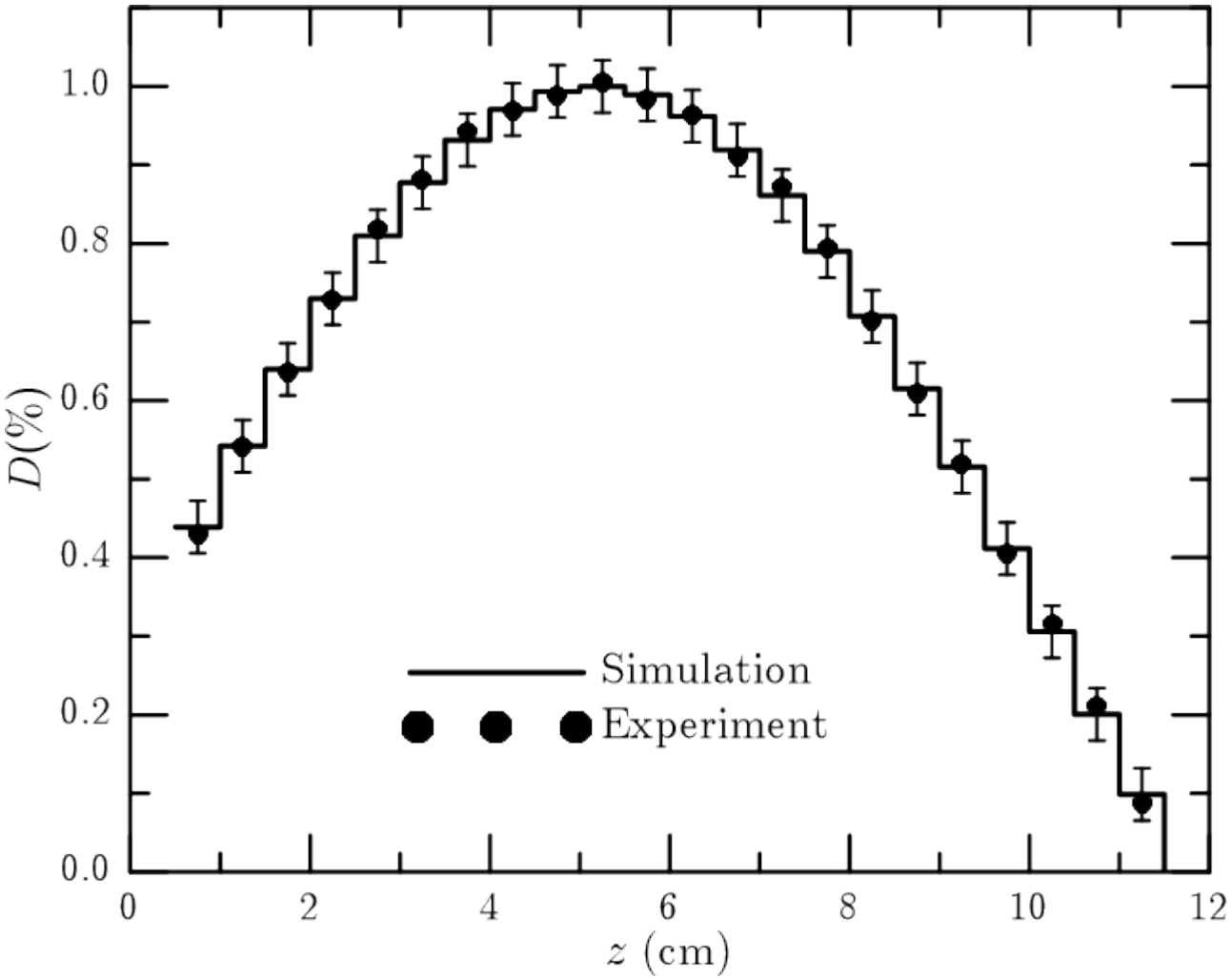

Key concepts: statistical uncertainty



Simulation unc. coverage factor k=1

if k=1 then ~68.3%

if k=2 then ~95.4%

if k=3 then ~99.7%

Key concepts: statistical uncertainty

Monte Carlo results mean NOTHING without the associated statistical uncertainty

Key concepts: variance-reduction techniques

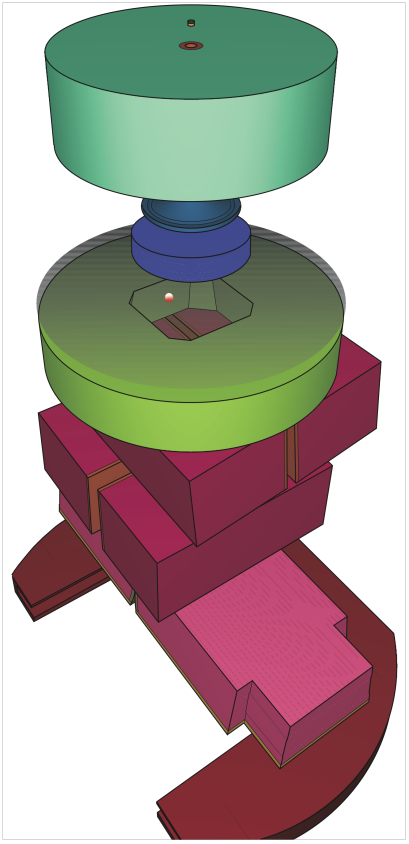
Variance-reduction techniques are aimed at improving the simulation efficiency

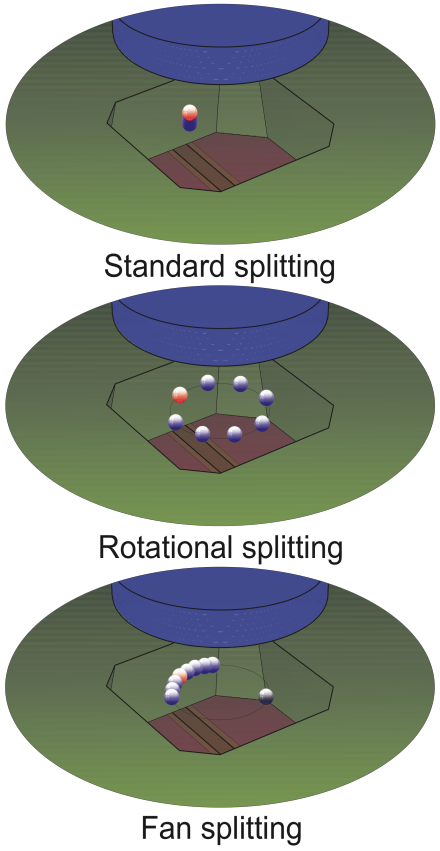
$$\epsilon = \frac{1}{T\sigma^2}$$

with T the simulation time and σ the relative standard deviation of the mean, while keeping the simulation unbiased.

Key concepts: variance-reduction techniques

- Movable skins[1]
- Standard splitting
- Rotational splitting[2,3]
- Fan splitting[2]
- Splitting roulette[4]
- Russian roulette
- Interaction forcing





1

IOP Publishing — Physics in Medicine and Biology
Phys. Med. Biol. **54** (2009) 4131–4149 — doi:10.1088/0031-9155/54/13/011

Efficient Monte Carlo simulation of multileaf collimators using geometry-related variance-reduction techniques

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2

A PENELOPE-based system for the automated Monte Carlo simulation of clinacs and voxelized geometries—application to far-from-axis fields

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On the efficiency of azimuthal and rotational splitting for Monte Carlo simulation of clinical linear accelerators

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A combined approach of variance-reduction techniques for the efficient Monte Carlo simulation of linacs

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[3] NCTeam, Strahlenklinik, Universitätsklinikum Essen, Hufelandstr 55, D-45122 Essen, Germany

Statistical weight

[PHASE SPACE FILE FORMAT penEasy v.2008-05-15]

```
# [PHASE SPACE FILE FORMAT penEasy v.2008-05-15]
#KPAR:  E     :      X     :      Y     :      Z     :      U     :      V     :      W     :   WGHT     :DeltaN:ILB(1..5)
 2  5.53157E+06  4.54723E+00 -8.53211E+00  6.68000E+01  6.73731E-02 -1.26413E-01  9.89687E-01  5.91716E-05 2 2 1 4 0 0
 2  1.00973E+05  4.65926E+00 -6.32448E+00  6.68000E+01  7.44427E-02 -8.18501E-02  9.93861E-01  5.91716E-05 2 2 1 4 0 0
 2  1.00973E+05  4.42096E+00 -6.49329E+00  6.68000E+01  7.13488E-02 -8.45605E-02  9.93861E-01  5.91716E-05 0 2 1 4 0 0
 2  1.00973E+05  4.17654E+00 -6.65313E+00  6.68000E+01  6.81564E-02 -8.71541E-02  9.93861E-01  5.91716E-05 0 2 1 4 0 0
 2  1.00973E+05  3.92636E+00 -6.80378E+00  6.68000E+01  6.48698E-02 -8.96273E-02  9.93861E-01  5.91716E-05 0 2 1 4 0 0
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 2  1.00973E+05  3.41007E+00 -7.07666E+00  6.68000E+01  5.80323E-02 -9.41987E-02  9.93861E-01  5.91716E-05 0 2 1 4 0 0
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 2  1.00973E+05  2.60121E+00 -7.41225E+00  6.68000E+01  4.71869E-02 -1.00073E-01  9.93861E-01  5.91716E-05 0 2 1 4 0 0
 2  2.06650E+05  4.51939E+00 -8.11293E+00  6.68000E+01  6.62699E-02 -1.19732E-01  9.90592E-01  5.91716E-07 1 4 1 4 0 0
 2  2.06650E+05  4.21471E+00 -8.27531E+00  6.68000E+01  6.17737E-02 -1.22112E-01  9.90592E-01  5.91716E-07 0 4 1 4 0 0
 2  2.06650E+05  3.90420E+00 -8.42625E+00  6.68000E+01  5.71921E-02 -1.24324E-01  9.90592E-01  5.91716E-07 0 4 1 4 0 0
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 2  8.44930E+05  3.43546E+00 -6.80856E+00  6.68000E+01  5.10947E-02 -1.01287E-01  9.93544E-01  5.91716E-05 0 2 1 4 0 0
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```
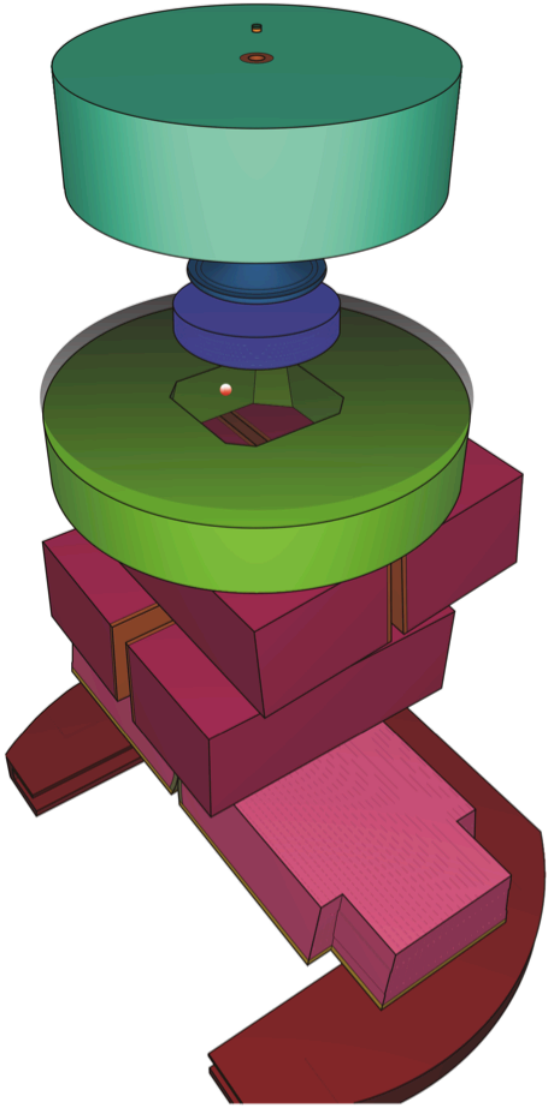
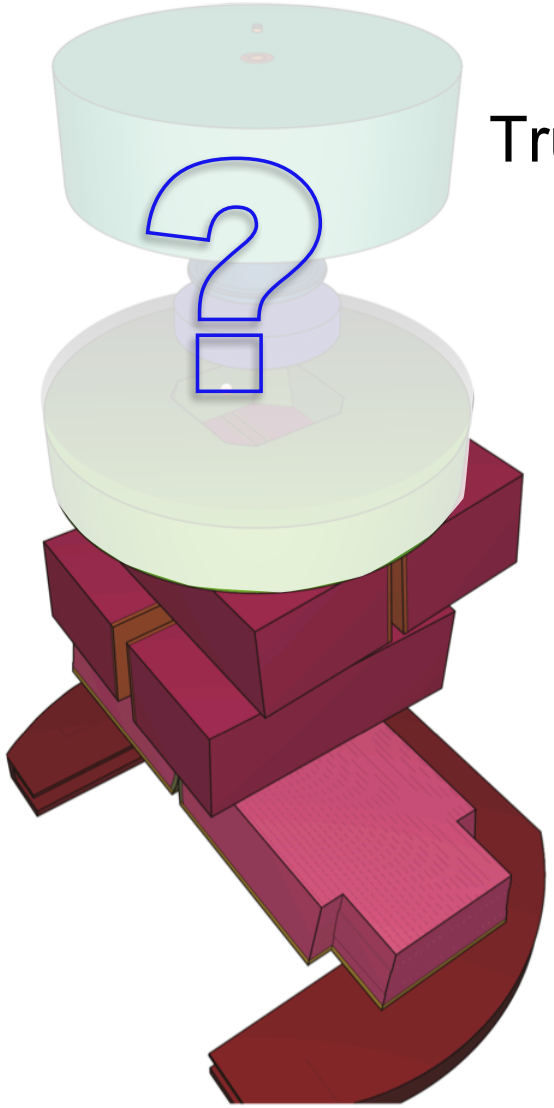

Available geometries of Varian linacs

2100 C/D



TrueBeam



FakeBeam (ungenuine geometry) vs. TrueBeam (PSF distributed by Varian)

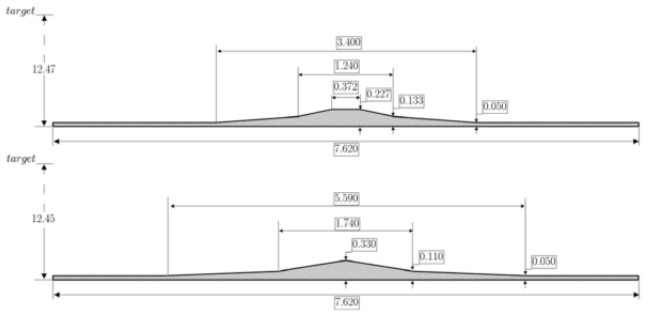


Figure 1. Cross-section of the *ad hoc* 6-FFF (above) and 10-FFF (below) filters. The materials are bronze and tantalum, respectively. Cylindrical symmetry applies. All dimensions are given in centimeters.

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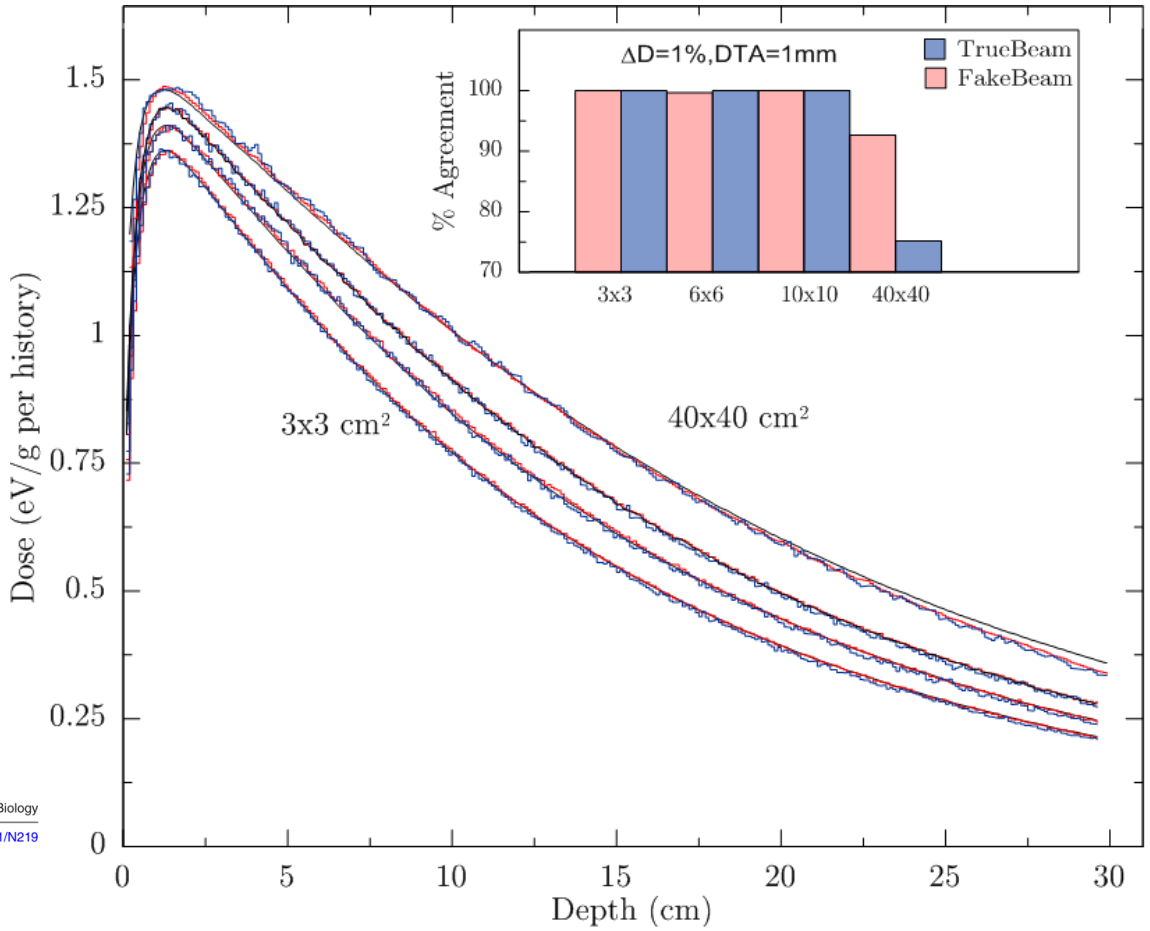
Phys. Med. Biol. **60** (2015) N219–N229 — doi:10.1088/0031-9155/60/11/N219

Note

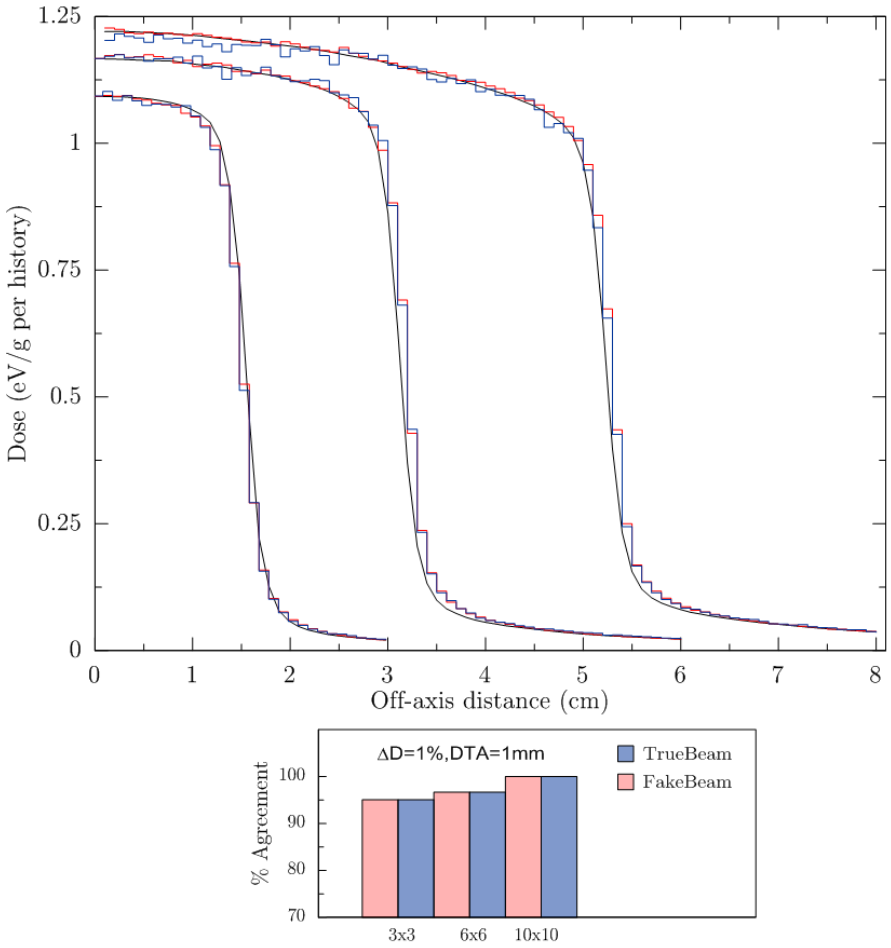
A geometrical model for the Monte Carlo simulation of the TrueBeam linac

M Rodriguez[1], J Sempau[1], A Fogliata[2], L Cozzi[2], W Sauerwein[3] and L Brualla[3]

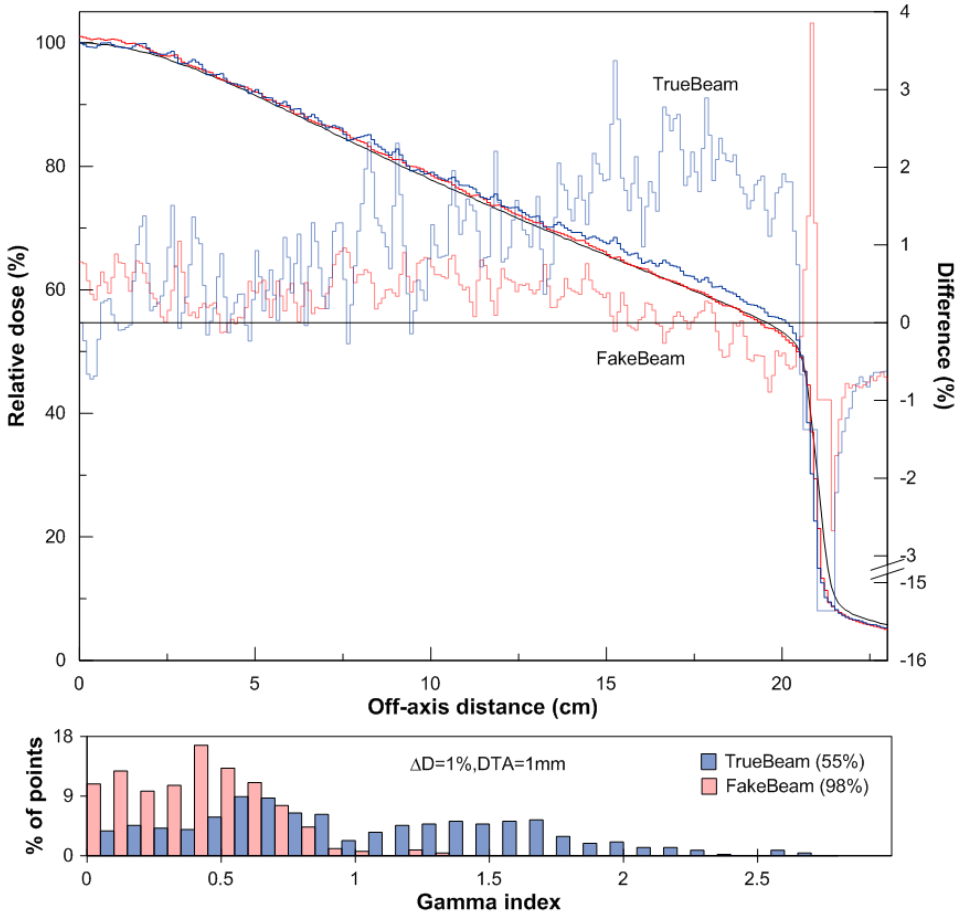


Depth dose curves for a 6MV FFF beam and fileds of 3x3 cm², 6x6 cm², 10x10 cm² and 40x40 cm². Black lines: experimental data. Red lines: MC estimated results from Varian´s TrueBeam PSF. Red line: MC estimated results using FakeBeam geometry. Gamma analysis appears in the inset.

FakeBeam (ungenuine geometry) vs. TrueBeam (PSF distributed by Varian)



Lateral crossplane profiles for a 6 MV FFF beam and fields of 3X3, 6x6 and 10x10 cm^2 at 5 cm depth. Black Line: experimental data; Blue line: MC estimated results from Varian´s TrueBeam PSF; Red line: MC estimated results using FakeBeam geometry. Gamma analysis appears in the lower panel.



Lateral crossplane profile (left ordinate axis) from a 6 MV FFF beam of a 40X40 cm^2 field at 5 cm depth. Black Line: experimental Golden Beam Data; Blue line: MC estimated results from Varian´s TrueBeam PSF. Red line: MC estimated results using FakeBeam geometry. Relative difference curves respect to the maximum experimental dose are plotted using the right ordinate axis. Notice that this axis is broken. Gamma analysis appears in the lower panel.

Strahlenther Onkol (2017) 193:243–259
DOI 10.1007/s00066-016-1075-8

REVIEW ARTICLE

Monte Carlo systems used for treatment planning and dose verification

Lorenzo Brualla[1] · **Miguel Rodriguez**[2] · **Antonio M. Lallena**[3]

Received: 4 May 2016 / Accepted: 25 October 2016 / Published online: 25 November 2016

Ultra-accurate Monte Carlo based dose calculation algorithm.

(Webpage of the product)

Similar accuracy to and faster calculation times than Monte Carlo.

(Brochure of the product)

[It] calculates a fraction of the total stopping power stochastically using a specially constructed energy straggling cross section.

(Algorithm's technical manual)

Types of MC codes for radiation transport

Accuracy

Speed

General-purpose

- Wide range of energy (~1 keV up to ~1 GeV)
- Any material. Any geometry
- Examples: PENELOPE, EGSnrc, Geant, MCNP

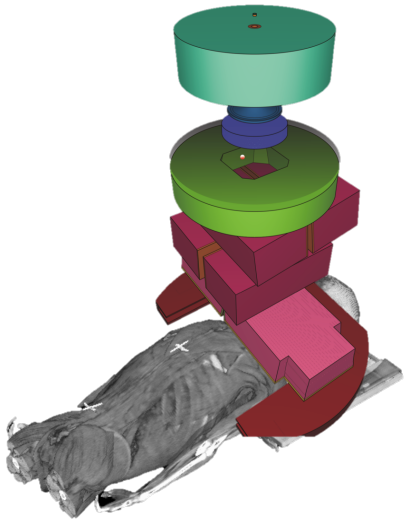
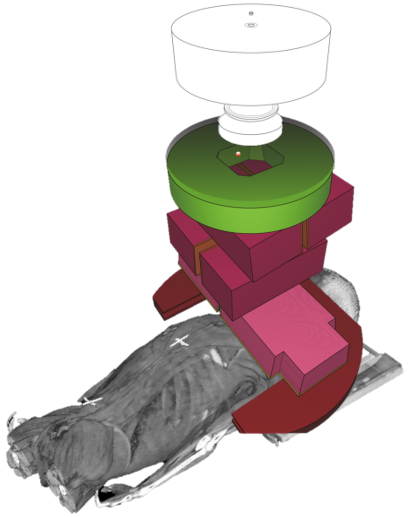
Fast

- Only energies with clinical interest (~MeV)
- Only low Z materials. Only binned geometries
- Examples: DPM, XVMC, VMC, PENFAST

Pre-computed

- Use pre-calculated data
- Only energies with clinical interest (~MeV)
- Only low Z materials
- Examples: MMC, eMC, SMC

Classification criteria

Purpose	*Reach*	*Algorithm*	*Self-contained*
Treatment planning	Full 	General purpose	Yes
		Fast	
Dose verification	Virtual source 	Pre-computed	No

MC systems according criteria

System	Purpose	Reach	Algorithm linac	Algorithm patient	Self-contained	Distributed
CARMEN	tp	full	gp (EGSnrc)	gp (EGSnrc)	no	no
CERR	dv	-	-	fast (VMC++)	no	free
Corvus	tp	vsm	-	fast (PEREGRINE)	yes	no
Eclipse	tp	vsm	-	pc (MMC)	yes	pay
eIMRT	dv	full	gp (EGSnrc)	gp (EGSnrc)	yes	free
iPlan	tp	vsm	-	fast (XVMC)	yes	pay
ISOgray	tp	full	gp (PENELOPE)	fast (PENFAST)	yes	no
MCDE	tp	full	gp (EGSnrc)	gp (EGSnrc)	no	no
MCDOSE	tp	vsm	-	gp (EGS4)	no	no
MCV	dv	full	gp (EGS4)	gp (EGS4)	no	no
MCVS	dv	full	gp (EGSnrc)	gp (EGSnrc)	no	no
MMCTP	dv	full	gp (EGSnrc)	gp (EGSnrc)	no	free
Monaco	tp	vsm	-	fast (XVMC)	yes	pay
MSKCC	dv	vsm	-	gp (EGS4)	yes	no
Oncentra	tp	vsm	-	fast (VMC++)	yes	pay
Pinnacle	tp	-	-	fast (DPM)	yes	no
PLanUNC	dv	full	gp (EGSnrc)	gp (EGSnrc)	no	free
PRIMO	dv	full	gp (PENELOPE)	gp (PENELOPE)/fast (DPM)	yes	free
RTGrid	tp	full	gp (EGSnrc)	gp (EGSnrc)	no	no
SMCP	tp	vsm	-	gp (EGSnrc)/fast (VMC++)	no	no
VIMC	dv	full	gp (EGSnrc)	gp (EGSnrc)/fast (VMC++)	no	no
XiO	tp	vsm	-	fast (XVMC)	yes	pay

MC systems according criteria

System	Purpose	Reach	Algorithm linac	Algorithm patient	Self-contained	Distributed
CERR	dv	-	-	fast (VMC++)	no	free
Eclipse	tp	vsm	-	pc (MMC)	yes	pay
eIMRT	dv	full	gp (EGSnrc)	gp (EGSnrc)	yes	free
iPlan	tp	vsm	-	fast (XVMC)	yes	pay
MMCTP	dv	full	gp (EGSnrc)	gp (EGSnrc)	no	free
Monaco	tp	vsm	-	fast (XVMC)	yes	pay
Oncentra	tp	vsm	-	fast (VMC++)	yes	pay
PLanUNC	dv	full	gp (EGSnrc)	gp (EGSnrc)	no	free
PRIMO	dv	full	gp (PENELOPE)	gp (PENELOPE)/fast (DPM)	yes	free
XiO	tp	vsm	-	fast (XVMC)	yes	pay

MC systems according criteria

System	Purpose	Reach	Algorithm linac	Algorithm patient	Self-contained	Distributed
Eclipse	tp	vsm	-	pc (MMC)	yes	pay
eIMRT	dv	full	gp (EGSnrc)	gp (EGSnrc)	yes	free
iPlan	tp	vsm	-	fast (XVMC)	yes	pay
Monaco	tp	vsm	-	fast (XVMC)	yes	pay
Oncentra	tp	vsm	-	fast (VMC++)	yes	pay
PRIMO	dv	full	gp (PENELOPE)	gp (PENELOPE)/fast (DPM)	yes	free
XiO	tp	vsm	-	fast (XVMC)	yes	pay

Features of distributed MC systems

		Eclipse	elMRT	iPlan	Monaco	Oncentra	PRIMO	XiO
Algorithm	**Linac upper**	vsm	gp (BEAMnrc)	vsm	vsm	vsm	gp (PENELOPE)	vsm
	Linac lower	vsm	gp (BEAMnrc)	fast	transmission filter	vsm	gp (PENELOPE) fast (DPM)	pc
	Dose	pc (MMC)	gp (DOSXYZnrc)	fast (XVMC)	fast (XVMC)	fast (VMC++)	gp (PENELOPE) fast (DPM)	fast (XVMC)
Beams	**Electrons**	yes	no	no	no	yes	yes	yes
	Photons	no	yes	yes	yes	no	yes	no
Beam QA tools in water		yes	no	no	yes (optional)	yes	yes	yes
Modalities	**3D-CRT**	n/a	yes	yes	yes	n/a	yes	n/a
	IMRT	n/a	yes	yes	yes	n/a	yes	n/a
	VMAT	n/a	no	no	yes	n/a	yes	n/a
Linacs	**Varian**	C-Series	C-Series	600, C-Series, Novalis	600, C-Series	C-Series	600, Unique, C,TrueBeam	C-Series
	Elekta	-	-	MLCi, MLCi2	MLCi, MLCi2	SLi, MLCi, MLCi2	SLi, MLCi	SLi, MLCi, MLCi2
	Siemens	-	Primus, Oncor	Meva, Primus, Oncor, Artiste	-	Mevatron, Primus, Oncor	-	Mevatron, Primus, Oncor
Inverse TP optimization		n/a	no	pbc	pbc	n/a	no	n/a
Dose referred to		water	water	medium/water	medium/water	water	medium	medium/water
Beam configuration		auto	auto	manufacturer	manufacturer	manufacturer	manual	manufacturer
Operating system		Windows	Linux	Windows	Windows	Windows	Windows	Linux
FDA approval		yes	no	yes	yes	yes	no	yes

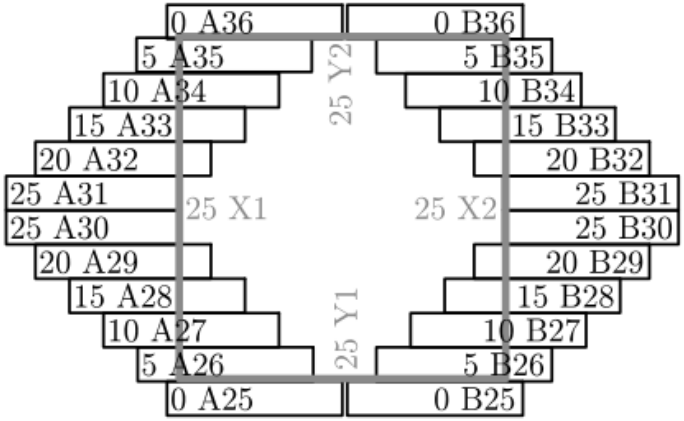
Benchmarks

Field 1 (photons)

- *6 MV*
- *water phantom*
- *voxel 3x3x3 mm³*
- *uncertainty 2% (k=1)*
- *field 10x10 cm²*

Field 2 (photons)

- *field 5x5 cm²*



Field 3 (electrons)

- *6 MeV*
- *water phantom*
- *voxel 3x3x3 mm³*
- *uncert 2% (k=1)*
- *field 10x10 cm²*

Field 4 (electrons)

- *16 MeV*
- *water phantom*
- *voxel 3x3x3 mm³*
- *uncert 2% (k=1)*
- *field 10x10 cm²*

Benchmarks

Simulation time in minutes

	Eclipse	elMRT	iPlan	Monaco	Oncentra	PRIMO (DPM)	PRIMO (PENELOPE)	XiO
Field 1 (10x10)	-	372 (57)	0.5	0.4	-	5	30	-
Field 2 (MLC)	-	361 (17)	0.2	0.5	-	3	24	-
Field 3 (6 MeV e^-)	0.1	-	-	-	0.5	-	21	0.1
Field 4 (16 MeV e^-)	0.2	-	-	-	0.9	-	31	0.2

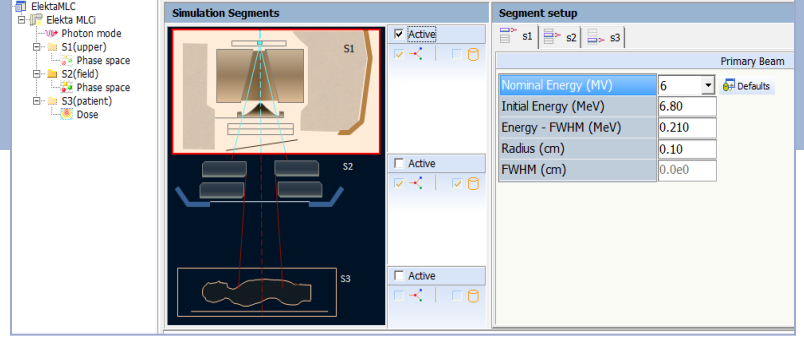
PRIMO

PRIMO is a computer software that simulates linacs and dose distributions in water phantoms and computerized tomographies. It combines a graphical user interface and a computation engine based on the Monte Carlo code PENELOPE.

www.primoproject.net

particularity, easiness

PRIMO



penEasyLinac

```
MODEL  2100  [Model of the Varian Clinac:'600C','600CD','2100','2300'. REQUIRED]
TITLE  Gantry=0 and Collimator=0 => in BEV patient head up in gview2d (z-screen)
MODEEP 1       [Operation mode. Possible values: 1=electron. 2=photon. REQUIRED]
SNOMEN 6       [Nominal energy in MeV. Pos val: 6,9,12,15,16,18,20,22  REQUIRED]
SERVIC 0                        [Working mode: 0=Patient, 1=Service. REQUIRED]
APPSXY 10 10     [Appli Pos val:6 6, 6 10, 10 10, 15 15, 20 20, 25 25. REQUIRED]
ROTSPL 0       [Usage of rotational splitting: 0=No. 1=Yes. Yes for faster sim.]
POSPSF 1   [Position of PSF. 1=3rd scraper, 2=2nd scraper. REQUIRED if SERVIC=0]
SYSTEM 1                    [Operating system: 1=Unix-like. 2=Windows. REQUIRED]
```

PENGEOM

```
0000000000000000000000000000000000000000000000000000000000000000000000000000
SURFACE (  17) Inclined lower plane of support plate for Ta
INDICES=( 0, 0, 0, 1,-1)
  OMEGA=( 9.000000000000000E+01,   0) DEG
  THETA=(-5.561283191310000E+01,   0) DEG
    PHI=( 9.000000000000000E+01,   0) DEG
Z-SHIFT=( 5.834971000000000E+00,   0)
0000000000000000000000000000000000000000000000000000000000000000000000000000
BODY    (   5) Inclined support Al plate for Ta foil (Right)
MATERIAL(   5)
SURFACE (  16), SIDE POINTER=( 1)
SURFACE (  17), SIDE POINTER=(-1)
SURFACE (  12), SIDE POINTER=( 1)
```

penEasy

```
[SECTION TALLY PHASE SPACE FILE v.2009-06-15]
 OFF                            STATUS (ON or OFF)
 0                              PSF FORMAT (0=STANDARD penEasy ASCII; 1=IAEA BINARY)
 1                              DETECTION MATERIAL (NOT EQUAL 0)
 output.psf                     PSF FILENAME, REMOVE EXTENSION IF FORMAT=1
[END OF PSF SECTION]
```

```
      write(*,'(a)')
     &  'Spectrum limits [Emin,Emax] (eV) and no. bins:'
      read(*,*) emin,emax,nbin
      write(*,'(2(1x,1pe12.5),1x,i5)') emin,emax,nbin
      ebin = (emax-emin)/nbin
      iebin = 1.0d0/ebin
      ! Add one bin to store, separately, counts with E=Emax:
      nbin = nbin+1
```

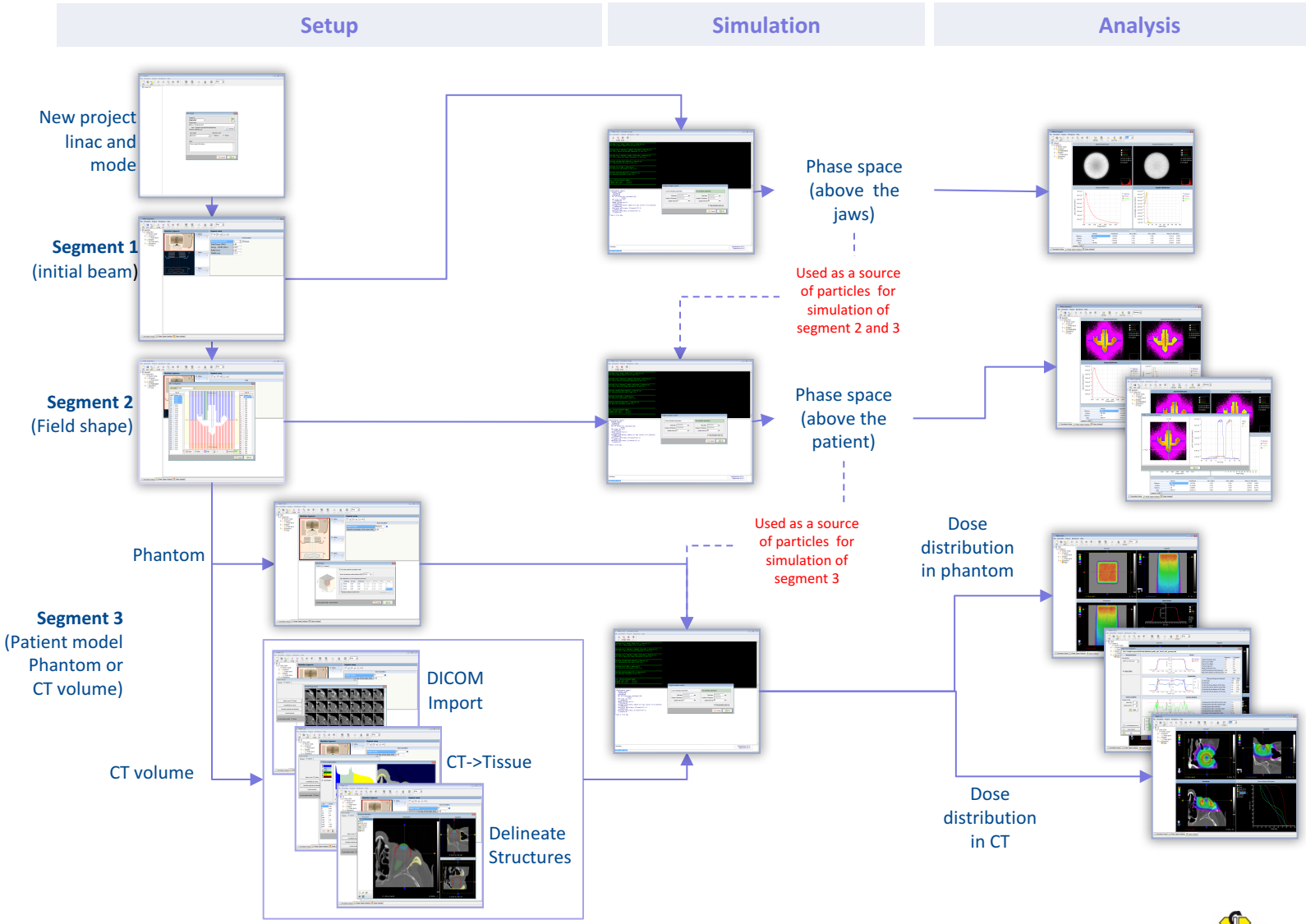
PENELOPE

```
C  ****  1st order correction, integral of Pz times the Compton profile.
C        Calculated approximately using a free-electron gas profile.
      PF=3.0D0/(4.0D0*FJ0(M,IO))
      IF(ABS(PIMAX).LT.PF) THEN
        QCOE2=1.0D0+ECOE**2-2.0D0*ECOE*CDT
        P2=PIMAX**2
        DSPZ=SQRT(QCOE2)*(1.0D0+ECOE*(ECOE-CDT)/QCOE2)
     1       *FJ0(M,IO)*0.25D0*(2*P2-P2**2/PF**2-PF**2)
        SIA=SIA+MAX(DSPZ,-SIA)
      ENDIF
```

Linac-GLASS	Graphical user interface
penEasyLinac	Input files preparation for linacs
penEasy	MAIN: sources+tallies+VRTs
PENGEOM / penVox	Geometry
PENELOPE	Physics

generality, difficulty

Workflow of PRIMO



Main tool bar

Structure tree

structure selection

Plan and dose

Import & review

Dose evaluation

(dose comparison)

Segment Setup

Primary Beam | Fields | Patient model

+ Field | -Field | Edit Field

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	Elekta SL	STATIC	1.0000	0.0	0.0	0.0	0.0	5.0	5.0	10.0	5.0	5.0	10.0	None	None	0.00	0.00	0.00

Segment Setup

Primary Beam | Fields | Patient model

	Size (cm)	Minimum (cm)	Maximum (cm)	Bin size (cm)	Size (bins)
Sagittal	40.50	-20.25	20.25	0.50	81
Axial	40.50	-20.25	20.25	0.50	81
Coronal	40.00	0.00	40.00	0.50	80

It is not editable

- An homogeneous (water) CT volume is created by default for the project
- A slab phantom can be created or a CT can be imported in DICOM format

New project

Open project

Save project

Import a phase-space file (copy)

Link a phase-space file (no copy)

Import a CT (DICOM)

Import contours (DICOM)

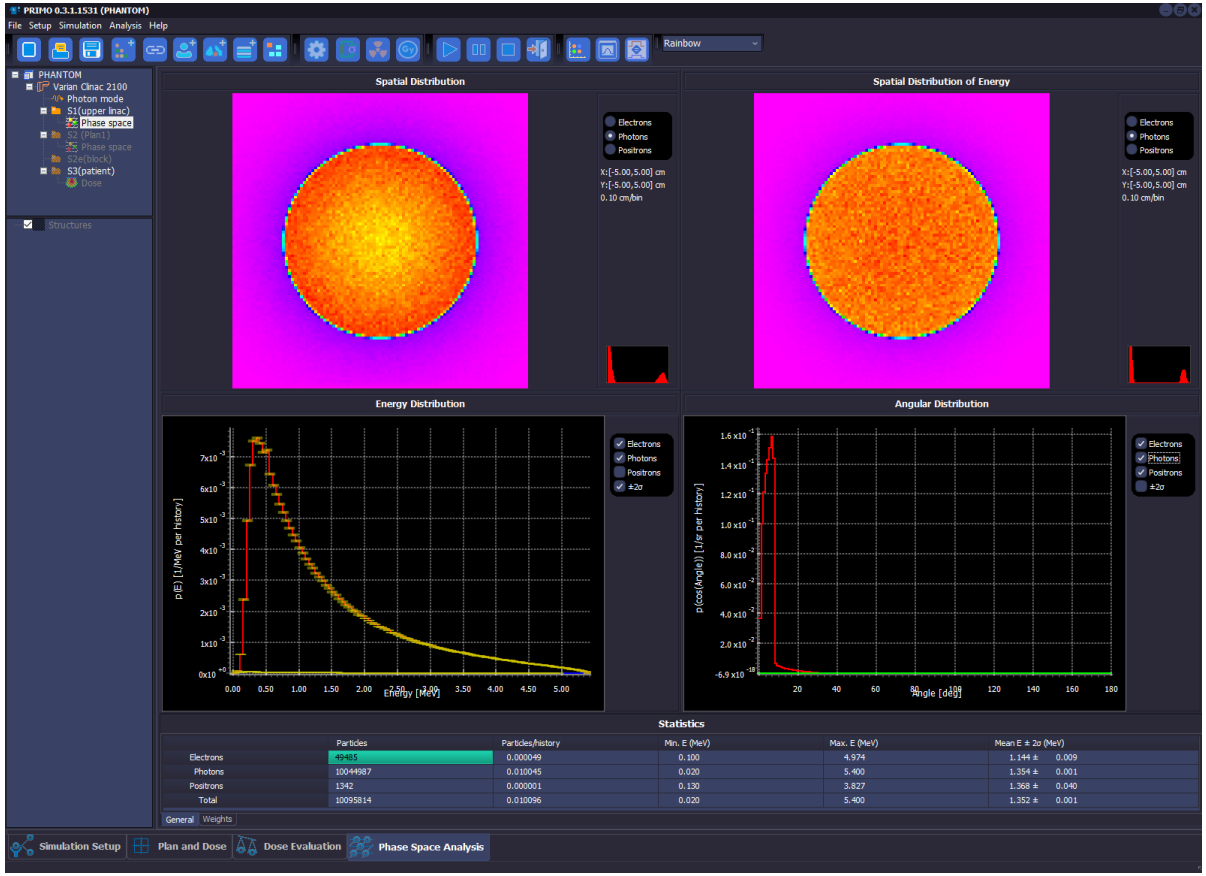
Create a slab phantom

Create simulation geometry (segmentation)

Analyze the source phase-space

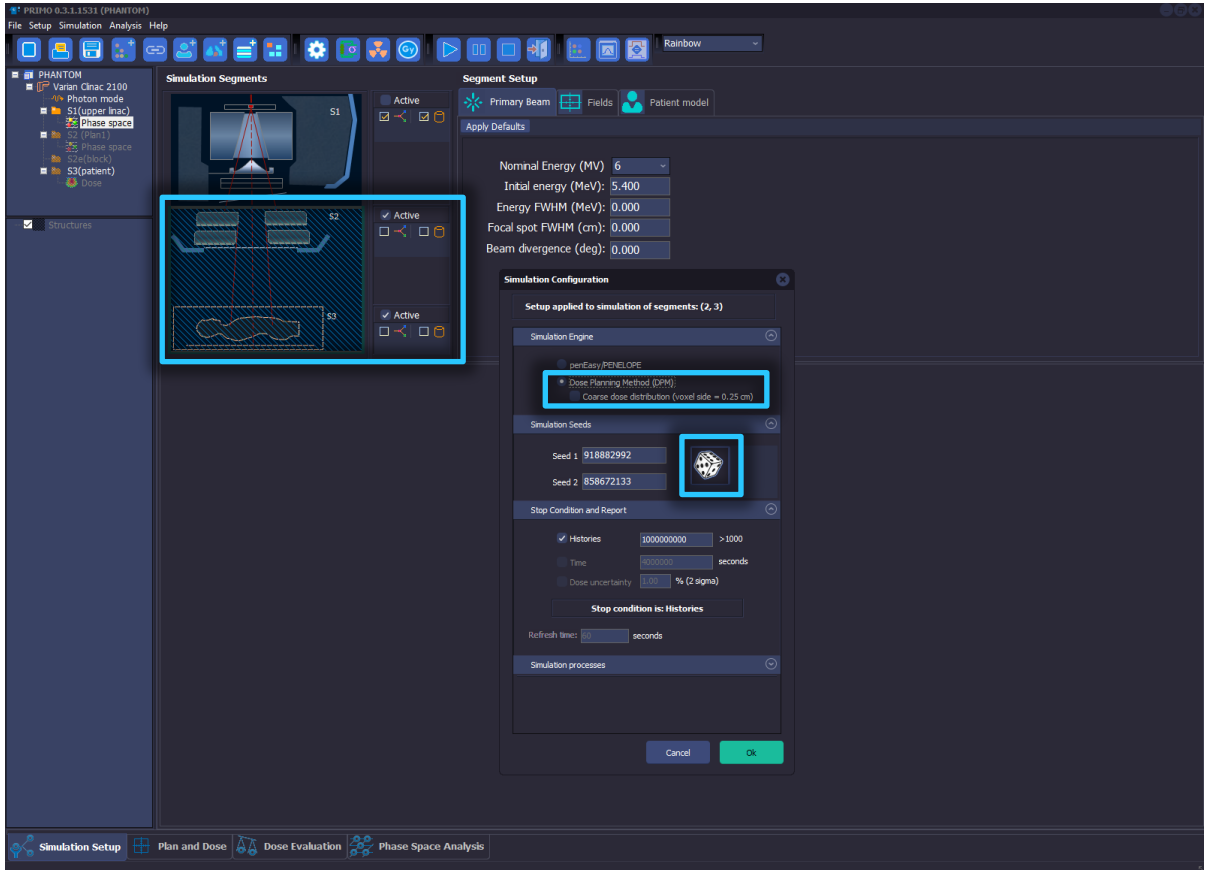
Analyze the source phase-space

- Toggle among electrons, photons or positrons.
- View maps in as a 3D graph
- Zoom curves in/out
- Explore the contextual menus



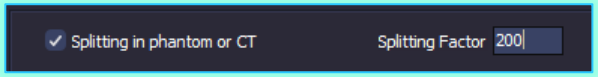
Simulation setup

- Activate segments S2 and S3
- On the simulation config dialog chose:
  - DPM as simulation engine
  - Press the dice to change the RNG seeds

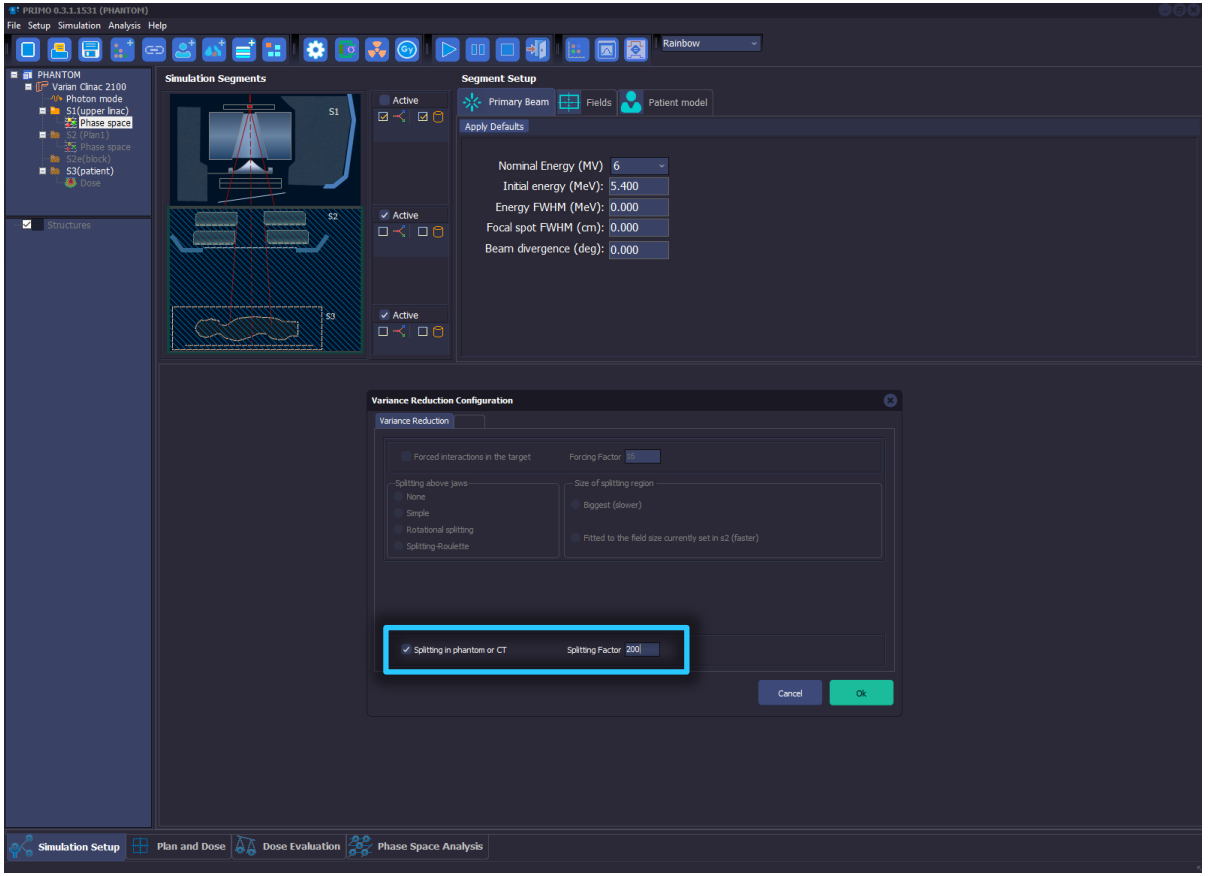


Variance-reduction technique setup

- Select 
- On the variance reduction configuration window set:



- Save the project 

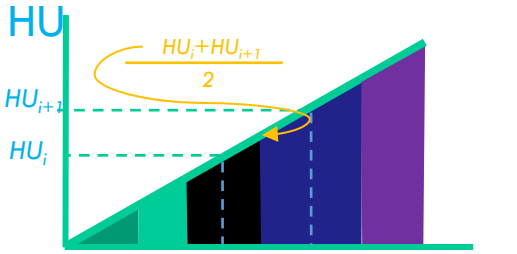


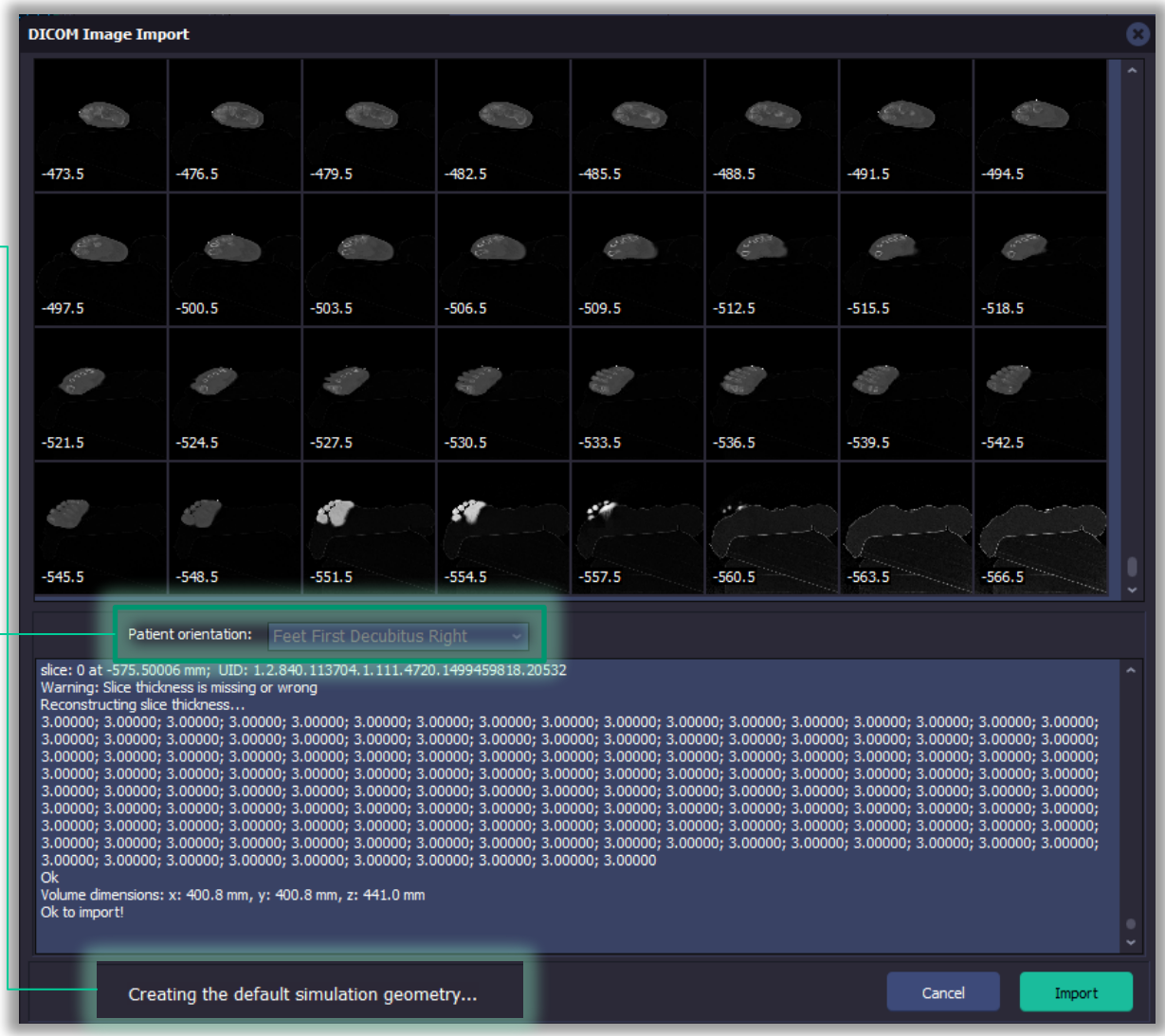
Import a CT

Patient orientation (not editable)

A default segmentation is created on import

- Materials:
  - Air, lung ICRP, adipose tissue, muscle skeletal, cartilage ICRP, compact bone
- Range of HU for a material taken from the CT calibration curve.

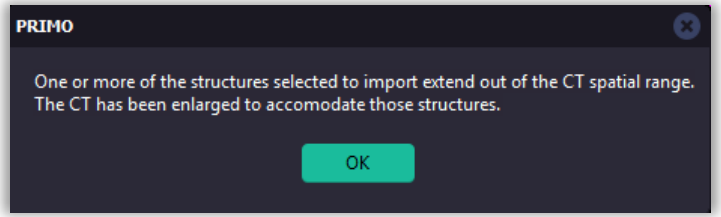


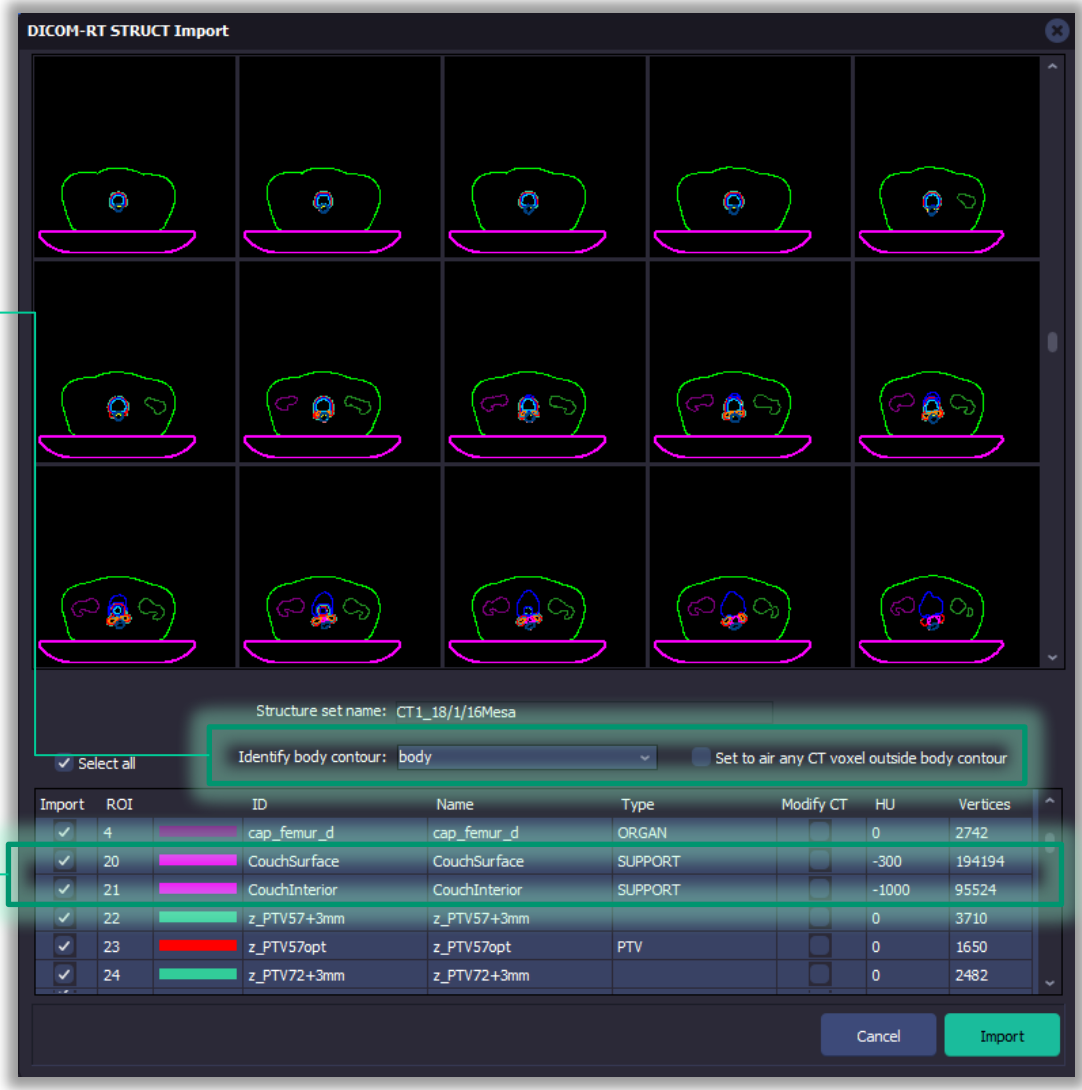


Import contours

All the voxels outside a selected contour can be set to air. To avoid accessories used in simulation that interfere with dose calculation

Support structures can be imported and its HU “written” on the CT





Plan and Dose

Default field: 10 ×10 cm^2 isocenter at (0,0,0), the center of the CT surface

Plans are imported from this window

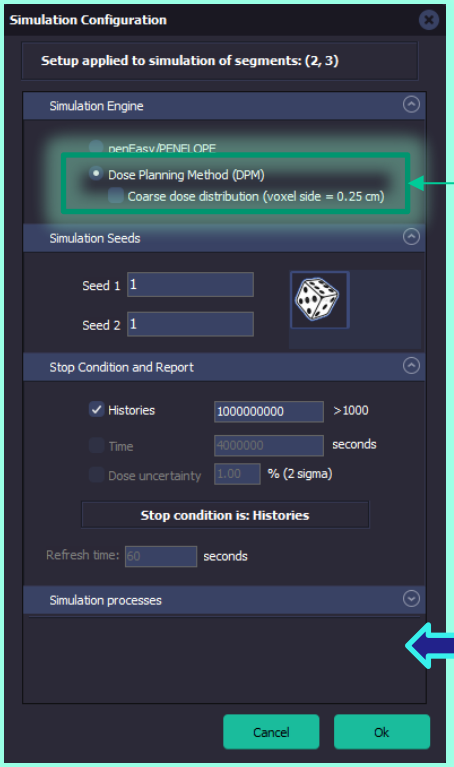
Dynamic plans cannot be edited (only the isocenter can be repositioned)

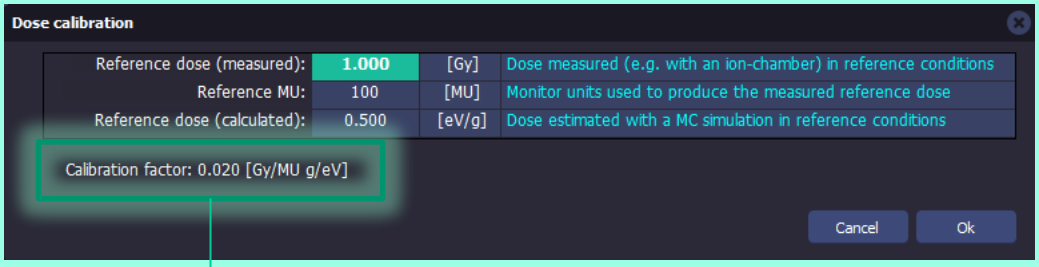
Simulati on config

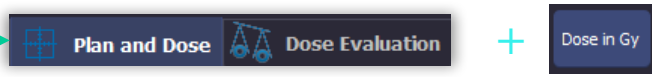
Variance reduction

Transport parameters

Dose calibration







DPM uses all the cores available

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DPM, a fast, accurate Monte Carlo code optimized for photon and electron radiotherapy treatment planning dose calculations

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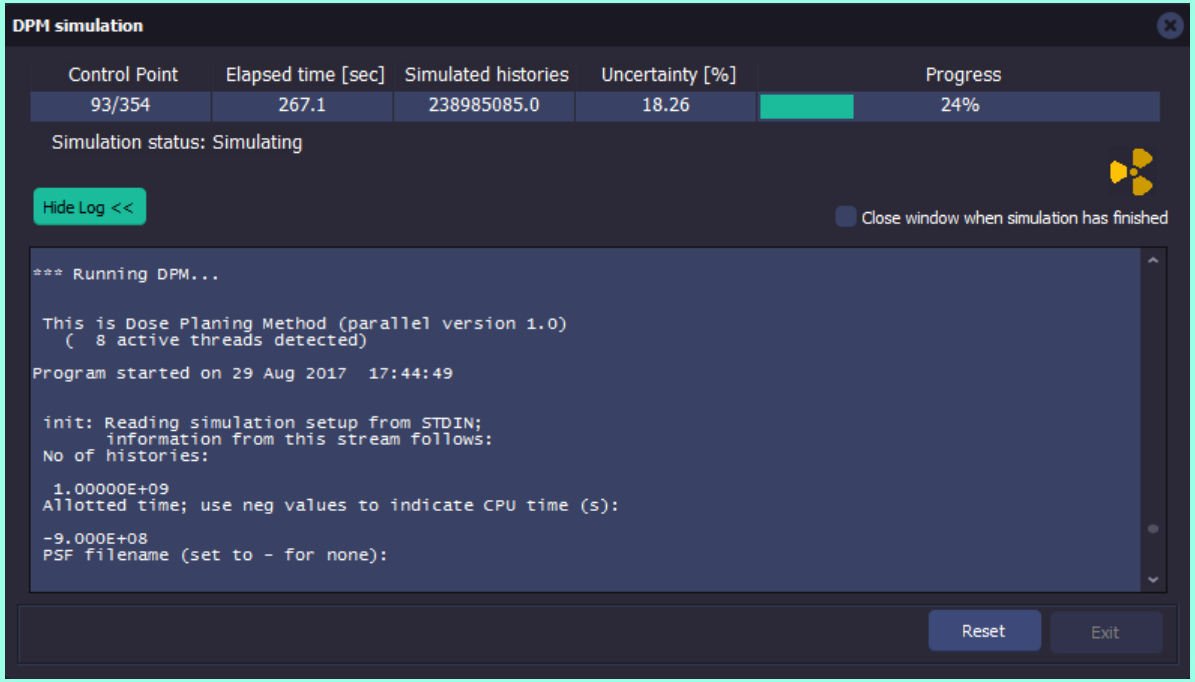
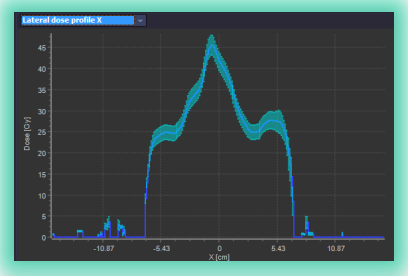
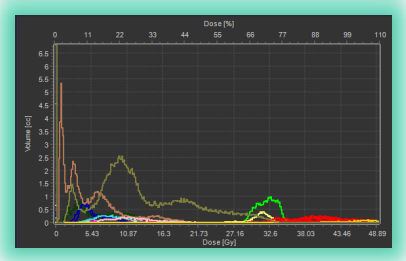
‡ Institut de Tècniques Energètiques, Universitat Politècnica de Catalunya, Diagonal 647, 08028 Barcelona, Spain

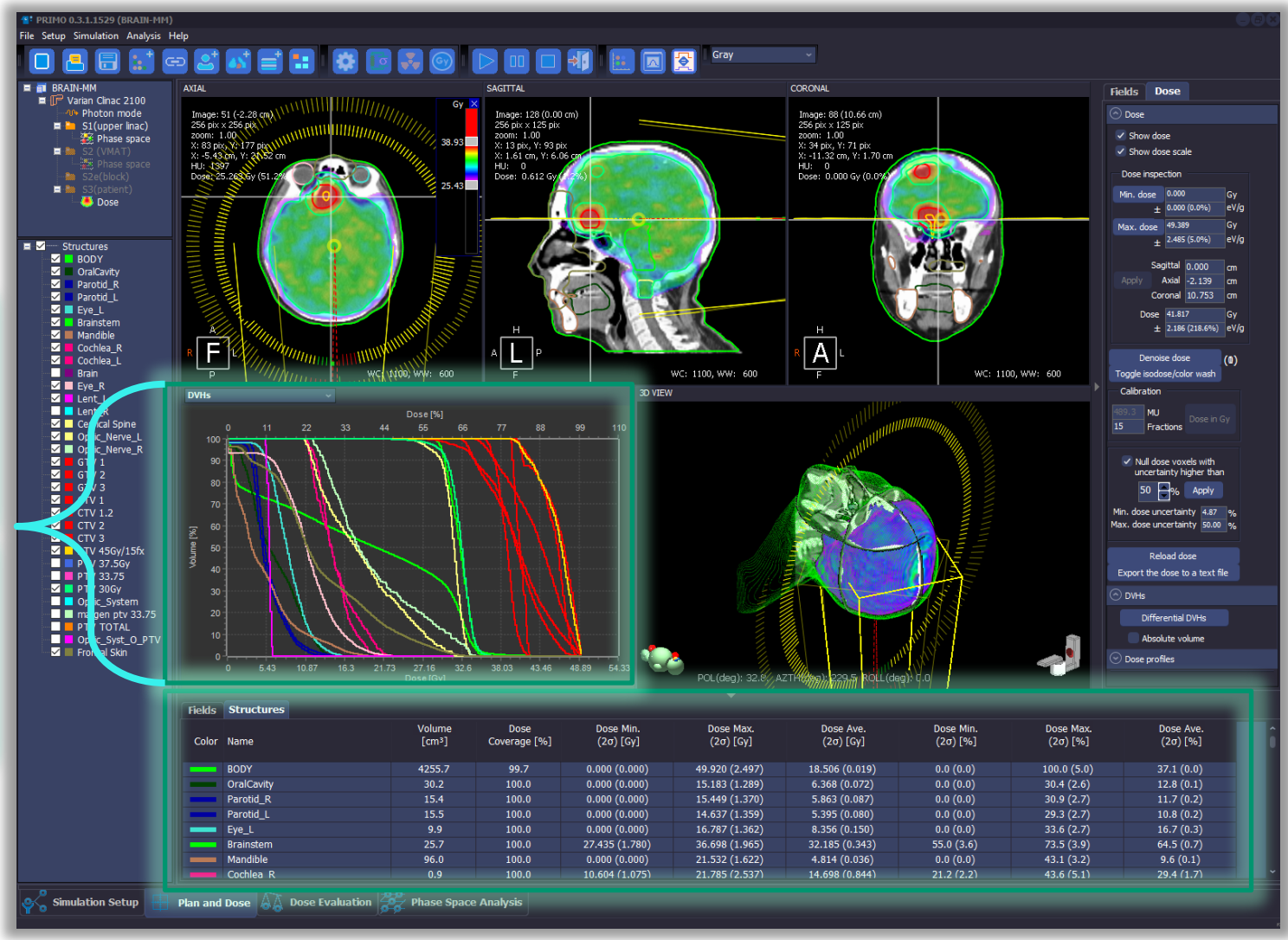
Play simulation



Plan and Dose



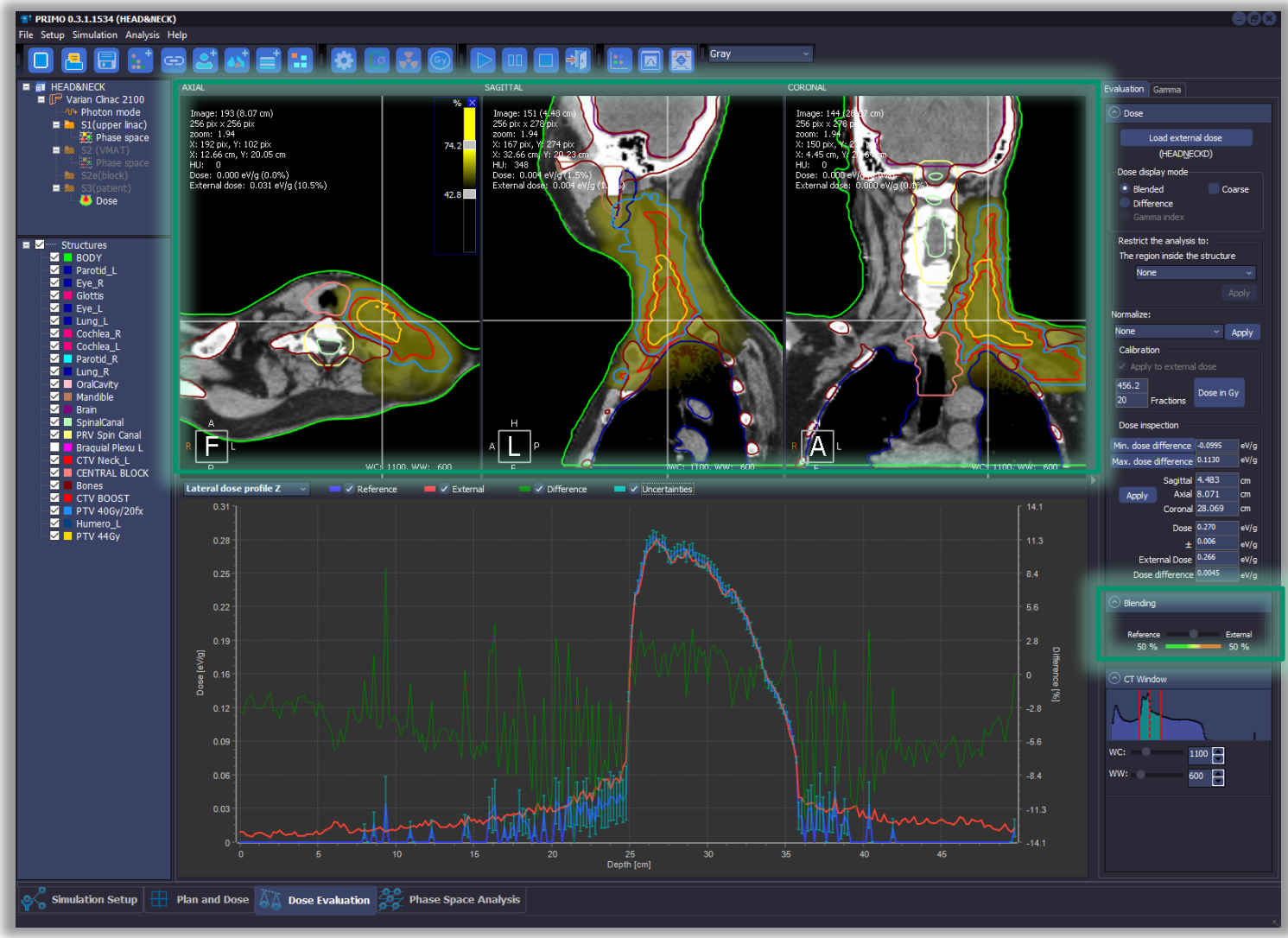




Dose evaluation
(dose comparison)

- Blending
- Difference
- Gamma

- Dose profiles w/ difference profile
- DVHs



Dose evaluation
(dose comparison)

- Blending
- Difference
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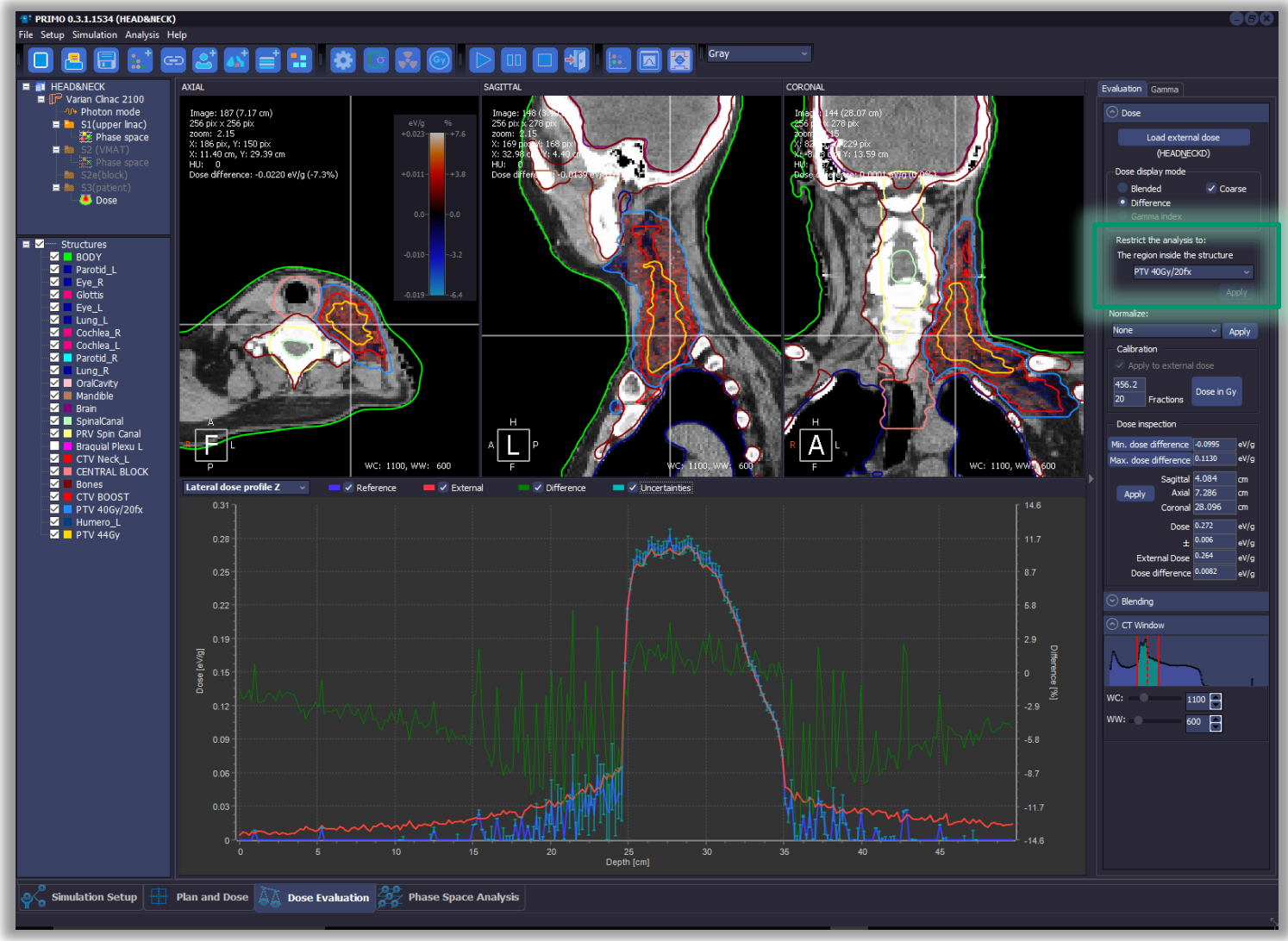
- Dose profiles w/ difference profile
- DVHs

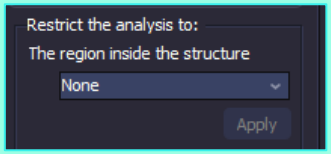


Dose evaluation
(dose comparison)

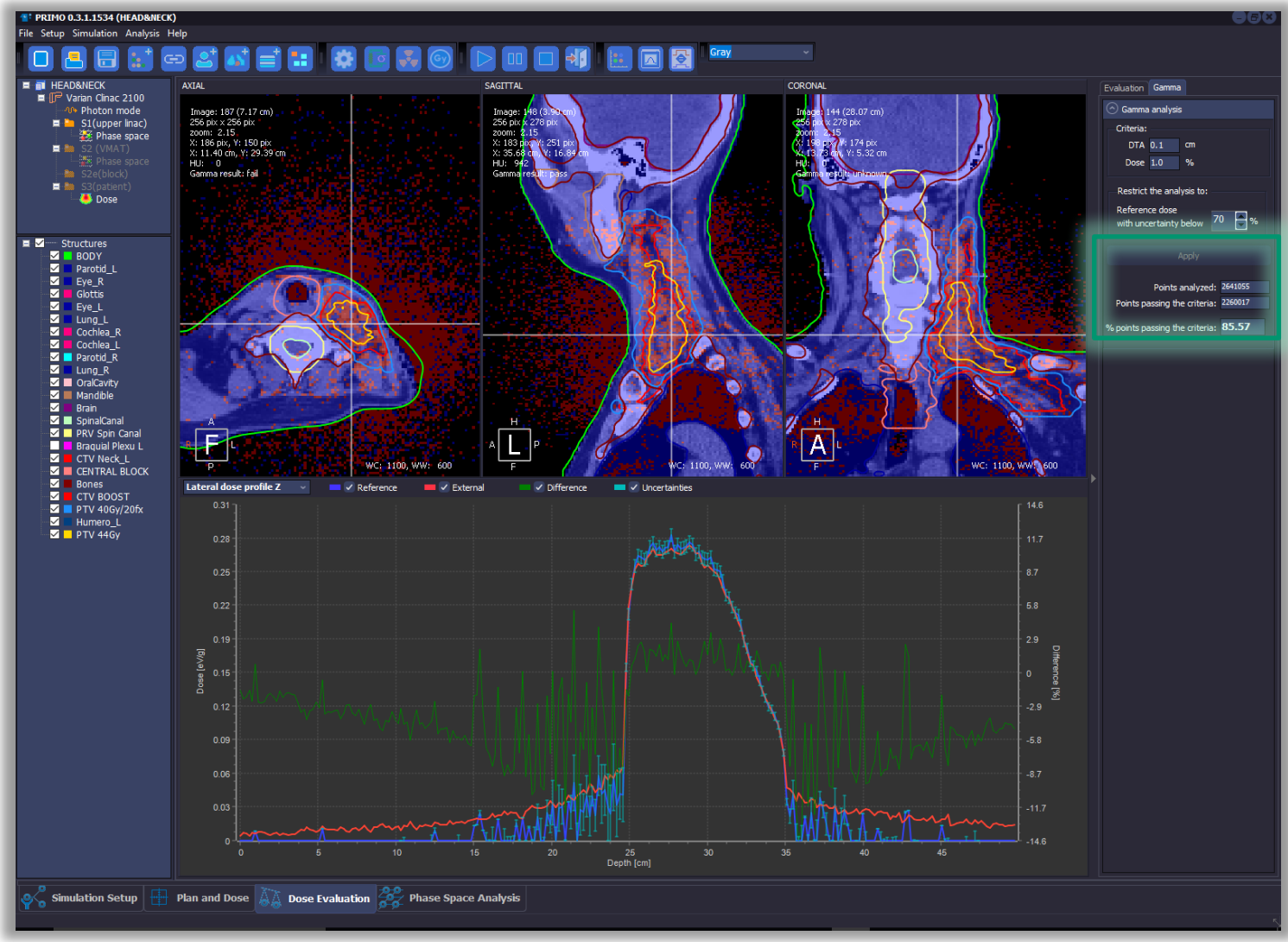
- Blending
- Difference
- Gamma

T~30 s

18.2 ×10⁶ voxels



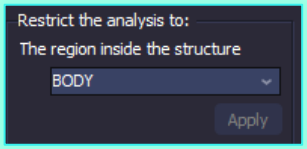
- Dose profiles w/ difference profile
- DVHs



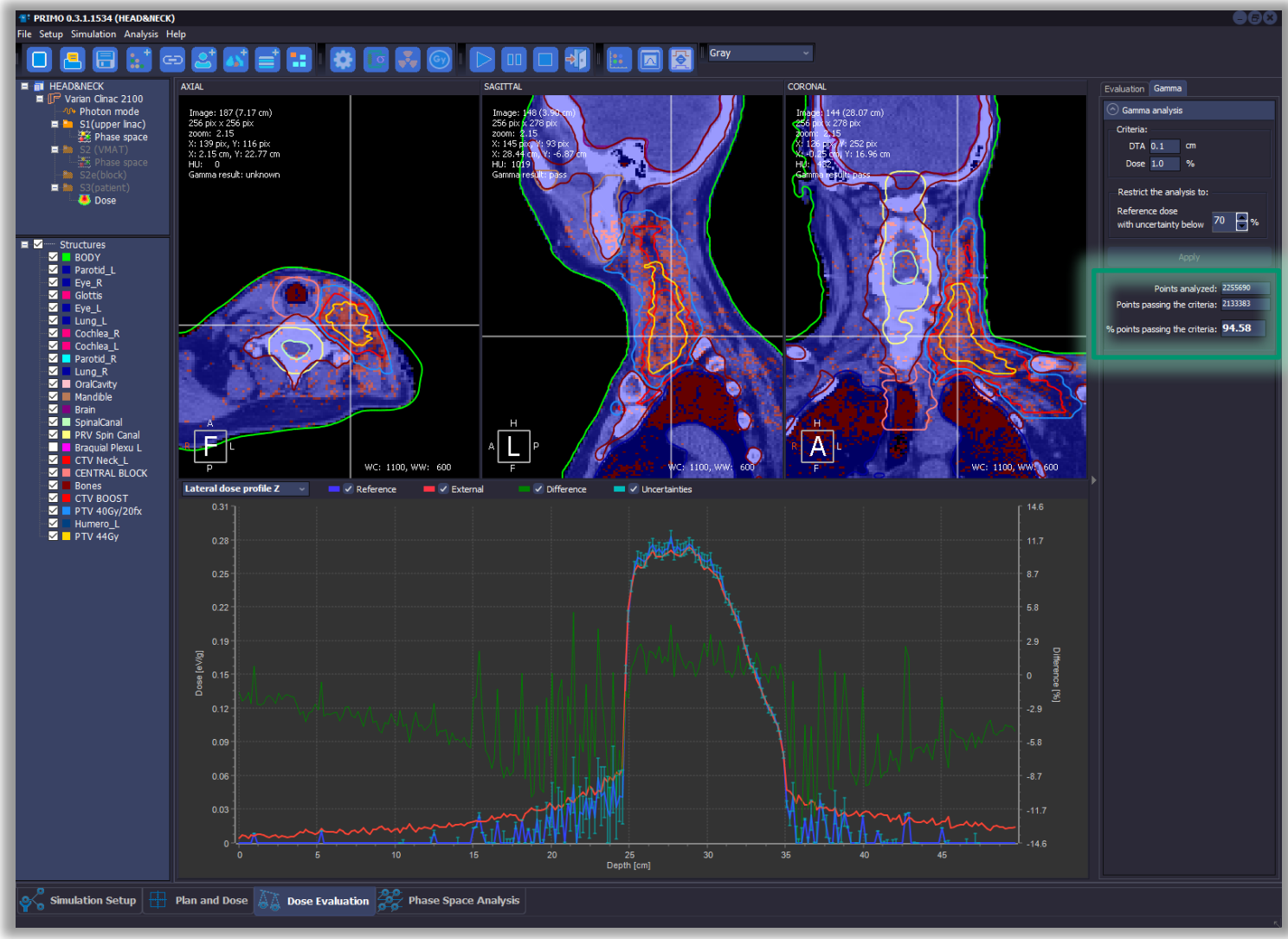
Dose evaluation
(dose comparison)

- Blending
- Difference
- Gamma

t~20 s



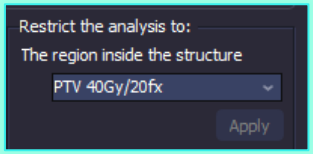
- Dose profiles w/ difference profile
- DVHs



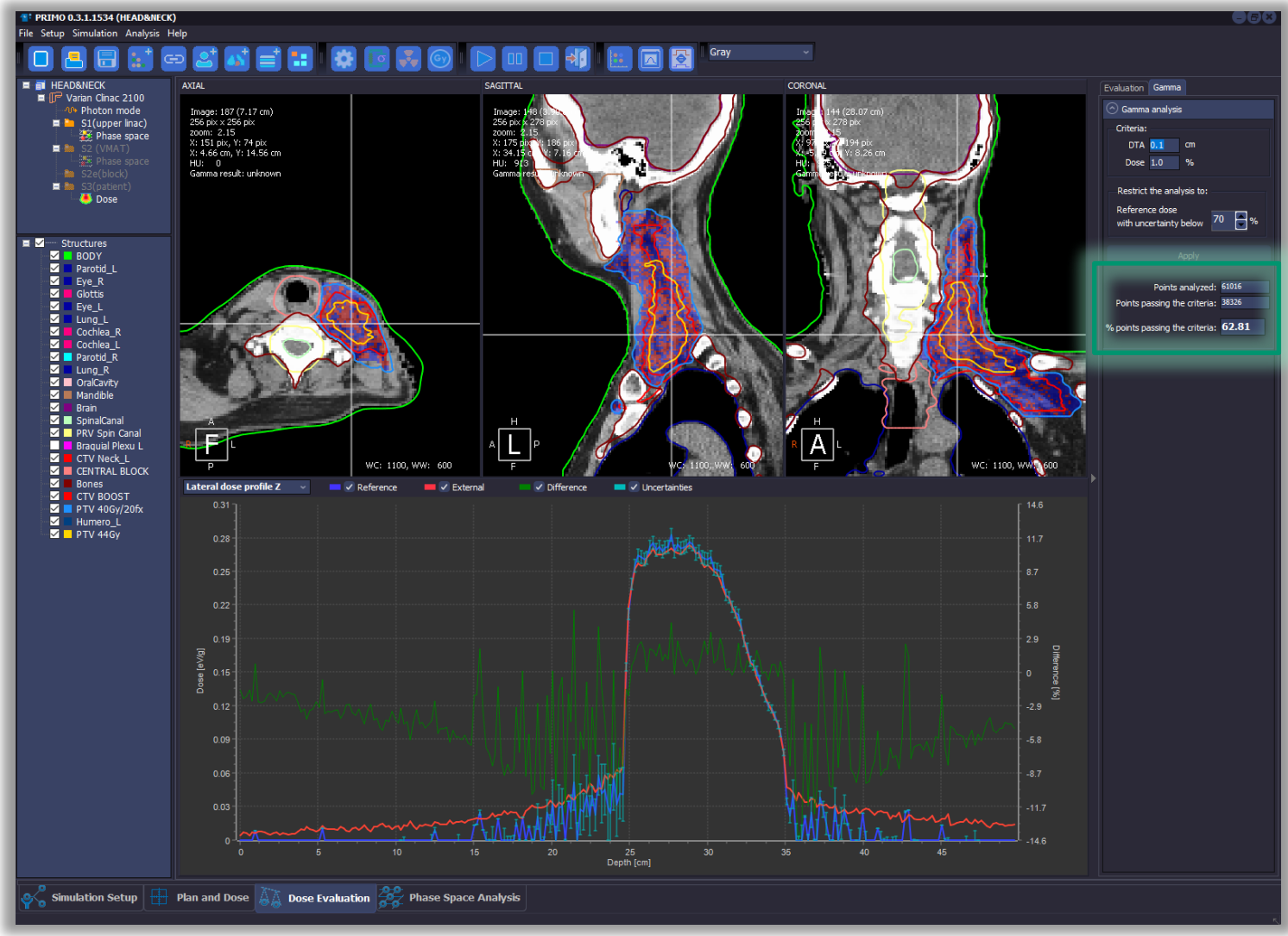
Dose evaluation
(dose comparison)

- Blending
- Difference
- Gamma

T~3 s



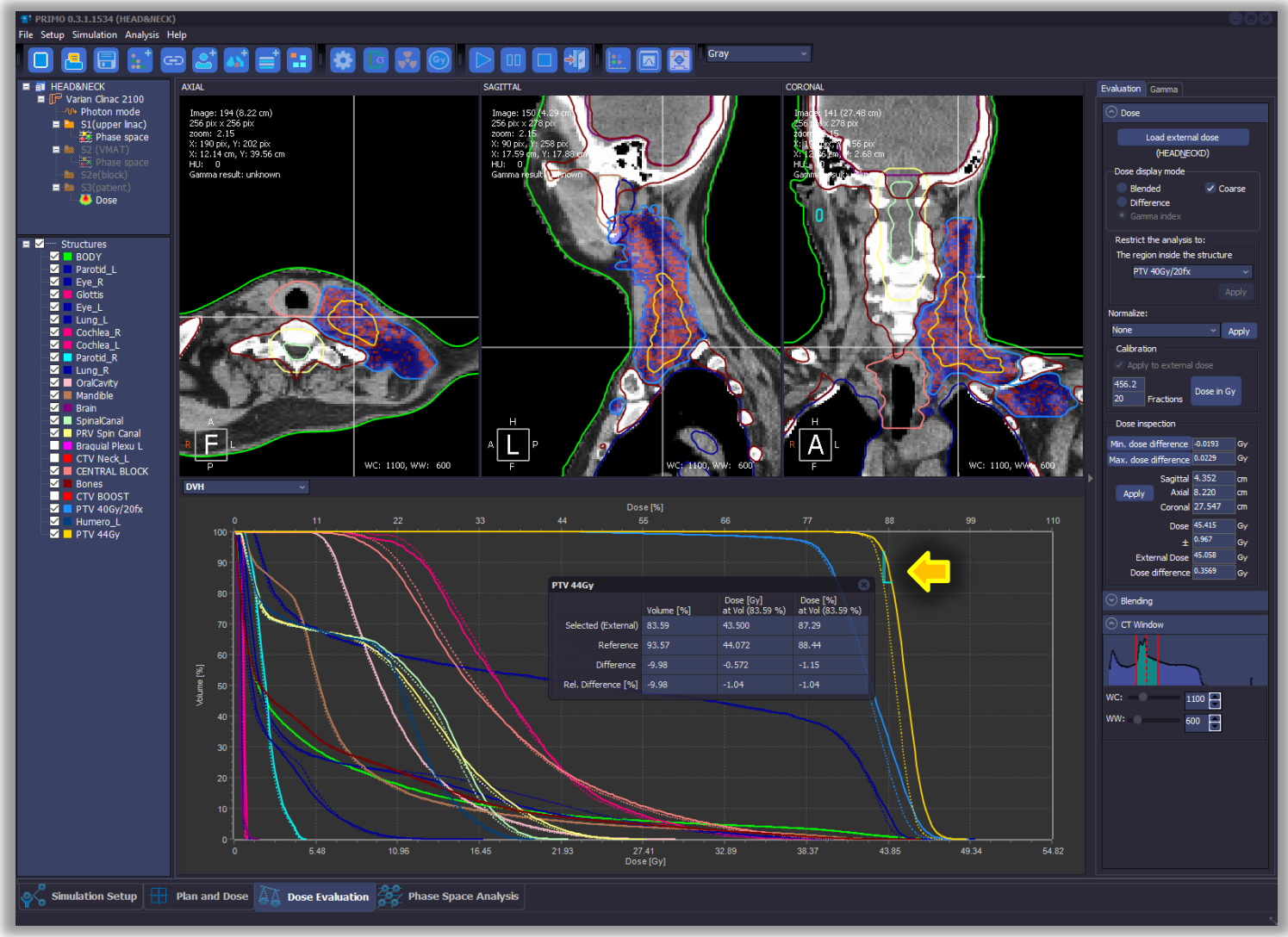
- Dose profiles w/ difference profile
- DVHs



Dose evaluation
(dose comparison)

- Blending
- Difference
- Gamma

- Dose profiles w/ difference profile
- DVHs



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