RAYSTATION PHOTON DOSE ENGINE - CC

RayStation 11B

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OVERVIEW

- Input to dose calculation
- Collapsed Cone (CC) dose algorithm:
  1. TERMA
  2. PSK superposition
- Electron contamination dose algorithm
- GPU computation
- Singular Value Decomposition (SVD) dose engine

INPUT TO DOSE CALCULATION

Geometry and density

- Effective density: Essentially a 3D distribution of relative electron density slightly modified to take effects of pair production into account.

Fluence

- Primary source
- Flattening filter source
- (Wedge scatter source)
- Electron sources

Machine parameters (from commissioning)

- Effective energy spectrum on central axis
- Flattening filter attenuation (Off-axis softening)
- (Wedge attenuation)

TOTAL CLINICAL DOSE CALCULATION

- Photon dose computation is performed in 3 steps:
  1. The energy fluence computation (see *Photon fluence model PPT*)
  2. TERMA computation
  3. Point Spread Kernel (PSK) tracing dose computation

- An electron contamination component is computed separately and added to the dose

$$D(x,y,z) = D(x,y,z)_{photon} + D(x,y,z)_{contamination\ electrons}$$

COLLAPSED CONE DOSE COMPUTATION

- Collapsed Cone dose algorithm:

1. TERMA distribution by ray trace of primary radiation through the patient, taking inhomogenities into account

2. Superposition of Point Spread Kernel (PSK) – describing the secondary scatter – collapsed along radial rays, taking inhomogenities into account

$$D(\vec{r}) = \sum_{\vec{r_i}'} TERMA(\vec{r_i}', \dots) PSK(\vec{r_i} - \vec{r_i}', \dots)$$

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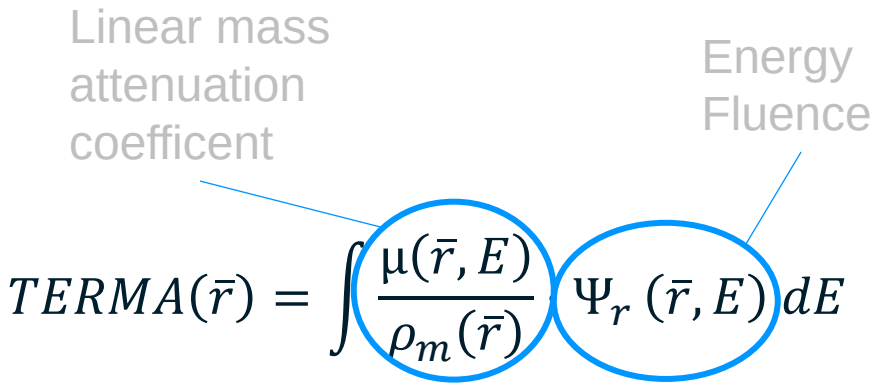
TERMA

- TERMA is the

Total Energy Released per unit Mass



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TERMA

- TERMA is the

Total energy released per unit mass

Linear mass attenuation coefficent

Energy Fluence

$$TERMA(\bar{r}) = \int \frac{\mu(\bar{r}, E)}{\rho_m(\bar{r})} \Psi_r(\bar{r}, E) dE$$

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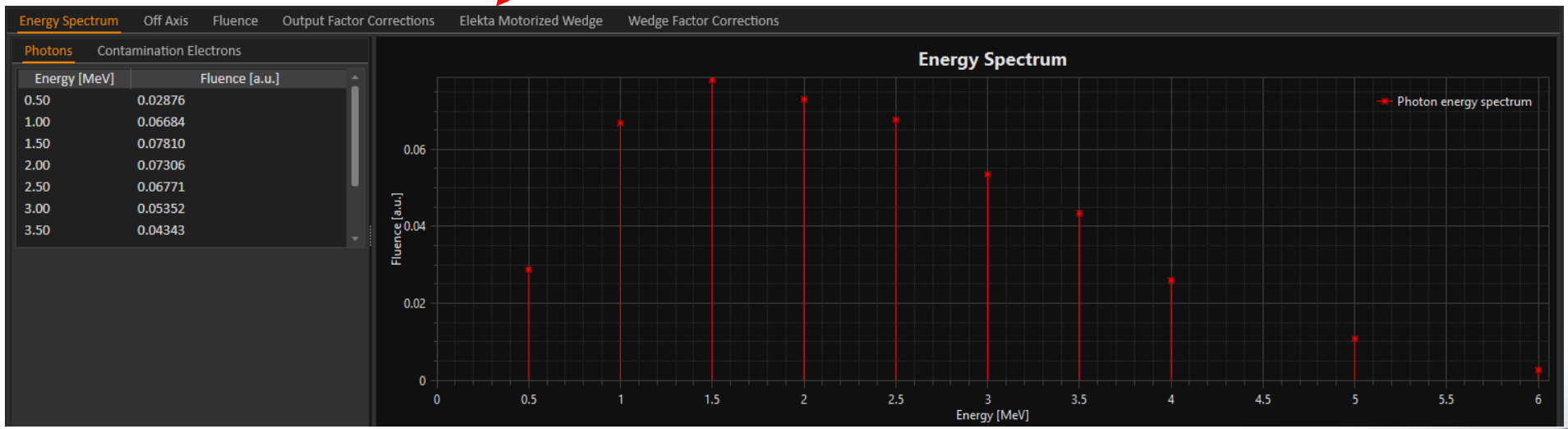
TERMA – ENERGY FLUENCE

$$\Psi(\bar{r}, E_i) = \Psi_0(E_i) \cdot \frac{\bar{r}_0^2}{\bar{r}^2} \cdot \exp\left(-\int_{\bar{r}_0}^{\bar{r}} \mu(\bar{r}, E_i) dl\right)$$

TERMA – ENERGY FLUENCE

- Ψ_0 from beam model

$$\Psi(\bar{r}, E_i) = \Psi_0(E_i) \cdot \frac{\bar{r}_0^2}{\bar{r}^2} \cdot \exp\left(-\int_{\bar{r}_0}^{\bar{r}} \mu(\bar{r}, E_i) dl\right)$$



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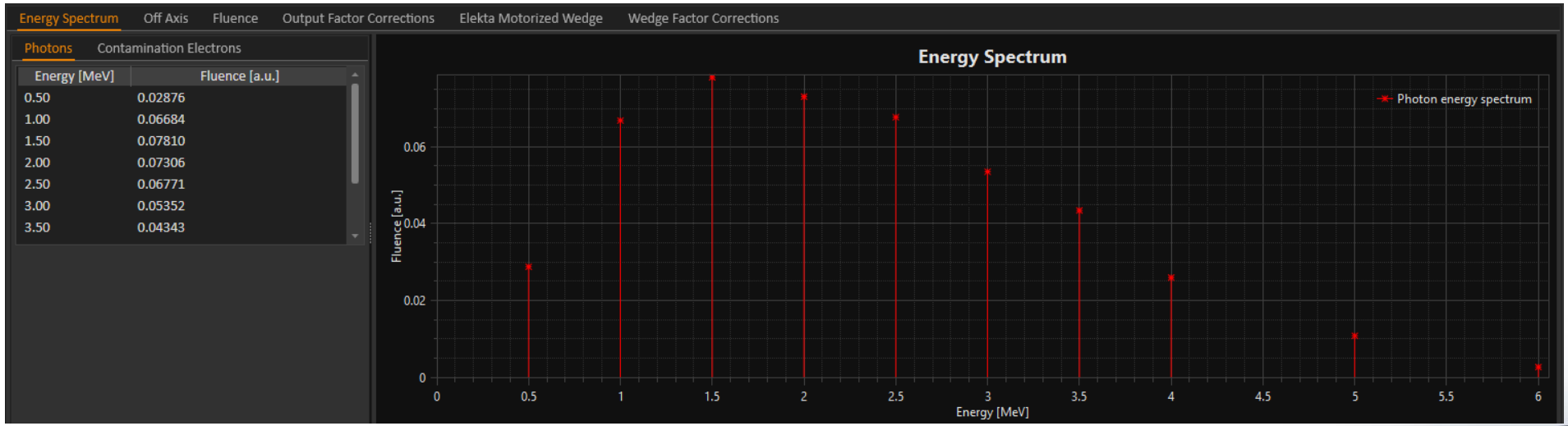
TERMA – ENERGY FLUENCE

- Ψ_0 from beam model
- Takes divergence into account

Inverse square law

$$\Psi(\bar{r}, E_i) = \Psi_0(E_i) \cdot \frac{\bar{r}_0^2}{\bar{r}^2} \cdot \exp\left(-\int_{\bar{r}_0}^{\bar{r}} \mu(\bar{r}, E_i) dl\right)$$



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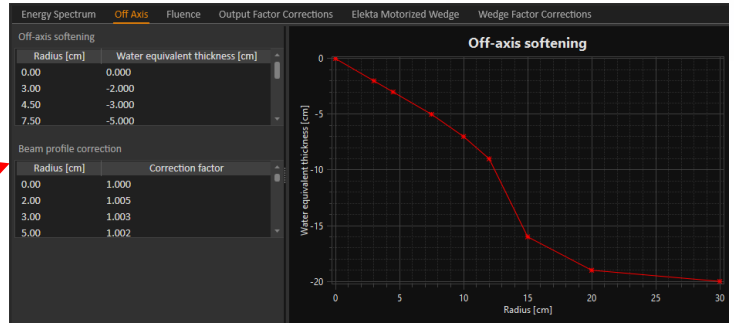
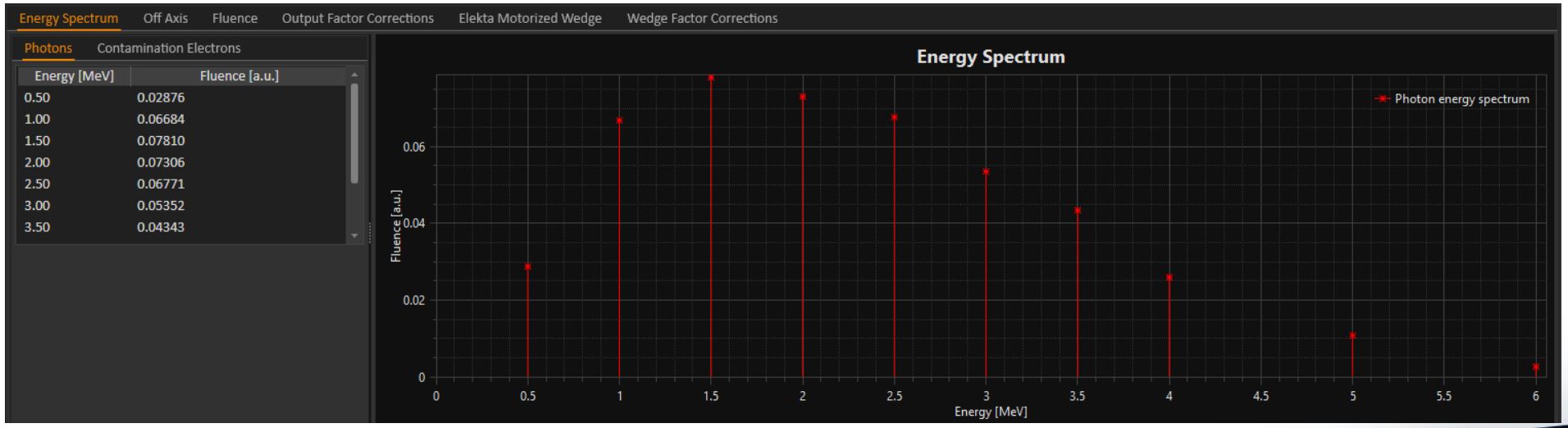
TERMA – ENERGY FLUENCE

- Ψ_0 from beam model
- Takes divergence into account
- Off-axis softening TOTAL energy fluence



$$\Psi(\bar{r}, E_i) = \Psi_0(E_i) \cdot \frac{\bar{r}_0^2}{\bar{r}^2} \cdot \exp\left(-\int_{\bar{r}_0}^{\bar{r}} \mu(\bar{r}, E_i) dl\right)$$



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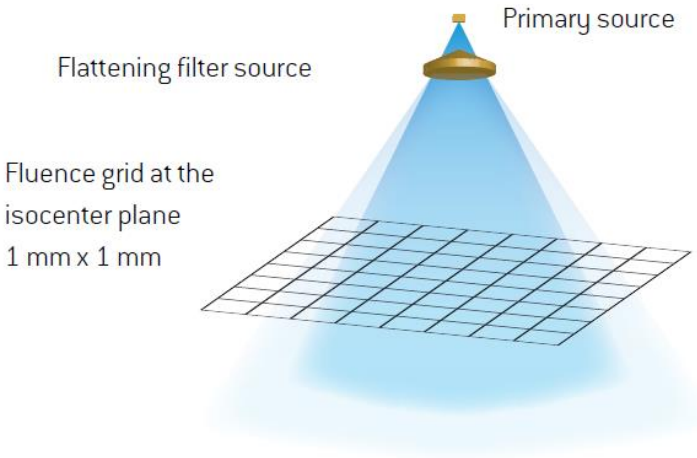
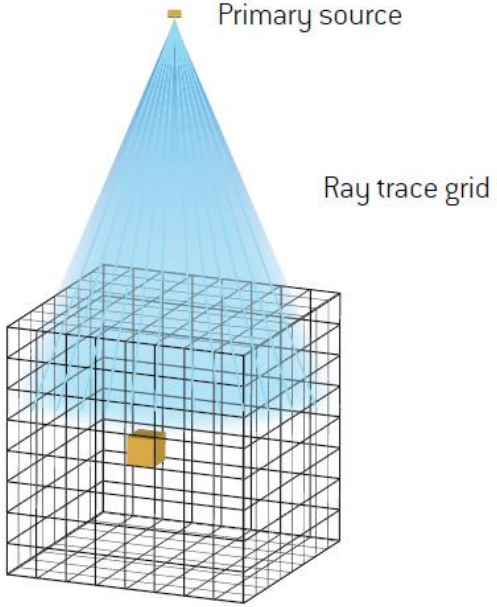
TERMA- ENERGY FLUENCE

Energy Fluence



VS

TERMA



- TERMA is computed using the fluence distribution at isocenter level, tracing it back to the surface and then down into the patient
- As if all rays originate from the primary source
- TERMA is then calculated for each voxel intersected by a ray trace in the dose grid

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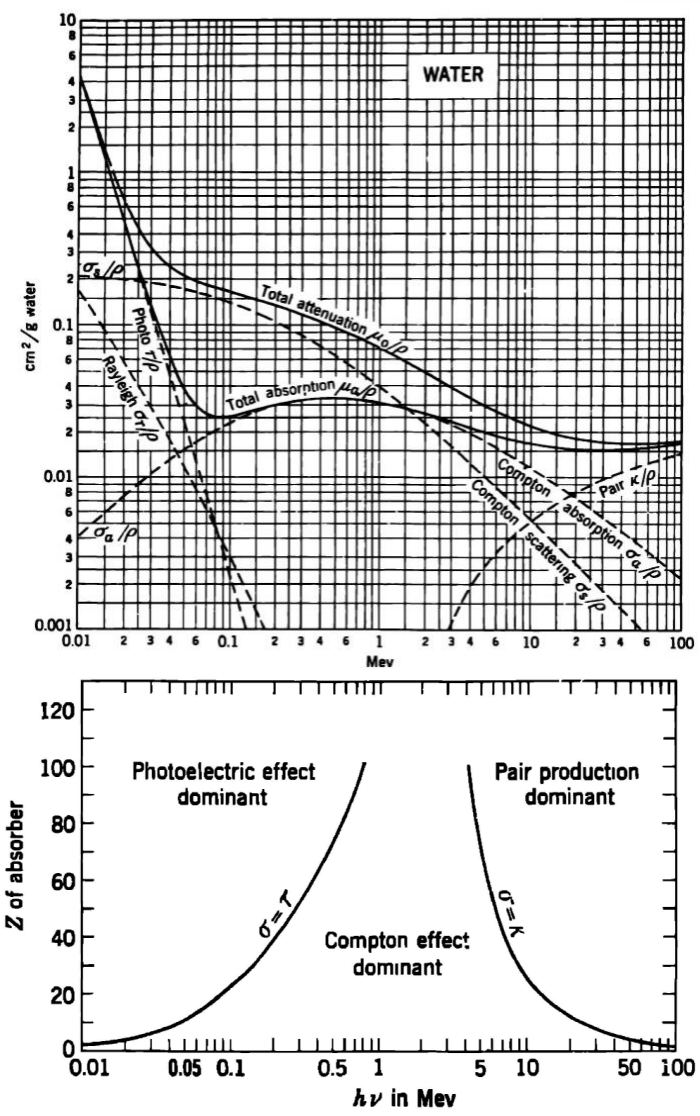
TERMA

- TERMA is the

Total Energy Released per unit Mass

- Describes the distribution of the primary energy deposit, i.e. energy released by primary photons to secondary particles:
  - Electrons from photoelectric effect
  - Electrons from Comptom scattering
  - Scattered Compton photons
  - Electrons and positrons from pair production

- No explicit separation into interaction components, but taken into account calculating the effective density of materials in the linear attenuation coefficient



R. D. Evans, The Atomic Nucleus (1955)

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TERMA

- TERMA is the

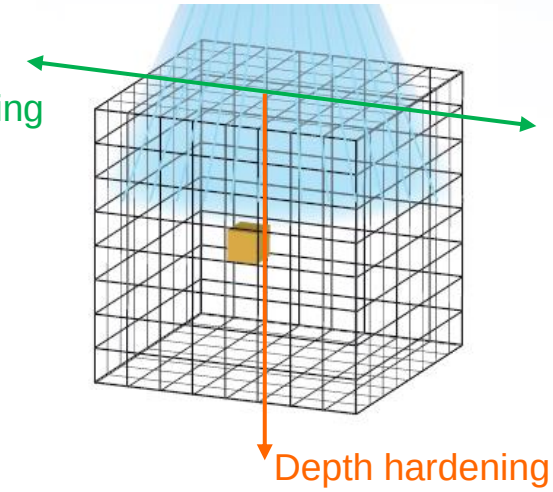
Total Energy Released per unit Mass

Linear mass attenuation coefficent

Energy Fluence

$$TERMA(\bar{r}) = \int \frac{\mu(\bar{r}, E)}{\rho_m(\bar{r})} \Psi_r(\bar{r}, E) dE$$

TERMA – LINEAR MASS ATTENUATION COEFFICIENT

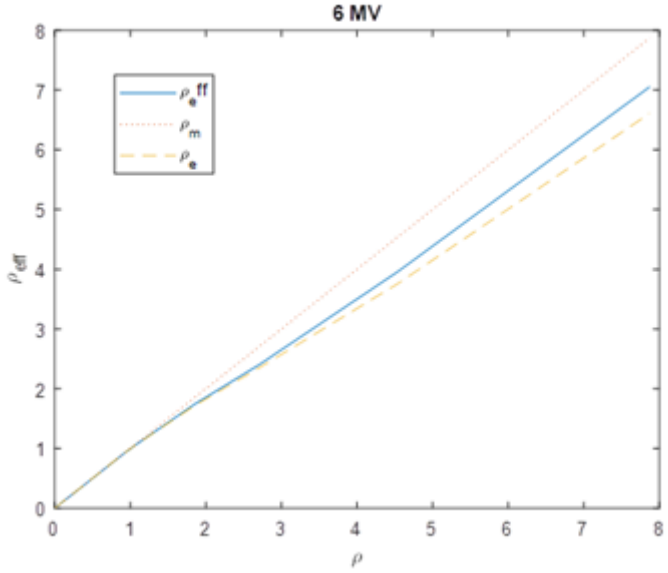


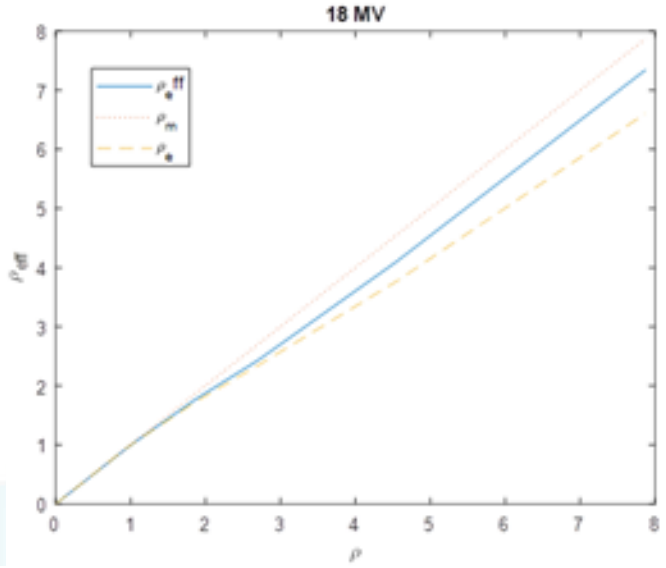
- Water:

  The linear attenuation of water, $\mu_0(E)$, uses the energy spectrum that takes both off-axis softening and depth hardening into account

- Materials other than water:

Effective density calculation: using beam energy spectrum at isocentre, NO depth hardening or off-axis softening is taken into account





$$\mu(\bar{r}, E) = \frac{\mu_0(E) \cdot \rho_{effective}(\bar{r}, \mathrm{E})}{\rho_{effectiveH_2O}(E)}$$

A typical conversion from mass density to electron and effective density for a 6 MV beam. The effective density is used both in TERMA-tracing, point spread kernel tracing and electron dose computation.

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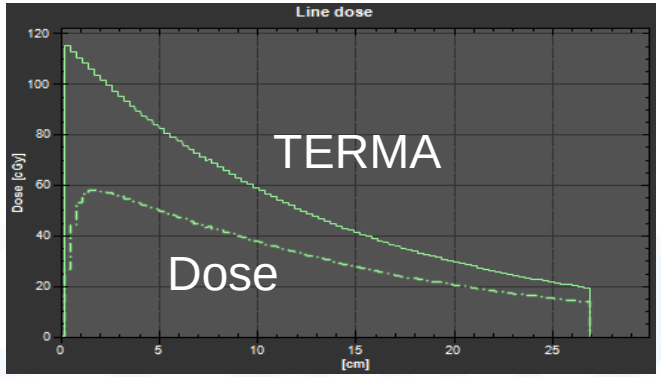
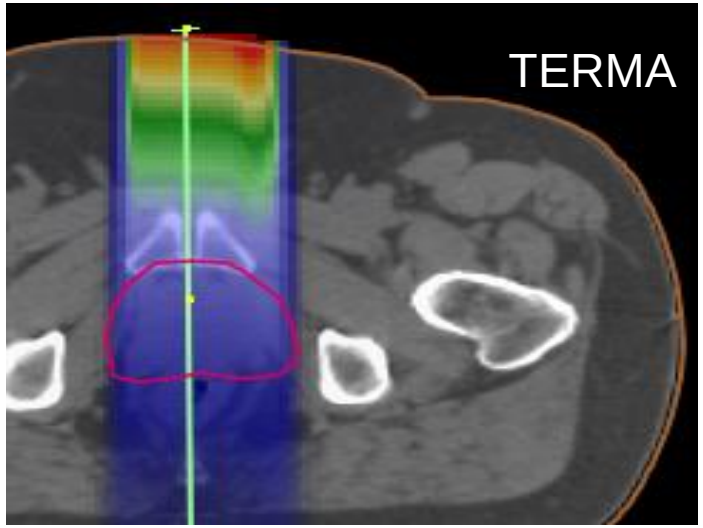
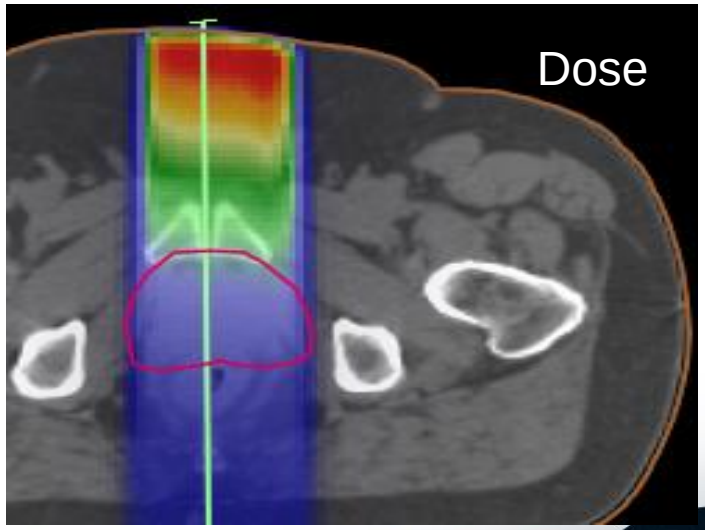
COLLAPSED CONE (CC)

- The CC dose engine calculates dose by means of a convolution-superposition method which is thoroughly described in literature by:
  - Mackie et. al., 9th ICCR (1987)
  - Ahnesjö, Med. Phys. 16 577 (1989)

- Once TERMA is determined describing the primary interaction taking place, the secondary scatter will be described using Point Spread Kernels (PSK)





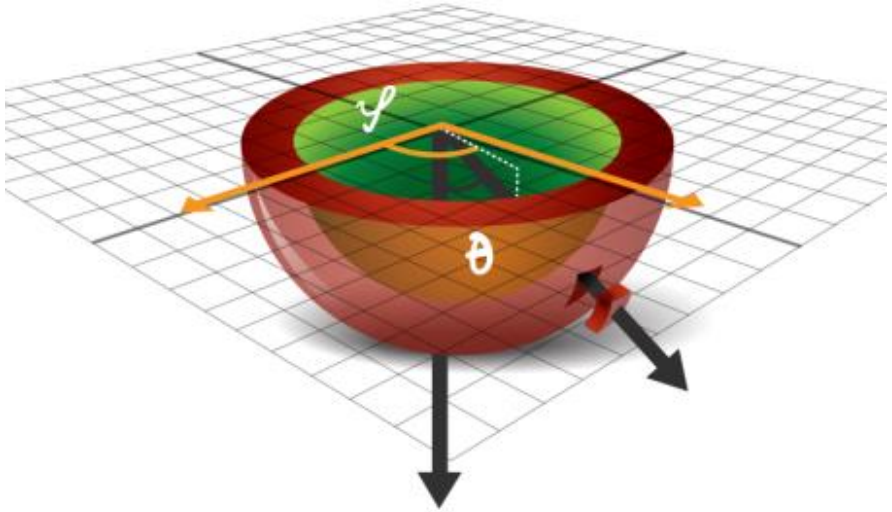


POINT SPREAD KERNELS

- Primary interaction usually Compton
  - Short range free electron, ionize tissue in a surrounding volume
  - Long range lower energy photon

- The point spread kernel, *PSK(r,θ,E)* describes the *statistical energy deposit distribution* in an 3D spherical grid from a primary energy deposit, i.e. the spread of secondary particles

- In RayStation, PSK(r,θ,E) are *Monte Carlo pre-calculated using EGSnrc*



The origin of the spherical coordinate system is the interaction point. The photon enters the plot from above

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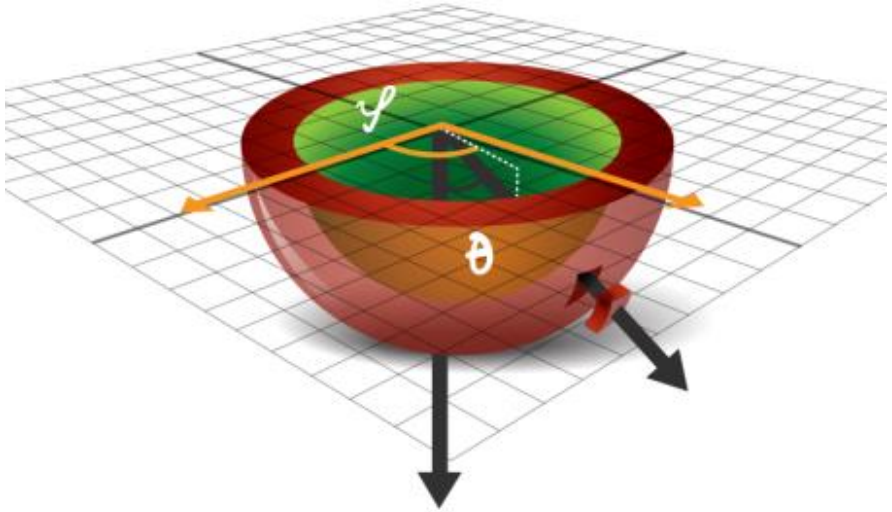
POINT SPREAD KERNELS

- Monte Carlo pre-computed using EGSnrc:
  - In water
  - One simulation per energy level

- The simulated *mono-energetic kernels* are *combined into poly-energetic kernels*. These are weighted so that they correspond to the beam energy distribution at different radiological depths

- When applied to a heterogenous geometry, the radial distance *r* is replaced by the *radiological distance d*



The origin of the spherical coordinate system is the interaction point. The photon enters the plot from above

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COLLAPSED CONE – CONVOLUTION

- The point kernels are divided into a number of cones, each emenating from its origin, where he energy deposited within a cone is collapsed to the central ray of that cone

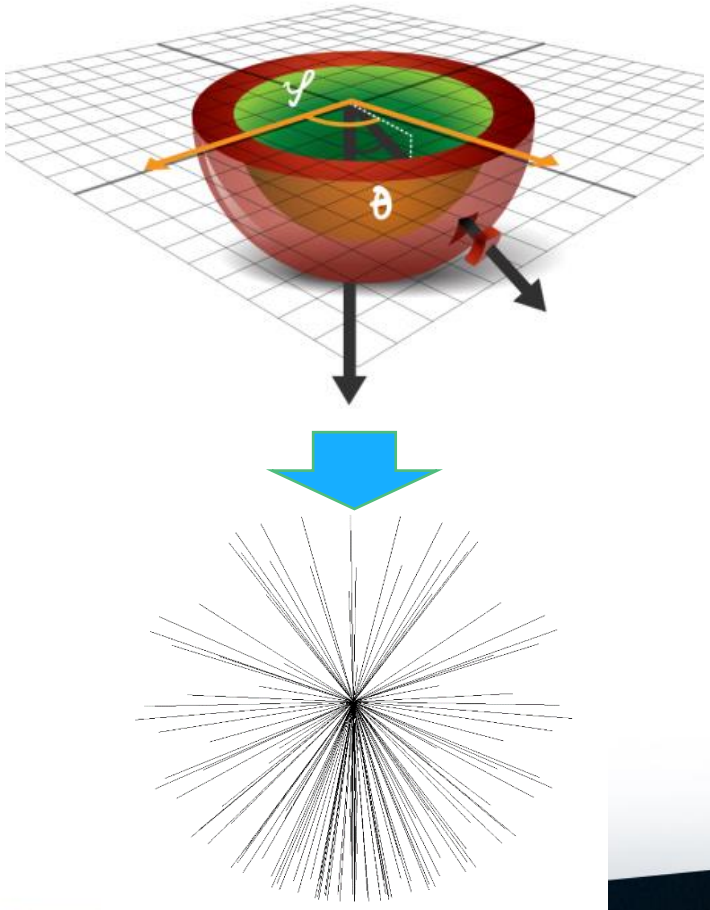
- This will speed up the calculation significantly

- 8 angular intervals are used in θ and 16 angular intervals in φ, resulting in 128 rays in total

- To achieve adequate dose accuracy for the lowest beam energies: 12 angular intervals in θ for energies below 6 MV, resulting in 192 rays in total

- Since more energy is directed in forward direction, the number of rays are also more frequent in this direction

$$PSK(r, \theta_i, \varphi_j, d_{TERMA-voxel})$$



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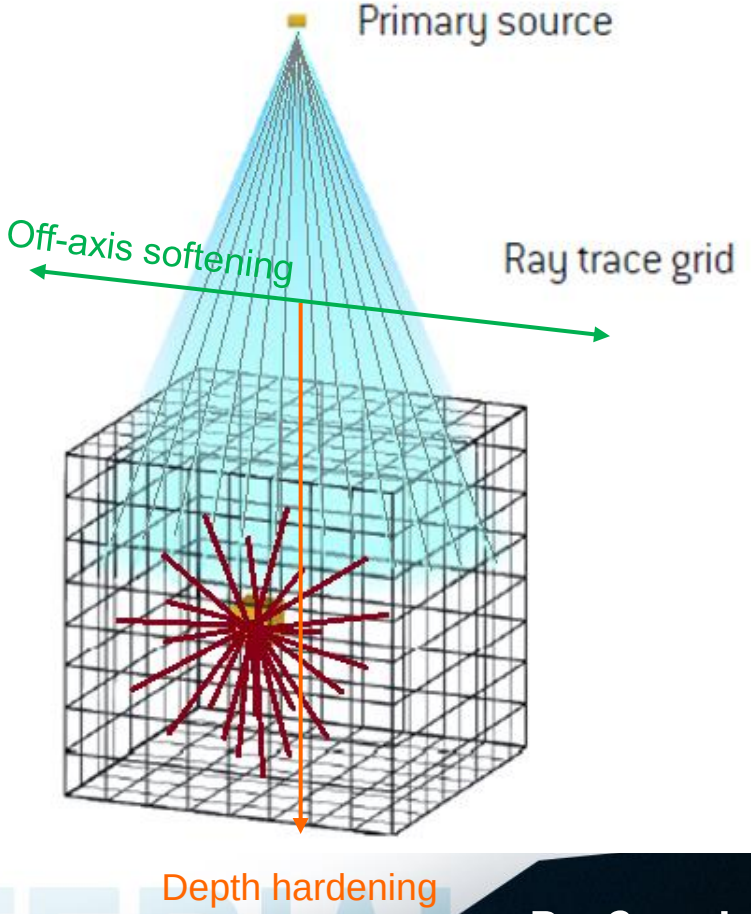
COLLAPSED CONE – SUPERPOSITION

- For each voxel with significant TERMA, a point kernel is created and aligned along the z-axis (no kernel tilt approximation).
- The energy spectrum of each point kernel is chosen to correspond to correct radiological distance of the TERMA voxel, this way the off-axis softening and beam hardening is taken into consideration
- The point spread kernels are then collapsed into ray traces which will collect dose contributions from the intersected surrounding TERMA voxels
- The dose is finally computed as a set of dose contributions summed over the trace directions



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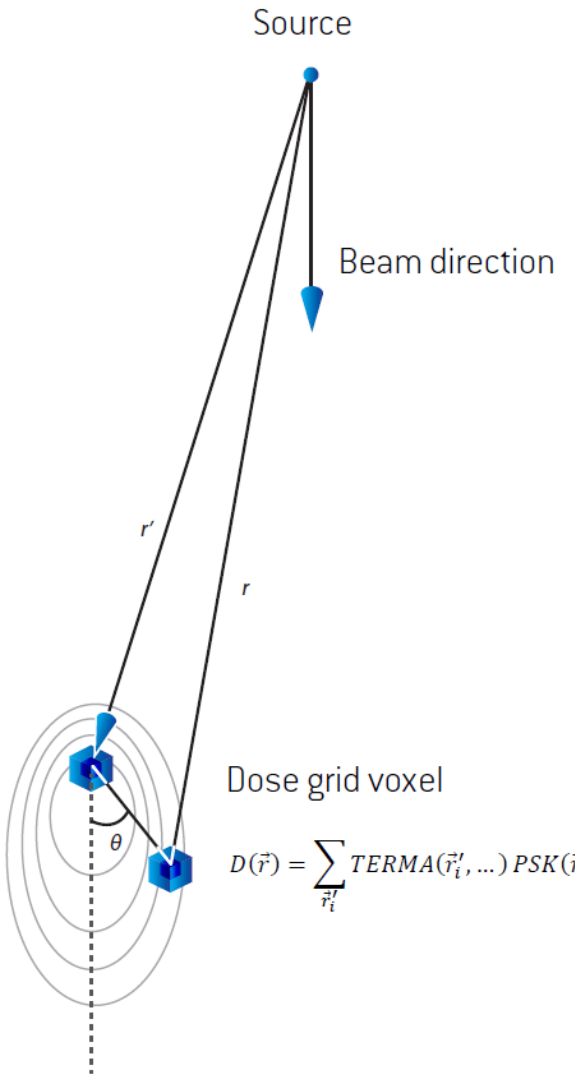
SUMMARY OF CC DOSE CALCULATION



TERMA voxel

$$\Psi_{E_i}(\vec{r}') = \Psi_{0E_i} \times \frac{\vec{r}_0^{\,2}}{\vec{r}'^{2}} \times exp\left(-\mu_{0E_i} d(\vec{r}')\right)$$

$$TERMA\ (\vec{r}') = \frac{\mu\left(E_{spectrum}(\vec{r}')\right)}{\rho_m(\vec{r}')} \times \sum_{E_i} \Psi_{E_i}(\vec{r}')$$

Dose grid voxel

$$D(\vec{r}) = \sum_{\vec{r}_i'} TERMA(\vec{r}_i', \dots)\, PSK(\vec{r} - \vec{r}_i', \dots)$$

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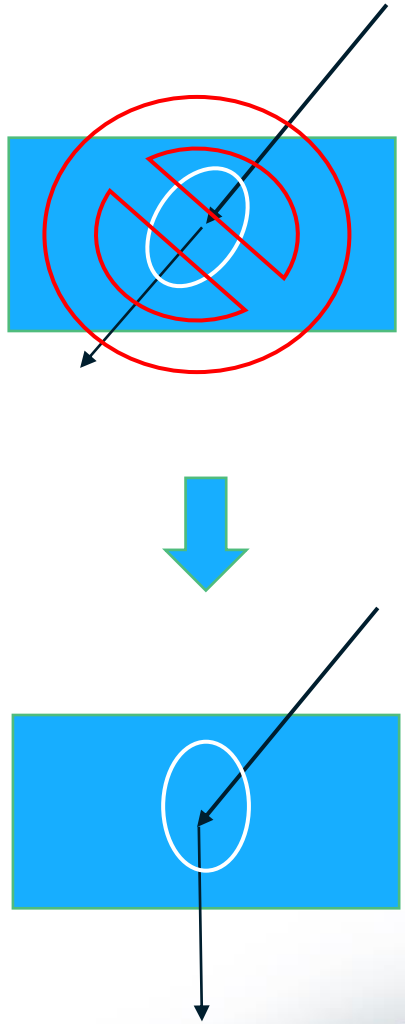
CC ALGORITHM – NO KERNEL TILT APPROXIMATION

- At the edges of a large field, the forward direction of beam photons will not be parallel to the central axis

- In the sphere point kernel tracing in RayStation all kernels are aligned with the central beam axis in order to speed up the calculation time

- This is done by:
  - Rescaling the TERMA dose to remove divergence
  - Computing the CC dose on the rescaled TERMA
  - Rescaling the dose to re-apply the divergence

- Using this no kernel tilt approximation will make the dose contribution narrower than it actually is



DOSE ENGINE SPEED-UPS

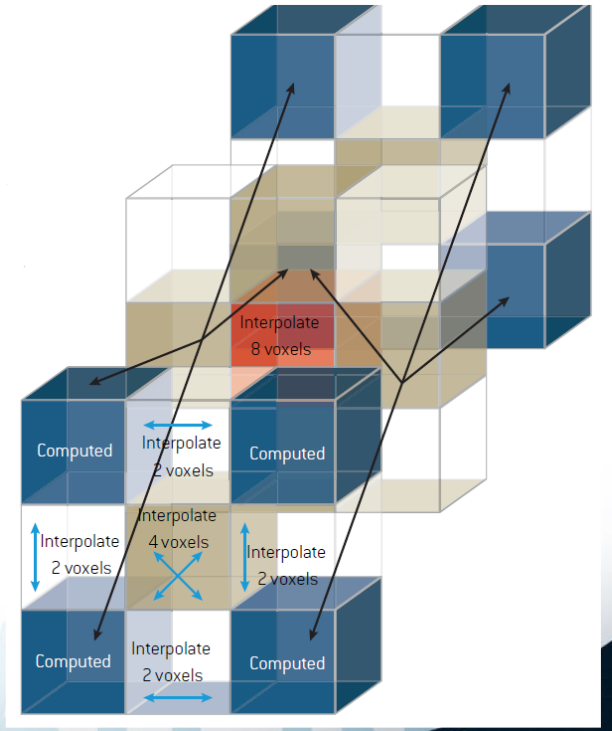
Calculation mask:

- Unnecessary computation is avoided by application of a calculation mask around the TERMA region
- When there is no TERMA above 0.5% of the maximum TERMA within a 5 cm radiological distance: the ray trace is terminated and the dose in remaining voxels further away are taken as TERMA dose.
- Calculate TERMA ebery voxel of the dose grid

Adaptive dose interpolation

- Computing dose in some voxels: every 4th (2nd) voxel

  if resolution is better than 0.26 cm (0.51 cm)
- In remaining voxels:
  - Interpolate the dose if TERMA gradient is low
  - Compute dose by CC if TERMA gradient is high



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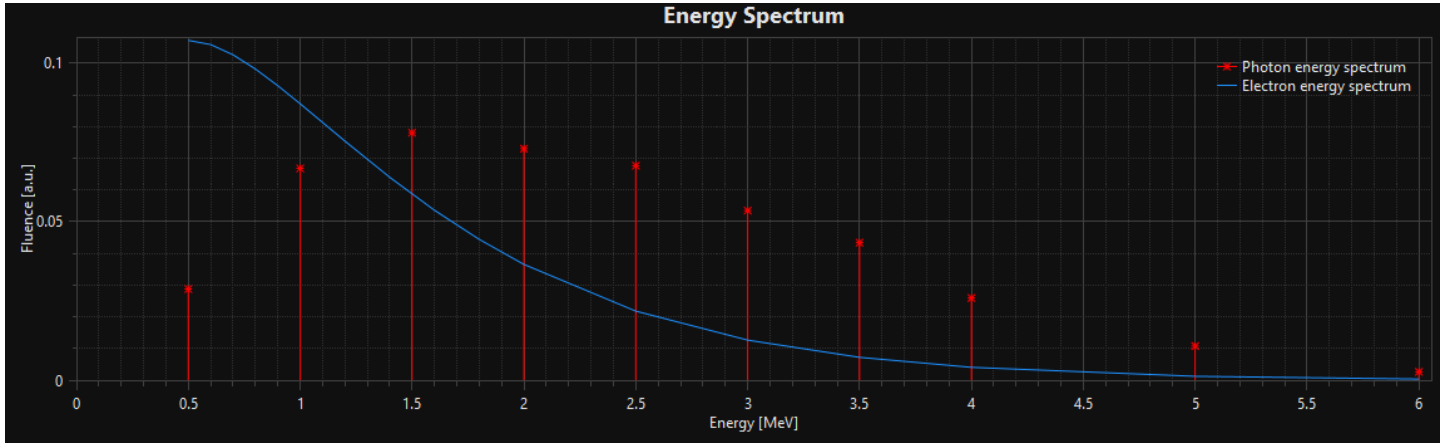
ELECTRON CONTAMINATION

Electron energy distribution

$$f(E) \propto E^c e^{-E/E_0}$$



- The contamination electrons arise due to interactions between the photons of the beam, the machine head and the air

- The electron contamination component is calculated separately and added to the dose

$$D(x,y,z) = D(x,y,z)_{photon} + D(x,y,z)_{contamination\ electrons}$$

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ELECTRON CONTAMINATION

- The electron interactions for the electron contamination are computed using pencil beam kernels with effective density scaling
- Cylindrical electron kernel *A(E,r,d)* pre-computed for a set of electron energies by the EGSnrc Monte Carlo package (DOSRZnrc)
- Mono-energetic pencil kernels are used to create a poly-energetic electron depth dose curve
- Semi-infinite slab approximation: lateral inhomogeneities not accounted for in the electron contamination dose. Important for:
  - Inclined beam arrangements
  - Inhomogeneous regions in the beam entry region
- Voxel electron dose is then computed as the product of the electron fluence and the electron depth dose at the voxel radiological depth

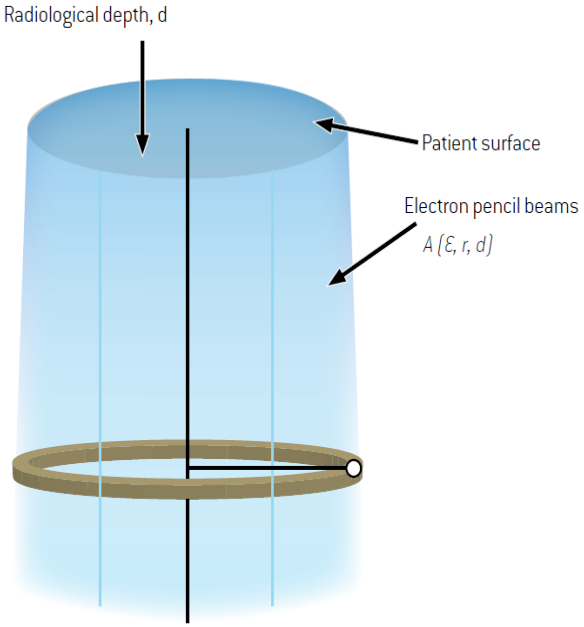

Figure 28. The electron pencil beam.

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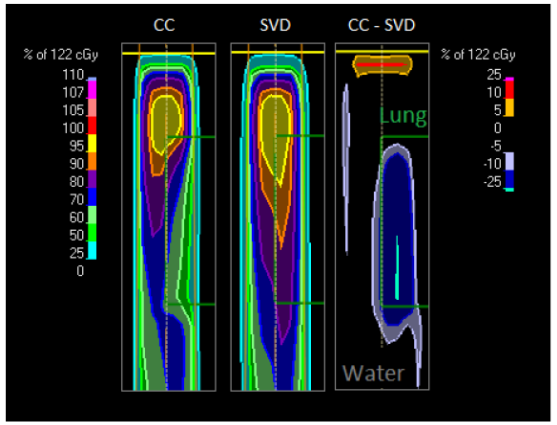
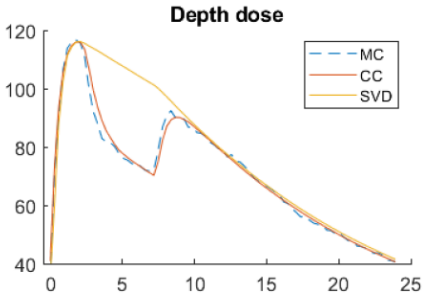
GPU COMPUTATION

- From RayStation 8B, both fluence and CC dose computed only on GPU
- From RayStation 9B, photon optimization and gradient algorithm (SVD or Singular Value Decomposition) moved to GPU computation
- ~ 3-7 times faster than CPU (depends on hardware, dose grid resolution, treatment technique)
- Source code implementation → identical for different GPU models
- No major differences between doses computed on different GPU models
- Minor differences of up to 0.2% of dose maximum possible due to differences in precision of floating-point operations on various hardware
- Minor differences can be expected, in some cases, between different operating system versions and GPU driver versions

SINGULAR VALUE DECOMPOSITION DOSE ENGINE

- Used for optimization
- Pencil beam convolution technique with a more simplified fluence model compared to collapsed cone
  - Primary source fluence
  - Scattering source fluence
  - NO contamination electrons, reduces the accuracy in the build-up region
- Cylindrical pencil beam kernels where the radial components are convolved with the energy fluence.
- Scaling of kernel by radiological path length only in depth, taking inhomogeneities into account only in depth and not laterally
- Lateral dose cut-off close to the border of the fluence field.
  - For treatments with many control points, the sum of the missing out-of-field dose can become significant
- Dose computed with the singular value decomposition (SVD) dose engine is always considered unclinical in RayStation





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