MCTPS: a new Monte Carlo-based treatment planning tool for hadrontherapy

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A Monte Carlo based Treatment planning?

- Currently treatment planning for hadron therapy are commonly based on fast analytic dose engines using Pencil Beam algorithms.

- MC calculation of doses and fluences could be superior in accuracy because they take into account heterogeneities, large densities, geometry details. They can predict secondary particle production to be used for imaging, range control, etc.
- *However they require much longer execution times…*

Project: an integrated MC+optimization tool

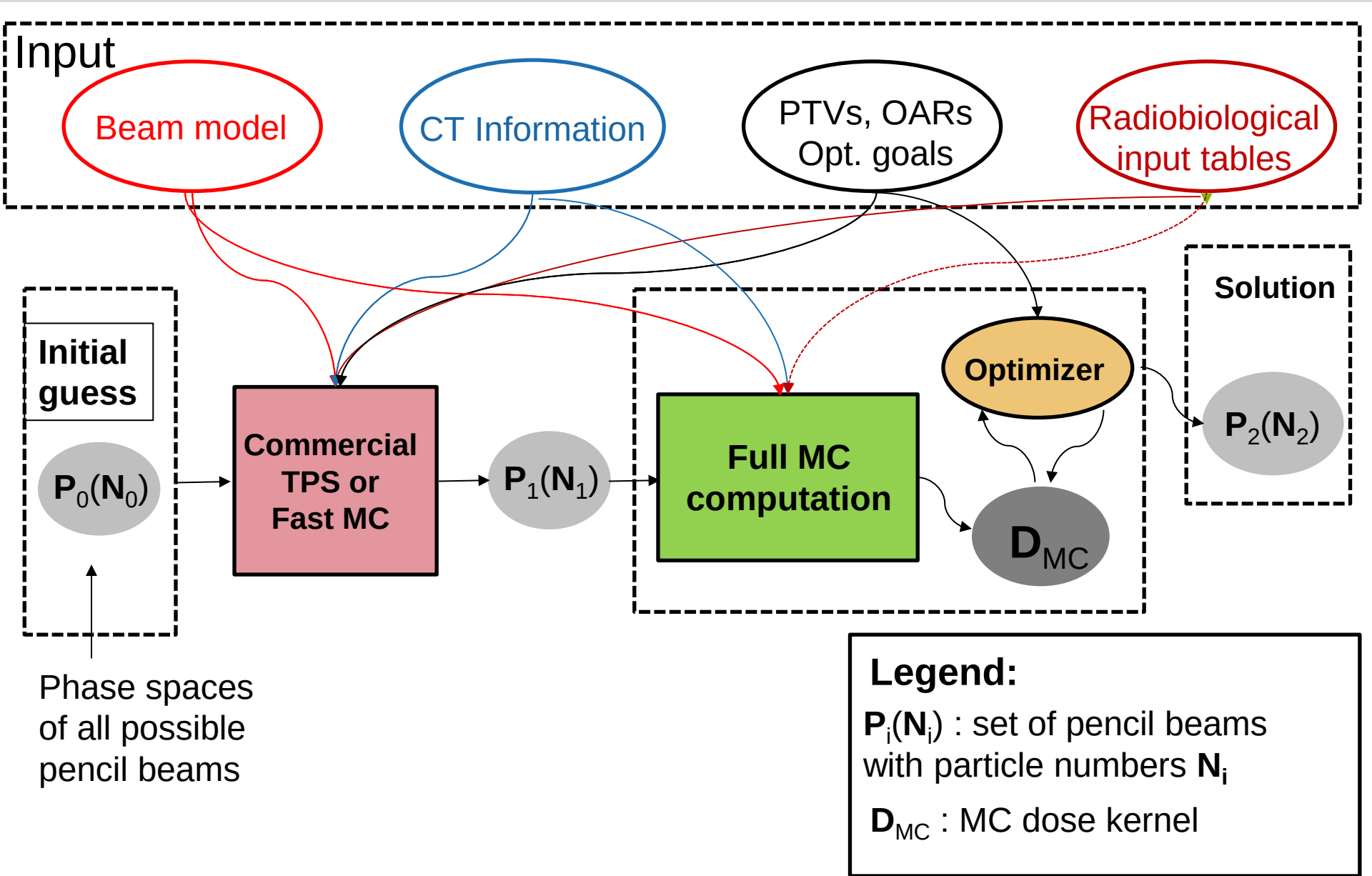
- To take into account all details about geometry and materials, overcoming the “water-equivalent” approach
- Tool to be applied to realistic treatment conditions with acceptable CPU time
- That can be applied in planning for ions with 1<Z<8 (at CNAO and HIT)
- A tool which not only allows to recheck a given plan, but which also suggests a better solution
- To be used stand-alone (using some pre-processing code) or as post re-optimization of plans obtained from commercial TPS (here examples as applied at CNAO and HIT)
- To be used in research: **New ions and combined ion fields, testing of new bio-models and algorithms, to predict secondary fluxes: β^+ emitters, prompt γ, etc.**

Basic principles of MCTPS

Multistep procedure:

1. start from a a given set of PBs $\mathbf{P}_1(\mathbf{N}_1)$ with pre-optimized initial particle numbers $\mathbf{N}_1$
2. This set can be obtained from a pre-selection and pre-optimization of available PBs deliverable by the "*accelerator beam library*": $\mathbf{P_0}$ for a given treatment and beam port:
   Two alternatives: - an already available certified TPS\
   - a fast simulator
3. Starting from $\mathbf{P}_1(\mathbf{N}_1)$ the MC allows to calculate a Dose Kernel ($\mathbf{D_{MC}}$) using the **fully detailed case geometry, composition and machine setting**
4. An optimization code will derive iteratively from $\mathbf{D_{MC}}$ the optimized solution $\mathbf{P}_2(\mathbf{N}_2)$

Components and program flow



Choice of the MC code

FLUKA (INFN-CERN property) **is the baseline choice for this project**

(http://www.fluka.org)

- Presently used in hadron therapy context
- Includes sound physical models
- Capability of being coupled to CT scans to import geometry, to import volume/organ definitions
- Possibility to be coupled to a radiobiological model

See talk at this conference by P.R. Sala

Optimization procedure

$$D_j(\mathbf{N}) = \sum_{i \in \mathrm{PB}} d_{i,j} \cdot N_i$$ Absorbed dose in voxel j from PBs (running on i index)

N has to be determined by minimizing the following cost function:

$$\chi^2(\mathbf{N}) = \sum_{j \in \mathrm{PTV}} \frac{w_j(\hat{D}_j - D_j)^2}{\hat{D}_j^2} + \sum_{j \in \mathrm{OAR}} \frac{w_j(\hat{D}_j - D_j)^2}{\hat{D}_j^2} \Theta(\hat{D}_j - D_j)$$

Prescribed dose in dose grid voxel

Weight associated to grid voxel j based on planner's prescription

$D_{RBE,j}$ can replace D_j

Two optimization methods tested:

1) Gradient-Based optimization ("Steepest Descent")
2) "Dose-Difference Optimization" approach described in *Lomax, PMB 44 (1999) 185*

Calculation choices

- In order to compare to standard TP calculation Dose has to be expressed as Dose-To-Water. TP rescale depth-dose profiles in water using Water Equivalent Path Length (WEPL) approximantion. In MC we can score Dose-To-Water as derived directly from Dose-To-Medium.
- RBE alternatives:
  - fixed (fort instance ~ 1.1 for protons)
  - Radiobiological input tables computed with LEM are interfaced with FLUKA to calculate RBE-weighted doses D_{RBE}
  - Values of non-constant RBE are obtained by a re-implementation of the “local effect model” (LEM, version IV) developed in Heidelberg .*Elsasser T. et al., Int. J. Radiat. Oncol. 78 (2010) 1177-1184*

Warning: using for the moment a the reference V79 cell line (non-human) typical in radiobiology studies

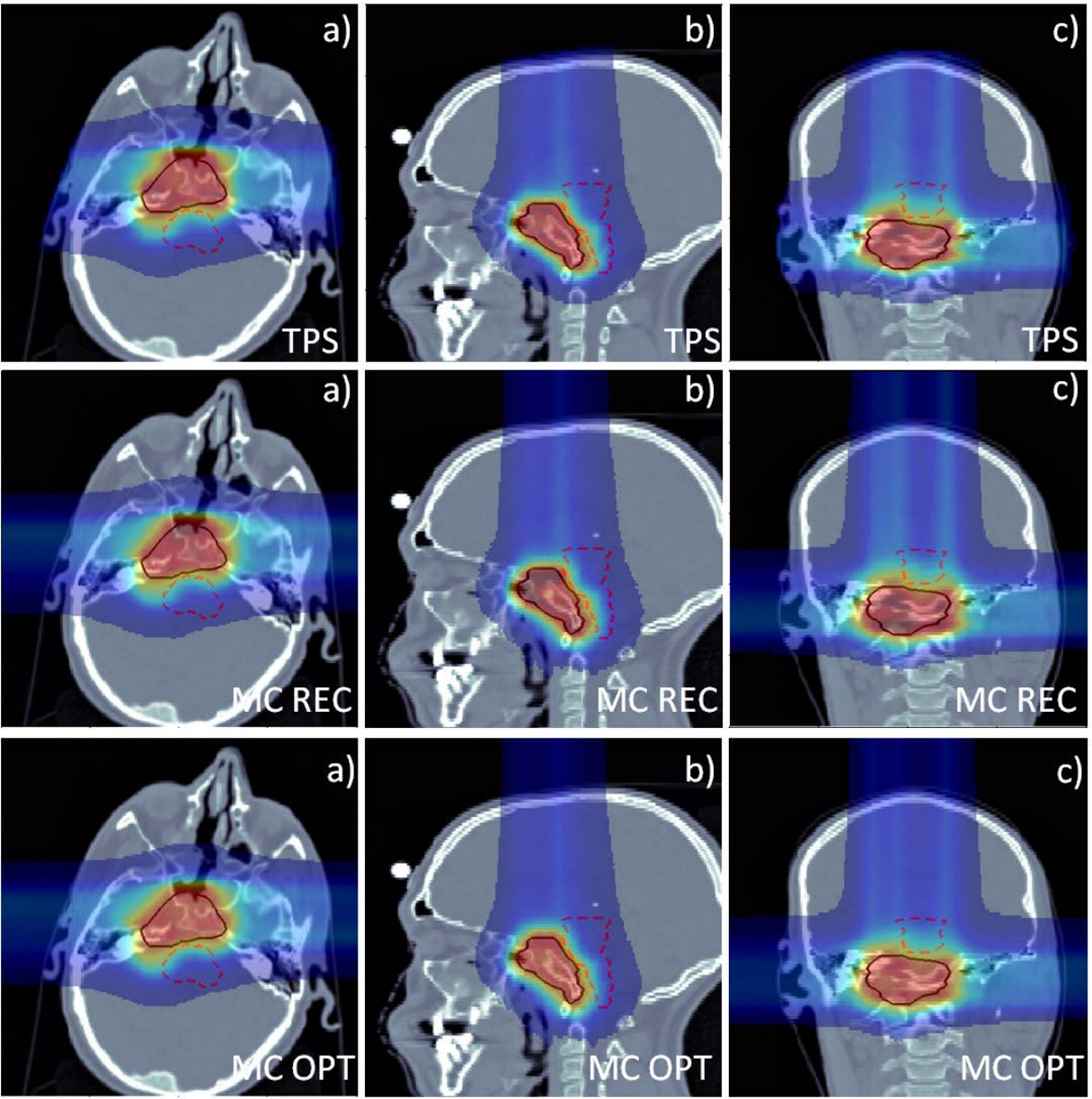
Verification of MCTPS Plans.
Protons at CNAO

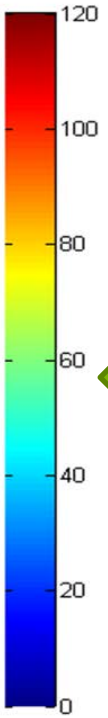
- Cases:
  - Phantoms for which we used as pre-optimizer Syngo RT Planning by Siemens AG (CNAO standard) and alternatively, a fast MC skimmer (FRED, by A. Schiavi)
  - Patient caes at CNAO with 2 or 3 beam ports for protons. D=2 Gy for PTV either with fixed RBE=1.1 or variable RBE as predicted by LEM. PTVs of 32.5 ml and 103.5 ml. Pre-optimizier: the Syngo TPS

MC Set-up

- Simulation set up includes CNAO Nozzle so to generate “PB” with actual phase space distribution: lateral FWHM ~ 1.0 cm at isocenter, lateral spacing of 3 mm. Spacing between Bragg peak position of 2 neighbouring beam energies 2 mm.
- Simulation includes voxelized water phantom or CT patient image: 2x2 mm^2 transaxial pixels and 2 mm slices (as for the certified default TPS at CNAO). This defines transport and scoring granularity in MC
- Materials and Composition (see talk about FLUKA) assigned to voxels according to *Schneider et al, PMB 45 (2000) 459* and *Parodi et al. PMB 52 (2007) 3369*
- In order to build the Dose Kernel Matrix $D_{MC} \equiv (d_{j,i}; a_{j,i}; b_{j,i})$ **a total no. of PB to be simulated: 3438 for the cube-shaped PTV to 6257 and 13920 for the 2 patient cases**
- **5 10^3 primary protons per PB at the given granularity ➔ mean statistical uncertainty on PTV ~ 1% (max 2%)**

A 3-port chordoma case treated with protons at CNAO





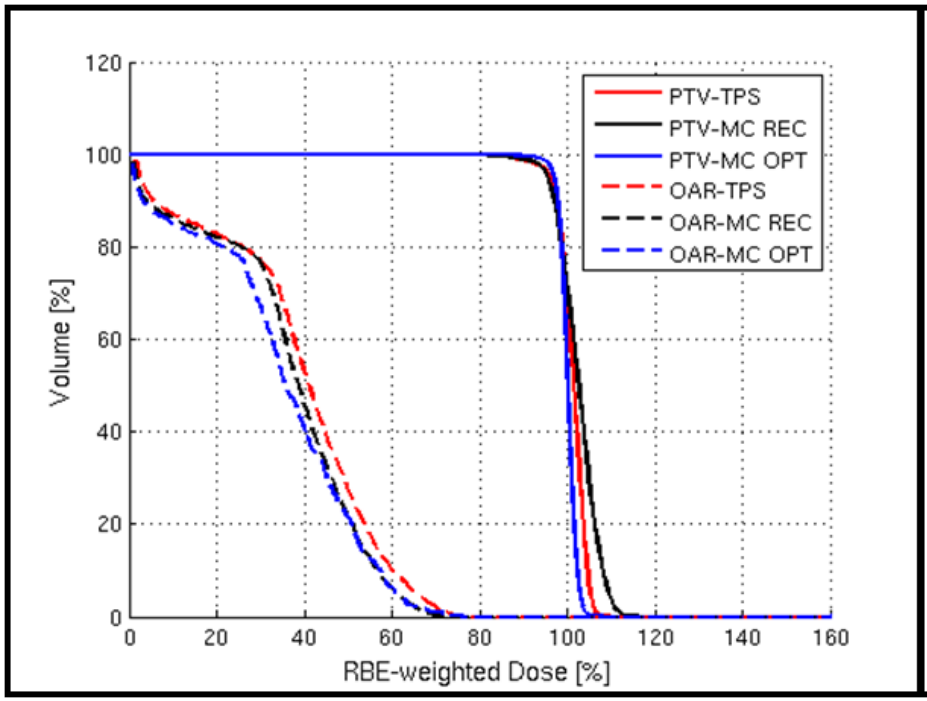
The Syngo TPS prescription

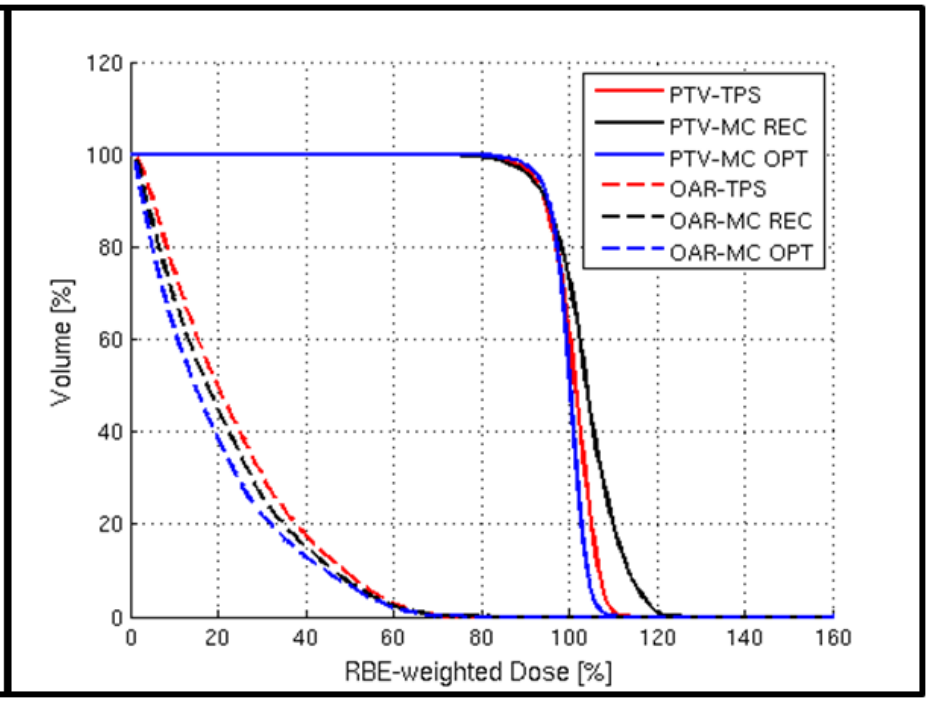
MC fw simulation of TPS prescription

Mairani A, et al.
PMB 58 (2013) 2471-2490

Result of our MCTPS Optimization

DVHs for PTV and OAR





2-port

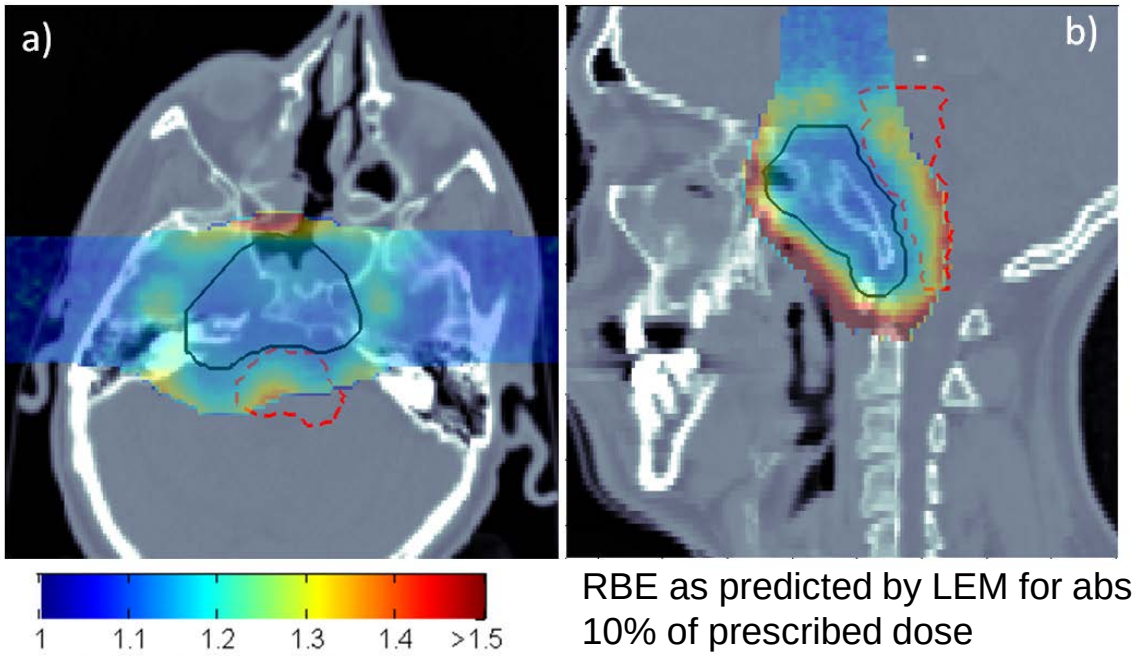
3-port

By comparing MCTPS with MC fw simulation of TPS prescription:

The % of volume fulfilling gamma index criterion for PTV is 91% and 81% for OAR

The % of volume fulfilling gamma index criterion for PTV is 72% and 90% for OAR

RBE as predicted by LEM for abs. doses larger than 10% of prescribed dose

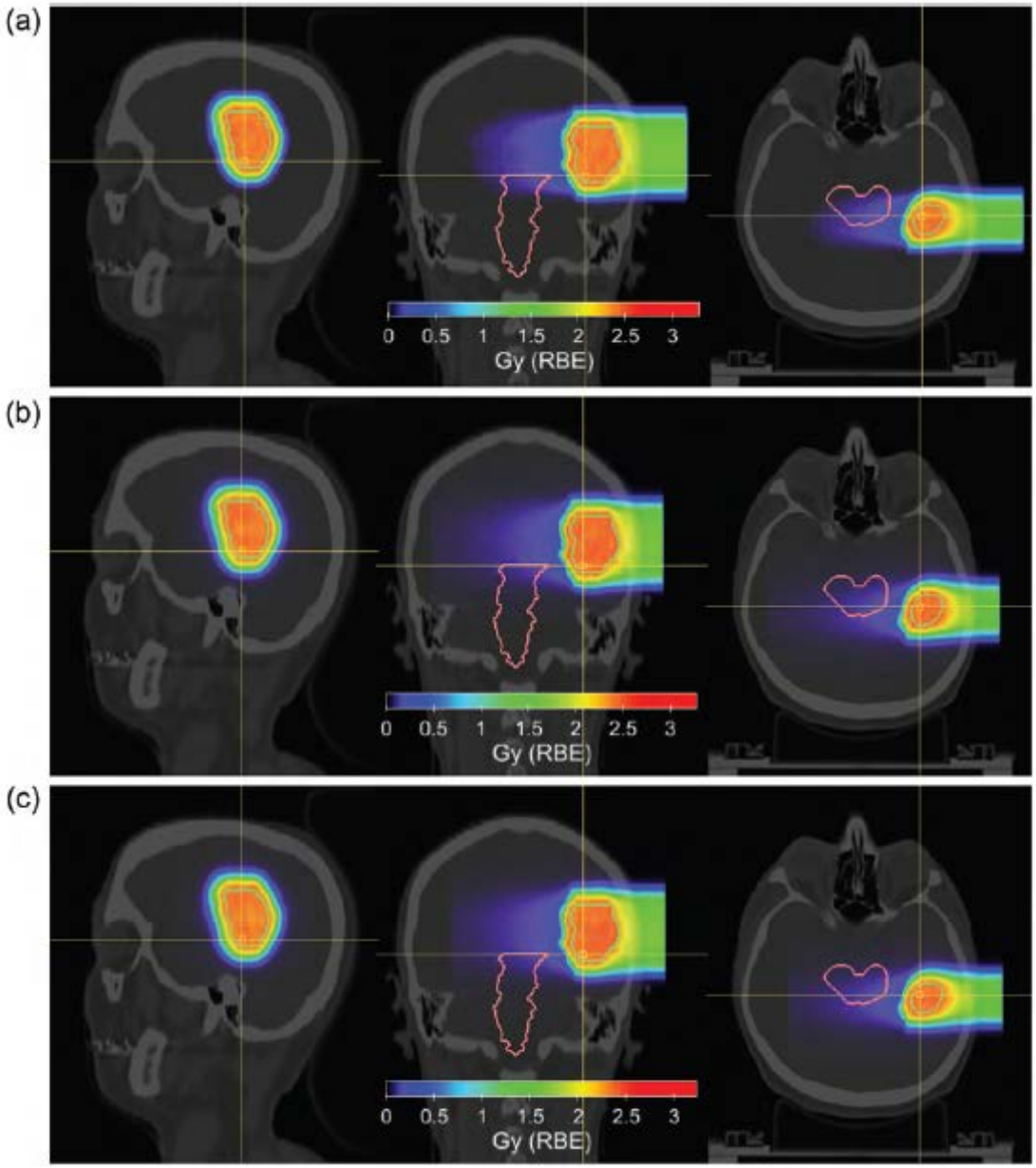


RBE as predicted by LEM for abs. doses larger than 10% of prescribed dose

3-port case

A Carbon Case study

MCTPS implemented @HIT



Boehlen TT, et al.
Journal of Radiation Research
54, i77-i81 (2013)

Result of MCTPS Optimization

Computing effort

Example: for the 2-port patient case:

MC calc. of RBE-weighted dose matrixes (5 k MC histories per PB) =
50 h (20 CPUs, 10 CPUs/field

Optimization time = 2h (1 CPU)

52 hours

A local cluster ~100 cores would be recommended

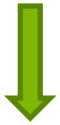
Essential a development of accelerating techniques in MC calculation

Simulation speed-up in FLUKA: see POSTER by C. Mancini et al

Cloud approach: the cost of 1000 hour of CPU can be estimated around 100 Euros (no prioritary service)

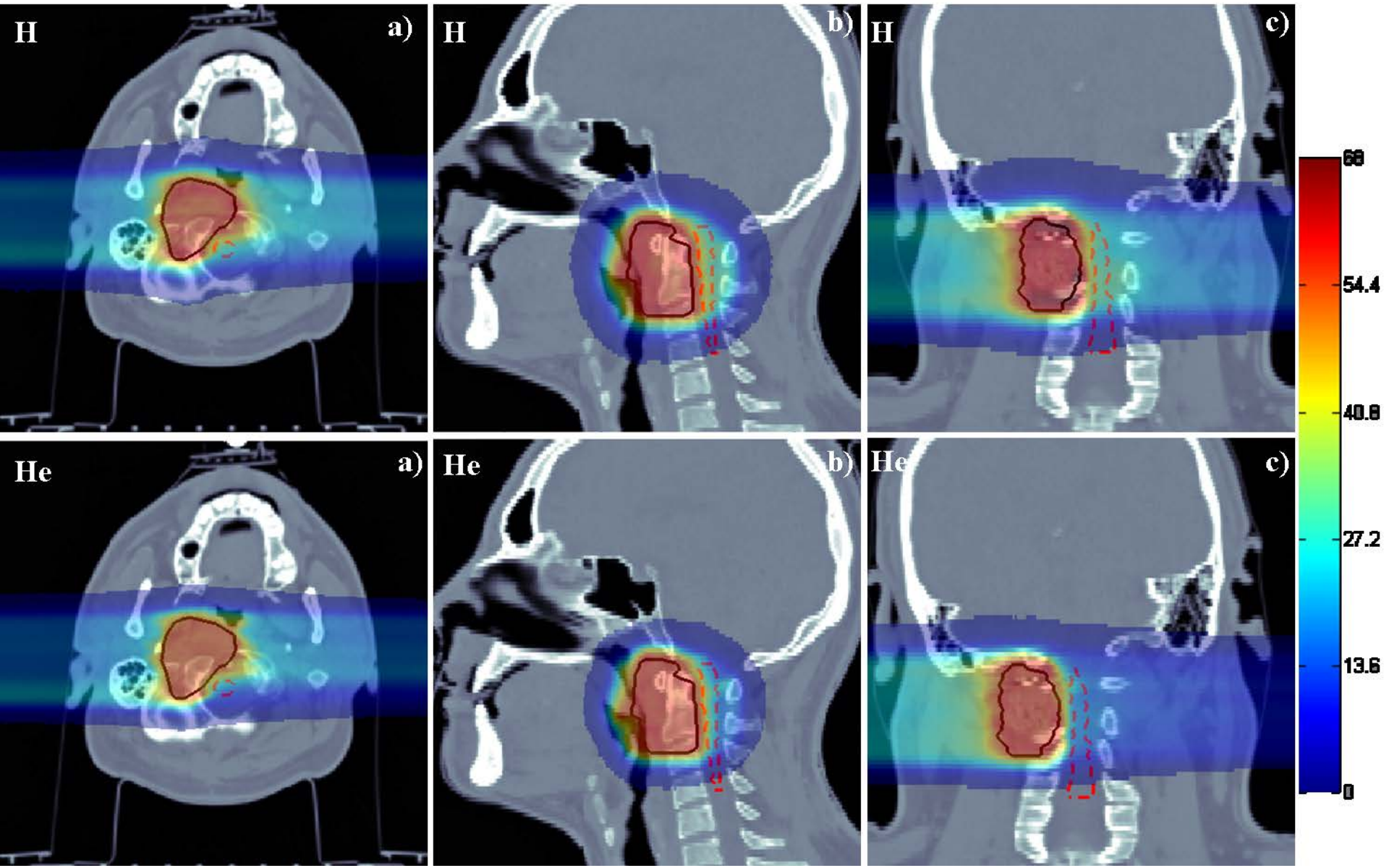
A new case: exploring use of He ions

- Very preliminary results.
- RBE fixed ~1.3 (*A. Brahme 2004*) as a starting point. In future variable RBE
- The nuclear model of FLUKA for He interactions is in development: *~good for E≤100 MeV/u (BME); to be improved for 100<E<few 1000 MeV/nucleon(RQMD*)

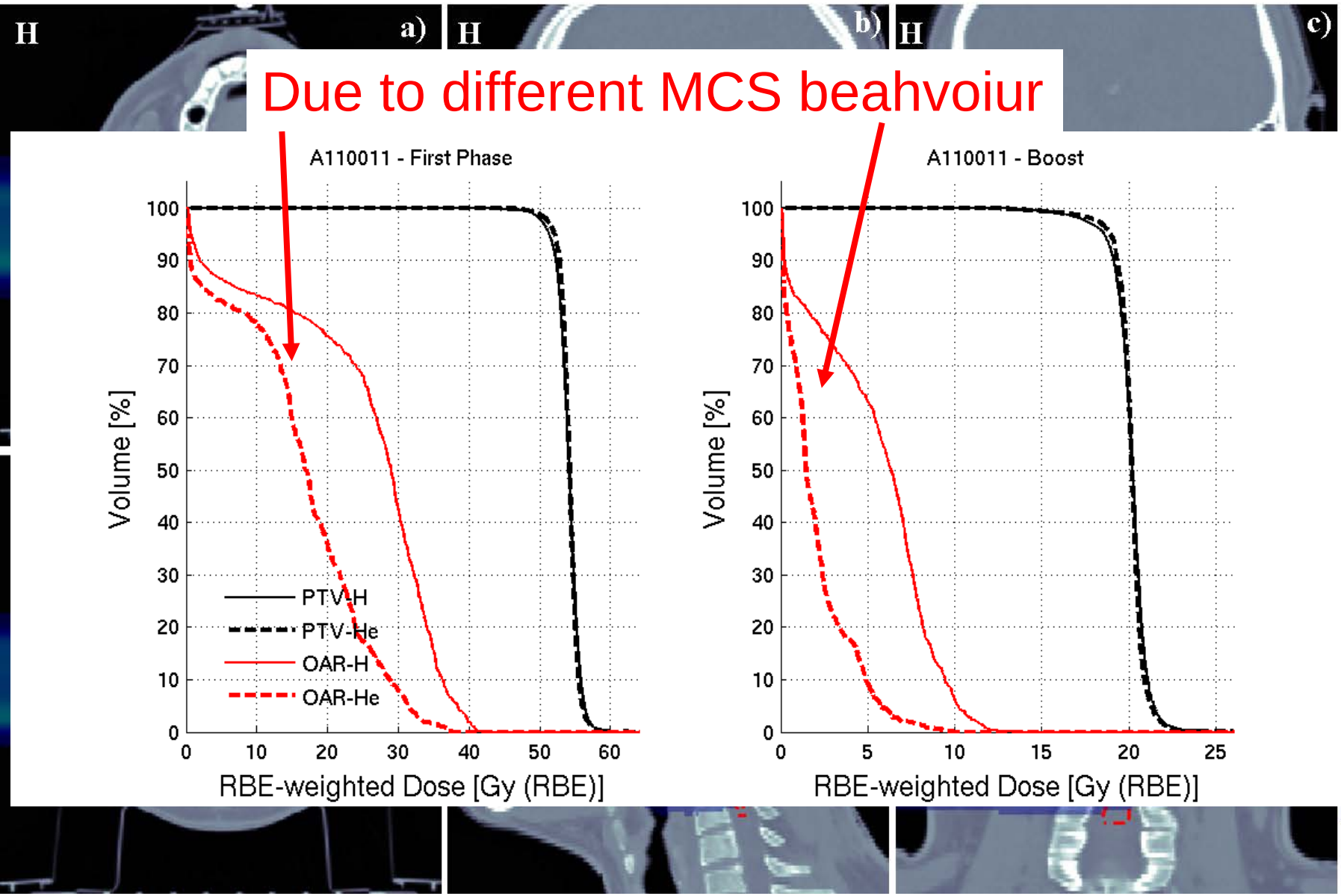


- No clinically oriented study yet
- The study is aimed:
  - to show capabilities of MCTPS
  - to study Multiple Coulomb Scattering effects on dose distribution comparison between ^{4}He and ^{1}H

A new case: exploring use of He ions



A new case: exploring use of He ions



Some Conclusions about the MCTPS

- The achieved results are very promising
- Computation speed is actually acceptable only for a research tool, for the moment
- In progress:
  - Study robustness of MCTPS plans
  - Integrate the different pieces together including graphical tools

Acknowlegments

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