



A fast - Monte Carlo platform on GPU for treatment plan dose recalculation in proton therapy

Martina Senzacqua

PhD student in “Accelerator Physics” in University of Rome “La Sapienza”

Department of Basic and Applied Sciences for Engineering (SBAI), Via A. Scarpa 14, Roma

email: martina.senzacqua@uniroma1.it



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Particle therapy (PT)

Cancer treatment technique using accelerated beams of protons or positive ions to treat solid tumor volumes.

Dose
$$D = \frac{dE}{dm} \quad \text{Gy [J/Kg]}$$



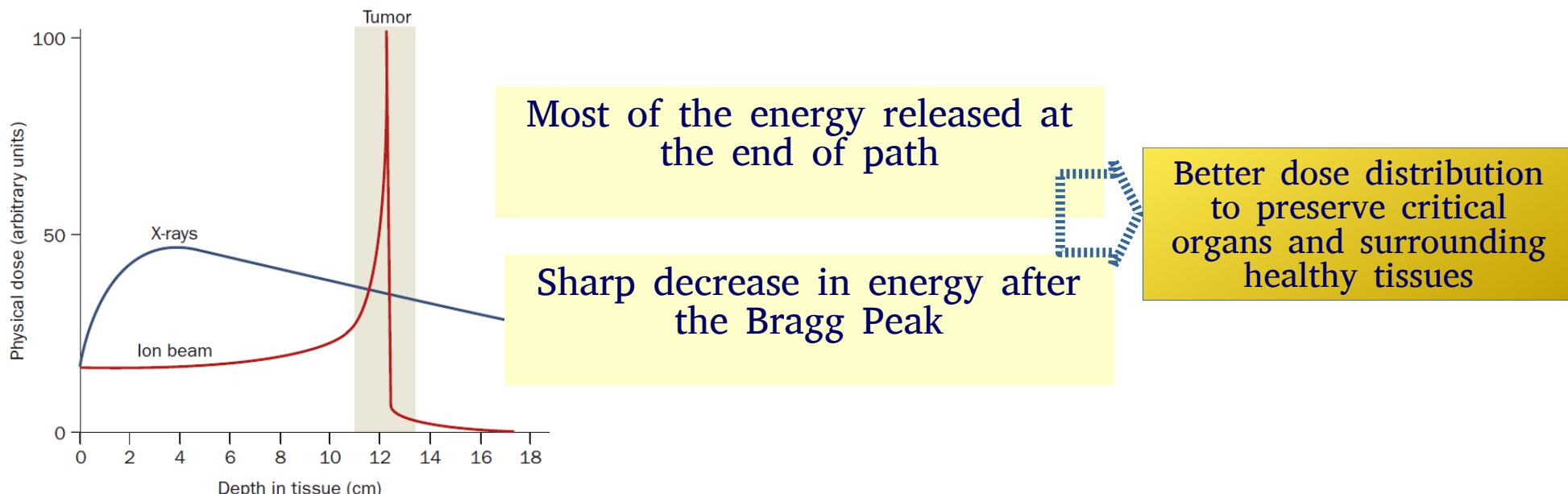
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Radiotherapy vs particle therapy

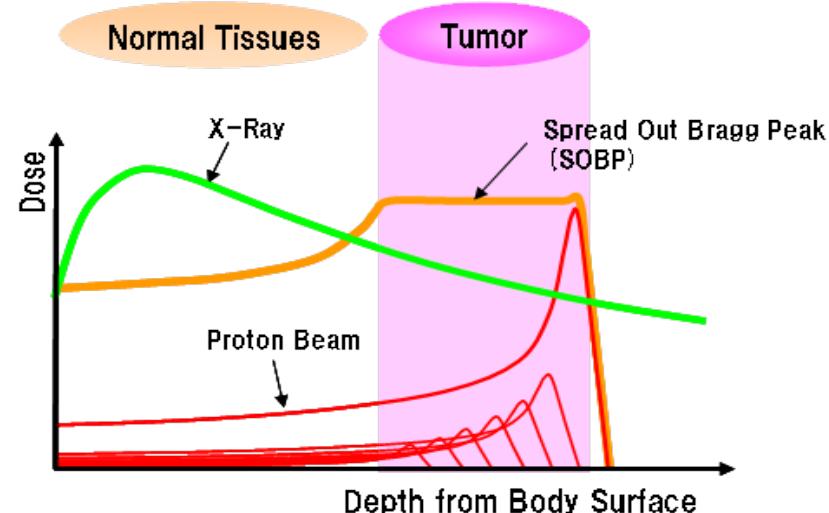


Cancer irradiation techniques goal:

Conformal dose distribution

concentrate all the dose to tumor and spare healthy tissues

- Standard radiotherapy → Intensity Modulated Radiation Therapy (IMRT)
 - Different beam directions (**fields**)
 - Dynamic delivery (Different beams fluences, tissue compensator)
- Particle therapy → Spread Out Bragg Peak (SOBP)
 - Active tumor volume scanning
 - Superposition of beams with different energies



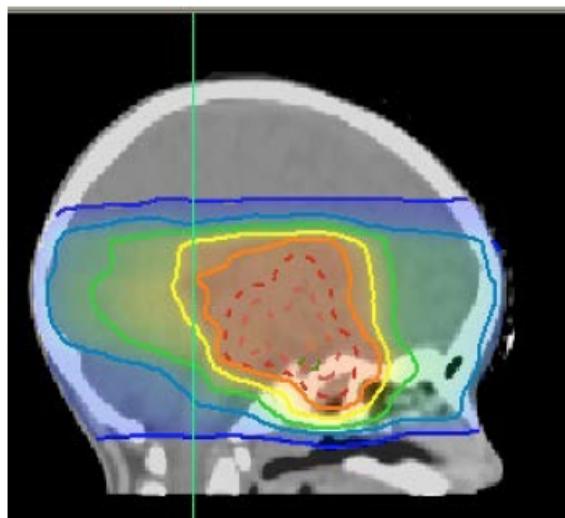
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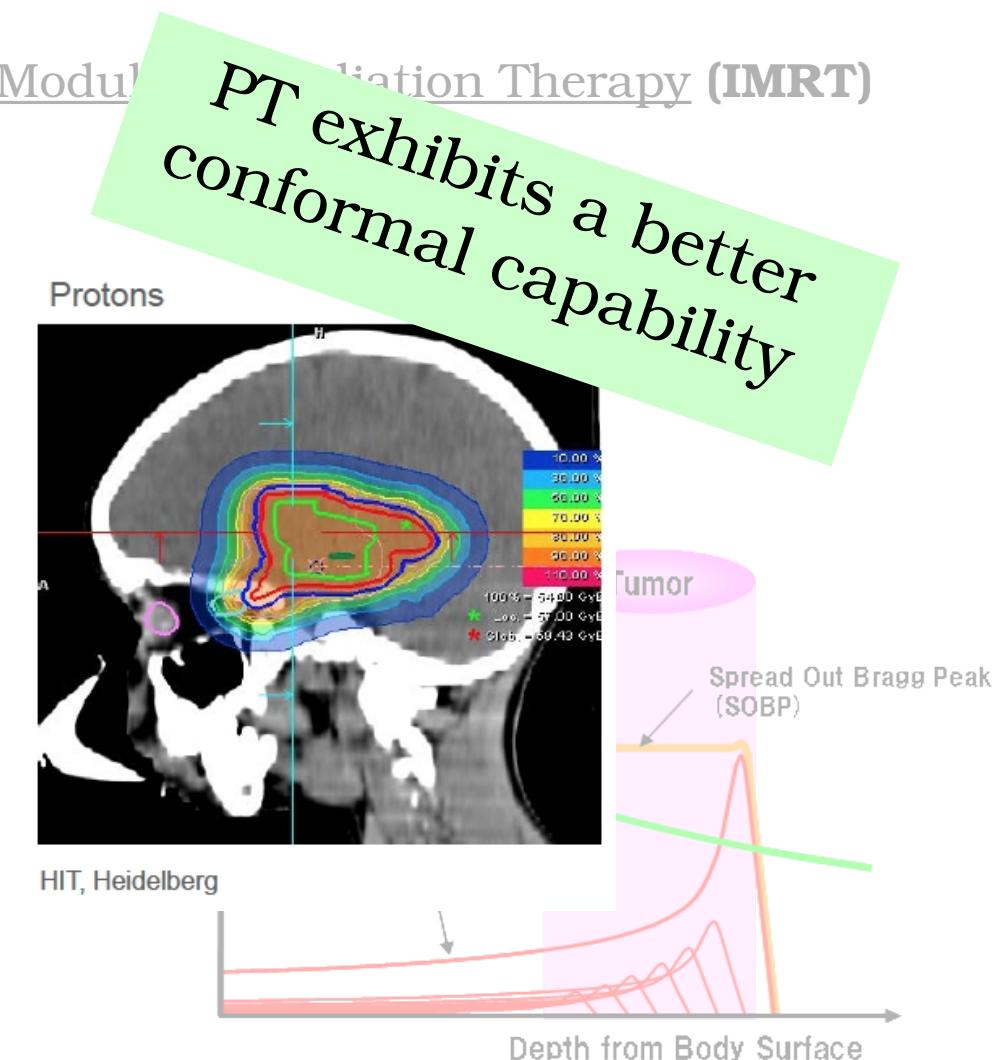
- Standard radiotherapy → Intensity Modulated Radiation Therapy (IMRT)

- Different beam directions (**fields**)
- Dynamic Photon-IMRT



Universitätsklinikum Dresden

- Particle therapy
- Active tumor
- Superimposition

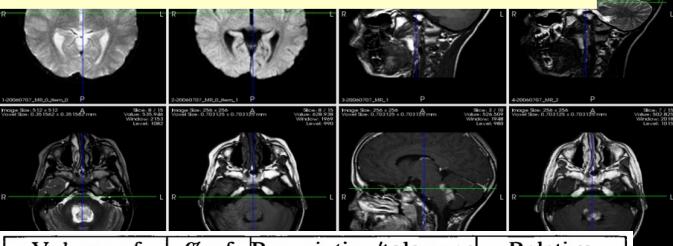


The high **selectivity** in energy release asks for an high level of **accuracy** in the computation of beams to be sent to the patient



Treatment Planning System (TPS)

patient anatomic data (CT, MRI, PET)



Radiotherapist prescriptions

Organ	% of Volume	Prescription/tolerance dose (Gy)	Relative importance
Bladder	50.0	20.0	0.2
Bladder	10.0	30.0	0.2
Femoral heads	90.0	10.0	0.2
Femoral heads	50.0	20.0	0.2
Femoral heads	10.0	40.0	0.2

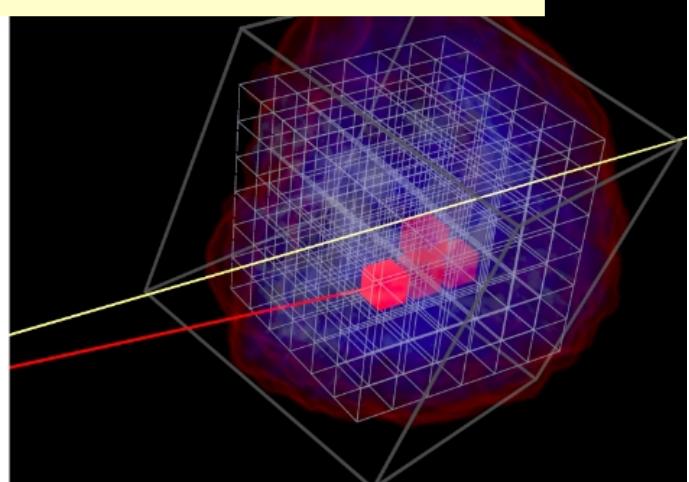
Accelerator parameters



TPS

Treatment Plan (TP) For each beam:

- Fluence Φ_i
- Energy E_{ki}
- Direction θ_i



CCP2016
XXVIII IUPAP Conference
on Computational Physics
10–14 July 2016
St George Hotel and Conference Centre,
Cape Town, South Africa



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Nowadays one of the major issues related to the TPS in Particle therapy is the **large CPU time** needed.

Options:

- FULL-MC recalculation using standard codes ~ 72 h/core
- Commercial TPS using analytical pencil beam algorithm
 ~ 1 h/core

FRED

is a fast MC able to perform a complete recalculation of **proton** TP in **less than 1 minute**

How?!?



NVIDIA Graphic Process Units

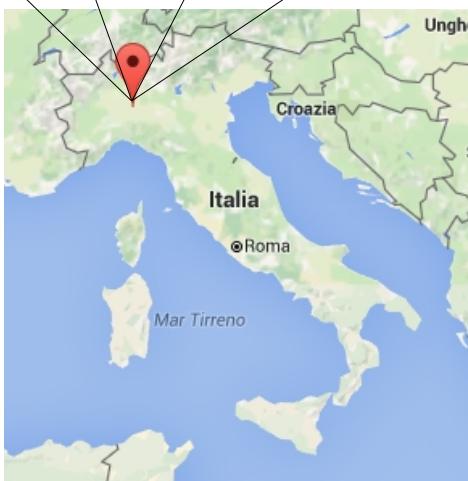
- Low budget
- Redundancy
- In-house maintenance



fondazione **CNAO**

Centro Nazionale di Adroterapia Oncologica per il trattamento dei tumori

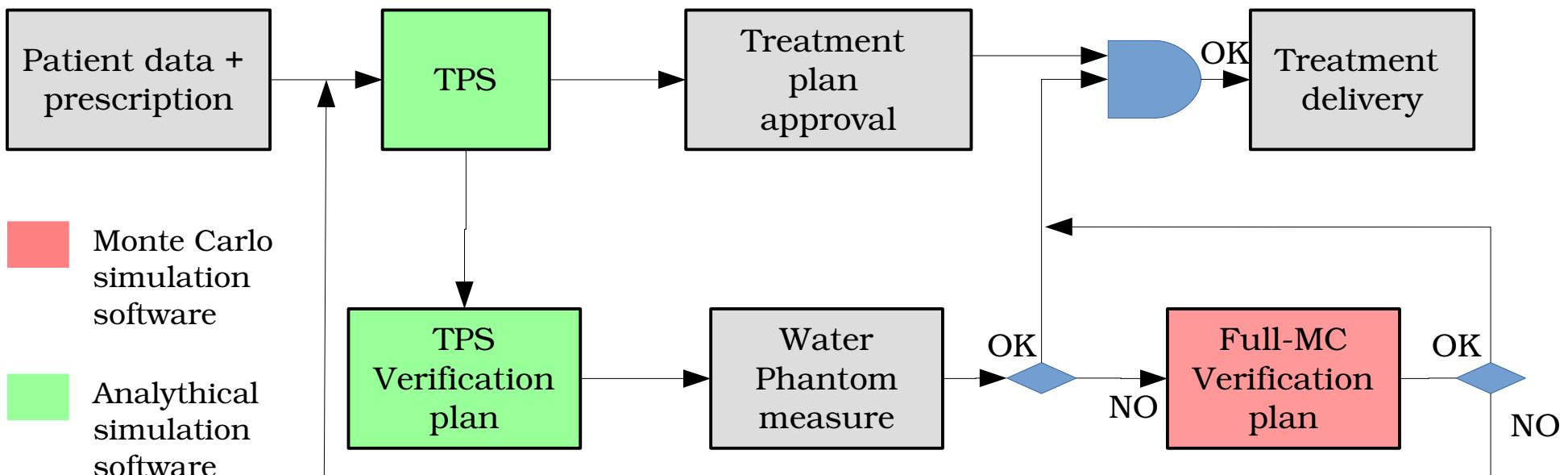
- Both **carbons ions** and **protons** beam
- One of the 10 worldwide centers using carbon ions beams to treat tumor
- First patient treated in 2014
- ~ 900 patients treated





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CNAO clinical protocol





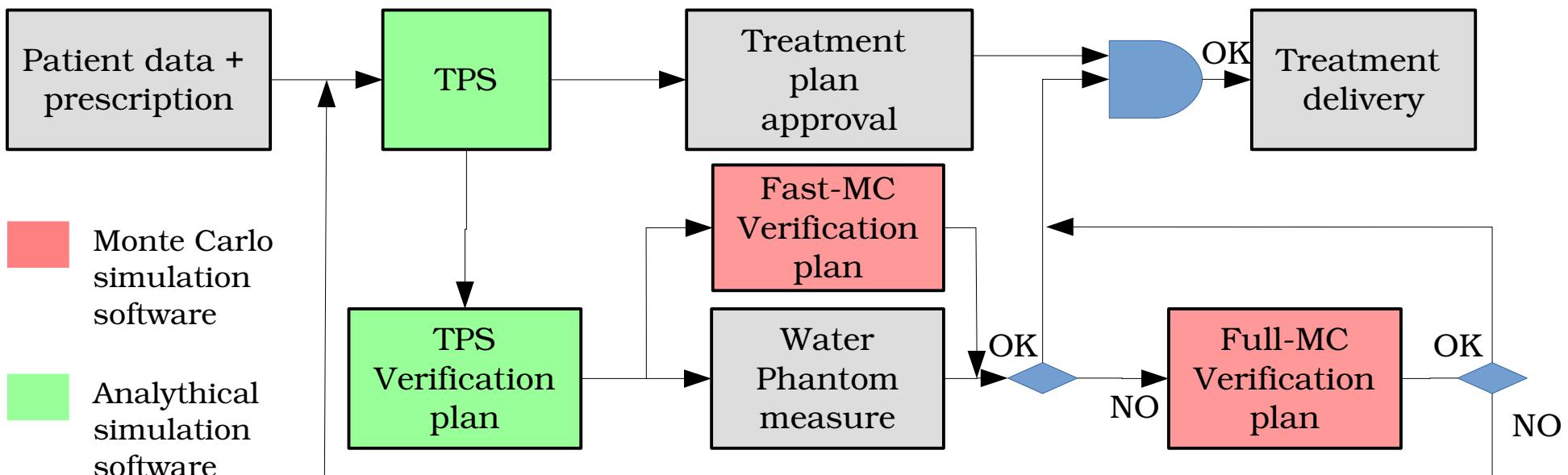
Pavia, PV

fondazione CNAQ

Centro Nazionale di Adroterapia Oncologica per il trattamento dei tumori

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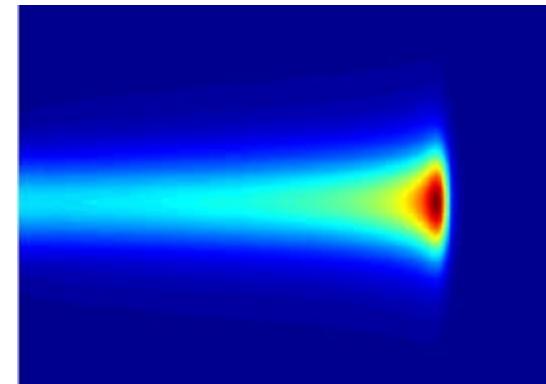
CNAO clinical protocol



Physics models

Physics models implemented in the code are:

- **Stopping Power**
- **Energy Fluctuations**
- Multiple Coulombs Scattering (**MCS**)
- **Nuclear interactions** (elastic and inelastic)



Stopping power and energy fluctuations

Bethe formula^[1]

$$\frac{dE}{dx}(x, N_e, v, E, \beta, \gamma, I)$$

Mean energy loss
per travelled distance

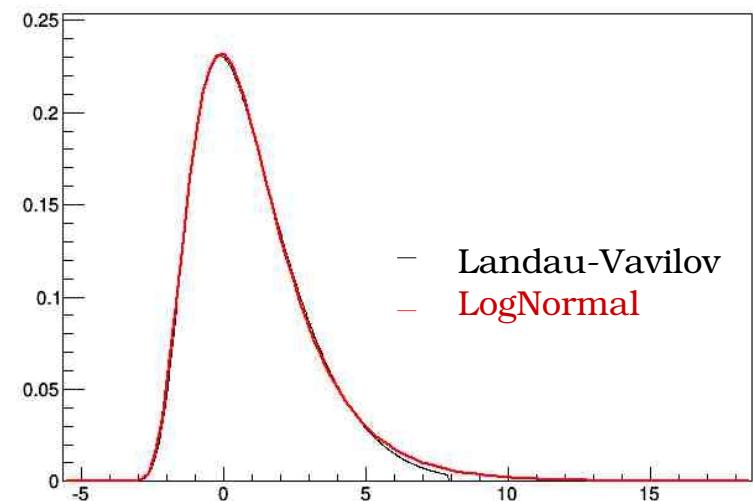
**Thick
absorber**

Gaussian distribution of energy loss

**Thin
absorber**

Landau-Vavilov
distribution of energy loss

↓
Approximation with
logarithmic normal function



λ_V

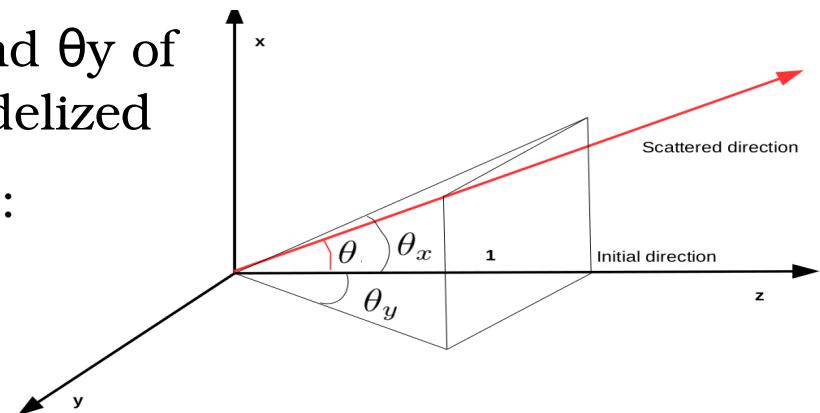
[1] H. Bethe und J. Ashkin in "Experimental Nuclear Physics", ed. E. Segré, J. Wiley, New York, 1953, p. 253

Multiple coulomb scattering

Distributions of **projected angles** θ_x and θ_y of the angle θ have been studied and modeled

Small angles approximation: $\sin(\theta) \sim \theta$:

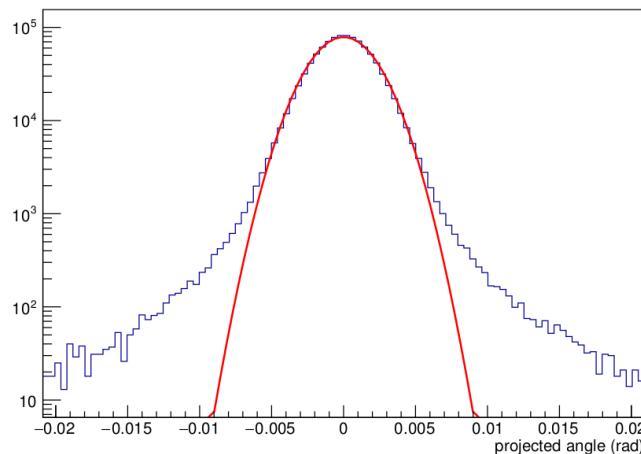
$$\theta = \sqrt{\theta_x^2 + \theta_y^2}$$



Three different models implemented:

Single Gaussian

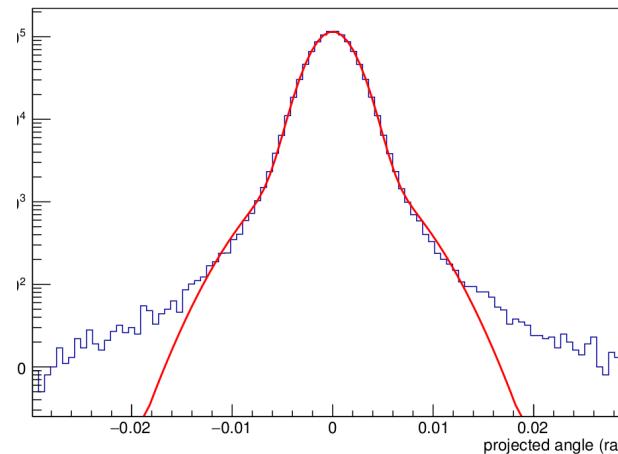
Energy=151MeV step=10^{-1.0}cm



Double Gaussian

(used in clinical analytic TPS)

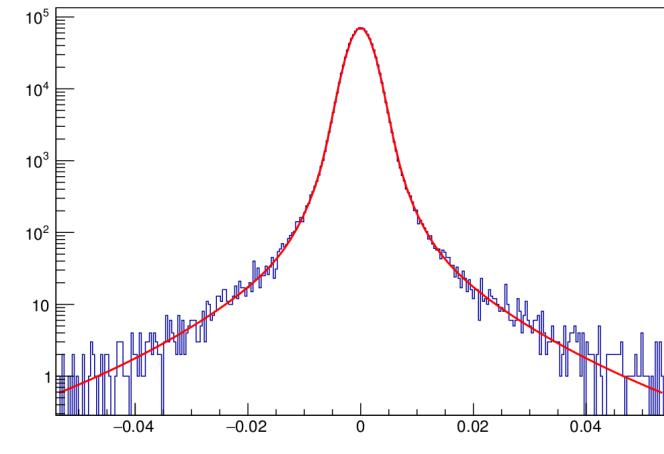
Energy=151MeV step=10^{-1.0}cm



Gauss- Rutherford like

$$f_{GR}(\theta_{x,y}) = (1-w)G(\theta_{x,y}, \sigma) + w \frac{a}{(\theta_{x,y}^2 + b)^c}$$

Energy=151MeV step=10^{-1.0}cm

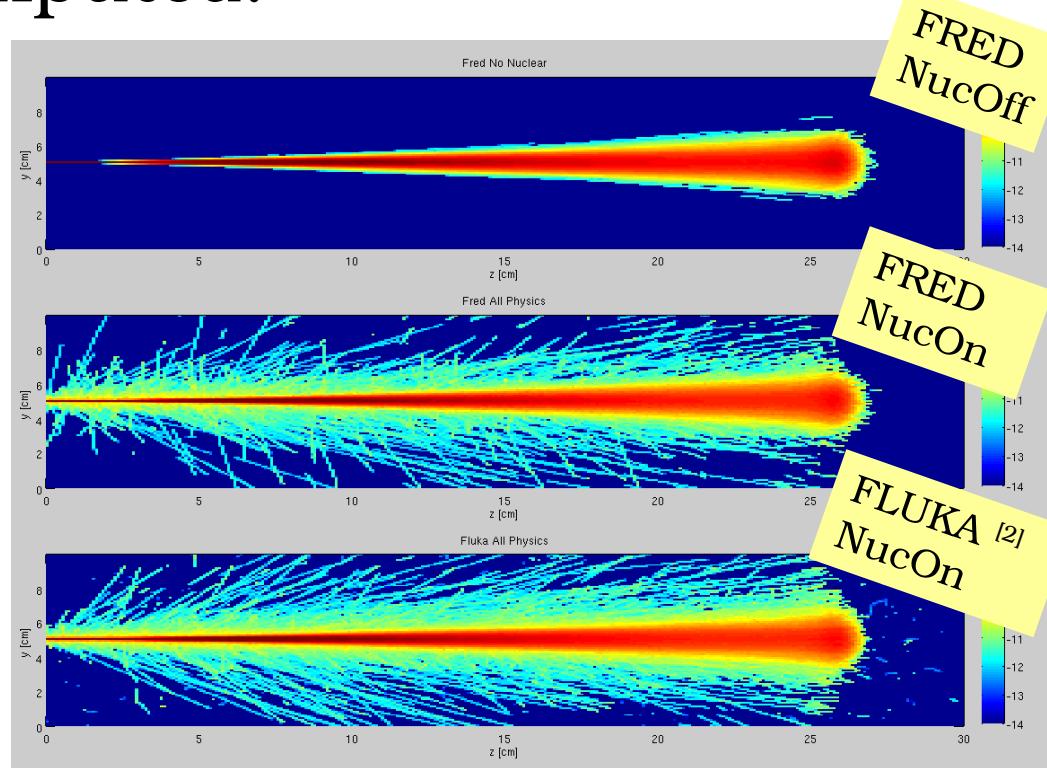


Nuclear interaction

Nuclear cross sections from ICRU report of 2003

Secondary fragments computed:

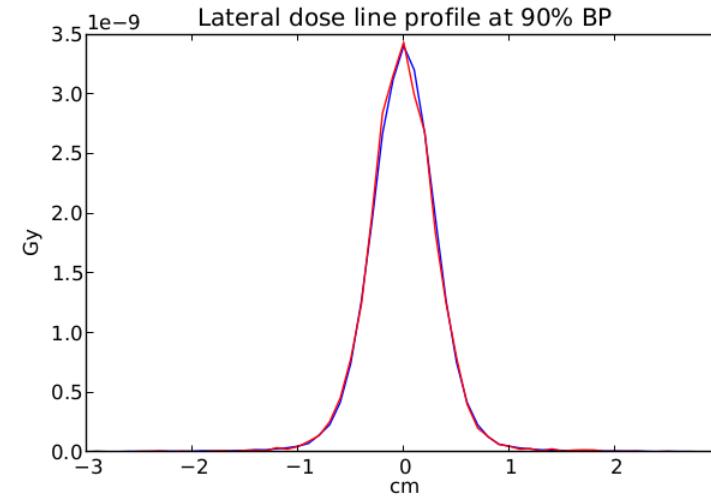
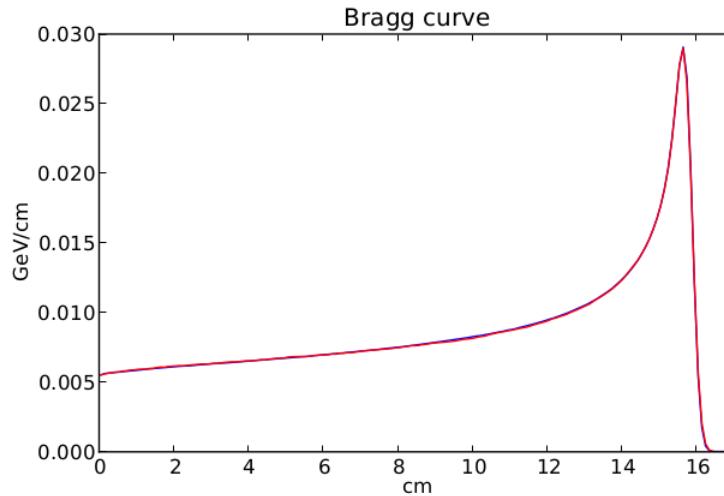
- ✓ **Protons**, tracked
- ✓ **Deuterons**, tracked
- ✗ **Neutrons**, neglected
- **Heavier ions**, locally deposited



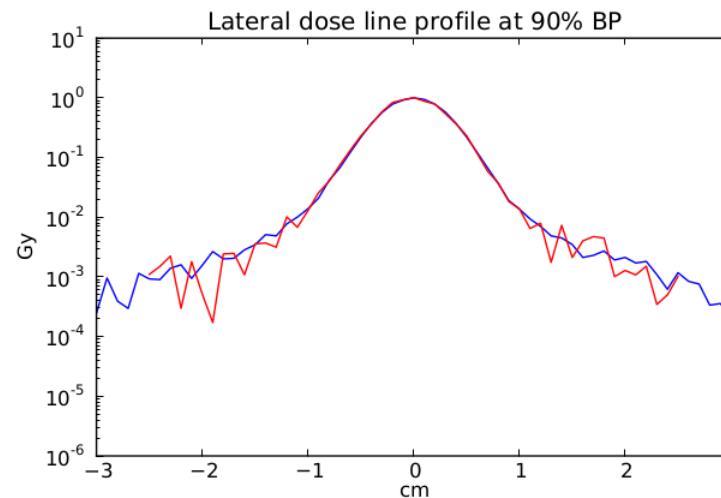
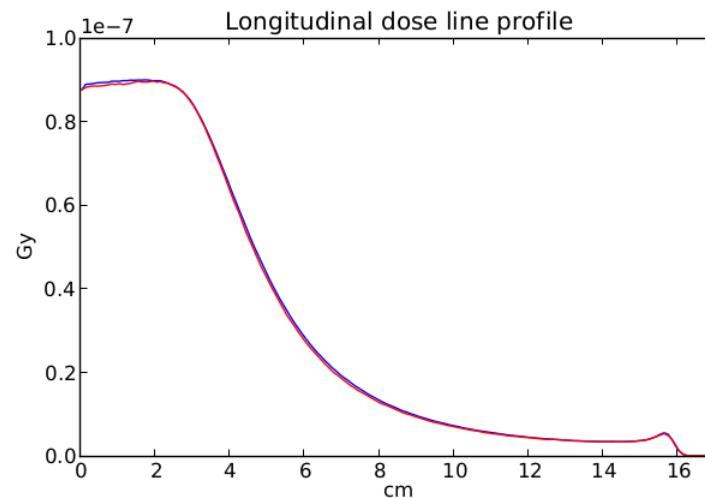
[2] <http://www.fluka.org/fluka.php>

Single PB dose profiles

150 MeV protons in water (FWHM=0.0)



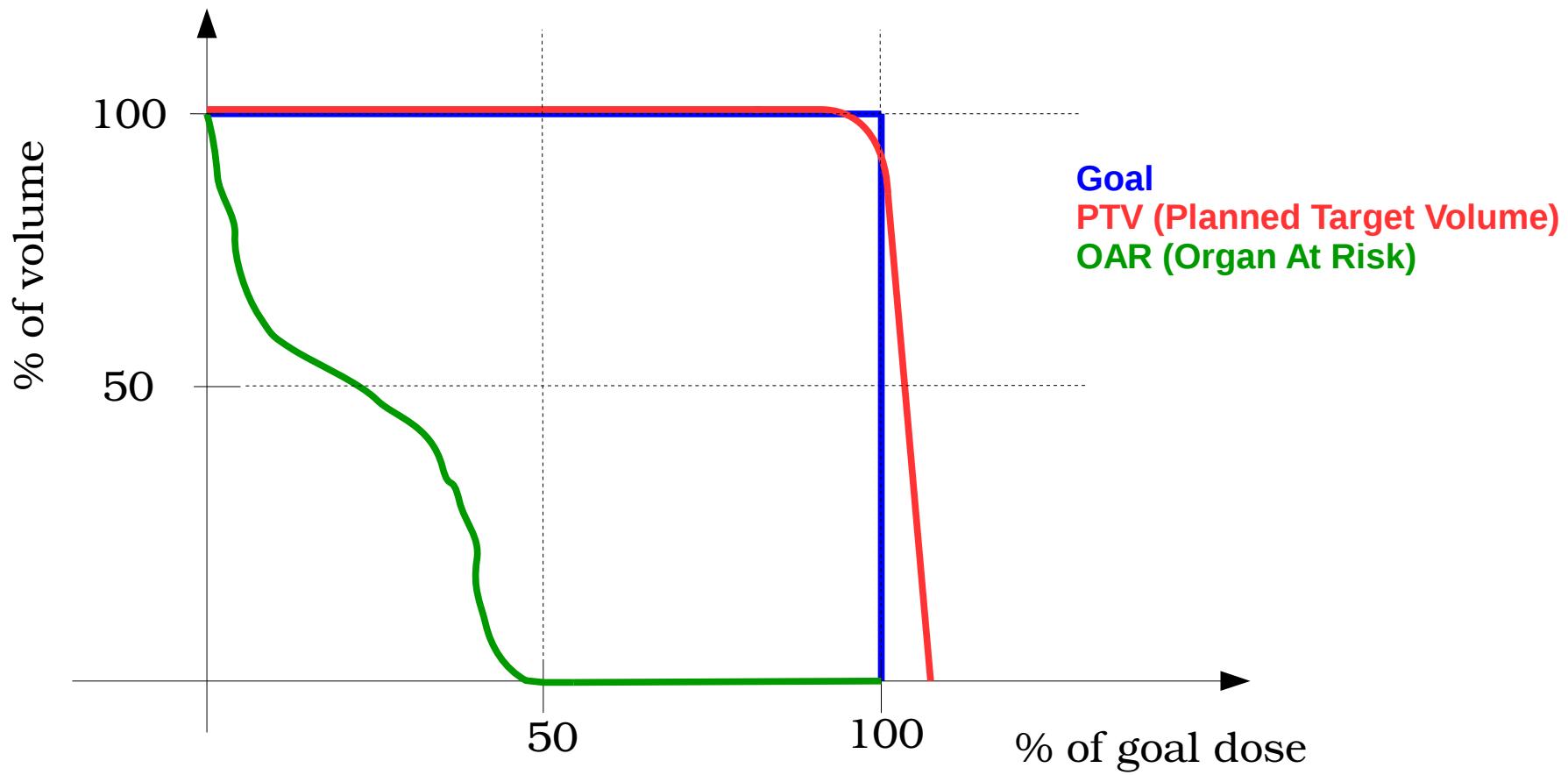
Full Monte Carlo
(FLUKA)
Fast Monte Carlo
(FRED)



DVH quality indicator

DVH (Dose Volume Histogram)

DVH is an histogram where each bin's high represents the percentage of volume receiving a dose greater or equal to the value of the center of the bin.

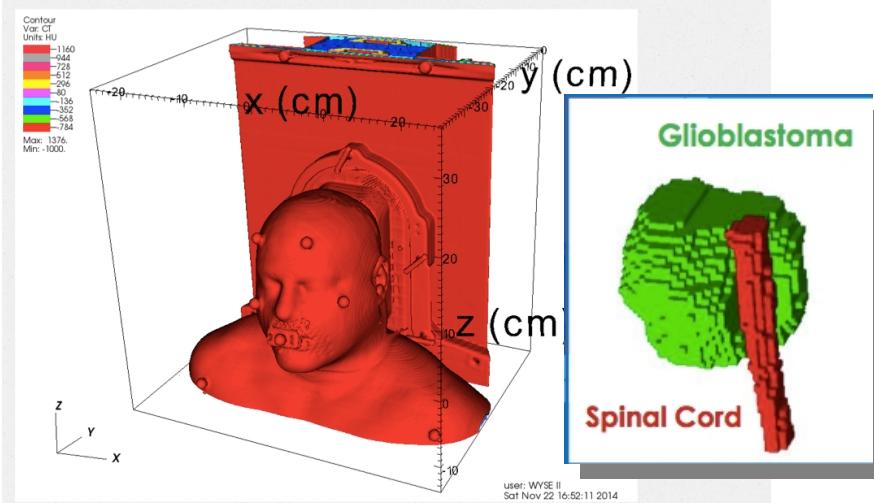


Clinical case: Glioblastoma

HU conversion in voxel density ρ and elemental composition from

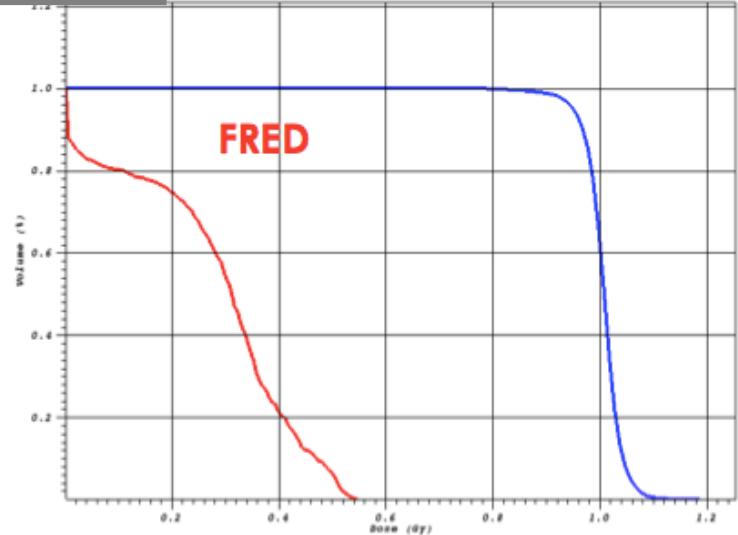
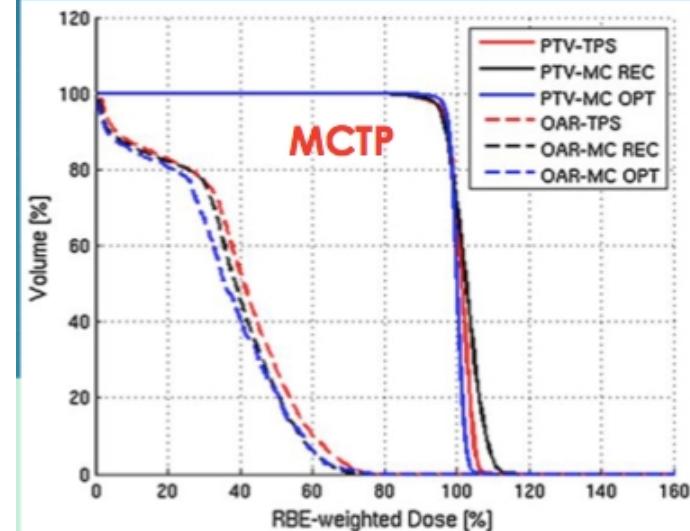
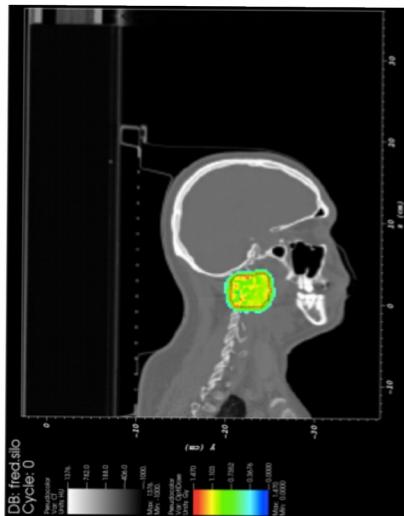
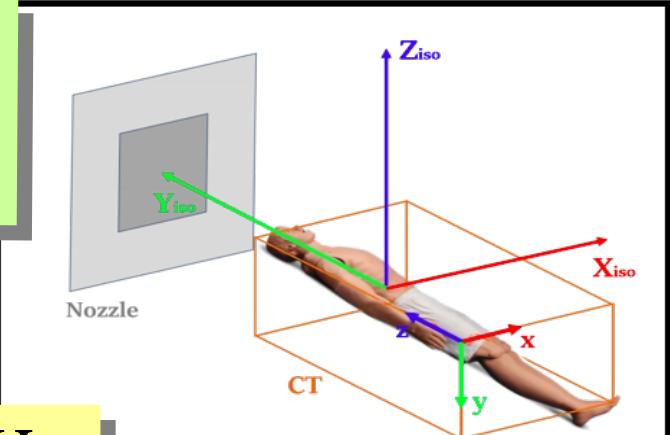
"The Calibration of CT of CT Hounsfield units for radiotherapy treatment planning",

Schneider, Pedroni, Lomax, 1996 Phys. Med. Biol. 41 111



6400 pencil beams,
5000 primary each
Dose scoring
volume resolution
 $2 \times 2 \times 2$ mm

DVH



Hardware and performance



Under sustained raytracing workload, in order to keep temperature of all GPU cards below 70°, we obtain:

AIR-COOLED 2X NVIDIA GTX TITAN

30% duty cycle

WATER-COOLED 4X NVIDIA GTX 980

100% duty cycle

		THREADS	primary/s	µs/primary
C P U	FLUKA	1	0.75 K	1340
	FRED	1	15K	68
	FRED	16	48K	21
	FRED	32	80K	12.5
G P U	FRED	1 GPU*	800K	1.35
	FRED	2 GPU**	3500K	0.3
	FRED	4 GPU***	20000K	0.05

*LAPTOP: MacBookPro(AMD Radeon R9 M370X)

** DESKTOP: Mac Pro (AMD FirePro D300)

***LINUX WorkStation with 4 NVIDIA GTX 980 GPUs

Conclusions and future developments

- Good dose maps agreement with TPS data and Full-MC simulations
- Time computing expense > 1000 times less than a full MC tool

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- Clinical validation of fast-recalculation tool
 - Applications to clinical routine
 - Extensions to include other ions (Carbon, Helium)
 - Improvement of radiobiological models (RBE)
 - Dose monitoring using secondary particles

Thank you for your attention!



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UNIVERSITÀ DI ROMA

Martina Senzacqua
martina.senzacqua@uniroma1.it

Prof. Vincenzo Patera
vincenzo.patera@uniroma1.it

Prof. Angelo Schiavi
angelo.schiavi@uniroma1.it



Prof. Giuseppe Battistoni
giuseppe.battistoni@mi.infn.it

Stefano Pioli
stefano.pioli@uniroma1.it

fondazioneCNAO
Centro Nazionale di Adroterapia Oncologica per il trattamento dei tumori

Andrea Mairani
andrea.mairani@cnao.it

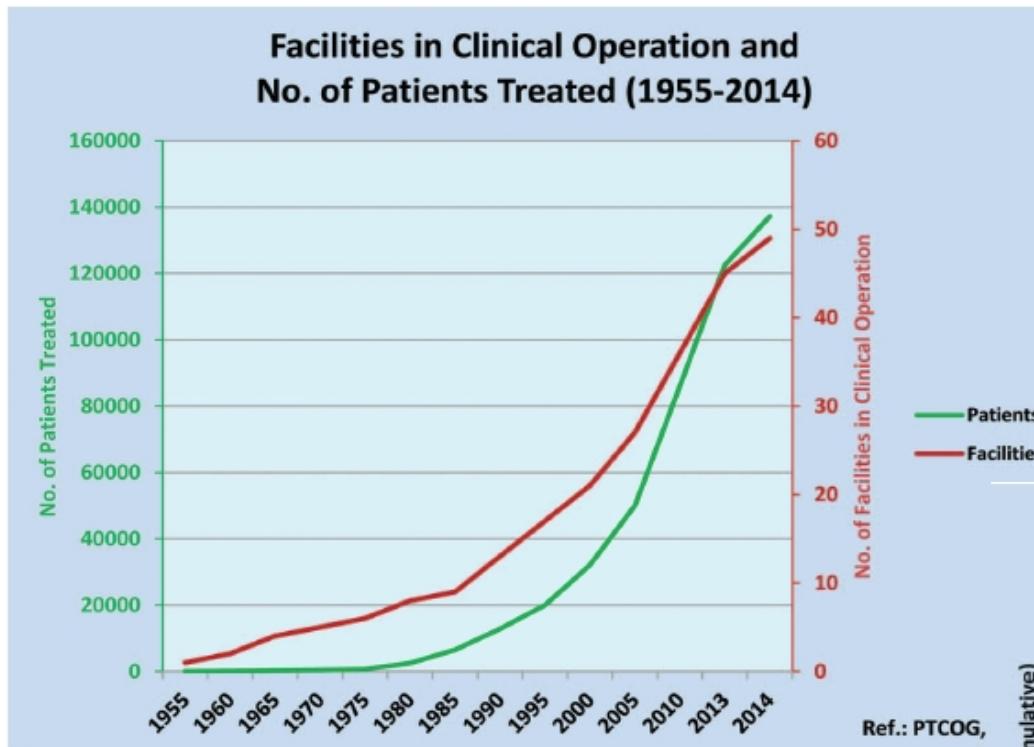
Mario Ciocca
mario.ciocca@cnao.it

Silvia Molinelli
silvia.molinelli@cnao.it

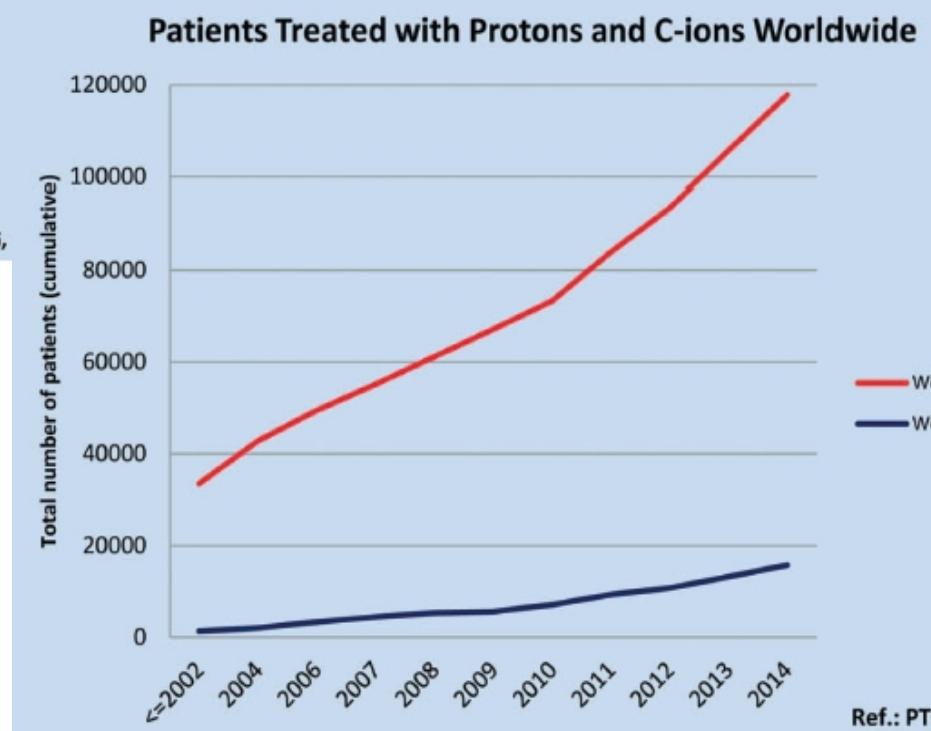
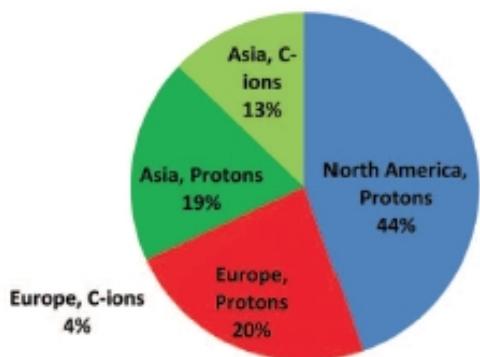
Giuseppe Magro
giuseppe.magro@cnao.it



Patient statistic

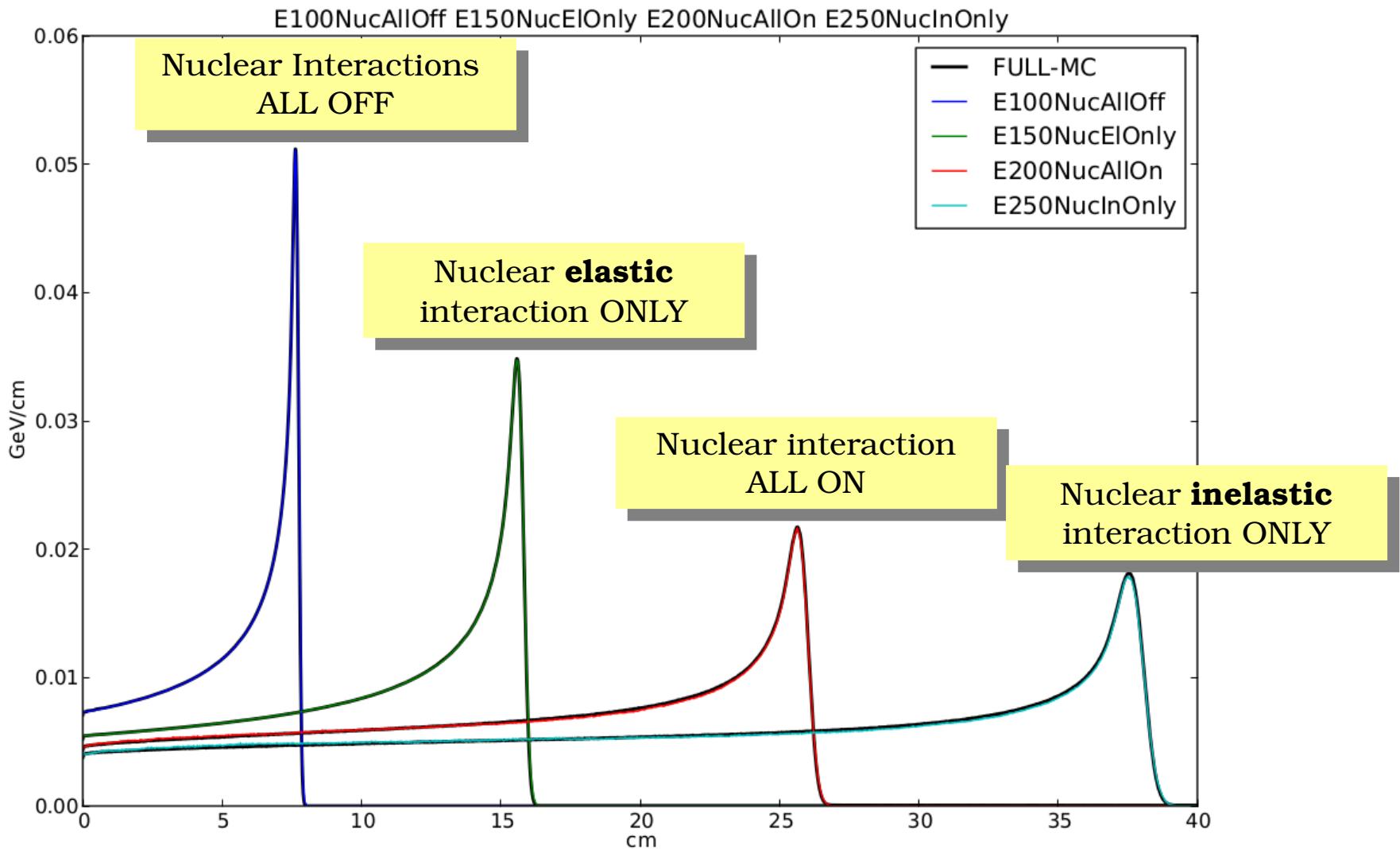


Patients Treated in 2014, Protons and C-ions
Total of 15 400



www.ptcog.ch

Bragg Peaks



Gamma Index pass rate^[3]

DTA = Distance to agreement

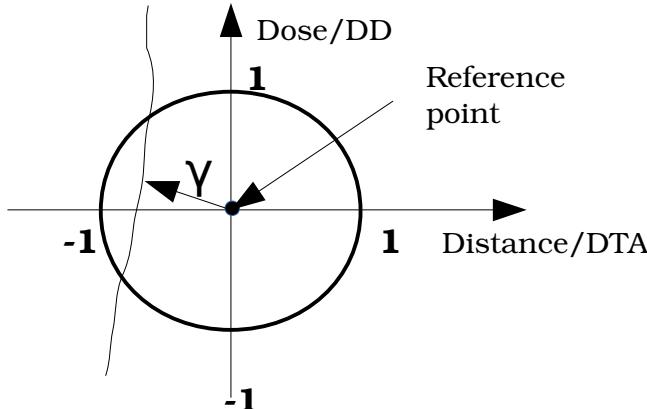
DD = Dose Difference

*_r = reference dose map

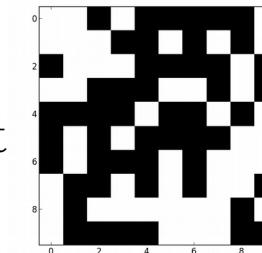
*_e = evaluated dose map

$$\Gamma(\vec{r}_e, \vec{r}_r) = \sqrt{\frac{|\vec{r}_e - \vec{r}_r|^2}{DTA^2} + \frac{[D_e(\vec{r}_e) - D_r(\vec{r}_r)]^2}{DD^2}}$$

$$\gamma(\vec{r}_r) = \min \{\Gamma(\vec{r}_e, \vec{r}_r)\} \forall \{\vec{r}_e\}$$

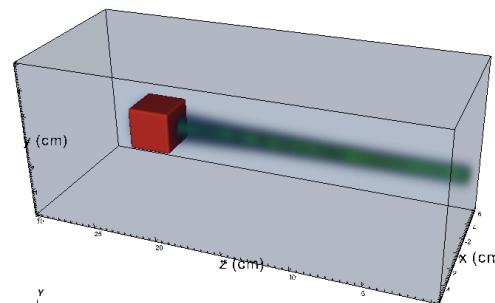


If $\gamma < 1$, the reference point passes the γ -test otherwise it fails.



[3] Daniel A. Low, William B. Harms, Sasa Mutic, and James A. Purdy, "A technique for the quantitative evaluation of dose distributions", Medical Physics, Vol. 25, No. 5, May 1998

Quality assurance cube



SOBP 3 cm cube @ 20 cm depth
20000 primary protons per PB

— FRED
— TPS

