Towards efficient and accurate particle transport simulation in medical applications

L. Grzanka^{1,2}, M. Kłodowska¹, N. Mojżeszek¹, N. Bassler³

¹ Cyclotron Centre Bronowice, Institute of Nuclear Physics (IFJ PAN), Kraków, Poland,

² AGH University of Science and Technology, Kraków, Poland,

³ Stockholm University, Stockholm, Sweden







Cancer and radiotherapy

PROTONS CONVENTIONAL RADIATION Prostate Bladder Top of Hip Bone

Tumor

TREATMENT

FIELD 2

Rectum

These images show the areas exposed to radiation during treatment.



- New and innovative technique
- Rare (1 center in Poland)
- <200 patients per year
- Proton beam generated by cyclotron large facility
- No exit-beam, more healthy tissue spared

Tumor

TREATMENT

FIELD 1

More complexity in physics of the beam

- Long history
- Popular (~120 accelerators)

Tumor

MULTIPLE TREATMENT

FIELDS

- ~70000 patients per year
- Beam of X-rays, compact linear accelerator in use
- Simpler physics involved

Proton therapy is booming

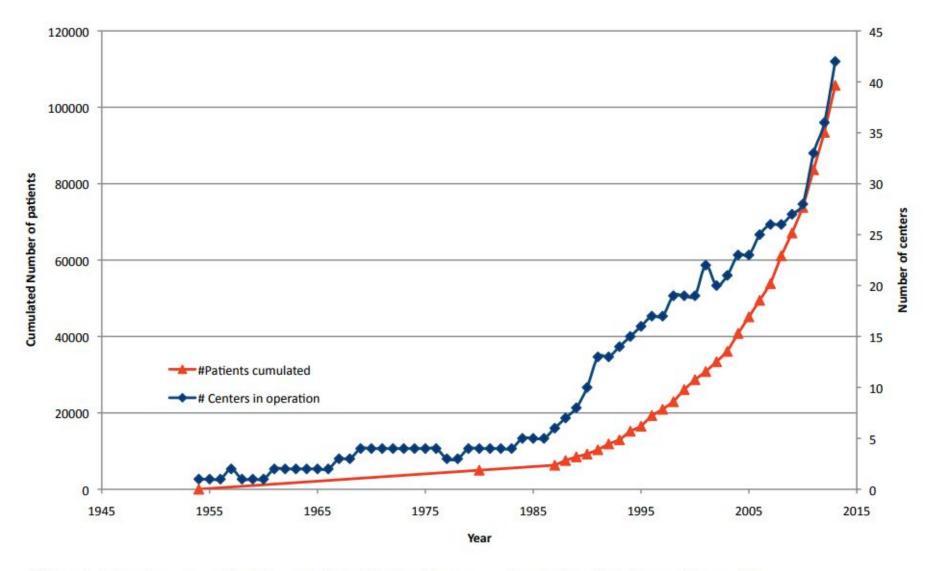


Figure 1.1: Graph representing the evolution of proton therapy centers under clinical operation and the cumulated number of patients treated using proton therapy (Source: PTCOG Website)

Cyclotron Center Bronowice in Krakow



1990 - proton therapy plans

2009 - CCB project starts

2011 - first patients with eye tumors

2012 - new cyclotron and building

2016 - first patient treated on gantry

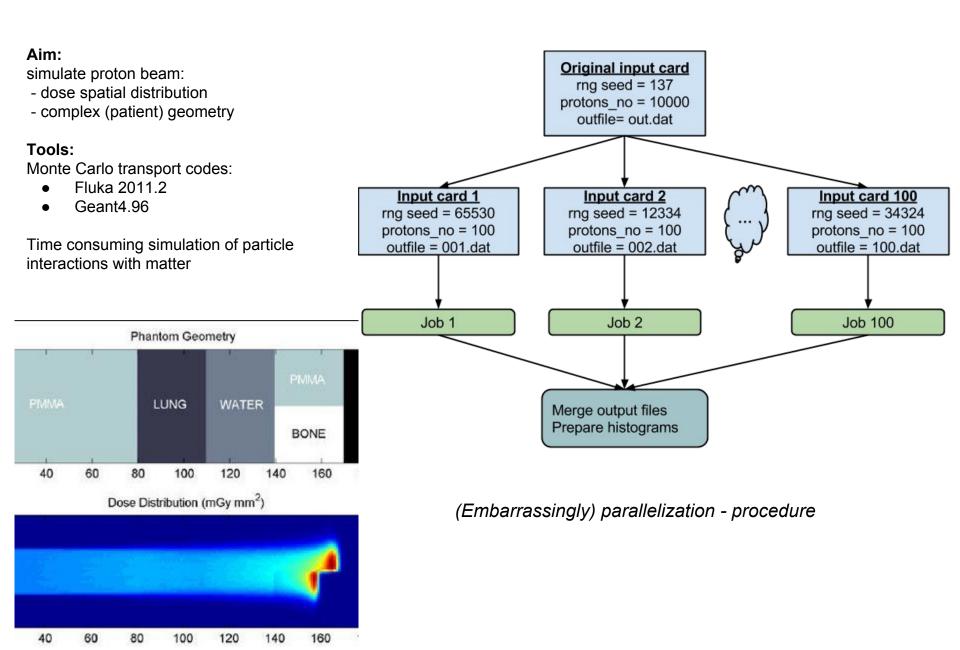
Robotic gantry rotates around the patient

Cyclotron delivers beam of protons with max energy 230 MeV (~30 cm range in water)

CCB: patient treatments, experimental physics research, applied physics

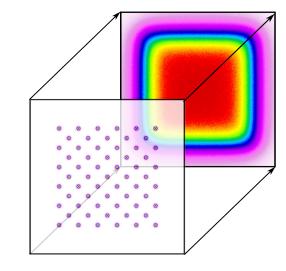


Monte Carlo Simulation of a proton beam



Proton microbeam radiotherapy

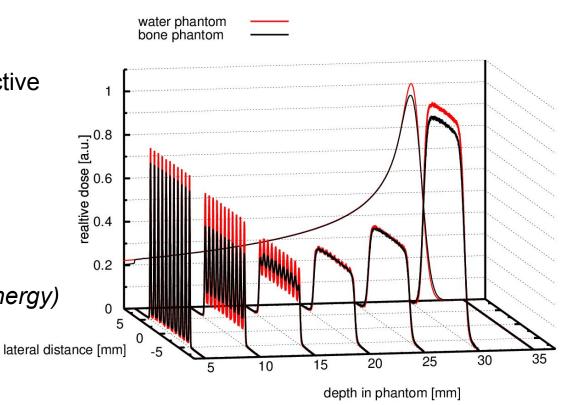
 New concept: broad beam filtered by slits.
 Close to skin damage in narrow channels - benefit from dose-volume effect.
 Beam scattering with depth.



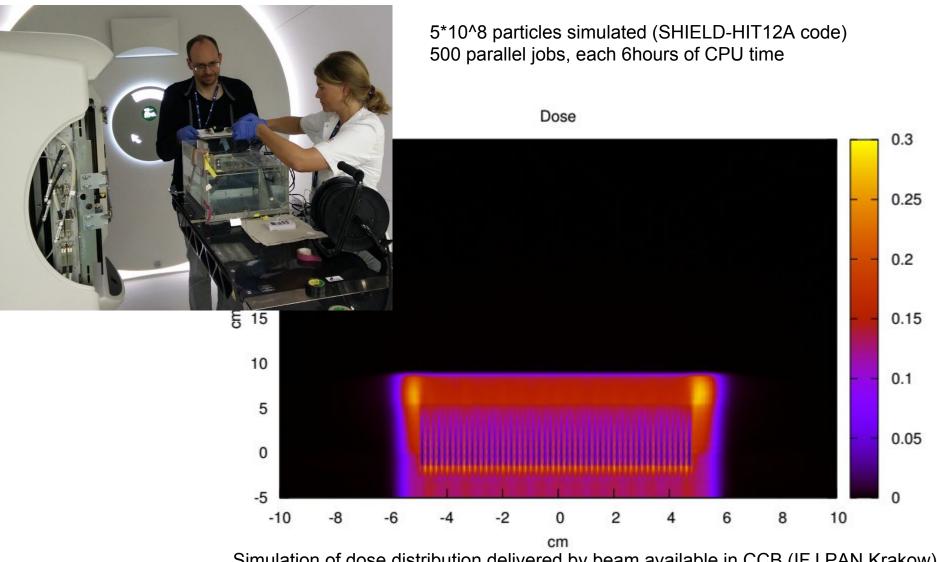
FLUKA MC code:

100 µm proton beam with active pencil-beam scanning mode 60-120 MeV, 1-8 mm beam spacing

10^5 protons/spot in 10 runs (60-221 spots / energy)

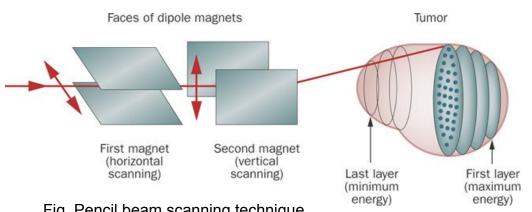


Proton spatially fractionated radiotherapy



Simulation of dose distribution delivered by beam available in CCB (IFJ PAN Krakow), filtered by 1mm slit collimator. Geometry represents setup used in radiobiology experiment.

Verification of a proton pencil beam model in the treatment planning system (TPS)



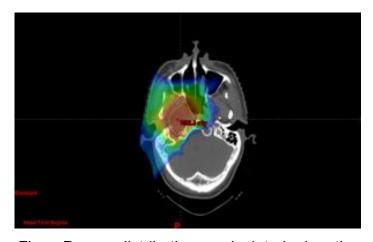
Parameters like **position**, **energy** and weight of each proton pencil **beam** are calculated in the treatment planning system (TPS) and optimized to achieve uniform dose distribution in the tumour while sparing healthy organs in close region to the irradiated volume.

Fig. Pencil beam scanning technique.

http://www.nature.com/nrclinonc/journal/v7/n1/images/nrclinonc.2009.183-f4.jpg

Dose distribution calculated in the TPS

TPS - analytical algorithms based on simplified physical models (gaussian scattering in water and air). Some disagreement with measurement is observed.



Dose distribution calculated treatment planning system.

Verification of a proton pencil beam model in the treatment planning system (TPS)

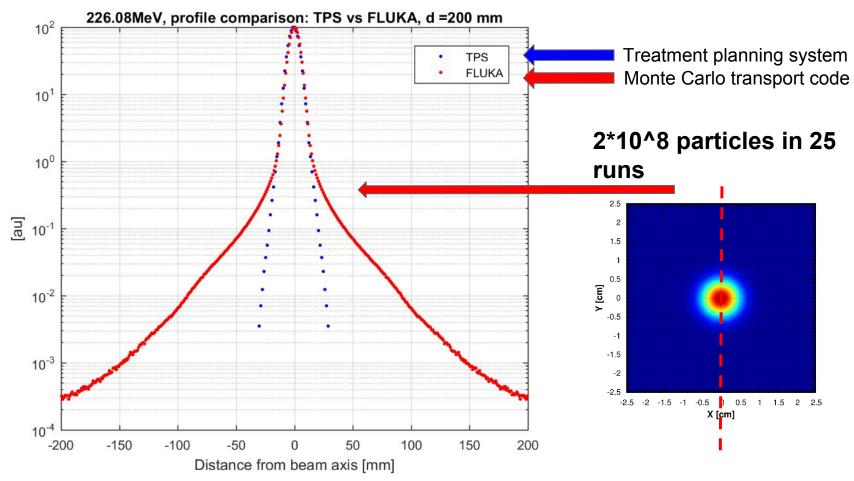
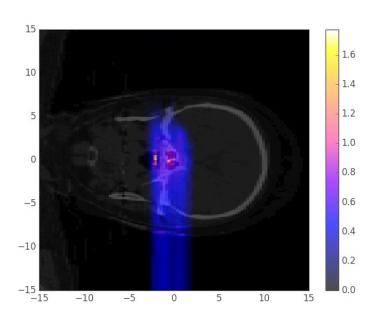


Fig. Lateral beam profiles in water at depth of 200 mm of a single pencil beam of energy 226.08 MeV calculated in FLUKA Monte Carlo code and in Eclipse treatment planning system.

Towards Monte-Carlo based treatment planning



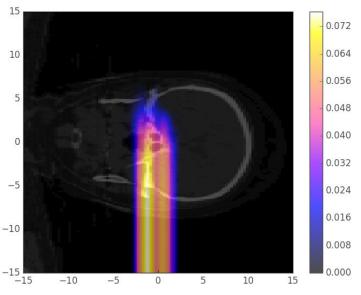
Simulations of particle interaction in geometries based on patient CT scans.

Novel algorithm implemented in SHIELD-HIT12A MC transport code.

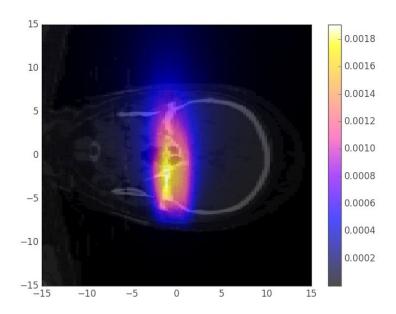
Time and memory consuming calculations:

- ~ 10GB RAM per node
- 10⁸ particles
- 3h of CPU time on 100 nodes





Proton fluence



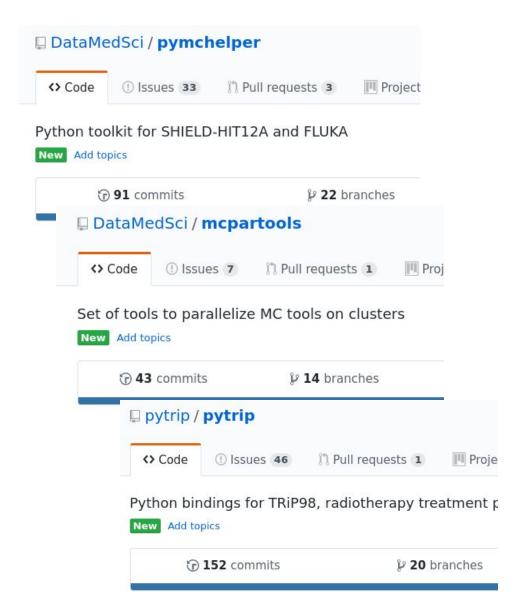
Neutron fluence

Ecosystem of tools, codes and projects

Monte Carlo particle transport codes:

Tools and toolkits essential for users





Simplifying "embarassing" parallelization

Input card 1

rng seed = 65530 protons no = 100

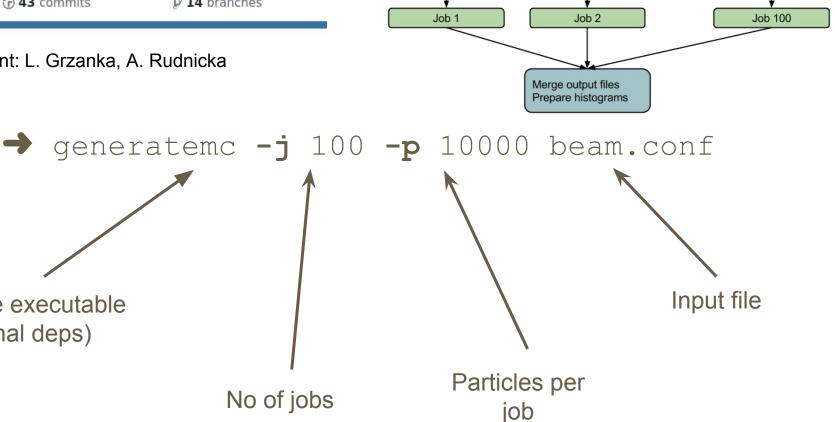
outfile = 001.dat



Development: L. Grzanka, A. Rudnicka

Single-file executable

(no external deps)



Original input card rng seed = 137

protons no = 10000 outfile= out.dat

Input card 2

rng seed = 12334

protons no = 100

outfile = 002.dat

Input card 100

rng seed = 34324

protons no = 100

outfile = 100.dat

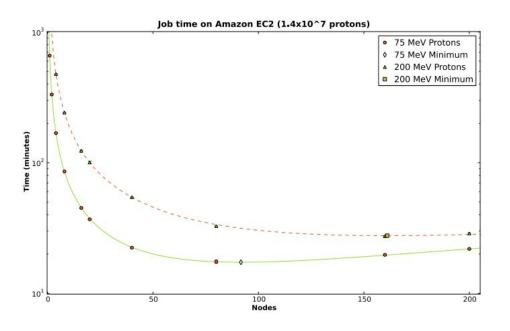
Minimizing total computing time

How to parallelize?

- 10⁶ protons on 1000 nodes, or
- 10^7 protons on 100 nodes, or
- 10^8 protons on 10 nodes?

Concept from https://arxiv.org/pdf/1009.5282.pdf

Implementation in mcpartools - in progress (P. Ociepka)



$$T(n) = \frac{\alpha p}{n} + \beta n + \gamma$$

T(n) - total computing time

n - number of nodes

p - number of particles

α - calc. time per particle

β*n - initialization and merging results time (linear)

γ - initialization time (fixed)

Figure 4. Calculation time versus number of virtual nodes for proton depth-dose curves on Amazon's EC2 cloud service. The calculation time is modelled with Eq.1.

