



Implementation and benchmarking of radiobiological models for the prediction of biological dose in hadrontherapy

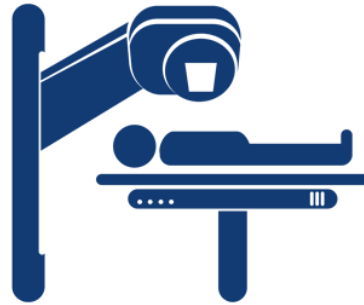
Y. Ali, L. Auzel, C. Monini, J.M. Létang, E. Testa, L. Maigne, M. Beuve.



Context

Biophysical models implementation in Gate

For hadrontherapy applications, biological dose prediction will enhance treatments optimization.



Why using an approximative RBE value for ions isn't relevant?

What would be the tools for an accurate RBE estimation?

In which ways our work contribute to this purpose?

Biophysical Models

The biophysical models requires several types of data to lead to the relative biological effectiveness

Microkinetic model

Cell survival fraction

$$S = e^{-\langle L_n \rangle}$$

Number of damages in the nucleus

$$\langle L_n \rangle = (\alpha + \beta z)D + \beta D^2$$

Inaniwa T. et al. (2010)

NanOx

Cell survival fraction

$$S = S_{local\ events} \cdot S_{non\ local\ events}$$

LOCAL EVENTS

Effective lethal function

$$F(z) = -N \ln(1-f(z))$$

NON LOCAL EVENTS

Oxidative stress

$$F(Y) = e^{(-\langle \alpha Y + \beta Y^2 \rangle)}$$

C. Monini et al. (2017)



Biological data

α, β : constants of the linear and quadratic components of cell killing



Physical data

z : specific energy deposited in a target
 N : targets distributed in sensitive volume



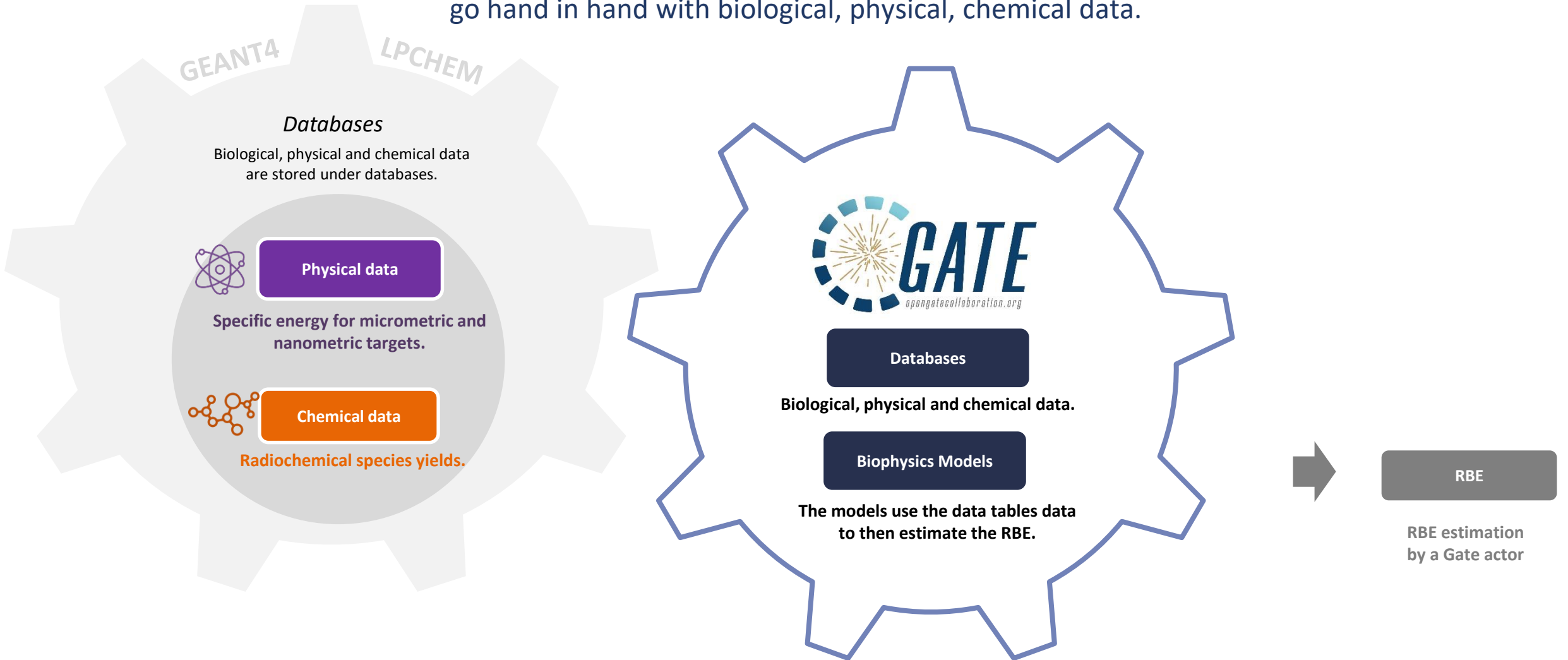
Chemical data

Y : yield of OH· the sensitive volume

Models implementation

Our methodology

To estimate the biological effectiveness, Monte Carlo simulations go hand in hand with biological, physical, chemical data.



G4DNA vs. LPCHEM

Differences between the codes

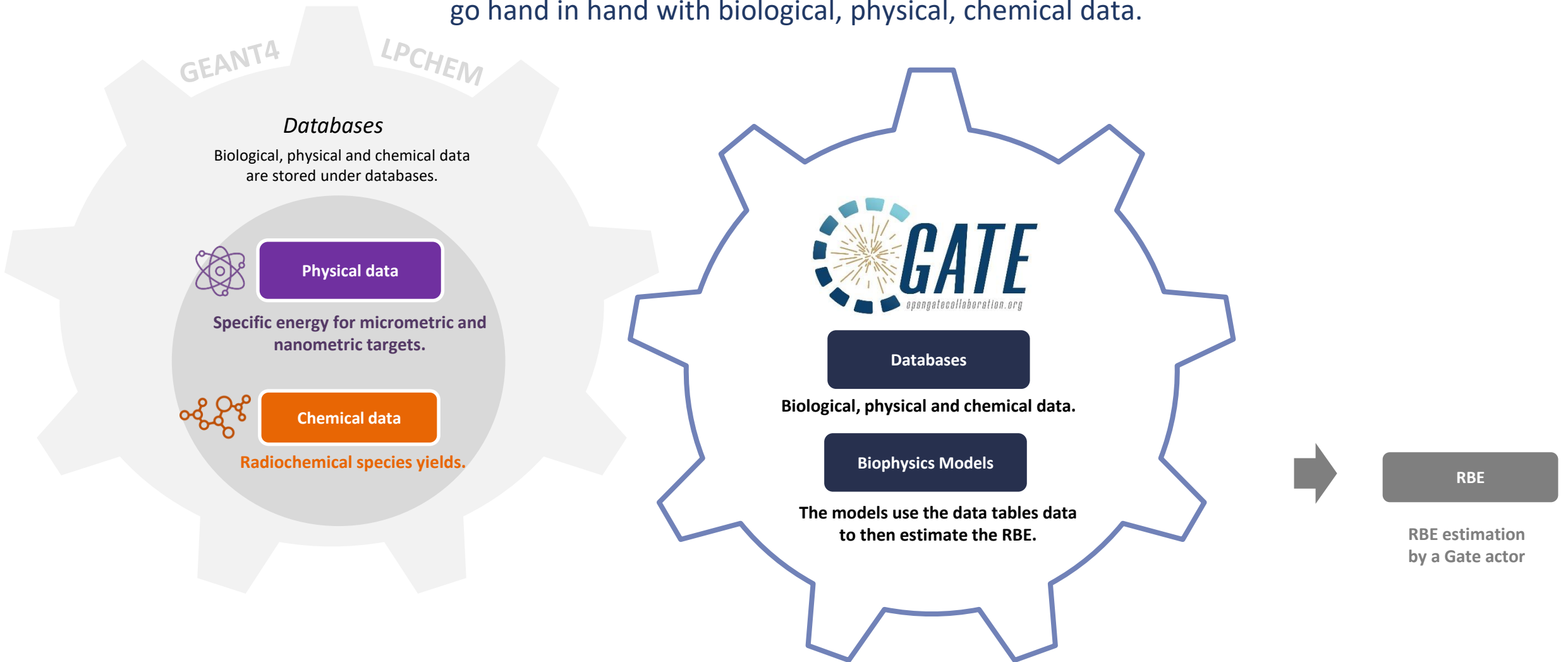
We use similar simulation parameters for both LPCHEM and GEANT4DNA, however a few differences can be noted between the codes.

	Physics Models	Simulated interactions		Stored interactions	Energies	
		Electrons	Protons		Electrons	Protons
LPCHEM 1.11	CDW-EIS calculations	Ionizations Electronic excitation Vibrational excitation Attachment	Ionization Excitation	80% of deposited energy, events relevant for the biological effect of radiation	10 keV to 100 keV	10 MeV to 250 MeV
G4DNA 10.5	G4DNA_Option 0 G4DNA_Option 2 G4DNA_Option 6	Ionizations Electronic excitation Vibrational excitation Attachment	Ionization Excitation Capture	100% of deposited energy	10 keV to 100 keV	10 MeV to 100 MeV

Models implementation

Our methodology

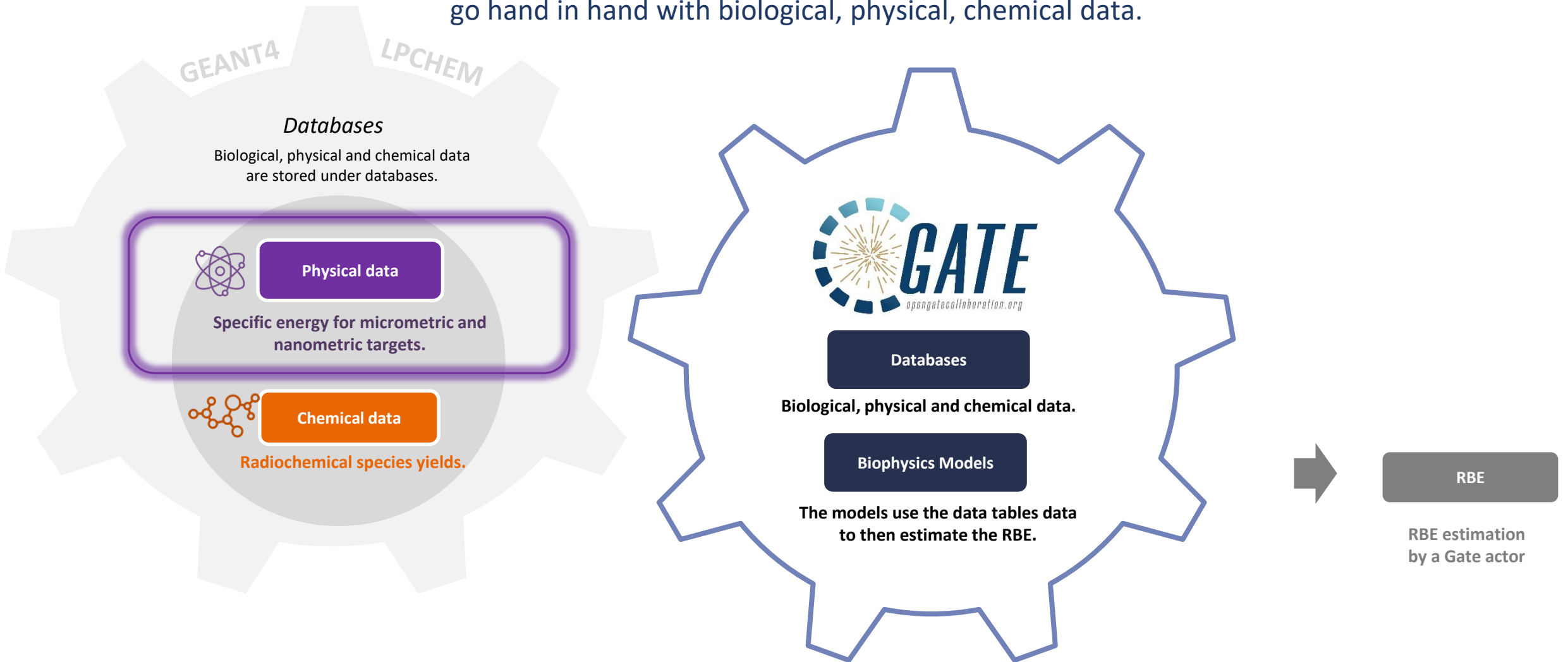
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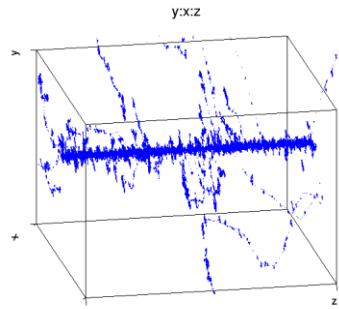


Physical data simulation

From energy transfer points to the specific energy distributions in micrometric and nanometric targets

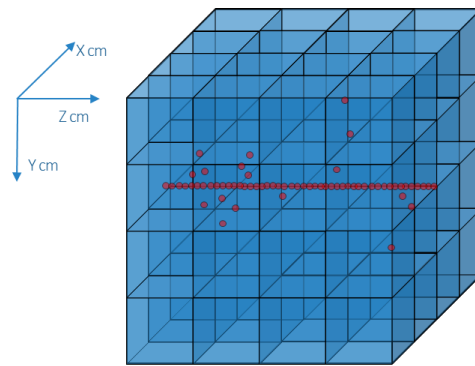
ENERGY TRANSFER POINTS

From LPCHEM or G4DNA



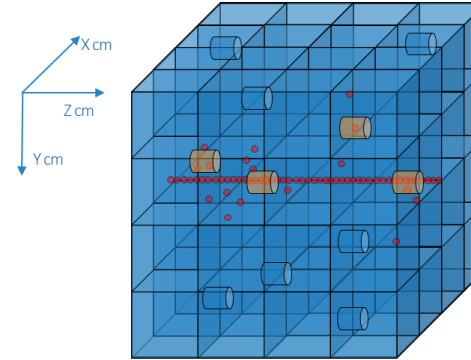
THE MESH AND 3D MATRIX

Calculation time saving biased method



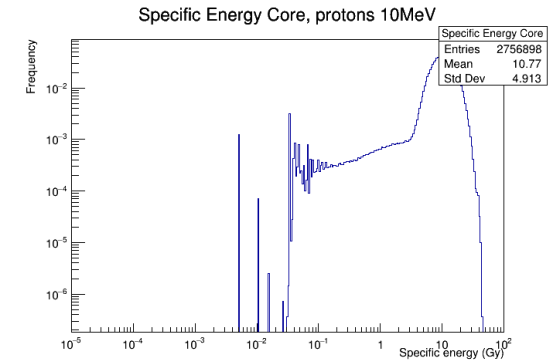
THE TARGETS

1 μ m micrometric and 10nm nanometric targets



PROBABILITY DISTRIBUTIONS

Specific energy



The LPCHEM and G4DNA physical modules simulate the energy transfer points.

The track volume is divided into voxels.

Targets are generated in the voxels containing energy transfer points.

The probability distributions of specific energy are calculated.

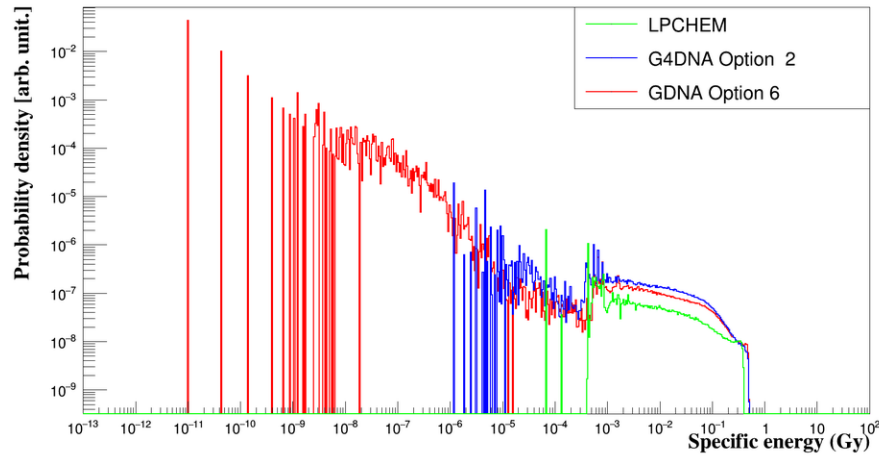
Specific energy probability distribution

for 1 μ m micrometric and 10nm nanometric targets

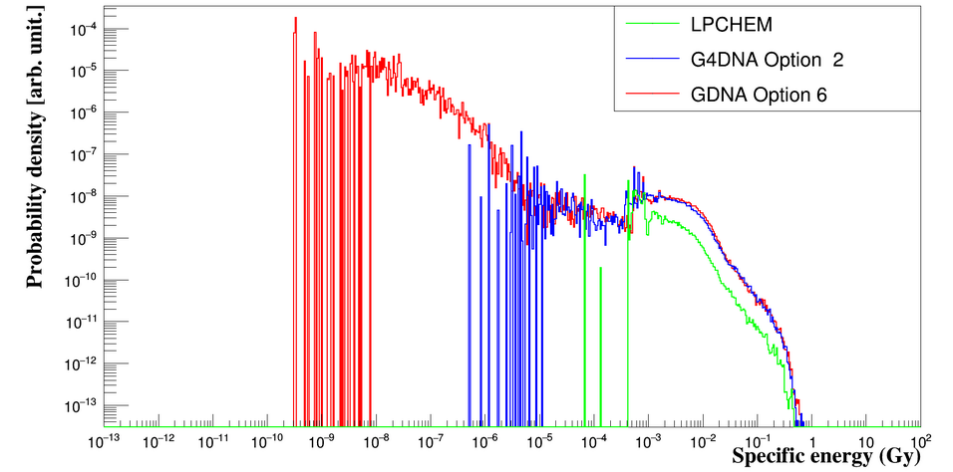
Electrons 10 keV

Electrons 100 keV

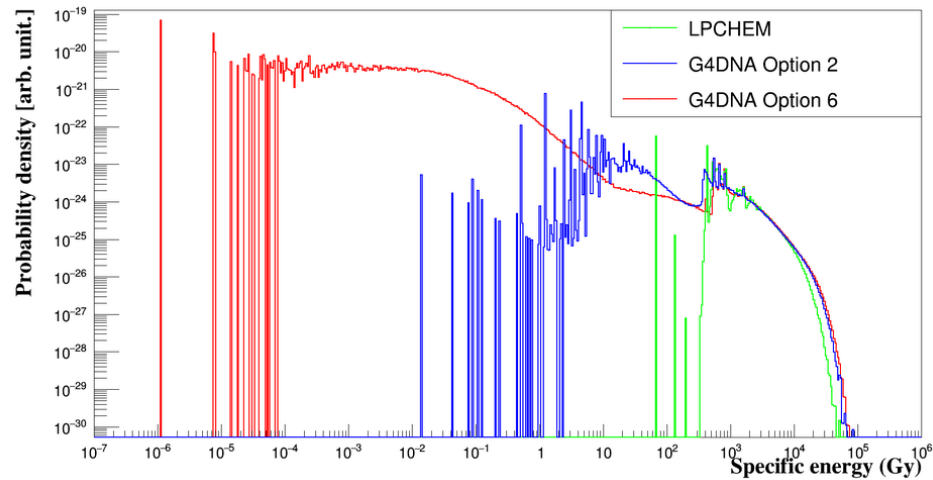
Micrometric



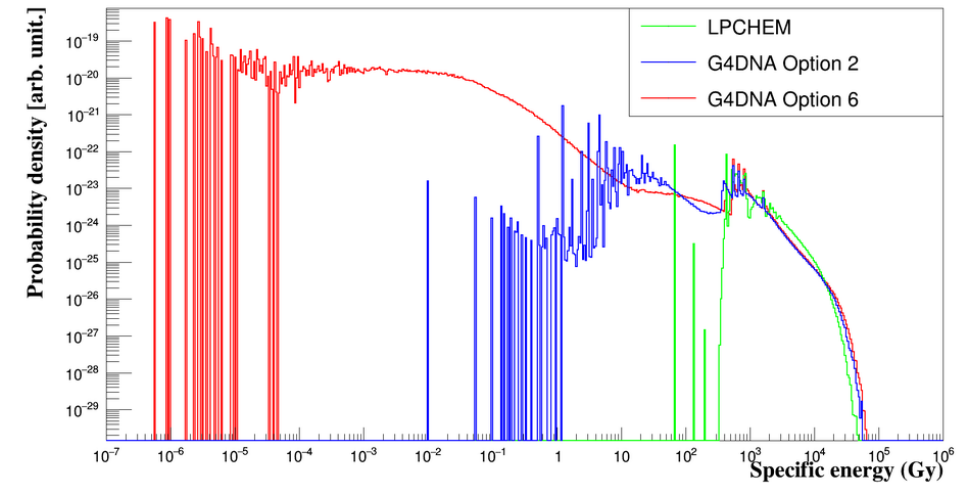
Micrometric



Nanometric



Nanometric



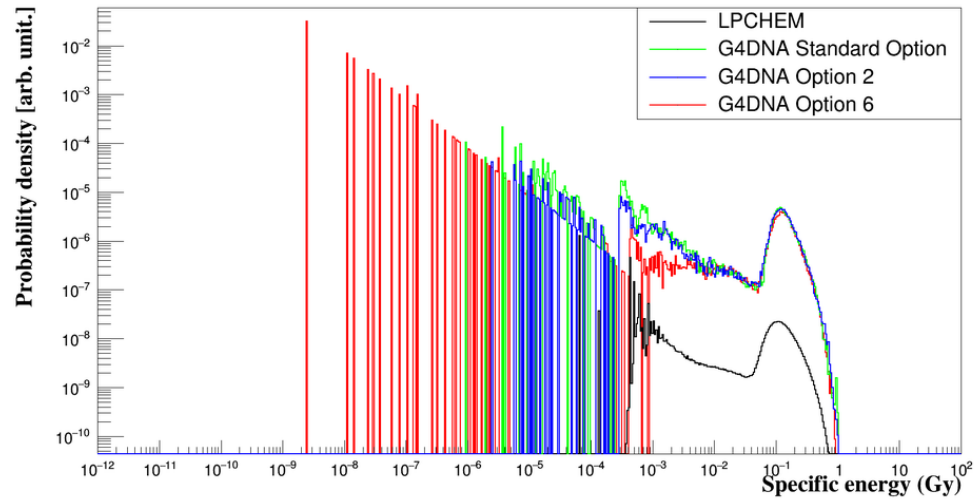
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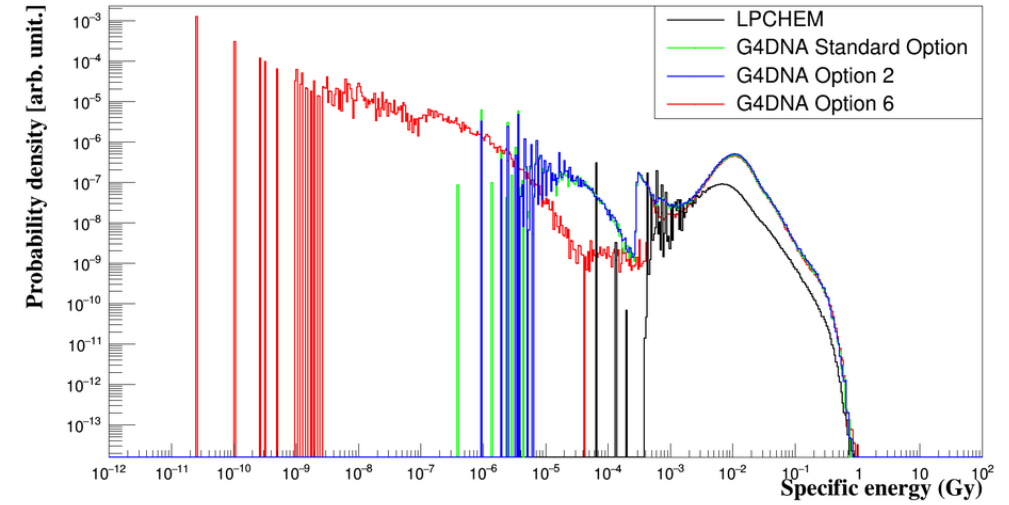
Protons 10 MeV

Protons 100 MeV

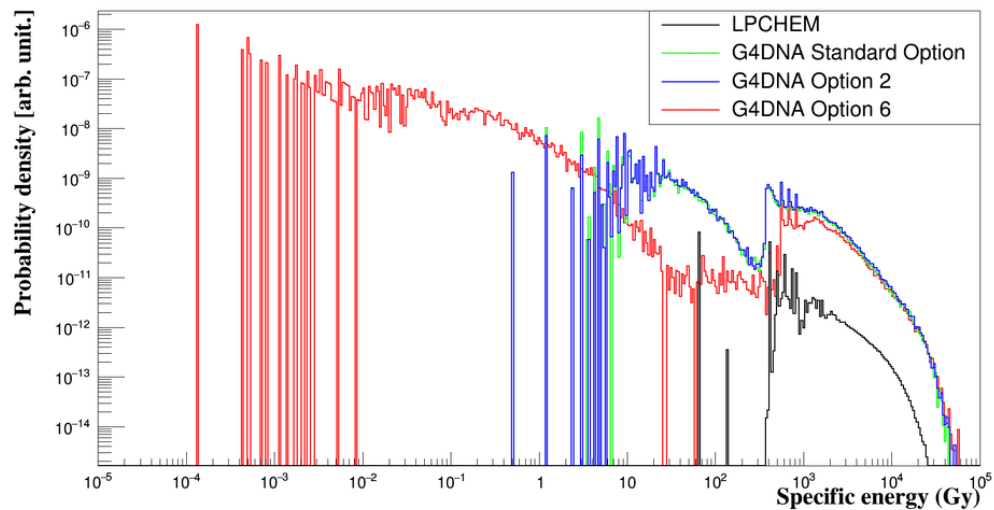
Micrometric



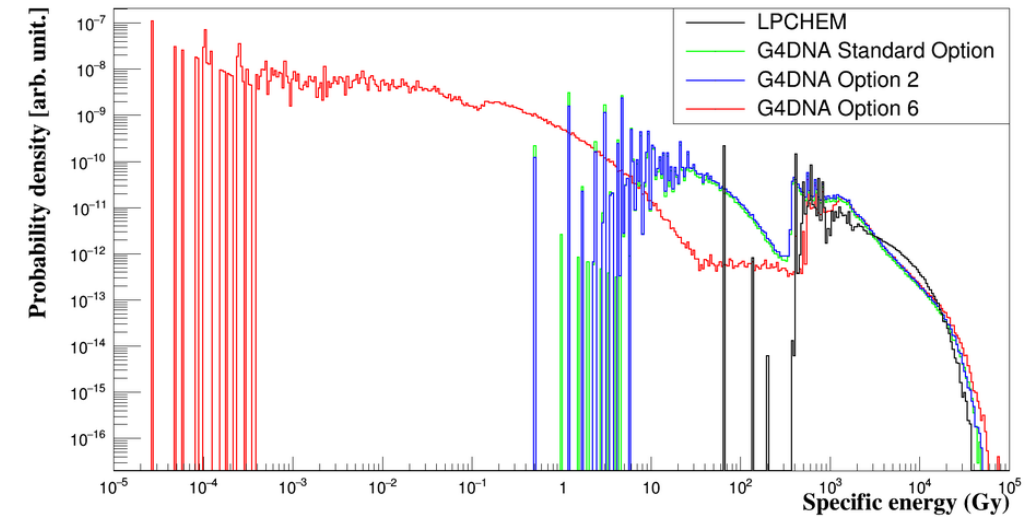
Micrometric



Nanometric



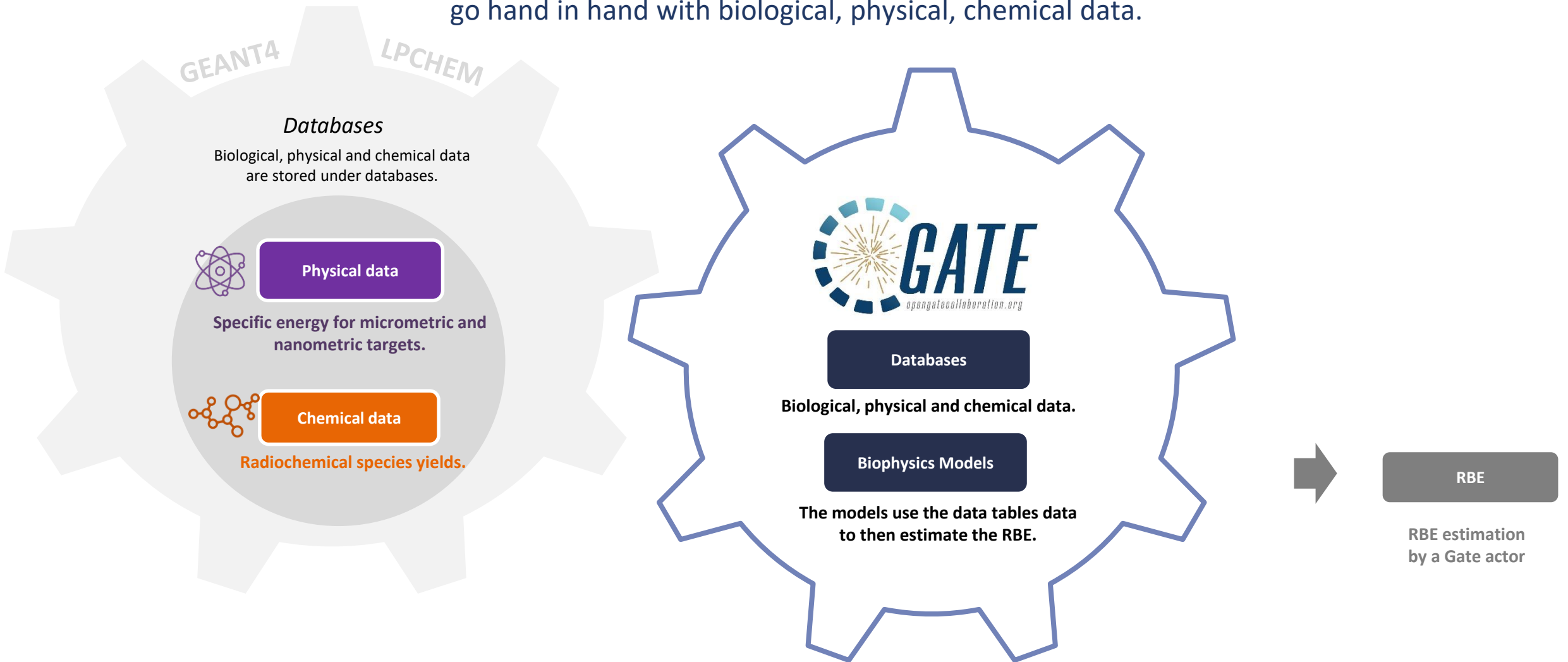
Nanometric



Models implementation

Our methodology

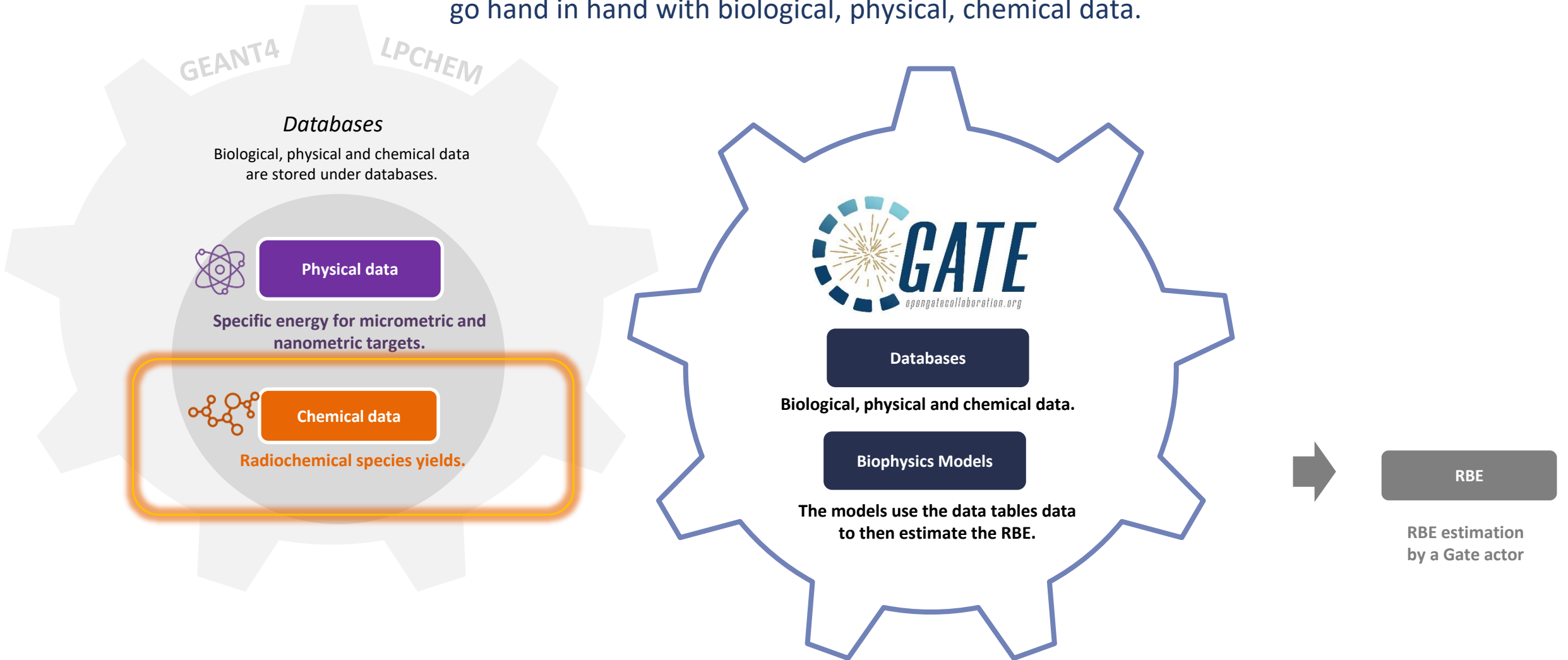
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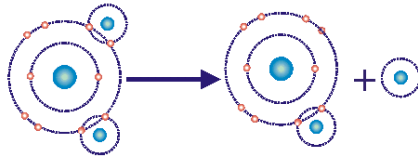


Chemical data simulation

To estimate the type, the quantity of free radicals with the chemistry modules

PHYSICOCHEMICAL STAGE

By LPCHEM and G4DNA



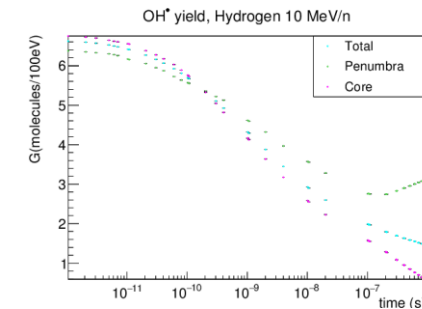
In the physicochemical stage of LPCHEM and G4DNA chemistry modules, the radiochemical products are generated.

CHEMICAL STAGE

Radiochemical products

FREE RADICAL YIELDS

OH Yield



The average yield of OH molecules between 10⁻¹² and 10⁻⁰⁶ second for a 100eV deposited energy is estimated.

G4DNA vs. LPCHEM

Differences between the codes

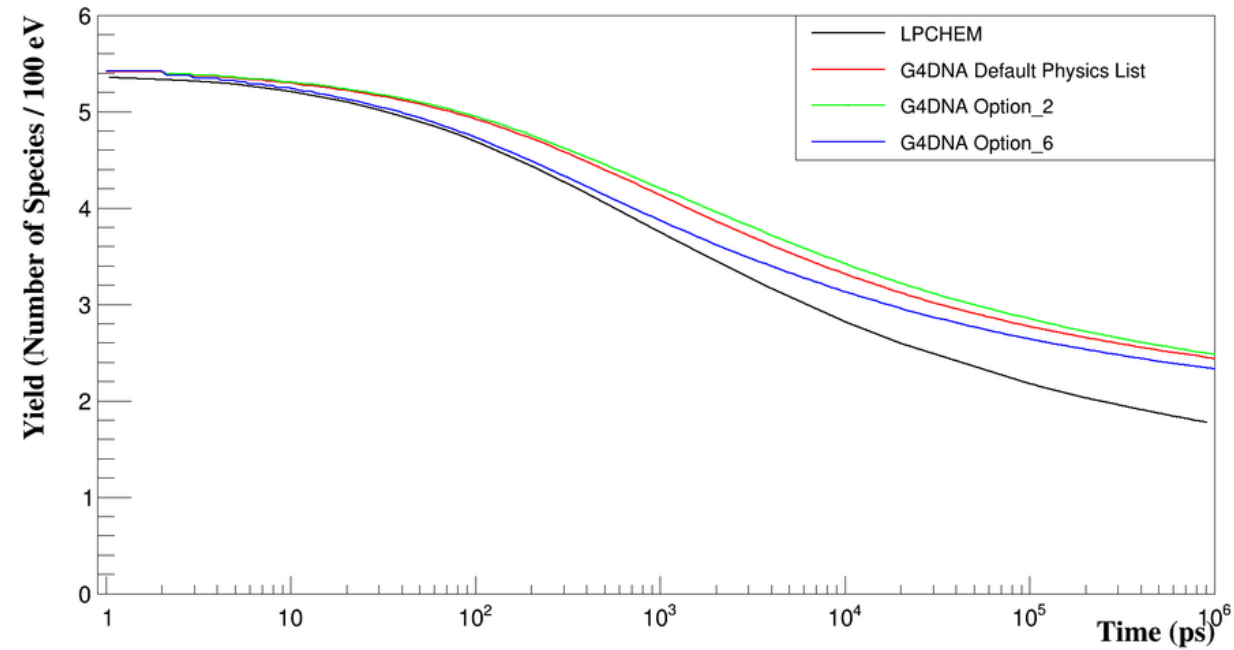
We use similar simulation parameters for both LPCHEM and GEANT4DNA, however a few differences can be noted between the codes.

	Chemical stage	Simulated interactions
LPCHEM 1.11	IRT (Independent Reaction Times)	A maximum time step is chosen, only the couples requiring less time to interact are taken into account. The brownian movement isn't simulated for time saving purposes so the position of the species between the time steps isn't considered.
G4DNA 10.5	Step by Step	The distance between the radicals as well as their probability of interaction is estimated. The brownian movement is simulated for the particles, based on the Smoluchowski equation. Unlike LPCHEM, the position of the species can be known between the time steps.

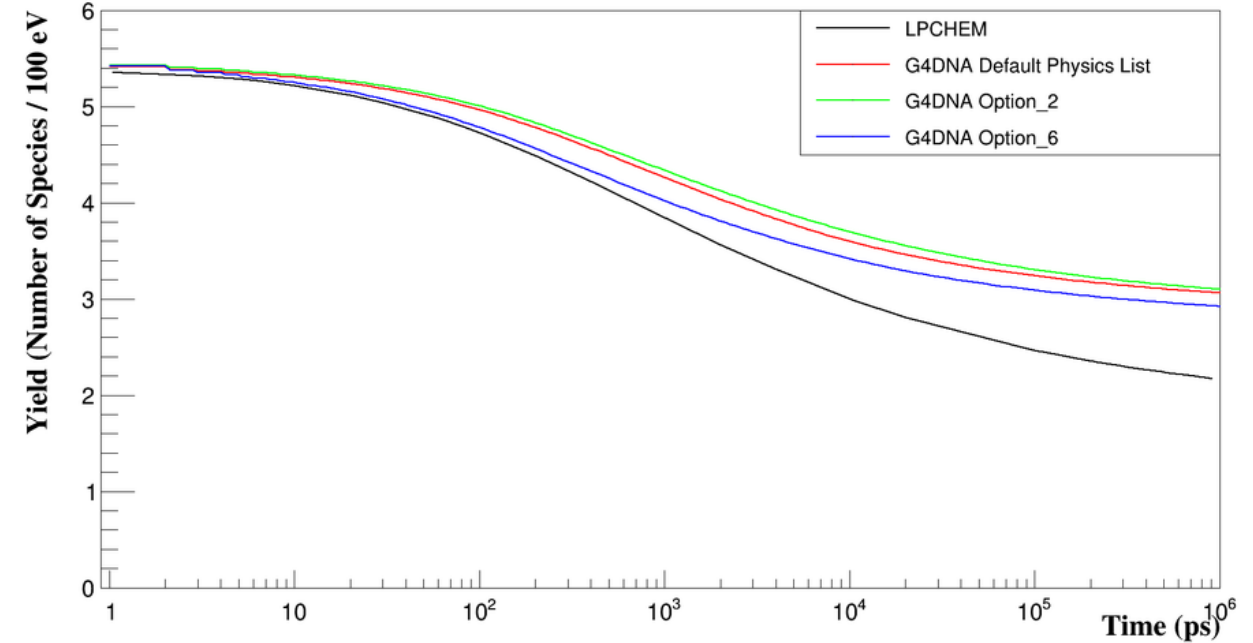
Hydroxyl radical yield

OH radical products yields for a 100 eV deposited energy

Protons 10 MeV



Protons 100 MeV

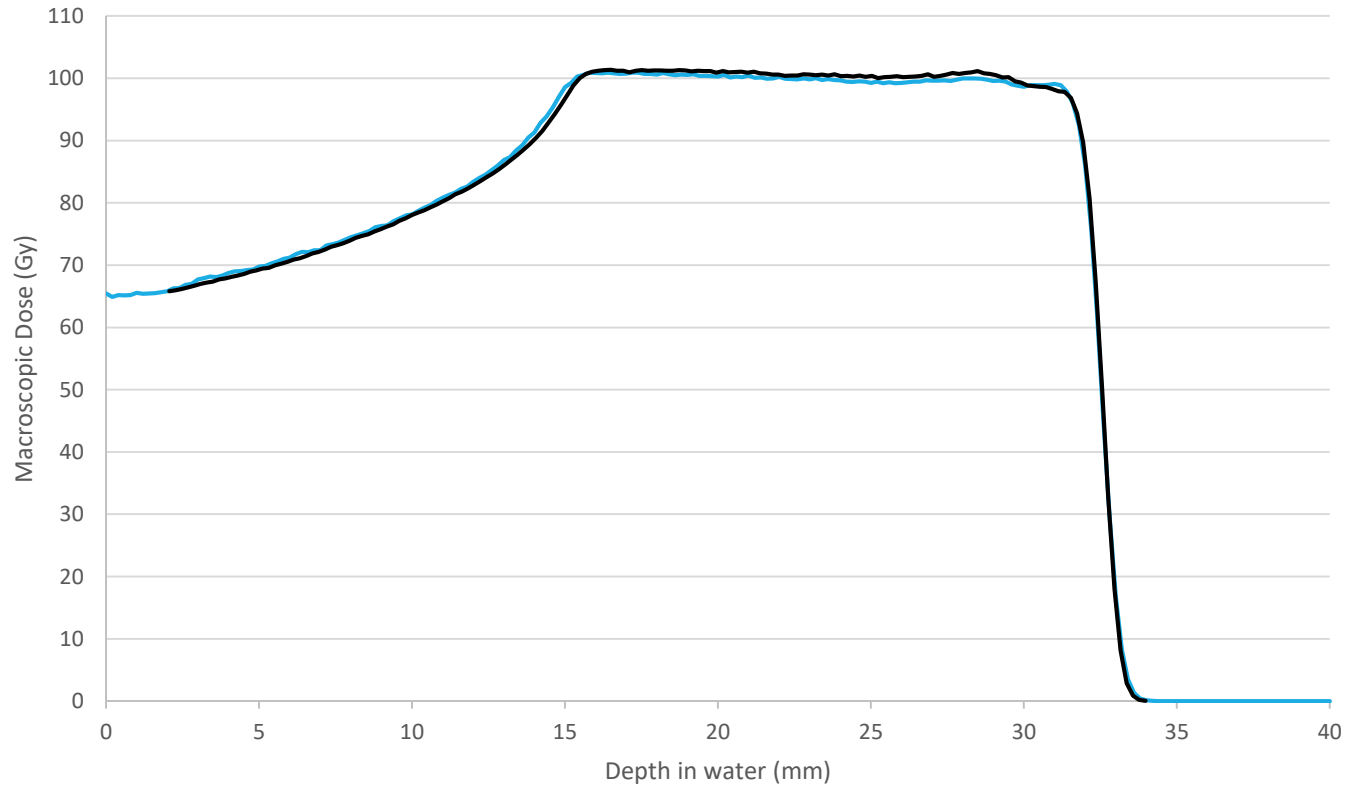


Spread out bragg peak

Our methodology

Physical and chemical data have been simulated for monoenergetic beams, the next step will be to perform the same work for a clinical beam SOBP.

Spread out bragg peak for 65 MeV protons.



— GATE 8.1 simulation (Y. Ali, 2018)
— Ionization chamber dose measurements (F. Smekens, 2017)

GATE ACTOR

The actor collects, for each voxel :

- the particles atomic number
- the deposited energy for each particle
- the proportion of each type of particles

DATA TABLES

We use data tables of biological, physical and chemical data calculated for monoenergetic beams, summed, to obtain the equivalent data for a SOBP.

Collaborations

We would like to thank



THANK YOU.
