

Development of chemistry and biodose actors in GATE 10

Alexis Pereda¹, Hermann Fuchs⁴, Dietmar Georg⁴, Jean Michel Létang², Étienne Testa³,
Michael Beuve³, Lydia Maigne¹, Geant4-DNA collaboration

¹LPCA, ²CREATIS, ³IP2I, ⁴Medical University of Vienna/MedAustron

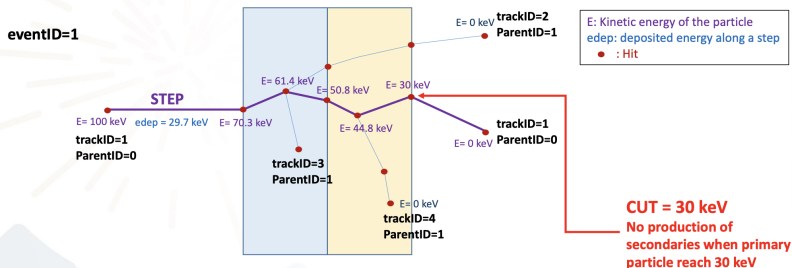
<alexis.pereda@clermont.in2p3.fr>

Laboratoire de Physique Clermont Auvergne, UCA, CNRS, France

GATE Scientific Meeting 2025

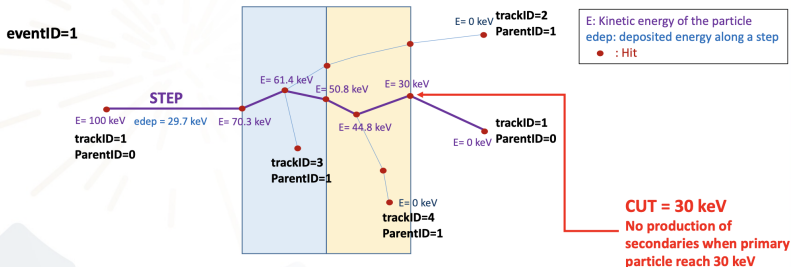
- 1 GATE
- 2 Biodose actor
- 3 Chemistry actor

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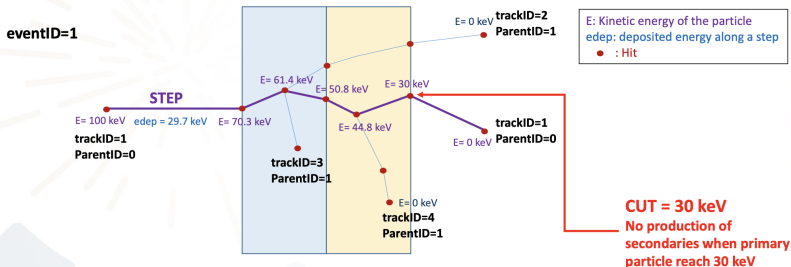
Geant4 actions

	BeginOfRun	BeginOfEvent	Stepping	EndOfEvent	EndOfRun	NewStage
compute dose	✓		✓		✓	
compute fluence	✓	✓	✓		✓	
compute biodose	✓	✓	✓	✓	✓	
apply chemistry				✓	✓	✓



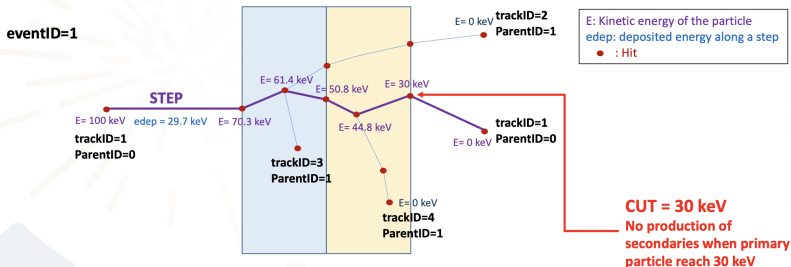
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compute biodose	✓	✓	✓	✓	✓	
apply chemistry				✓	✓	✓



Geant4 actions

	BeginOfRun	BeginOfEvent	Stepping	EndOfEvent	EndOfRun	NewStage
compute dose	✓		✓		✓	
compute fluence	✓	✓	✓		✓	
compute biodose	✓	✓	✓	✓	✓	
apply chemistry				✓	✓	✓



Geant4 actions

GATE actors ↓	BeginOfRun	BeginOfEvent	Stepping	EndOfEvent	EndOfRun	NewStage
DoseActor	✓		✓		✓	
FluenceActor	✓	✓	✓		✓	
BioDoseActor	✓	✓	✓	✓	✓	
ChemistryActor				✓	✓	✓

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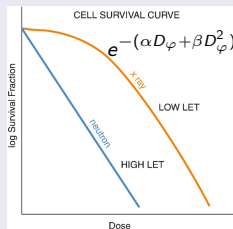
Objective of the biological dose

effects of the physical dose on biological tissues

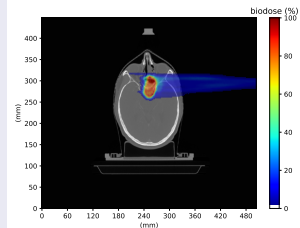
nano/micro scale

- mMKM
(Kase et al., 2006)
- NanOx
(Cunha et al., 2017)

cellular scale



macro scale



Biophysical model databases

Cell line Human Salivary Glands (HSG): HSG_mMKM.db or HSG_NanOx.db
 $\Rightarrow$ easy to provide new cell lines or biophysical models

Example:

α, β : from Geant4-DNA/LPCHEM simulations

// Ion type

H

...

He

...

C

...

O

...

Li

...

// energy

// (MeV)

alpha

(Gy⁻¹)

beta

(Gy⁻²)

H

0.1

3.528

0.059

0.125

3.584

0.022

0.15

3.642

0.098

...

1

0.932

0.059

...

10

0.376

0.063

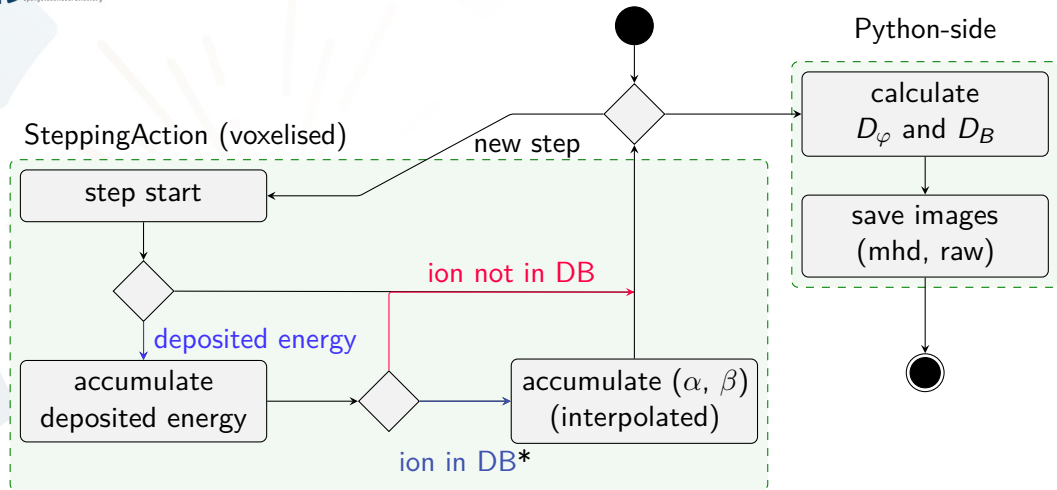
...

300

0.339

0.109

BioDoseActor process diagram



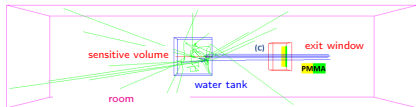
* provided databases (DB) contain values for {H, He, C, O, Li}

```
biodose = sim.add_actor("BioDoseActor", "biodose")

biodose.attached_to      = volume
biodose.output_filename  = "biodose.mhd"
biodose.translation      = [0, 0, 0]
biodose.spacing          = [1 * mm, 60 * mm, 60 * mm]
biodose.size             = [400, 1, 1]

biodose.cell_line        = "HSG"
biodose.biophysical_model = "NanOx"
biodose.alpha_ref        = 0.313
biodose.beta_ref         = 0.0615
biodose.uncertainty.active = True
```

Clinical and pre-clinical simulations

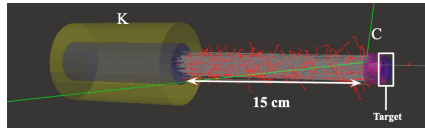


- Pencil Beam Scanning:

- H: 95.9 – 113 MeV
- C: 120 – 402 MeV/u

- PhysicsList:

- H: QGSP_BIC_EMZ
- C: Shielding_EMZ



- Pulsed beam:

- He²⁺: 67 MeV

- PhysicsList:

G4EmDNAPhysics_option2

Results – dose profiles

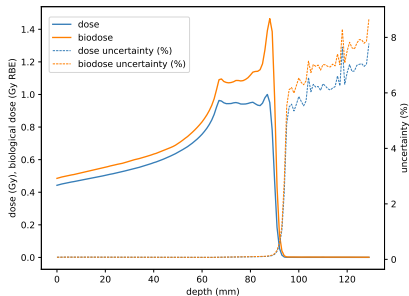


Figure: H-ion in water with 1×10^7 primaries, production cut 100 m, step limiter 10 μ m (HSG, NanOx)

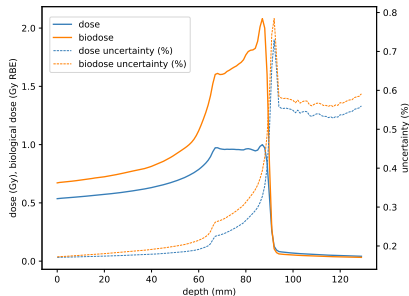
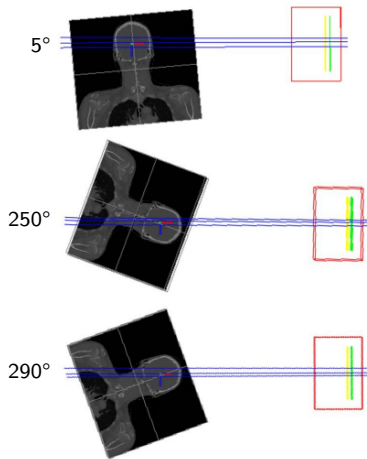


Figure: C-ion in water with 1×10^6 primaries, production cut 100 m, step limiter 10 μ m (HSG, mMKM)

C-ion clinical PBS beams in patient

- Human Salivary Glands
- Pencil Beam Scanning
- CT: $50 \times 50 \times 44 \text{ cm}^3$
- Voxel size:
 $0.97 \times 0.97 \times 2 \text{ mm}^3$
- PhysicsList:
Shielding_EMZ
- 3 beams
- sinonasal chordoma



Results – C-ion, biological dose (NanOx)

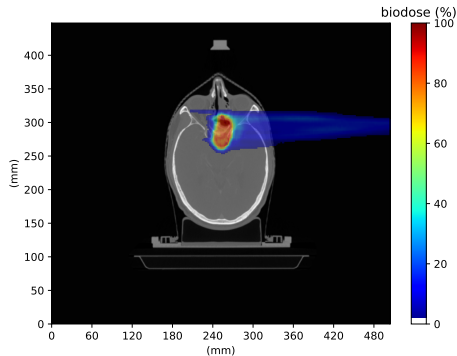


Figure: biological dose with C-ion in patient, 1×10^6 primaries per beam, production cut 100 m, step limiter $10 \mu\text{m}$ (HSG, NanOx)

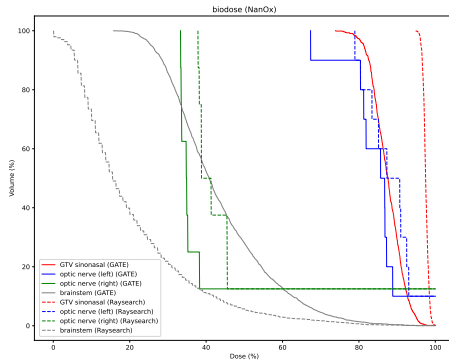


Figure: Cumulative biological DVH comparison GATE/NanOx (solid lines) and Raysearch (dashed lines)

Results – Arronax Helium SOBP (NanOx)

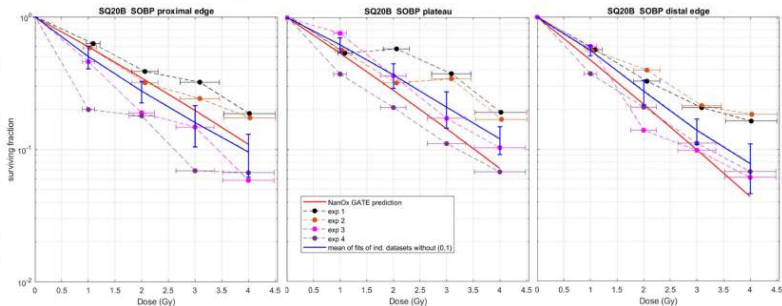
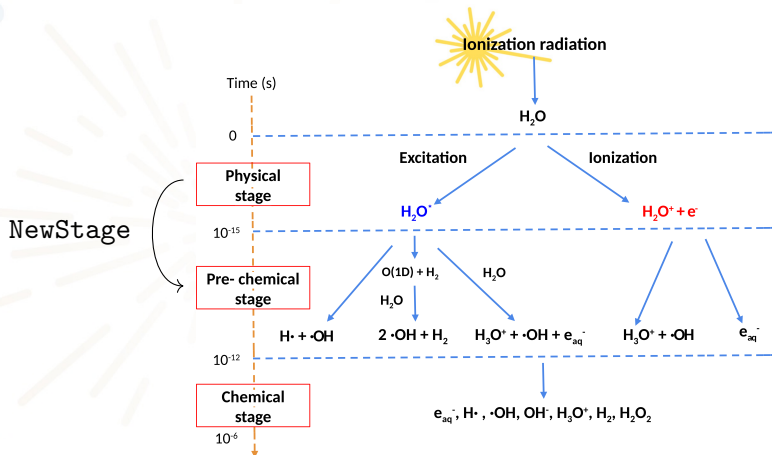


Figure: Irradiation of SQ20B (Human Squamous Cell Carcinoma) cells in a helium SOBP: comparison of measured surviving fractions with NanOx predictions for three irradiation settings (Berger et al., in preparation).

Slide content by Mario Alcocer (Berger et al.) [preliminary results]

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Geant4-DNA chemistry



Main figure from Da Eun Kwon (Ph.D. student)

Main purpose

Being able to use Geant4-DNA chemistry directly in GATE
(e.g. to study water radiolysis for FLASH therapy)

This requires:

- handling physics/chemistry lists
- triggering the chemical stage
- new user code to record chemical reactions
- (wip) being able to configure the simulation (pH, scavengers, ...)
- (wip) output handling

Chemistry lists

```
sim = gate.Simulation()  
  
# G4EmDNAPhysics, G4EmDNAPhysics_option1..8  
sim.physics_manager.physics_list_name = "G4EmDNAPhysics_option2"  
  
# G4EmDNACchemistry, G4EmDNACchemistry_option1..4  
sim.physics_manager.chemistry_list_name = "G4EmDNACchemistry_option3"
```

Chemistry actor – interface

```
chemistry = sim.add_actor("ChemistryActor", "chemistry")
chemistry.attached_to      = volume
chemistry.timestep_model   = "IRT"  # "IRT", "IRT_syn", "SBS"
chemistry.end_time         = 1 * ns
chemistry.time_bins_count  = 50
chemistry.pH               = 7
chemistry.reactions        = [
    # totally diffusion-controlled (TDC)
    [["H", "H"], ["H2"], "Fix", 0.5e10, 0],
    [["e_aq", "H"], ["H2", "OHm"], "Fix", 2.5e10, 0],
    [["e_aq", "e_aq"], ["H2", "OHm", "OHm"], "Fix", 0.636e10, 0],
    # partially diffusion-controlled (PDC)
    [["OH", "H"], ["H2O"], "Fix", 1.55e10, 1],
    # ...
]
```

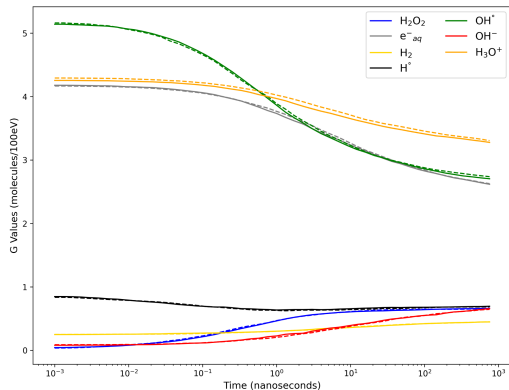
Chemistry actor – output – work in progress

```
chemistry.get_times()  
# [0.001, ..., 754.311, 999.999]  
  
chemistry.get_data_v()  # species count, G values, ...  
# {  
#   'H2O2~0': {'count': [...]}, 'g': [...]},  
#   ...,  
# }  
  
chemistry.get_reactions()  # all reactions by time  
# {  
#   0.001: [{'reactants': ['OH~-1', '°OH~0'], 'products': ['O~-1']}, ...]  
#   ...,  
# }
```

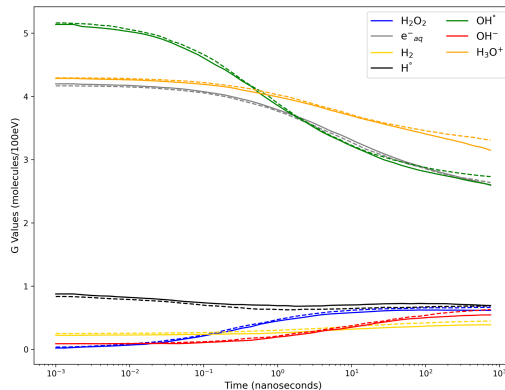
Chemistry actor – results

Geant4-DNA (chem6) dashed; GATE 10 plain

IRT (Independent Reaction Time)



SBS (Step by Step)



Simulation and analysis by Da Eun Kwon

BioDose actor

- available in current GATE release (9.4.1)
- work in progress version in GATE 10 (branch biodoseactor)
- paper in preparation

Chemistry actor

- work in progress version in GATE 10 (branch dnachemistry)
- ongoing validation for UHDR ion beam lines

Thank you for your attention