Chemistry examples

geant4-dna.org

UHDR example

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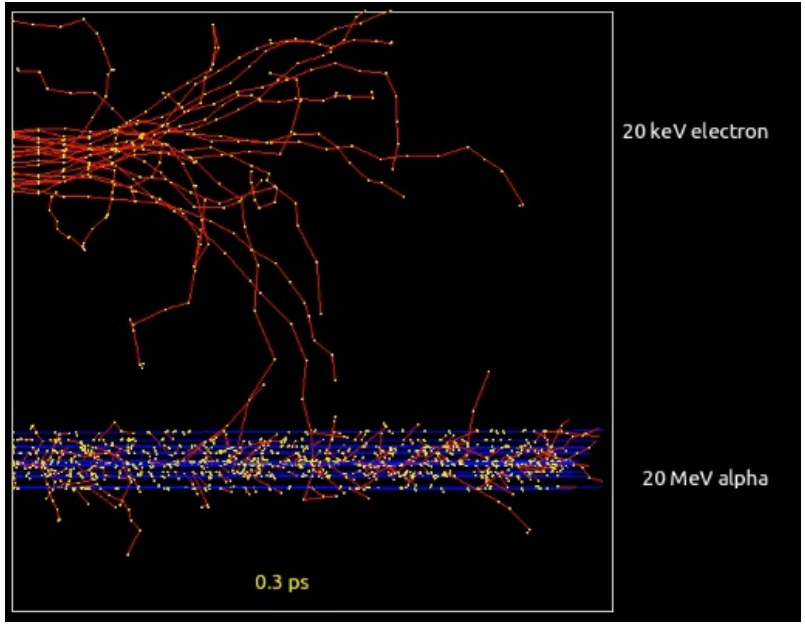
Processes in the Physical Stage

Geant4-DNA simulation



			Branching ratio (%)		
Ionization	H_2O^+	$H_3O^+ + {}^{\bullet}OH$	100	100	Ionization
Excitation	A^1B_1	$H^{\bullet} + {}^{\bullet}OH$	65	65	A1B1_DissociationDecay
		$H_2O + \Delta E$	35	35	No displacement
	B^1A_1	$H_3O^+ + {}^{\bullet}OH + e_{aq}^-$	50	55	Auto-Ionization
		$H^{\bullet} + {}^{\bullet}OH$	25.35	-	A1B1_DissociationDecay
		$H_2 + 2{}^{\bullet}OH$	3.25	15	B1A1_DissociationDecay
		$2H^{\bullet} + O(^3P)^*$	3.9	-	B1A1_DissociationDecay2
		$H_2O + \Delta E$	17.5	30	No displacement
	Rydberg A+B, C+D, Diffuse bands	$H_3O^+ + {}^{\bullet}OH + e_{aq}^-$	50	50	Auto-Ionization
		$H_2O + \Delta E$	50	50	No displacement
Electron capture	DEA	$OH^- + {}^{\bullet}OH + H_2$	100	100	Dissociative attachment
	Recombinat-ion	$H^{\bullet} + {}^{\bullet}OH$	35.75	55	A1B1_DissociationDecay
		$H_2 + 2{}^{\bullet}OH$	13.65	15	B1A1_DissociationDecay
		$2H^{\bullet} + O(^3P)$	15.6	-	B1A1_DissociationDecay2
		$H_2O + \Delta E$	35	30	No displacement

W.-G. Shin, et al., Phys. Med. (2021)

Processes in the Chemical Stage

Chemical Species: DIFFUSION

Species	Diffusion coefficient D (10^{-9} m^2 s^{-1})
H_3O^+	9.0
H•	7.0
OH^-	5.0
e^-_{aq}	4.9
H_2	5.0
•OH	2.8
H_2O_2	1.4

REACTIONS

REACTION BUILDERS

Reaction lists are collected by builders for specific applications.

ChemNO2_NO3ScavengerBuilder

→ build reaction list with NO2-/NO3-

ChemPureWaterBuilder

→ build the reaction list with pH

ChemOxygenWaterBuilder

→ build the reaction list with ROS.

ChemFrickeReactionBuilder

→ build the reaction list of Fricke Dosimeter

Water Molecules:

→ Electron Hole Recombination

→ Water Dissociation

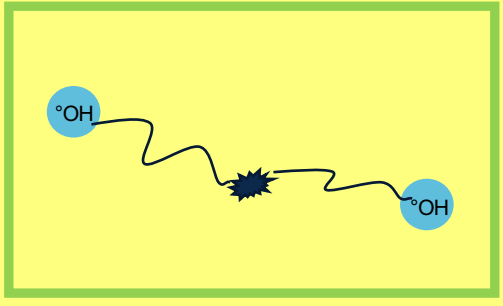
Chemistry Models

SBS model

At each step (bigger than a Minimum Time Step) the separation distance "d" of all pairs of reactants is checked.

Two species react with each other when d is below a given threshold "R", called reaction radius.

The Brownian bridge technique compensate for possible missed reactions.



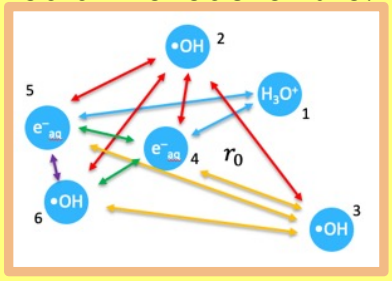
Karamitros, M. et al. (**2014**) Diffusion-controlled reactions modeling in Geant4-DNA. Journal of Computational Physics, 274, 841-882. https://doi.org/10.1016/j.jcp.2014.06.011

IRT model

An event table is constructed with the initial chemical species positions and reaction times (calculated with probability functions) for each reactant pair of interest.

Table's entries are sorted in ascending reaction time order and then processed.

Reaction product positions are randomly sampled within a sphere centred at the reaction site.



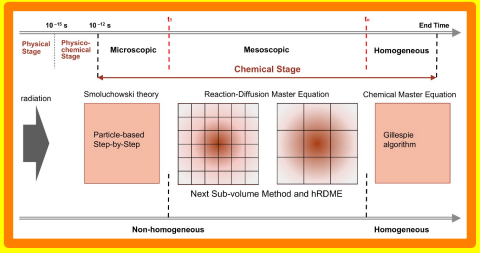
Karamitros, M. et al. (**2020**) Implementing the Independent Reaction Time method in Geant4 for radiation chemistry simulations. https://doi.org/10.48550/arXiv.2006.14225

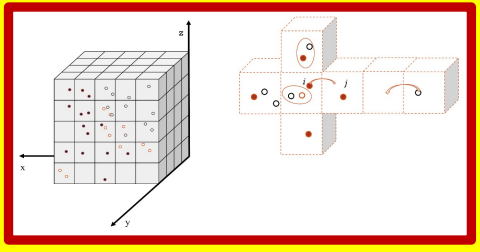
Ramos-Méndez, J. et al. (**2020**) Independent reaction times method in Geant4-DNA: Implementation and performance. https://doi.org/10.1002/mp.14490

SBS-RDME model

Combination of:

- SBS model
- Compartment-based model using RDME (Reaction-Diffusion Master Equation)





Tran, H. N. et al. (**2021**) Geant4-DNA Modeling of Water Radiolysis beyond the Microsecond: An On-Lattice Stochastic Approach. International Journal of Molecular Sciences, 22(11), 6023. https://doi.org/10.3390/ijms22116023

The Chemistry Examples

example/extended/medical/dna

- The « chem1 » example illustrates how to activate the simulation of water radiolysis (step-by-step method).
- The « chem2 » example illustrates how to set minimum time step limits on water radiolysis (step-by-step method).
- The « chem3 » example illustrates how to implement user actions in the chemistry module (step-by-step method).
- The « chem4 » example illustrates how to compute radiochemical yields ("G") versus time, including a dedicated ROOT graphical interface (step-by-step method).
- The « chem5 » example illustrates how to compute radiochemical yields ("G")versus time, using alternative physics and chemistry lists (step-by-step method).
- The « chem6 » example illustrates how to compute radiochemical yields ("G")versus time and LET using IRT method.
- The « scavenger » example illustrates how to simulate scavenging using an easy-to-use interface and the IRT method.
- The « UHDR » extended/medical/dna example illustrates how to activate the chemistry mesoscopic model in combination with the step-by-step model, and allows to simulate chemical reactions beyond 1 us post-irradiation.

UHDR example

AUTHOR: Hoang N. Tran

UHDR Example

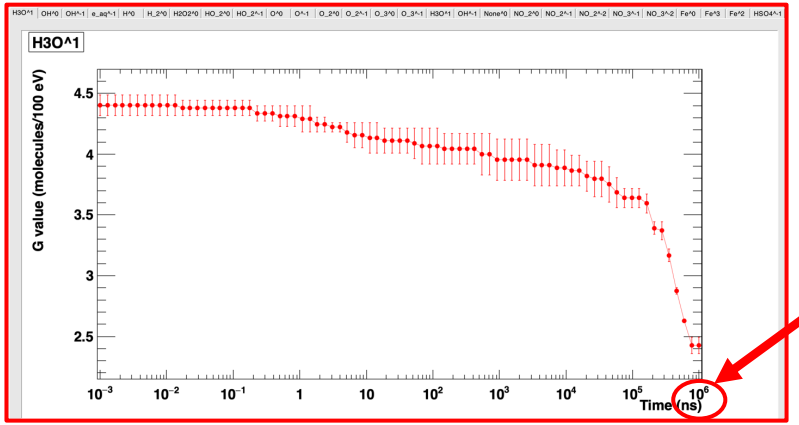
Tran, H. N. et al. (**2021**) Geant4-DNA Modeling of Water Radiolysis beyond the Microsecond: An On-Lattice Stochastic Approach. International Journal of Molecular Sciences, 22(11), 6023. https://doi.org/10.3390/ijms22116023

- ✅ The world is a water box with two possible optimized dimensions
- ✅ The example implements the mesoscopic approach (SBS-RDME)
- ✅ Chemical reactions implemented by builders for specific applications)
- ✅ Scavenger molecules
- ✅ Chemical evolution vs. ph
- ✅ Each event consists of multiple incident particles

As chem6 provides scoring of the radiochemical yield G:

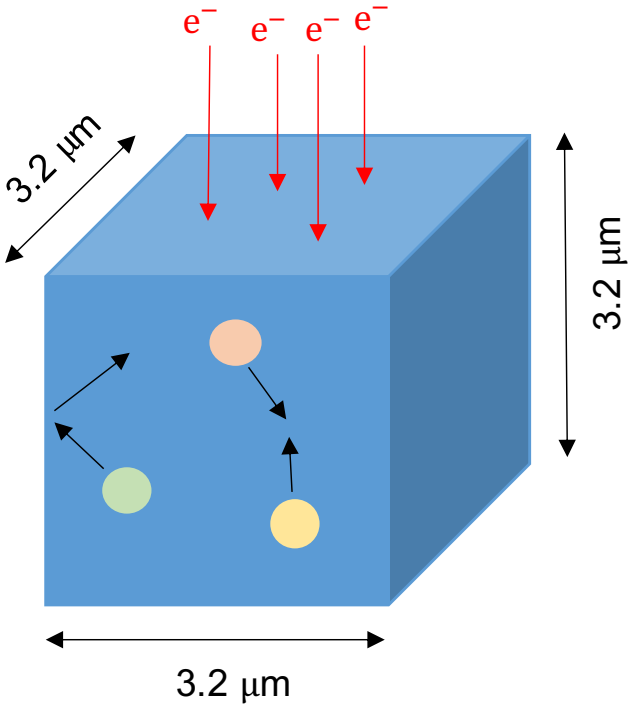
$$G = \frac{\text{Number of species X}}{\text{100 eV of deposited energy}}$$

as a function of time.



Geometry

- Two cubic water volumes of 3.2 x 3.2 x 3.2 μm^3 and 1.6 x 1.6 x 1.6 μm^3 are used for CONV and UHDR simulations respectively
- Chemical molecules diffuse and react in a bound volume that is, the diffusion is limited by geometrical boundaries.
- The bouncing of chemical molecules on the volume border is applied for both microscopic and mesoscopic sub-stages, depicting a closed system of test cells for in vitro measurements

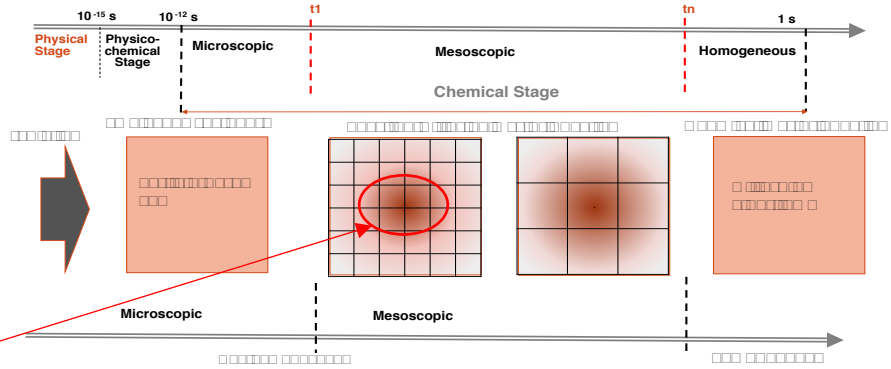


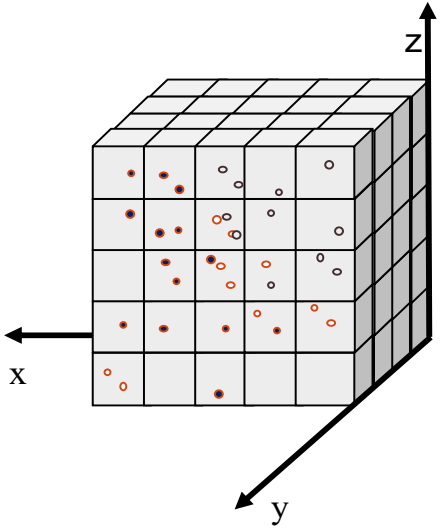

```
# Set the simulation volume (half Side Length)
#/UHDR/env/volume 0.8 um # for UHDR
/UHDR/env/volume 1.6 um # for CONV
```

The Mesoscopic approach

Tran et al., Int. J. Mol. Sci. (2021) 22
https://doi.org/10.3390/ijms22116023

- Coarse-grained model: compartment based ("on-lattice")
- Simulation from heterogeneous to homogeneous states
- pH-dependence of $HO_2^{\bullet}$ / $O_2^{\bullet-}$ kinetics in water
- Developed in Geant4-DNA by the MAGIC Collaboration (CHUV, Switzerland & CNRS/LP2i, France)

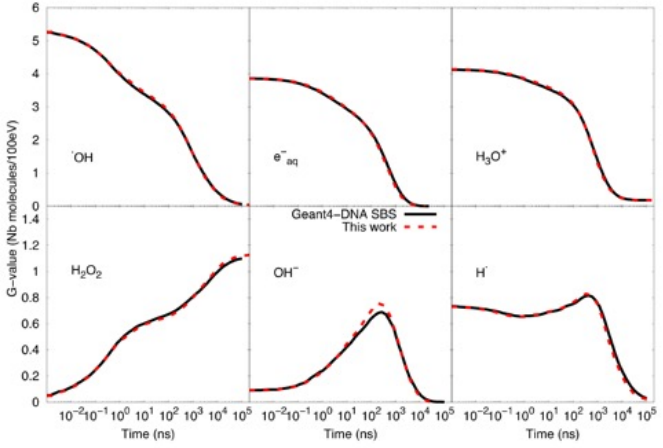




1. ***Well mixed species in voxels***
2. ***Species can react with each other in the voxels***
3. ***Diffusion is modelled by jumps between adjacent voxels***

- Next sub-volume algorithm
- Hierarchical algorithm for the RDME ("hRDME")
- Spatial distributions are simulated at voxel level.
- Coarser meshes over time until we reached the coarsest mesh → 1single voxel.

Principle of the combination of the particle-based SBS model with the compartment-based model



Chemistry Builders

Chemical reactions can be grouped by different chemistry builders. Depend on user application, these builder can be used. UHDR provides 5 default builders.

- ChemPureWaterBuilder::WaterScavengerReaction to simulate acid-base reactions associated with pH
- ChemOxygenWaterBuilder::OxygenScavengerReaction to simulate the reactions with oxygen.
- ChemOxygenWaterBuilder:: SecondOrderReactionExtended to simulate secondary reaction
- ChemNO2_NO3ScavengerBuilder::NO2_NO3ScavengerReaction to simulate NO2+/NO3+
- ChemFrickeReactionBuilder::FrickeDosimeterReaction to simulate Fricke dosimeter

Scavenger: Dissolved Oxygen in Water

Modelling oxygen as a continuum

- Homogeneous distribution of oxygen:
  - Scavengers are added in the chemistry stage,;
  - They have no effect on the physical stage.
- Variation of $[O_2]$ over time

$$\frac{dX}{dt} = -k\,[O_2]\,X$$

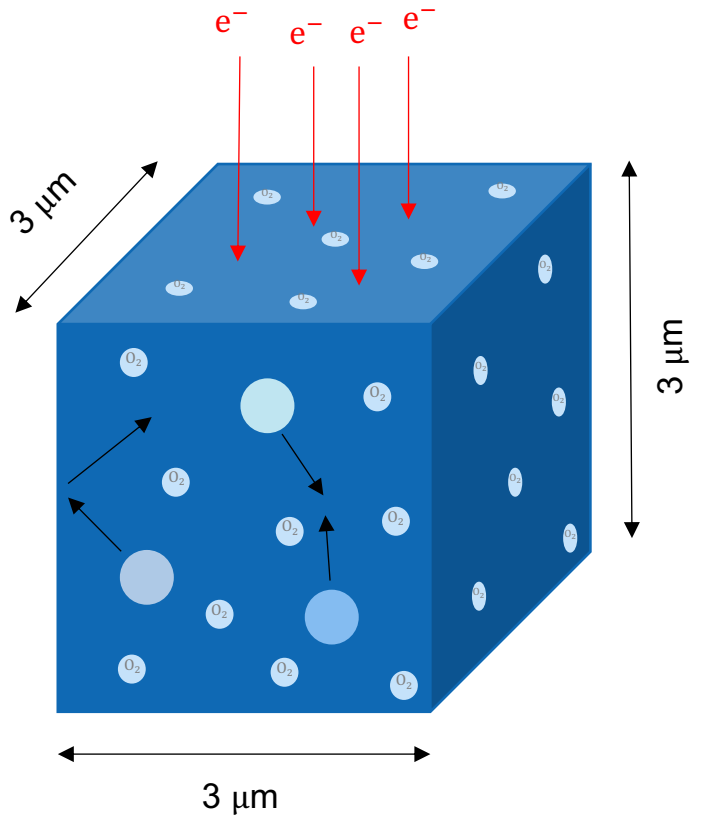
X = concentration of species X [M]

k = reaction rate $[M^{-1}s^{-1}]$

$[O_2]$ = concentration of oxygen [M]

- Partially oxygenated water is converted to concentration

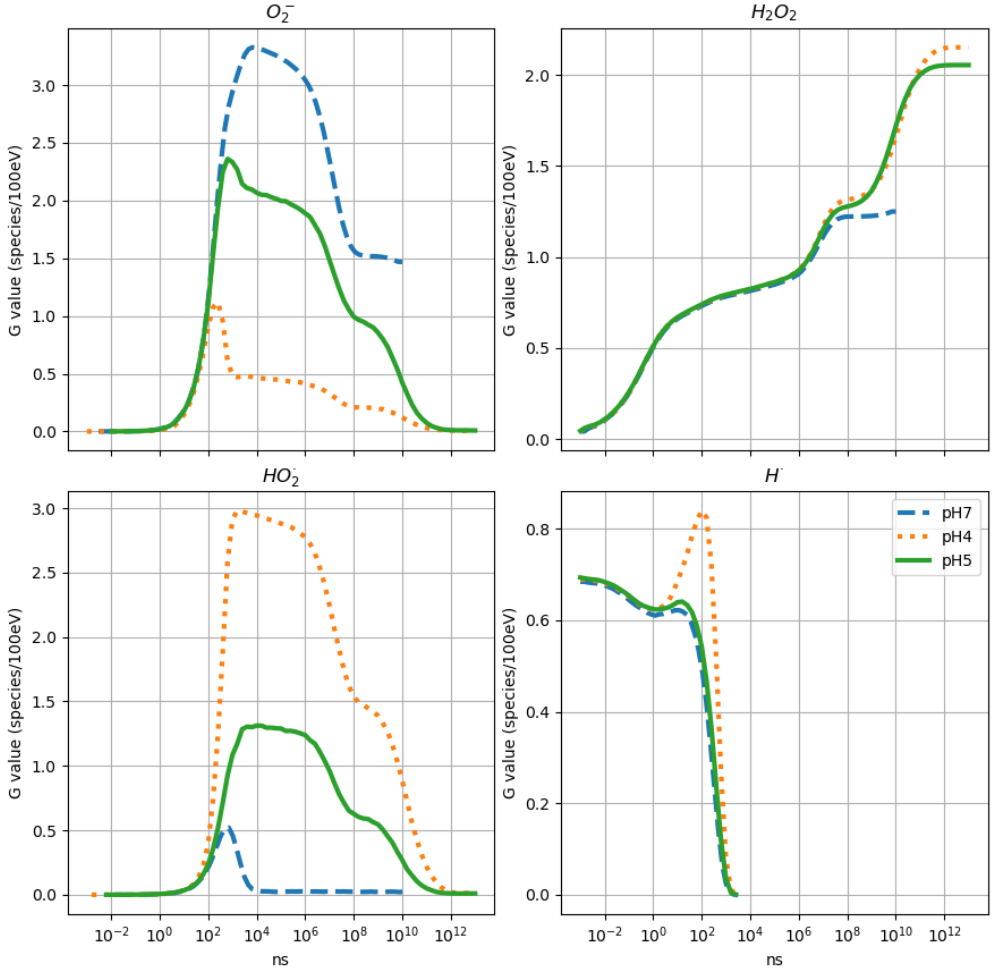
```
# Oxygen concentration
/UHDR/env/scavenger O2 19 %
```



pH simulation

#	Equilibrium	pKa
1	$2H_2O \leftrightarrow OH^- + H_3O^+$	13.999
2	$H_2O_2 + H_2O \leftrightarrow HO_2^- + H_3O^+$	11.65
3	$^{\bullet}OH + H_2O \leftrightarrow O^- + H_3O^+$	11.9
4	$HO_2 + H_2O \leftrightarrow O_2^- + H_3O^+$	4.57
5	$H + H_2O \leftrightarrow e^-_{aq} + H_3O^+$	9.77

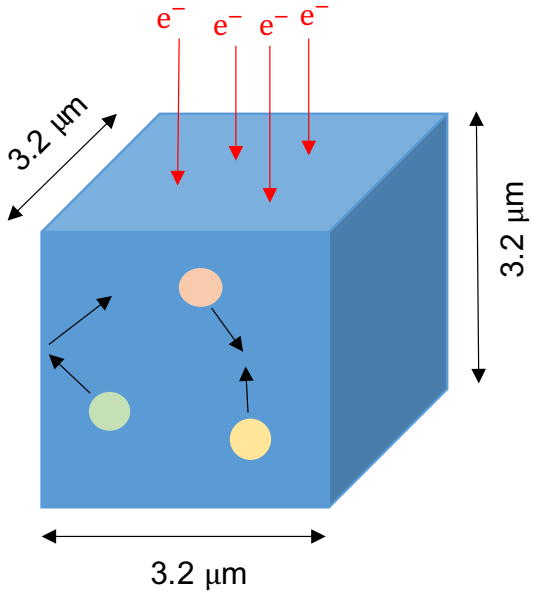
- The products of primary and secondary reactions can participate in equilibrium reactions which are associated with pKa (see the table)
- Based on the H3O+ and OH- ion concentrations determined by the pH, acid-base reactions associated with these pKa are simulated



Particle Source

Modelling of ultra-high dose rate (UHDR) electron beams

- Default source: 1 MeV electron beam
- Instantaneous pulse:
  - Each event consists of multiple incident particles shot at the same time.
  - All species are produced simultaneously at 1 ps.
  - **Pulse duration is not considered**.
- Cut-off dose: Primary particles are shoot until the sum of all energy deposits in the volume reaches a given absorbed dose:
  - 0.01 Gy is considered for conventional irradiation
  - 1-10 Gy is considered for UHDR irradiation



Modalities	Volume (µm³)	Dose rates (Gy/pulse)	Incident electrons (tracks)	deposit energy (keV)
CONV	3.2 x 3.2 x 3.2	0.0109812	6	2.246
UHDR	1.6 x 1.6 x 1.6	1.00273	110	25.637
		5.01636	562	128.254
		10.0076	1063	255.866

User interface: beam.in macro

UHDR example provides user interface to control the simulation:

- Irradiated geometries
- pH control
- Oxygen concentration
- Cut-off dose

```
#/run/numberOfThreads 10
/process/dna/e-SolvationSubType Meesungnoen2002
#/process/dna/e-SolvationSubType Ritchie1994
#/process/dna/e-SolvationSubType Terrisol1990

# Set the simulation volume (half Side Length)
#/UHDR/env/volume 0.8 um # for UHDR
/UHDR/env/volume 1.6 um # for CONV

/run/initialize

# time structure (not available)
#/UHDR/pulse/activate true

# pH and Scavenger
/UHDR/env/pH 5.5

# Oxygen concentration
/UHDR/env/scavenger O2 19 %

/chem/reaction/print

#/run/verbose 1
/tracking/verbose 0
/scheduler/verbose 0
/scheduler/endTime 1 ms

# set false if many beamOn in medium
/scheduler/ResetScavengerForEachBeamOn true

/scorer/Gvalues/nOfTimeBins 80

/run/printProgress 10

/scorer/Dose/cutoff 0.01 Gy
/UHDR/source/particle e-
/UHDR/source/energy 0.999 MeV
/run/beamOn 2
```

Irradiated geometries

pH control

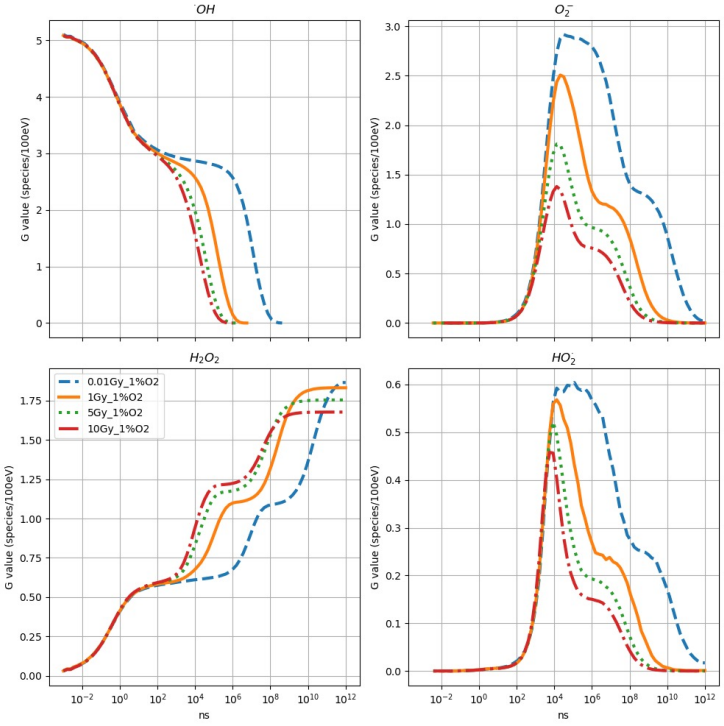
oxygen control

Cut-off Dose

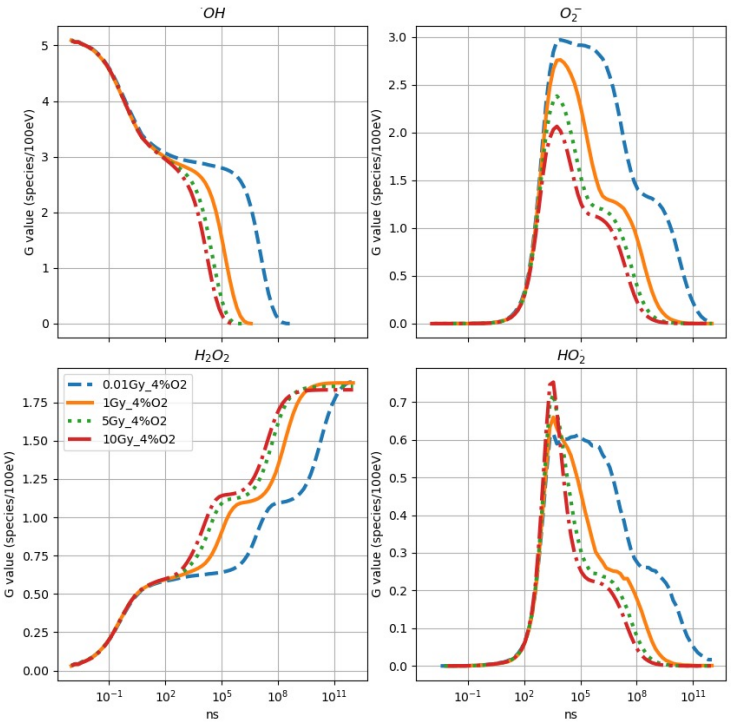
Some Simulations Outputs

Modelling of ultra-high dose rate (UHDR) electron beams 1 MeV

1% O2



4% O2



More Information

Welcome to the web page of the Geant4-DNA project !

The Geant4 general purpose particle-matter Monte Carlo simulation toolkit is being extended with processes for the **modeling of biological damage induced by ionising radiation at the DNA scale**. Such developments are on-going in the framework of the Geant4-DNA project. This project was originally initiated by the European Space Agency (ESA). Developments are undertaken by an international collaboration, coordinated since 2008 by the National Institute of Nuclear and Particle Physics (IN2P3) of the National Centre for Scientific Research (CNRS) in France, in collaboration with the Geant4@IN2P3 activities.

Once published, all developments are freely accessible in **full open access** through the Geant4 toolkit or through our freely accessible Geant4 Virtual Machine.

Recent posts

June 27th, 2023 : **Geant4 11.1.2** LP2i Virtual Machine has been released, see link.