Overview of the Geant4-DNA Project

geant4-dna.org

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Geant4-DNA tutorial
Pohang Accelerator Laboratory, Republic of Korea
07/02/2025

Geant4 version 11.3
Released in December 2024

Contents of this talk

- Context of the Geant4-DNA project
- Physical stage
- Physico-chemical & chemical stage
- Geometrical models
- DNA damage and biological models
- Tips

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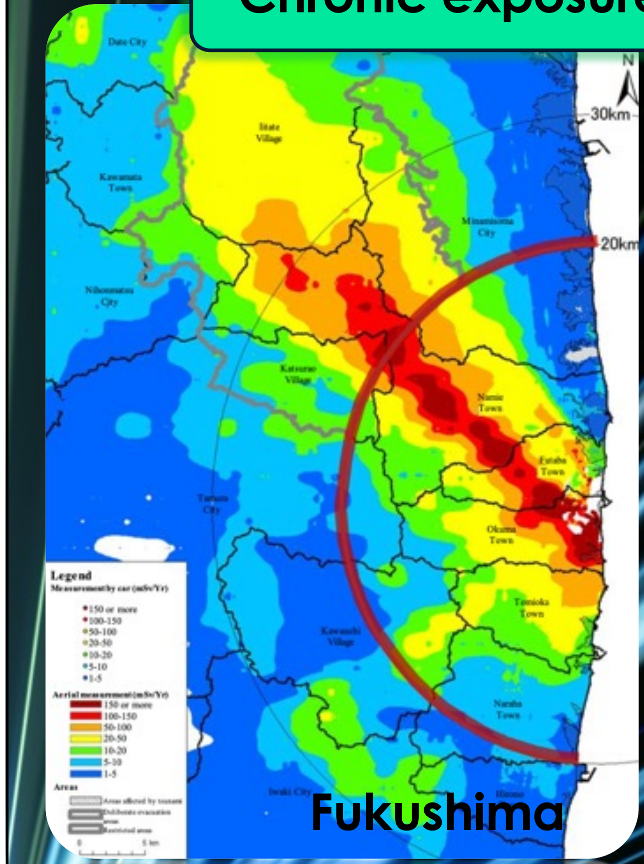
Modeling biological effects of ionising radiation remains a major scientific challenge

Chronic exposure



IAEA

Diagnosis

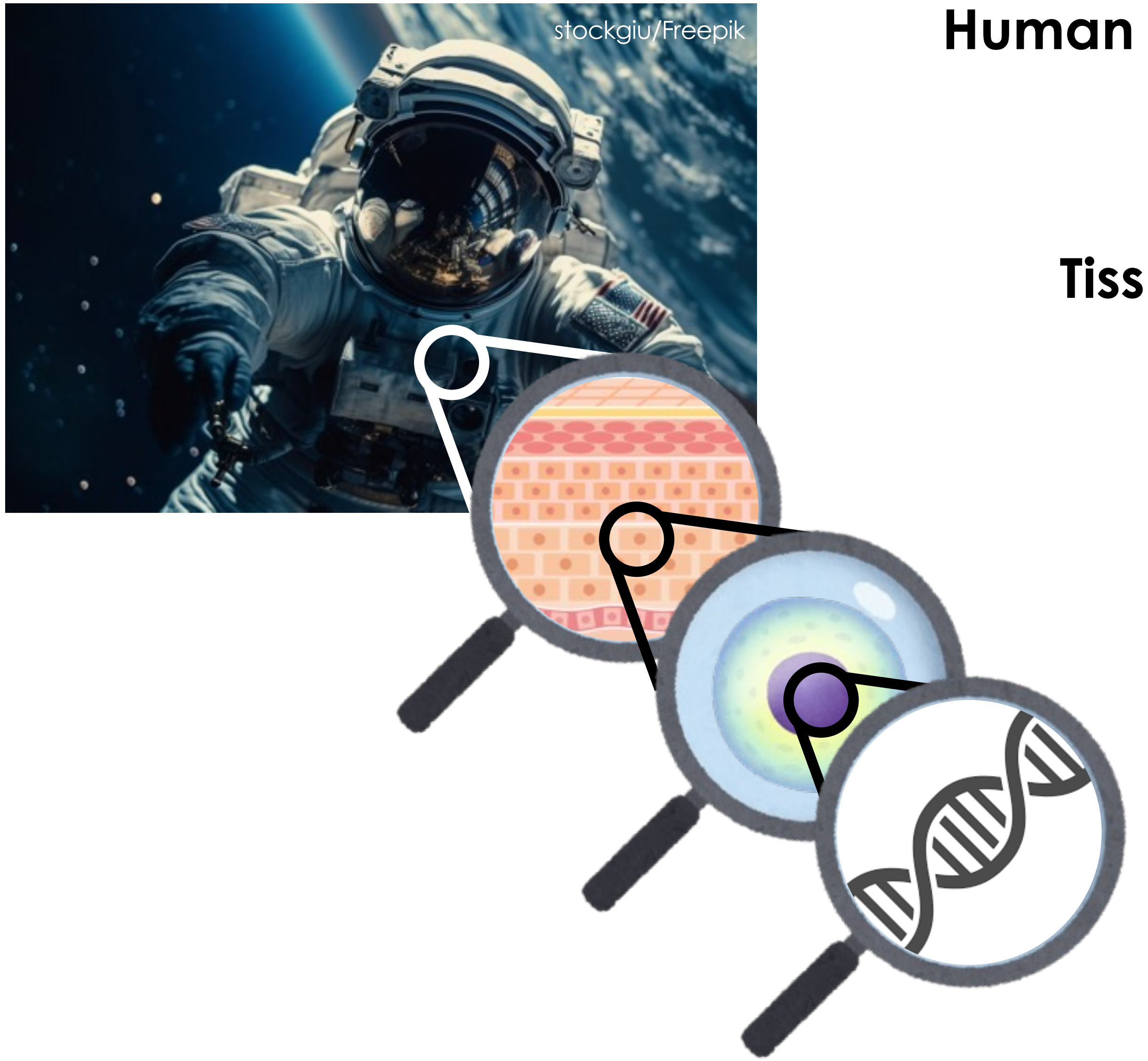
Proton & ion-therapy

Space missions

Space exploration

ESA & NASA

Radiation effects scales



Human body: ~ 1cm - 100 cm

Radiation sickness (organ-level effects)

Tissue: ~ 1 mm - 10 mm

Radiation injury

Cell: ~ 1 µm - 10 µm

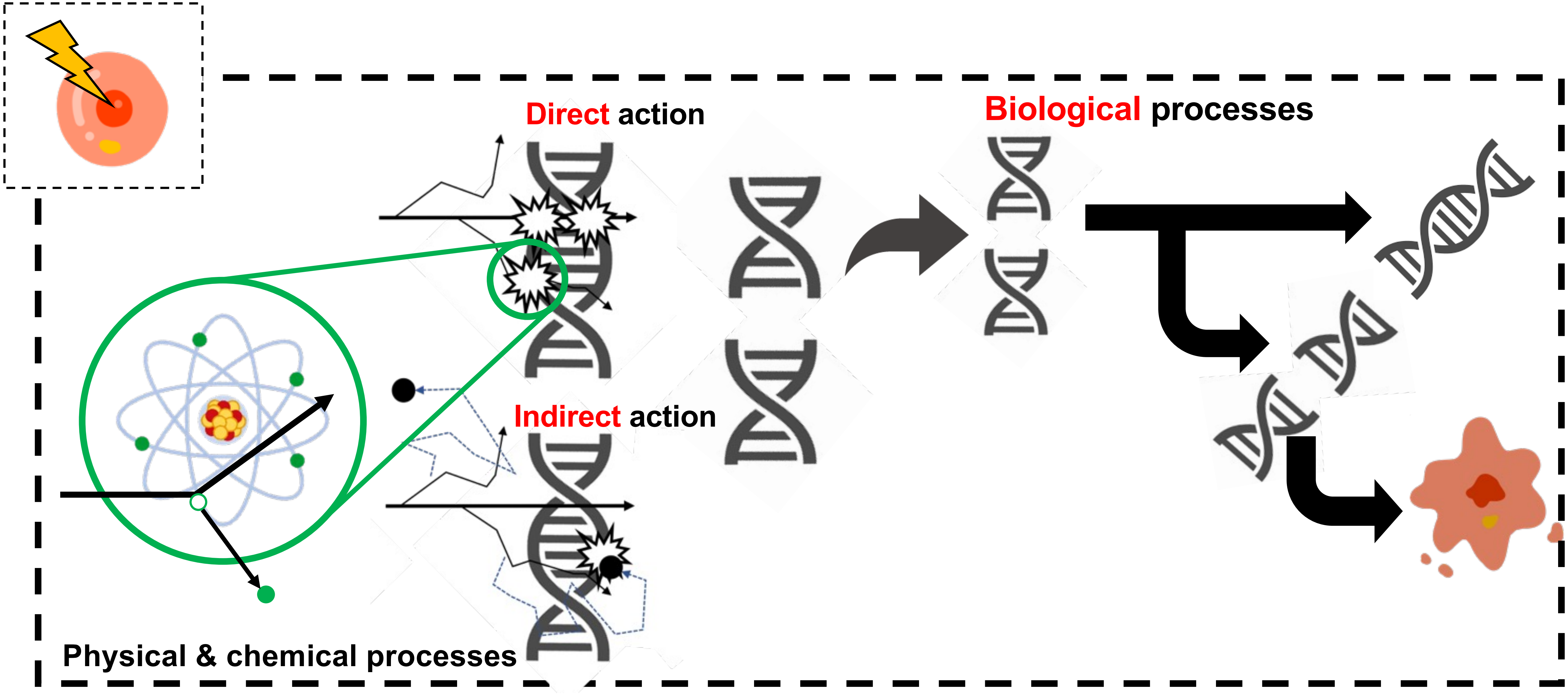
Cell death

DNA: ~ 1 nm - 10 nm

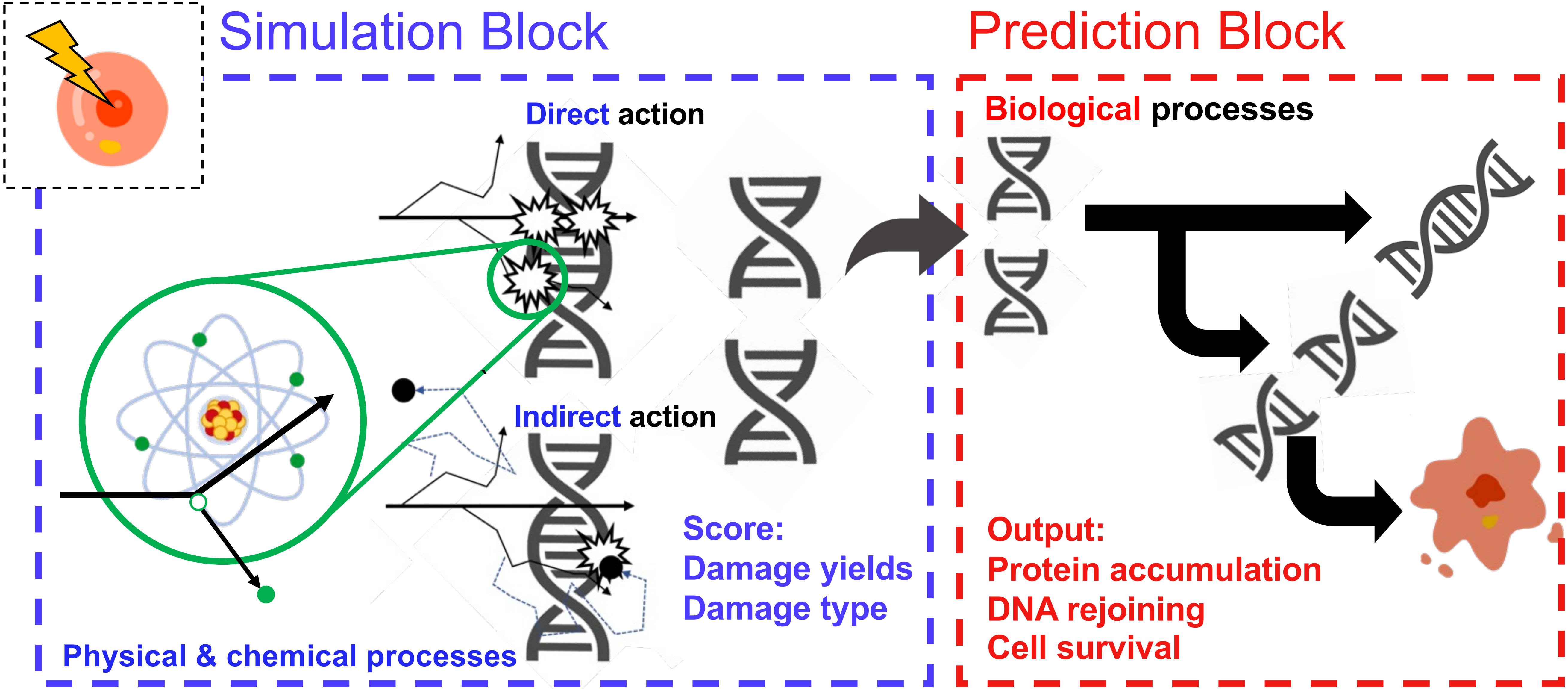
DNA damage, mutation, …

Geant4-DNA main target

Radiobiological processes after irradiation



Conceptual design of the Geant4-DNA approach



Simulation Block

Prediction Block

Direct action

Indirect action

Score:
Damage yields
Damage type

Physical & chemical processes

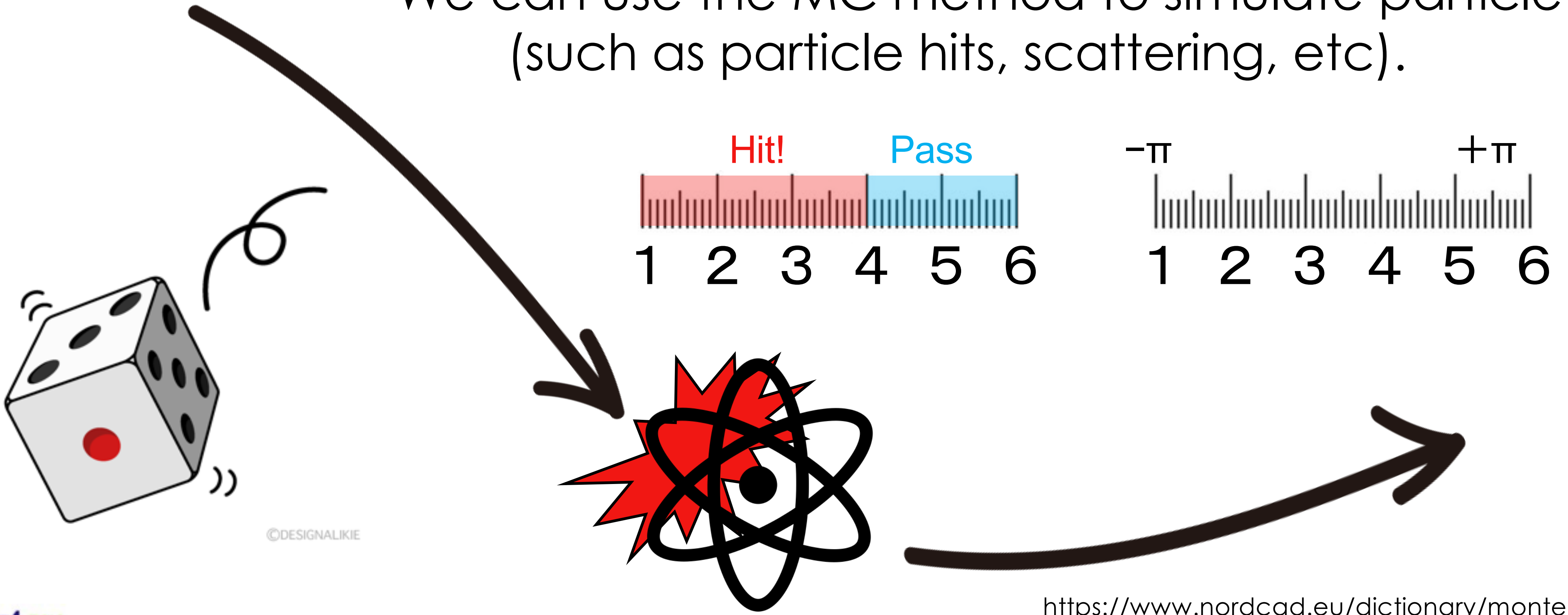
Biological processes

Output:
Protein accumulation
DNA rejoining
Cell survival

Monte Carlo methods in particle & molecule transport

“Monte Carlo simulation is a model used to predict the probability of various events when the potential for random variable is present”

We can use the MC method to simulate particle transport (such as particle hits, scattering, etc).



https://www.nordcad.eu/dictionary/monte-carlo-simulation-2/

The Monte Carlo approach

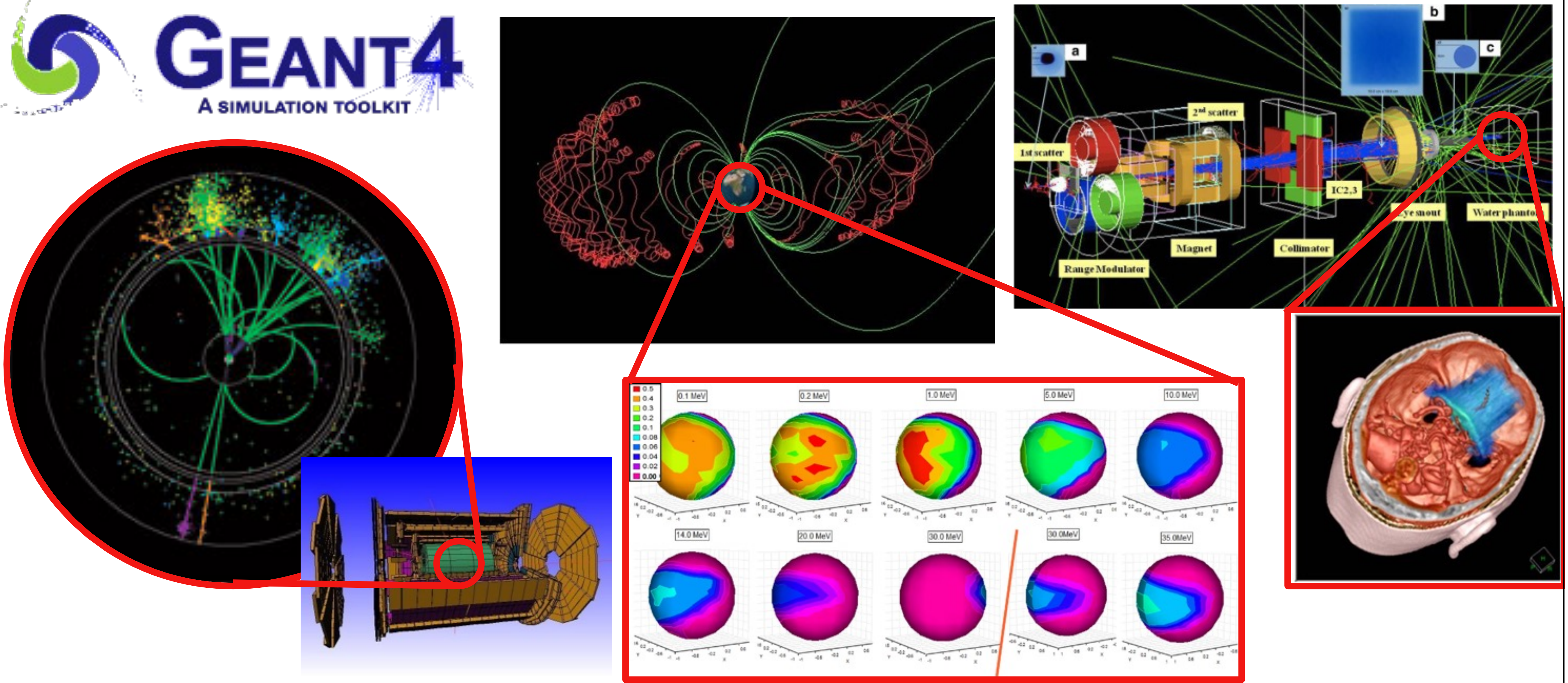
- Many **Monte Carlo codes** are already available today in radiobiology for the simulation of track structures at the molecular scale in biological medium
    - E.g. **PARTRAC**, **MC4***, **KURBUC**, **RETRACKS/RITRACKS**, **NOREC**, …
    - Include **physics & physico-chemistry** processes, detailed **geometrical** descriptions of biological targets down to the DNA size, **DNA and chromosome damage** simulation and even **repair** mechanisms (PARTRAC)…
- Usually designed for very specific applications
- Not always easily accessible
    - Is it possible to access the source code?
    - Are they adapted to recent OSs?
    - Are they extendable by the user?

Open-source track structure MC codes for radiobiological simulations is in high demand

https://geant4.org

What is Geant4?

GEANT4
A SIMULATION TOOLKIT



https://geant4-dna.org

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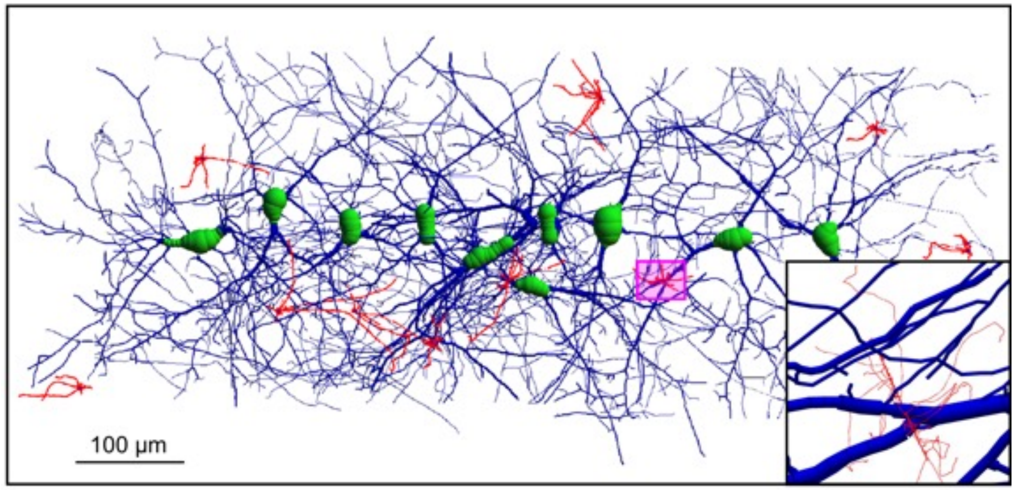
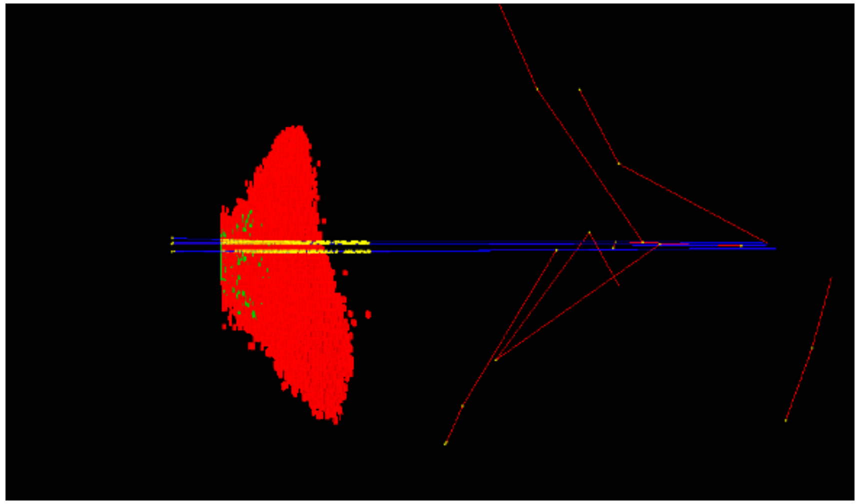
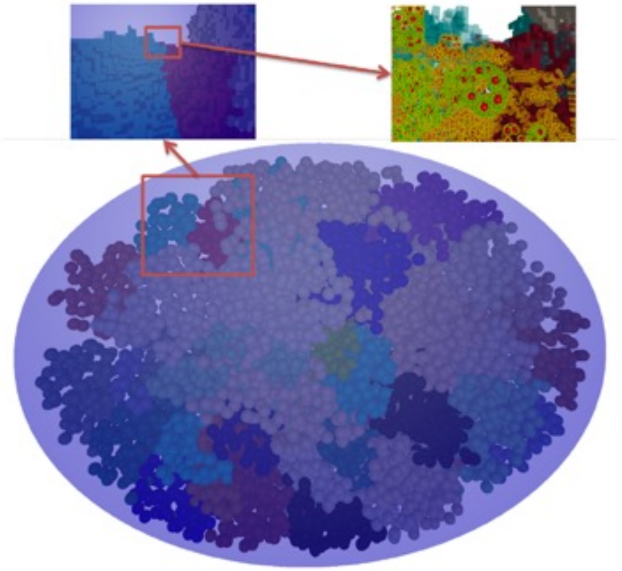
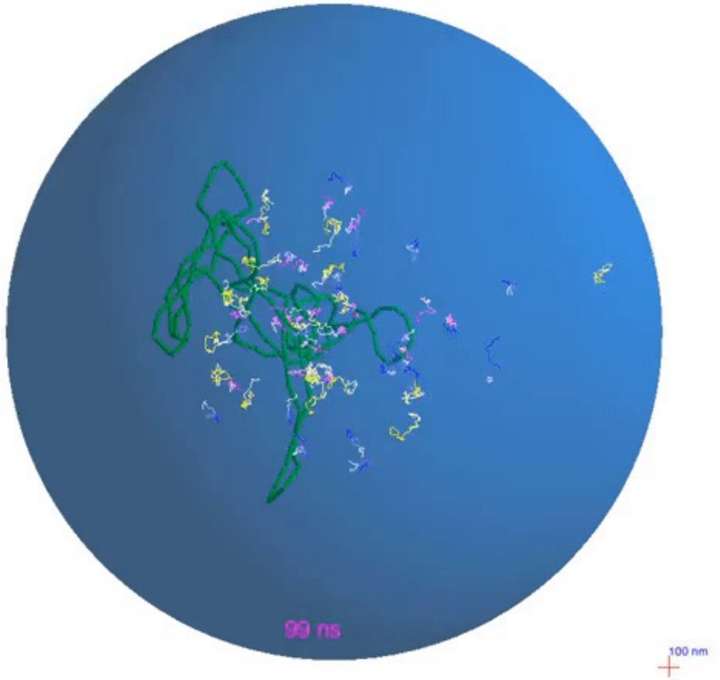
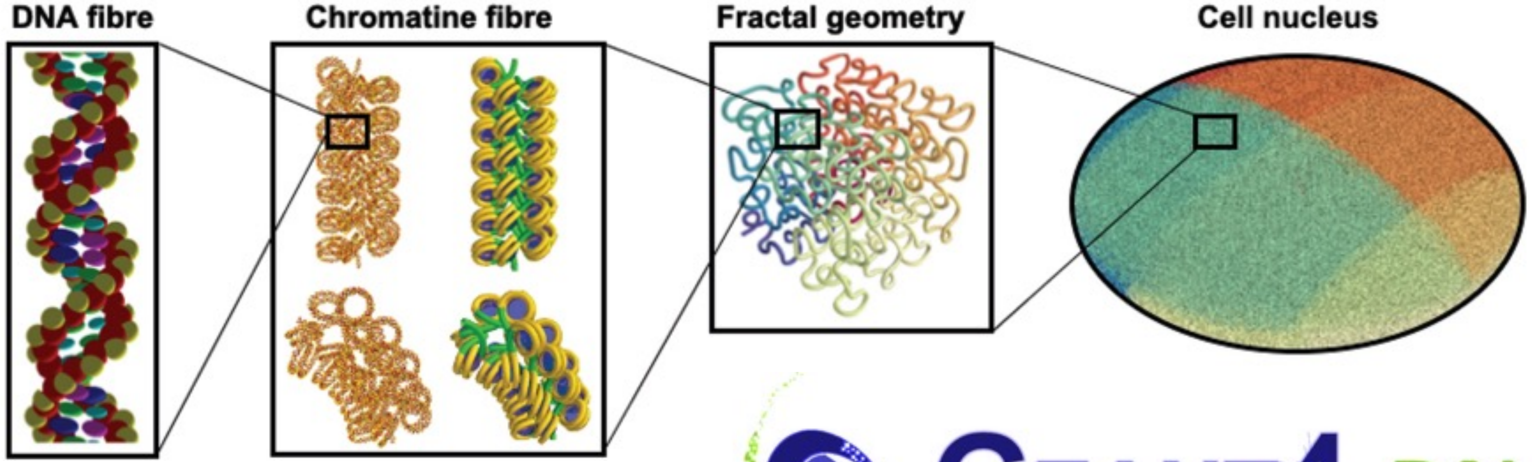










GEANT4-DNA
A SIMULATION TOOLKIT

Why Geant4-DNA?
- Requirements for radiobiological simulations -

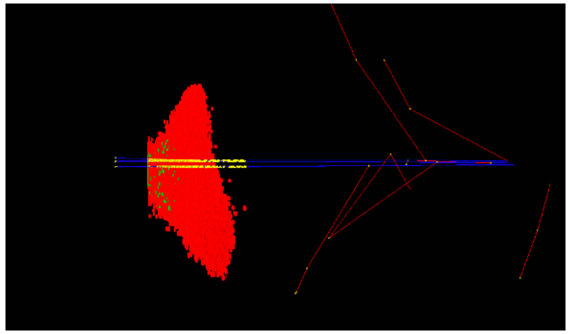
- **High spatial resolution (few μm, nm), low energy limit, reliable physics for sub-keV energies**

  Geant4:

  Fast / Low spatial resolution, E_{limit} ~ 250eV

  Geant4-DNA:

  Slow/ High spatial resolution, E_{limit} ~ 10eV



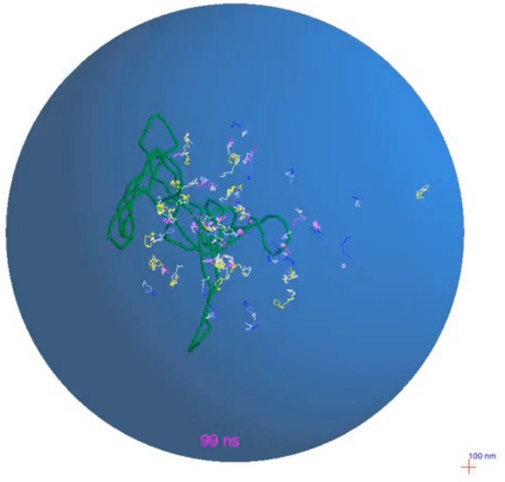
- **Interface for water radiolysis**

  Geant4:

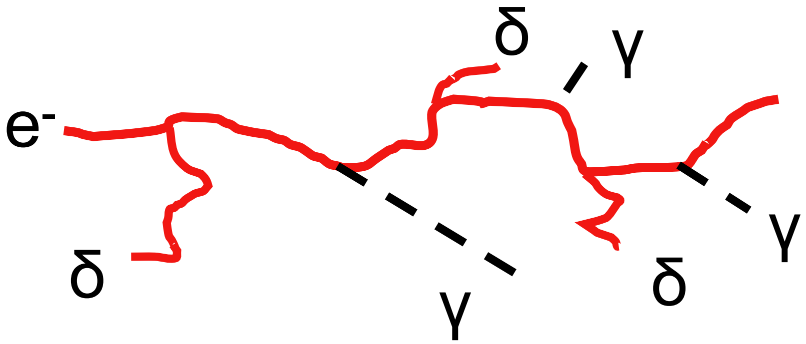
  No interface

  Geant4-DNA:

  Production/Diffusion of chemical molecules



Requirement for physics: ① High spatial resolution

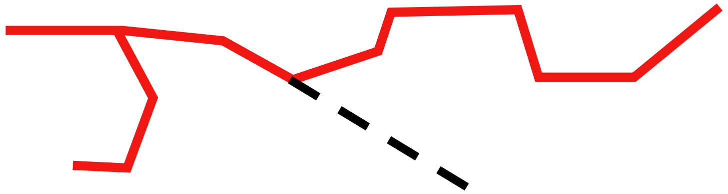


Trajectory in real world

High accuracy/Slow computing

Track-Structure approach

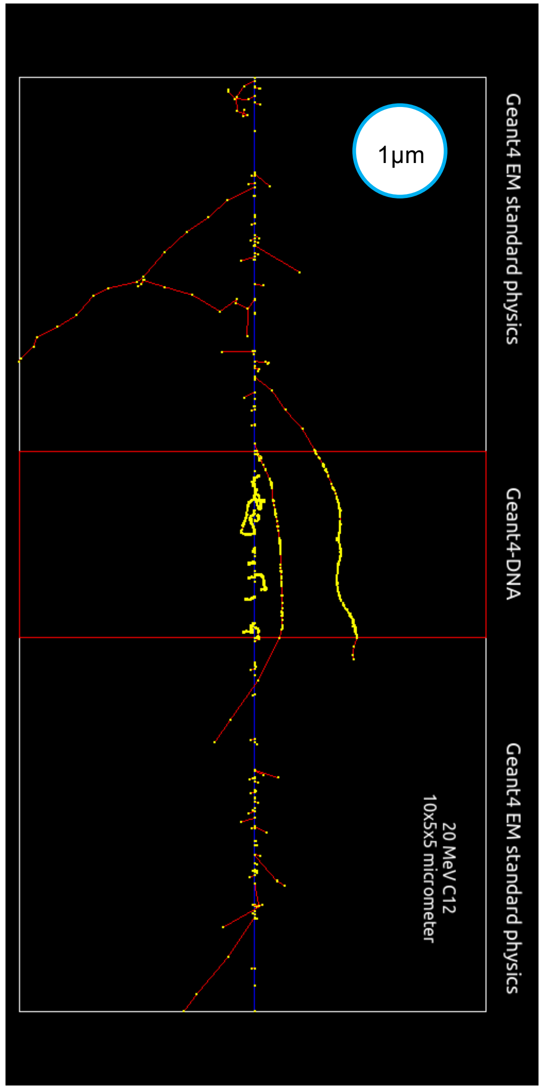
- All physical interactions are simulated individually in a sequential manner
- Example: **Geant4-DNA**, PARTRAC, RITRACKS, NOREC, KURBUC, PHITS-TS…



Low accuracy /**Fast computing**

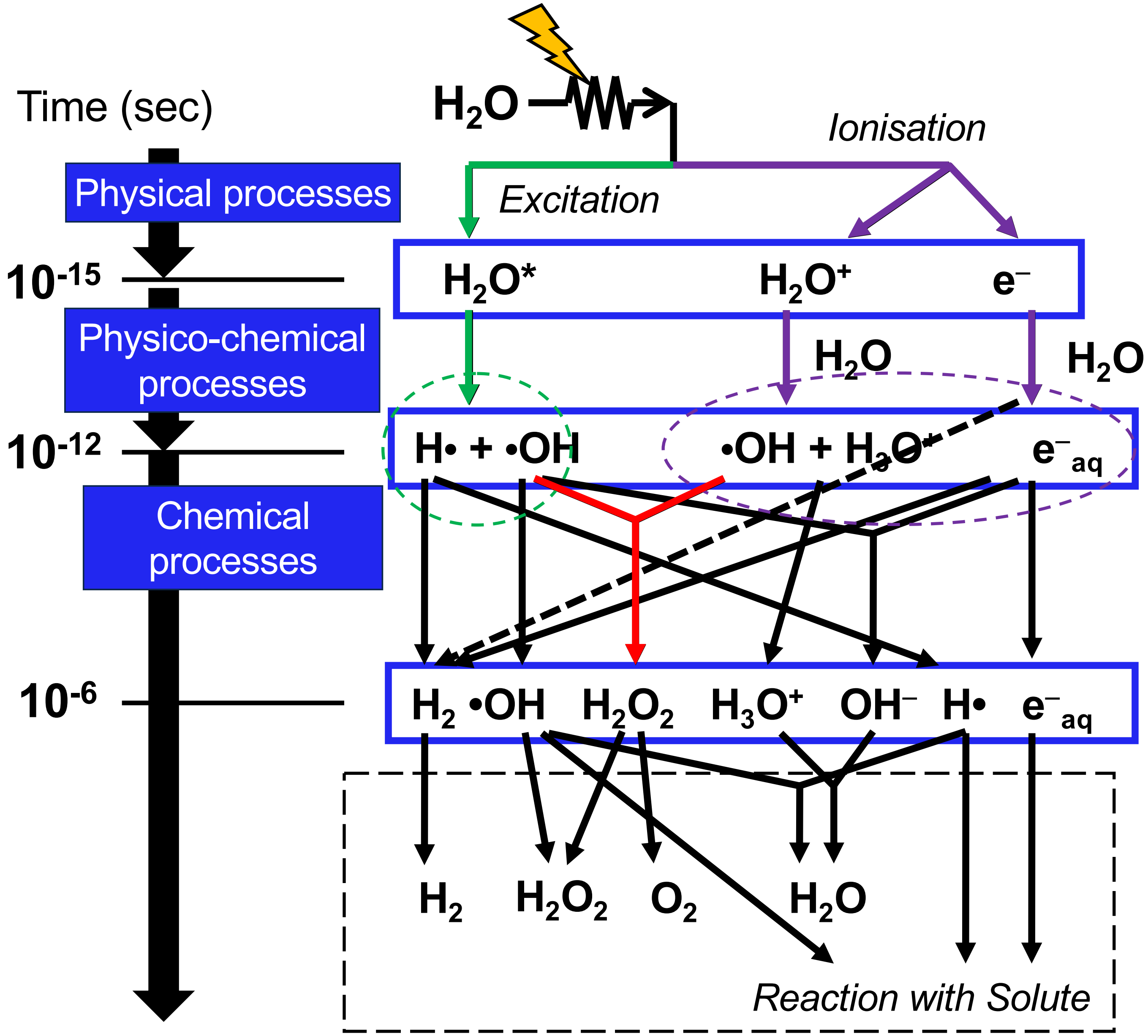
Condensed-History approach

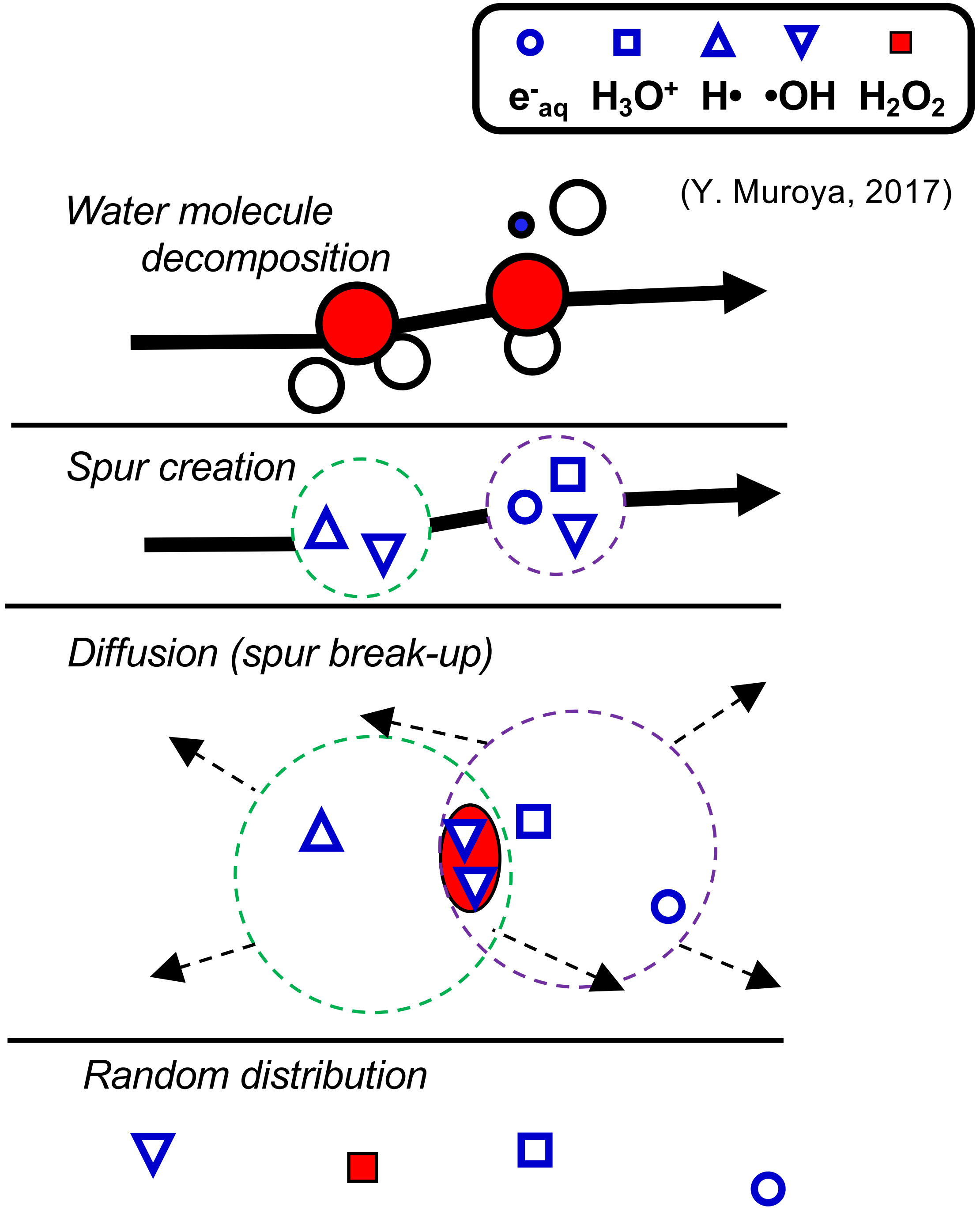
- Several discrete physical interactions are “condensed” into a single transport step
- Multiple-scattering approximation
- Example: **Geant4**, PHITS, EGS, FLUKA, PENELOPE, MCNP…



Ref.: Nucl. Instrum. and Meth. B 273, 95-97 (2012), Prog. Nucl. Sci. Tec. 2, 898-903 (2011)

Requirement: ② Water radiolysis





(Y. Muroya, 2017)

Geant4-DNA history

2001

Initiated by the
European Space Agency/ESTEC

2007

First prototypes of
physics models
for liquid water
added to Geant4 **9.1**

2008

Re-engineered
to be coherent with
Geant4 EM physics
in Geant4 **9.3**

2014

Chemistry stage
extension
ready for end users in
Geant4 **10.1**

2014

First extended examples
applicable to **"DNA-scale" geometries**
released in Geant4 **10.4**

2019 - 2023

Development of fully integrated radiobiological applications

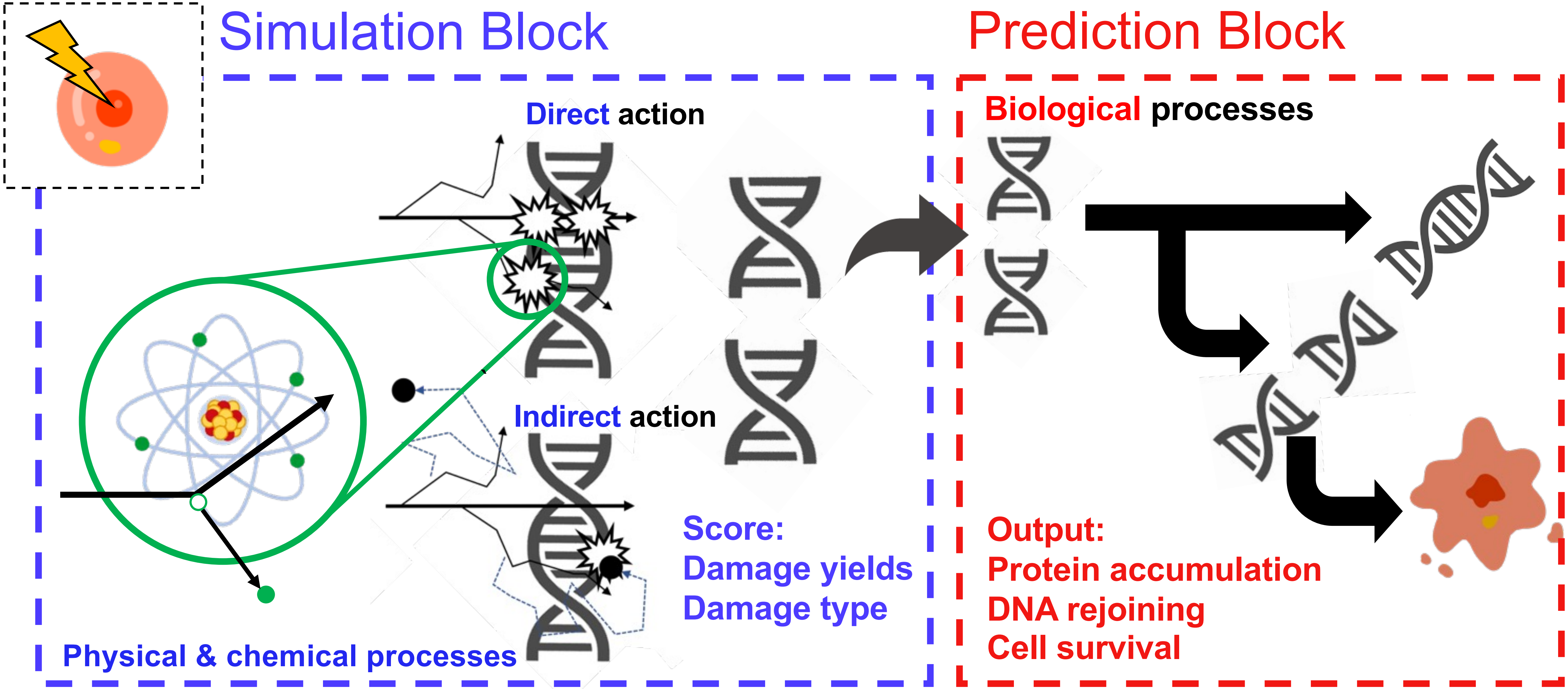
Integration of Phys. + Chem. + Geometry in **10.5**

Integration with biological prediction models in **11.1**

dnaphysics
microdosimetry
pdb4dna
wholeNuclearDNA

dnadamage1 in 10.5 (2019)
dnadamage2 in 11.1 (2022)
moleculardna in 11.1 (2022)
dsbandrepair in 11.2 (2023)

Conceptual design of the Geant4-DNA approach



Simulation Block

Direct action

Indirect action

Score:
Damage yields
Damage type

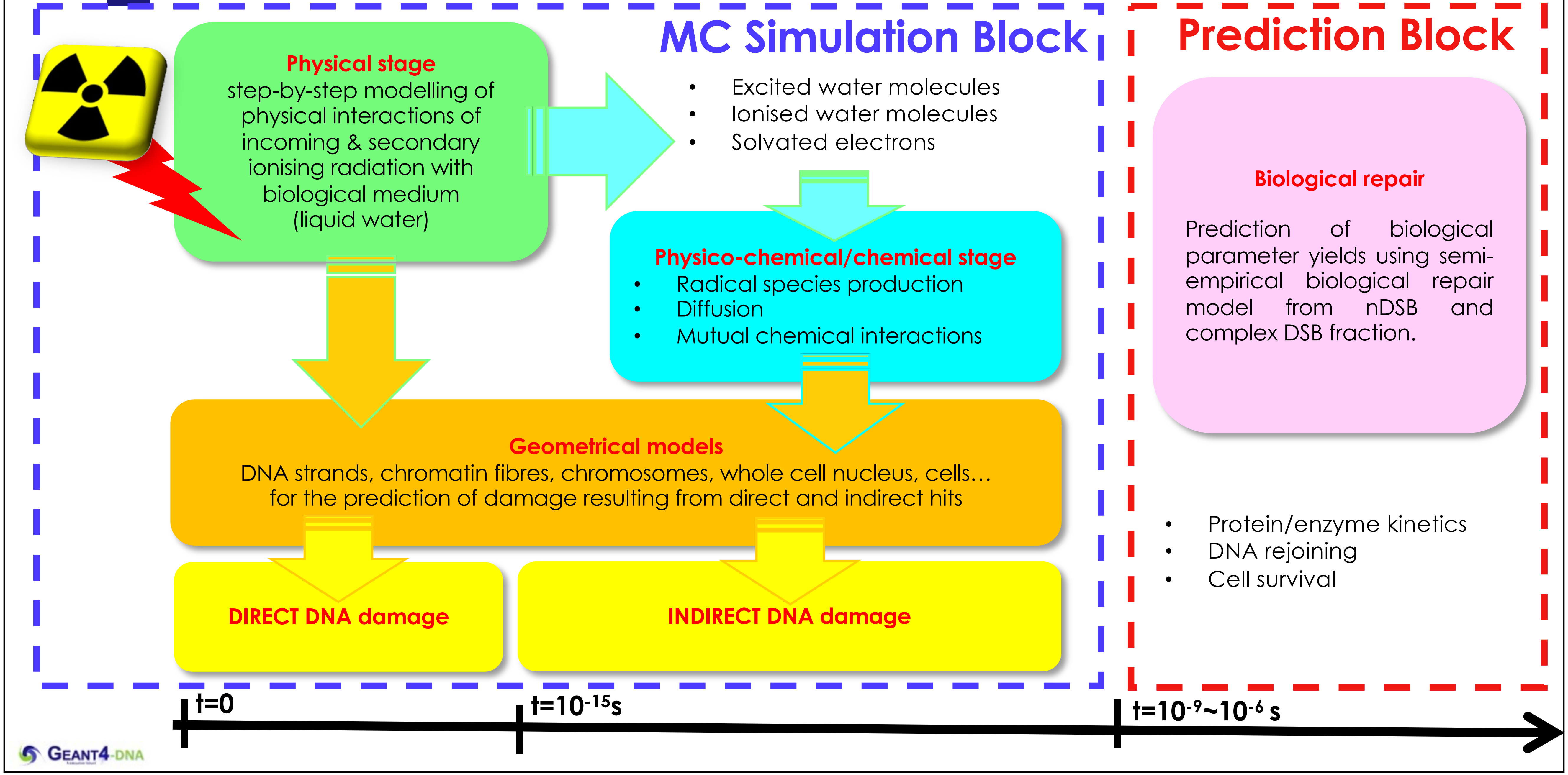
Physical & chemical processes

Prediction Block

Biological processes

Output:
Protein accumulation
DNA rejoining
Cell survival

The Geant4-DNA approach



MC Simulation Block

Physical stage

step-by-step modelling of physical interactions of incoming & secondary ionising radiation with biological medium (liquid water)

- Excited water molecules
- Ionised water molecules
- Solvated electrons

Physico-chemical/chemical stage

- Radical species production
- Diffusion
- Mutual chemical interactions

Geometrical models

DNA strands, chromatin fibres, chromosomes, whole cell nucleus, cells… for the prediction of damage resulting from direct and indirect hits

DIRECT DNA damage

INDIRECT DNA damage

Prediction Block

Biological repair

Prediction of biological parameter yields using semi-empirical biological repair model from nDSB and complex DSB fraction.

- Protein/enzyme kinetics
- DNA rejoining
- Cell survival

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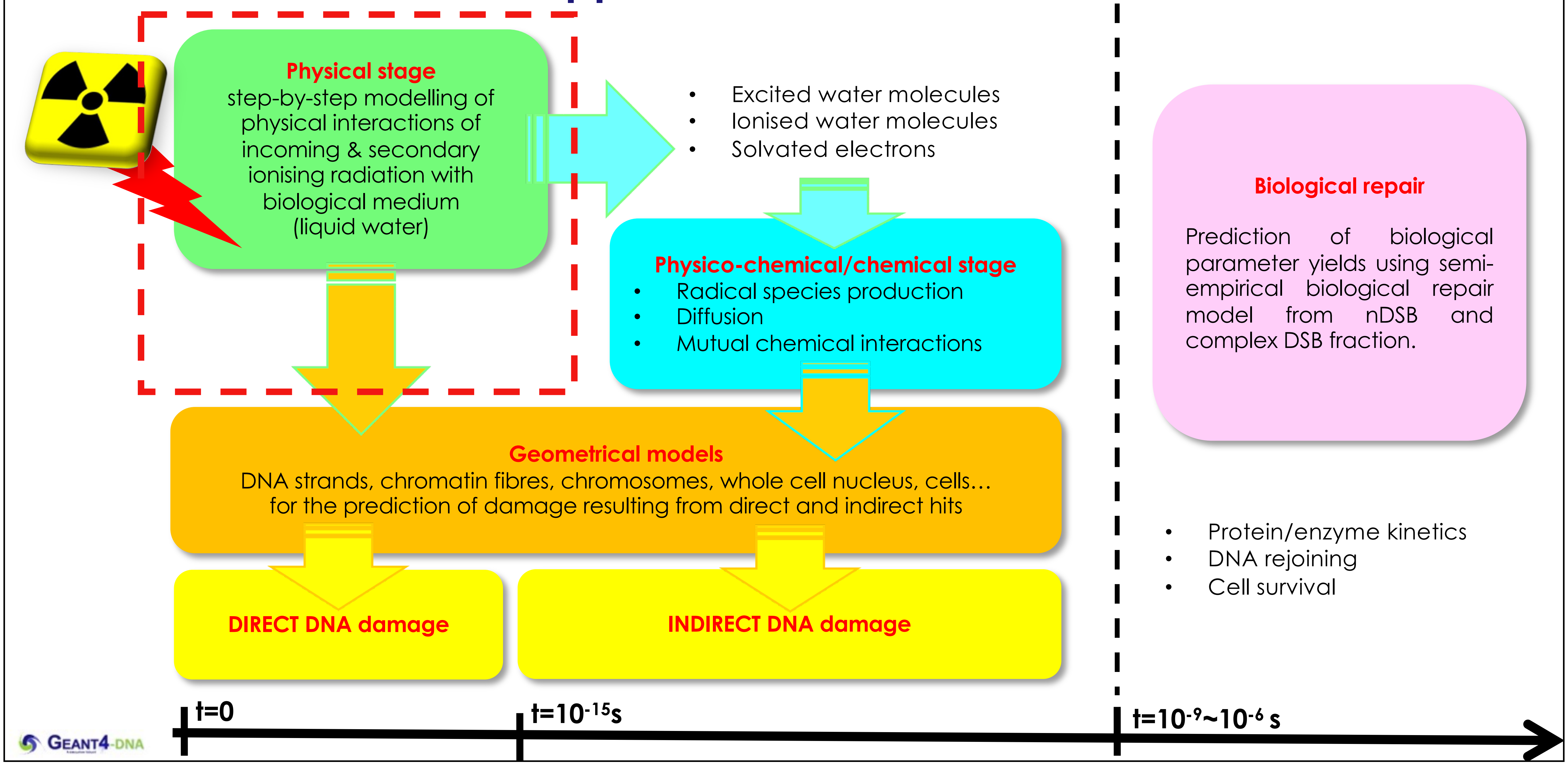

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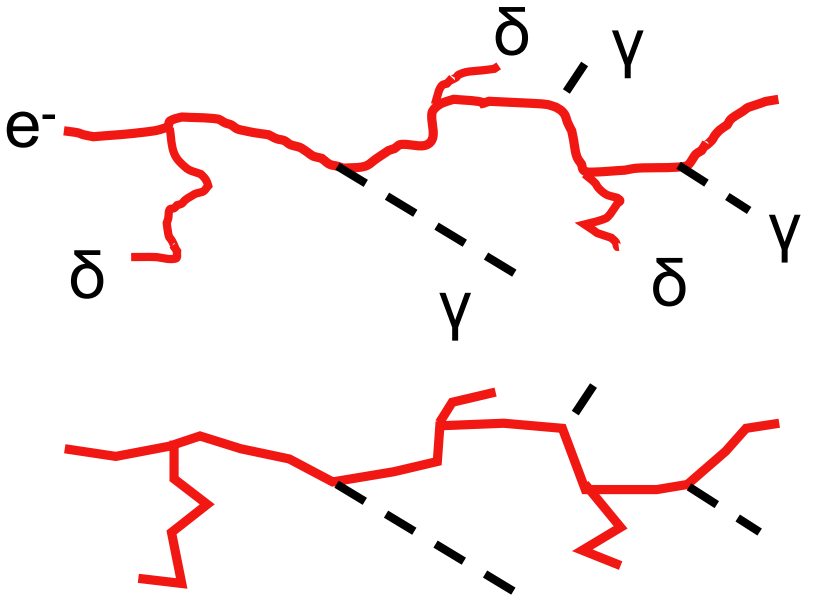
t=0

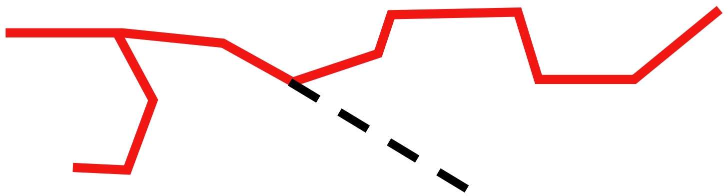
t=10^{-15}s

t=10^{-9}~10^{-6} s

Requirement: ① High spatial resolution



High accuracy/Slow computing



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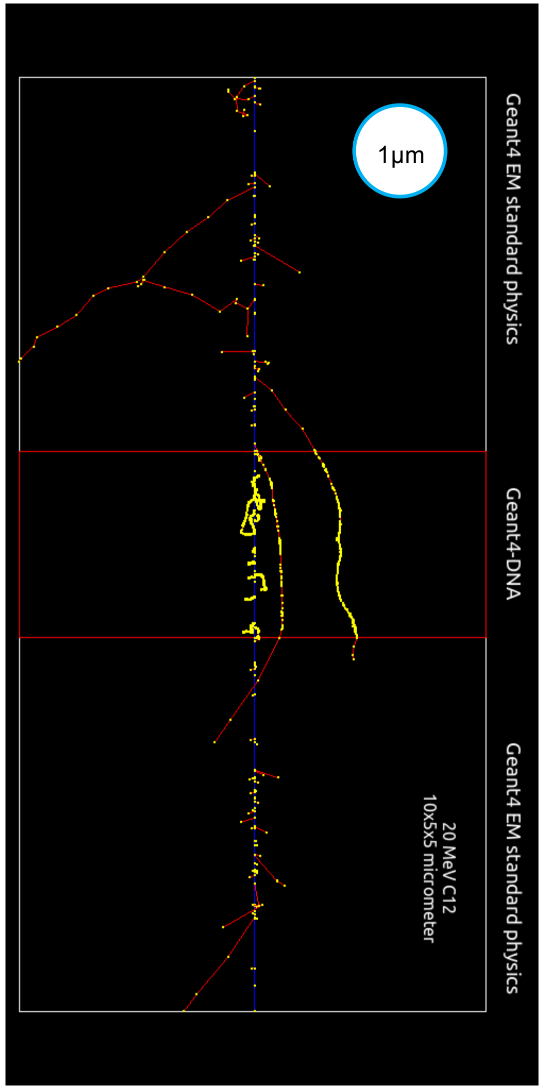

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Geant4-DNA physics for liquid water

Other materials are available:
DNA precursors, DNA bases & S-P, solid gold,…
see Physics talk

- **Geant4-DNA processes and models allows the transport in liquid water**
  - Electrons: ionisation, excitation, elastic scattering, vibrational excitation, electron attachment
  - Protons, H (0,+): ionisation, excitation, elastic, charge increase/decrease processes
  - Alpha, He(0,+,2+): ionisation, excitation, elastic, charge increase/decrease processes
  - Generic ions: ionisation

- **Geant4-DNA Physics constructors for simulations in liquid water**
  - `G4EmDNAPhysics_option2` (since version 9.1): accelerated default constructor, simulating electron interactions (elastic, inelastic, dissociative attachment, vibrational excitation) **up to 1 MeV**, as well as other particle interactions
  - `G4EmDNAPhysics_option4` (since version 10.2): contains electron elastic and inelastic models, **up to 10 keV**; extended up to 10 MeV (to be released)
  - `G4EmDNAPhysics_option6` (since version 10.4): contains CPA100 electron elastic and inelastic models, **up to 256 keV**

NOTE

- Protons can be tracked up to 300 MeV
- Option4 and option6 can go up to 1 MeV (beyond the default limits, Born models are used)

Multi-scale combination of physics processes

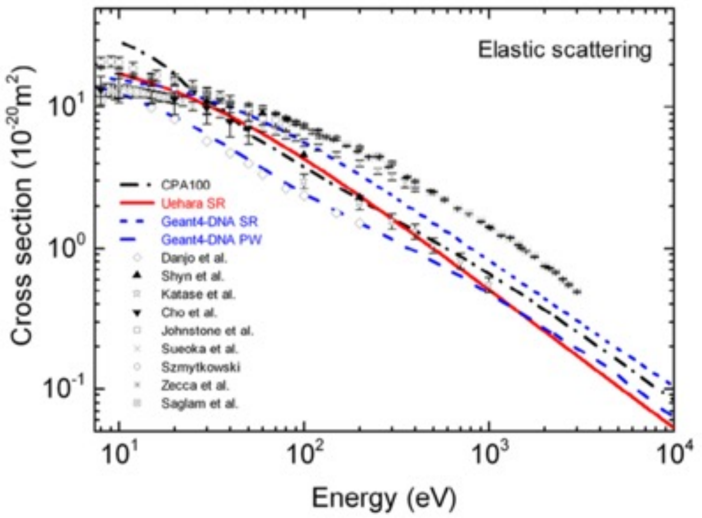
- Geant4-DNA is mainly dedicated to **(very) low energy charged particles**
  - Is it possible to simulate neutral particles such as photons?
  - Can we include the physics processes for high-energy particles?

- Any Geant4-DNA process can be combined with other Geant4 process such as:
  - Geant4 **photon** processes: photoelectric effect, Compton scattering, Rayleigh scattering, pair production
    - Livermore (EPDL97) included by default
  - Geant4 **alternative EM** processes for charged particles
    - E.g. bremsstrahlung
  - Geant4 **atomic de-excitation** (fluorescence + Auger emission, including cascades)
    - EADL97
    - Bearden
  - …and also Geant4 **hadronic physics**

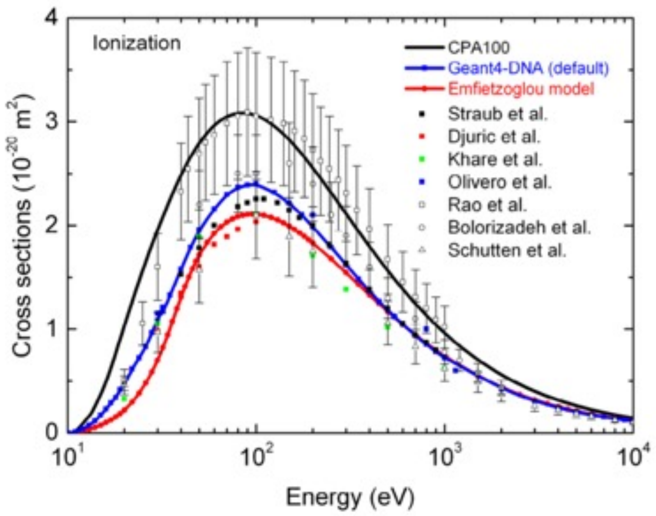
E.g. of validation and verification of Physics : total cross sections

Electron CS:

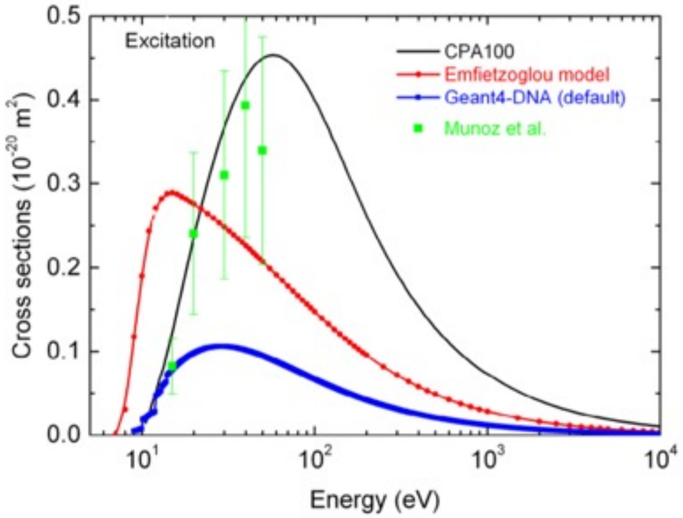
Elastic



Ionisation

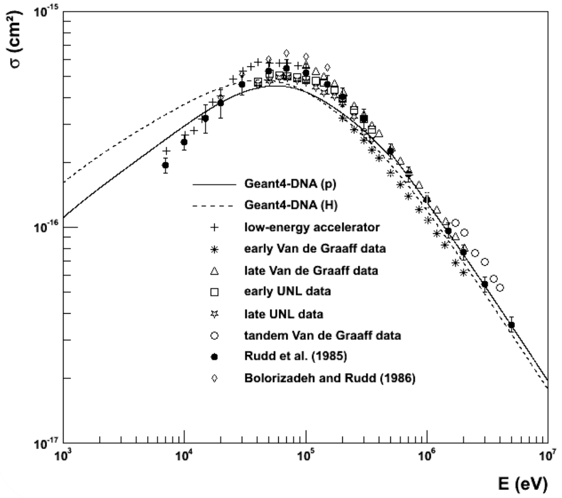


Electronic excitation

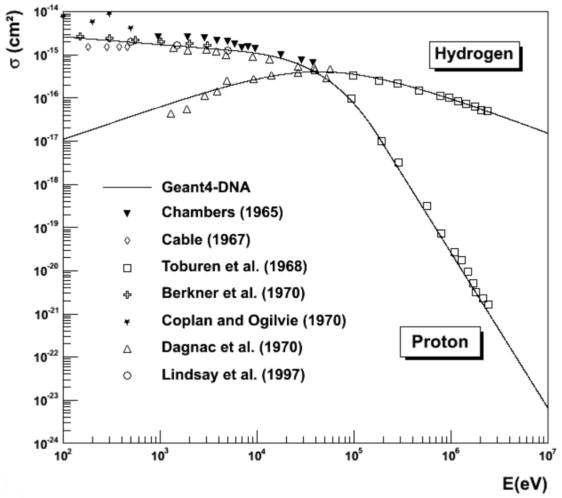


Proton CS:

Ionisation

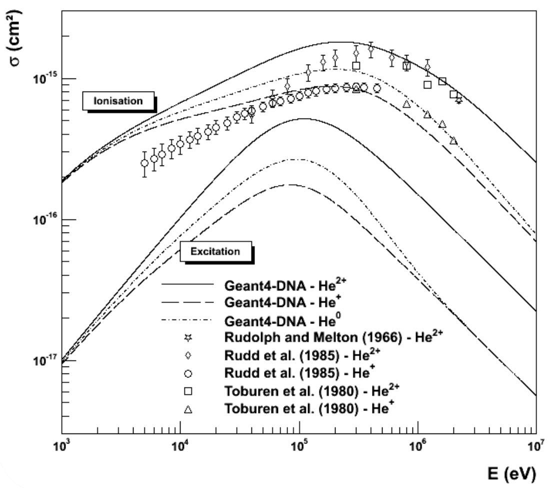


Charge exchange



Helium CS:

Ionisation



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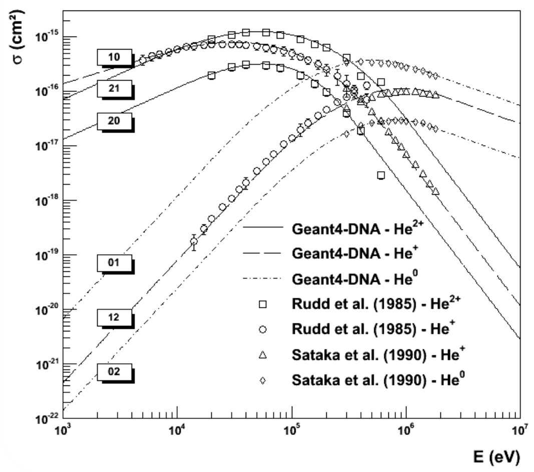
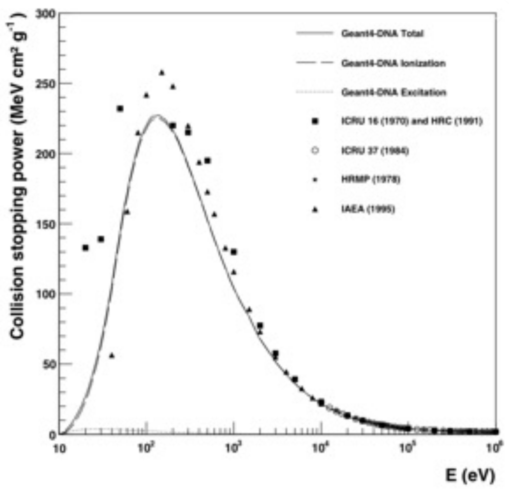


Ref.: Med. Phys. 37, 4692-4708 (2010), Phys. Med. 31, 861-874 (2015)

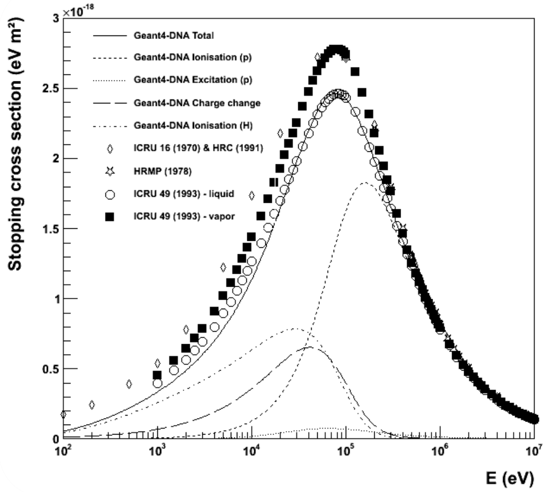
E.g. of validation and verification of Physics: range and stopping power

Stopping power:

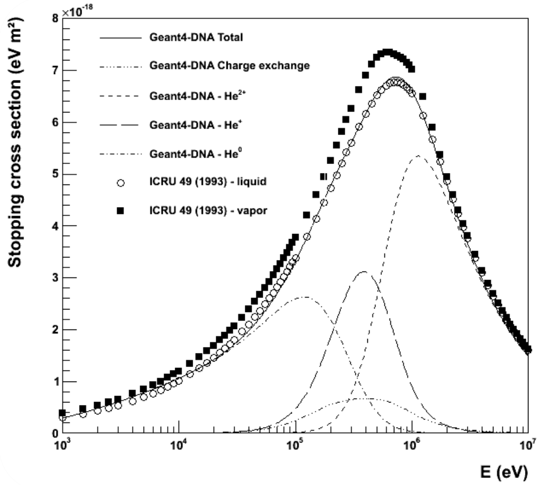
Electron



Proton

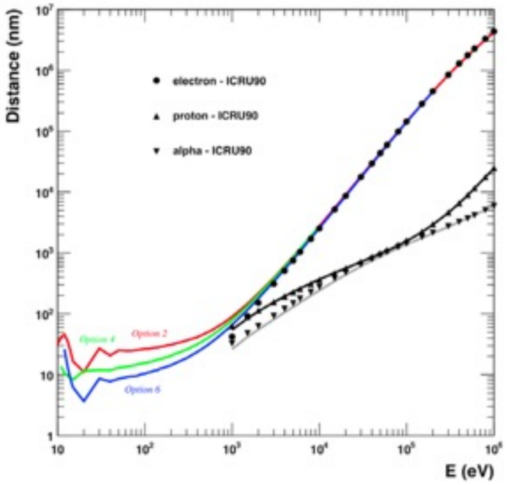


Helium

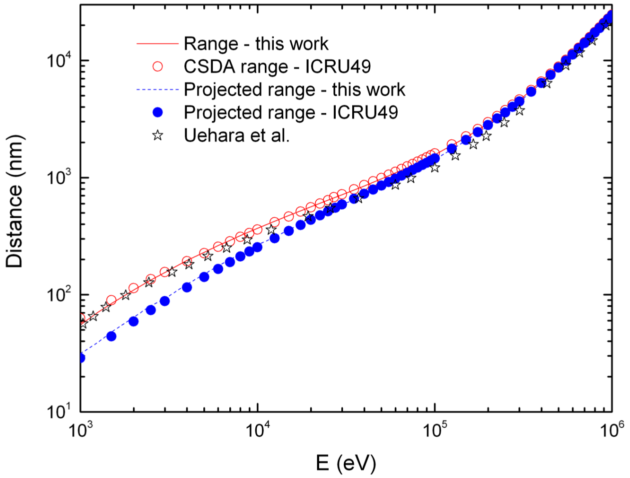


Range:

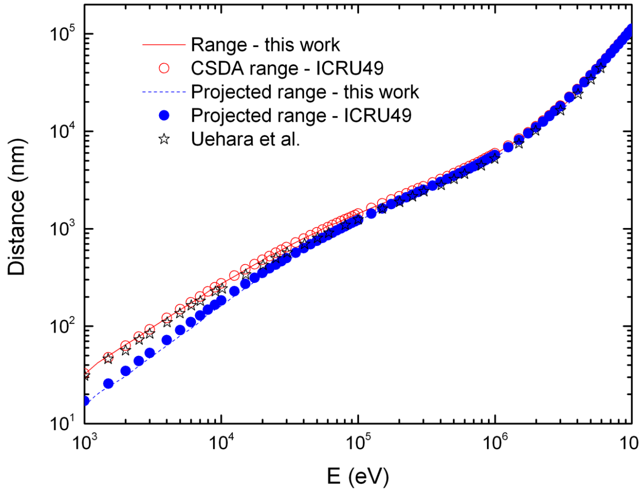
Electron



Proton



Helium



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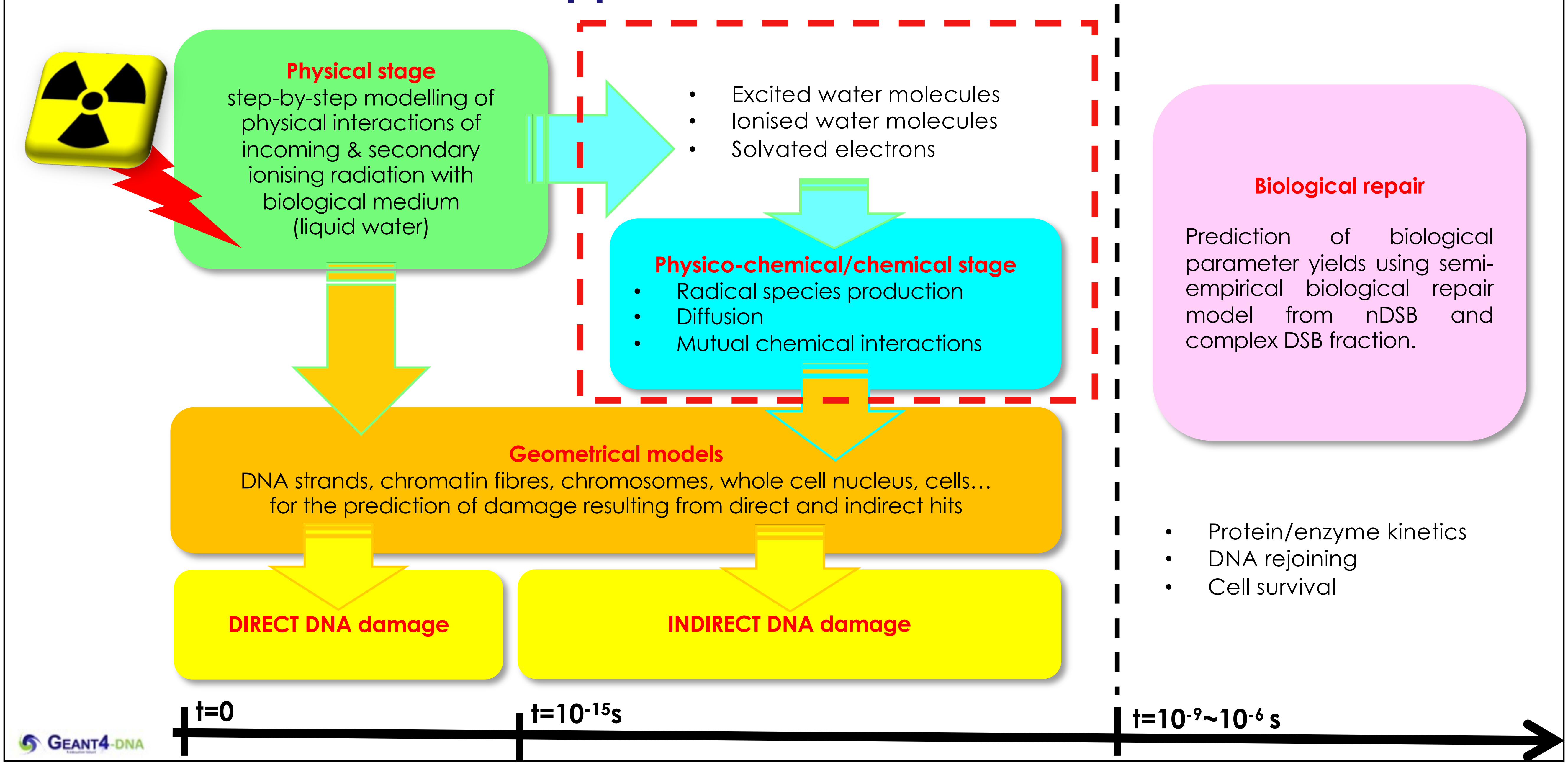

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DNA strands, chromatin fibres, chromosomes, whole cell nucleus, cells… for the prediction of damage resulting from direct and indirect hits

DIRECT DNA damage

INDIRECT DNA damage

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Prediction of biological parameter yields using semi-empirical biological repair model from nDSB and complex DSB fraction.

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- Cell survival

Geant4-DNA chemistry models

- **Geant4-DNA chemistry allows the water radiolysis simulation:**
  - **Production of molecules**: e.g, place decomposed molecules at 1 ps
  - **Diffusion**: Geant4-DNA offers 3 types of diffusion algorithm
    - **Step-by-Step (SBS)**: Fixed time step molecular transport method.
    - **Independent Reaction Time (IRT)**: Calculates the reaction times between all possible pairs. Reactions occur one by one, starting with the pair with the shortest reaction time.
      - **IRT-sync**: IRT-sync stores all molecular positions **at each time step**, as the SBS approach.
    - **Mesoscopic**: A compartment-based representation that describes the evolution of species through their concentrations in different compartments.
  - **Reaction**: Geant4-DNA handles reactions between molecules.
- **Geant4-DNA chemistry constructors:**
  - **`G4EmDNAChemistry`**: First constructor implemented with parameter values from Karamitros et al. – from PARTRAC
  - **`G4EmDNAChemistry_option1`**: Implements a revisited set of chemistry parameters from Shin et al. – from TRACs + Burns et al. (1981) + Rowe et al. (1988)
  - **`G4EmDNAChemistry_option2`**: Includes chemistry parameters for reactions with DNA components – from Buxton et al. (1988)
  - **`G4EmDNAChemistry_option3`**: Implements the IRT approach from Ramos-Mendez et al. (2020) – from RITRACKS & Elliot et al. (1994)

Geant4-DNA chemistry extended examples

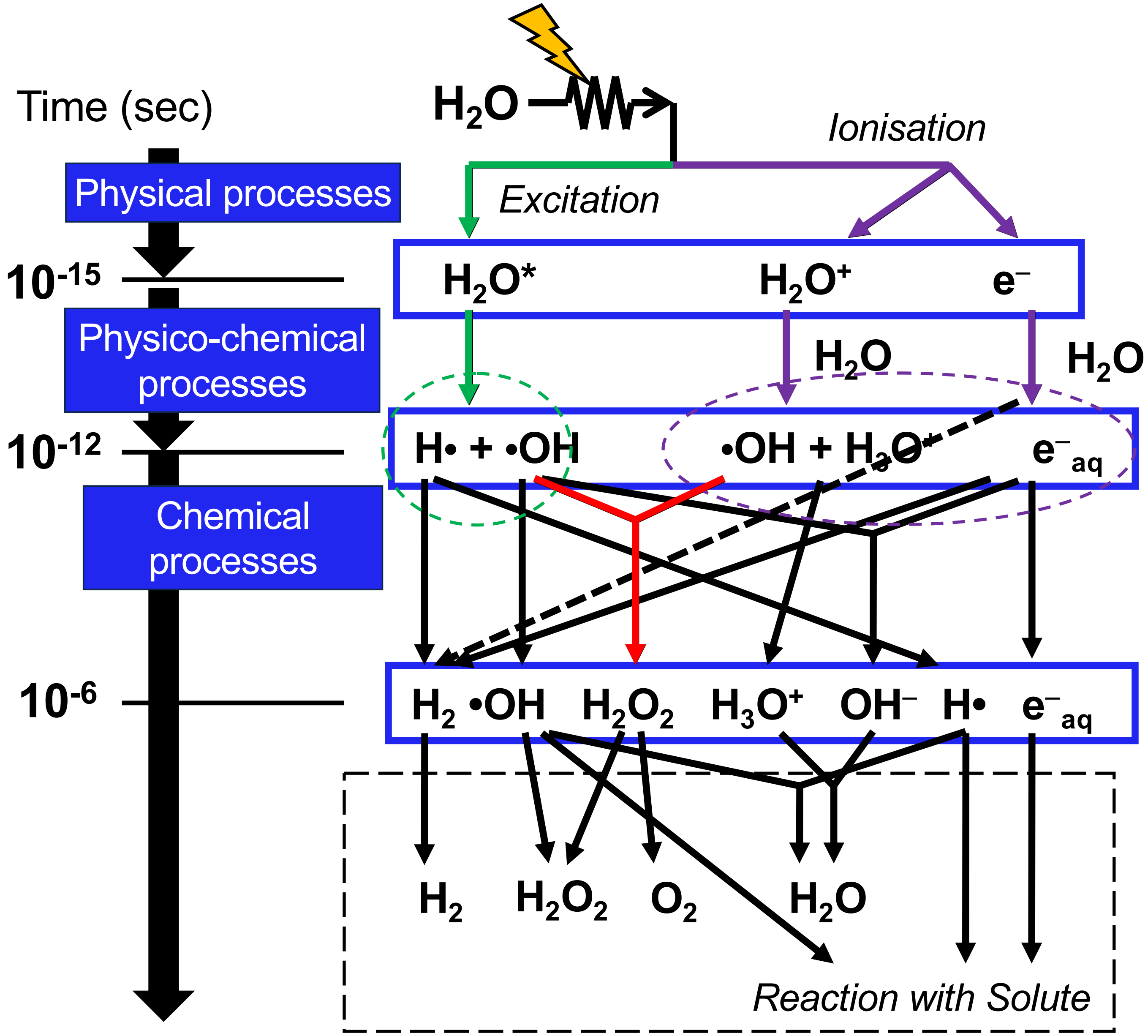
Located in $G4EXAMPLES/extended

- The « **chem1** » **extended/medical/dna** example illustrates how to **activate** the simulation of water radiolysis (step-by-step method).
- The « **chem2** » **extended/medical/dna** example illustrates how to **set minimum time step** limits on water radiolysis (step-by-step method).
- The « **chem3** » **extended/medical/dna** example illustrates how to **implement user actions** in the chemistry module (step-by-step method).
- The « **chem4** » **extended/medical/dna** example illustrates how to **compute radiochemical yields ("G") versus time**, including a dedicated ROOT graphical interface (step-by-step method).
- The « **chem5** » **extended/medical/dna** example illustrates how to **compute radiochemical yields ("G") versus time**, using alternative physics and chemistry lists (step-by-step method).
- The « **chem6** » **extended/medical/dna** example illustrates how to **compute radiochemical yields ("G") versus time and LET** using IRT method.
- The « **scavenger** » **extended/medical/dna** 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 µs post-irradiation.

Towards FLASH simulations…

You remember, chemistry interface needed

○ e^-_{aq} □ H_3O^+ △ H• ▽ •OH 🟥 H_2O_2



Time (sec)

Physical processes

10^{-15}

Physico-chemical processes

10^{-12}

Chemical processes

10^{-6}

H_2O

Excitation

Ionisation

H_2O^* H_2O^+ e^-

H_2O H_2O

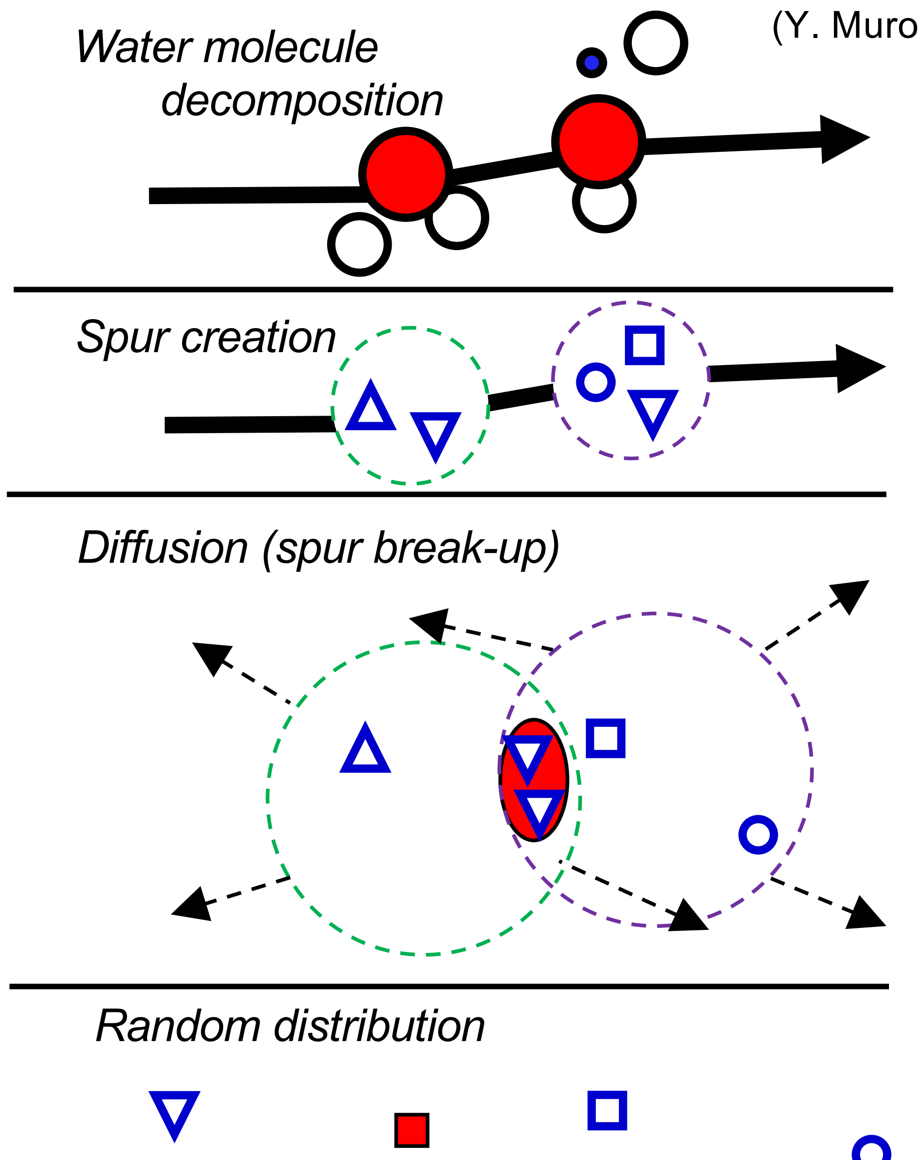
H• + •OH •OH + H_3O^+ e^-_{aq}

H_2 •OH H_2O_2 H_3O^+ OH^- H• e^-_{aq}

H_2 H_2O_2 O_2 H_2O

Reaction with Solute

(Y. Muroya, 2017)



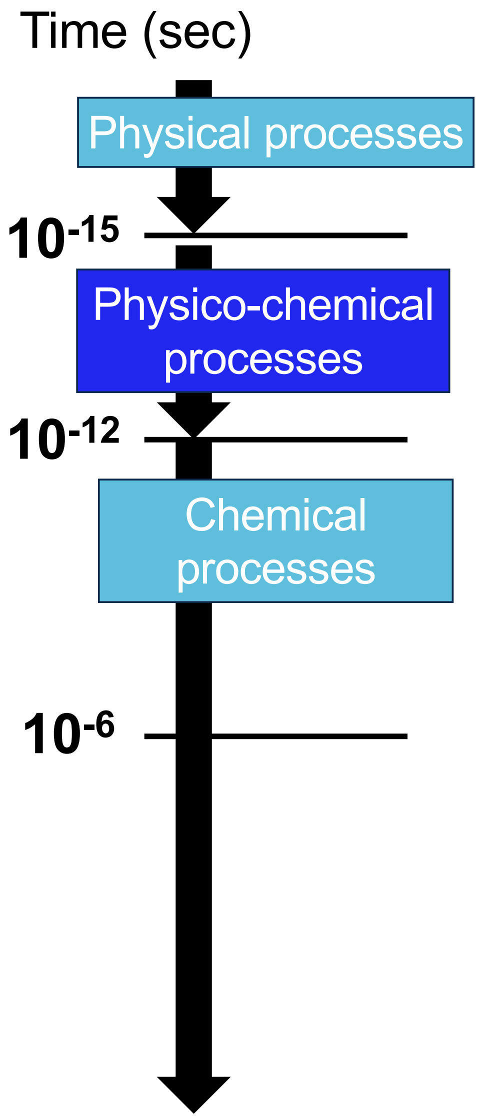
Water molecule decomposition

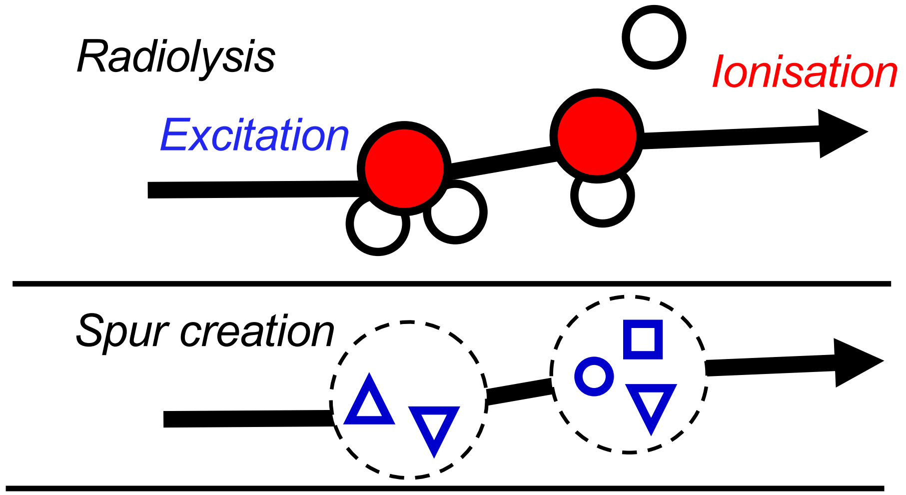
Spur creation

Diffusion (spur break-up)

Random distribution

Chemistry / Physico-chemical stage: Molecule production



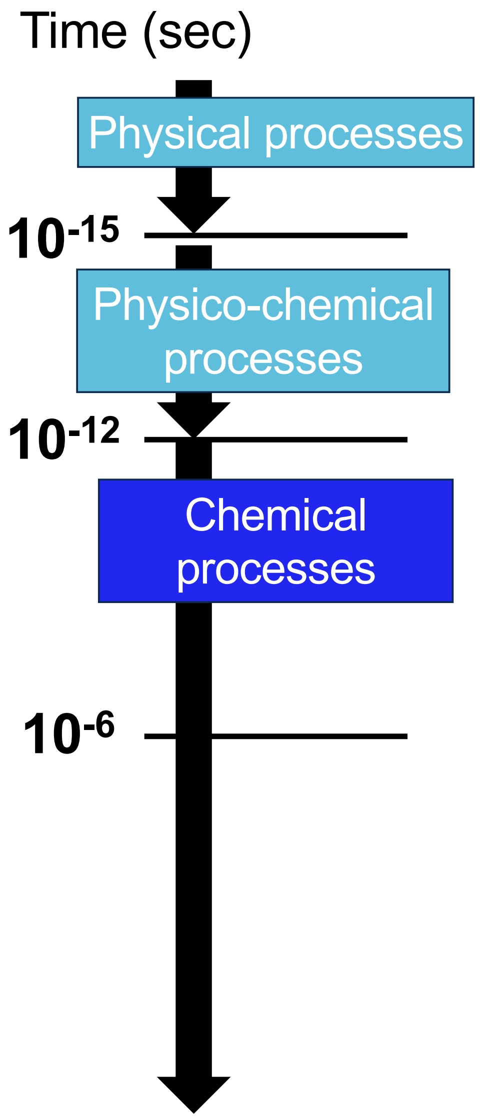


- Geant4-DNA starts from **altered water molecules** which underwent changes in their electronic configuration from physical processes occuring during the **physical stage**.
- Dissociation of water molecules by ionising radiation **during physico-chemical stage**, **creating molecules** in **« spur »**.

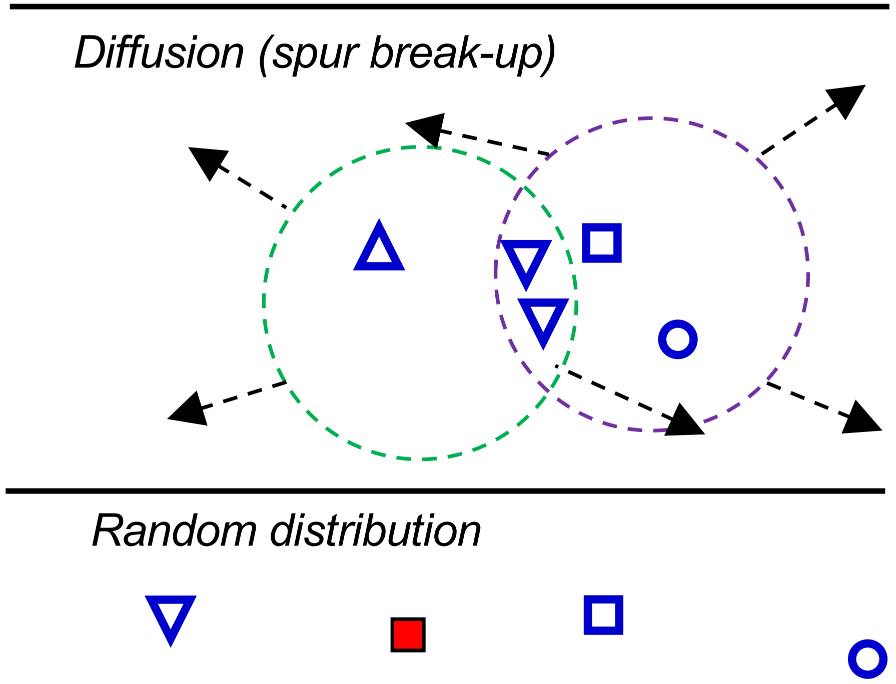
Electronic state	**Dissociation channels**	**Fraction (%)**
All single ionisation states	$H_3O^+ + \bullet OH$	100
Excitation state A1B1: (1b1) → (4a1/3s)	$\bullet OH + H\bullet$	65
	$H_2O + \Delta E$	35
Excitation state B1A1: (3a1) → (4a1/3s)	$H_3O^+ + \bullet OH + e^-_{aq}$	55
	$\bullet OH + \bullet OH + H_2$	15
	$H_2O + \Delta E$	30
Excitation state: Rydberg, diffusion bands	$H_3O^+ + \bullet OH + e^-_{aq}$	50
	$H_2O + \Delta E$	50
Dissociative attachment	$\bullet OH + OH^- + H_2$	100

Ref: J. Comput. Phys. 274, 841-882 (2014)

Chemistry / Chemical stage: Diffusion of molecules



- After the physico-chemical stage, molecules **diffuse, breaking-up spurs**.
- Finally, the molecules are distributed **homogeneously**, after 1 µs from irradiation.
- Geant4-DNA uses a table to control the diffusion speed. The user can change these values.



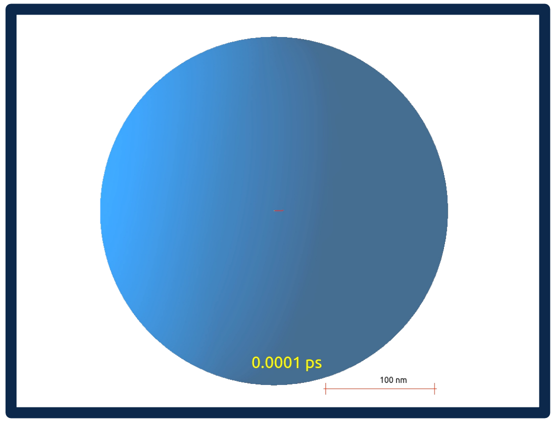
Species	Diffusion coefficient D $(10^{-9}\ m^2\ s^{-1})$
H_3O^+	9.0
H•	7.0
OH^-	5.0
e^-_{aq}	4.9
H_2	5.0
•OH	2.8
H_2O_2	1.4
H_2O	2.0

Ref: J. Comput. Phys. 274, 841-882 (2014)

Chemistry / Chemical stage: Diffusion of molecules

SBS (Step-By-Step)

- **Brownian transport** of molecules using the Smoluchowski model
- Chemical species are represented by point objects which diffuse in the liquid medium (continuum). Chemical reactions are « **controlled by diffusion** »: two reactants interact when their separation is smaller than the reaction radius, which is calculated from the rate constant of the reaction.
- *8 species, 9 chemical reactions*

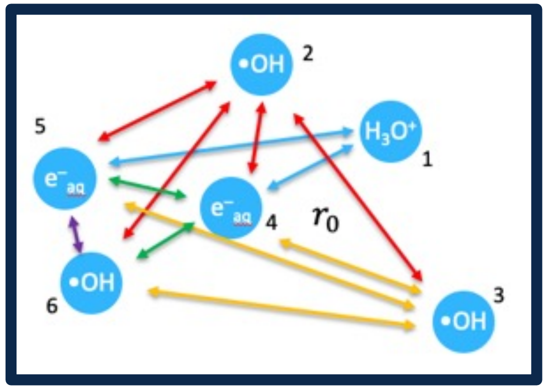


+: Tracking of species

-: Very slow & memory cons.

IRT (Independent Reaction Time)

- From the 1980’s by Clifford, Green et al., **widely used today**.
- Iterative process where the approximation of « **independent pairs** » is assumed: calculates the reaction times between all possible pairs of reactive species, as if they were isolated. Then, reactions occur one by one, starting with the pairs having the **shortest reaction times**.
- No longer necessary to diffuse the chemical species and to calculate the possible reactions between the species at each time step.
- *15 species, 72 chemical reactions (totally & partially diff. controlled)*
- A « **synchronous** » alternative hybrid version (« IRT-sync ») which gives all spatio-temporal info. on radicals required for combination with geometries

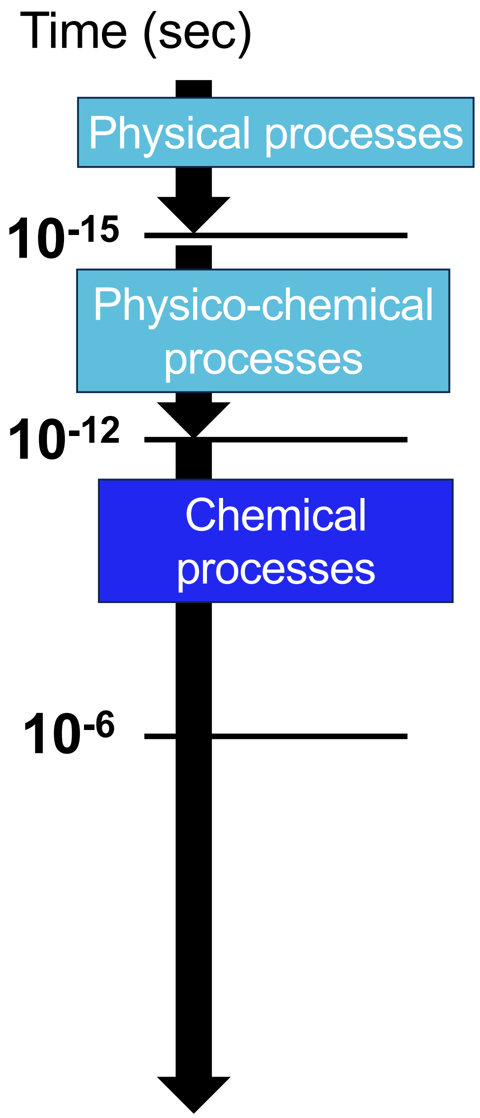


Clifford et al. (1986)

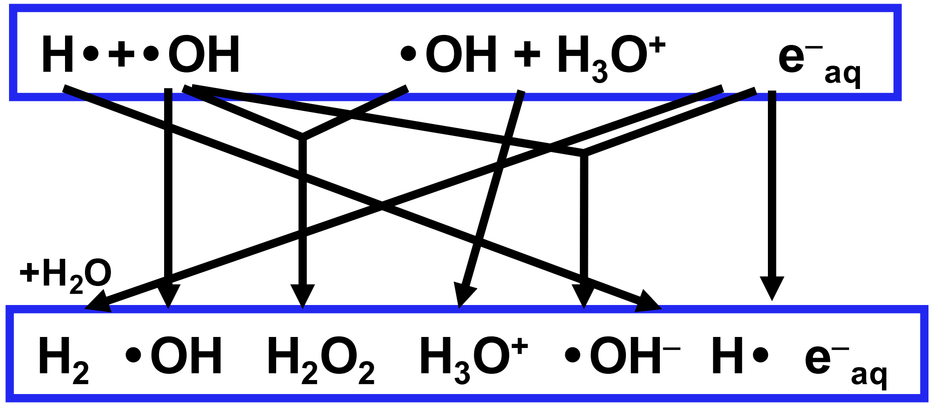
+: Very fast

-: Tracking of species

Chemistry / Chemical stage: Reactions



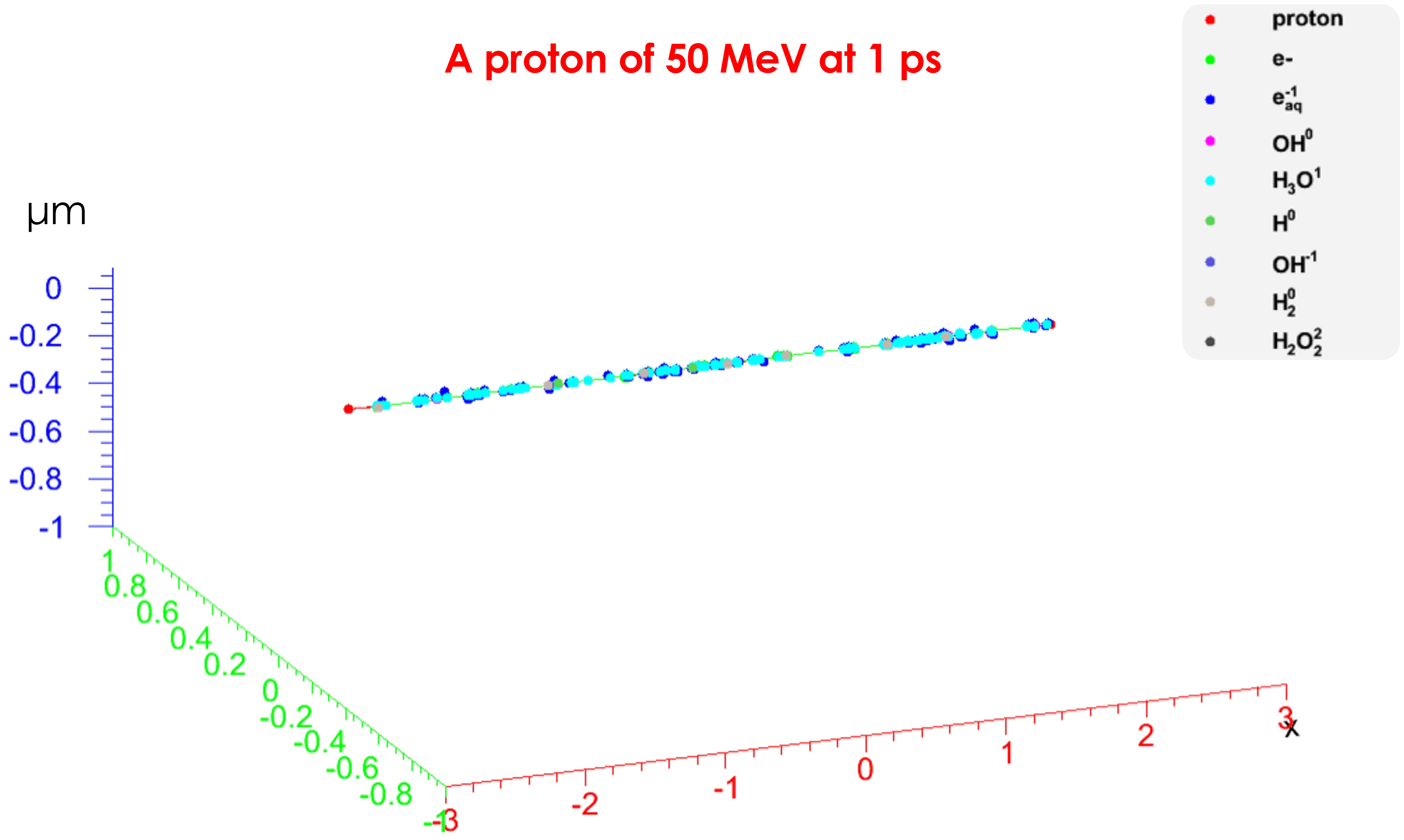
- During the chemical stage, a molecule can encounter and react with another molecule, creating a new molecule.
- Geant4-DNA uses a table to manage the reaction probabilities, e.g. as listed.



Reaction	Reaction rate (10^7 m^3 mol^{-1} s^{-1})
$H_3O^+ + OH^- \rightarrow 2\ H_2O$	14.3
$\bullet OH + e^-_{aq} \rightarrow OH^-$	2.95
$H\bullet + e^-_{aq} + H_2O \rightarrow OH^- + H_2$	2.65
$H_3O^+ + e^-_{aq} \rightarrow H\bullet + H_2O$	2.11
$H\bullet + \bullet OH \rightarrow H_2O$	1.44
$H_2O_2 + e^-_{aq} \rightarrow OH^- + \bullet OH$	1.41
$H\bullet + H\bullet \rightarrow H_2$	1.20
$e^-_{aq} + e^-_{aq} + 2\ H_2O \rightarrow 2\ OH^- + H_2$	0.50
$\bullet OH + \bullet OH \rightarrow H_2O_2$	0.44

Ref: J. Comput. Phys. 274, 841-882 (2014)

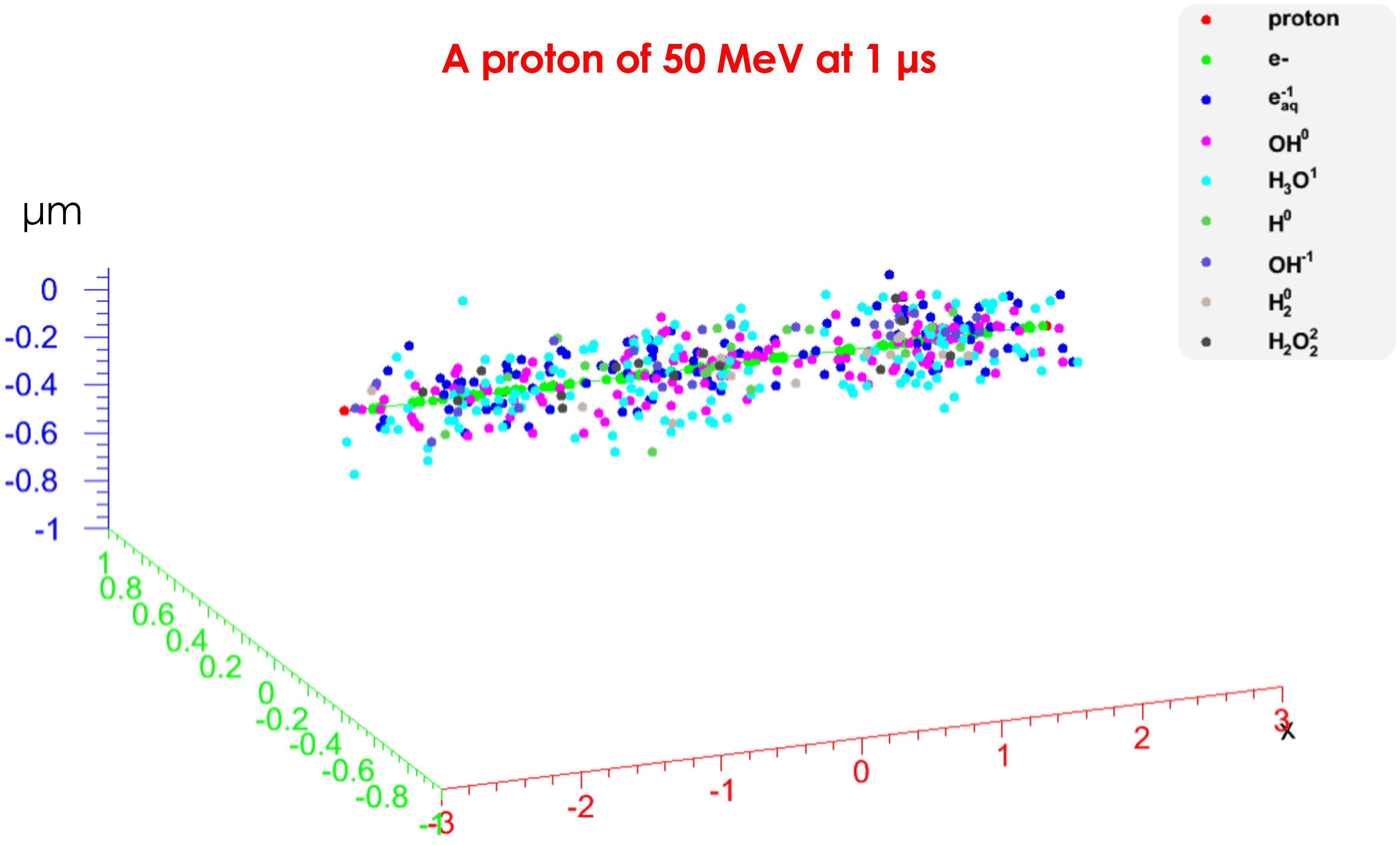
Distribution of chemical molecules using Geant4-DNA



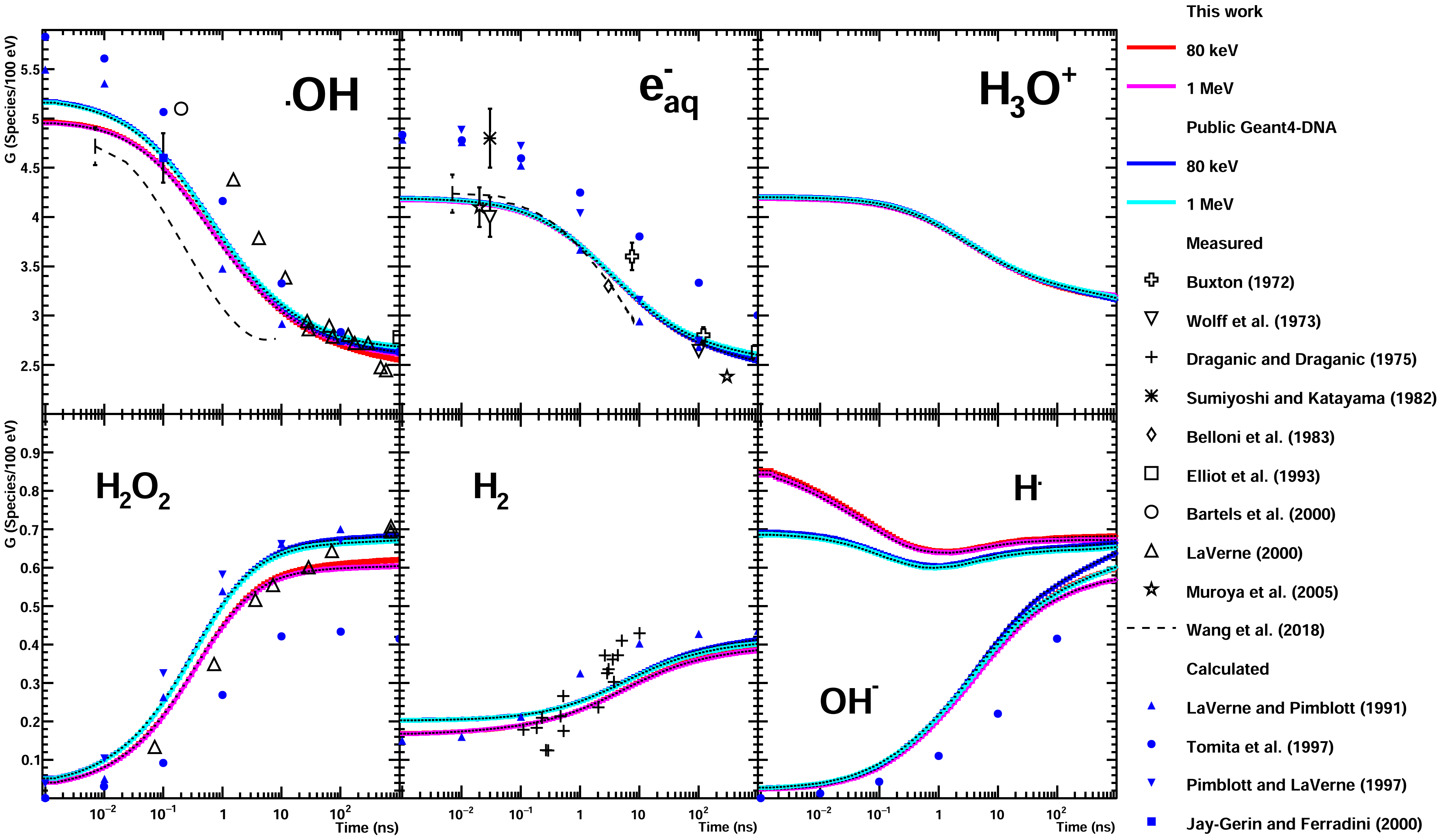
A proton of 50 MeV at 1 ps

Distribution of chemical molecules using Geant4-DNA

A proton of 50 MeV at 1 μs

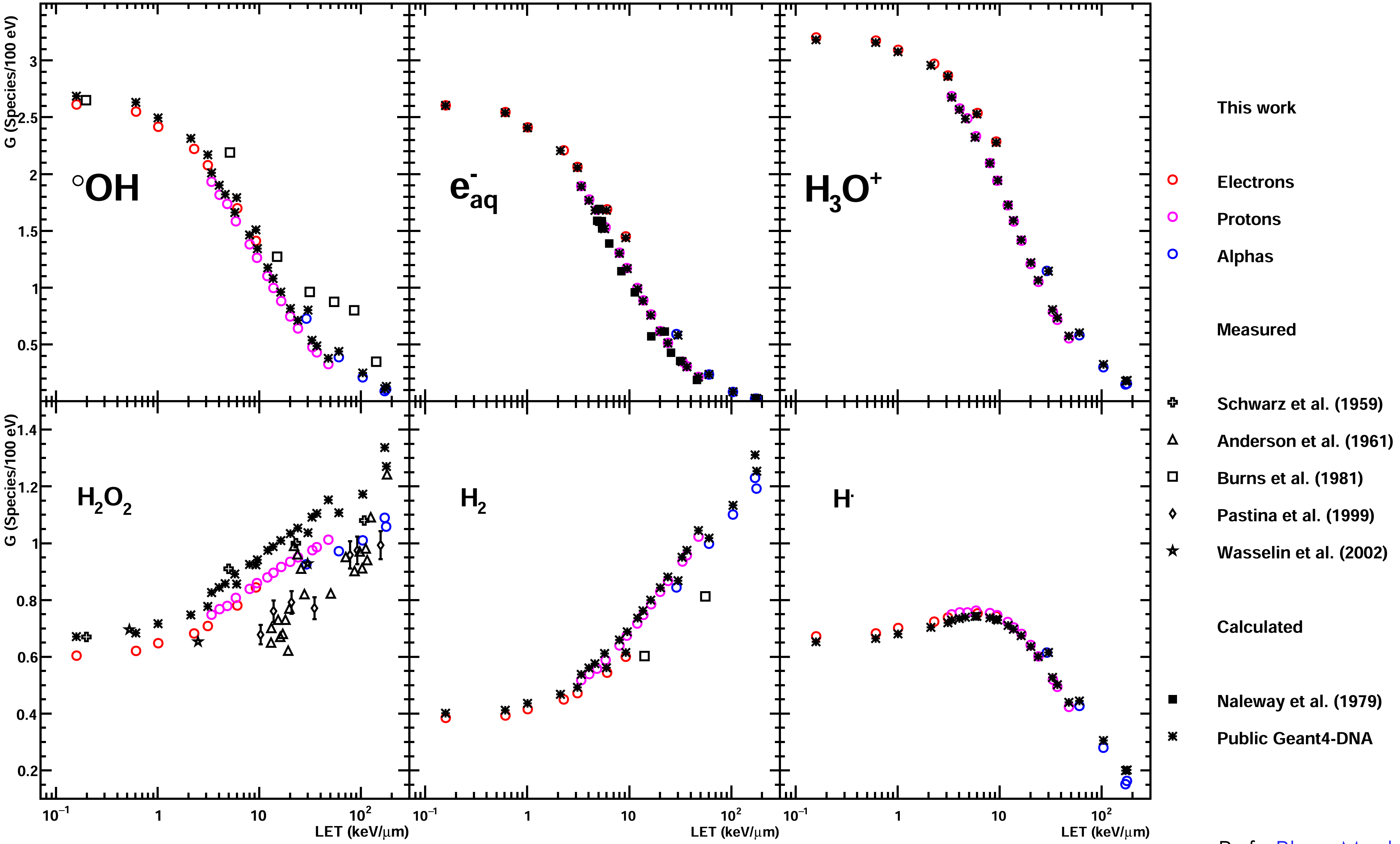


Validation and verification of chemistry: G-value vs time



Ref.: Phys. Med. 88, 86-90 (2021)

Validation and verification of chemistry: G-value vs LET

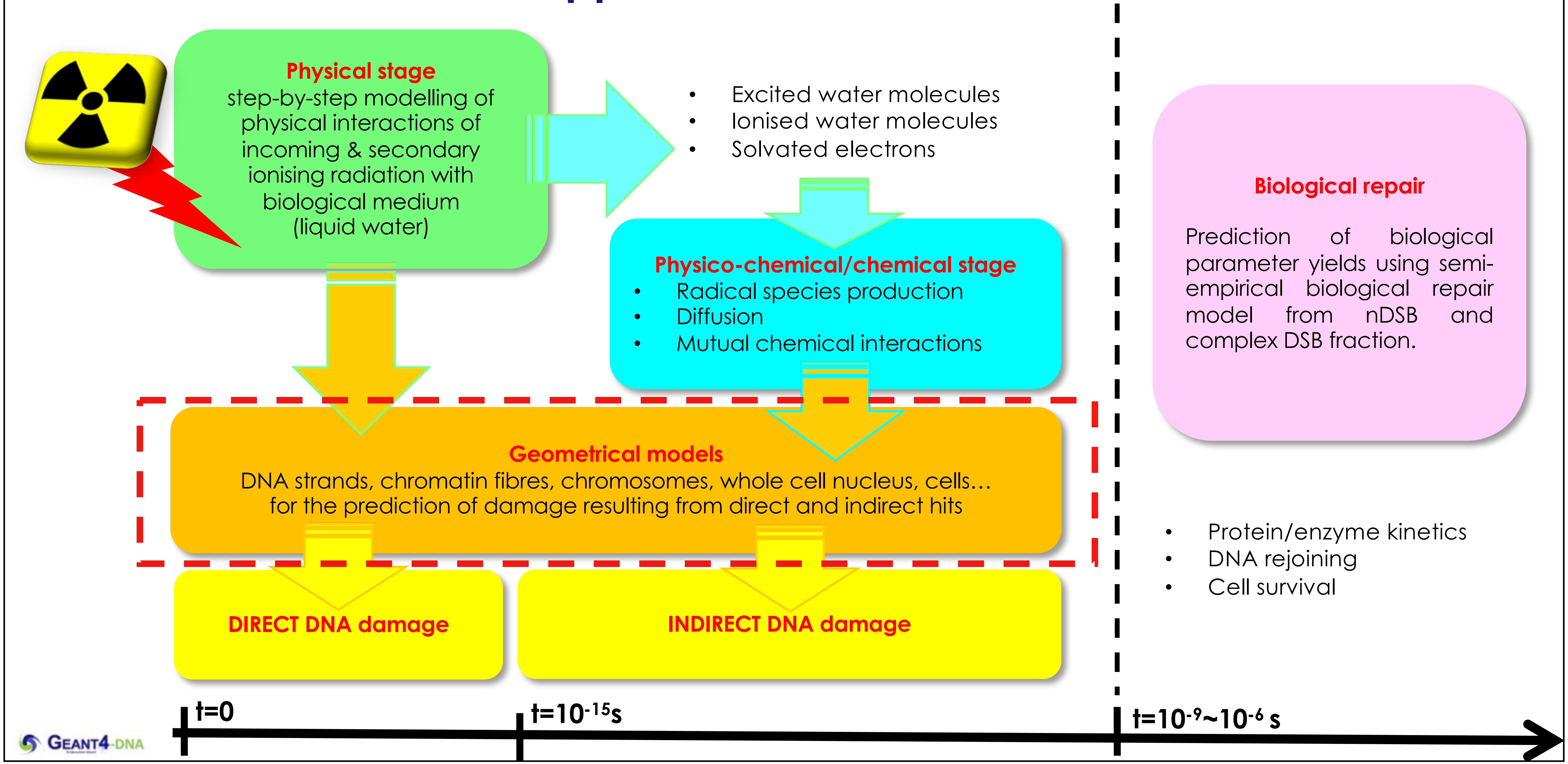


Ref.: Phys. Med. 88, 86-90 (2021)

Contents of this talk

- Context of the Geant4-DNA project
- Physical stage
- Physico-chemical & chemical stage
- Geometrical models
- DNA damage and biological models
- Tips

The Geant4-DNA approach



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step-by-step modelling of physical interactions of incoming & secondary ionising radiation with biological medium (liquid water)

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DNA strands, chromatin fibres, chromosomes, whole cell nucleus, cells…
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DIRECT DNA damage

INDIRECT DNA damage

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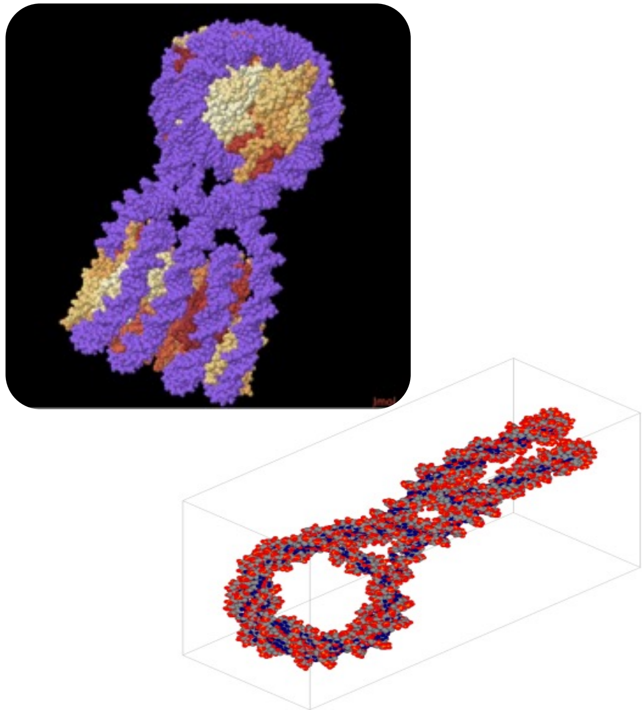
Prediction of biological parameter yields using semi-empirical biological repair model from nDSB and complex DSB fraction.

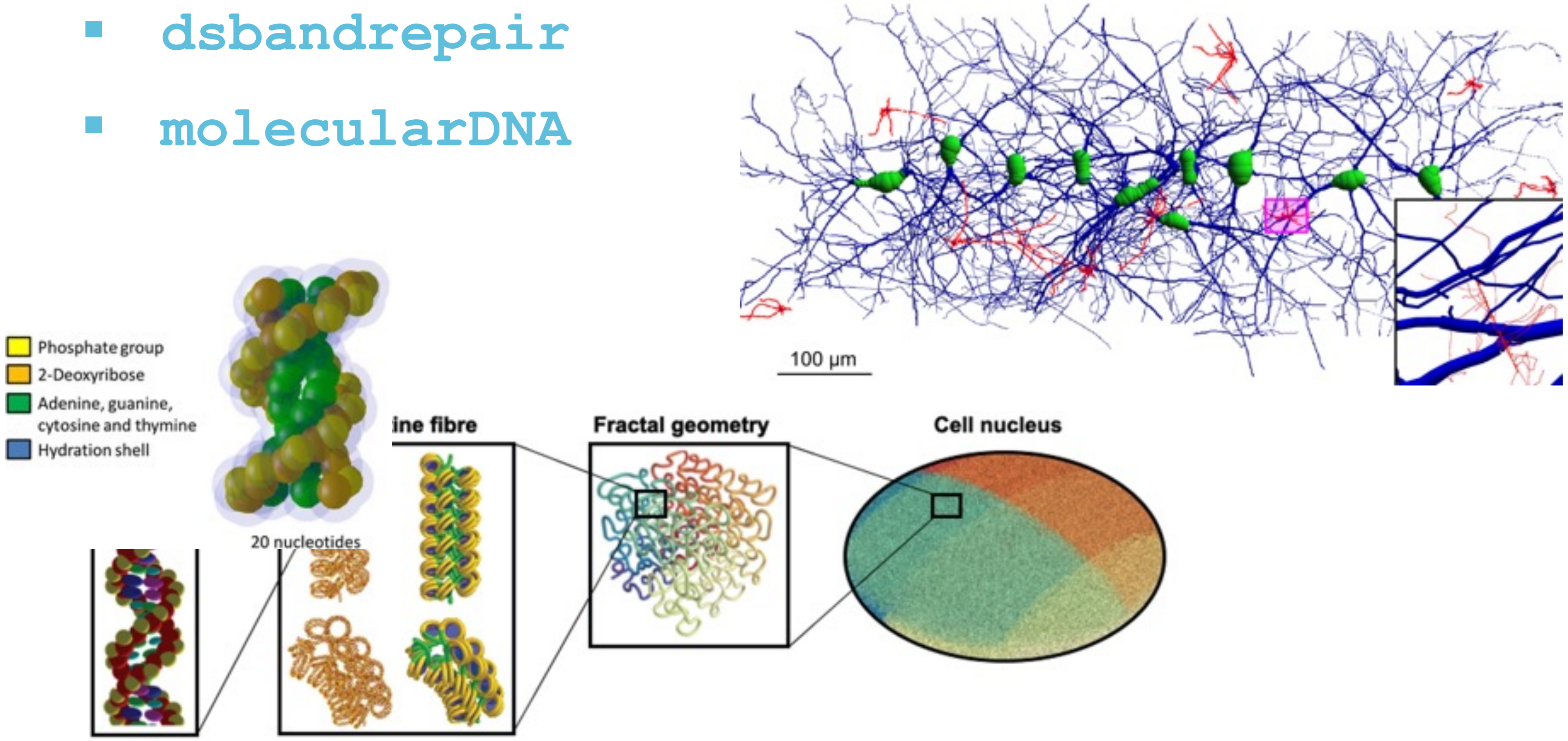
- Protein/enzyme kinetics
- DNA rejoining
- Cell survival

Geant4-DNA **geometry models** (in examples)

10^{-10} 10^{-9} 10^{-6} [m]

- **Atomic** scale
  - `pdb4dna`
- **Molecular** scale
  - `wholeNuclearDNA`
  - `dnadamage1,2`
  - `dsbandrepair`
  - `molecularDNA`
- **Cellular** scale or larger
  - `microbeam`
  - `neuron`

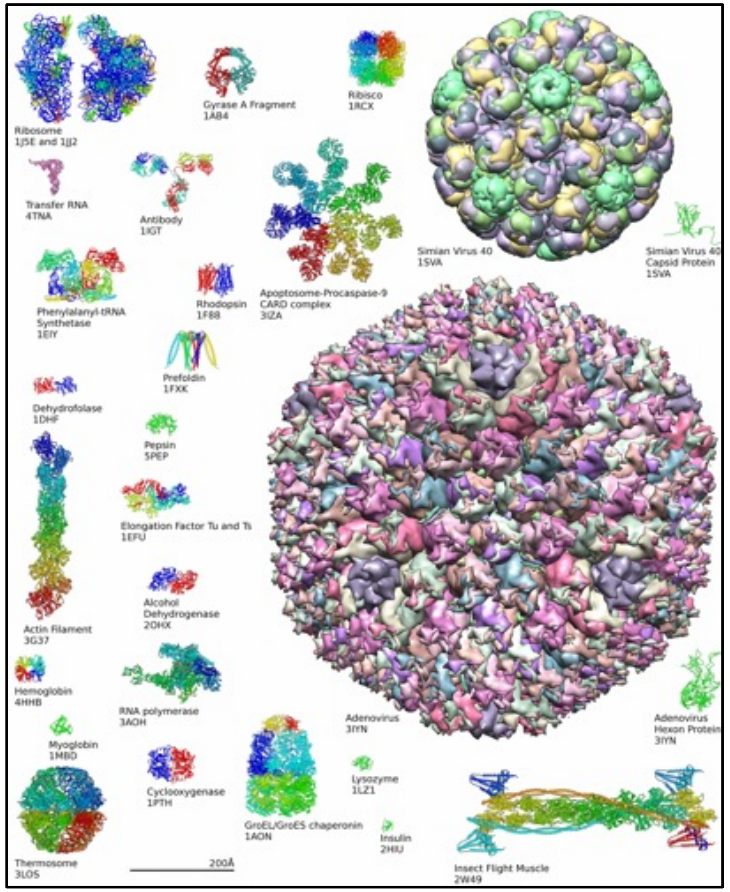




Geometry: Atomic scale
pdb4dna example

Ref.: [Comput. Phys. Commun. 192, 282-288 (2015)]

- **Protein Data Bank (PDB)** http://www.rcsb.org/pdb/
  - 3D structure of molecules
  - Proteins
  - Nucleic acids



E.g.: 1ZBB.pdb
- Tetranucleosome
- 2 nucloosomes: 347 pairs of bases
- (9,5 x 15,0 x 25,1 nm^3)

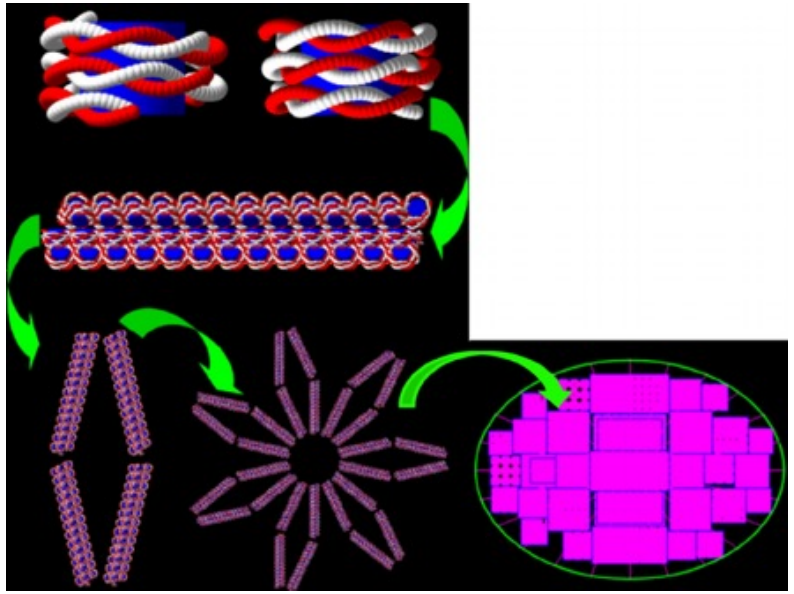
```
HEADER    STRUCTURAL PROTEIN/DNA                08-APR-05   1ZBB
TITLE     STRUCTURE OF THE 4_601_167 TETRANUCLEOSOME
...
ATOM      1  O5'  DA I   1     70.094  16.969 123.433  0.50238.00     O
ATOM      2  C5'  DA I   1     70.682  18.216 123.054  0.50238.00     C
ATOM      3  C4'  DA I   1     69.655  19.289 122.776  0.50238.00     C
...
TER   14223       DT J 347
...
HELIX    1   1 GLY A   44  SER A   57  1                          14
HELIX    2   2 ARG A   63  ASP A   77  1                          15
...
SHEET    1   A 2 ARG A  83  PHE A  84  0
SHEET    2   A 2 THR B  80  VAL B  81  1  O  VAL B  81   N  ARG A  83
```

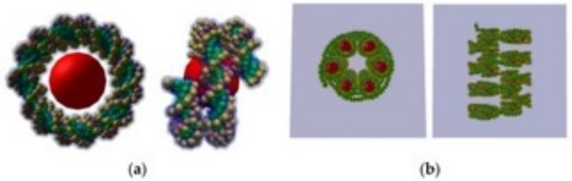
See implementation in
`geant4/examples/extended/medical/dna/pdb4dna`

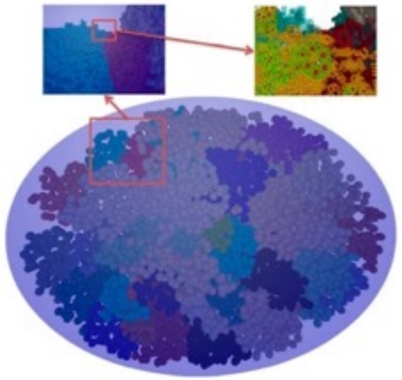
See http://geant4-dna.org → Examples

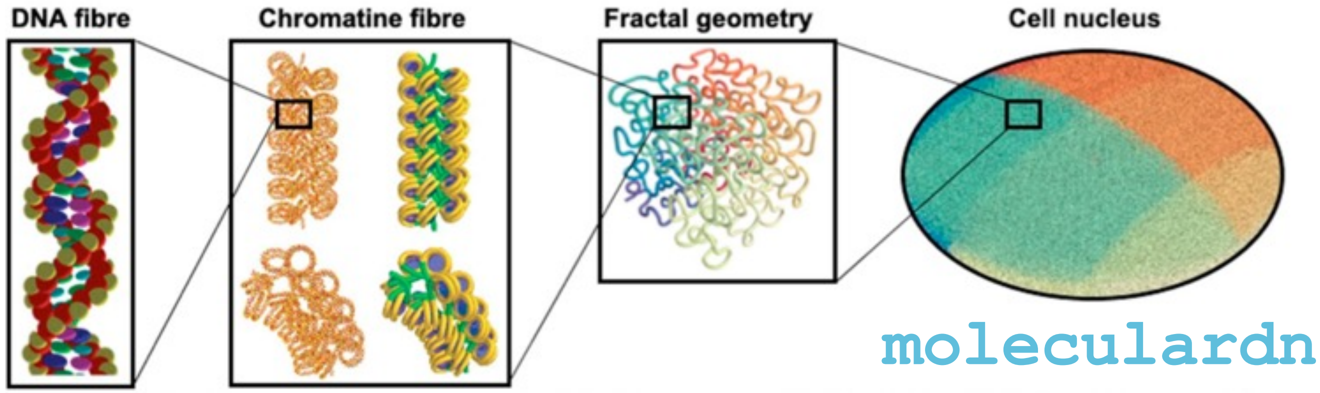
Geometry: Molecular scale

`wholeNuclearDNA`







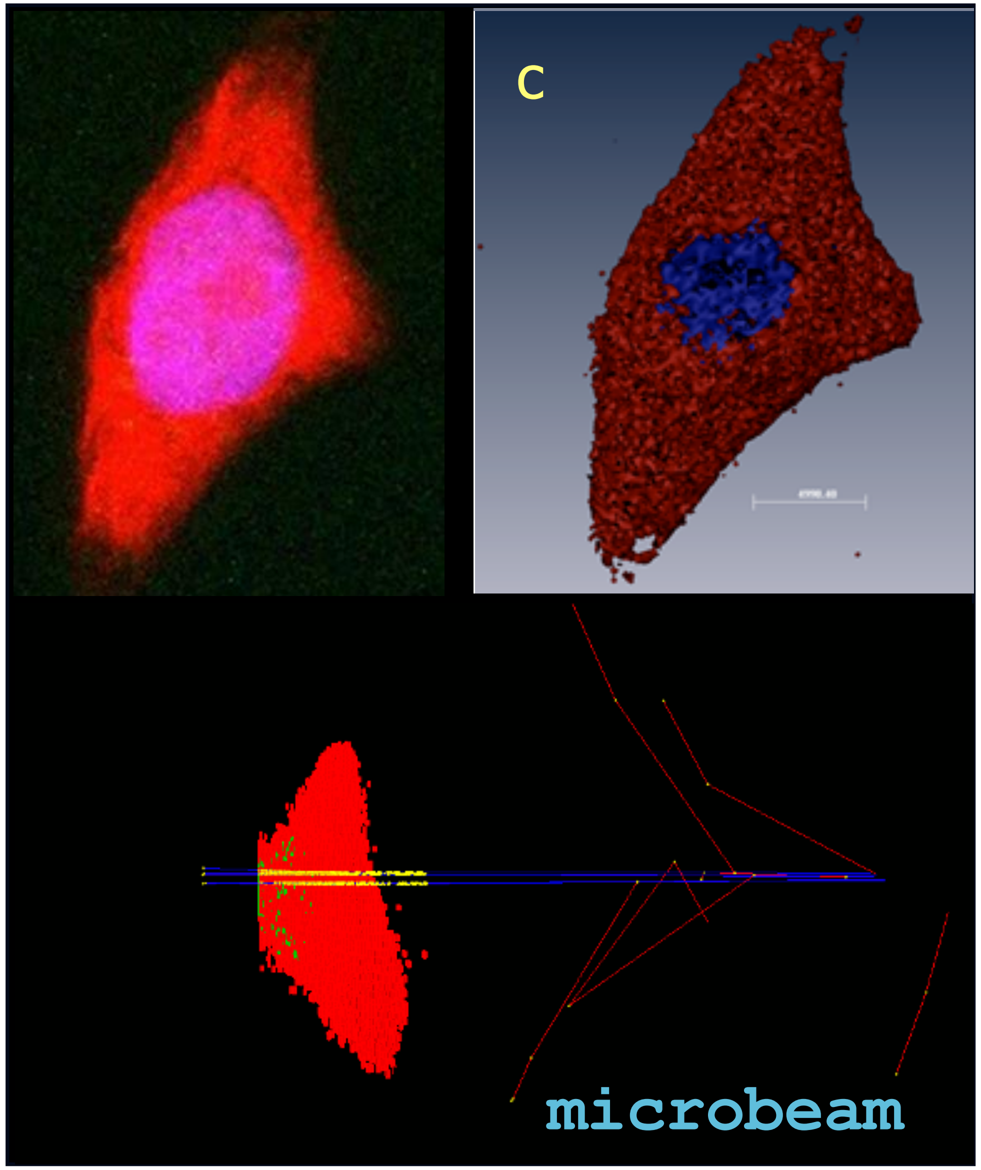


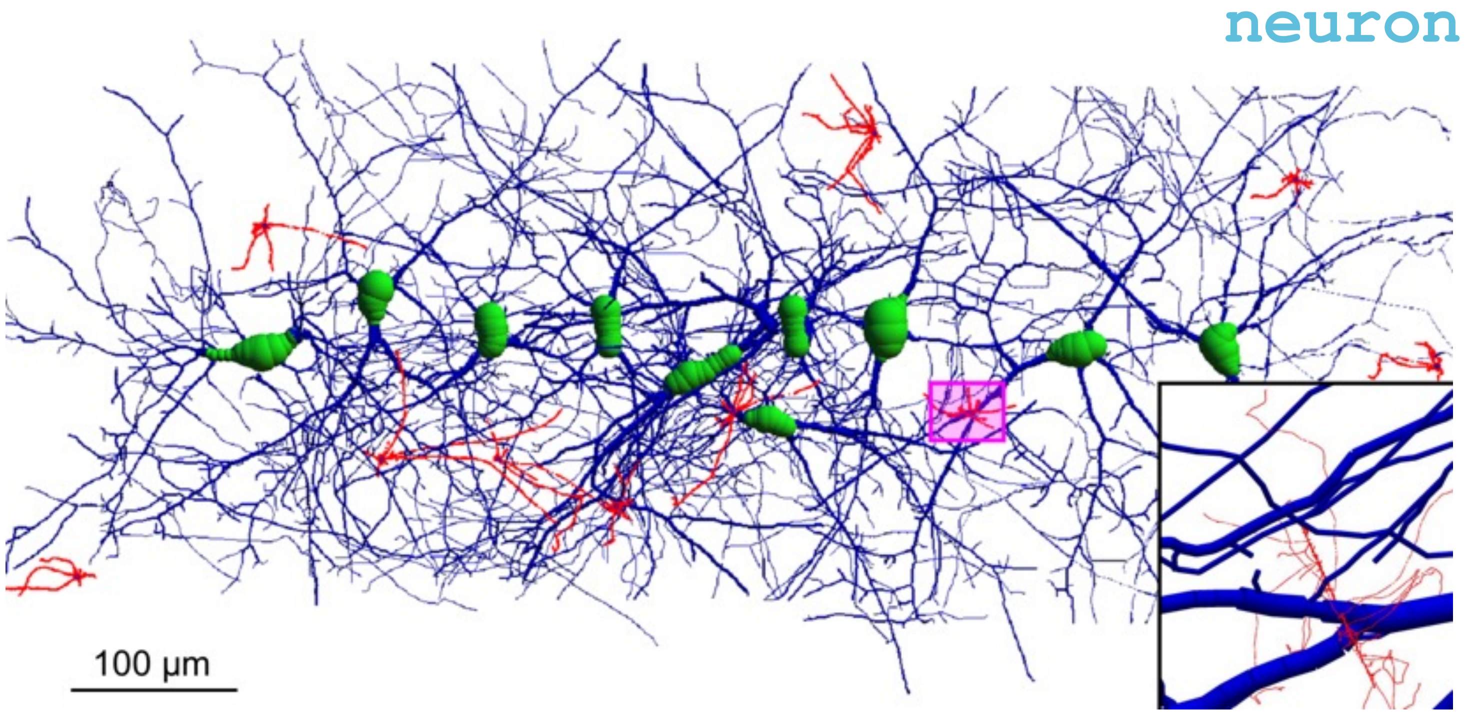
`moleculardna`

- Geant4-DNA offers **5 examples** of cell nucleus models, which consist of molecular-based DNA geometry models
  - `wholeNuclearDNA`*
  - `dnadamage1,2`
  - `dsbandrepair`
  - `moleculardna`
- These examples offer the possibility of simulating the **water radiolysis*** as well as the **energy deposition** of ionizing radiation at a nanometric scale within a geometrical representation of the **whole DNA molecule contained in a cell nucleus**.

See http://geant4-dna.org → Examples

Geometry: Cellular scale or Larger



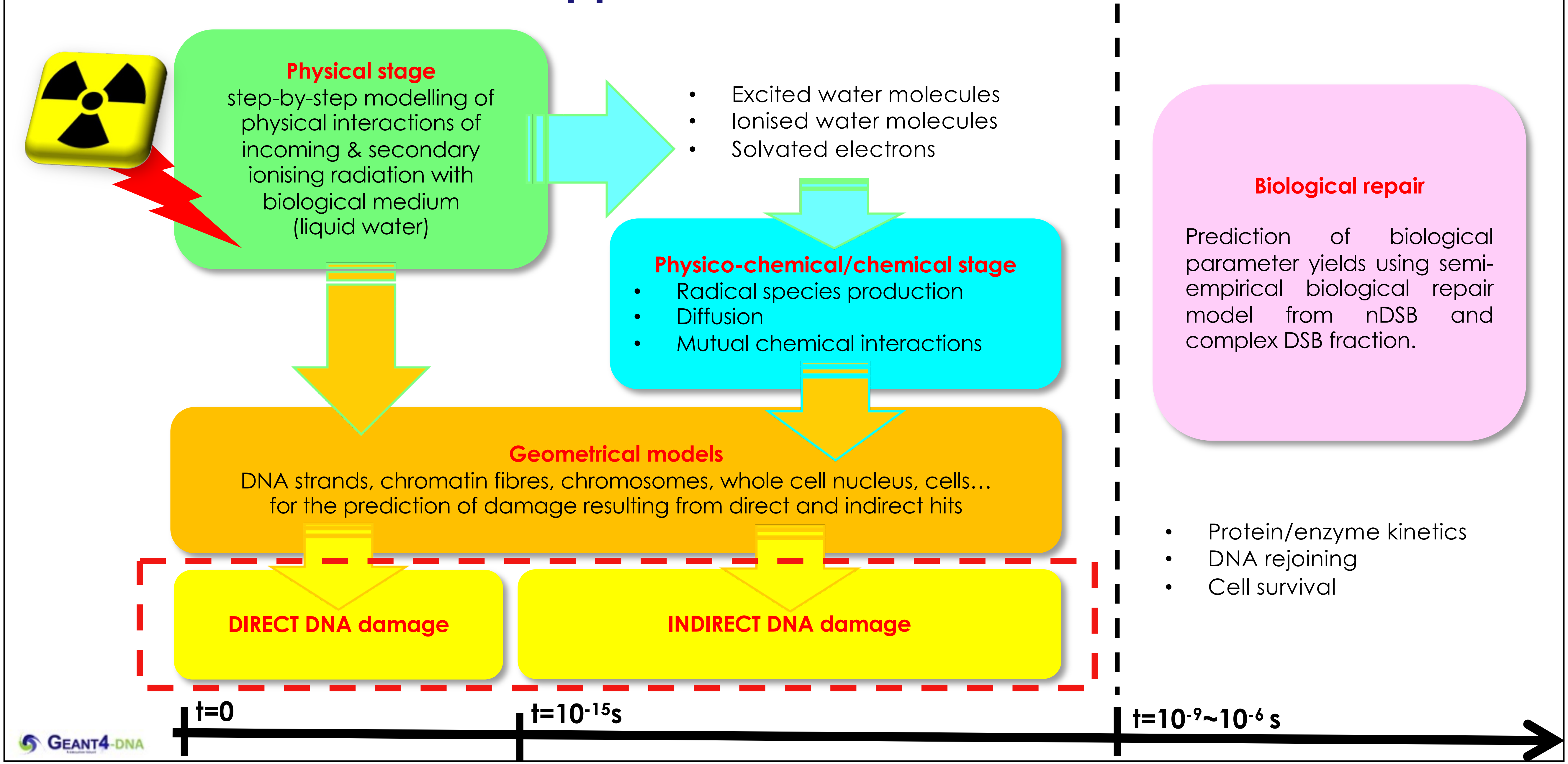


- Geant4-DNA also offers 2 examples that provide realistic geometry of a cell and neurons:
  - `microbeam`
  - `neuron`

See http://geant4-dna.org → Examples

Contents of this talk

The Geant4-DNA approach



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DIRECT DNA damage

INDIRECT DNA damage

Biological repair

Prediction of biological parameter yields using semi-empirical biological repair model from nDSB and complex DSB fraction.

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- DNA rejoining
- Cell survival

t=0

t=10^{-15}s

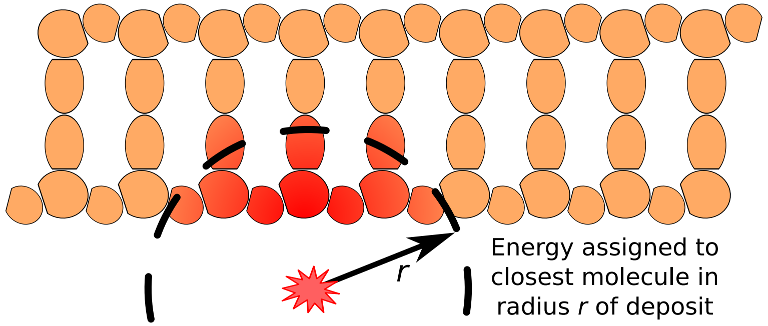
t=10^{-9}~10^{-6} s

DNA damage and biological models

- Geant4-DNA follows a **standard** DNA damage calculation approach:
  - **Direct action: Structural damage to DNA molecules induced by excitation/ionisation processes**
    - Score local energy deposition in a nanoscopic domain: nanodosimetric approach
    - Two damage probability models are commonly used:
      - Threshold model (KURBUC model)
      - Proportional model (PARTRAC model)
  - **Indirect action: Structural damage to DNA molecules induced by a chemical process**, typically interaction with reactive oxygen species
    - A constant probability model can be used (the probability should be adjusted)
- **DNA damage classification**:
  - The complexity of the DNA damage structure affects the subsequent biological repair process and its endpoint. In particular, two strand breaks within a short distance (leading to physical disconnection of the DNA fiber), so-called **Double Strand Break (DSB)**, induce crucial radiobiological effects such as cell death.
  - Thus, the classification of DNA damage is one of the most important issues in evaluating the radiobiological effects.
  - So far, two classification models are proposed: Nikjoo's model and the Standard DNA Damage (SDD) model.

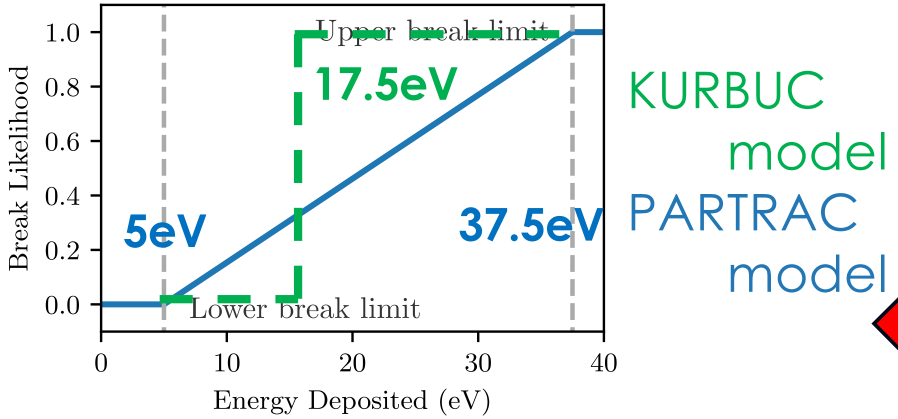
How can we score DNA damage?
- DNA damage model – (e.g. `moleculardna`)

Direct action model

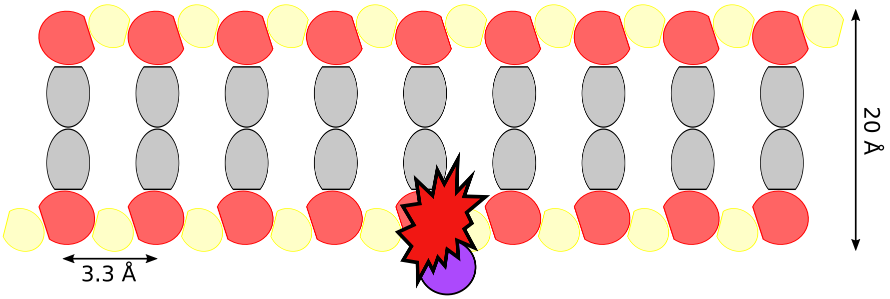


R_{direct} (R of nucleotides: 2.3~2.6 Å)

E_{dep} assigned to closest strand molecule



Indirect action model

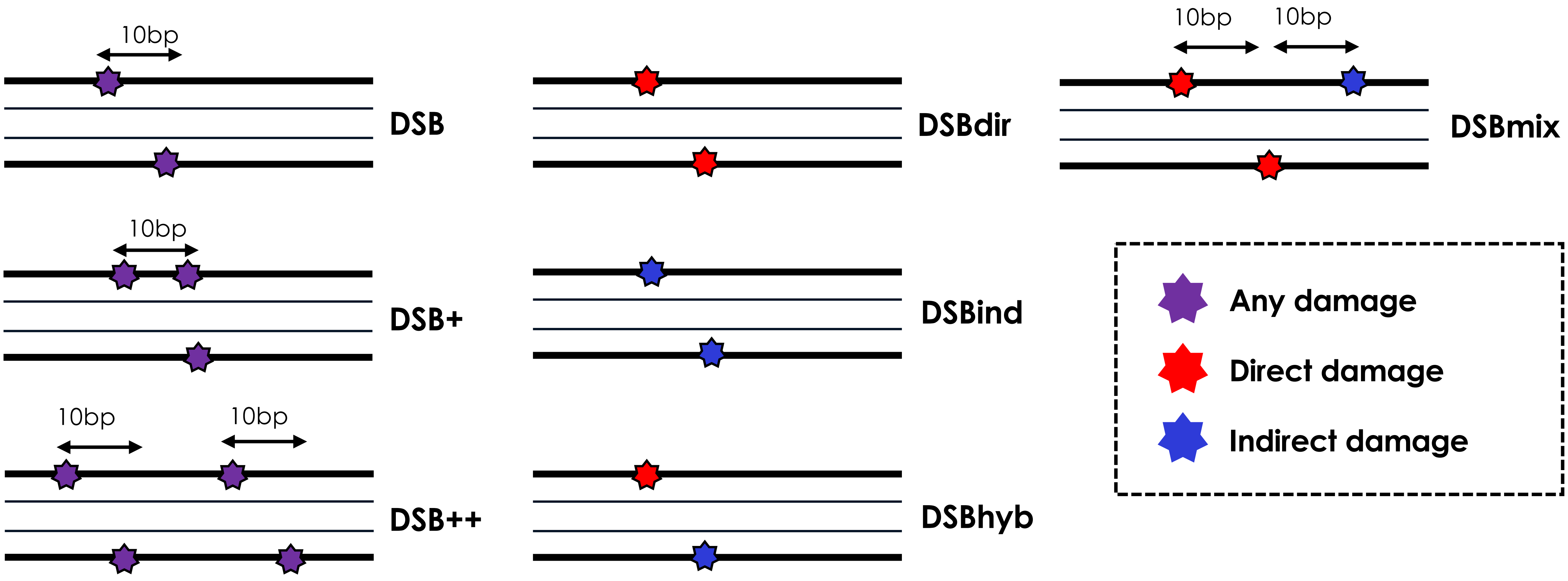


$\mathrm{DNA} + {\cdot}\mathrm{OH} \rightarrow \mathrm{SSB}$

P_{OH}: possible range (measured) 40 – 80%

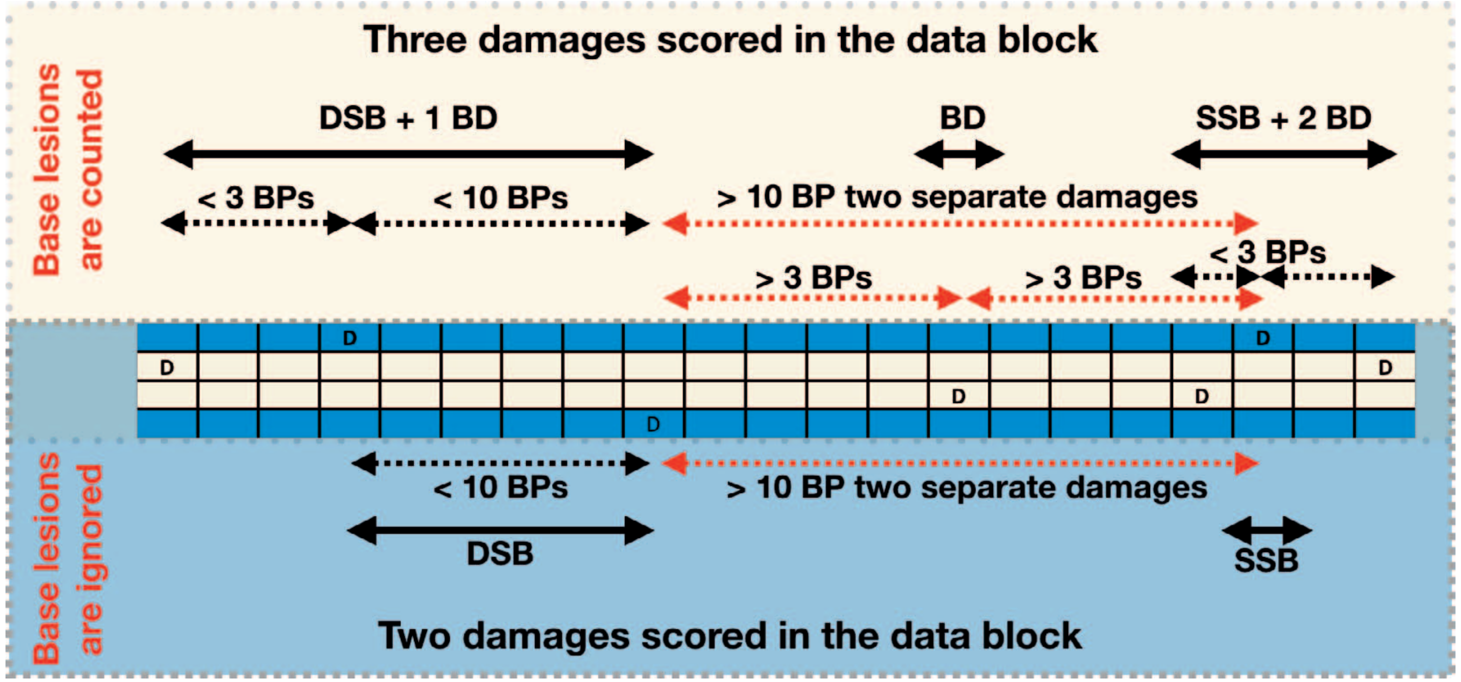
Each single damage is regarded as a strand break.

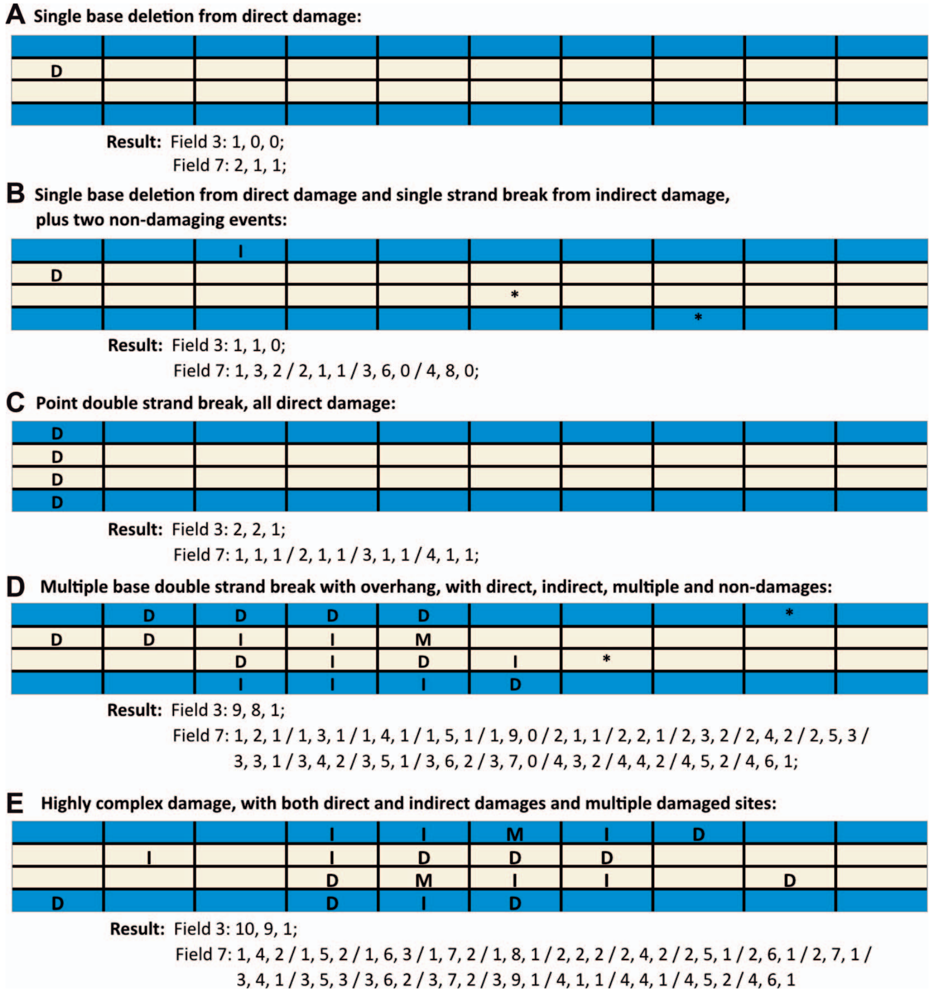
Damage classification: Nikjoo's classification



Ref.: [Radiat. Res. 156, 577–583 (2001)]

Damage classification: SDD classification





A Single base deletion from direct damage:

D									

Result: Field 3: 1, 0, 0;
Field 7: 2, 1, 1;

B Single base deletion from direct damage and single strand break from indirect damage, plus two non-damaging events:

		I							
D									
					*				
							*		

Result: Field 3: 1, 1, 0;
Field 7: 1, 3, 2 / 2, 1, 1 / 3, 6, 0 / 4, 8, 0;

C Point double strand break, all direct damage:

D									
D									
D									
D									

Result: Field 3: 2, 2, 1;
Field 7: 1, 1, 1 / 2, 1, 1 / 3, 1, 1 / 4, 1, 1;

D Multiple base double strand break with overhang, with direct, indirect, multiple and non-damages:

	D	D	D	D				*	
D	D	I	I	M					
		D	I	D	I	*			
		I	I	I	D				

Result: Field 3: 9, 8, 1;
Field 7: 1, 2, 1 / 1, 3, 1 / 1, 4, 1 / 1, 5, 1 / 1, 9, 0 / 2, 1, 1 / 2, 2, 1 / 2, 3, 2 / 2, 4, 2 / 2, 5, 3 /
3, 3, 1 / 3, 4, 2 / 3, 5, 1 / 3, 6, 2 / 3, 7, 0 / 4, 3, 2 / 4, 4, 2 / 4, 5, 2 / 4, 6, 1;

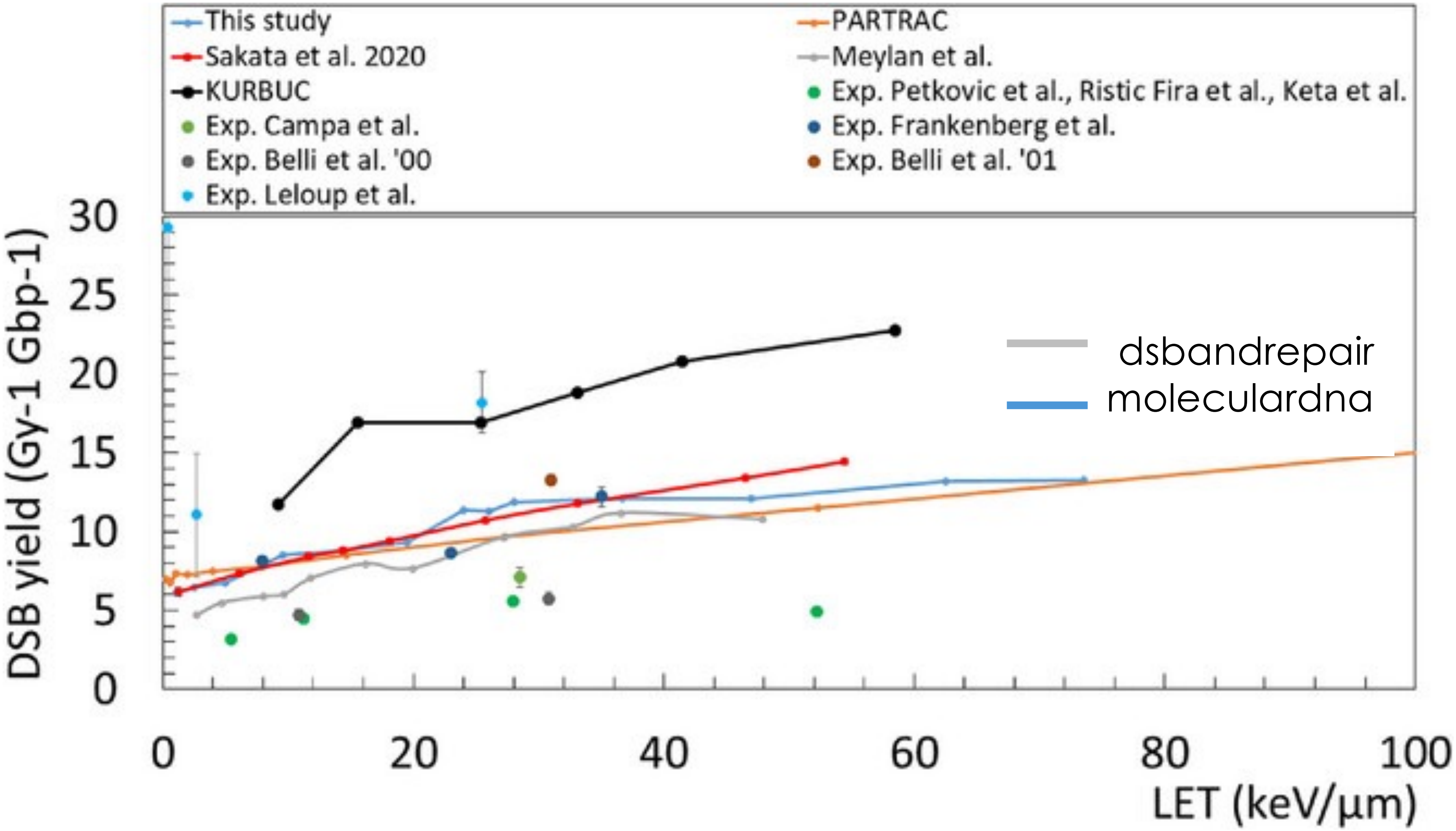
E Highly complex damage, with both direct and indirect damages and multiple damaged sites:

			I	I	M	I	D		
	I		I	D	D	D			
			D	M	I	I		D	
D			D	I	D				

Result: Field 3: 10, 9, 1;
Field 7: 1, 4, 2 / 1, 5, 2 / 1, 6, 3 / 1, 7, 2 / 1, 8, 1 / 2, 2, 2 / 2, 4, 2 / 2, 5, 1 / 2, 6, 1 / 2, 7, 1 /
3, 4, 1 / 3, 5, 3 / 3, 6, 2 / 3, 7, 2 / 3, 9, 1 / 4, 1, 1 / 4, 4, 1 / 4, 5, 2 / 4, 6, 1

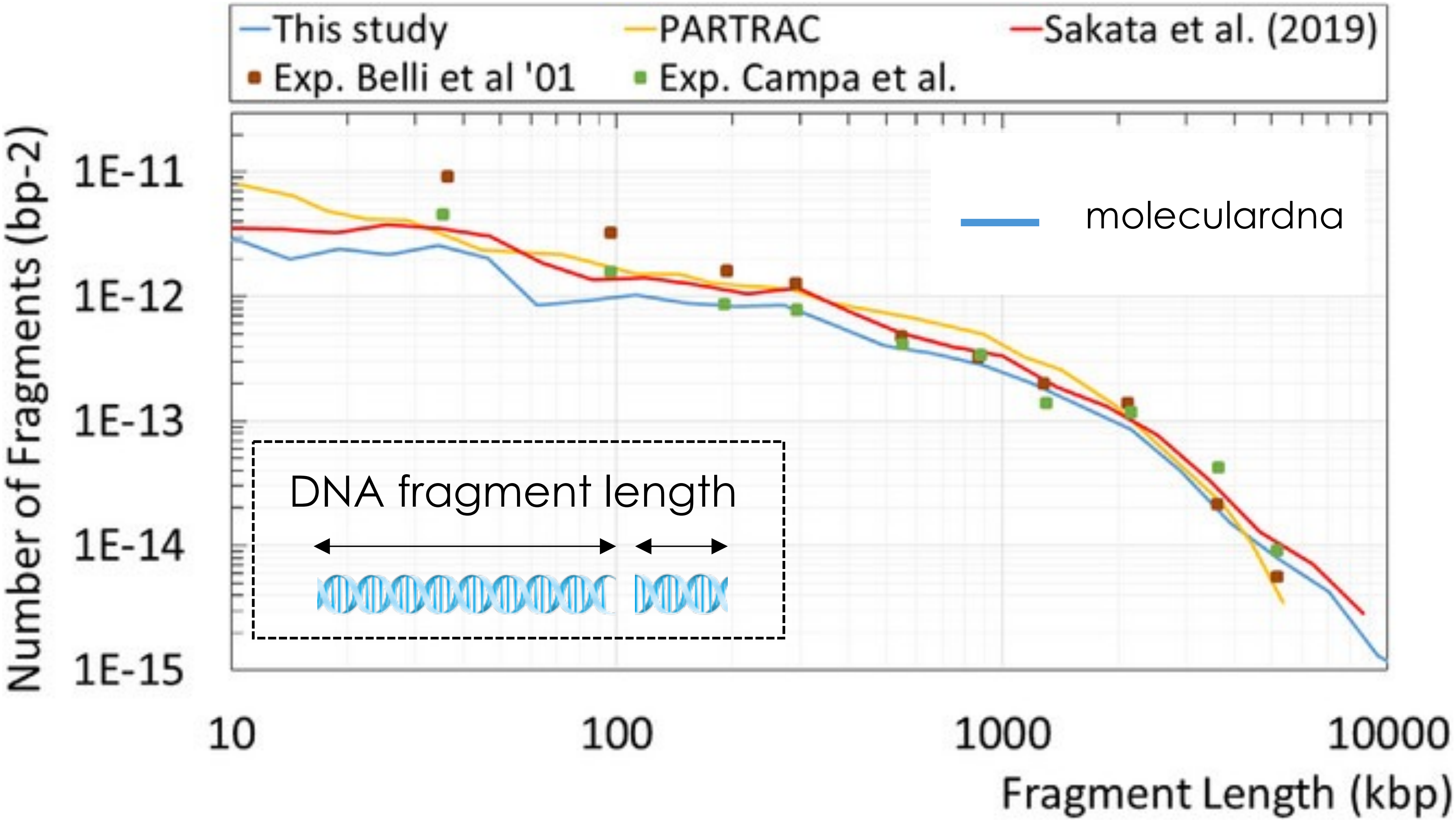
Ref.: Radiat. Res. 191(1), 76-92 (2019)

Validation and verification: Damage yield



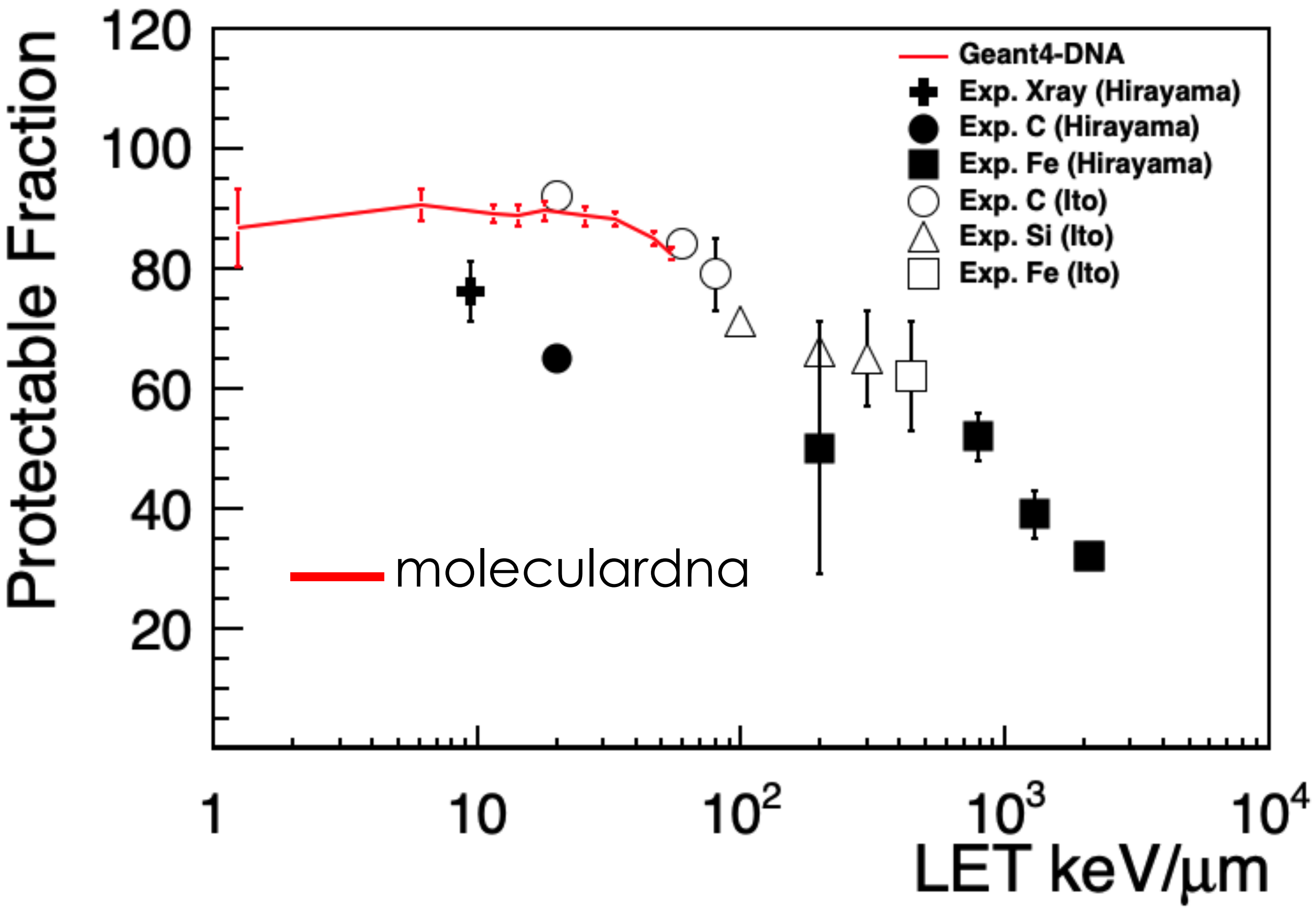
Ref.: Prec. Radiat. Oncol. 7, 4-14 (2023)

Validation and verification: Fragment yield



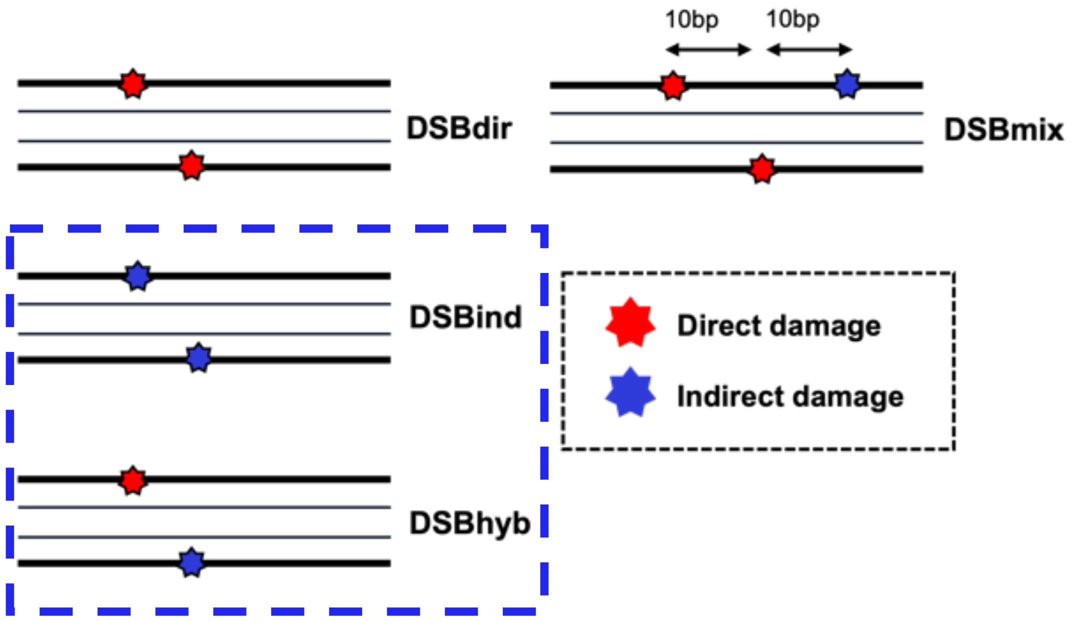
Ref.: Prec. Radiat. Oncol. 7, 4-14 (2023)

Validation and Verification: Indirect damage fraction



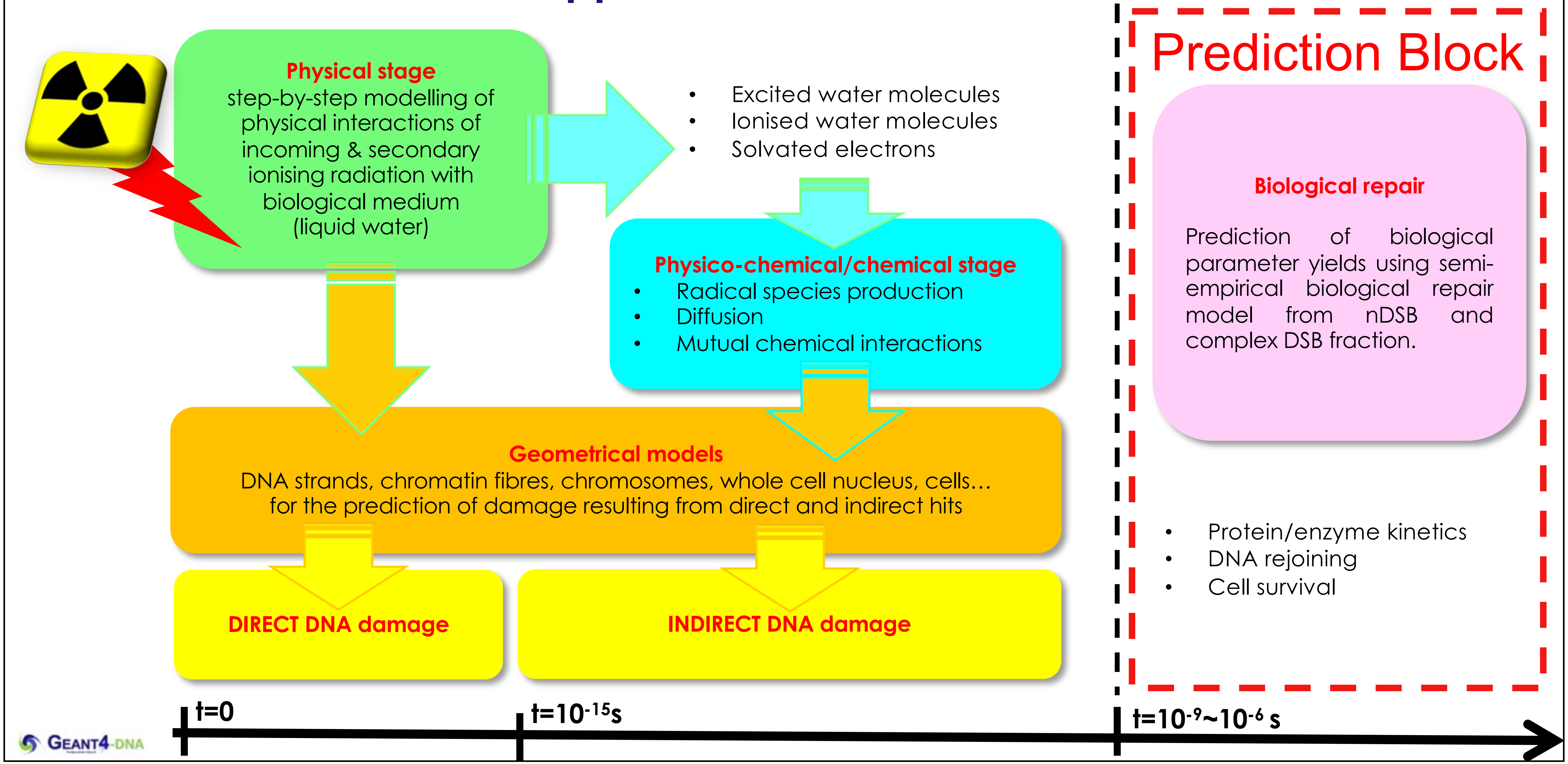
Protectable fraction
(damage type based)

$$\frac{\boxed{N_{\mathrm{DSB}_{ind}} + N_{\mathrm{DSB}_{hyb}}}}{N_{\mathrm{DSB}_{dir}} + N_{\mathrm{DSB}_{mix}} + N_{\mathrm{DSB}_{ind}} + N_{\mathrm{DSB}_{hyb}}}$$



Ref.: Sci. Rep. 10, 20788 (2020)

The Geant4-DNA approach



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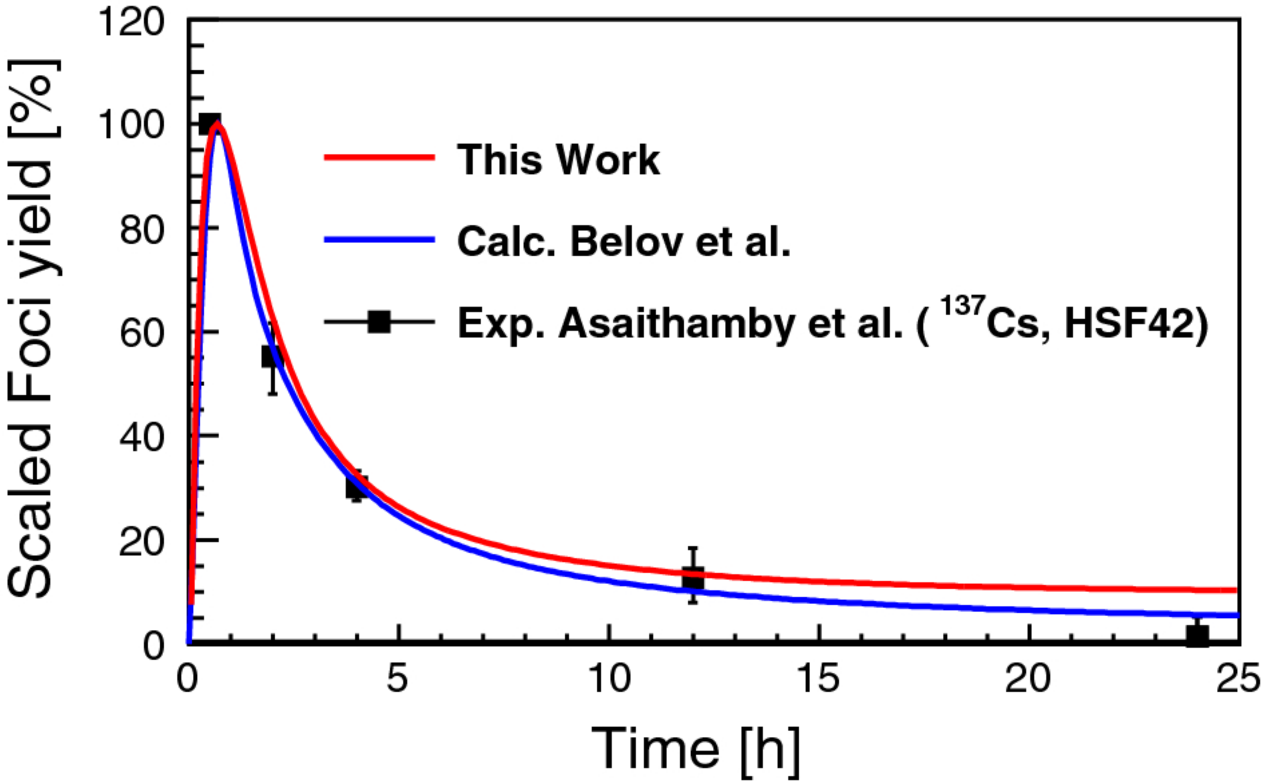
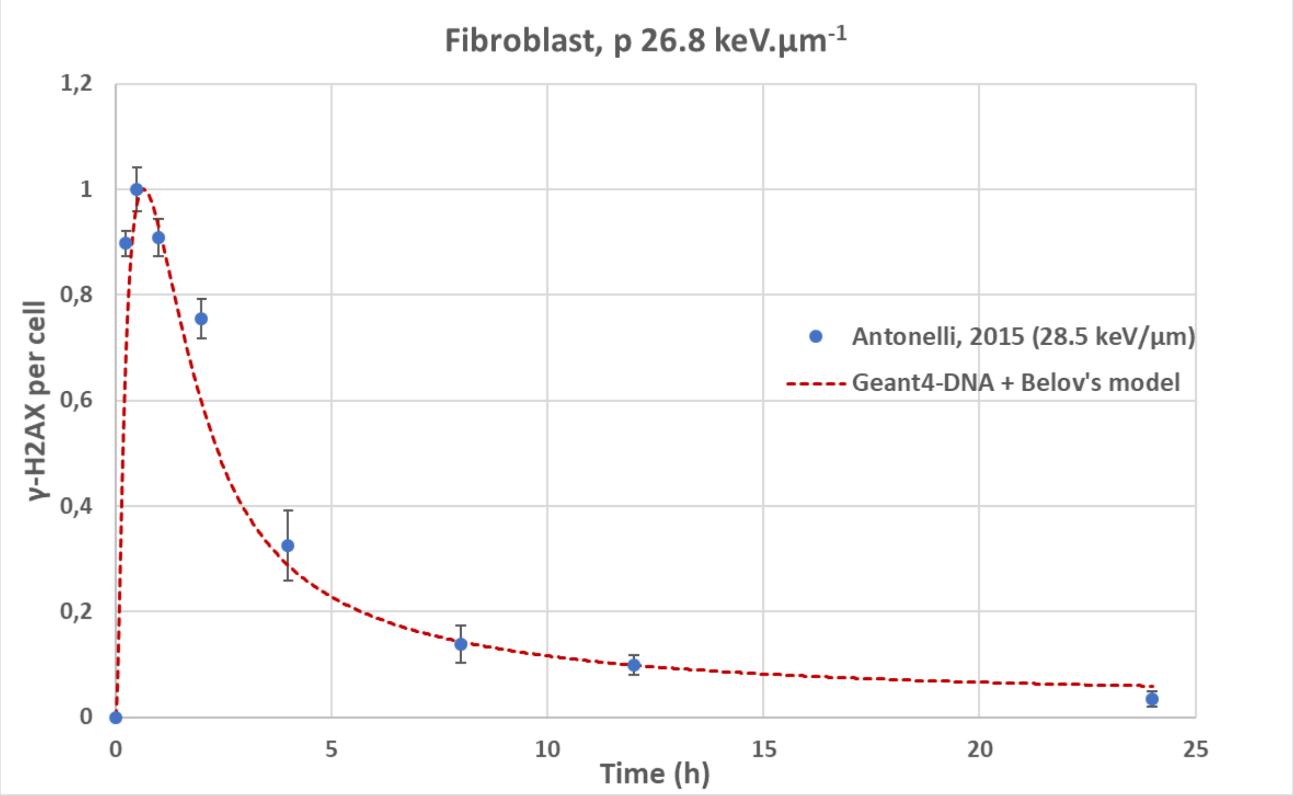
DNA damage and biological models

- Prediction models are able to **link DNA damage to biological endpoints**:
  - **Belov model**: Prediction model of **protein/enzyme accumulation yield** from the number of DSBs and **irreparable fraction**. In Geant4-DNA applications, the irreparable fraction is assumed to be the fraction of complex DSBs w.r.t the total number of DSBs.
  - **Two-Lesion kinetic (TLK)** model: The TLK model model links the number of simple-/complex-DSBs and **cell survival**, considering the rejoining of DSBs and lethality of the residual DNA damage.
  - **Local Effect Model (LEM)-IV**: The LEM-IV calculates **cell survival** from a number of lethal damage that considers the induction of DSBs and their spatial distribution and fast-/slow-rejoining of DSBs.
- Geant4-DNA examples offer such biological prediction models:
  - `wholeNuclearDNA`: No biological prediction model provided (Physics only)
  - `dsbandrepair`: Oleg model, TLK model and LEM-IV model
  - `moleculardna`: Oleg model, TLK model

Validation and verification: time evolution of foci yields





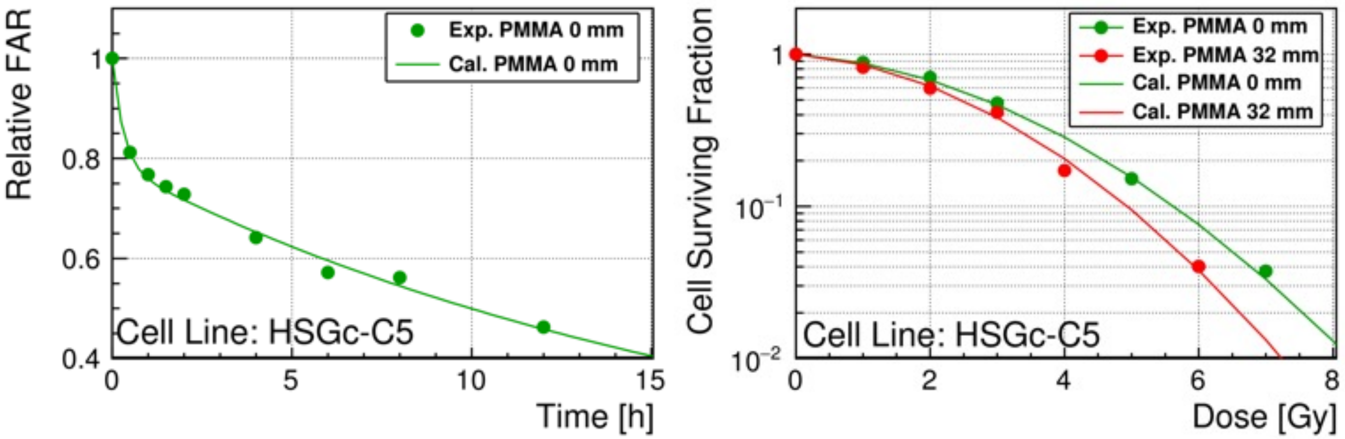
`moleculardna`: for gamma-ray (^{137}Cs)

`dsbandrepair`: for proton

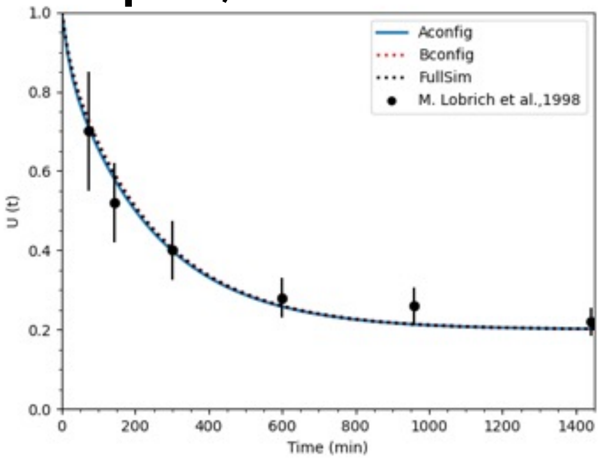
Ref.: Sci. Rep. 10, 20788 (2020)

Validation and verification: DNA rejoining & cell survival

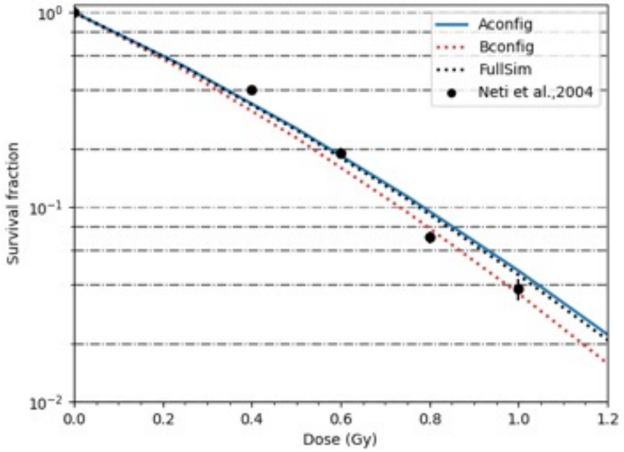
`moleculardna`: proton, TLK model, HSGc-G5 cell



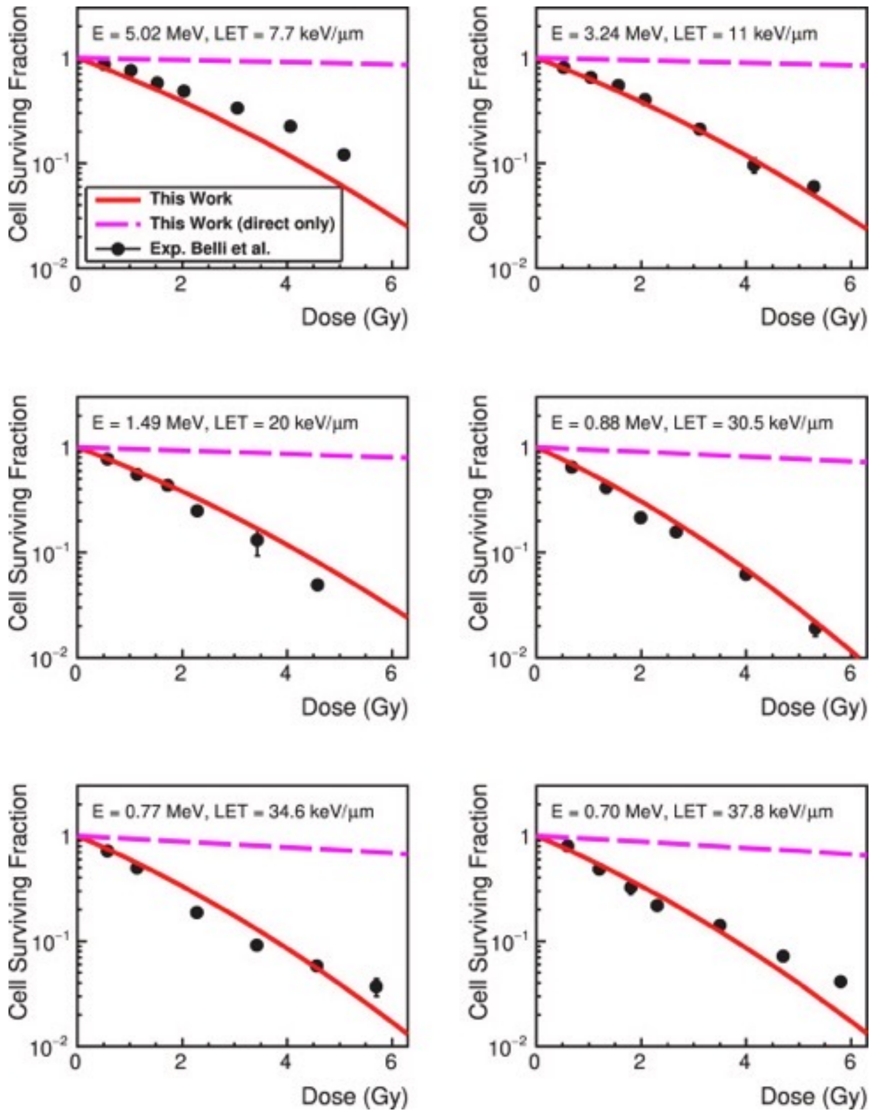
`dsbandrepair`: alpha, LEM-IV model



`dsbandrepair`: alpha, TLK model



`moleculardna`: proton, TLK model, V79 cell



Ref.: [Cancers 13, 6046 (2021)](), [Phys. Med. 105, 102508 (2023)](), [Phys. Med. 124 (2024) 103422]()

Contents of this talk

Where to find more information ?

https://geant4-dna.org/

Our publications are also announced on X and Bluesky

X

Geant4-DNA
@geant4_dna Vous suit
This is the official X account of the Geant4-DNA project and international collaboration
Traduire la biographie
Bordeaux, France geant4-dna.org A rejoint X en octobre 2016
4 Abonnements **353** Abonnés
Suivi par Geant4

Geant4-DNA @geant4_dna · 22 h
Geant4-DNA is now also available on Bluesky: @geant4-dna.bsky.social

Geant4-DNA a reposté
Geant4VM @Geant4VM · 17/12/2024
The new Geant4 Virtual Machine 11.3.0 for VMware Workstation & Fusion with AlmaLinux 9 is now available! - See extra.lp2ib.in2p G4/download/

@geant4_dna

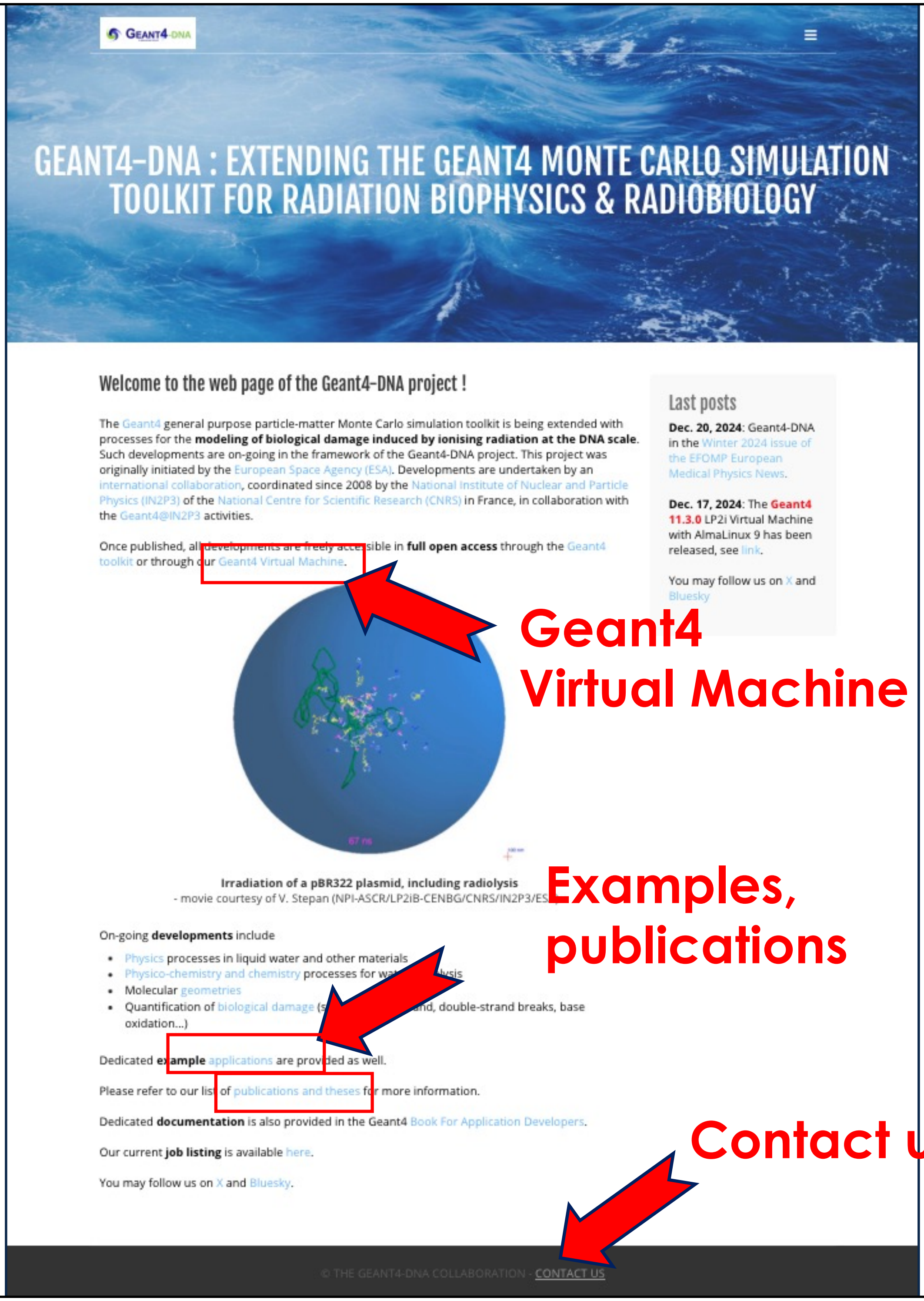
Bluesky

Geant4-DNA
@geant4-dna.bsky.social
2 abonné·e·s **1** abonnement **0** post
This is the official Bluesky account of the Geant4-DNA project and international collaboration

Republié par vous
Geant4VM @geant4vm.bsky.social · 1j
The new Geant4 Virtual Machine 11.3.0 for VMware Workstation & Fusion with AlmaLinux 9 is now available! - See extra.lp2ib.in2p3.fr/G4/downloa

Downloads – Geant4 Virtual

@geant4-dna.bsky.social



GEANT4-DNA : EXTENDING THE GEANT4 MONTE CARLO SIMULATION TOOLKIT FOR RADIATION BIOPHYSICS & RADIOBIOLOGY

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 Geant4 Virtual Machine.

Last posts

Dec. 20, 2024: Geant4-DNA in the Winter 2024 issue of the EFOMP European Medical Physics News.

Dec. 17, 2024: The Geant4 11.3.0 LP2i Virtual Machine with AlmaLinux 9 has been released, see link.

You may follow us on X and Bluesky

Irradiation of a pBR322 plasmid, including radiolysis
- movie courtesy of V. Stepan (NPI-ASCR/LP2iB-CENBG/CNRS/IN2P3/ES

On-going **developments** include

- Physics processes in liquid water and other materials
- Physico-chemistry and chemistry processes for wa lysis
- Molecular geometries
- Quantification of biological damage (s nd, double-strand breaks, base oxidation...)

Dedicated **example** applications are provided as well.

Please refer to our list of publications and theses for more information.

Dedicated **documentation** is also provided in the Geant4 Book For Application Developers.

Our current **job listing** is available here.

You may follow us on X and Bluesky.

© THE GEANT4-DNA COLLABORATION · CONTACT US

Geant4 Virtual Machine

Examples, publications

Contact us

Thank you for your attention!

Backup

Extensions of Geant4-DNA

- **GATE** (http://www.opengatecollaboration.org/)
  - GATE is a particle transport simulation toolkit based on Geant4 and dedicated to numerical simulations in medical imaging and radiotherapy. GATE can perform Geant4-DNA physics and chemistry simulations, directly in the platform which proposes a Python interface.
- **TOPAS-nBio** (https://github.com/topas-nbio/TOPAS-nBio)
  - TOPAS-nBio is based on Geant4-DNA. The goal is to provide user friendly interface, making Monte Carlo simulations easy-to-use with focus on radiation biology at sub-cellular scales.
- **MPEXS-DNA** (https://wiki.kek.jp/display/mpexs/MPEXS+Project)
  - MPEXS-DNA is a newly developed MC code based on Geant4-DNA physics/chemistry models that offer high computing performance by using a GPU.