





MINAS TIRITH: A GEANT4-DNA-BASED TOOL FOR MODELING DAMAGE AT THE CELL POPULATION SCALE

<u>Y. Thibaut¹</u>, C. Villagrasa¹, S. Incerti², Y. Perrot¹

¹ IRSN, PSE-SANTE/SDOS/LDRI, Fontenay-aux-Roses, France ² Univ. Bordeaux, CNRS, LP2I, UMR 5797, Gradignan, France

IV Geant4 International User Conference



MODELING THE RADIATION INDUCED DNA DAMAGE AT THE CELL NUCLEUS SCALE *

A nanodosimetric simulation chain based on SEANT4-DNA to model the early radiation-induced DNA damage at the cell nucleus scale.



Calculation of early radiation-induced damage in modeling

* Meylan et al., Sci. Rep. (7) 2017



MODELING THE RADIATION INDUCED DNA DAMAGE AT THE CELL NUCLEUS SCALE *

A nanodosimetric simulation chain based on SCANT4-DNA to model the early radiation-induced DNA damage at the cell nucleus scale.



Calculation of early radiation-induced damage in modeling

* Meylan et al., Sci. Rep. (7) 2017



MODELING THE RADIATION INDUCED DNA DAMAGE AT THE CELL NUCLEUS SCALE *

A nanodosimetric simulation chain based on S GEANT4-DNA to model the early radiation-induced DNA damage at the cell nucleus scale.



* Meylan et al., Sci. Rep. (7) 2017

https://bitbucket.org/sylMeylan/opendnafabric/src/master/ ** Meylan et al., Comput. Phys. Commun. (204) 2016 / Tang et al., Med. Phys. (46) 2019 / Thibaut et al., Int. J. Mol. Sci. 2022



MODELING THE RADIATION INDUCED DNA DAMAGE AT THE CELL NUCLEUS SCALE *

A nanodosimetric simulation chain based on SEANT4-DNA to model the early radiation-induced DNA damage at the cell nucleus scale.





COMPARISON WITH EXPERIMENTAL RESULTS



At present, the comparison is not performed at the same level:

- Simulations performed for one single cell
- Comparison in terms of mean number of DNA damages (DSB, SSB..)
- No consideration of damage distributions
- Induction of possible biases in the comparison (co-located foci)



COMPARISON WITH EXPERIMENTAL RESULTS



At present, the comparison is not performed at the same level:

- Simulations performed for one single cell
- Comparison in terms of mean number of DNA damages (DSB, SSB..)
- No consideration of damage distributions
- Induction of possible biases in the comparison (co-located foci)

Scaling-up DNA damage modeling to the cell population level, several options:

- Increase the scale of our simulation chain
- Multiscale Monte Carlo simulation approach *



* Douglass et al., Phys. Med. Biol. (60) 2015 / Baiocco et al., Sci. Rep. (6) 2016



COMPARISON WITH EXPERIMENTAL RESULTS



At present, the comparison is not performed at the same level:

- Simulations performed for one single cell
- Comparison in terms of mean number of DNA damages (DSB, SSB..)
- No consideration of damage distributions
- Induction of possible biases in the comparison (co-located foci)

Scaling-up DNA damage modeling to the cell population level, several options:

- Increase the scale of our simulation chain
- Multiscale Monte Carlo simulation approach *



A new Geant4-DNA-based tool is proposed:

MINAS TIRITH

MIcrodosimetry and NAnodosimetry to Simulate The Initial Radiation-Induced damage Topology's Heterogeneity

* Douglass et al., Phys. Med. Biol. (60) 2015 / Baiocco et al., Sci. Rep. (6) 2016



TRACK DISTRIBUTION IN THE CELL POPULATION

- Variability in the responses of cells from the same population, exposed to a given macroscopic absorbed dose, could be related to the variation in energy imparted to each cell.
- Track distribution in the cell population must be done according to the microdosimetry formalism.

PLOS ONE

RESEARCH ARTICLE

Cell to Cell Variability of Radiation-Induced Foci: Relation between Observed Damage and Energy Deposition

Gaëtan Gruel * °, Carmen Villagrasa °, Pascale Voisin, Isabelle Clairand, Marc Benderitter, Jean-François Bottollier-Depois, Joan Francesc Barquinero"



TRACK DISTRIBUTION IN THE CELL POPULATION

- Variability in the responses of cells from the same population, exposed to a given macroscopic absorbed dose, could be related to the variation in energy imparted to each cell.
- Track distribution in the cell population must be done according to the microdosimetry formalism.

PLOS ONE

RESEARCH ARTICLE

Cell to Cell Variability of Radiation-Induced Foci: Relation between Observed Damage and Energy Deposition

Gaëtan Gruel*[©], Carmen Villagrasa[©], Pascale Voisin, Isabelle Clairand, Marc Benderitter, Jean-François Bottollier-Depois, Joan Francesc Barquinero[®]

 Construction of a database of f₁(y) and f(CL) microdosimetric spectra by Monte Carlo simulations over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in a volume representing an endothelial cell nucleus.



TRACK DISTRIBUTION IN THE CELL POPULATION

- Variability in the responses of cells from the same population, exposed to a given macroscopic absorbed dose, could be related to the variation in energy imparted to each cell.
- Track distribution in the cell population must be done according to the microdosimetry formalism.

PLOS ONE

RESEARCH ARTICLE

Cell to Cell Variability of Radiation-Induced Foci: Relation between Observed Damage and Energy Deposition

Gaëtan Gruel*[©], Carmen Villagrasa[©], Pascale Voisin, Isabelle Clairand, Marc Benderitter, Jean-François Bottollier-Depois, Joan Francesc Barquinero[®]

- Construction of a database of f₁(y) and f(CL) microdosimetric spectra by Monte Carlo simulations over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in a volume representing an endothelial cell nucleus.
- Interpolation between the spectra of the database for calculating the non-simulated spectra.



TRACK DISTRIBUTION IN THE CELL POPULATION

- Variability in the responses of cells from the same population, exposed to a given macroscopic absorbed dose, could be related to the variation in energy imparted to each cell.
- Track distribution in the cell population must be done according to the microdosimetry formalism.

PLOS ONE

RESEARCH ARTICLE

Cell to Cell Variability of Radiation-Induced Foci: Relation between Observed Damage and Energy Deposition

Gaëtan Gruel*[©], Carmen Villagrasa[©], Pascale Voisin, Isabelle Clairand, Marc Benderitter, Jean-François Bottollier-Depois, Joan Francesc Barquinero[®]

- Construction of a database of f₁(y) and f(CL) microdosimetric spectra by Monte Carlo simulations over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in a volume representing an endothelial cell nucleus.
- Interpolation between the spectra of the database for calculating the non-simulated spectra.
- Combining the spectra, depending on the quality of the irradiating beam, to obtain the f₁(z) spectrum of the cell population.



TRACK DISTRIBUTION IN THE CELL POPULATION

- Variability in the responses of cells from the same population, exposed to a given macroscopic absorbed dose, could be related to the variation in energy imparted to each cell.
- Track distribution in the cell population must be done according to the microdosimetry formalism.

PLOS ONE

RESEARCH ARTICLE

Cell to Cell Variability of Radiation-Induced Foci: Relation between Observed Damage and Energy Deposition

Gaëtan Gruel*[©], Carmen Villagrasa[©], Pascale Voisin, Isabelle Clairand, Marc Benderitter, Jean-François Bottollier-Depois, Joan Francesc Barquinero[®]

- Construction of a database of f₁(y) and f(CL) microdosimetric spectra by Monte Carlo simulations over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in a volume representing an endothelial cell nucleus.
- Interpolation between the spectra of the database for calculating the non-simulated spectra.
- Combining the spectra, depending on the quality of the irradiating beam, to obtain the f₁(z) spectrum of the cell population.
- Calculation of the mean value $\overline{z_f}$ of the $f_1(z)$ spectrum.



TRACK DISTRIBUTION IN THE CELL POPULATION

- Variability in the responses of cells from the same population, exposed to a given macroscopic absorbed dose, could be related to the variation in energy imparted to each cell.
- Track distribution in the cell population must be done according to the microdosimetry formalism.

PLOS ONE

RESEARCH ARTICLE

Cell to Cell Variability of Radiation-Induced Foci: Relation between Observed Damage and Energy Deposition

Gaëtan Gruel*[©], Carmen Villagrasa[©], Pascale Voisin, Isabelle Clairand, Marc Benderitter, Jean-François Bottollier-Depois, Joan Francesc Barquinero[®]

- Construction of a database of f₁(y) and f(CL) microdosimetric spectra by Monte Carlo simulations over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in a volume representing an endothelial cell nucleus.
- Interpolation between the spectra of the database for calculating the non-simulated spectra.
- Combining the spectra, depending on the quality of the irradiating beam, to obtain the f₁(z) spectrum of the cell population.
- Calculation of the mean value $\overline{z_f}$ of the $f_1(z)$ spectrum.
- Distribution of the number of tracks per cell in the population from a Poisson law with parameter $\frac{\overline{Z_f}}{D_{abs}}$ with D_{abs} the value of the macroscopic absorbed dose delivered to the population.



ASSOCIATING A DNA DAMAGE TOPOLOGY TO EACH TRACK

Once the number of tracks is assigned to each cell of the population, each tracks is associated to a DNA damage topology.



- Once the number of tracks is assigned to each cell of the population, each tracks is associated to a DNA damage topology.
- **Construction of a database** of damage spectra, using the IRSN's Geant4-DNAbased simulation chain, over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in the volume of an **endothelial** cell nucleus.





ASSOCIATING A DNA DAMAGE TOPOLOGY TO EACH TRACK

- Once the number of tracks is assigned to each cell of the population, each tracks is associated to a DNA damage topology.
- **Construction of a database** of damage spectra, using the IRSN's Geant4-DNAbased simulation chain, over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in the volume of an **endothelial** cell nucleus.



For each track distributed in the cell population:



- Once the number of tracks is assigned to each cell of the population, each tracks is associated to a DNA damage topology.
- **Construction of a database** of damage spectra, using the IRSN's Geant4-DNAbased simulation chain, over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in the volume of an **endothelial** cell nucleus.



- For each track distributed in the cell population:
 - Sampling in the phase space of the irradiation the track type (particle, initial energy, direction, entrance point in the nucleus).



- Once the number of tracks is assigned to each cell of the population, each tracks is associated to a DNA damage topology.
- **Construction of a database** of damage spectra, using the IRSN's Geant4-DNAbased simulation chain, over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in the volume of an **endothelial** cell nucleus.



- For each track distributed in the cell population:
 - Sampling in the phase space of the irradiation the track type (particle, initial energy, direction, entrance point in the nucleus).
 - Calculation of CL according to the nucleus geometric characteristics and the track type.



- Once the number of tracks is assigned to each cell of the population, each tracks is associated to a DNA damage topology.
- **Construction of a database** of damage spectra, using the IRSN's Geant4-DNAbased simulation chain, over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in the volume of an **endothelial** cell nucleus.



- For each track distributed in the cell population:
 - Sampling in the phase space of the irradiation the track type (particle, initial energy, direction, entrance point in the nucleus).
 - Calculation of *CL* according to the nucleus geometric characteristics and the track type.
 - Calculation of the z value based on the CL and the interpolated $f_1(y)$ spectrum.



- Once the number of tracks is assigned to each cell of the population, each tracks is associated to a DNA damage topology.
- **Construction of a database** of damage spectra, using the IRSN's Geant4-DNAbased simulation chain, over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in the volume of an **endothelial** cell nucleus.



- For each track distributed in the cell population:
 - Sampling in the phase space of the irradiation the track type (particle, initial energy, direction, entrance point in the nucleus).
 - Calculation of *CL* according to the nucleus geometric characteristics and the track type.
 - Calculation of the z value based on the CL and the interpolated $f_1(y)$ spectrum.
 - Determination of the number of *DSB* and *SSB* by sampling in the damage spectra as a function of *z*.



- Once the number of tracks is assigned to each cell of the population, each tracks is associated to a DNA damage topology.
- **Construction of a database** of damage spectra, using the IRSN's Geant4-DNAbased simulation chain, over a large range of energies (1 keV to 20 MeV) for different types of particles (e-, p+, α) in the volume of an **endothelial** cell nucleus.



- For each track distributed in the cell population:
 - Sampling in the phase space of the irradiation the track type (particle, initial energy, direction, entrance point in the nucleus).
 - Calculation of *CL* according to the nucleus geometric characteristics and the track type.
 - Calculation of the z value based on the CL and the interpolated $f_1(y)$ spectrum.
 - Determination of the number of *DSB* and *SSB* by sampling in the damage spectra as a function of *z*.
 - Localization of each *DSB* and *SSB* by sampling in the damage spectra based on the geometric characteristics of the track (entrance point, direction, particle type).
 - Determination of the complexity and type (direct, indirect or hybrid) of damage by sampling.



- The method cannot be validated by direct comparison with a simulation performed using the Monte-Carlo method with Geant4 because the scale is too important.
- A step-by-step validation is therefore required:



- The method cannot be validated by direct comparison with a simulation performed using the Monte-Carlo method with Geant4 because the scale is too important.
- A step-by-step validation is therefore required:

MATHEMATICAL EVALUATION OF THE SPECTRUM RECONSTRUCTION BY INTERPOLATION

Performed using the Mean Absolute Percentage Error (MAPE) statistical indicator.

- Less than 4% for microdosimetric spectra.
- Less than 8% for ion damage spectra.
- Less than 15% for electron damage spectra.



- The method cannot be validated by direct comparison with a simulation performed using the Monte-Carlo method with Geant4 because the scale is too important.
- A step-by-step validation is therefore required:

MATHEMATICAL EVALUATION OF	DOSE DISTRIBUTION EVALUATION
THE SPECTRUM RECONSTRUCTION	IN A CELL POPULATION BY
BY INTERPOLATION	COMPARISON WITH MC-MODELING
Performed using the Mean Absolute	Performed by making a comparison
Percentage Error (MAPE) statistical	between the microdosimetric
ndicator.	spectra obtained by MINAS TIRITH
Less than 4% for microdosimetric	and by Monte-Carlo simulation for
spectra.	the same irradiation.
Less than 8% for ion damage	The number of tracks attributed to
spectra.	each nucleus of the cell population in
Less than 15% for electron	MINAS TIRITH is directly correlated
damage spectra.	to the dose distributed to each cell.



- The method cannot be validated by direct comparison with a simulation performed using the Monte-Carlo method with Geant4 because the scale is too important.
- A step-by-step validation is therefore required:

MATHEMATICAL EVALUATION OF THE SPECTRUM RECONSTRUCTION BY INTERPOLATION

Performed using the Mean Absolute Percentage Error (MAPE) statistical indicator.

- Less than 4% for microdosimetric spectra.
- Less than 8% for ion damage spectra.
- Less than 15% for electron damage spectra.

DOSE DISTRIBUTION EVALUATION IN A CELL POPULATION BY COMPARISON WITH MC-MODELING

Performed by making a comparison between the microdosimetric spectra obtained by MINAS TIRITH and by Monte-Carlo simulation for the same irradiation.

The number of tracks attributed to each nucleus of the cell population in MINAS TIRITH is directly correlated to the dose distributed to each cell.

EVALUATION OF THE DAMAGE ASSOCIATED PER TRACK BY COMPARISON WITH MC-MODELING

If the tracks are well distributed in the cell population, it remains to evaluate that each track is assigned the correct damage topology, according to its characteristics.

To validate this point, we compare the mean number of damages computed by MINAS TIRITH for different track types, compared to the one obtained with the simulation chain based on Geant4-DNA.



DOSE DISTRIBUTION EVALUATION IN A CELL POPULATION BY COMPARISON WITH MC-MODELING

- In order to evaluate the method over the whole energy range and for each particle type, the phase space chosen for this validation is the one of a monoenergetic neutron irradiation of 15.1 MeV.
 - Containing alphas, electrons and protons.
 - Covers the whole energy range of the tool.
 - Provides a wide range of particle incidence (angle).



DOSE DISTRIBUTION EVALUATION IN A CELL POPULATION BY COMPARISON WITH MC-MODELING

- In order to evaluate the method over the whole energy range and for each particle type, the phase space chosen for this validation is the one of a monoenergetic neutron irradiation of 15.1 MeV.
- Containing alphas, electrons and protons.
- Covers the whole energy range of the tool.
- Provides a wide range of particle incidence (angle).



Comparison of $f_1(z)$ (left) and $zf_1(z)$ (right) spectra obtained using the MINAS TIRITH tool (red) and by Monte Carlo simulation with the Geant4 and Geant4-DNA simulation codes (blue)



Electrons Alphas Protons 0.08 MC Geant4-DNA MC Geant4-DNA MC Geant4-DNA r of DSB/track 0.00 2000 2000 2000 **O MINAS TIRITH O MINAS TIRITH O MINAS TIRITH** o 0.04 0.03 0.02 Wean 0.01 ð 🖌 0 🧳 0 4 3.5 MC Geant4-DNA MC Geant4-DNA MC Geant4-DNA Mean number of SSB/track 5.0 c SSB/track 5.0 c SSB/track O MINAS TIRITH **O MINAS TIRITH O MINAS TIRITH** ο 🖕 0 1 Energy (keV) Energy (keV) Energy (keV)

EVALUATION OF THE DAMAGE ASSOCIATED PER TRACK BY COMPARISON WITH MC-MODELING

Comparison of the mean number of DSB/track (top) and SSB/track (bottom)

IRSN

CONCLUSION ET PERSPECTIVES

CONCLUSION



Time saving by MINAS TIRITH compared to the Geant4-DNA based simulation chain over the whole energy range and for each particle type without damage location



CONCLUSION ET PERSPECTIVES

CONCLUSION



Time saving by MINAS TIRITH compared to the Geant4-DNA based simulation chain over the whole energy range and for each particle type without damage location

- MINAS TIRITH has been validated by comparison:
- Well distributed dose in the population
- Successful calculation of the mean number of damages per track
- Time saving allows to scale-up the simulation to the cell population level.



CONCLUSION ET PERSPECTIVES

CONCLUSION



Time saving by MINAS TIRITH compared to the Geant4-DNA based simulation chain over the whole energy range and for each particle type without damage location

- MINAS TIRITH has been validated by comparison:
- Well distributed dose in the population
- Successful calculation of the mean number of damages per track
- Time saving allows to scale-up the simulation to the cell population level.

PERSPECTIVES

- Some observables that can influence the repair are, like damage location, not validated yet
- An experimental validation is planned by comparison with IRSN biological experiments.



Thank you for your attention!

More questions?

 \longrightarrow

yann.thibaut@irsn.fr

