gMicroMC: Accelerating Microscopic Monte Carlo Simulation Using Rapid Parallel Processing Platforms

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Motivation

 Ionizing radiation causes damage through water radiolysis, with DNA as the primary target of the generated radiolytic molecules.

 Accurate modeling of water radiolysis is essential to understand the radiobiological mechanisms and quantitatively test the related hypotheses







· Physical and physico-chemical stage:

· Computationally acceptable

- Chemical stage is highly time-consuming on conventional CPU because:
- Simulation of a dynamic process over several orders of magnitude in time $(10^{12}\,s \sim 10^{\,6}\,s)$
- An ionizing particle can generate a large number of radiolytic molecules in water
- A highly correlated many-body simulation problem due to the mutual chemical reactions: algorithm complexity $O(N^2)$
- This time limitation hinders a number of related research studies, particularly cell-level simulations

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GPU Acceleration

A huge boost of GPU application in scientific computing

What is GPU?

Graphics Processing Unit, co-processor, needs a host (General-purpose CPU)



• GPU vs CPU:

- CPU: a few cores optimized for sequential serial processing
 GPU: thousands of smaller, more efficient cores designed for handling multiple tasks
 simultaneously
- Data level parallelism: Single Instruction, Multiple Data



We have successfully applied GPU in radiotherapy problems:

- Image reconstruction
- Treatment planning

Monte Carlo Dose Calculation (external radiotherapy, brachytherapy, proton, carbon)

GPU is also known to successfully accelerate the simulation of fluid system, contacting particle system, cell biological system

We initiated the development on a GPU-based fast microscopic MC simulation package, named
gMicroMC

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Simulation methods of physical stage



Simulation methods of physical stage

Currently, our physical stage simulation only supports electron transport in water (1 eV~10 MeV)

Ionization

Considered five ionization shells: 1b1, 3a1, 1b2, 2a1, K-shell

- Relativistic binary-encounter-Bethe model(BEB) (Phys Rev A 2000, 62: 052710–52711)
- Energy loss: Composition sampling method (Physica Medica 2016, 32:1833–1840)

Excitation

Considered five excited states: A¹B¹, B¹A¹, Ryd A+B, Ryd C+D, diffuse bands

A semi-analytic model (Journal of Geophysical research, 1972, 77(25): 4797-4811)

Elastic scattering

 <200 eV: a semi-empirical parameterization method (Brenner, D.J. & Zaider, M. Phys. Med. Biol. (1983), 29 443-447)

 200 eV: Rutherford cross section with a screening parameter (Uehara, S et al Phys. Med. Biol. (1992) 37, 1841-1858)

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Simulation methods of physico-chemical stage

Simulation methods of physico-chemical stage



Simulation methods of chemical stage



Simulation methods of chemical stage1

Step-by-step method: Dividing the dynamic chemical stage into small consecutive time steps
 Diffusion model: Each molecule was considered as an individual Brownian object with random and independent motion, following a 3D Gaussian distribution

$$p(x,y,z) \mathrm{d}x \mathrm{d}y \mathrm{d}z = \frac{1}{(4\pi D \Delta t)^{3/2}} \exp \Biggl(- \frac{(x-x_0)^2 + (y-y_0)^2 + (z-z_0)^2}{4D \Delta t} \Biggr) \mathrm{d}x \mathrm{d}y \mathrm{d}z,$$

• Δt : step size of time step

Reaction model: Assuming diffusion-controlled reactions, i.e. a reaction would only occur when the distance of the reactants was no greater than its reaction radius

1. M. Karamitros, et al. Journal of Computational Physics 274 (2014) 841–882

$$\label{eq:restion} \begin{split} & \frac{\text{Reaction}^3}{\text{III} + c_{01} + (160) \rightarrow 01\Gamma + 1l_2}, \\ & \text{III} + c_{01} - (160) \\ & \text{III} + 1II - 1l_3, \\ & \text{III} + 0II - 1II + 1(L0) \\ & \text{R}/D + c_{01}^2 - 1II + 1(L0) \\ & \text{R}/D + c_{01}^2 - 1II + 1(L0) \\ & \text{R}/D + 10I + 01H_0 \\ & \text{R}/D + 10I + 01H_0 \\ & \text{OH} + c_{01} + 0H - 1H_0 \\ & \text{OH} + c_{01} + 0H - 1H_0 \\ & \text{OH} + c_{01} + (2160) + 201\Gamma + 1l_2 \\ & \text{OUT} \text{Southworstern} \end{split}$$

Simulation methods of chemical stage

Dynamic time step:

- Prefer small time step in order not to miss any interactions, but results in longer simulation time
- Dynamic time step is to improve simulation efficiency without sacrificing accuracy
- For each potential reactant pair, we calculated a time interval during which the reaction would not occur with a 95% confidence interval
- The step size was set as the minimum step size between all the pairs at the current step
 Brownian bridge: Considering the "crossing" event and estimate the probability of crossing
 effect diffusion
 after diffusion



GPU Implementation

Physical stage

- Each GPU thread was responsible for simulating the transport of one incident radiation particle
- The generated ionized and excited water molecules were recorded using atomic operation to avoid GPU writing conflict
- Secondary particles generated during the simulation were stored in a stack temporally
- Once the simulation of the incident radiation particles were finished, the secondary particles were simulated, one particle per thread

Physico-chemical stage

Each GPU thread was responsible for simulating the decay and thermalization of one molecule

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GPU Implementation

Chemical stage:

- Each GPU thread was responsible for simulating the diffusion and chemical reactions of one molecule
- A molecule array was allocated to record the evolution (species, spatial locations) of the radiolytic molecules during chemical stage
- · A buffer array was also allocated to record the third product of the reactions if existed
- A tag array was used to inform the GPU regarding the status of each molecule ("alive"/ "dead") during simulation to avoid reaction conflicts

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array indicating the index of each cell's first molecule in the sorted molecule array

For each molecule, only search for its potential reactants within the same cell and the neighboring cells

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A non-empty-cell array storing cell IDs of the non-empty cells, and an associated start-position array indicating the index of each cell's first molecule in the sorted molecule array

Cell size: the largest reaction radius out of all the reaction types considered in our simulation
 Rearrange the molecules in the molecule array according to their cell IDs

Grid data approach: reduce algorithm complexity in the simulation of the chemical stage
 Divide the volume of interest into a grid of uniformly sized cells

Grid data approach

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Table 1. Yield values (molecules/100 eV) of radiolytic species present at the end of chemical stage for 750 keV electron (depositing all its energy in a sphere of 3mm diameter) and 5 MeV proton (depositing –0.5MeV in a sphere of 50 µm).

	Geant4-DNA	2.51	3.03	3.00	0.66	0.49	0.39	0.45
750 keV	gMicroMC	2.51	3.07	3.06	0.72	0.53	0.36	0.41
electron	Difference (%)	0.00	1.32	2.00	9.09	8.16	7.69	8.89
	Geant4-DNA	1.38	1.97	2.05	0.73	0.63	0.66	0.70
5MeV proton	gMicroMC	1.40	1.97	2.15	0.80	0.60	0.70	0.67
	Difference (%)	1.45	0.00	4.88	9.59	4.76	6.06	4.29

Table 2. Efficiency test results, including the amount of radiolytic molecules at the beginning of the chemical stage in the two cases, denated as N(O), t=1pc, total simulation time taken by Genard-DNA on CPU and our gMicroMC on GPU; the speed-up factor achieved by our package compared to the Genard-DNA.

		Simulation time (s)		Speedure
		Geant4-DNA (CPU)	gMicroMC (GPU)	factor
750 keV electron	101829	102865.4	599.2	171.1
5MeV proton	56122	96446.5	489.0	197.2

Summary

- We have validated the simulation of each individual stage implemented in gMicroMC
- End-to-end test to validate gMicroMC as an entire package is ongoing
- Simulation of DNA damage will be implemented into our package
- Fast simulation of the water radiolysis will facilitate many radiobiology related research:

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- Cell-level simulation of radiation damage
- Effect of nano-particle in radiotherapy
- Mechanism of ultrahigh dose rate FLASH irradiation
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