



GENESIS Hands-on Part 2-2:

High performance computation with GENESIS

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IUPAB2024 Hands-on Training Program CHARMM-GUI/GENESIS MD Tutorial

Schedule of GENESIS parts (6/30-7/2)

06/30 Part1	
13:30 – 15:00	GENESIS basics and GENESIS on Fugaku (Kobayashi) Lecture
	Hands-on tutorial on Fugaku
07/01 Part 2	
14:30 – 15:30	Coarse-grained simulations in GENESIS (Tan)
15:30 – 16:30	High-performance computation with GENESIS (Jung)
07/02 Part 3	
13:30 – 15:00	Generalized-ensemble simulations using GENESIS (Ito)

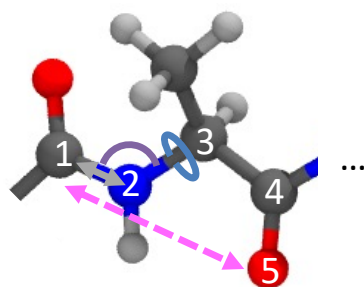


Contents

- Decision of Nonbonded interaction scheme
- Large time step integration with Hydrogen
Mass Repartitioning
- Others

Force calculation for biological systems

Force can be divided into bonding and nonbonding interactions.



Hydrogen: Light Gray
 Carbon: Dark Gray
 Oxygen: Red
 Nitrogen: Blue

$$E_{\text{potential}} = \sum_{\text{bonds}} k_b (b - b_0)^2 \quad \text{Bond (ex. 1-2, 2-3, ...)}$$

$$+ \sum_{\text{angles}} k_\theta (\theta - \theta_0)^2 \quad \text{Angle (ex. 1-2-3, 2-3-4, ...)}$$

$$+ \sum_{\text{dihedrals}} k_\phi [1 + \cos(n\phi - \delta)] \quad \text{Dihedral (ex. 1-2-3-4, ...)}$$

Bonding
 $O(N)$

$$+ \sum_{\text{non-bonded pairs}} \left[\epsilon_{ij}^{\min} \left\{ \left(\frac{R_{ij}^{\min}}{r_{ij}} \right)^{12} - \left(\frac{R_{ij}^{\min}}{r_{ij}} \right)^6 \right\} + \frac{q_i q_j}{r_{ij}} \right]$$

Nonbonding
 $O(N^2)$

van der Waals
 (ex. 1-5, ...) :

Coulomb
 (ex. 1-5, ...) :

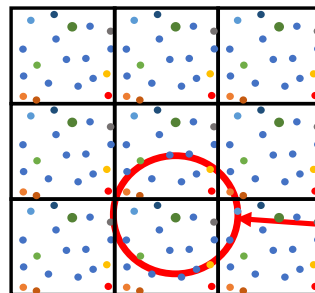
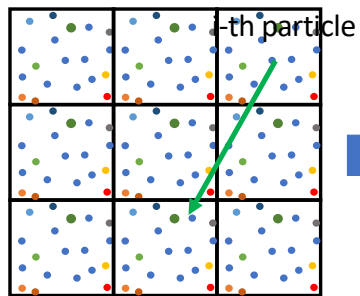


Nonbonded interactions

- Nonbonded interactions (Coulomb + vdW) are the main **bottleneck** of simulations.
- Nonbonded interactions are divided into those of real space with cutoff-distance and reciprocal lattice space.

Real space calculation

$$\sum_{ij,\mathbf{n}} \left[\varepsilon_{ij}^{min} \left\{ \left(\frac{R_{ij}^{min}}{r_{ij,\mathbf{n}}} \right)^{12} - \left(\frac{R_{ij}^{min}}{r_{ij,\mathbf{n}}} \right)^6 \right\} + \frac{q_i q_j}{r_{ij,\mathbf{n}}} \right] \rightarrow \sum_{ij,\mathbf{n}} \left[\varepsilon_{ij}^{min} \left\{ \left(\frac{R_{ij}^{min}}{r_{ij,\mathbf{n}}} \right)^{12} - \left(\frac{R_{ij}^{min}}{r_{ij,\mathbf{n}}} \right)^6 \right\} + \frac{q_i q_j \text{erfc}(\alpha r_{ij,\mathbf{n}})}{r_{ij,\mathbf{n}}} \right]$$



Range of j -th particle that interacts with i -th particle

$$\frac{1}{2\pi V} \sum_{\mathbf{k} \neq 0} \frac{\exp(-\pi^2 \mathbf{k}^2 / \alpha^2)}{\mathbf{k}^2} |S(\mathbf{k})|^2 - \frac{\alpha}{\sqrt{\pi}} \sum_{i=1}^N q_i^2$$

Reciprocal space calculation

Nonbonded interaction kernels in GENESIS

- In GENESIS, there are four interaction kernels for real space nonbonded interaction.
 1. Generic
 2. Fugaku
 3. Intel
 4. GPU
- Please choose the best calculation kernel from MD with small simulation time (We will do at this time).
- We also have four reciprocal space calculation schemes.
- Reciprocal space calculation scheme is decided by GENESIS by executing each scheme before starting MD.



Contents

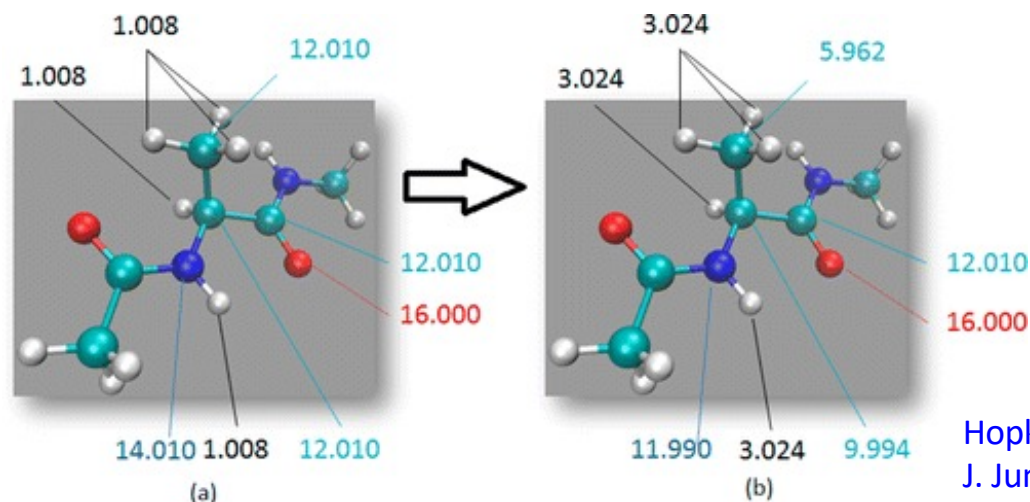
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- Large time step integration with Hydrogen

Mass Repartitioning

- Others

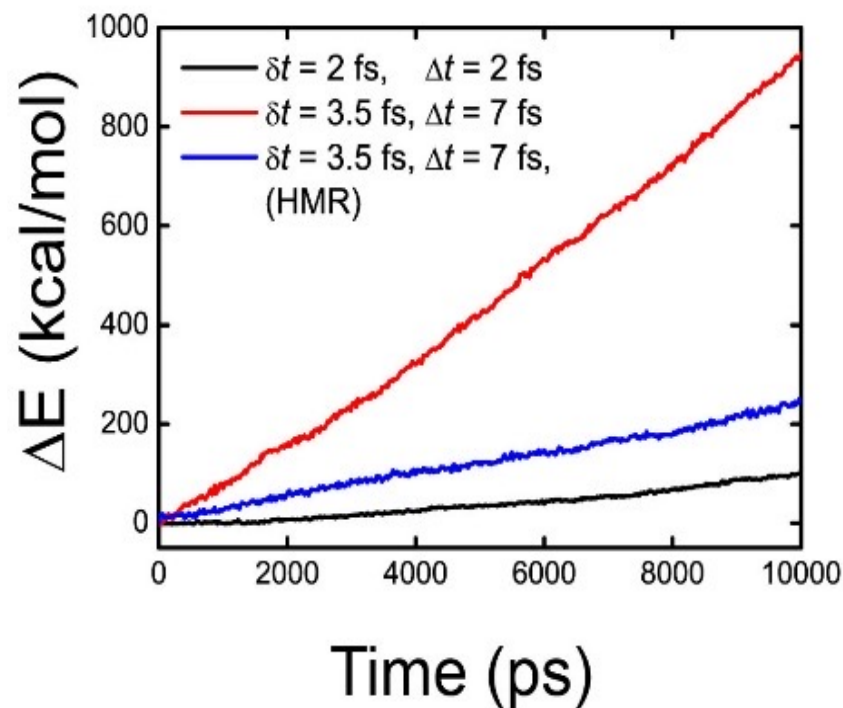
Hydrogen Mass Repartitioning (HMR) scheme



Hopkins *et al.*, JCTC. **11**, 1864 (2015))
J. Jung *et al.*, JCTC. **17**, 5312 (2021))

- Increase the mass of hydrogen atoms while reducing the mass of heavy atoms such that the total mass of one hydrogen group is not changed.
- With the HMR scheme, we can avoid the problem of SHAKE/RATTLE error by reducing the displacement of hydrogen atoms.
- We increase the mass of the hydrogen atoms three times.

HMR increases the stability (example of energy drift)

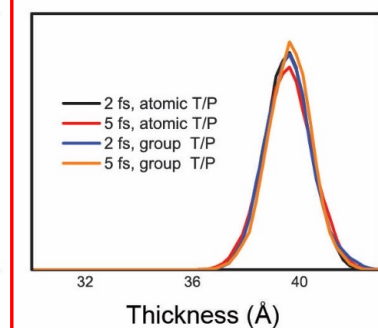
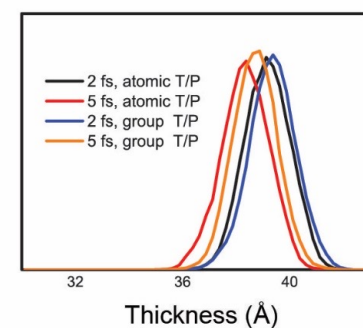
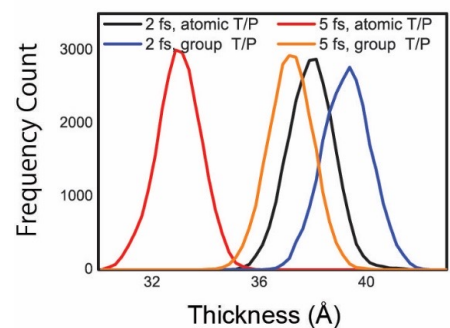
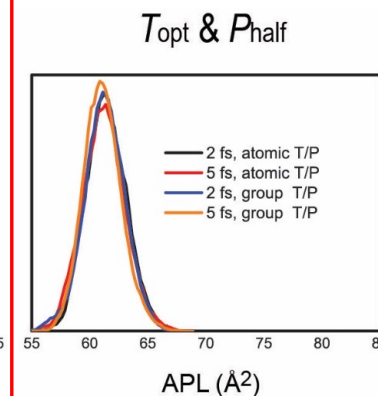
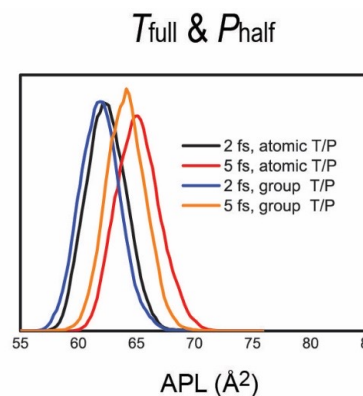
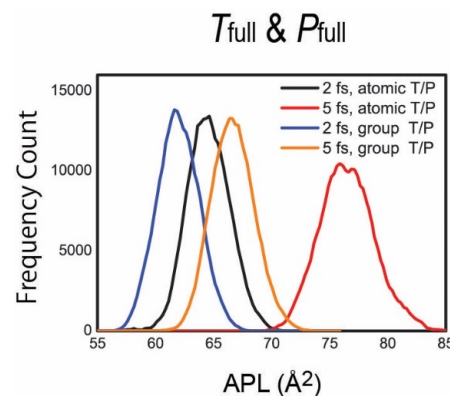
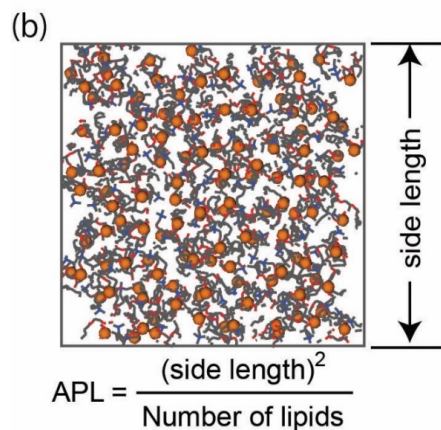
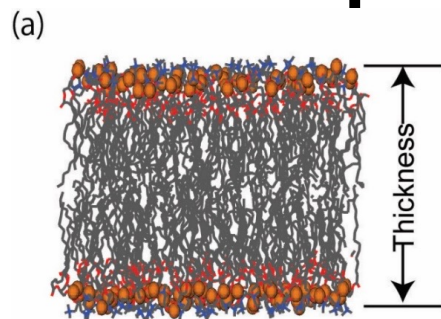


- HMR reduces the energy drift and increases the overall stability.

J. Jung et al., JCTC. 17, 5312 (2021))



Accurate temperature/pressure evaluation is important for large time step!!



Conventional temperature and pressure evaluation

Accurate temperature and pressure evaluation in GENESIS

J. Jung *et al.*, JCTC, **15**, 84 (2019))

J. Jung *et al.*, JCP, **153**, 234115



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Multiple time step integration

We can reduce the computational cost by skipping slow motion force every other step

