# Multiscale Modeling

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## Summary part 1

#### QM/MM

- many QM/MM algorithms and implementations
- electrostatic embedding
- mechanical coupling, link atoms, charge spilling
- polarization of MM environment
- many parameters, not a black box method

#### QM/QM, density embedding

- spectroscopy
- freeze-thaw cycles

Discreet reaction field

- polarizable MM environment
- self consistent procedure

PCM, COSMO

- implicit solvent model
- only electrostatics
- shape and size of cavity
- low computational cost



## content

- Lecture 1: Density embedding
- Lecture 2: QM/MM
- Lecture 3: Coarse-graining
- Lecture 4: Hybrid multiscale molecular dynamics



#### Multiscale methods



 $QM \longrightarrow MM$ 

Integration over electronic degrees of freedom

$$U(R) = -k_B T \ln \int \int \int dr \, d\dot{r} \, d\dot{R} \, e^{-\beta H(R, \dot{R}, r, \dot{r})}$$



 $QM \longrightarrow MM$ 

Integration over electronic degrees of freedom

$$U(R) = -k_B T \ln \int \int \int dr \, d\dot{r} \, d\dot{R} \, e^{-\beta H(R, \dot{R}, r, \dot{r})}$$



 $MM \longrightarrow CG$ 

Integration over non-essential degrees of freedom

$$U(R, V, T) = -k_B T \ln \int dr \, e^{-\beta V(R, r)}$$

 $QM \longrightarrow MM$ 

Integration over electronic degrees of freedom

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Integration over non-essential degrees of freedom

$$U(R, V, T) = -k_B T \ln \int dr \, e^{-\beta V(R, r)}$$

multi-dimensional free energy surface metadynamics of collective variables



 $QM \longrightarrow MM$ 

Integration over electronic degrees of freedom

$$U(R) = -k_B T \ln \int \int \int dr \, d\dot{r} \, d\dot{R} \, e^{-\beta H(R, \dot{R}, r, \dot{r})}$$

 $MM \longrightarrow CG$ 

Integration over non-essential degrees of freedom

$$U(R, V, T) = -k_B T \ln \int dr \, e^{-\beta V(R, r)}$$

$$U(R) \approx \sum_{i < j} u(r_i, r_j) = V(R)$$

#### Methods to coarse-grain

**Iterative Boltzmann Inversion** 

**Inverse Monte Carlo** 

Force matching

Maximum entropy method

Selected experimental and computer target properties

## CG to atomistic mapping



How to choose which degrees of freedom to keep or "integrate out"?

- very problem dependent
- arbitrary, chemical intuition
- or use maximum likelihood or Bayesian information criterion...
- 3-5 orders of magnitude saving in computational cost...

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#### The Henderson theorem

R. L. Henderson [Physics Letters **A49**, 197-198 (1974)]

A (classical or quantum) system described by the Hamiltonian

$$H = \sum_{i} \frac{p_i^2}{2m} + \frac{1}{2} \sum_{i \neq j} u(|r_i - r_j|)$$

will give rise to a unique pair correlation function (in the canonical ensemble). Henderson's theorem asserts that the reverse is also true: Two systems, which have a Hamiltonian of this form and which feature the same g(r) have pair potentials which differ at most by a trivial constant.



#### Iterative Boltzmann Inversion

A pair-potential is constructed in an iterative manner

- target is reference probability e.g. radial distribution
- useful for bonded and non-bonded interactions
- update potential until reference probability is matched
- requires a CG simulation for each cycle
- requires smooth function of V, e.g. splines or tabulated
- $\lambda$  [0, 1] stabilizes optimization

$$V^{n+1} = V^n + \lambda k_B T \ln \frac{P^n}{P_{\text{ref}}}$$

Sometimes the g(r) is used directly to construct a pair-potential. This is not correct.



#### Inverse Monte Carlo

A pair-potential U is constructed in an iterative manner

- target is histogram of CG property, Sref
- solving set of linear equations, gives improvement  $\Delta U$

$$\langle S_{\alpha} \rangle - S_{\alpha}^{\text{ref}} = A_{\alpha\gamma} \Delta U_{\gamma}$$

- Hamilonian can be written as a sum over a grid of pair distances

- S is an estimator of the RDF

$$H = \sum_{ij} U(r_{ij}) = \sum_{\alpha} U_{\alpha} S_{\alpha} \qquad \langle S_{\alpha} \rangle = \frac{N(N-1)}{2} \frac{4\pi r_{\alpha}^2 \Delta r}{V} g(r_{\alpha})$$
$$\frac{\partial \langle S_{\alpha} \rangle}{\partial U_{\lambda}} = \frac{\partial}{U_{\lambda}} \left( \frac{\int dq S_{\alpha}(q) \exp(-\beta \sum_{\lambda} U_{\lambda} S_{\lambda}(q))}{\int dq \exp(-\beta \sum_{\lambda} U_{\lambda} S_{\lambda}(q))} \right)$$
$$A_{\alpha\gamma} = \frac{\partial \langle S_{\alpha} \rangle}{\partial U_{\gamma}} = \beta \left( \langle S_{\alpha} \rangle \langle S_{\gamma} \rangle - \langle S_{\alpha} S_{\gamma} \rangle \right)$$

A Lyubartsev and A Laaksonen. Calculation of effective interaction potentials from radialdistribution functions - a reverse monte-carlo approach. *Phys. Rev. E*, **52**, 3730–3737, (1995)

#### Inverse Monte Carlo



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## Force Matching

Aims to reproduce the potential of mean force (not aiming to reproduce distribution functions)

- CG forcefield depends on M parameters:  $g_1, g_2, \dots, g_M$
- calculate reference forces for *L* snapshots
- force on CG bead is constructed from forces on atoms
- mapping coefficients d can be set to c

$$\mathbf{F}_{I}^{\text{ref}} = \sum_{j \in S_{I}} \frac{d_{Ii}}{c_{Ii}} \mathbf{f}_{j}(\mathbf{r}^{n})$$

- requires least squares fitting to find optimal parameters
- solve NxL equations

$$\mathbf{F}_{Il}^{CG}(g_1, \dots, g_M) = \mathbf{F}_{il}^{ref}, I = 1, \dots, N, l = 1, \dots, L$$

- F is non-linear function of  $g_i$ , --> use coefficients for spline or tabulated functions to linearize.

## Matching selected properties

Construct CG Forcefield that matches

- experimental properties: density, surface tension, affinities
- atomistic simulation data: RDF, PMF, free energy profiles

Example:

- MARTINI forcefield
- uses solvation free energies and phase partitioning
- requires optimization scheme
- can be better than atomistic forcefields
- limited to target thermodynamic state
- which properties are accurate?

#### Summary coarse-graining

Transferability What can you expect from the model? Dynamical properties?

# Lecture 4 Multscale Molecular Dynamics

## Reverse mapping problem





Reverse mapping (is difficult)

#### **NVE ensemble**



$$H = \sum_{i=1}^{n} \frac{p_i^2}{2m_i} + V(r^n)$$

## NVT ensemble



Nosé-Hoover thermostat

NH thermostat "potential"
is a book keeping term
non-Hamiltonian dynamics

$$E = \sum_{i=1}^{n} \frac{p_i^2}{2m_i} + V(r^n) + \frac{\epsilon^2 Q}{2} + L\frac{\ln s}{\beta}$$

Understanding Molecular Simulation, Frenkel & Smit (chapter 6)

#### Coarse grained MD



$$E = \sum_{\alpha=1}^{N} \frac{P_{\alpha}^2}{2M_{\alpha}} + V(R^N)$$



#### Atomistic + Coarse grained MD

non-interacting

• non-adaptive

$$E = \sum_{i=1}^{n} \frac{p_i^2}{2m_i} + V(r^n) + \sum_{\alpha=1}^{N} \frac{P_{\alpha}^2}{2M_{\alpha}} + V(R^N)$$

• interacting



$$E = \sum_{i=1}^{n} \frac{p_i^2}{2m_i} + V(r^n) + \sum_{\alpha=1}^{N} \frac{P_{\alpha}^2}{2M_{\alpha}} + V(R^N) + V^{\text{MIX}}(r^n, R^N)$$
$$V_{i\in\alpha} = \sum_{j} \Phi_{ij}(r_i, r_j) + \frac{m_i}{M_{\alpha}} \sum_{\beta}^{N} \Phi_{\alpha,\beta}(R_{\alpha}, R_{\beta})$$

- order parameter
- book keeping
- smooth transition



**)** 

 $\lambda_{\alpha\beta} = \max(s(q_{\alpha}), s(q_{\beta}))$ 

$$V = V(r^{n}) + V(R^{N}) + V^{\text{MIX}}$$
$$= \sum_{\alpha,\beta} \left( \lambda \Phi_{\alpha\beta}^{\text{CG}} + (1-\lambda) \sum_{\substack{i \in \alpha \\ j \in \beta}} \Phi_{ij}^{\text{A}} \right) + \sum_{\alpha} \sum_{\substack{i j \in \alpha \\ ij \in \alpha}} \Phi_{ij}^{\text{A}}$$

- order parameter
- book keeping
- smooth transition



$$\begin{aligned} q &\longrightarrow \\ V &= \sum_{\alpha,\beta} \left( \lambda \Phi_{\alpha\beta}^{\mathrm{CG}} + (1-\lambda) \sum_{\substack{i \in \alpha \\ j \in \beta}} \Phi_{ij}^{\mathrm{A}} \right) + \sum_{\alpha} \sum_{ij \in \alpha} \Phi_{ij}^{\mathrm{A}} - \Delta U(q^{\dagger}) \\ \Delta U_{\alpha}(q^{\dagger}) &= \Delta \lambda \sum_{\beta} \left( \Phi_{\alpha\beta}^{\mathrm{CG}^{\dagger}} - \sum_{\substack{i \in \alpha \\ j \in \beta}} \Phi_{ij}^{\mathrm{A}^{\dagger}} \right) \end{aligned}$$

- order parameter
- book keeping

#### smooth transition

## Constructing Hybrid MD



$$\begin{aligned}
q &\longrightarrow \\
V &= \sum_{\alpha,\beta} \left( \lambda \Phi_{\alpha\beta}^{\mathrm{CG}} + (1-\lambda) \sum_{\substack{i \in \alpha \\ j \in \beta}} \Phi_{ij}^{\mathrm{A}} \right) + \sum_{\alpha} \sum_{ij \in \alpha} \Phi_{ij}^{\mathrm{A}} - \Delta U(q^{\dagger}) \\
\Delta U_{\alpha}(q^{\dagger}) &= \Delta \lambda \sum_{\beta} \left( \Phi_{\alpha\beta}^{\mathrm{CG}^{\dagger}} - \sum_{\substack{i \in \alpha \\ j \in \beta}} \Phi_{ij}^{\mathrm{A}^{\dagger}} \right) \qquad \lambda_{\alpha\beta} &= \max(s(q_{\alpha}), s(q_{\beta}))
\end{aligned}$$

- order parameter
- book keeping

smooth transition

$$s(q) = 0 \qquad S = \frac{1}{N}, \frac{2}{N} \cdots \frac{N-1}{N} \qquad s(q) = 1$$

$$\Delta U_{\alpha}(q^{\dagger}) = \sum_{q_1}^{q_2} \Delta \lambda \sum_{\beta} \left( \Phi_{\alpha\beta}^{\mathrm{CG}^{\dagger}} - \sum_{\substack{i \in \alpha \\ j \in \beta}} \Phi_{ij}^{\mathrm{A}^{\dagger}} \right)$$

- order parameter
- book keeping

smooth transition

## Constructing Hybrid MD



$$\Delta U_{\alpha}(q^{\dagger}) = \lim_{N \to \infty} \sum_{q_1}^{q_2} \Delta \lambda \sum_{\beta} \left( \Phi_{\alpha\beta}^{\mathrm{CG}^{\dagger}} - \sum_{\substack{i \in \alpha \\ j \in \beta}} \Phi_{ij}^{\mathrm{A}^{\dagger}} \right)$$
$$= \int_{q_1}^{q_2} \frac{d\lambda}{dq} \sum_{\beta} \left( \Phi_{\alpha\beta}^{\mathrm{CG}^{\dagger}} - \sum_{\substack{i \in \alpha \\ j \in \beta}} \Phi_{ij}^{\mathrm{A}^{\dagger}} \right) dq'$$

## Healing Region

## **Switching Function**



 $S(r) = (r - R_{AA})^{2} * (3R_{CG} - R_{AA} - 2r)/(R_{CG} - R_{AA})^{3}$  $\lambda_{\alpha\beta} = \max(s(r_{\alpha}), s(r_{\beta}))$ 

## Conserved Quantity

$$V_{\alpha} = \sum_{\beta} \left( \lambda \Phi_{\alpha\beta}^{\text{CG}} + (1-\lambda) \sum_{\substack{i \in \alpha \\ j \in \beta}} \Phi_{ij}^{\text{A}} \right) + \sum_{ij \in \alpha} \Phi_{ij}^{\text{A}} - \sum_{\beta} \Delta U_{\alpha}(q)$$
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$$f_{\alpha} = -\frac{\partial V}{\partial r_{\alpha}}$$
$$= -\lambda \frac{\partial \Phi_{\alpha\beta}^{CG}}{\partial r_{\alpha}} - \frac{d\lambda}{dr_{\alpha}} \Phi_{\alpha\beta}^{CG} - \sum_{\substack{i \in \alpha \\ j \in \beta}} (1-\lambda) \frac{\partial \Phi_{ij}^{A}}{\partial r_{\alpha}} + \sum_{\substack{i \in \alpha \\ j \in \beta}} \frac{d\lambda}{dr_{\alpha}} \Phi_{ij}^{A} + \frac{\partial \Delta U_{\alpha}}{\partial r_{\alpha}}$$

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Energy function, E = K + V

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$$f_{\alpha} = -\frac{\partial V}{\partial r_{\alpha}} = -\lambda \frac{\partial \Phi_{\alpha\beta}^{\text{CG}}}{\partial r_{\alpha}} - \sum_{\substack{i \in \alpha \\ j \in \beta}} (1-\lambda) \frac{\partial \Phi_{ij}^{\text{A}}}{\partial r_{\alpha}}$$

## Healing region



Coupled atomistic and coarse-grain regions

- adaptive resolution
- smooth forces
- equilibration of AA degrees of freedom
- equilibration generates heat, which requires thermostating
- conserved total momentum
- conserved auxiliary total energy

## Simple Example

#### Switching a harmonic bond interaction by a factor 10



Hybrid atomistic/coarse grained MD: 8000 methane molecules

Spherical AA-region, R=8A (+ 4A) ca. 34 AA/78 HR/7889 CG molecules



B. Ensing, S. O. Nielsen, P. B. Moore, M. L. Klein and M. Parrinello J. Chem. Theor. Comp. 3 1100-1105 (2007)

Hybrid atomistic/coarse grained MD: 8000 methane molecules



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#### Switching resolution



#### Atoms

#### Coarse grain "blobs"



#### Switching resolution



#### Switching resolution



## **Rigid body rotation**

- Frozen atomic library function
- Match centers of mass
- The body frame can only rotate: SO(3) operations
- reduced energy function
- Verlet algorithm by P. Krysl and L. Endres
- remove CG-CG bond distance from inter-CG interactions

S. O. Nielsen, B. Ensing, P. B. Moore and M. L. Klein. Book chapter in: "Advances in Hierarchical and Multi-Scale Simulations of Materials" (publisher: Taylor and Francis; editors: Sanat Mohanty and Richard B. Ross).

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$$\begin{aligned}
\omega_{i+\frac{1}{2}} &= \omega_i + \frac{\Delta t}{2} \alpha_i \\
R_{i+1} &= \exp\left[\Delta t \omega_{i+\frac{1}{2}} + \frac{\Delta t^2}{2} \alpha_i\right] R_i \\
T &= f \times r_{i+1} \\
I_{\alpha\beta} &= \sum_i m_i (\delta_{\alpha\beta} r_i^2 - r_i^{\alpha} r_i^{\beta}) \\
\alpha_{i+1} &= I^{-1} (T - \omega_{i+1} \times I_{i+1} \omega_{i+1}) \\
\omega_{i+1} &= \omega_{i+\frac{1}{2}} + \frac{\Delta t}{2} \alpha_{i+1}
\end{aligned}$$



#### Poly ethylene chain (50 blobs - 150 CH2)



#### Poly ethylene chain (50 blobs - 150 CH2)



CGMD + Reverse Mapping on the Fly



CGMD + Reverse Mapping on the Fly



#### Combined hybrid MD and rotational dynamics

#### Polyethylene chain, 2 atomistic regions, RAR=6Å



#### Combined hybrid MD and rotational dynamics

Polyethylene chain, 2 atomistic regions, RAR=6Å



## Multiscale MD of hexane

Size: 2000 molecules AR: 2x 12 Å (2D slice) HR: 4 Å Temp: 300 K, NH/particle





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## Grand-canonical ensemble?

#### Average number of particles (blobs)

Expected  $N_{AR}$  = 2000x2 x 2x12/118.147 = 812.547

Measured  $N_{AR} = 810.979$ 

#### Particle fluctuations

$$\left\langle dN^2 \right\rangle_{\mu VT} = \frac{N^2}{V} * k_B T \beta_T = 67.98$$

 $\beta_T = \left\langle dV^2 \right\rangle_{NPT} (k_B T V)^{-1} = 2.17613 \cdot 10^{-9} P a^{-1}$ 

Measured  $dN^2_{AR} = 65.15$ 

## Swelling of C<sub>450</sub>H<sub>902</sub> polyethylene chain

2000 hexane molecules



spherical AR of radius 10 Å centered on 75th polymer bead





#### Difference-based Adaptive Solvation method







Sorted Adaptive Partitioning (SAP) A. Heyden, H. Lin and D. G. Truhlar, J. Phys. Chem. B, 2007, **III**, 2231 Toward a Practical Method for Adaptive QM/MM Simulations Rosa E. Bulo, Bernd Ensing, Jetze Sikkema, and Lucas Visscher J. Chem. Theory Comput. 2009, **5**, 2212–2221

#### radial distribution



#### radial distribution



#### radial distribution



## Summary part 2

#### Coarse-graining

- how to choose a atom-CG mapping
- Iterative Boltzmann Inversion
- Inverse Monte Carlo
- Force matching iterative Boltzman
- Targeting selected exp./sim properties

hybrid multiscale MD

- open boundaries/adaptive resolution
- healing region
- non-equilibrium process (equilibration of atoms)
- bookkeeping, auxiliary total energy
- works for spherical CG particles

reverse mapping

- rigid body rotation
- combined with hybrid MD

adaptive QM/MM



# fin