Monte Carlo simulation of differences in free energies of hydration

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What is Monte Carlo Technique?

The Monte Carlo method is a numerical method for solving mathematical problems using stochastic sampling.

Random Configuration generation

- Use of Random Number
- Importance Sampling
- Markov Chain
- Metropolis Algorithm

Averaging Method

- NVT Ensemble
- NPT Ensemble
- *uPT* Ensemble

Implemention of MMC in different ensemble MMC in different ensembles A very large number of systems for convenient calculation of time average macroscopic properties Common macroscopic attributes (N, V, E): Microcanonical ensemble (N, V, T): Canonical ensemble (N, V, T): Canonical ensemble (N, V, T): Grand canonical ensemble (M, V, T): Grand canonical ensemble Microcanonical ensemble cannot be used in MMC because constant-kinetic energy constraint cannot be assumed. In thermodynamic limit all ensembles are equivalent and it is also possible to transform between ensembles. The choice of ensemble is completely a matter of convenience.

Approximations

- Periodic Boundary Condition
- Minimum Image Convention
- Neighborhood List

Theoretical Basis of Molecular Monte Carlo Method

General MMC Scheme

Start

Generate initial configuration

Calculate Energy

PBC and MIC

Importance Sampling (Metropolis Algorithm)

Calculate Summation of Properties

Average Properties

Approaches to compute free energy differences.

- Umbrella sampling
- Perturbation approach

Umbrella Sampling

- The procedure was developed by Valleau and coworkers.
- Calculate a distribution function g(r) that is related to free energy change by $w(r) = -KT \ln g(r)$.

Perturbation approach

■It centers on the following relationship A1 –A0 = -KT in(exp[-B(E1 – E0)])0 . The equation expresses free energy difference between systems 0 and 1 by an average of function of their energy difference.

■Multiple simulations over intermediate systems between 0 and 1. Coupling parameter (lambda) is defined for smooth transition of system 0 to 1.

$$\zeta(\lambda) = \zeta_0 + \lambda (\zeta_1 - \zeta_0).$$

Perturbation approach

- Application of the approach is in free energy of cavity formation in water, free energy of hydration of methane, studying donoracceptor complexes, compute free energy change for converting one solute into another in solution.
- Intriguing parallelism to mutagenic experiments in biochemistry.

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Jorgensen et al Procedure

- Series of Monte Carlo simulations were carried out for the interconversion of methanol and ethane in dilute aqueous solution.
- A coupling parameter lambda was used to smoothly transform methanol (lambda = 0) to ethane (lambda = 1).
- Simulations were run for lambda_i = 0.0, 0.125, 0.25, 0.50, 0.75, 1.0.
- Double ended sampling Simulations were run in both directions to check the self consistency.
 lambda_i → lambda_{i+1} and lambda_{i+1} → lambda_i

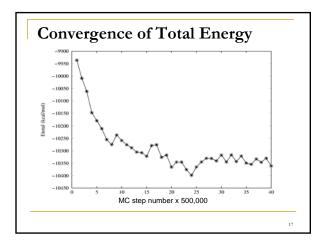
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Continuation of Jorgensen et al Procedure

- The simulations were run in NPT ensemble at 25 degrees C and 1 atm using standard procedures including periodic boundary conditions.
- The system had 125 water molecules plus solute in a cube.
- Metropolis sampling
- An attempt made to move solute on every 50th configuration and change in volume was tried on every 600th configuration.

Continuation of Jorgensen et al Procedure

- Ranges for attempted moves were the same in each simulation and provided ~40% acceptance probability for new configurations.
- Each simulation consisted of equilibrium phase for 0.5 *106 configurations, which was followed by averaging for properties over 1.5 *106 configurations.



Continuation of Jorgensen et al Procedure

■ The interaction energy between monomers was determined by Coulomb and Lennard -Jones interactions between all intermolecular pairs of sites.

Molecule	Group	q	$\sigma(\text{\AA})$	€ (kcal/mol
CH ₂ OH	CH,	0.265	3.775	0.207
CH ₁ OH	0	- 0.700	3.070	0.170
CH ₁ OH	H	0.435	0.0	0.0
CH ₁ CH ₁	CH,	0.0	3.775	0.207
H,0	0	0.0	3.1536	0.155 04
H,0	H	0.52	0.0	0.0
H,0	M'	- 1.04	0.0	0.0

Continuation of Jorgensen et al Procedure

- Standard geometries for monomers for ethane, r(CC) = 1.53 Angstrom, for methanol r(CO) = 1.43 Angstrom.
- The bond length gradually increases from 1.43 to 1.53 Angstrom.
- Smooth interconversion of geometries of the two systems.

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Hydration of Methanol

- 2CH3OH ←→ C2H6 + 2(OH)
- Carbon in yellow, Oxygen in blue(United atom model).





 Note the bond length gradually increases from 1.43 to 1.53 Angstrom.

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Results

- Thermodynamics
- Energy Distributions
- Radial distribution Functions

Radial distribution Functions

The rdf addresses the question, "given that I have one atom at some position, how many atoms can I expect to find at a distance raway from it?"—more precisely, we ask for the number of atoms at a distance between r to r + dr. The idea is demonstrated in this figure.



The darkened atom at the center is the reference atom, and the circles around it represent the other atoms. A ring centered on the reference is drawn with radius r and thickness dr, and in this example three other atoms are positioned within this ring and highlighted.

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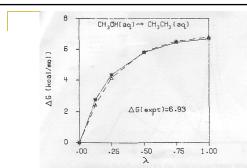


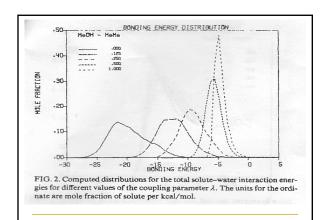
FIG. 1. Computed free energy changes for the interconversion of methanol $(\lambda=0)$ and ethane $(\lambda=1)$ in water. The solid and dashed lines correspond to the forward $(\lambda=0\rightarrow 1)$ and reverse $(\lambda=1\rightarrow 0)$ processes, respectively.

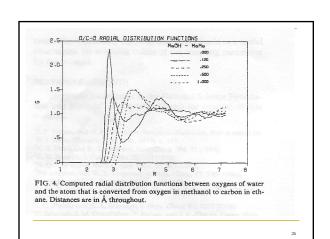
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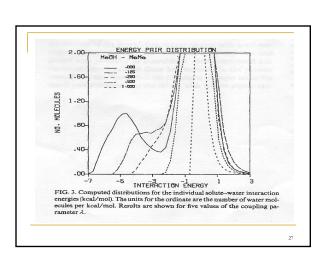
TABLE II. Free energy change for the interconversion of methanol and ethane in water.

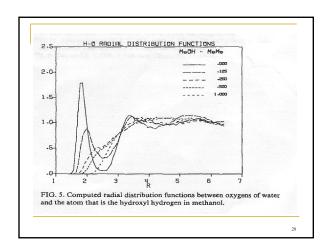
	State No. The state	ΔG (kcal/mol)	
λ_{l}	λ,	i→j	j→i
0.000	0.125	2.77 ± 0.10	- 2.45 ± 0.06
0.125	0.250	1.58 + 0.07	-1.70 ± 0.08
0.250	0.500	1.44 ± 0.14	-1.69 ± 0.10
0.500	0.750	0.67 + 0.08	-0.70 ± 0.08
0.750	1.000	0.24 + 0.05	-0.27 ± 0.05
Total		6.69 ± 0.21	-6.81 ± 0.17
	ptl.a	6.93	- 6.93

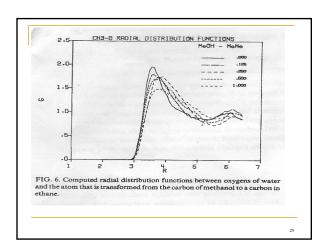
*Reference 28.











Summary

- Perturbation theory is investigated for interconversion of methanol and ethane in water. Results are encouraging for further chemical and biochemical applications.
- The results are in good accord with experimental differences in free energies of hydration for methanol and ethane.
- Double wide sampling along with 2 or 3 Monte Carlo simulations give good estimation of free energy change with good precision.
- Dominant changes occur for small perturbation near the solute with largest dipole moment.

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