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Conclusions and outlook

# A Level-Set Variational Implicit-Solvent Approach to Hydrophobic Interactions

# Zhongming Wang

#### Biochemistry and Mathematics, UCSD

Joint work with L.-T. Cheng, P. Setny, J. Dzubiella, B. Li and J. A. McCammon

UCSD Informal Seminars on Mathematics and Biochemistry-Biophysics, Jan 27, 2009

#### Introduction

Variational implicit or continuum solvent models

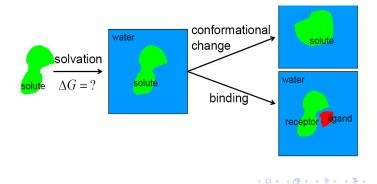
Level set method

Hydrophobic pocket

Conclusions and outlook

# **Basic facts**

- Biological processes, such as molecular recognition and protein folding, occur in solution
- Solute-solvent interactions are crucial in determining biomolecular structures and solvation free energies

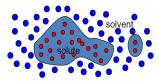


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# Explicit solvent vs implicit solvent

Explicit solvent: solvent atoms treated explicitly (e.g., MD, MC)



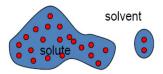
- Advantages
   First principle, accurate
- Disadvantages

Non-efficient, small portion of solutes (5-10%), boundary effects, uncertain convergence, statistical information

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# Explicit solvent vs implicit solvent cont'd

• Implicit solvent: solvent atoms are treated implicitly and solvent effects are coarse grained

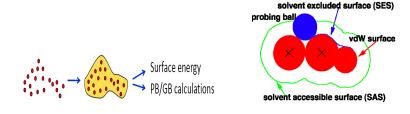


Advantages

Efficient, large systems, thermodynamical variables

• Disadvantages Mean field ion distribution, ignores details

#### Existing implicit solvent models



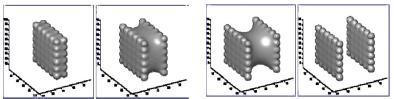
- Get atom positions
- Generate molecular surface(vdW surface, SES/SAS)
- Calculate surface energy
- Calculate electrostatic energy by PB/GB with the surface as dielectric boundary

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# Existing implicit solvent models cont'd

Issues of vdW surface, SAS/SES models

- Pre-defined dielectric interface
- Curvature correction
- Coupling of polar and nonpolar contributions
- Hydrophobicity <sup>1</sup>



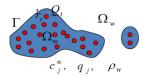
1 From Cheng, Dzubiella, McCammon, & Li, J. Chem. Phys., 2007 🔹 🖘 👘 🖉 🖉 🖉 🖉 🖓 🔍 🕐

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# Variational implicit solvent model facts

- Variational implicit solvent model (VISM)
  - Dzubiella, Swanson, & McCammon, Phys. Rev. Lett. 96, 087802 (2006); J. Chem. Phys. 124, 084905 (2006)
  - Che, Dzubiella, Li, & McCammon, J. Phys. Chem. B, 112, 3058 (2008)
- VISM ideas
  - Solvation structure = solutes position + solute-solvent interface
  - Free energy minimization determines solute-solvent interface
  - Free energy couples with different interactions: polar, nonpolar, dispersive, etc.

#### VISM geometry and parameters



- $\Omega_m$ ,  $\Omega_w$ ,  $\Gamma$ : solute region , solvent region, interface
- $r_i$ ,  $Q_i$ : center and fixed charged of  $i^{th}$  solute atom
- $c_i^{\infty}$ ,  $q_j$ : bulk density and bulk charge of  $j^{th}$  ionic specie

*ρ<sub>w</sub>*: solvent density

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# Free energy functional

$$G[\Gamma] = G_{geom}[\Gamma] + G_{vdW}[\Gamma] + G_{elec}[\Gamma]$$

• 
$$G_{geom}[\Gamma] = Pvol(\Omega_m) + \int_{\Gamma} \gamma(r) dS$$
  
 $\gamma(r) = \gamma_0[1 - 2\tau H(r)]$   
 $\tau$ : Tolman length,  $H$ : mean curvature  
 $G_{vdw}[\Gamma] = \rho_w \int_{\Omega_s} U(r) dV$   
 $U(r) = \sum_i U_i(|r - r_i|)$   
 $U_i(|r|) = 4\epsilon \left( \left(\frac{\sigma_i}{|r|}\right)^{12} + \left(\frac{\sigma_i}{|r|}\right)^6 \right)$ 

G<sub>elec</sub>[Γ] use PB/GB, Coulomb approximation, etc (not presented in this pocket project)

# Energy minimization

A Necessary condition for Γ to be a minimizer

 $\delta_{\Gamma}G[\Gamma] = 0, \forall r \in \Gamma$ 

• The energy minimizer  $\Gamma_{min}$  satisfies a PDE

$$P + 2\gamma_0(H(r) - \tau K(r)) - \rho_w U(r) + \left(\delta_{\Gamma} G_{elec}[\Gamma]|_{\Gamma_{min}}\right) = 0, \quad \forall r \in \Gamma_{min}$$

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• How to find the minimizer  $\Gamma_{min}$ ? Level set method

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## Level set method

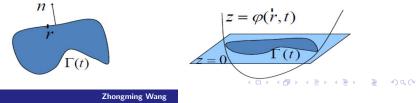
- Proposed by Sethian and Osher (1988); applied to image processing, computer vision, computational physics, etc.
- Interfaces (line, curve, surface, etc) are represented implicitly,

$$\Gamma(t) = \{r \in \Omega : \quad \Phi(r,t) = 0\}$$

 Motion of the interface is realized by evolution of the auxiliary function Φ(r, t)

$$\Phi_t + V_n |\nabla \Phi| = 0, \quad V_n = V_n(r, t) \text{ for } r \in \Gamma$$

• *V<sub>n</sub>* is the normal velocity, which may be given or depend on curvatures



# Geometric quantities in level set functions

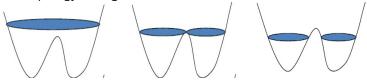
- Unit normal vector  $n = \frac{\nabla \Phi}{|\nabla \Phi|}$
- Mean curvature  $H = \frac{1}{2} \nabla \cdot n$
- Gaussian curvature  $K = n \cdot adj(\text{He}(\Phi))n$  $adj(\cdot)$ : adjoint matrix  $He(\cdot)$ : Hessian matrix
- Surface integral
- Volume integral
- $\int_{\Gamma} f(r) dS = \int_{\mathrm{IR}^3} f(r) \delta(\Phi) dV$  $\int_{\Omega} f(r) dV = \int_{\mathrm{IR}^3} f(r) (1 \mathrm{Heav}(\Phi)) dV$

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# Facts about level set method

- Uniform mesh grids may be used
- Automatically handles topological change: merging, breaking, etc., unlike ray tracing method which needs to relabel marks when topology changes



- Local level set method can be used to reduce computational cost
- Accuracy issue: interface approximation, conservation of mass, etc.

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#### Application to VISM

- Cheng, Dzubiella, McCammon, & Li, J. Chem. Phys., 2007
- Cheng, Xie, Dzubiella, McCammon, Che, & Li, J. Chem. Theory Comput.,(2008) accepted
- Cheng, Wang, Setny, Dzubiella, Li, & McCammon, 2008 (preprint)

Level set equation of relaxation:

$$\Phi_t + V_n |\nabla \Phi| = 0, V_n = -\delta_{\Gamma} G[\Gamma]$$

$$\delta_{\Gamma}G[\Gamma] = P + 2\gamma_0(H(r) - \tau K(r)) - \rho_w U(r) + \delta_{\Gamma}G_{elec}[\Gamma]$$

Motion of solute atoms due to interactions:

$$\frac{dx_i}{dt} = -\nabla_{x_i} G[\Gamma; x_1, \cdots, x_n]$$

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# Application to VISM cont'd

Decay of the free energy:

$$\frac{dG[V_n(t)]}{dt} = \int_{\Gamma(t)} \frac{\delta G[V_n(t)]}{\delta V_n} \left[ \frac{dr(t)}{dt} \cdot n \right] dS$$
$$= -\int_{\Gamma(t)} \left| \frac{\delta G[V_n(t)]}{\delta V_n} \right|^2 dS < 0$$

- Γ = Γ(t) and t is not the real dynamical time, but represents the minimization iteration
- The normal velocity does not represent the interface evolution in real dynamics of the system.

# Algorithm

- Step 1. Input parameters and initialize level-set function-signed distance function
- Step 2. Calculate the normal and curvatures
- Step 3. Calculate and extend the normal velocity
- Step 4. Solve the level-set equation
- Step 5. Reinitialize the level-set function
- Step 6. Solve ODEs for the motion of solute particles

• Step 7. Set  $t = t + \Delta t$  and go to Step 2

# Solving the level set equation numerically<sup>2</sup>

$$\Phi_t + V_n(r) |\nabla \Phi| = 0 \tag{1}$$
  
$$V_n(r) = -P - 2\gamma_0(H(r) - \tau K(r)) + \rho_w U(r)$$

- The mean curvature H and Gaussian curvature K are calculated from  $\Phi$
- Equation (1) is parabolic and may degenerate in certain parameter regimes. Computationally the degeneracy is removed by adding a small constant to the eigenvalues of the matrix that defines the parabolicity

<sup>&</sup>lt;sup>2</sup>See in Cheng, Dzubiella, McCammon, & Li, J. Chem. Phys., 2007 - 《 ㅁ 》 《 쿱 》 《 클 》 《 클 》 - 클 》 - 클 》 이 이 (?

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# Solving the level set equation numerically cont'd

- Reinitialization is used to keep  $\nabla \Phi$  away from zero while the interface  $\Gamma$  is unchanged
- The normal velocity  $V_n$  is only defined on  $\Gamma$  theoretically, and extended in normal direction both sides numerically
- For large system, U(r) = ∑<sub>i</sub> U<sub>i</sub>(|r r<sub>i</sub>|) is pre-computed and stored for each grid point (in the case of fixed solutes); a linear approximation is employed for any r ∈ Γ

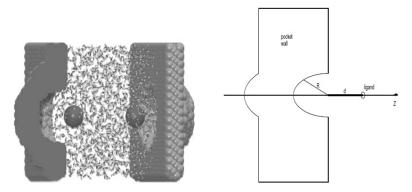
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# Solving the level set equation numerically cont'd

- When distance is small, LJ potential changes rapidly. To improve the accuracy, we can compute LJ on a fine grid while the level set function is evolved on a coarse grid
- Make proper initial guess based on a priori knowledge of the interface shape

These will drastically speed up the program. For the system of 4,243 solute atoms, with a  $50 \times 50 \times 50$  grid size and a good initial guess, it takes 5 minutes. Two hours with a bad initial guess and high resolution.

# Pocket system<sup>3</sup>



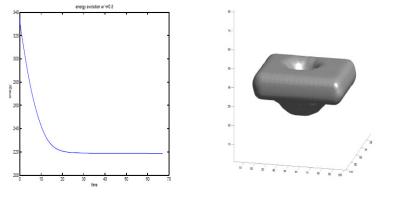
Each wall consists of 4,242 atoms.

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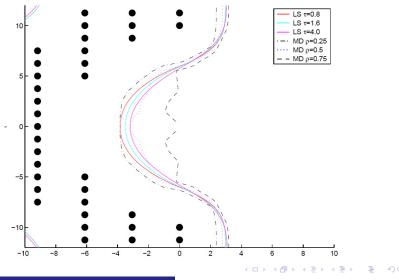
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# Wall (R8) without ligand

We first study the case of wall without ligand. We focus on the energy relaxation and interface with the effect of Tolman correction.



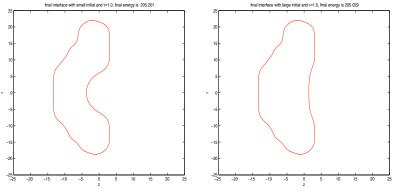
# Wall (R8) without ligand: effect of Tolman correction



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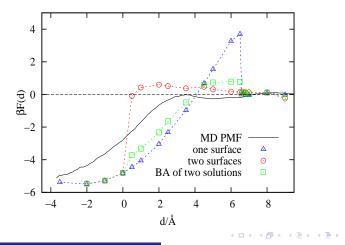
# Wall (*R*8) without ligand: effect of initial interface



Left: final interface with tight initial; right: final interface with loose initial

# Wall (R8) with ligand

In this case, we study the interface and energy with respect to the ligand position. Bi-mode is observed when  $d \in [0, 7]$ .

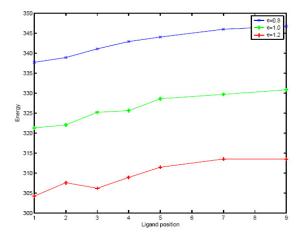


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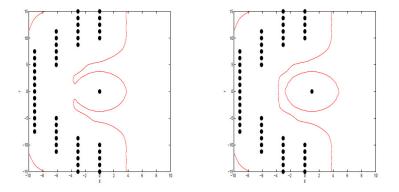
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# Wall (R8) with ligand: effect of Tolman correction



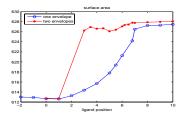
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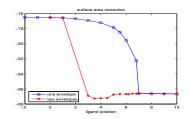
Wall (R8) with ligand: effect of initial interface (d = 0)

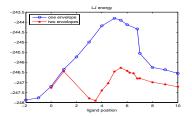


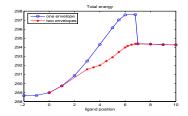
Left: final interface with loose initial; right: final interface with tight initial

# Wall (R5) with ligand: energy profile





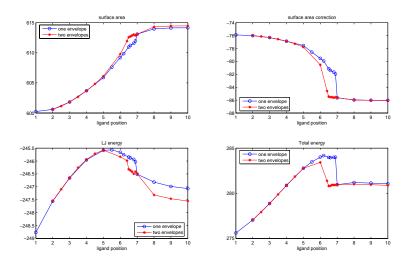




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# Wall (R0) with ligand: energy profile

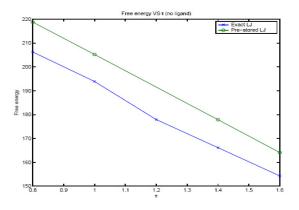


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# Efficiency vs accuracy

Efficiency is achieved at the cost of accuracy. Here is a figure showing the energy difference of the wall without ligand, computed with and without pre-computation of LJ potential.



#### Conclusion and outlook

#### Conclusions

- Tested the theory and method, and find that they work well to capture hydrophobic interactions
- Curvature correction has a stronger influence to the concave region than the convex region of solute-solvent interfaces
- Describe the bimodal behavior very well
- Very accurate free energy calculations
- Discussion
  - In terms of the model, how to choose the Tolman length
  - Comparison with SAS/SES type of implicit-solvent models
  - How to include the electrostatics efficiently?
  - The efficiency of the method compared with other implicit models?

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Conclusions and outlook

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# Thank you!

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• Reinitialization: solve

$$\Phi_t + sgn(\Phi)(\nabla \Phi - 1) = 0$$

to a steady state, where

$$sgn(\Phi) = rac{\Phi}{\sqrt{\Phi^2 + \epsilon}}$$

• Parabolicity: curvatures *H* and *K* are calculated from the second fundamental form

$$II = rac{1}{|
abla \Phi|} P_{
abla \Phi} 
abla^2 \Phi P_{
abla \Phi}, \quad P_{
abla \Phi} = I - rac{
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abla|^2}.$$

*II* is used to make sure the parabolicity