

3D-RISM Molecular Theory of Solvation

Tyler Luchko, Sergey Gusarov, David A. Case,
Andriy Kovalenko

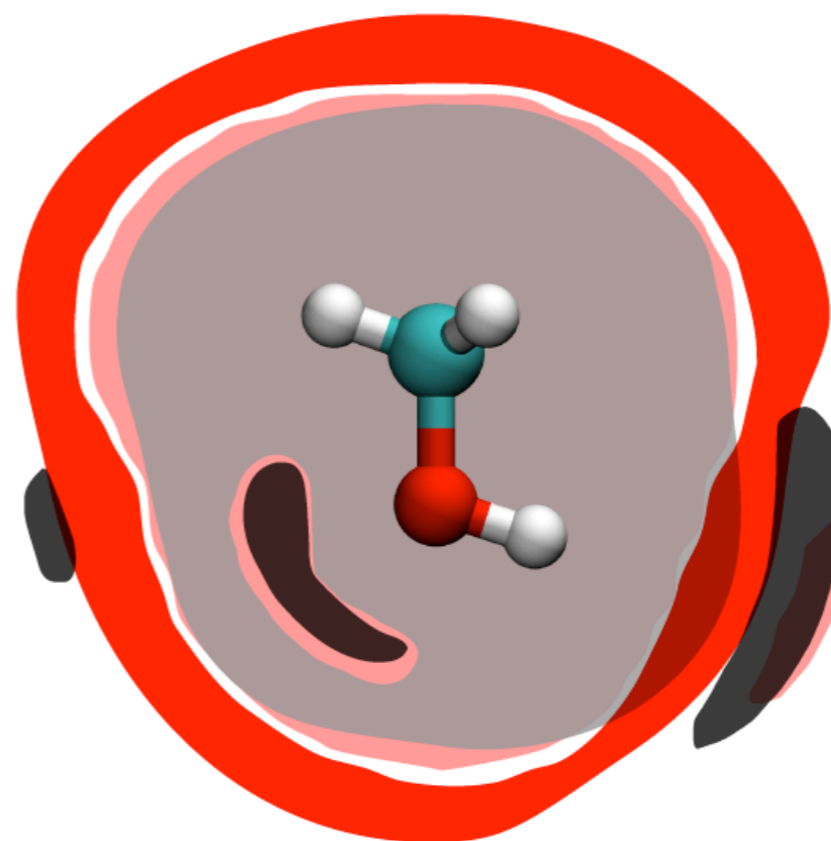
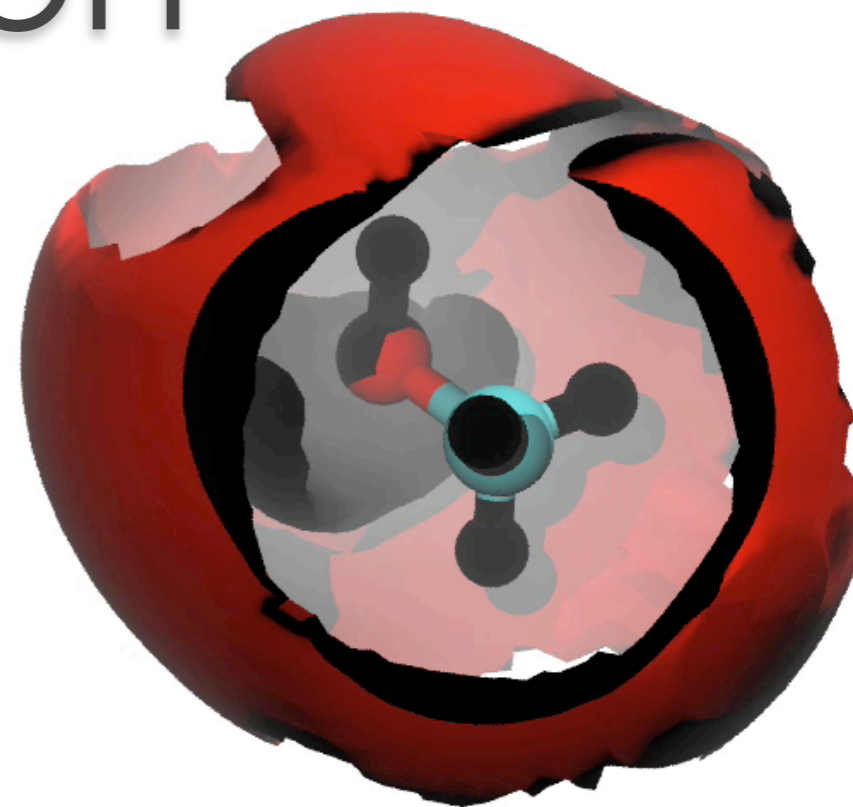
Rutgers University, University of Alberta, National
Institute for Nanotechnology

GPU Programming for Molecular Modeling
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Solvent Distribution

- Grid based calculation
- Orientations of an explicit solvent model are averaged
- Mean solvent distribution calculated

$$g_{\gamma}^{UV}(\mathbf{R})$$



3D-RISM

- Real space

$$h_{\gamma}^{\text{UV}}(\mathbf{R}) = \sum_{\alpha} \int d\mathbf{R}' c_{\alpha}^{\text{UV}}(\mathbf{R}' - \mathbf{R}) \chi_{\alpha\gamma}^{\text{VV}}(R')$$
$$\chi_{\alpha\gamma}^{\text{VV}}(R) = w_{\alpha\gamma}^{\text{VV}}(R) + \rho_{\alpha} h_{\gamma}^{\text{VV}}(R)$$

- K-space

$$h_{\gamma}^{\text{UV}}(\mathbf{k}) = c_{\alpha}^{\text{UV}}(\mathbf{k}) w_{\alpha\gamma}(k) + \rho^{\text{V}} c_{\alpha}^{\text{UV}}(\mathbf{k}) h_{\alpha\gamma}^{\text{VV}}(k)$$

- Coupled with a closure

$$g = \exp[-\beta u + h - c + b]$$

h → total correlation function

g → pair distribution function

c → direct correlation function

ω → intramolecular correlation

Kovalenko, A.; Hirata, F. Chem. Phys. Lett. 1998, 290, 237–244.

Kovalenko, A.; Hirata, F. J. Chem. Phys. 1999, 110, 10095–10112.

Thermodynamics

h → total correlation function
 g → pair distribution function
 c → direct correlation function
 b → bridge function

- From $g(\mathbf{R})$ we can get:

- Partial molar volume

$$\bar{V} = k_B T \chi_T \left(1 - \rho \sum_{\gamma} \int c_{\gamma} d\mathbf{r} \right)$$

- Solvation free energy

$$\Delta\mu_{\text{ex}} = \frac{\rho}{\beta} \int \left[h^2/2 - c + b - hc/2 + h \left(b - \int_0^1 b d\lambda \right) \right] d\mathbf{r}$$

- Entropy and energy

$$\Delta S = \frac{\Delta(\Delta\mu_{\text{ex}})}{\Delta T}, \quad \Delta E = \Delta\mu_{\text{ex}} + T\Delta S$$

- Mean solvation force

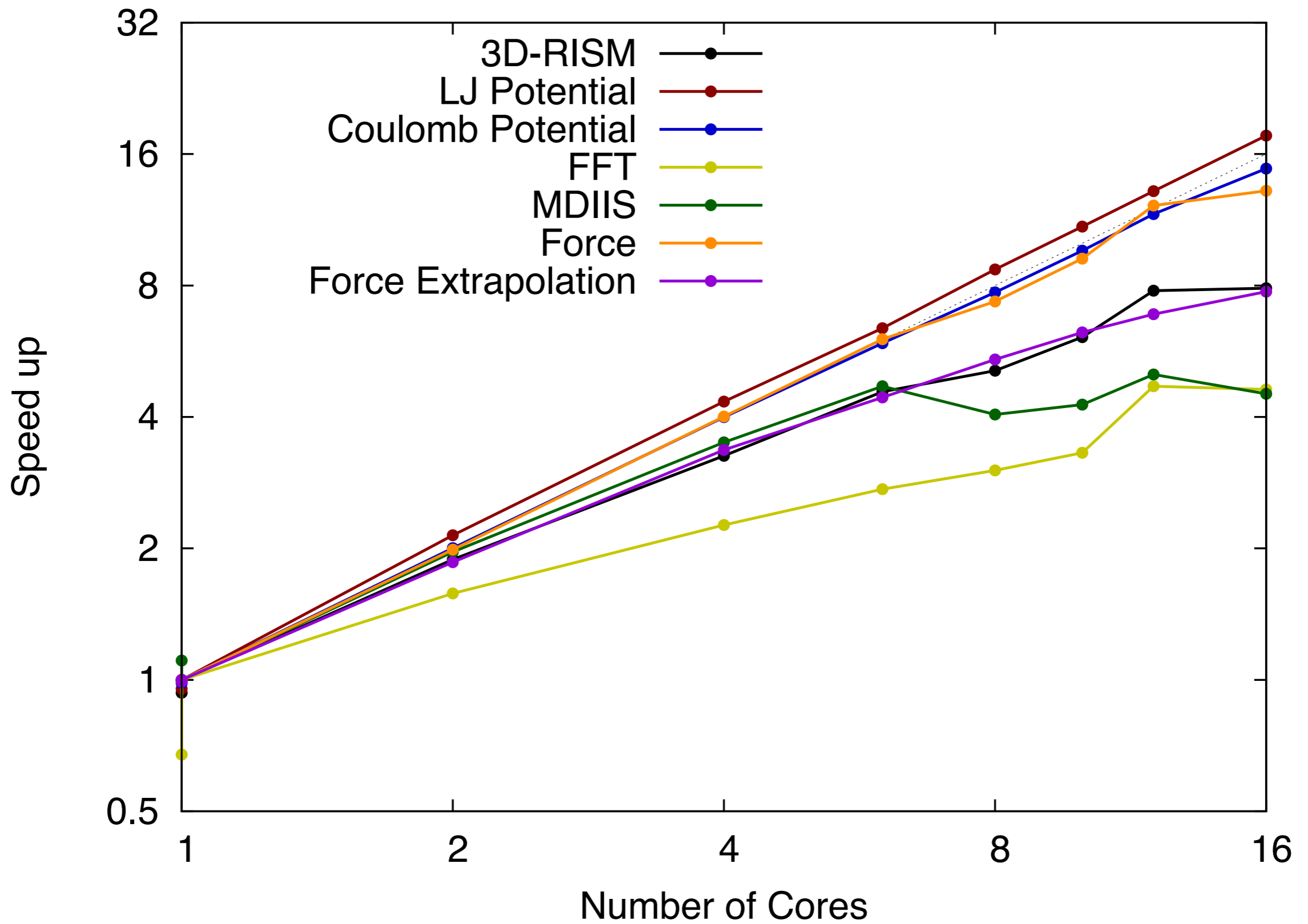
$$\mathbf{f}^{\text{UV}}(\mathbf{r}_i) = -\frac{\partial \Delta\mu_{\text{ex}}}{\partial \mathbf{r}_i} = -\sum_{\alpha} \rho_{\alpha} \int d\mathbf{R} g_{\alpha}^{\text{UV}}(\mathbf{R}) \frac{\partial u_{\alpha}^{\text{UV}}(\mathbf{R} - \mathbf{r}_i)}{\partial \mathbf{r}_i}$$

Computational Characteristics

- 3D arrays with 0.5 Å grid spacing

$$N = N_{\text{box}} \left[\underbrace{4}_{\text{asymptotics}} + N_{\text{solv}} \left\{ \underbrace{2N_{\text{MDIIS}}}_{\text{c,residual}} + \underbrace{2}_{g,h} \right\} \right]$$

- 24 base-pair DNA (~1500 atoms) in cTIP3P-Na⁺Cl⁻
 - 70 Å X 70 Å X 125 Å
 - ~ 3 GB RAM
 - ~1.5 CPU hours (Intel Core 2 Duo)
- MPI version uses distributed memory



MPI Scaling

Computational Considerations

- Largely consists of BLAS, FFT and LAPACK operations
- Typically 50% FFT, 25% MDIIS and 25% other
- Fortran 95

