



Adaptive Resolution Simulations for Soft Matter

Applications and New Developments

K. Kremer

Max Planck Institute for Polymer Research, Mainz



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COWORKERS:

Luigi Delle Site, FU Berlin
Matej Praprotnik , Ljubljana

Christoph Junghans , Los Alamos
Simon Poblete , FZ Jülich
Han Wang, Beijing, now FU Berlin
Adolfo Poma , La Sapienza Rome,
Sebastian Fritsch, MPIP

Debashish Mukherji, MPIP
Nico van der Vegt, TU Darmstadt

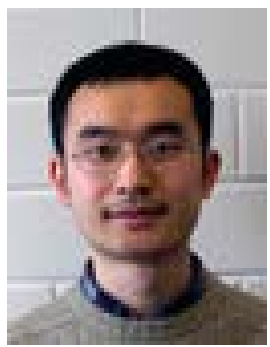
Raffaello Potestio, MPIP
Davide Donadio, MPIP

Ralf Everaers, ENS Lyon
Pep Espanol, Madrid
Rafa Delgado Buscalioni, Madrid

C. Clementi and her group (Rice),
G. Ciccotti (Rome), ...

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Outline

- **Motivation: Soft and Nanostructured Matter**
- **AdResS: Adaptive Resolution MD Simulation**
 - **Method, first Applications**
 - **Recent developments**
- **Particle-Continuum: AdResS + Hybrid MD**
- **Conclusions/Outlook**

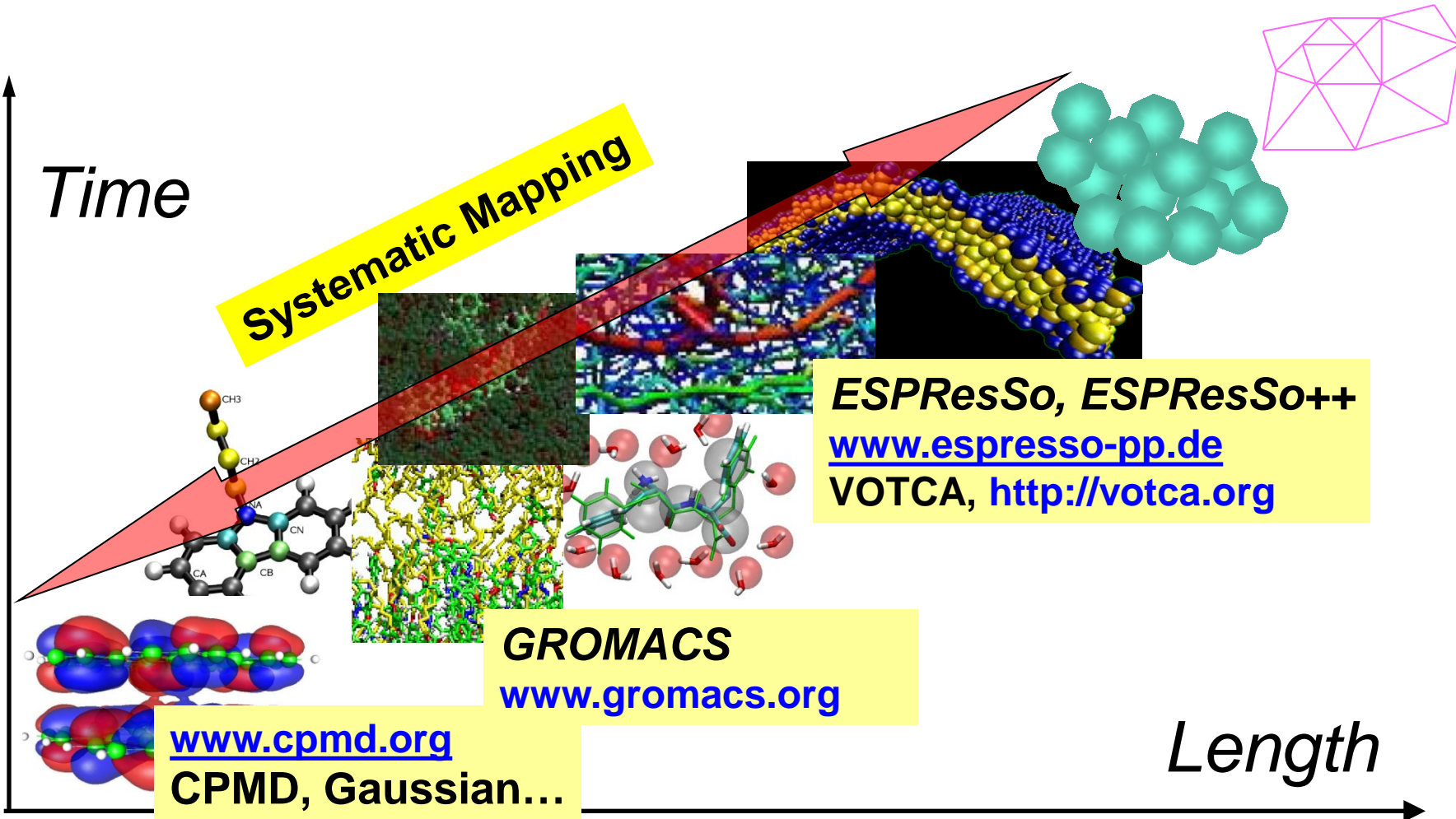
Soft Matter

“Soft” means:

- low energy density
- nanoscopic length scales
(10Å ... 1000Å)
- large (conformational) fluctuations
large *intra* molecular entropy
- thermal energy $k_B T$
relevant energy scale



Characteristic Time and Length Scales



Local Chemical Properties --- Scaling Behavior of Nanostructures
Energy Dominance --- Entropy Dominance of Properties

Energy Scale $k_B T$ for $T=300K$

$$E = 1.38 \cdot 10^{-23} J / K \cdot 300K$$

$$kT \approx 4.1 \cdot 10^{-21} J$$

$$kT \approx 2.5 \cdot 10^{-2} eV$$

$$kT \approx 9.5 \cdot 10^{-4} E_H$$

$$kT \approx 4.1 pNnm$$

$$kT \Rightarrow 200 cm^{-1}$$

$$kT \Rightarrow 0.6 kcal / mol$$

$$kT \Rightarrow 2.5 kJ / mol$$

$$E \approx 3 \cdot 10^{-19} J \approx 80kT$$

$$E \approx 4kT - 10kT$$

Electronic structure, CPMD

Quantum Chemistry

Biophysics Membranes, AFM

Spectroscopy

Chemical Bond

Hydrogen Bond

Energy Scale $k_B T$ for $T=300K$

$$E = 1.38 \cdot 10^{-23} \text{ J / K} \cdot 300 \text{ K}$$

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$$kT \approx 4.1 \text{ pNnm}$$

$$kT \Rightarrow 20$$

$$kT \Rightarrow 0.6 \text{ kcal / mol}$$

$$kT \Rightarrow 2.5 \text{ kJ / mol}$$

$$E \approx 3 \cdot 10^{-19} \text{ J} \approx 80kT$$

$$E \approx 4kT - 10kT$$

Electronic structure, MD

Quantum Chemistry

Biophysics Membranes, AFM

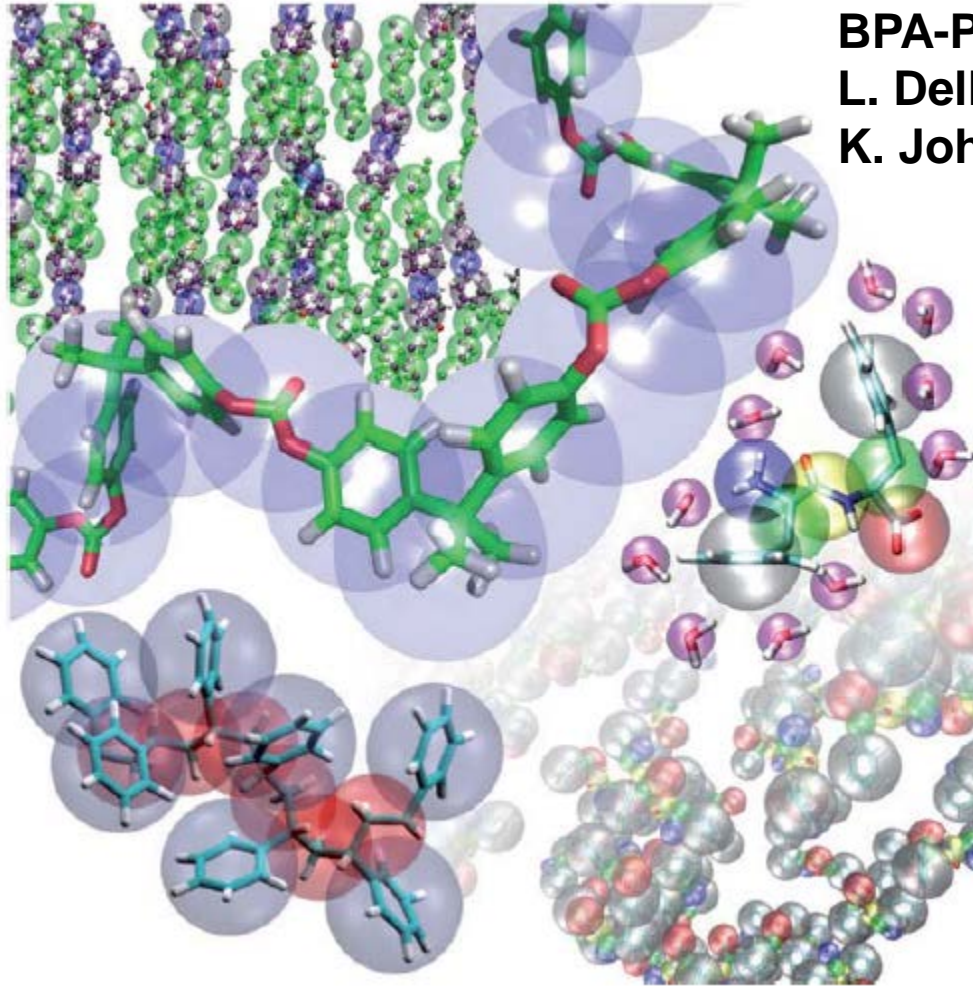
Spectroscopy

Green light photon $\approx 2-2.5 \text{ eV} \approx 100 kT$

**Chemical Bond
Hydrogen Bond**

Coarse Graining of Macromolecules: Examples

Azo Benzene LCs
C. Peter, L. Delle Site,
D. Marx



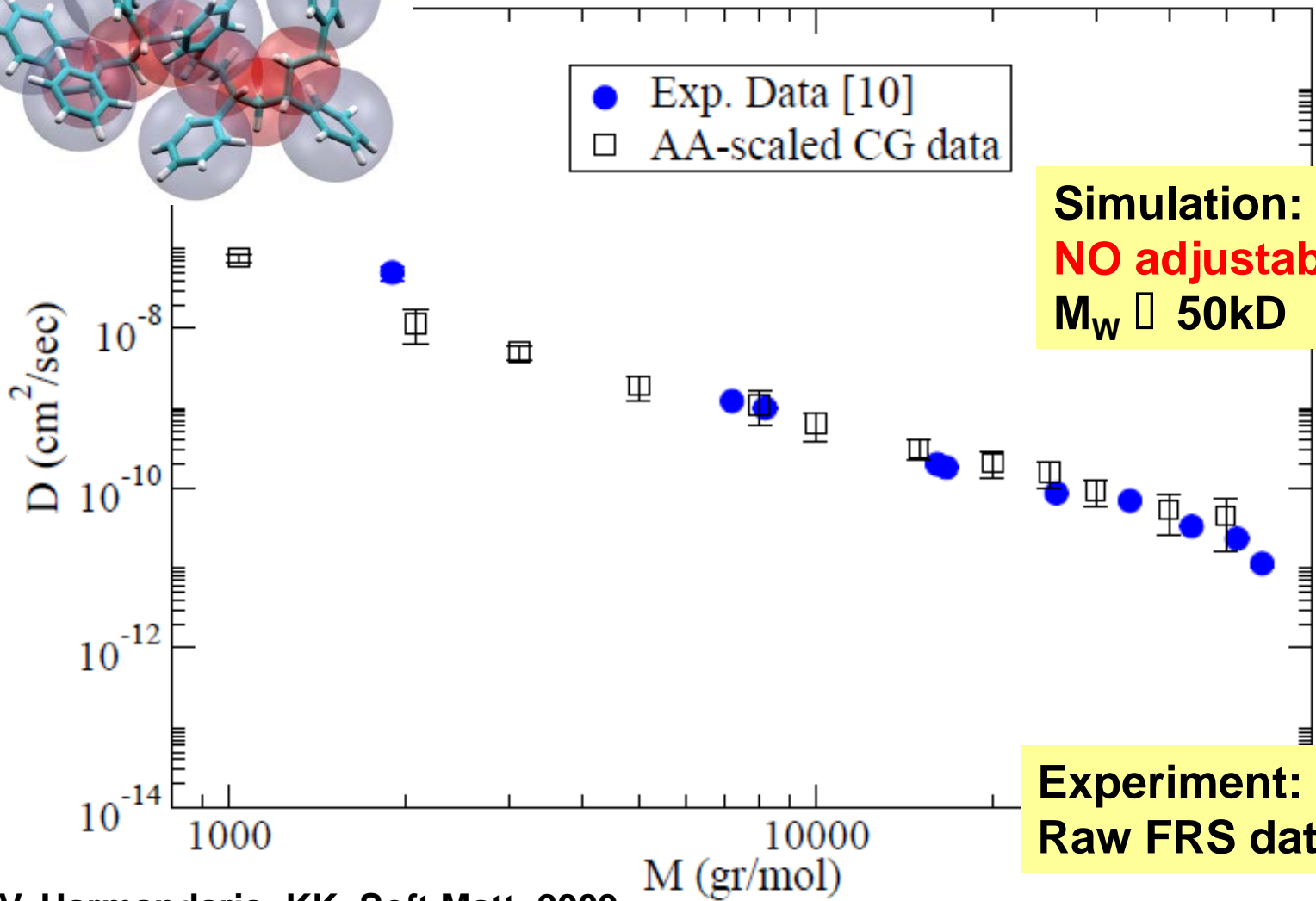
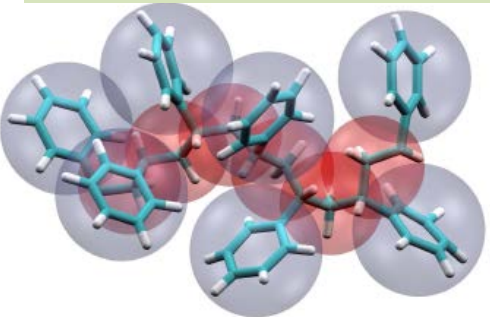
BPA-PC
L. Delle Site, C. Abrams
K. Johnston (1998ff)

**Polystyrene,
(w/wo additives)**
V. Harmandaris,
D. Fritz
N. Van der Vegt

Peptides
C. Peter

Application: Diffusion Constant of PS

(two step approach AA->UA->CG)



Simulation:
NO adjustable parameter
 $M_w \approx 50kD$

Experiment:
Raw FRS data, Sillescu

Standard Approach: Run whole system on one level of resolution.



Do we always need/want to do that?



M. Deserno et al.,
Nature, 2007

Andrienko et al,
PRL 98, 227402 (2007)

C. Peter et al, 2008ff

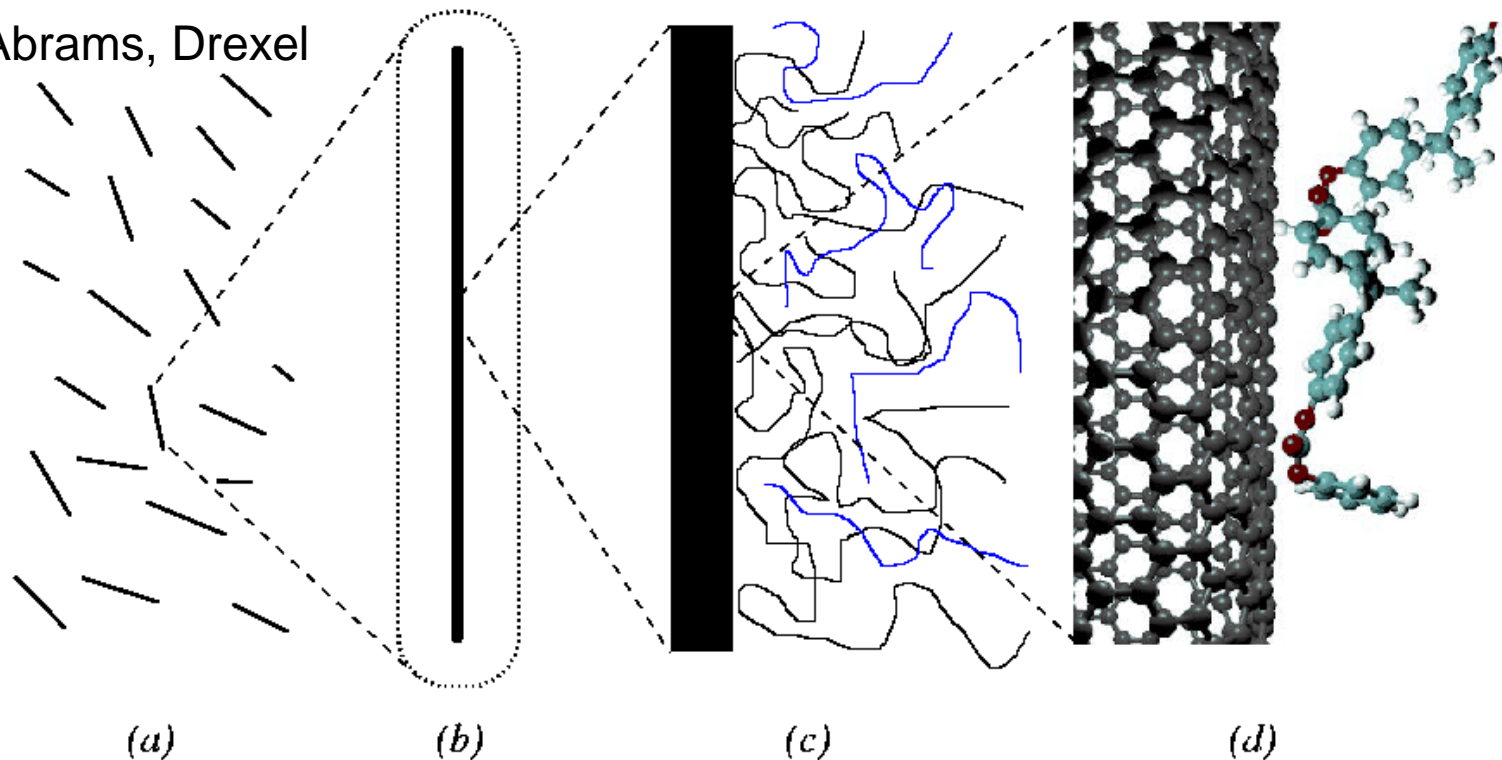
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Relevant Levels of Resolution

Example: Polymer/Nanotube Composites

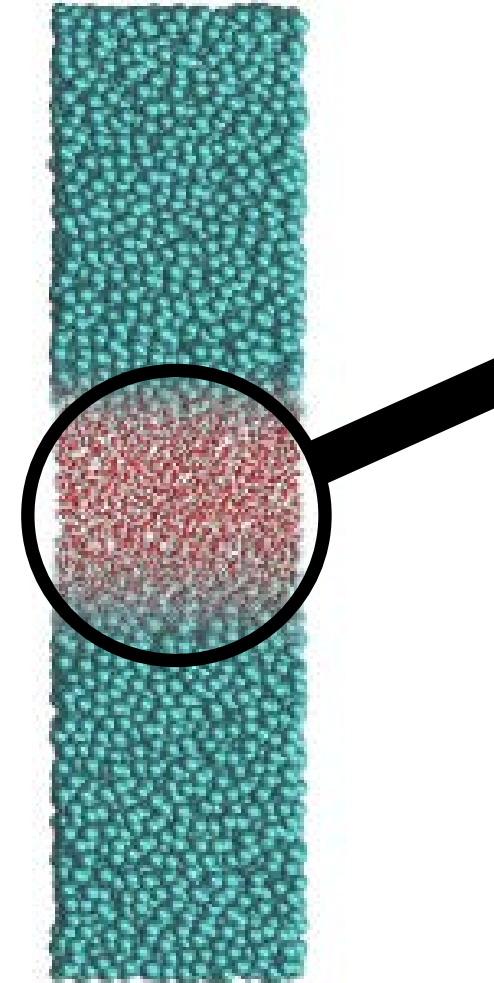
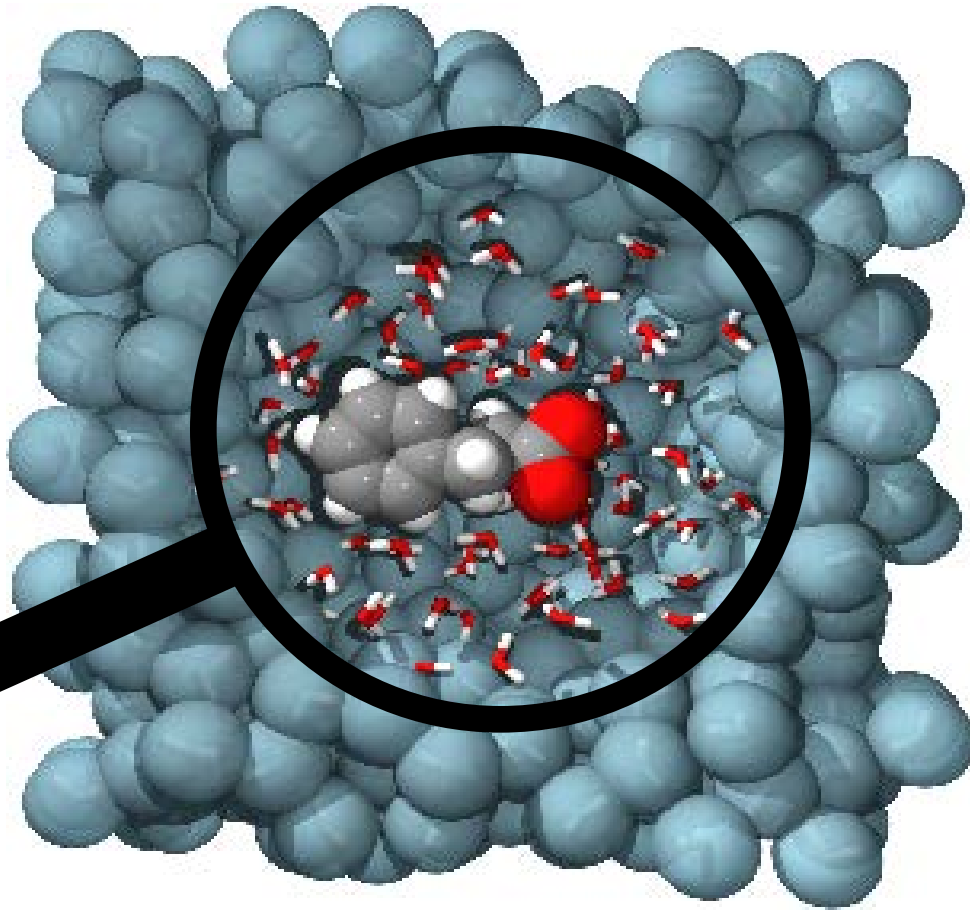
C. F. Abrams, Drexel



Aim at: Adsorption – Desorption, Flux of Chains, Additives, Structure Formation, grand canonical MD

AdResS

Adaptive Resolution MD Simulation

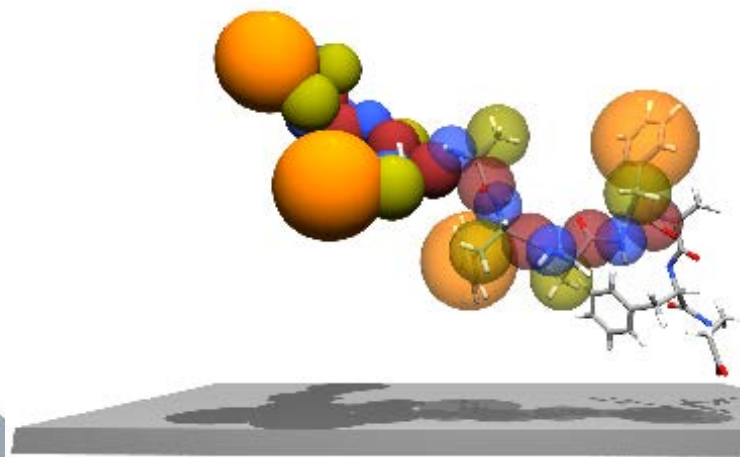
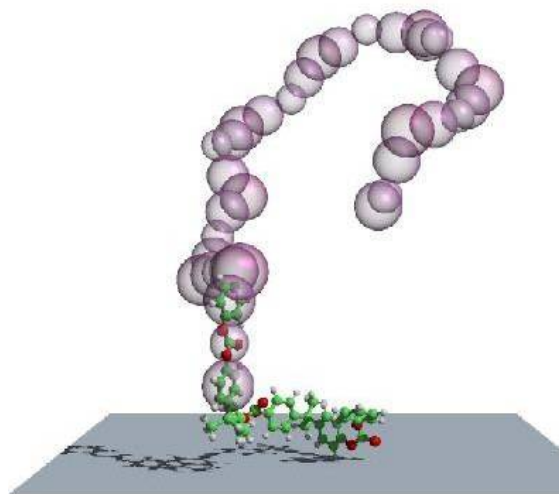
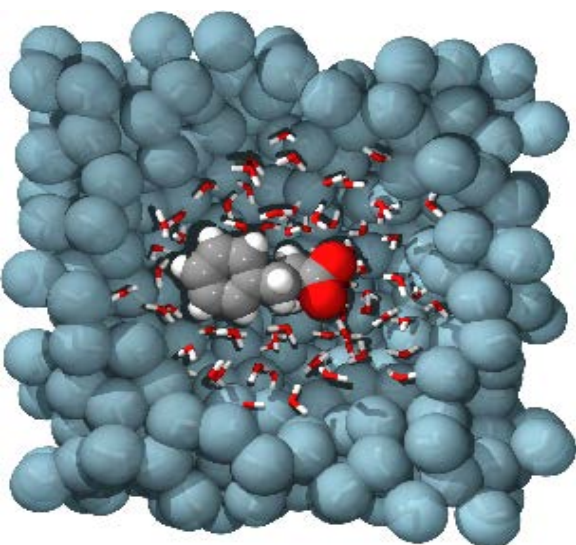


AdResS: **A**daptive **R**esolution **S**imulations

Free exchange of molecules/particles between regimes with different levels of resolution:



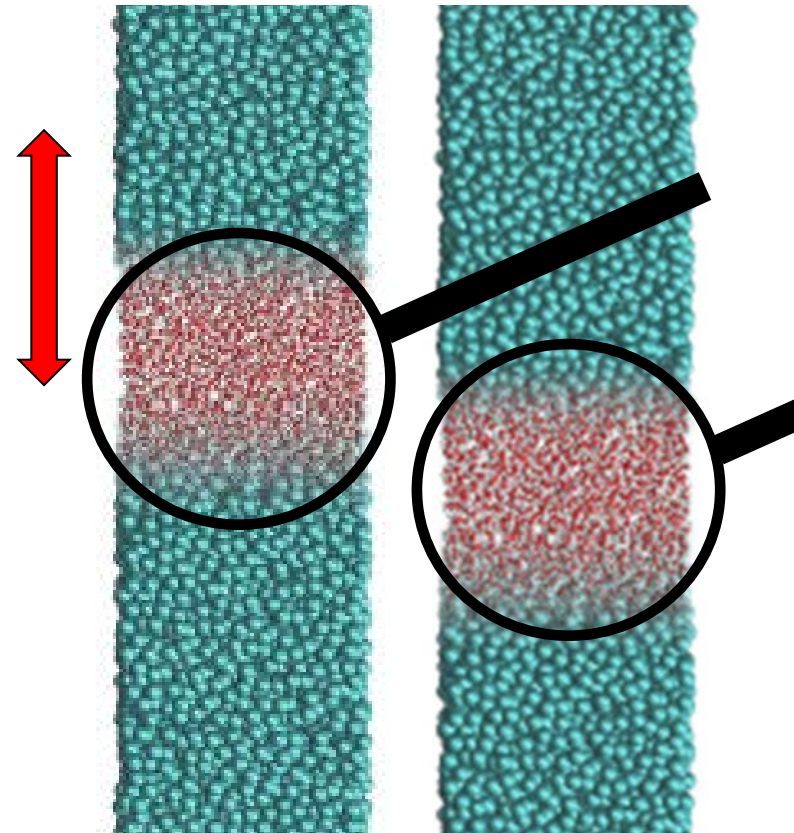
**equilibrium between both regimes,
no kinetic barrier**



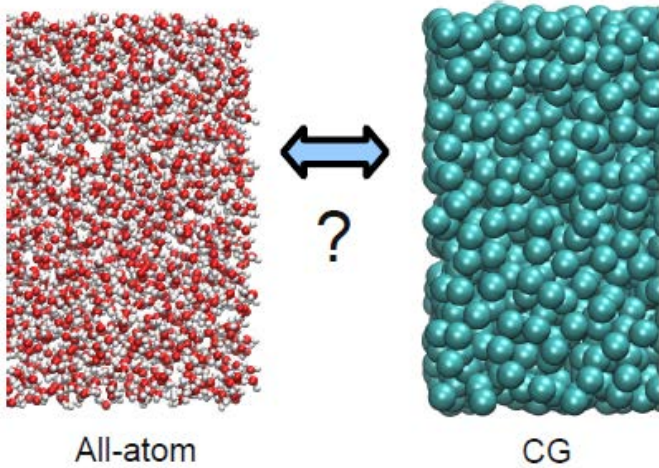
Adaptive Methods: Changing degrees of freedom (DOFs) on the fly

Requirements

- Same mass density
 - Same Pressure (\Rightarrow Eq. of state, ?)
 - Same temperature
 - **Free exchange between regimes**
 - Same center-center $g(r)$ (?)
 - (Simple two body potential)
- \Rightarrow “Some similarities” to 1st order phase transition
- \Rightarrow “Phase equilibrium”
- \Rightarrow Thermostat has to provide/take out latent heat due to change in degrees of freedom

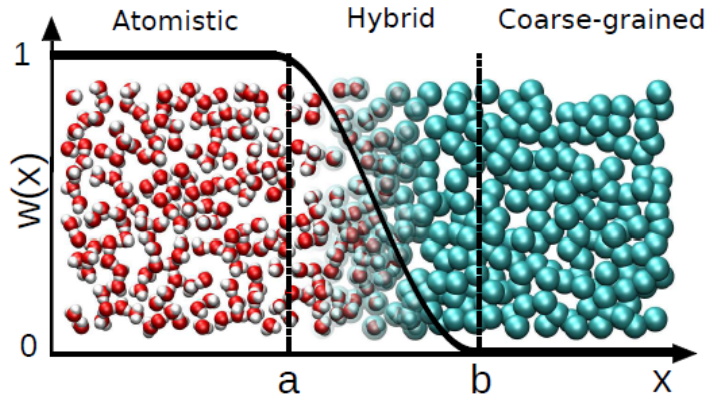


Adaptive Methods: Changing degrees of freedom (DOFs) on the fly



$$U_{\alpha\beta}^{AA}$$

$$U_{\alpha\beta}^{CG}$$



$$w(x) = \begin{cases} 1 & : \text{atomistic/explicit region} \\ 0 < w < 1 & : \text{hybrid region} \\ 0 & : \text{coarse-grained region} \end{cases}$$

Requirements:

- Free exchange of molecules
- NO (free) energy barriers
- Smooth transition forces
- Structure and dynamics preserved
 - (at least in all atom region)

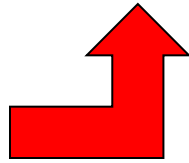
Newton's 3rd law:

- Force should be antisymmetric on exchange of particles $\alpha \leftrightarrow \beta$
- **Weight must depend on both particles**

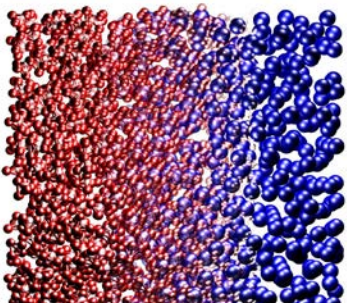
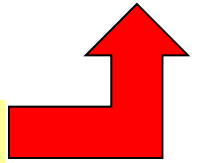
Transition Regime – Interpolation of Energy $U_{\alpha\beta}$?

$$U_{\alpha\beta} = w(X_\alpha)w(X_\beta)U_{\alpha\beta}^{atom} + [1 - w(X_\alpha)w(X_\beta)]U_{\alpha\beta}^{cg}$$

Full atomistic potential



Full coarse grained potential



$$\mathbf{F}_{\alpha\beta} = -\nabla_\alpha U = \mathbf{F}_{\text{Newton}} - [\nabla_\alpha w(\mathbf{X}_\alpha)]w(\mathbf{X}_\beta)(U_{\alpha\beta}^{AA} - U_{\alpha\beta}^{CG})$$

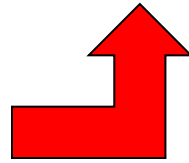
$$\mathbf{F}_{\beta\alpha} = -\nabla_\beta U = -\mathbf{F}_{\text{Newton}} - w(\mathbf{X}_\alpha)[\nabla_\alpha w(\mathbf{X}_\beta)](U_{\alpha\beta}^{AA} - U_{\alpha\beta}^{CG})$$

$$\mathbf{F}_{\alpha\beta} \neq -\mathbf{F}_{\beta\alpha}$$

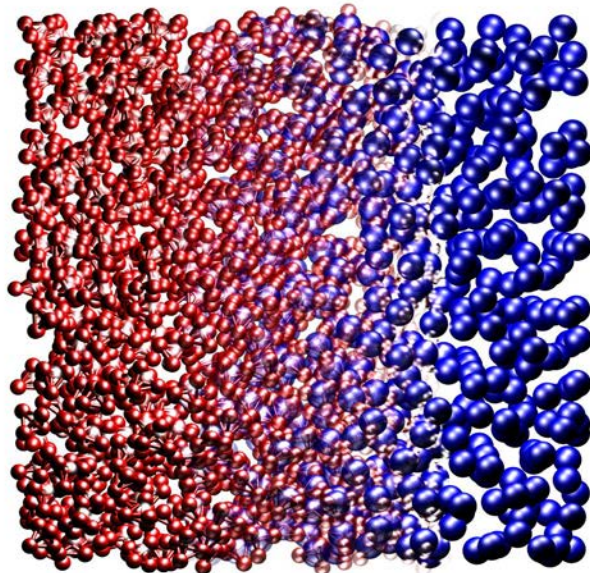
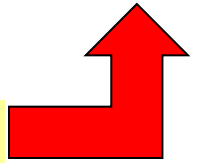
Transition Regime – Interpolation of Energy $U_{\alpha\beta}$?

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Full atomistic potential



Full coarse grained potential



- Drift terms from $W(x)$
- Violation of Newton's 3rd law
- Mathematical inconsistencies at boundaries
- There exists no $W(x)$, such that forces become conservative (L. Delle Site PRE 2007)

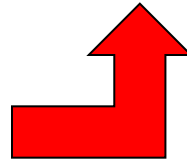
=> Force interpolation

AdResS:

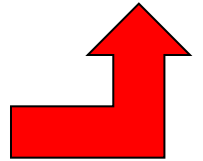
Transition Regime - Force Interpolation

$$F_{\alpha\beta} = w(X_{\alpha})w(X_{\beta})F_{\alpha\beta}^{atom} + [1 - w(X_{\alpha})w(X_{\beta})]F_{\alpha\beta}^{cg}$$

Full atomistic force



Full coarse grained force



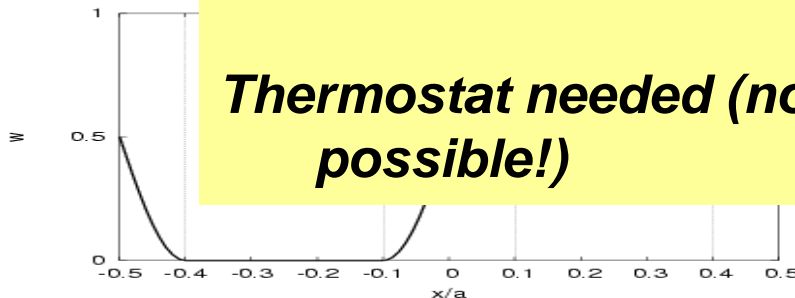
Transition regime: Force interpolation

(Newtons 3rd law fulfilled, no drift forces)

No transition energy function defined!

Pressure, Temperature, Density everywhere well defined

Thermostat needed (no microcanonical simulation possible!)

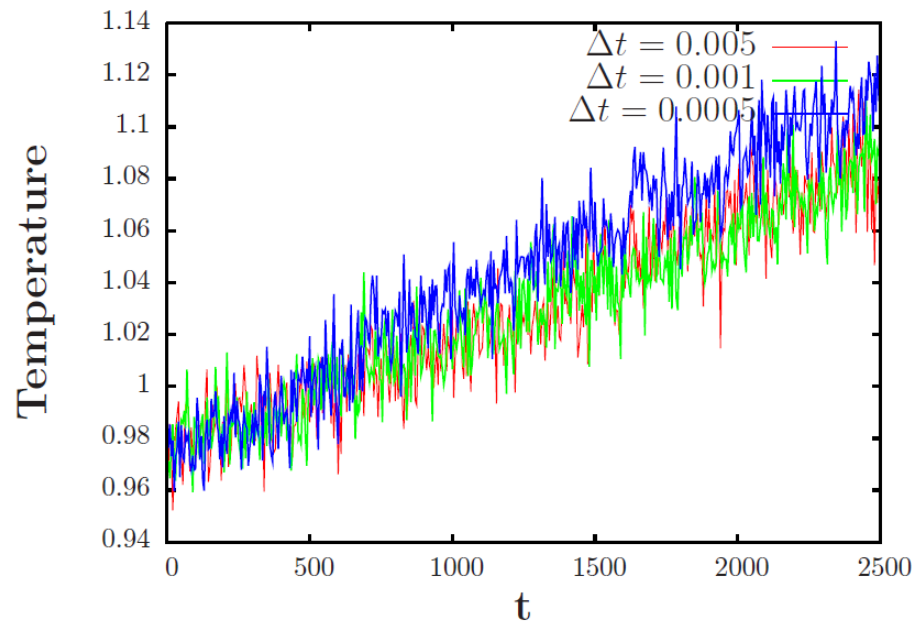
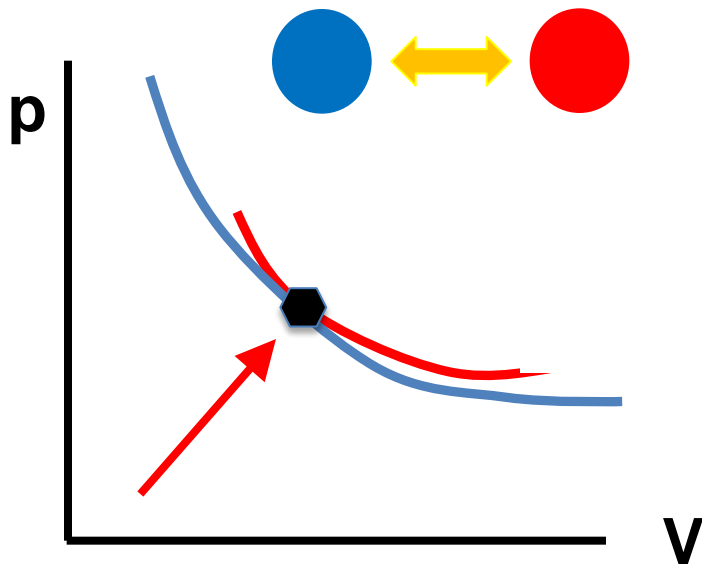


explicit hybrid: explicit explicit

* Similar problem already in H.C. Andersen, JCP **72**, 2384 (1979)

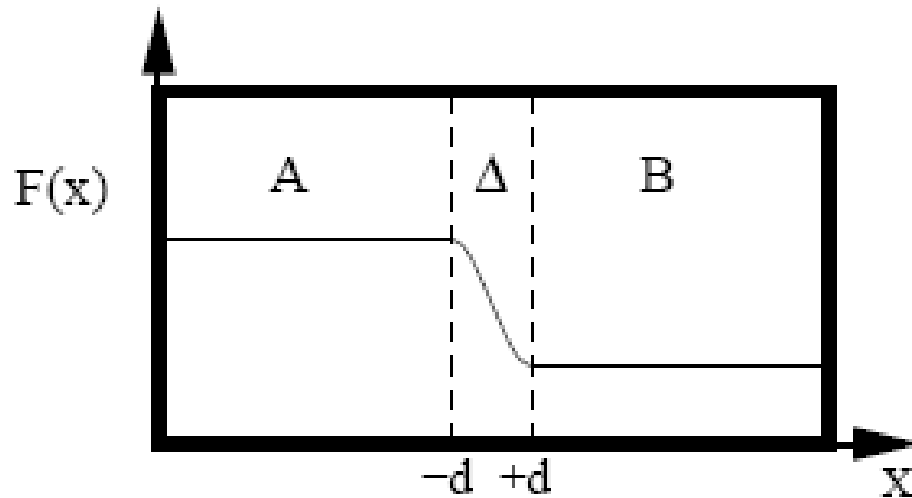
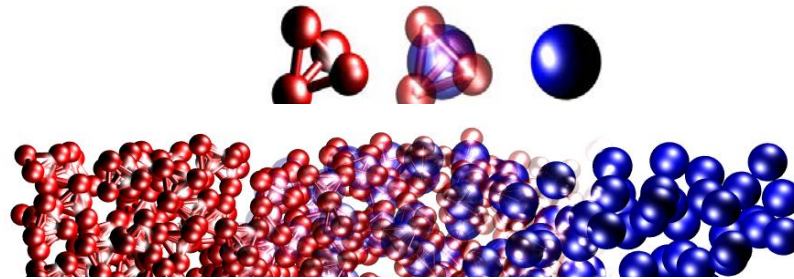
Theoretical Basis: Temperature... Necessity of Thermostat

Example: Two spherical Particles, no new DOFs



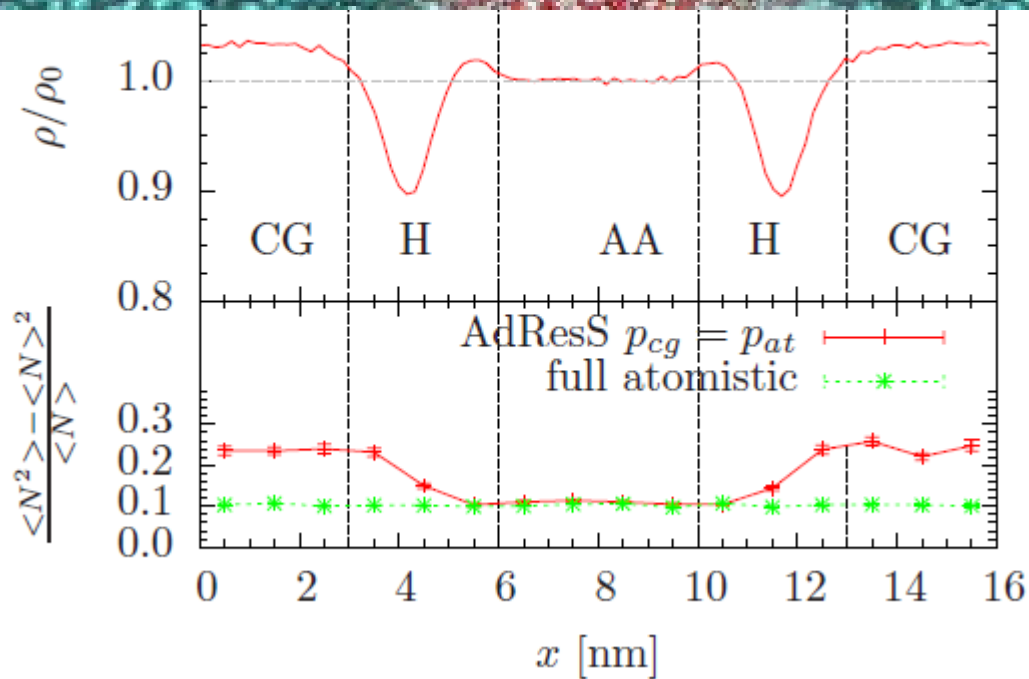
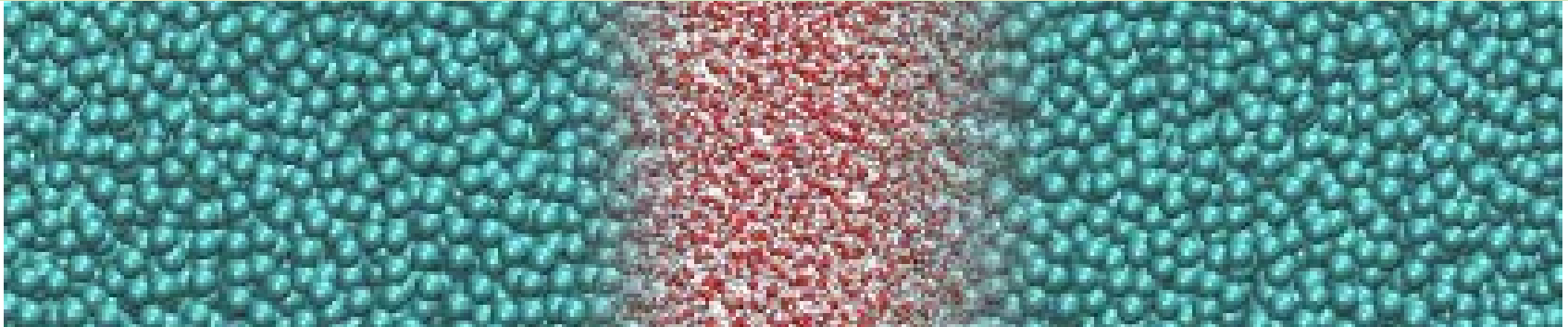
$$p_A(\mu_A, T)V = p_B(\mu_B, T)V; \quad \kappa_A = \kappa_B$$

Transition between models/levels of description => change in Free Energy



- Temperature well defined in whole box, fixed by thermostat
- Densities well defined
- Forces well defined => virial pressure well defined

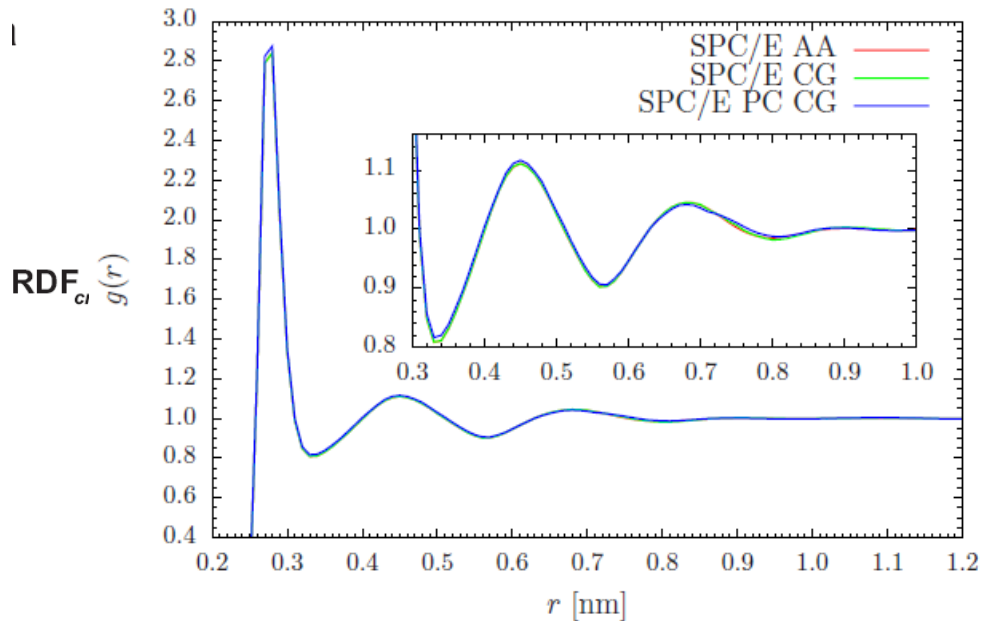
Transition between models/levels of description => change in Free Energy



System will adjust to constant pressure everywhere.

How to keep all atom region unperturbed?

Structure based CG - Compressibility



SPC/E water,
cg based on **matching $g(r)$**

Pressure

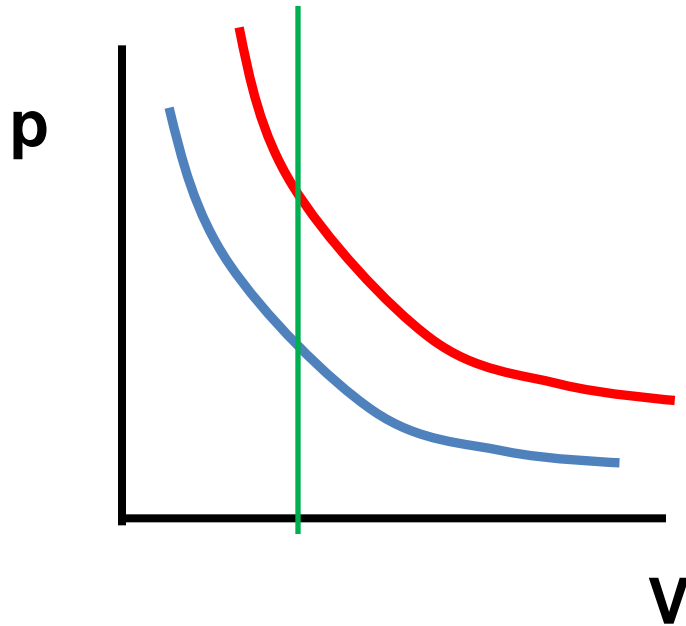
$$P = \rho k T - \frac{2}{3} \pi \rho^2 \int_0^{\infty} \underline{U'(r)g(r)r^3 dr}$$

Compressibility

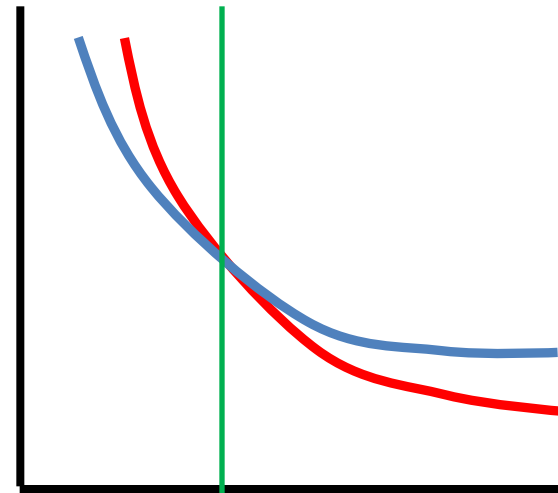
$$\kappa_T = \frac{1}{\rho k_B T} \left(1 + 4\pi\rho \int_0^{\infty} r^2 [g(r) - 1] dr \right) = \frac{1}{\rho k_B T} \frac{\langle N^2 \rangle - \langle N \rangle^2}{\langle N \rangle}$$

Equation of State: Pressure Correction

Structure based CG, based on $g(r)$ - pressure corrected



$$p_A(\mu_A, T) \neq p_B(\mu_B, T)$$
$$\kappa_A = \kappa_B$$



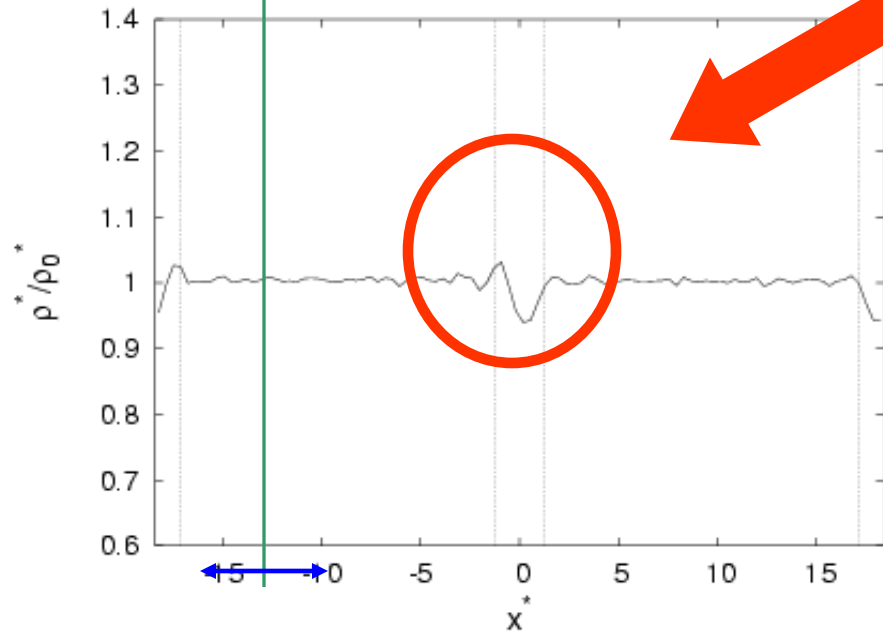
$$p_A(\mu_A, T) = p_B(\mu_B, T)$$
$$\kappa_A \neq \kappa_B$$

Pressure leverage causes density wiggles: special model with $p_{cg} = p_{AA}$



Equation of state in transition regime not the same!
(not surprising)

No energy function
but
well defined **forces** and thus
well defined **pressures**



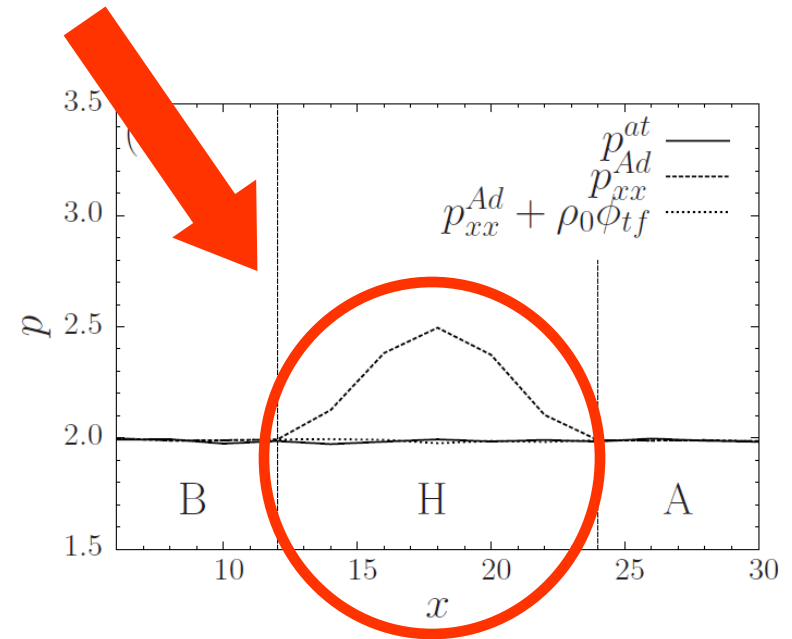
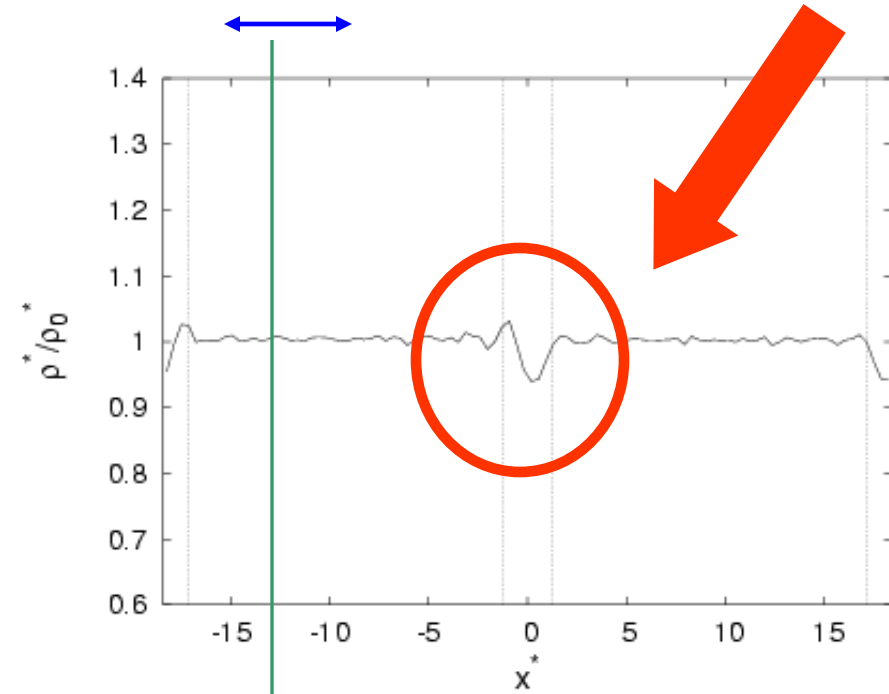
Calculate pressure in a plane \square x (Todd, Evans, Davies)

$$\bar{p}_{\beta\alpha}(\alpha) = \frac{1}{2A_{\alpha}\Delta\alpha} \left\langle \sum_{\alpha-\Delta\alpha \leq \alpha_i \leq \alpha+\Delta\alpha} m_i v_{i\beta} v_{i\beta} \right\rangle + \frac{1}{2A_{\alpha}} \left\langle \sum_{i=1}^N F_{i\beta} \text{sgn}(\alpha_i - \alpha) \right\rangle$$

Pressure

If density fixed to constant value

⇒ Pressure bump in hybrid zone



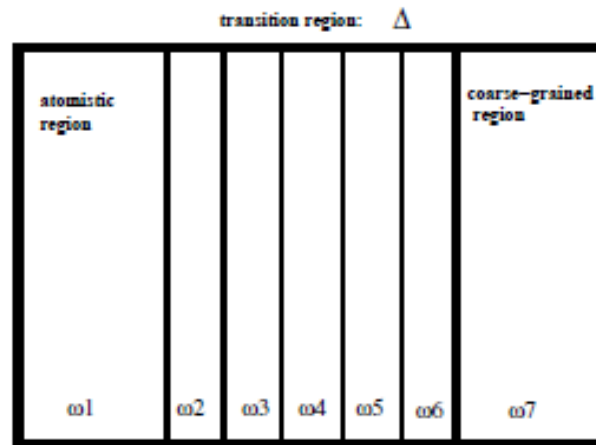
Calculate pressure in a plane \square x

(Todd, Evans, Davies)

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Effective Chemical Potential, at target density

- $\phi(x) = \mu_{atom} - \mu(w_i)$ (free energy per particle)

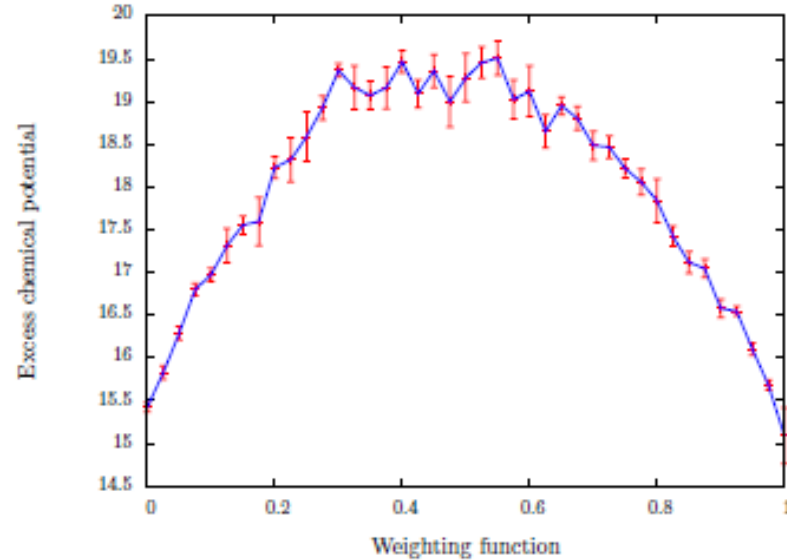
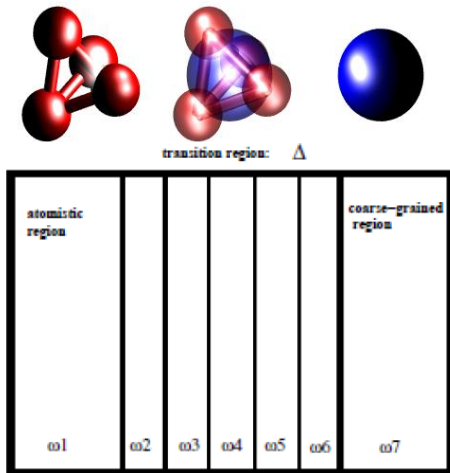


- Calculating $\mu(w_i)$ with $i = 2, 3, 4, 5, 6, 7$:
 - (a): **insertion particle method (IPM)** for each $i \implies$ Excess chemical potential $\mu^{exc}(w_i)$
 - (b): **fractional formula** \implies kinetic (ideal gas) contributions $\mu^{kin}(w)$

Effective Chemical Potential

at target density

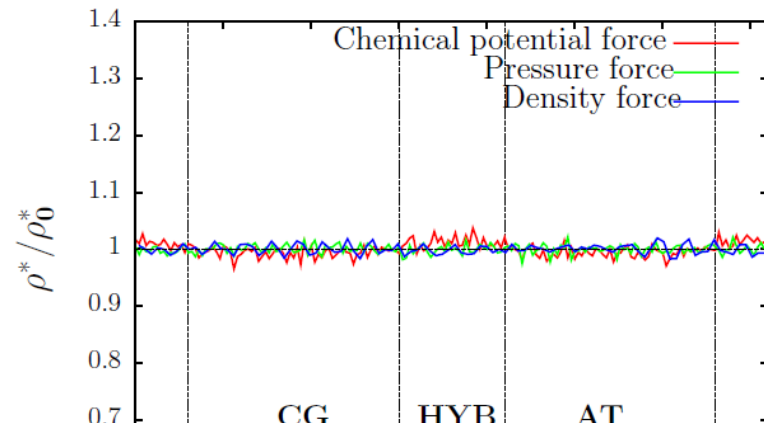
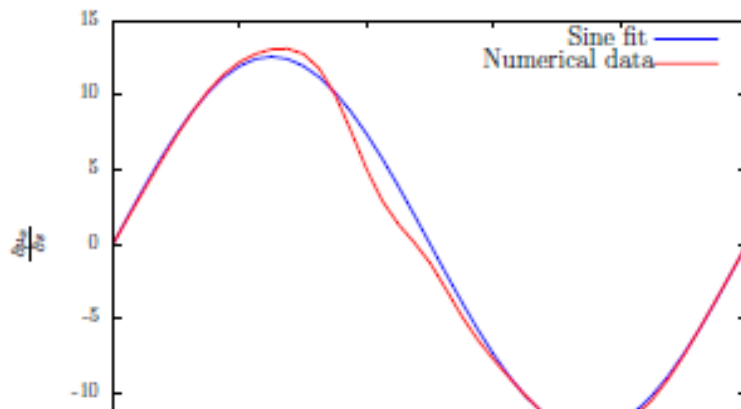
(a) Excess Chemical Potential μ^{exc}



(b) Kinetic contribution $:\mu^{kin} \propto \left(\frac{w}{2}\right) \lg(T) + \lg \frac{\Gamma\left(\frac{w}{2}\right)}{\Gamma(w)}$

Effective Chemical Potential: Thermodynamic Force F_{thm}

- “latent heat” leads to force: $F_{thm} = - \nabla_x \mu(x)$
- $-\nabla_x \mu^{exc} + \text{thermostat for kinetic part}$
-

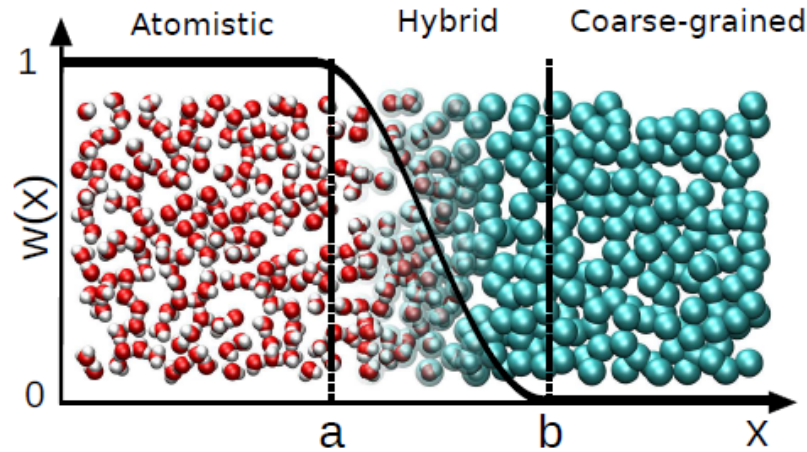


F_{thm} can perform work on the particles in transition regime

Allows to couple almost any system

No need to have same μ , same p in both regimes

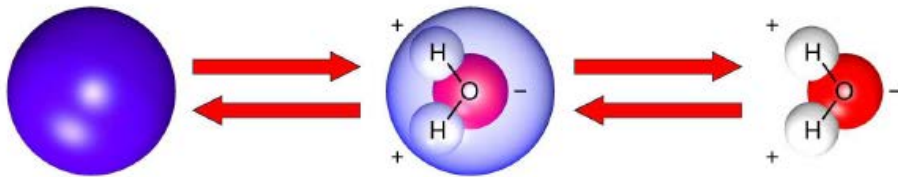
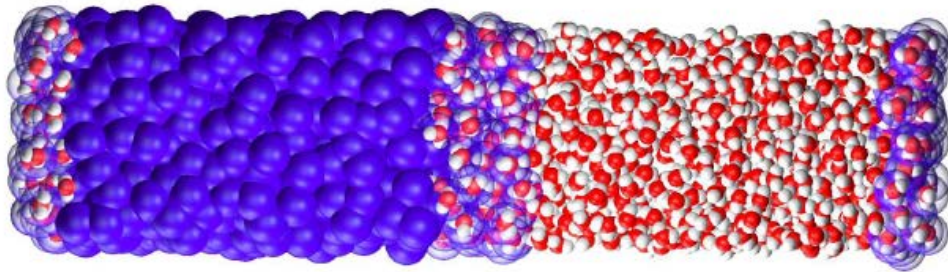
Variable pressure in AA and CG region: Thermodynamic Force F_{thm}



$$p_A(\mu_A, T)V \neq p_B(\mu_B, T)V; \quad \kappa_A = \kappa_B$$

$$\left(p_A(\mu_A, T) + \frac{\rho_0}{M_\alpha} \int_a^b \mathbf{F}_{th}(x) dx \right) V = p_B(\mu_B, T)V$$

Test case: Coarse Grained Water: SPC/E



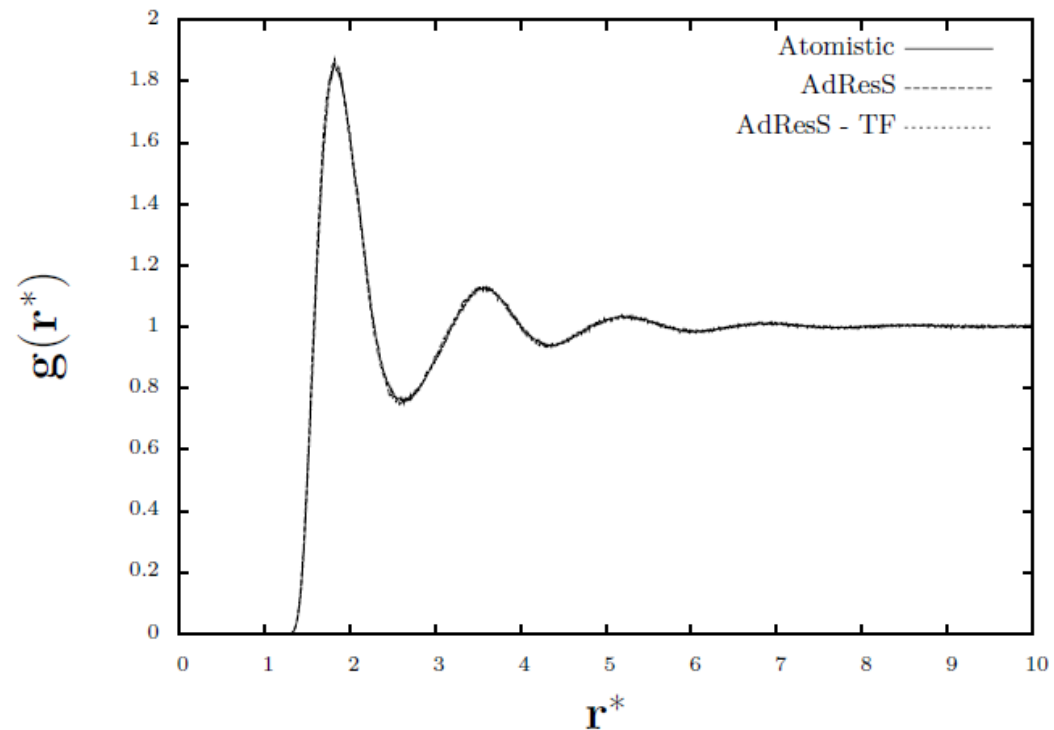
Structure based
Coarse Graining:

Perfect match of $g(r)$
all atom – coarse grained

$$K_{\text{atomistic}} = K_{\text{cg}}$$

BUT

$$p_{\text{cg}} = 6200 p_{\text{atomistic}}$$



Control of Thermodynamics in Explicit Region

Coarse-grained potentials usually don't match the atomistic system's virial pressure

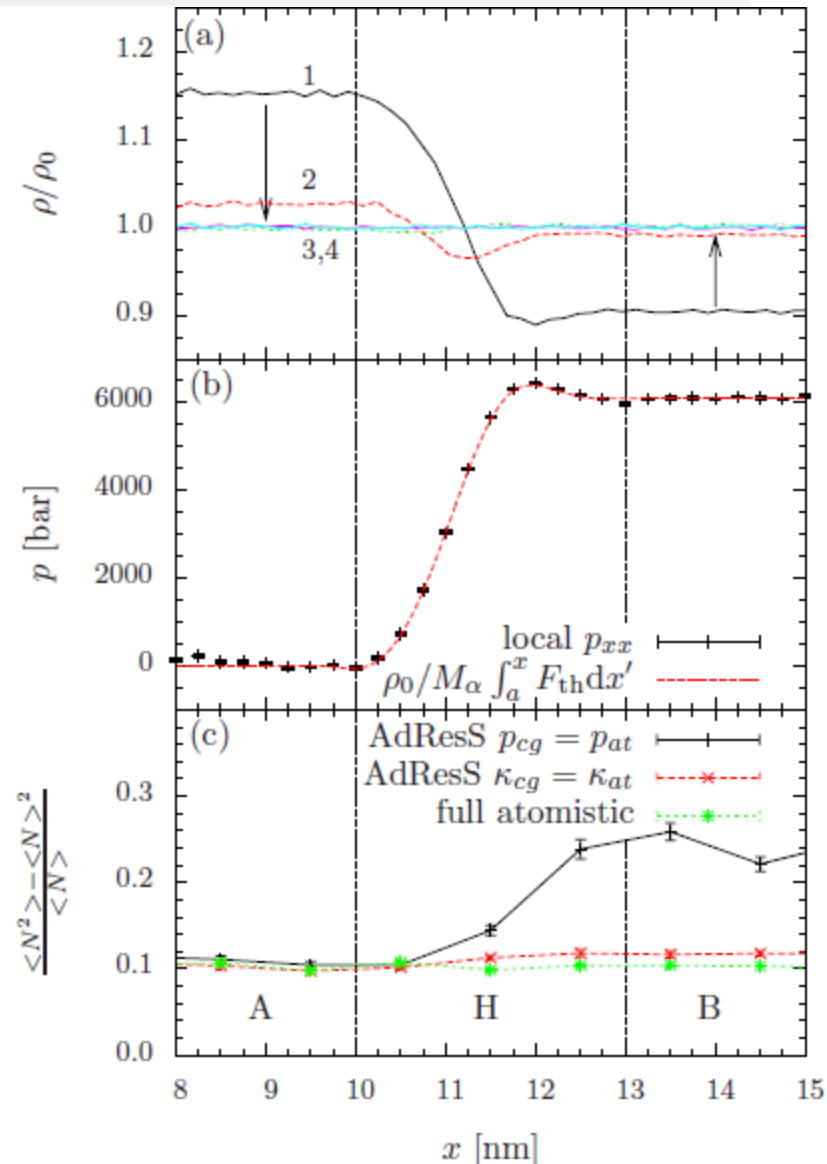


The difference can be balanced via an iteratively-refined thermodynamic force [1]

$$\mathbf{F}_{th}^{i+1}(x) = \mathbf{F}_{th}^i(x) - \frac{M}{\rho_0^2 \kappa_T} \nabla \rho^i(x)$$

Density and particle fluctuations are preserved

The explicit region behaves as an open system



[1] S. Fritsch, S. Pobleto, C. Junghans, G. Ciccotti, L. Delle Site, and K. Kremer, Phys Rev Lett 108, vol 108, 2012 [Figures from therein]

Some Applications

- Fullerene in Toluene
- Fullerenes in water

Kirkwood Buff integrals:

- Peptides in water urea mixtures
- **PNIPAM in water alcohol mixtures**

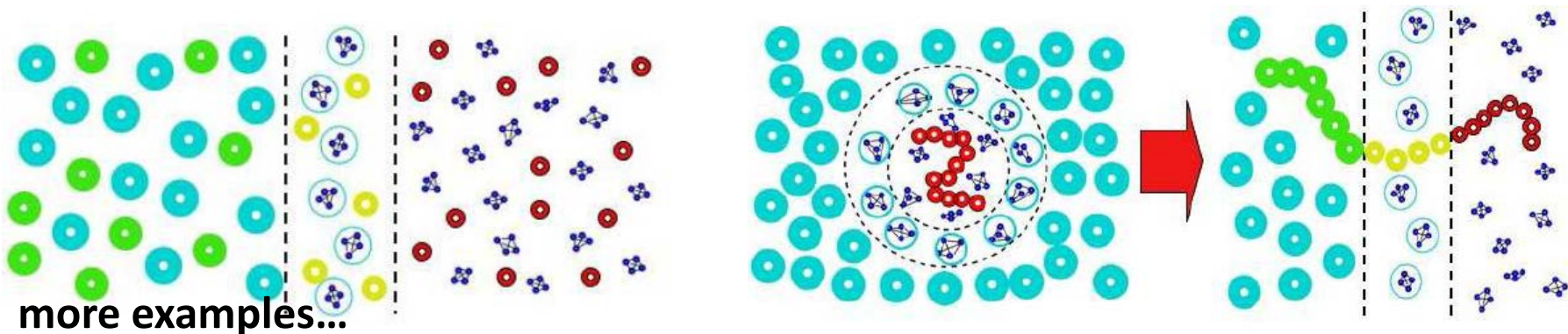
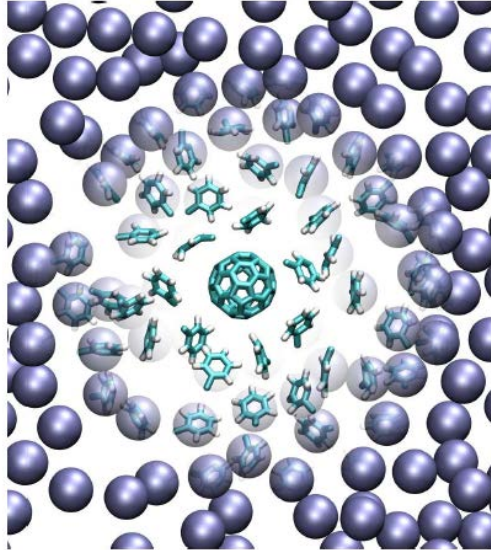


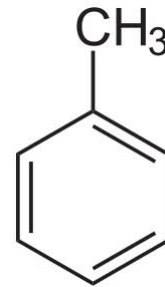
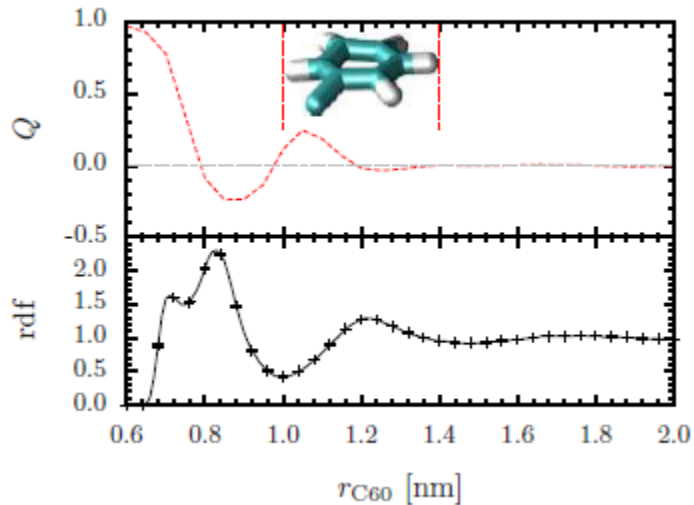
Table 1: Diffusion constants for the C60/toluene center of mass

C60 in Toluene

C. Junghans, S. Fritsch

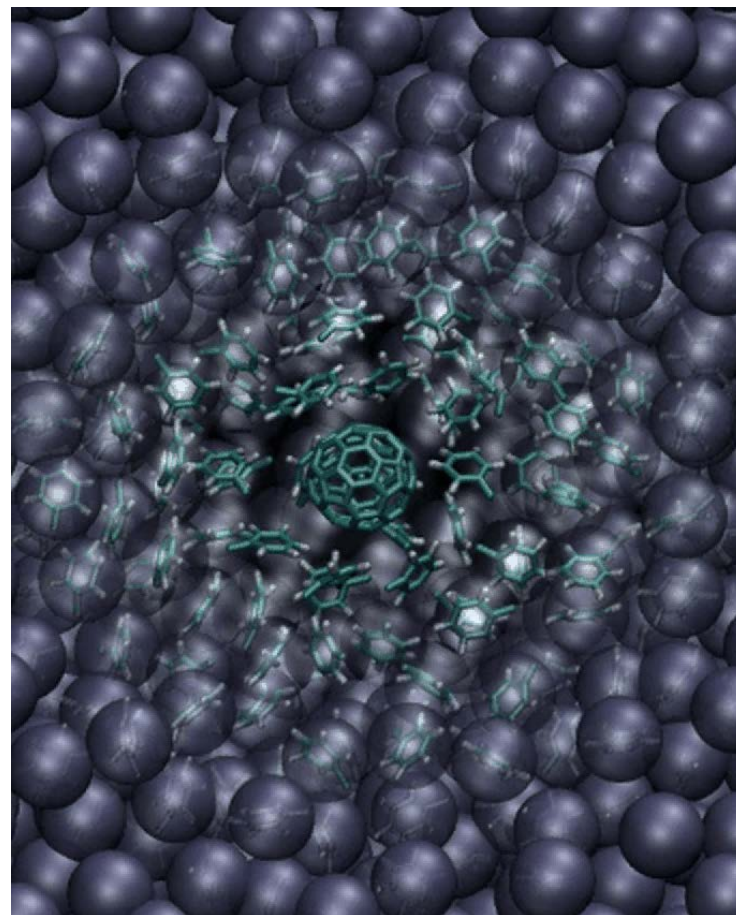
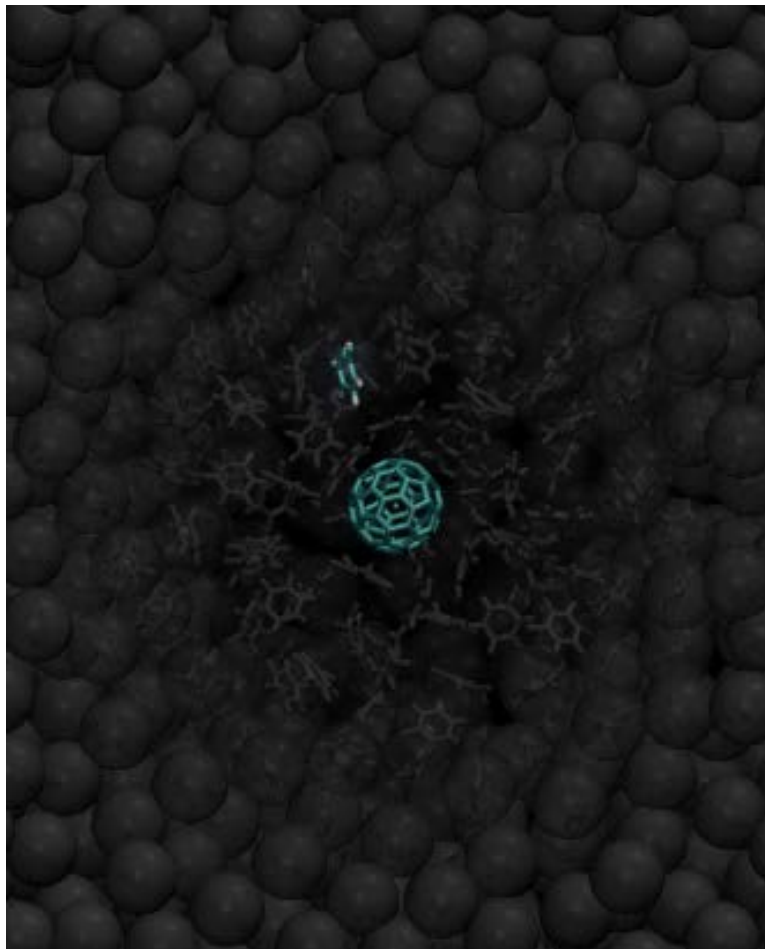


C ₆₀	Diffusion constants [nm ² /ps]
All-atom	$D = 6.3 \times 10^{-4}$
AdResS	
$r_{\text{at}} = 0.75 \text{ nm}$	$D = 9.0 \times 10^{-4}$
$r_{\text{at}} = 1.0 \text{ nm}$	$D = 8.2 \times 10^{-4}$
$r_{\text{at}} = 1.5 \text{ nm}$	$D = 7.9 \times 10^{-4}$
AdResS with TF	
$r_{\text{at}} = 0.75 \text{ nm}$	$D = 7.2 \times 10^{-4}$
Pure toluene	
All-atom	$D = 2.2 \times 10^{-3}$
Coarse-grained	$D = 8.6 \times 10^{-3}$



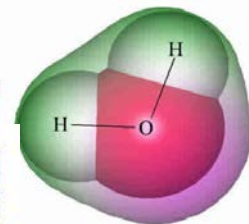
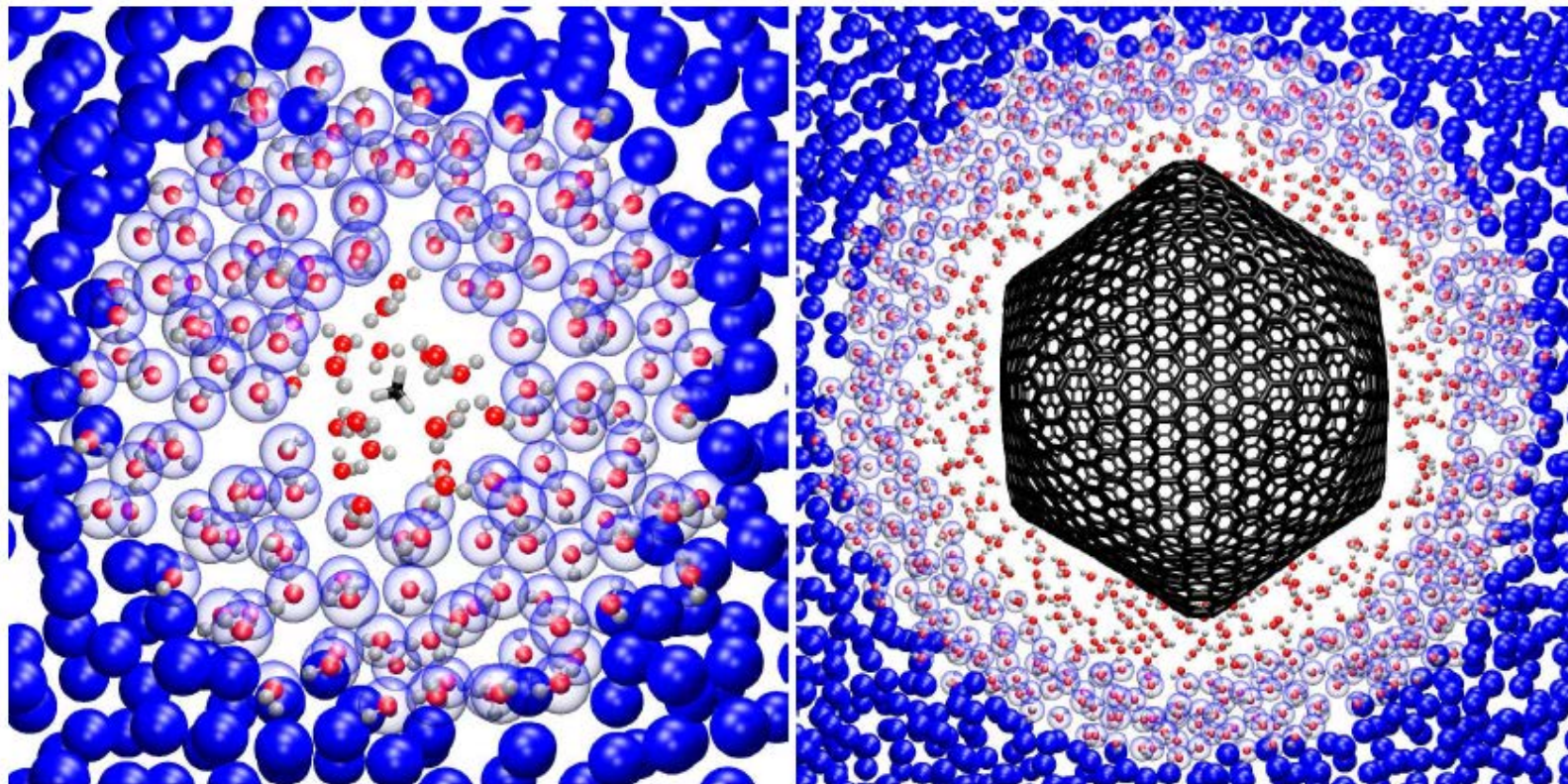
C60 in Toluene

C. Junghans, S. Fritsch



Example for
GROMACS implementation

Hydrophobic Solutes

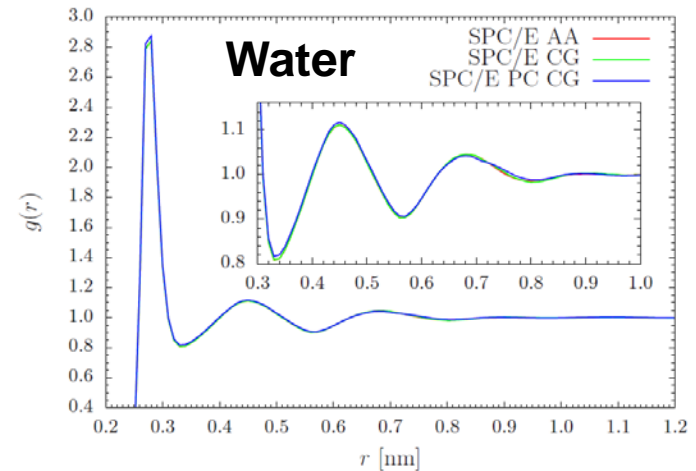
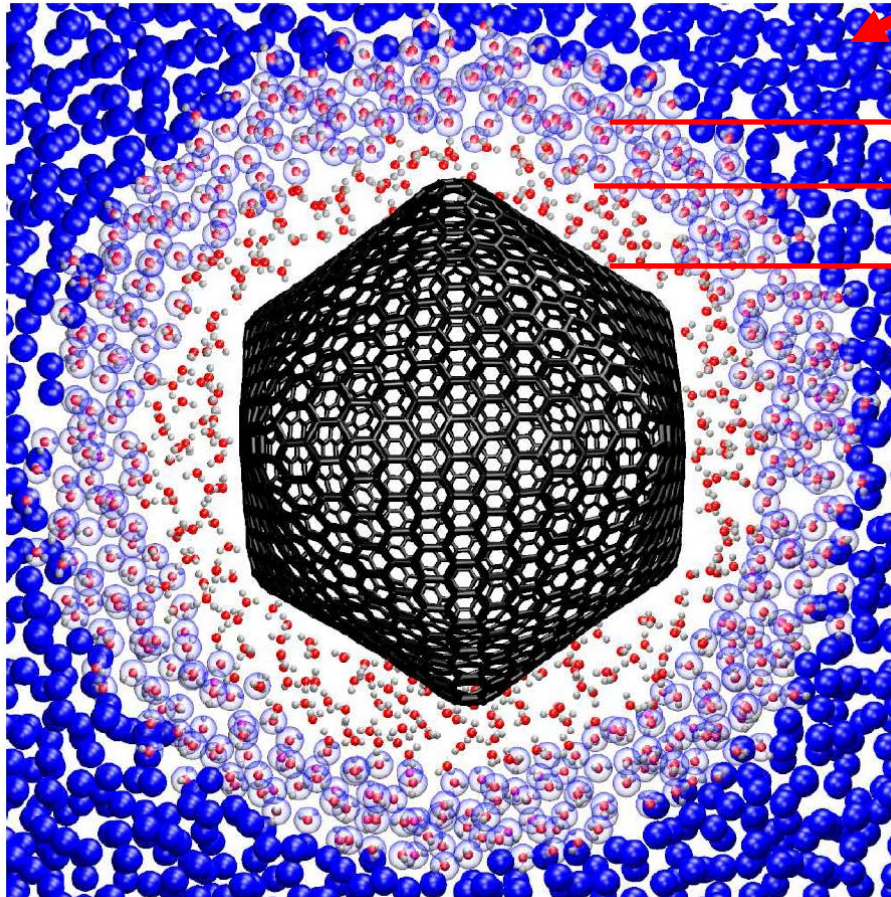


Hydrophobic Solutes: Surface vs Bulk

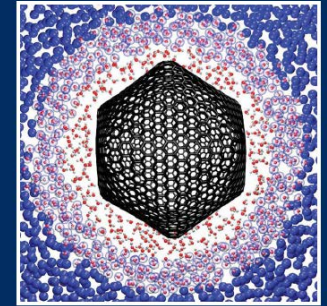
CG regime

Transition layer

All atom layer, d_{ex}



cg water reproduces $g(r)$
but NOT tetrahedral packing!



Hydrophobic Solutes

C₆₀



C₂₁₆₀

Influence of bulk H-bond structure on surface layer

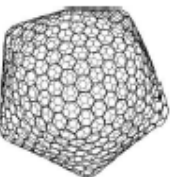
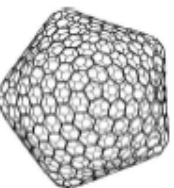
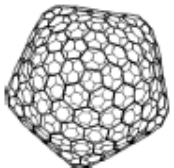
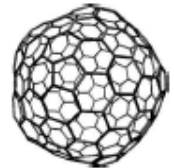
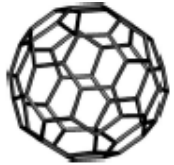
two surface potentials

- standard (weak) Lennard Jones

($\epsilon_{CO} \approx 0.2k_B T$, $\sigma_{CO} \approx 0.34\text{nm}$)

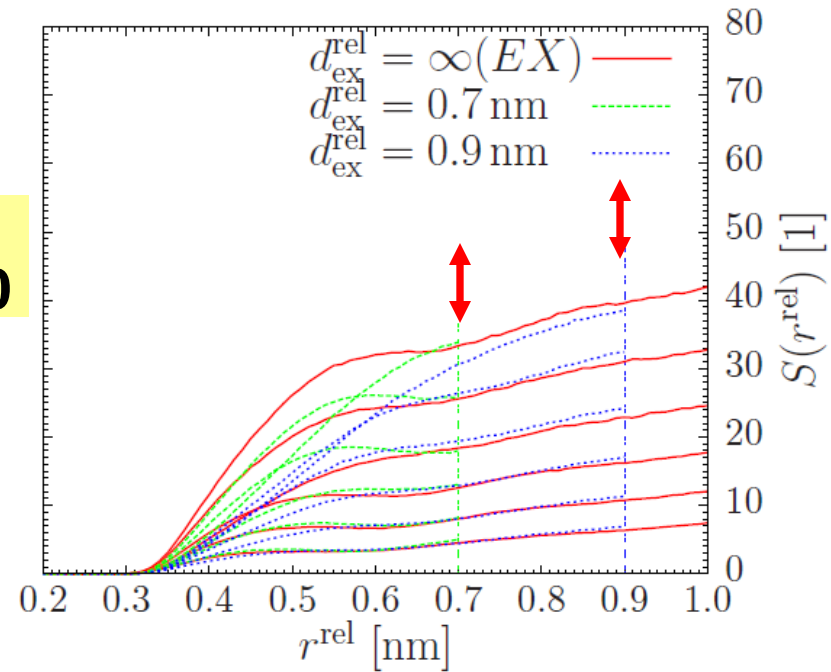
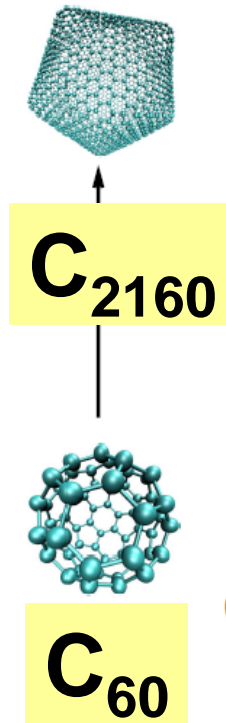
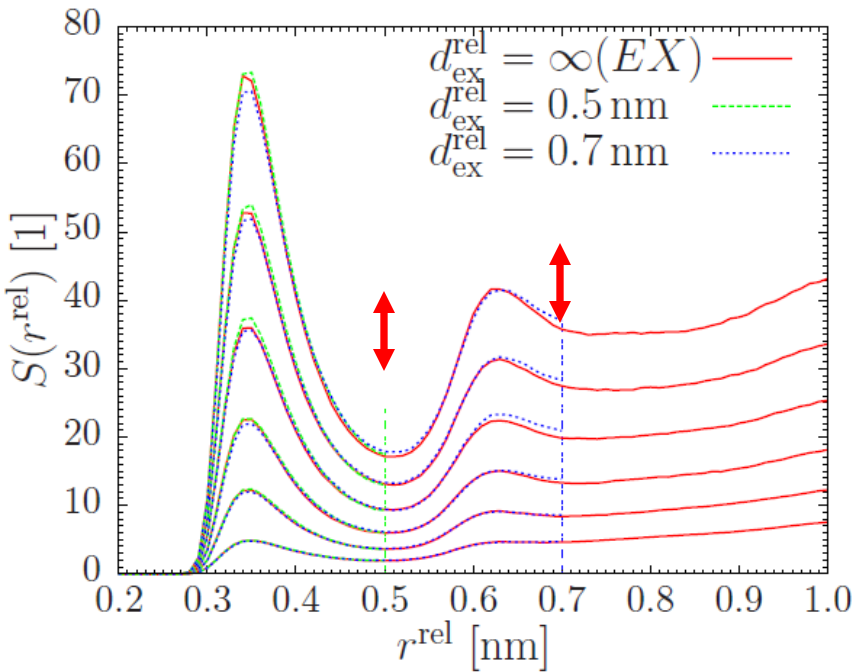
- purely repulsive (r^{-12})

variable width of explicit layer



of Water Molecules around Solute, variable all atom water layer

d_{ex} (\square 1st, 2nd shell, \square)



LJ interaction

dominated by surface
Interaction

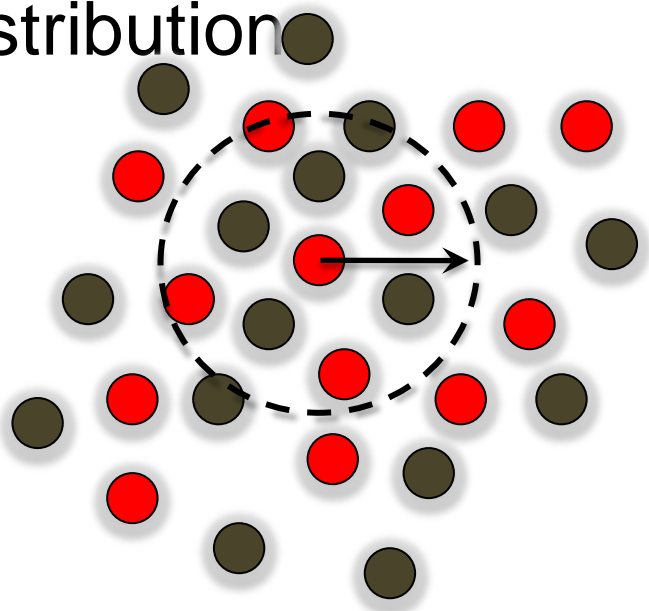
Repulsive

of waters close to surface
strongly depleted



Fluctuation theory of Kirkwood-Buff

Fluctuation theory: Global thermodynamic properties from microscopic (pair-wise) molecular distribution



Excess (depletion) coordination number

$$\Delta N_{ij} = \rho_j G_{ij}$$

$$G_{ij} = V \left[\frac{\langle N_i N_j \rangle - \langle N_i \rangle \langle N_j \rangle}{\langle N_i \rangle \langle N_j \rangle} - \frac{\delta_{ij}}{\langle N_j \rangle} \right]$$
$$= 4\pi \int_0^\infty \left[g_{ij}^{\mu VT}(r) - 1 \right] r^2 dr,$$

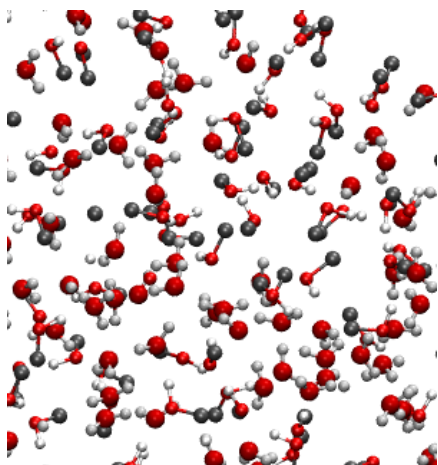
- Solvation energy
- Partial molar volume
- Activity coefficient
- Compressibility



MAX-PLANCK-GESELLSCHAFT

Fluctuation theory of Kirkwood-Buff

Solvation Free Energies



Activity coefficient

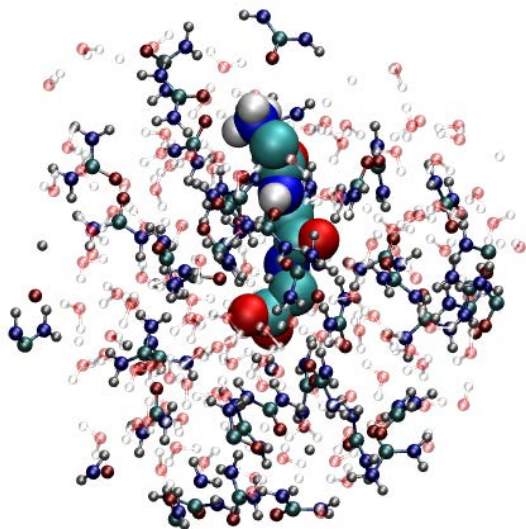
$$\gamma_{cc} = 1 + \left(\frac{\partial \ln \gamma_c}{\partial \ln \rho_c} \right)_{p,T} = \frac{1}{1 + \rho_c (G_{cc} - G_{cw})}$$

$$k_B T \ln \gamma_c$$

Solvation free energies

$$\lim_{\rho_s \rightarrow 0} \left(\frac{\partial \Delta \mathcal{G}_s}{\partial x_c} \right)_{p,T} = \frac{RT (\rho_w + \rho_c)^2}{\eta} (G_{sw} - G_{sc})$$

$$\eta = \rho_w + \rho_c + \rho_w \rho_c (G_{ww} + G_{cc} - 2G_{cw})$$



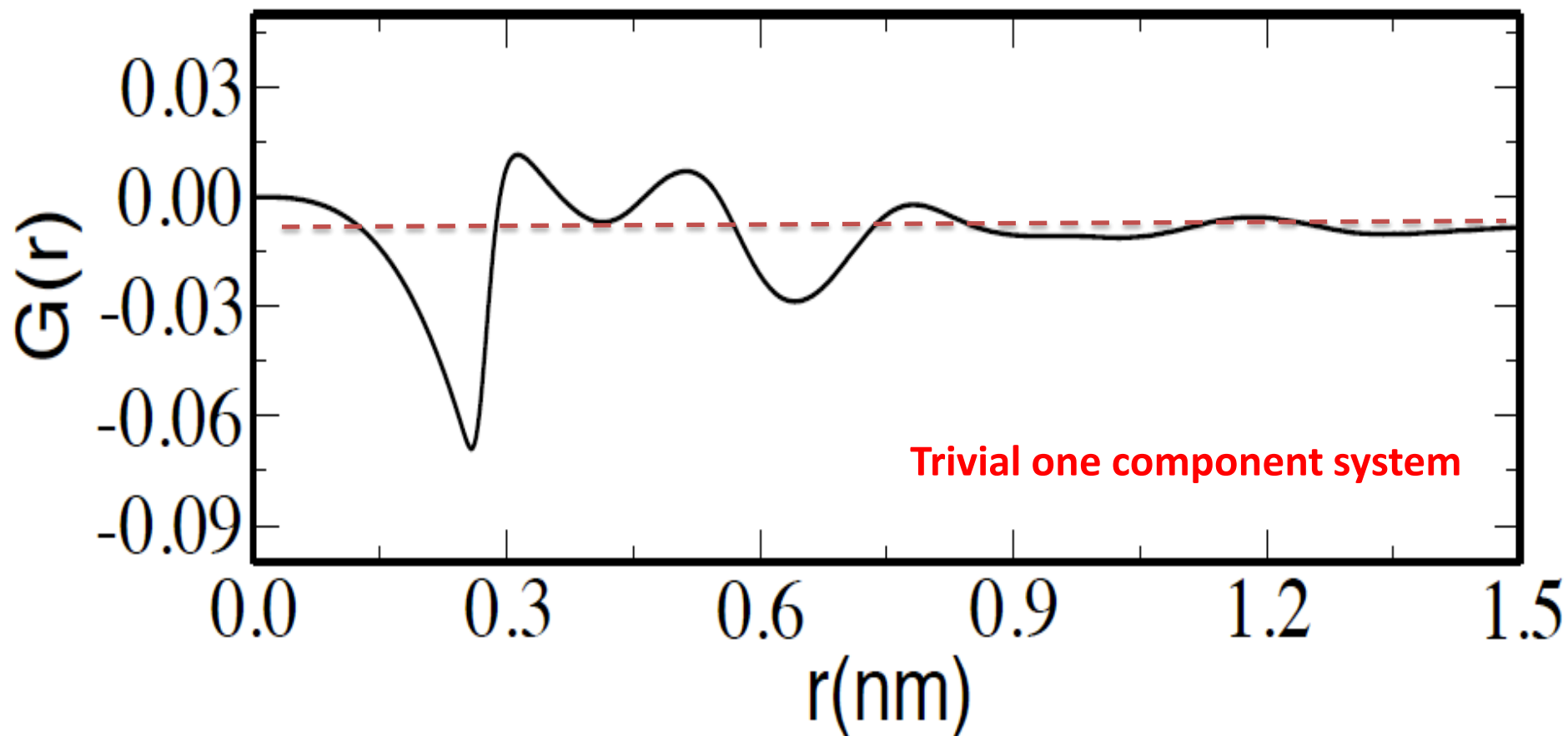
Kirkwood and Buff, J. Chem. Phys. 19, 774 (1951).



MAX-PLANCK-GESELLSCHAFT

Kirkwood-Buff integrals

$$G_{ij}(r) = 4\pi \int_0^r [g_{ij}(r') - 1] r'^2 dr'$$



Kirkwood and Buff, J. Chem. Phys. 19, 774 (1951).



Problems with closed boundary simulation

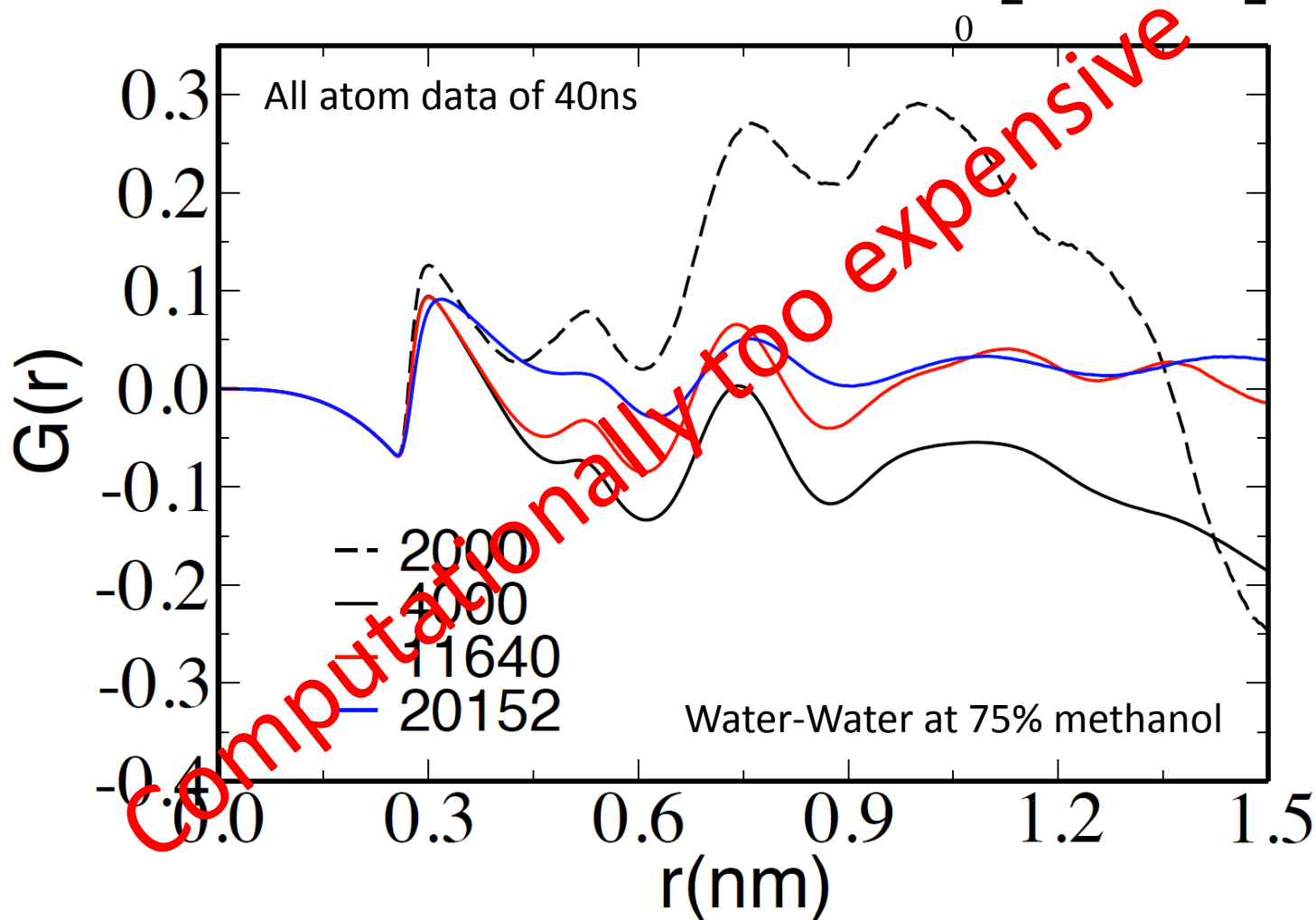
- Non-ideal mixture (**water-cosolvent**)
- Biophysical processes are intimately linked with large density fluctuations (**conformational transition**)
- Excess in one region leads to depletion elsewhere
- KBI does not converge
- Thermodynamics away from a protein structure is ill-defined



MAX-PLANCK-GESELLSCHAFT

Test case: methanol water mixture

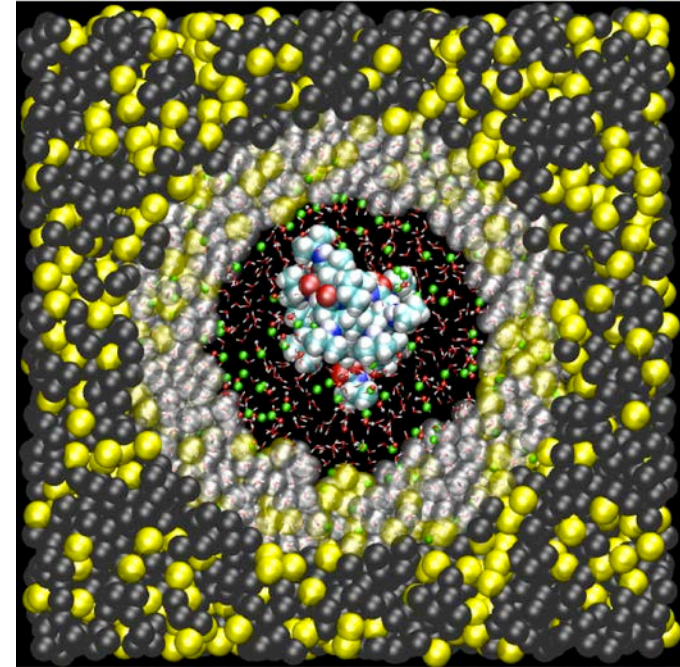
Where to take the value? $G_{ij}(r) = 4\pi \int_0^r [g_{ij}(r') - 1] r'^2 dr'$





Our Goal

- Study solvation of large (bio)macromolecules
- Device an efficient method
- Correct concentration fluctuations
- Solvent equilibrium

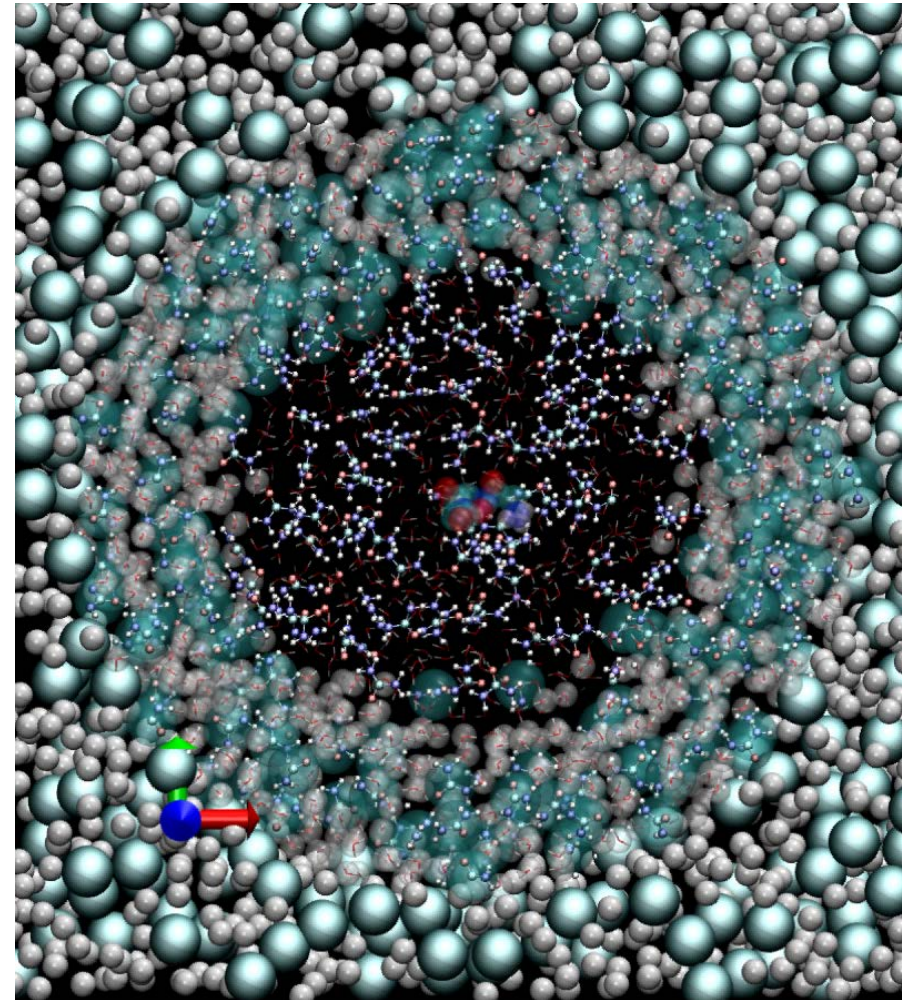
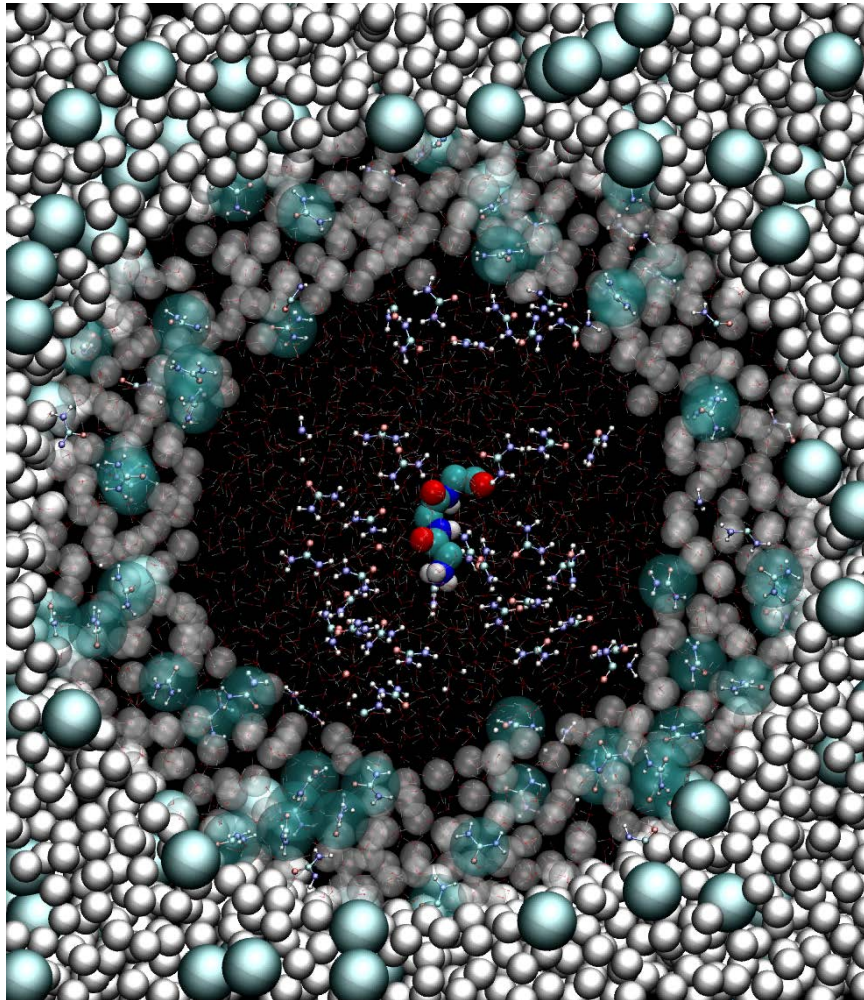


“Effective” open boundary

Why not go open boundary?

Make use of Kirkwood-Buff theory!

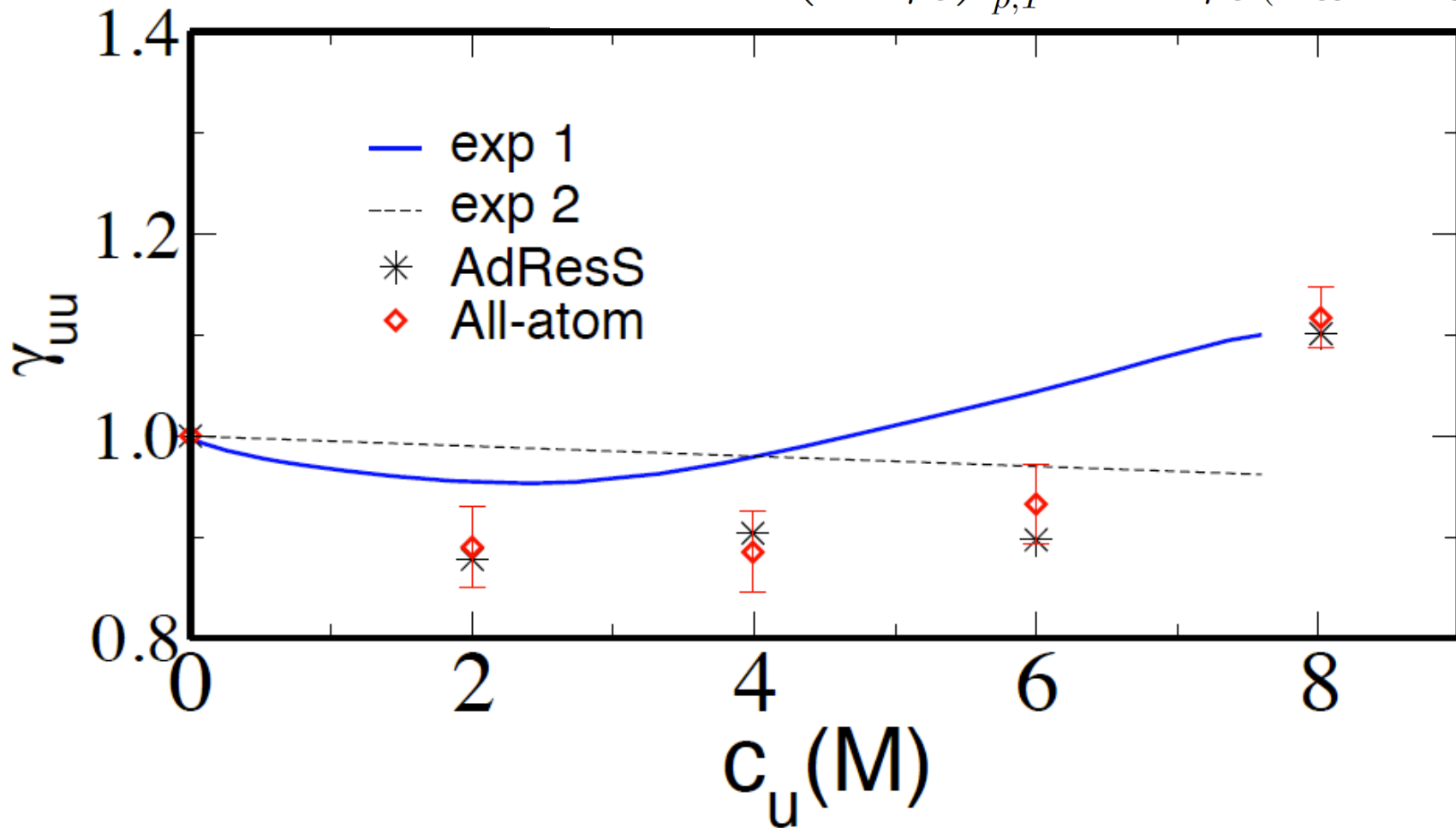
Tri-glycine in Urea-Water Mixture





Urea-Water

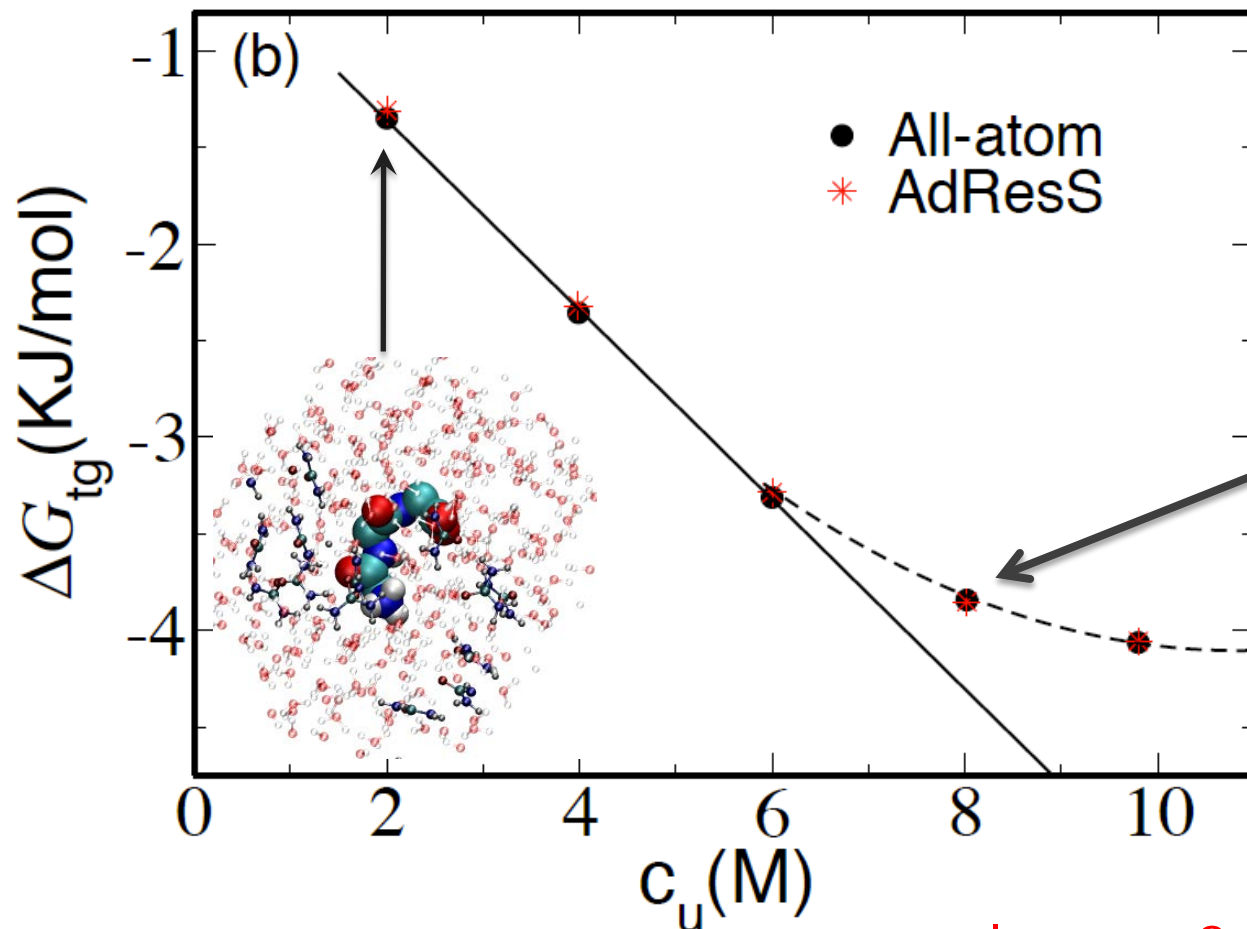
$$\gamma_{cc} = 1 + \left(\frac{\partial \ln \gamma_c}{\partial \ln \rho_c} \right)_{p,T} = \frac{1}{1 + \rho_c (G_{cc} - G_{cw})}$$





MAX-PLANCK-GESELLSCHAFT

Solvation free energy of tri-glycine



m-value = - 0.163 KJ mol⁻² L (sim)
= - 0.164 KJ mol⁻² L (exp)

Auton and Bolen, PNAS 102, 15065 (2005).

Mukherji, van der Vegt, and Kremer, J. Chem. Theory Comp. 8, 3635 (2012).

Some Applications

- Fullerene in Toluene
- Fullerenes in water

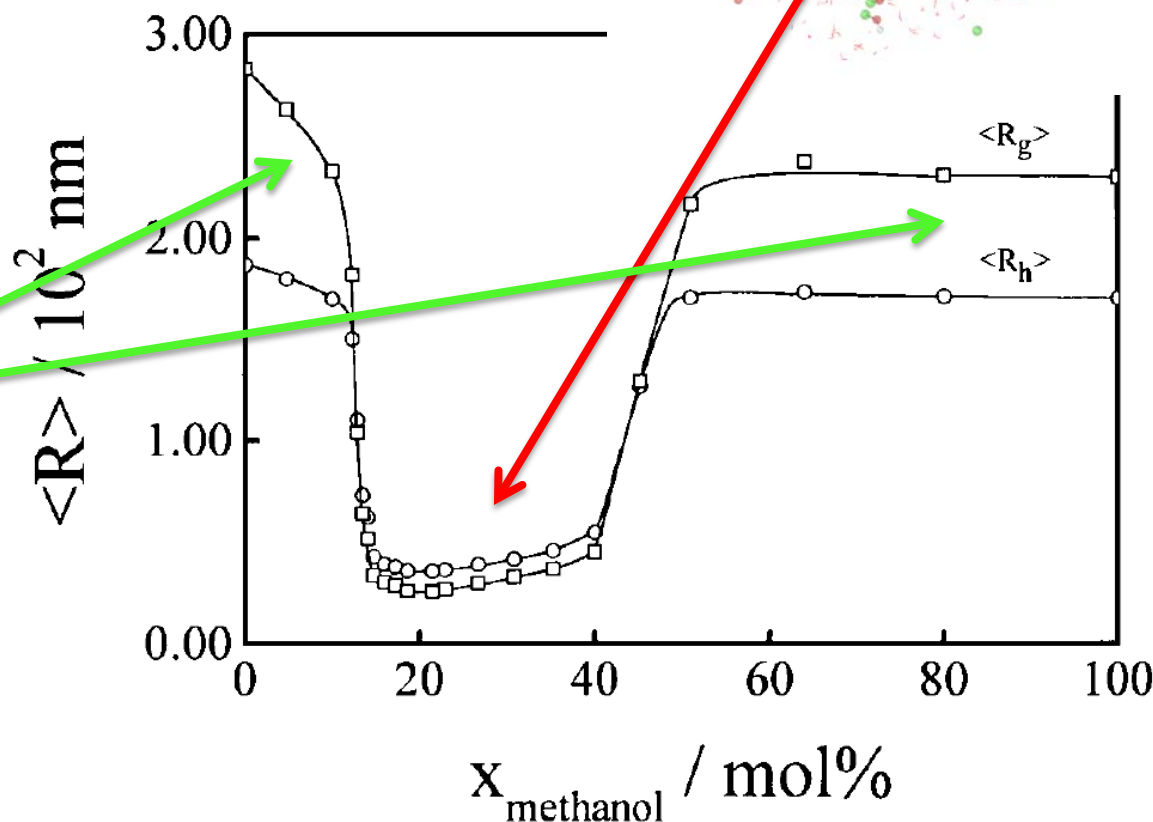
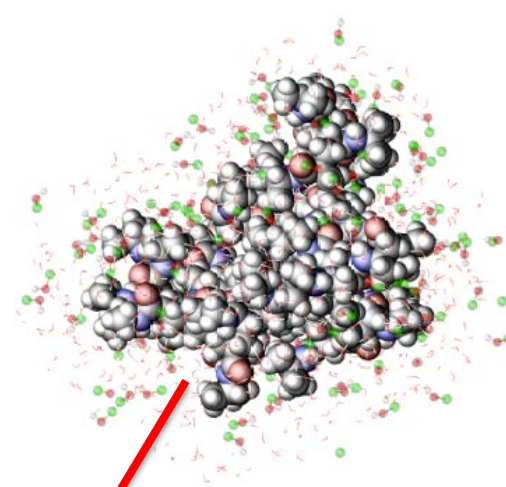
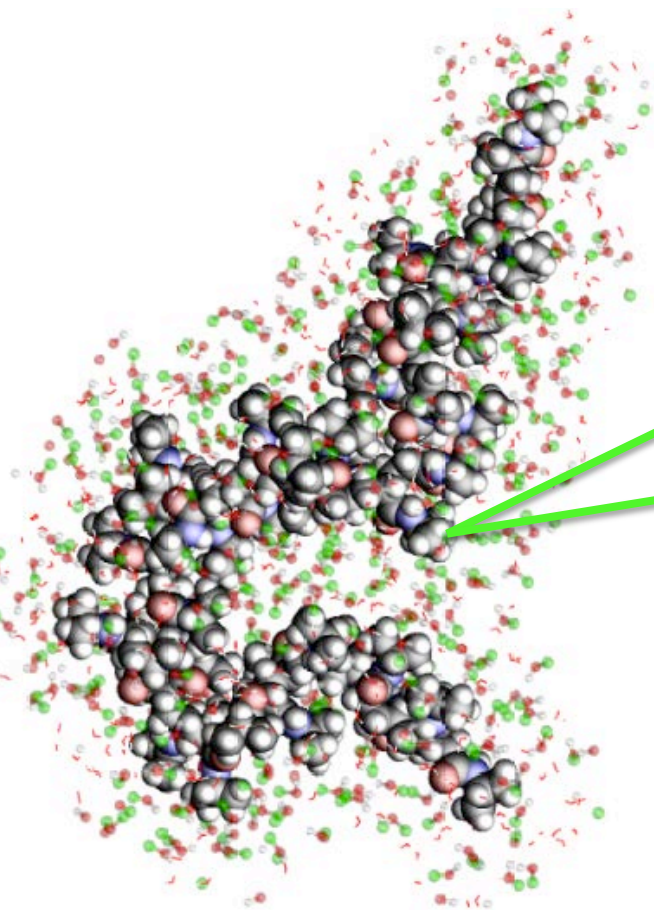
Kirkwood Buff integrals:

- Peptides in water urea mixtures
- **PNIPAM in water alcohol mixtures:**
“Grand Canonical” AdResS



MAX-PLANCK-GESELLSCHAFT

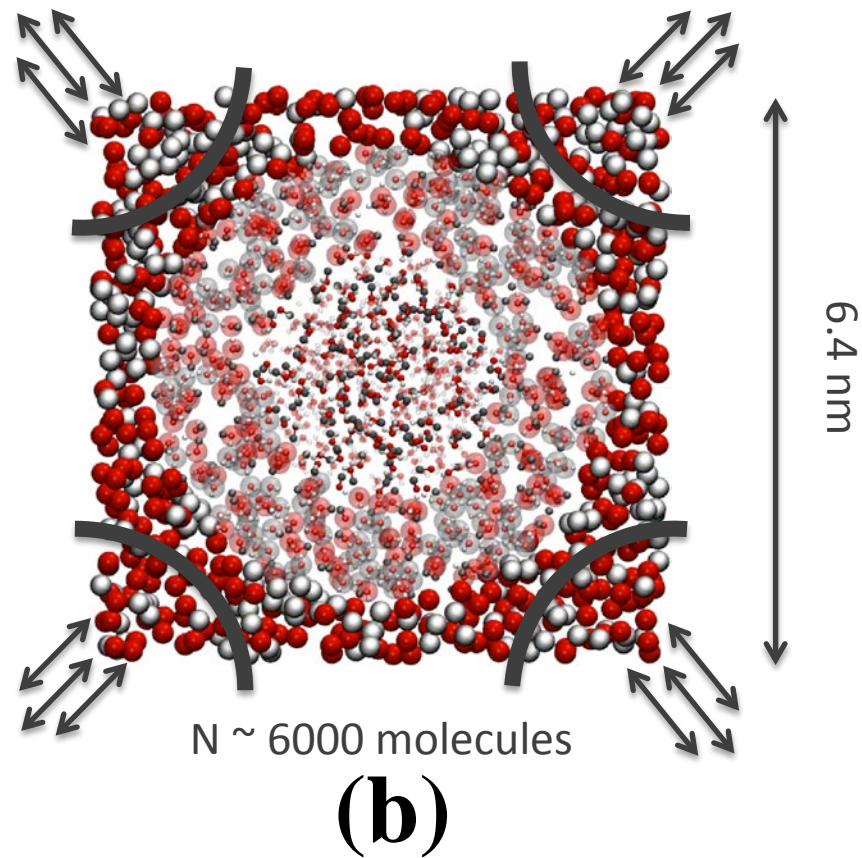
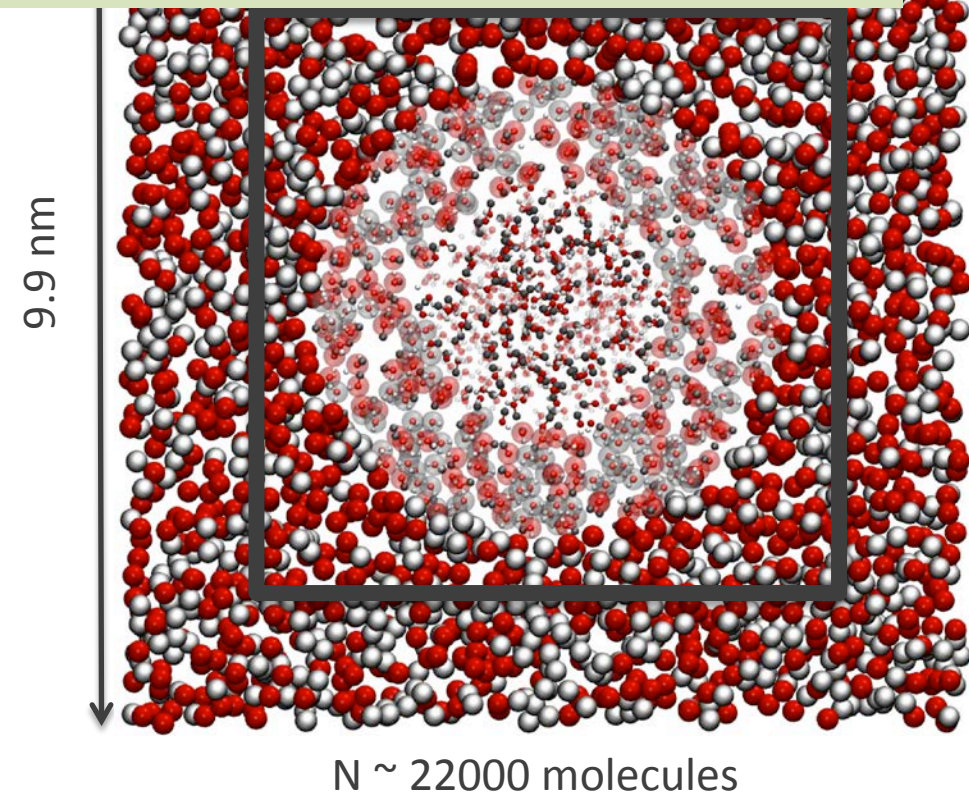
PNIPAm + CH₃OH + H₂O Problem: Depletion effects



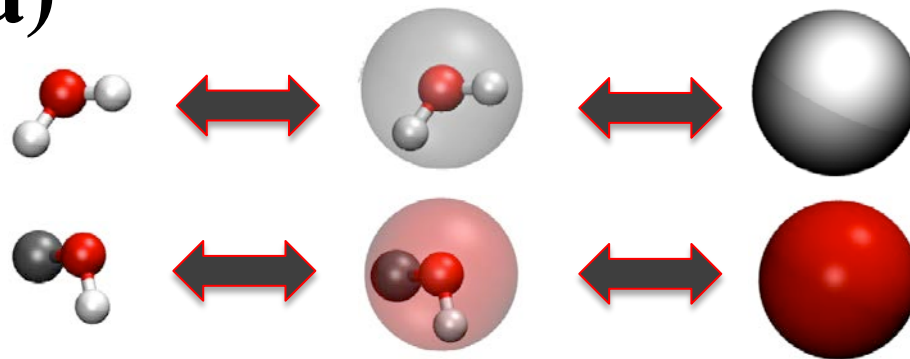
Zhang and Wu, Physical Review Letters 86, 822 (2001).

Mukherji and Kremer, submitted (2013).

Grand Canonical AdResS



(a)

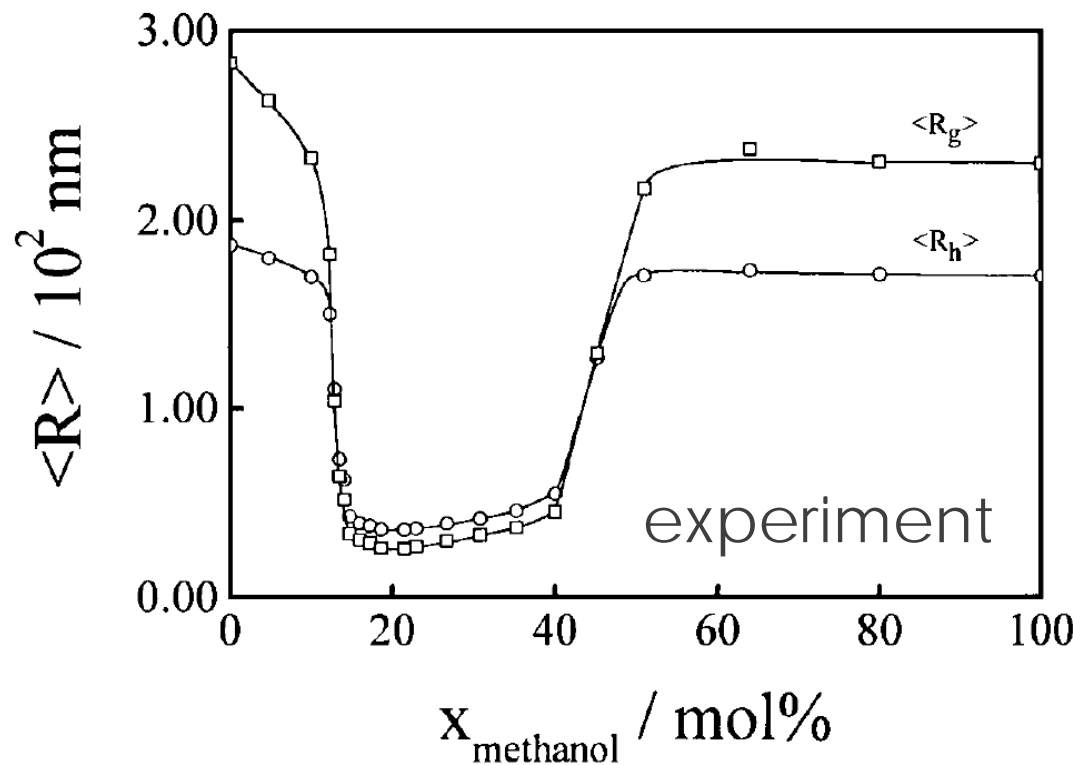
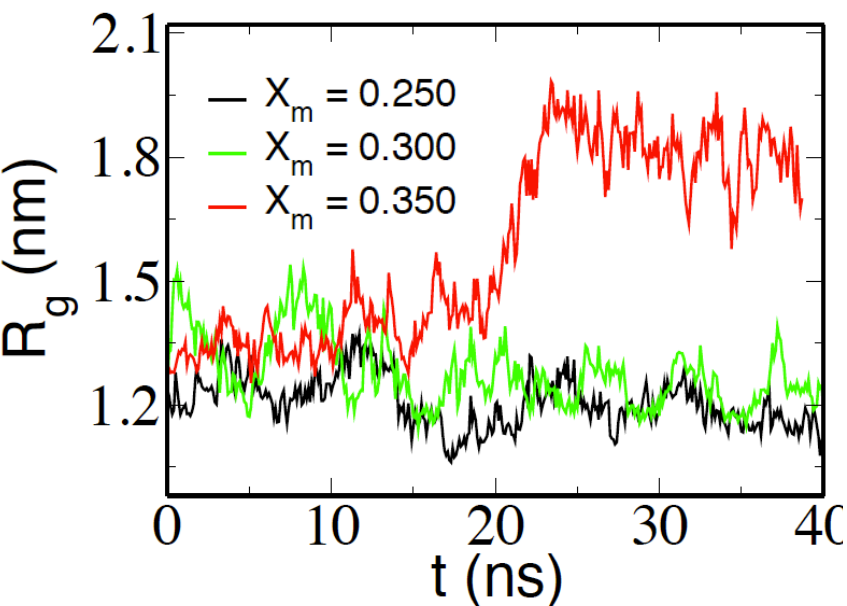
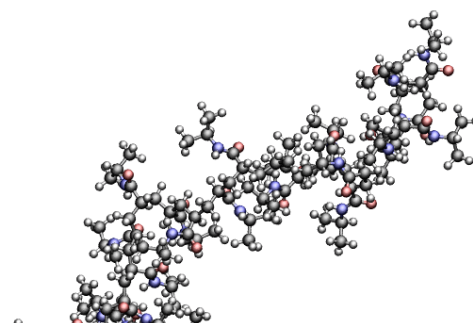
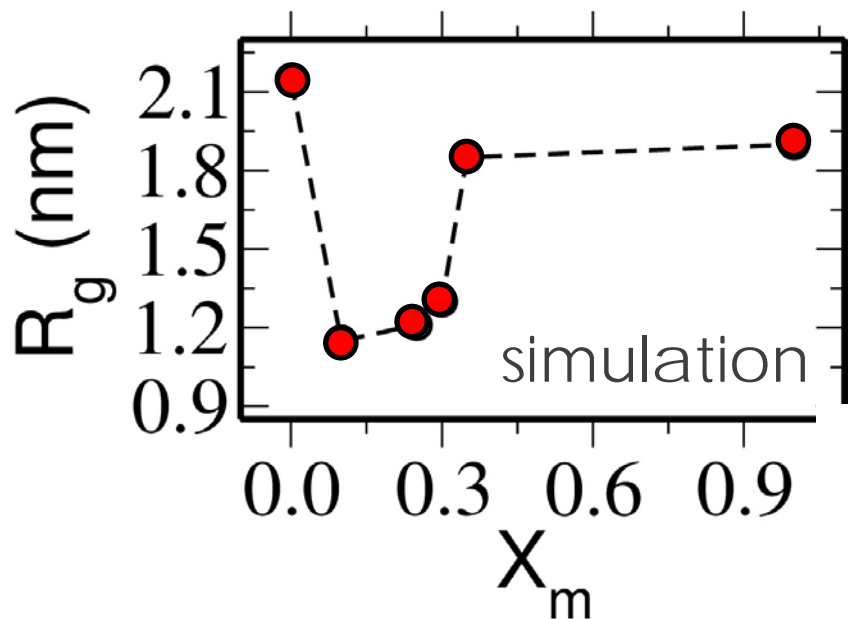


(c)



MAX-PLANCK-GESELLSCHAFT

Poly-NIPAm in aqueous methanol

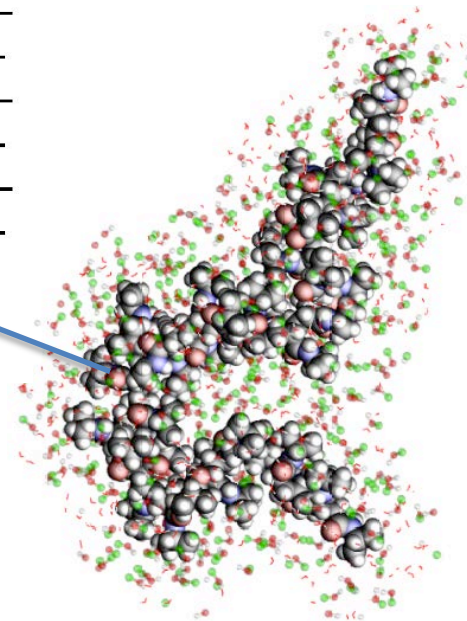
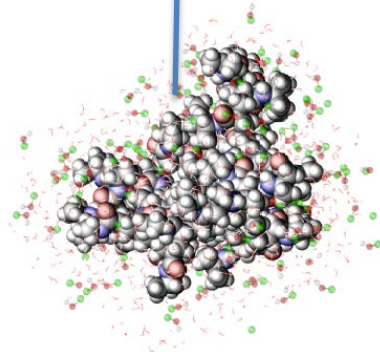
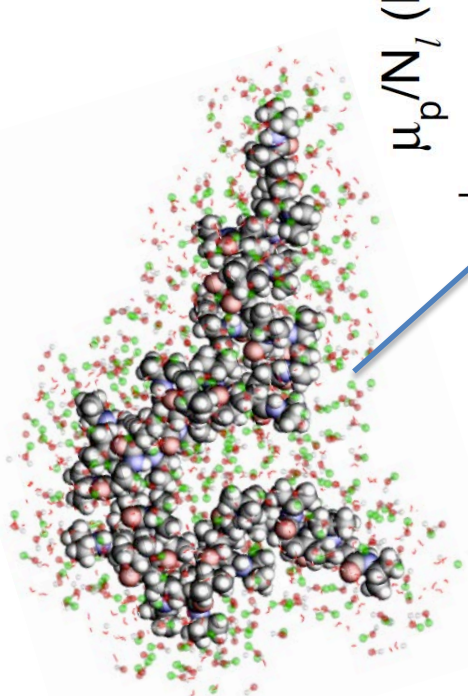
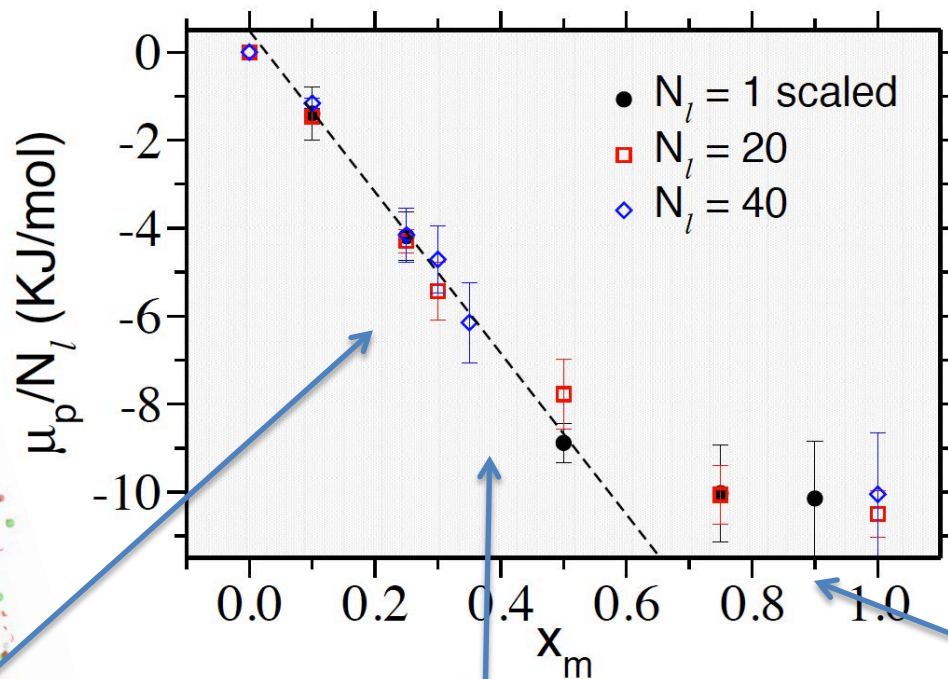


MIUKNERJI and KREMER, submitted (2013).



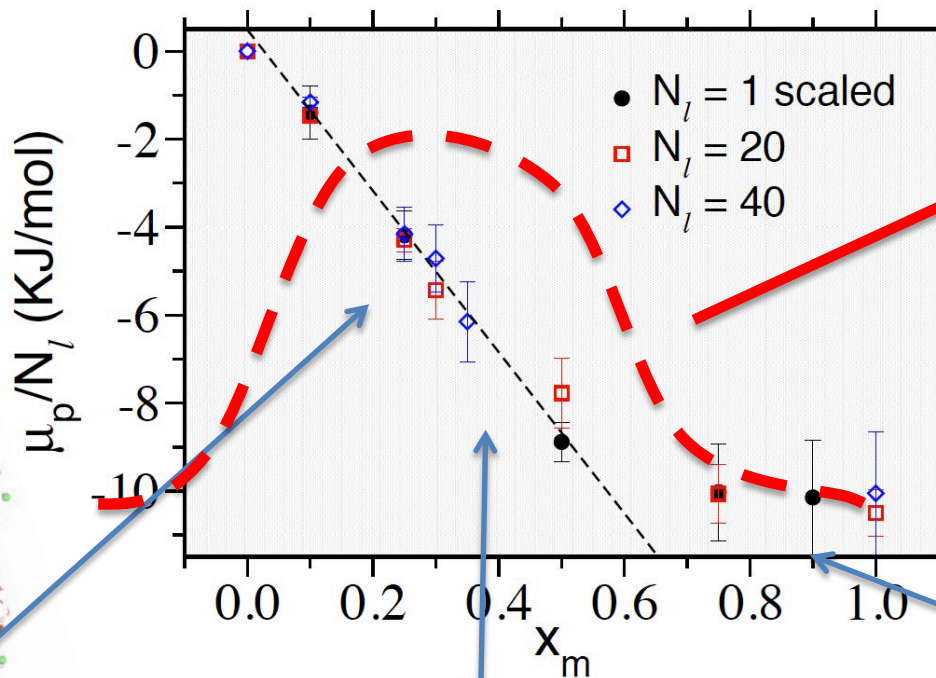
MAX-PLANCK-GESELLSCHAFT

Poly-NIPAm chemical potential

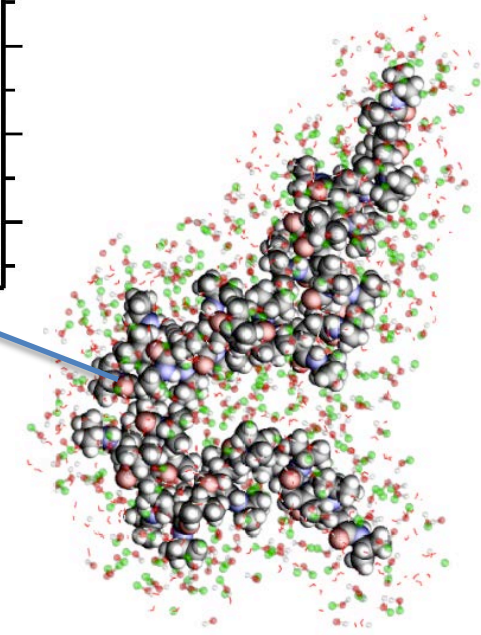
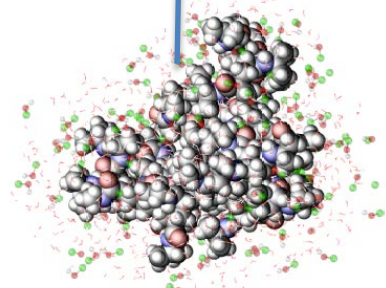
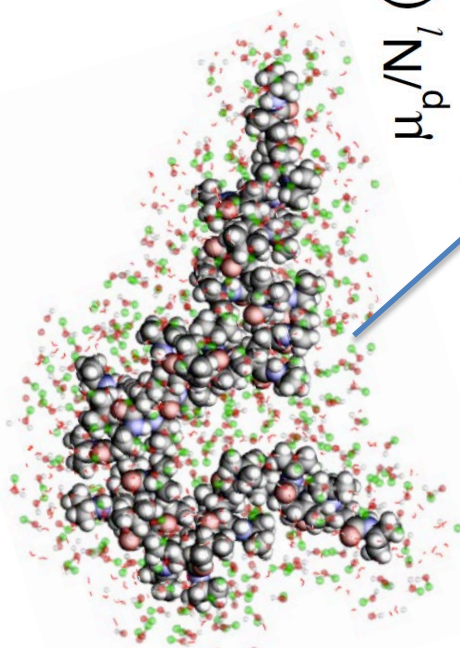




Poly-NIPAm chemical potential



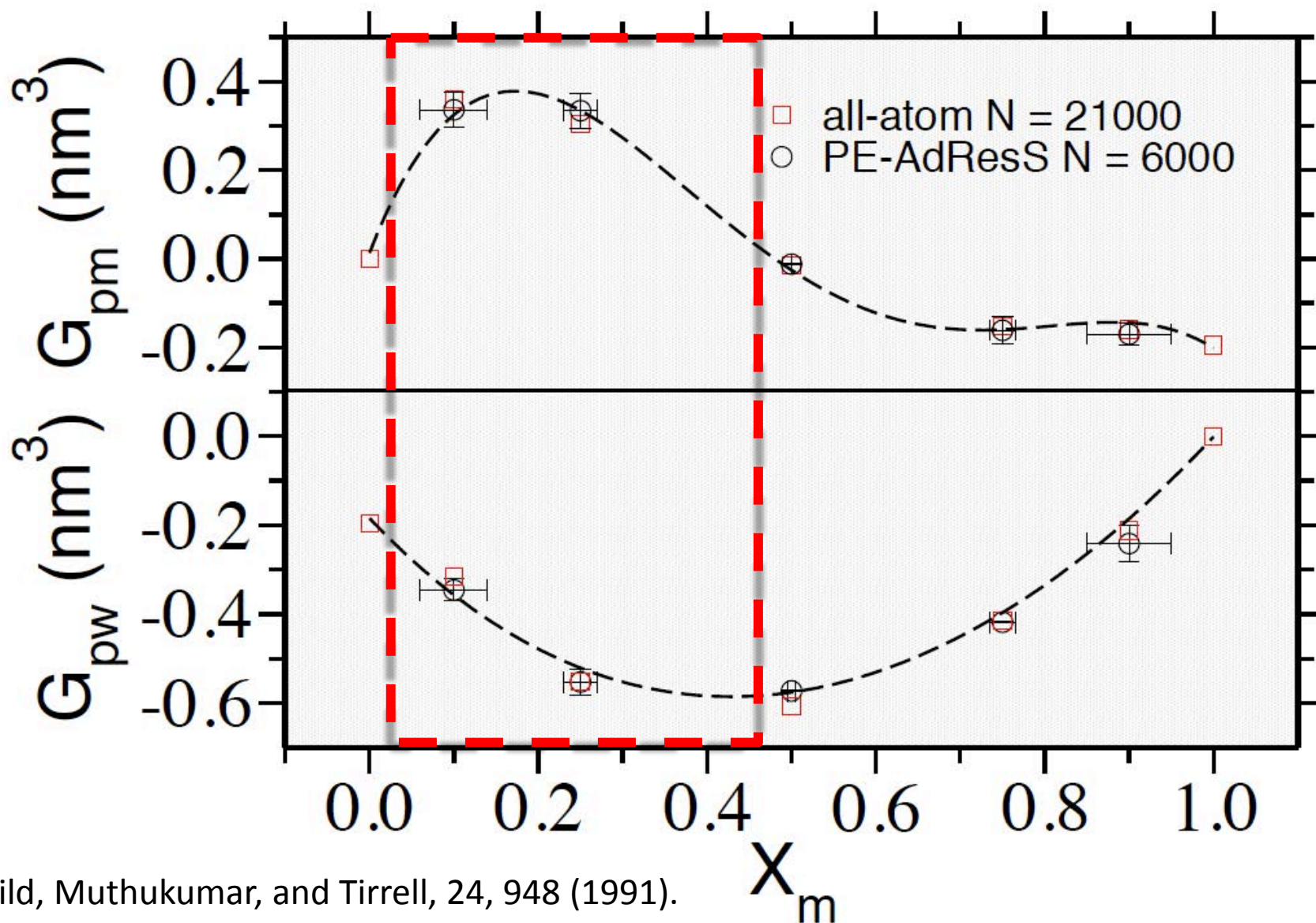
“expected shape”





MAX-PLANCK-GESELLSCHAFT

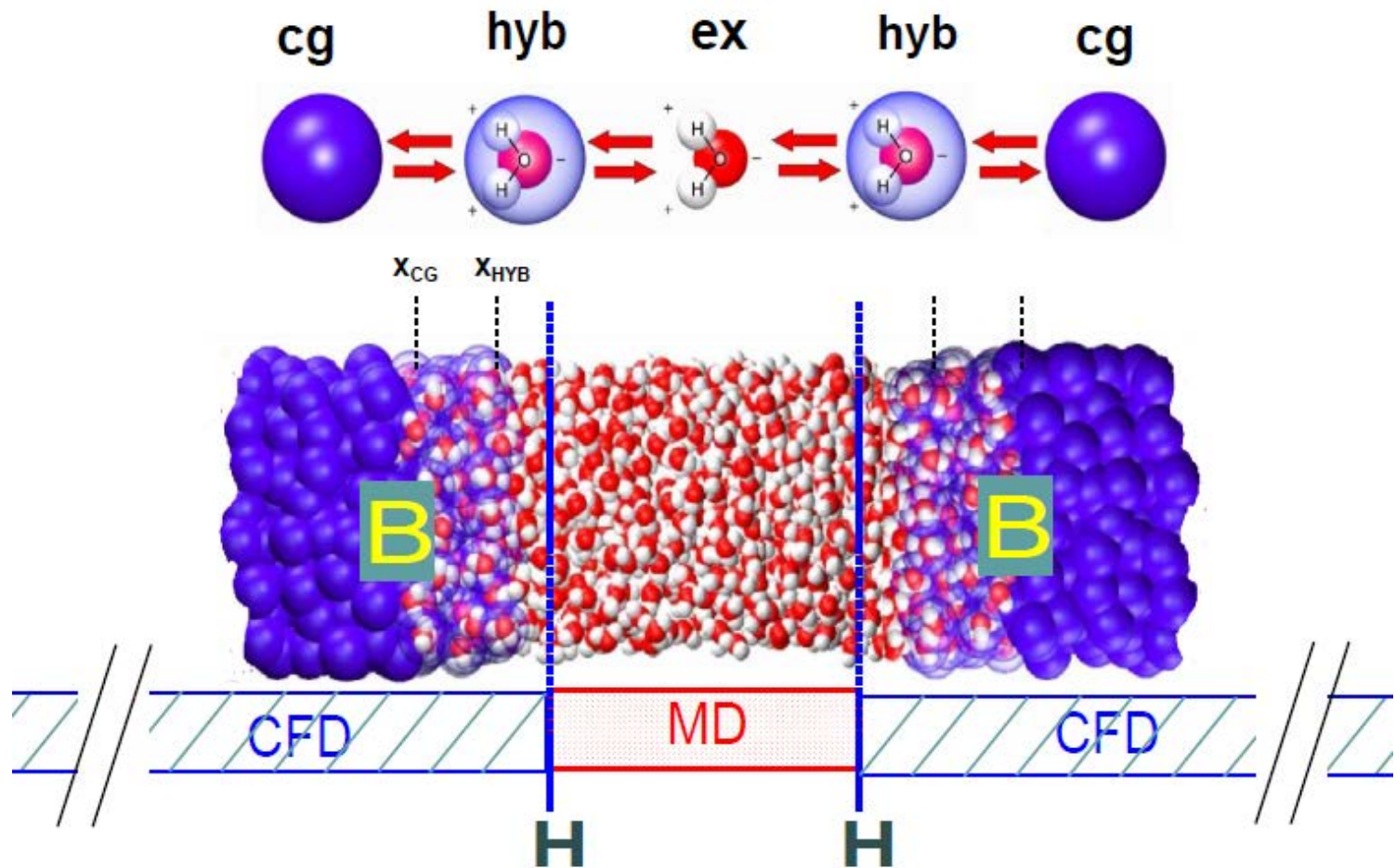
NIPAm in aqueous methanol



Schild, Muthukumar, and Tirrell, 24, 948 (1991).

Mukherji and Kremer, submitted (2013).

AdResS-HybridMD: Water



HybridMD: Coupling Particle-Based and Continuum Descriptions

→ The hybrid particle-continuum scheme (HybridMD) is designed to connect the dynamics of a “molecular domain” with that obtained from a continuum description of the surrounding fluid flow.

→ The method is based on flux-exchange.

→ The system is divided in (at least) two domains, described via classical molecular dynamics (MD) and continuum fluid dynamics (CFD), i.e., solving the Navier-Stokes equations.

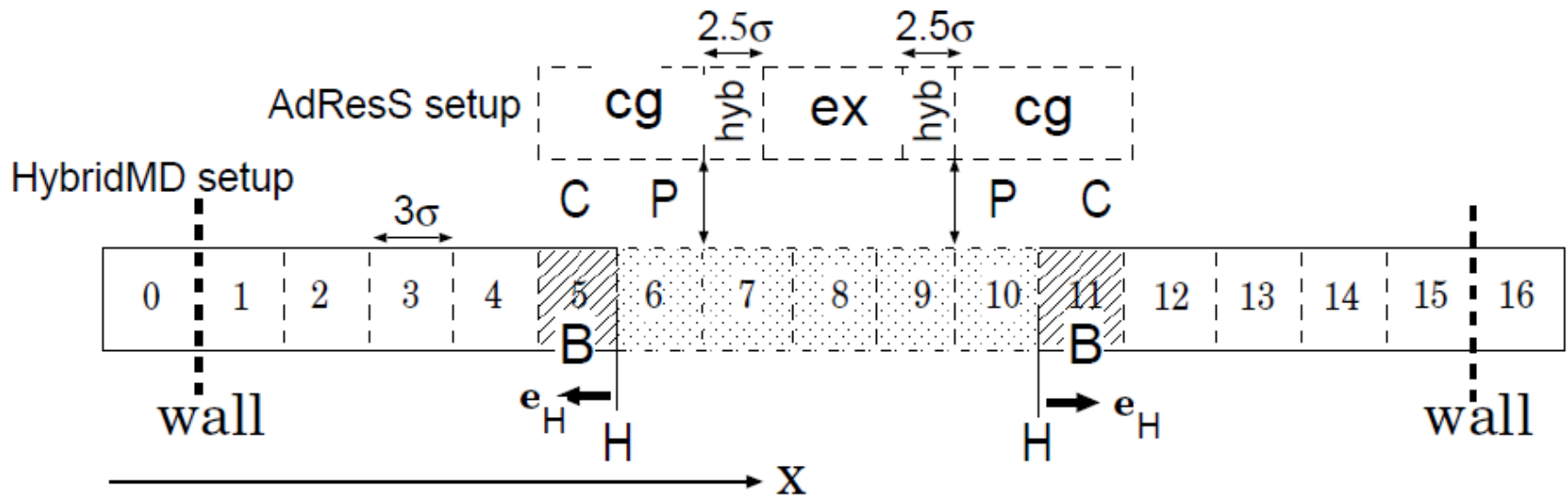
→ The MD and CFD domains share one unique “hybrid interface”, H : Flux balance implies the conservation of mass and momentum across H .

PROBLEM: Particle Insertion into Buffer

G. De Fabritiis, R. Delgado Buscalioni, P. Coveney, Phys. Rev. Lett 97, 134501 (2006).

R. Delgado Buscalioni, G. De Fabritiis, Phys. Rev. E 76, 036709 (2007).

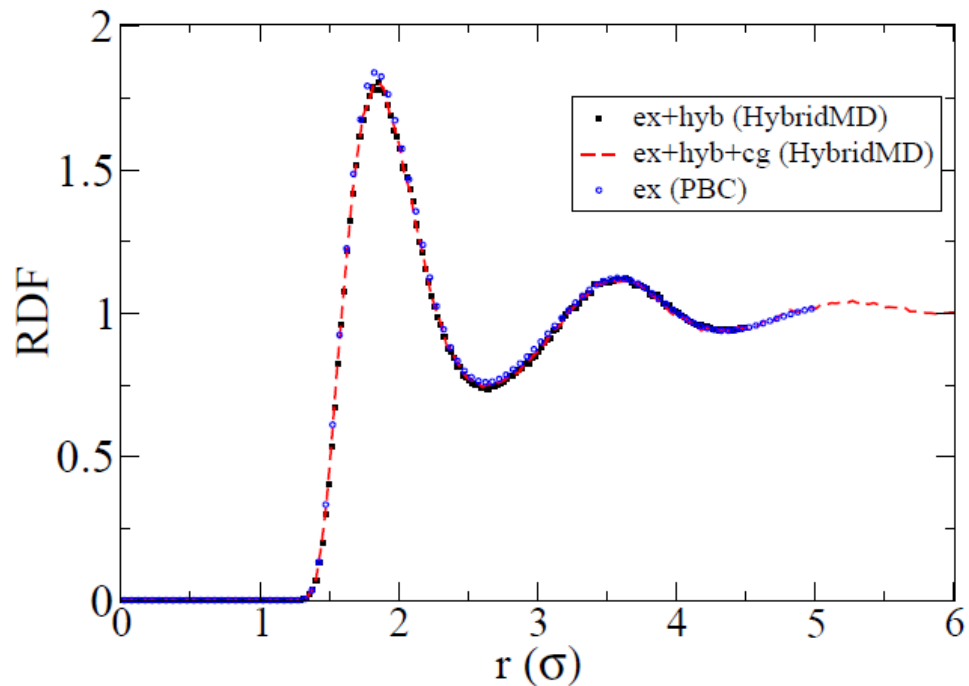
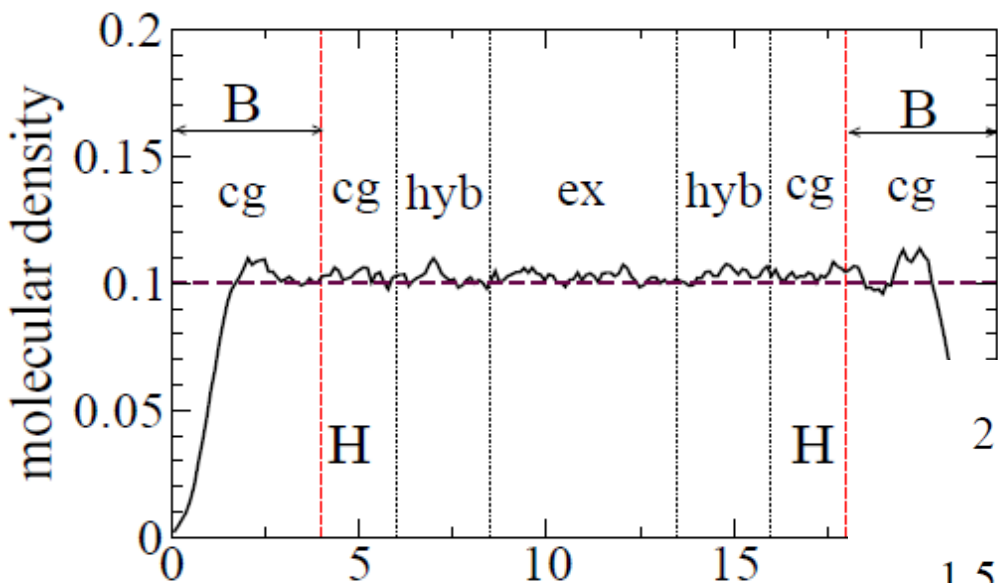
AdResS-HybridMD combined



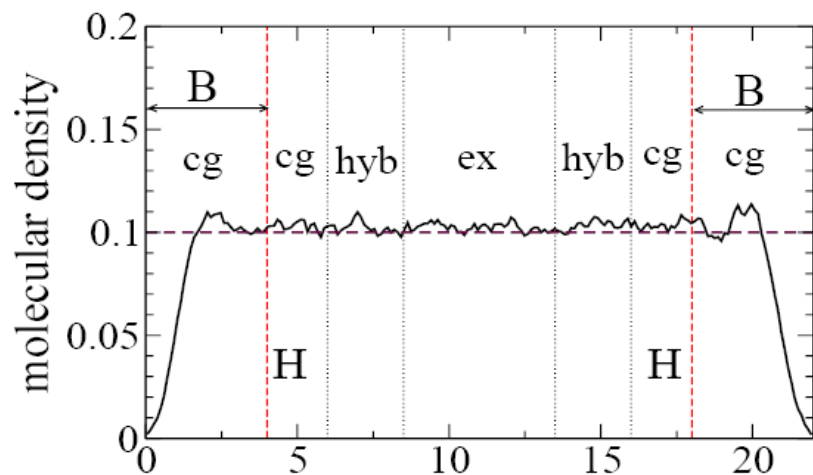
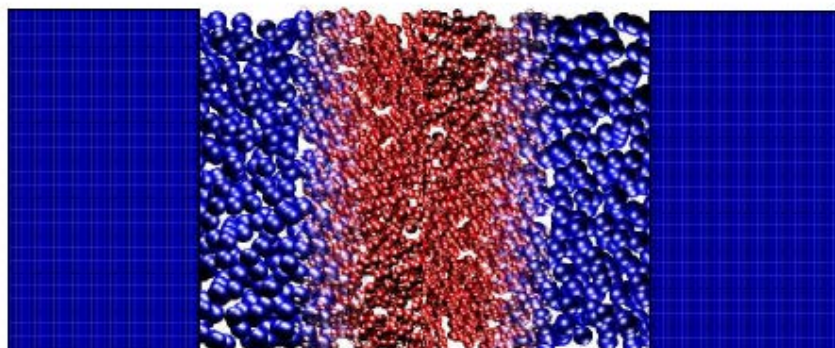
Domain decomposition of the combined scheme. The top part of the figure shows the location of the fluid model layers (*cg*, *hyb* and *ex*) within the HybridMD setup. The bottom part of the figure shows the set of control cells used in the HybridMD setup.

Particle Insertion into Buffer SIMPLE

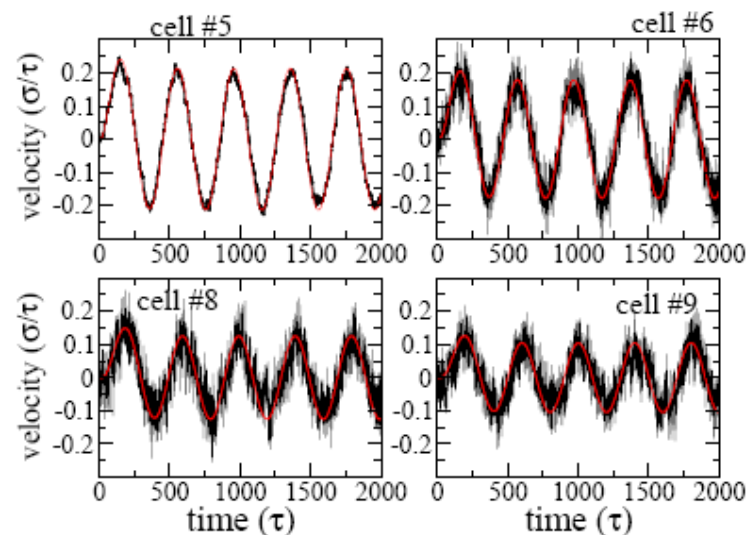
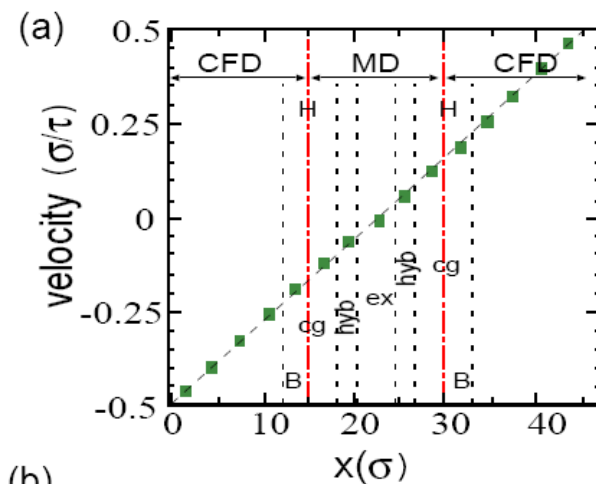
AdResS-HybridMD combined



Concurrent Triple-Scale Simulation of Molecular Liquids



Simple shear



Oscillatory shear
 (- - - - exact solution)

Conclusion / Challenges

- **Dual-Triple... Scale Simulations/Theory**
 - **Adaptive** quantum \leftrightarrow force field \leftrightarrow coarse grained ...
 - **Grand Canonical** i.e. salt etc
 - **Thermodynamic Force/ compensation scheme:** couple rather different systems
 - **H-AdResS:** adaptive Monte Carlo possible
- **Nonbonded Interactions: NEMD, Structure Formation, Morphology...**
- **Conformations \leftrightarrow Electronic Properties**
- **Structure Formation, Aggregation**
- **Online Experiments:**
 - **Nanoscale Experiments, long Times**

