



Adaptive Resolution Simulation of Molecular Liquids

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- Introduction: molecular liquids and soft matter, length- and time-scales, multiscale modeling
- 6 Hybrid Adaptive Resolution Scheme (AdResS): linking atomic and mesoscopic length-scales
- 6 Triple-scale AdResS-HybridMD method: coupling particle-based and continuum descriptions of a liquid

Molecular systems



- **G gases**: intermolecular distances are large in comparison with molecular sizes \rightarrow the intermolecular interactions are negligible
- 6 hard condensed matter: strong intermolecular interactions, long-range orientational and positional order
- 6 **molecular liquids and soft matter**: energy-entropy interplay. The free-energy scale: k_BT . The relevant properties of the system are determined by the interplay of the various **temporal** and **spatial scales** involved.





Length-scales



Wide range of characteristic length-scales:

- 6 bond length: $\sim 0.1 nm$
- 6 persistence length of polymers: $\sim 1 nm$
- 6 radius of gyration: $\sim 10 nm$
- 6 macroscopic domains' size: $\sim 1 \mu m$





Time-scales

Wide range of characteristic time-scales:

- \circ covalent bond vibrations: $\sim 10 \cdot 10^{-15} s$
- 6 angle bending: $\sim 20 \cdot 10^{-15} s$
- 6 atom dynamics governed by torsional and van der Waals interactions: $\sim 40 \cdot 10^{-15} s$
- ⁶ atom dynamics governed by long-range Coulomb interactions: $\sim 10^{-12}s$
- 6 relaxation times of macromolecular segments: $10^{-12} 10^{-9}s$
- 6 maximal macromolecular relaxation times: $\sim 1s$



Multiscale modeling







Adaptive resolution simulation



6 Motivation:

- to treat in a simulation only as many degrees of freedom (DOFs) as absolutely necessary for the problem considered.
- 6 **Method:** AdResS (Adaptive Resolution Scheme)
 - allows for an dynamical switching between the atomistic and mesoscopic levels of detail => on-the-fly changing of the number of DOFs
 - tailor-made for molecular systems where spatially localized domains with required atomistic resolution exchange particles with the remainder of the system sufficiently described on the mesoscopic scale.

6 Results:

 accurately reproduces the statistical properties of the reference all-atom system.



Molecular Dynamics (MD) simulation



MD simulation





All-Atom MD simulation:

- allows to study processes at the atomic level of detail
- is often incapable to bridge a gap between a wide range of length and time scales involved in molecular systems

Mesoscopic MD simulation:

- ⁶ reduces the number of DOFs by retaining only those that are relevant for the property of interest \implies longer length and time scales can be reached
- Specific chemical details are usually lost in the coarse-graining procedure

Combining the best from both approaches:

6 Hybrid Adaptive MD Schemes



Hybrid atomistic/mesoscopic liquid



MP, L. Delle Site, K. Kremer, J. Chem. Phys. **123**, 224106, 2005. MP, L. Delle Site, K. Kremer, Phys. Rev. E **73**, 066701, 2006.



- △ 3 translational
- △ 3 rotational
- $a \quad 3N-6 = 6 \text{ vibrational}$
- One particle mesoscopic molecule has no defined spatial orientation and only 3 translational DOFs.



MP, L. Delle Site, K. Kremer, J. Chem. Phys. **123**, 224106, 2005. MP, L. Delle Site, K. Kremer, Annu. Rev. Phys. Chem. **59**, 545, 2008.



In thermodynamical equilibrium, boundary conditions analogous to to two-phase coexistence must be satisfied:

$$\mu_{ex} = \mu_{cg}, \quad p_{ex} = p_{cg}, \quad T_{ex} = T_{cg}.$$

The rotational and vibrational parts of the free energy can be viewed as the latent heat, which is supplied or taken by the thermostat, at this transition.



Transition region





- 6 Molecules in A and B are physically identical but differently represented.
- 6 The number of DOFs is n = n(x) with: $n_A = const_A$; $n_B = const_B$; and $n_\Delta = n(x)$

6 The system is in equilibrium which implies: $\lim_{x \to d^{-}} \frac{\partial F_A(x)}{\partial x} = \lim_{x \to d^{+}} \frac{\partial F_B(x)}{\partial x} = 0 \Longrightarrow$ $\lim_{x \to d^{-}} \frac{\partial n_A(x)}{\partial x} = \lim_{x \to d^{+}} \frac{\partial n_B(x)}{\partial x} = 0$



Weighting Function = Order Parameter





⁶ The values w = 1 and w = 0 correspond to the atomistic and coarse-grained regions, respectively, while the values 0 < w < 1 correspond to the transition (*hyb*) regime.



AdResS: Linking atomic and mesoscopic length-scales



AdResS consists of two main steps:

- 1. Derive the effective pair potential U^{cm} between coarse-grained molecules on the basis of the reference all-atom system.
- 2. Couple the atomistic and mesoscopic scales:

$$\mathbf{F}_{\alpha\beta} = w(X_{\alpha})w(X_{\beta})\mathbf{F}_{\alpha\beta}^{atom} + [1 - w(X_{\alpha})w(X_{\beta})]\mathbf{F}_{\alpha\beta}^{cm},$$

where

$$\mathbf{F}^{atom}_{lphaeta} = \sum_{ilpha,jeta} \mathbf{F}^{atom}_{ilpha jeta}$$

is the sum of all pair interactions between explicit atoms of molecules α and β and

$$\begin{aligned} \mathbf{F}_{i\alpha j\beta}^{atom} &= -\frac{\partial U^{atom}}{\partial \mathbf{r}_{i\alpha j\beta}}, \\ \mathbf{F}_{\alpha\beta}^{cm} &= -\frac{\partial U^{cm}}{\partial \mathbf{R}_{\alpha\beta}}. \end{aligned}$$

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May the Force be with you





One must interpolate the **forces** and not the interaction potentials if the **Newton's Third Law** is to be satisfied!

MP, K. Kremer, L. Delle Site, J. Phys. A: Math. Theor. 40, F281, 2007.





- ⁶ The switching procedure implies that in the transition regime, where 0 < w(x) < 1, we deal with fractional DOFs, i.e., by switching on/off a DOF we continously change the dimensionality of the phase space.
- 6 To proper describe this situation we resort here to the fractional calculus.
- Solution Let us consider a given $w(x) = \alpha$ and use α as a variable parameter.
- ⁶ The infinitesimal volume element of the fractional configurational space is defined as $dV_{\alpha} = d^{\alpha}x \Gamma(\alpha/2)/2\pi^{\alpha/2}\Gamma(\alpha) = |x|^{\alpha-1}dx/\Gamma(\alpha) = dx^{\alpha}/\alpha\Gamma(\alpha)$ where the positive real parameter α denotes the order of the fractional coordinate differential.

MP, K. Kremer, L. Delle Site, Phys. Rev. E 75, 017701, 2007.

The extension of equipartition theorem to non-integer DOFs



6 For the fractional quadratic DOF Θ with the weight $w = \alpha$ we can write the partition function as:

$$\exp(-\beta F_{\alpha}) = C \int \exp(-\beta \alpha p_{\Theta}^2/2) \, dV_{\alpha} =$$
$$= 2C \int_0^{\infty} \exp(-\beta \alpha p_{\Theta}^2/2) \, |p_{\Theta}|^{\alpha-1} \frac{dp_{\Theta}}{\Gamma(\alpha)} =$$
$$= \frac{2^{\alpha/2} C \Gamma(\alpha/2)}{\Gamma(\alpha)} \alpha^{-\alpha/2} \beta^{-\alpha/2} \sim \beta^{-\alpha/2}.$$

$$(K_{\alpha}) = \frac{d(\beta F_{\alpha})}{d\beta} = \frac{\alpha}{2\beta} = \alpha \frac{k_B T}{2}$$

6 In equilibrium $T_A = T_B = T_\Delta = T$ and thus: $n_\alpha \sim \alpha$.

MP, K. Kremer, L. Delle Site, Phys. Rev. E **75**, 017701, 2007. MP, K. Kremer, L. Delle Site, J. Phys. A: Math. Theor. **40**, F281, 2007.



Langevin thermostat



Equation of motion for the i-th particle:

$$m_i \frac{d^2 \mathbf{r_i}}{dt^2} = \mathbf{F}_i - m_i \Gamma \frac{d \mathbf{r}_i}{dt} + \mathbf{W}_i(t).$$

Fluctuation-dissipation theorem:

$$\langle \mathbf{W}_i(t) \cdot \mathbf{W}_j(t') \rangle = \delta_{ij} \delta(t - t') 6 \sqrt{m_i m_j} k_B T \Gamma_i$$





Mapping of structural properties



Effective pair potential that reproduces the structure of the all-atom system as closely as possible is determined using the RDF_{cm} of the reference all-atom system via the potential of mean force (*PMF*) as

$$U^{cm}(r) \approx PMF(r) = -k_BT \log g_{ex}^{cm}(r),$$

 $g_{ex}^{cm}(r)$ is the all-atom RDF_{cm} and $U^{cm}(r)$ is the effective potential.

Effective potential is:

- in general temperature and density dependent
- **softer** than the interatomic potentials



Iterative Boltzmann inversion



In the limit $\rho = 0$:

$$U^{eff}(r) = F(r) = -k_B T \ln g(r).$$

For systems with $\rho > 0$ the above relation is used as an initial approximation in the iteration scheme:

$$U_{i+1}^{eff}(r) = U_i^{eff}(r) + k_B T \ln \frac{g_i(r)}{g_{target}(r)}$$

Ramp pressure correction:

$$\Delta U_{lin} = A(1 - \frac{r}{r_{cut}}).$$

D. Reith, M. Pütz, F. Müller-Plathe, J. Comput. Chem., 24, 1624, 2003.



Tetrahedral liquid: effective potential



0.5

0

0

1

(c) Tabulated effective potential.

2.4

r

2.6

2.8

3

3.2 3.4

 $\mathbf{2}$

1

0

1.4 1.6

1.8

2

2.2

(d) RDF_{cm} .

2

r

3

4

5







(e) EOS for $\rho = 0.175$ and T = 1. (f) RDF_{cm}.



Density profile profile



(g) Radius of the explicit regime:(h) Radius of the explicit regime: $r_0 = 6.0.$ $r_0 = 11.0.$



Artifacts of the method





Interface pressure correction (ic)

$$\mathbf{F}_{\alpha\beta}^{cm} = s[w(R_{\alpha})w(R_{\beta})]\mathbf{F}_{\alpha\beta_{o}}^{cm} + (1 - s[w(R_{\alpha})w(R_{\beta})])\mathbf{F}_{\alpha\beta_{ic}}^{cm}$$

 $s \in [0,1]$ is defined as

$$s[x] = 4(\sqrt{x} - \frac{1}{2})^2,$$

where s[0] = 1, s[1] = 1 and s[1/4] = 0



Density profile with ic correction

(m) $\rho = 0.1$.

(n) $\rho = 0.175$.

Macromolecule in solvent

MP, L. Delle Site, K. Kremer, J. Chem. Phys. 126, 134902, 2007.

Maximal monomer distance

Static properties of the solvent

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Static properties of the polymer

$$S(q) = \frac{1}{N} \left\langle \sum_{ij} \exp(i\mathbf{q} \cdot (\mathbf{r}_i - \mathbf{r}_j)) \right\rangle$$

 $S(q) \propto q^{-1/\nu} \rightarrow q^2 S(q) \propto q^{2-1/\nu}, \nu \approx 0.57$

Dynamic properties of the polymer

Diffusion constant of the chain

N	10	20	30
D(<i>ex</i>)	0.008	0.005	0.003
D(<i>ex-cg</i>)	0.009	0.006	0.0045
$D(ex-cg_{ic})$	0.0085	0.006	0.0035

$$D_{bulk_{ex}} = 0.036, D_{bulk_{cg}} = 0.057$$

$$D_{polymer} \ll D_{solvent}$$

Liquid water

The simulation speed-up is $\sim 17 - 20$ compared to atomistic simulations.

MP, S. Matysiak, L. Delle Site, K. Kremer, C. Clementi, J. Phys.: Condens. Matter, 19, 292201, 2007. Universität Stuttgart - SFB 716, Pforzheim-Hohenwart, September 8-10, 2008 – p. 36/59

Electrostatics: Reaction field method

The electrostatic forces interactions are described using the Reaction field (RF) method:

$$\mathbf{F}_{C_{i_{\alpha}j_{\beta}}}^{atom}(\mathbf{r}_{i_{\alpha}j_{\beta}}) = \frac{e_{i_{\alpha}}e_{j_{\beta}}}{4\pi\epsilon_0} \left[\frac{1}{r_{i_{\alpha}j_{\beta}}^3} - \frac{1}{R_c^3}\frac{2(\epsilon_{RF}-1)}{1+2\epsilon_{RF}}\right]\mathbf{r}_{i_{\alpha}j_{\beta}}.$$

The RF is suitable to be used with AdResS because:

- it is pairwise
- like AdResS it must also be applied with a thermostat

Weighting function for flat geometry

Static properties

The transition regime neutralizes the interface effect of the cg water \implies the structure of water in the explicit regime is the same as in the bulk.

Diffusion across the transition

regime I.

Diffusion coefficient across the simulation box

Position dependent Langevin thermostat

The Langevin equation with a position dependent coefficient $\Gamma(x)$ can be written as:

$$m_i dv_i/dt = F_i - m_i \Gamma(x) v_i + R_i(x, t) \tag{1}$$

where $R_i(x,t)$ is:

$$\langle R_i(x,t)\rangle = 0, \tag{2}$$

$$\langle R_i(x,t_1)R_j(x,t_2)\rangle = 2\Gamma(x)m_ikT\delta(t_1-t_2)\delta_{ij}$$
(3)

$$\Gamma(x) = \begin{cases} \Gamma_{cg} & \text{if } x \le 0.6\\ \alpha x + \beta & \text{if } 0.6 < x \le 1.0 \end{cases}$$
(4)

This choice provides a simple interpolation between the two limit values of $\Gamma(0.6) = \Gamma(0) = \Gamma_{cg} = 15ps^{-1}$ and $\Gamma(1) = \Gamma_{all-atom} = 5ps^{-1}$. The parameters α and β are $-25ps^{-1}$ and $30ps^{-1}$, respectively.

Diffusion coefficient in the hybrid

Diffusion coefficient across the simulation box II.

Transverse DPD Thermostat

Friction Strength

⁶ The variation of the dissipative particle dynamics (DPD) thermostat includes the damping of the perpendicular components of the relative velocity, yet keeping the advantages of conserving Galilei invariance and within our error bar also hydrodynamics. It allows for controlling transport properties of molecular fluids.

C. Junghans, MP, K. Kremer, Soft Matter 4, 156, 2008.

AdResS: Conclusions

6 Adaptive Resolution MD simulation:

- Changing resolution is formally equivalent to a phase transition \rightarrow latent heat.
- For a smooth variation of the resolution we introduce a transition regime.
- The temperature in the transition region can be obtained by extending the equipartition theorem to non-integer dimensions.

6 Hybrid method AdResS:

- Allows for a dynamical switching of the spatial resolution.
- We treat only as many DOFs as absolutely necessary for the problem considered.
- AdResS was so far applied to MD simulations of a simple tetrahedral liquid, a macromolecule in an explicit solvent, and liquid water at standard conditions.
- A The simulation speed-up for liquid water is $\sim 17 20$ compared to atomistic simulations.

6 Review:

MP, L. Delle Site, K. Kremer, Annu. Rev. Phys. Chem. 59, 545, 2008. Universität Stuttgart - SFB 716, Pforzheim-Hohenwart, September 8-10, 2008 – p. 47/59

AdResS: Future work

Concurrent triple-scale simulation

6 Motivation:

to simplify the model to the largest extend possible while keeping all the necessary details where this is required

6 **Method:** *Triple-scale AdResS-HybridMD scheme*

- is a combination of two dual-scale models: a particle-based Adaptive Resolution
 Scheme (AdResS), which couples the atomic and mesoscopic scales, and a hybrid
 continuum-molecular dynamics scheme (HybridMD)
- covers the length-scales ranging from the micro- to macro-scale
- successfully sorts out the problem of large molecule insertion in the hybrid particle-continuum simulations of molecular liquids
- opens up the possibility to perform efficient grand-canonical molecular dynamics simulations of truly open molecular liquid systems

6 Results:

the structural and dynamical properties of the liquid are accurately captured

R. Delgado Buscalioni, K. Kremer, MP, J. Chem. Phys. 128, 114110, 2008.

HybridMD: Coupling particle-based and continuum descriptions

- 6 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.
- 6 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.
- ⁶ The MD and CFD domains share one unique "hybrid interface", H: Flux balance implies the conservation of mass and momentum across H.

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.

- 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.
- R. Delgado Buscalioni, K. Kremer, MP, J. Chem. Phys. 128, 114110, 2008.

Molecular density profile

 \circ (a) $ho_m=0.1\sigma^{-3}$. (b) $ho_m=0.175\sigma^{-3}$ (b) $ho_m=0.175\sigma^{-3}$

Radial distribution functions

⁶ RDF_{cm}s of the liquid in the atomistic and transition domains (ex + hyb) and in the total molecular region (ex + hyb + cg) of the triple-scale model together with the reference RDF_{cm} of the all-atom system (ex(PBC)) at $\rho = 0.175/\sigma^3$.

Couette flow

S Velocity profile at the particle region of an hybrid simulation of a Couette flow.

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Stokes flow

Velocity in the y-direction at some selected cells in a hybrid simulation of a Stokes flow.
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AdResS-HybridMD: Conclusions

6 AdResS-HybridMD Scheme:

- We performed a triple-scale simulation of a molecular liquid.
- Length scales from the micro- to macro-scale are concurrently coupled.
- The method allows us to perform efficient grand-canonical molecular dynamics simulations of molecular liquids.

5 Future work:

Application to realistic systems, e.g., liquid water.

Triple-scale liquid water

URL: http://www.mpip-mainz.mpg.de/~praprot/

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