

# Supporting Information for Adaptive resolution simulation of MARTINI solvents

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## 1 Bundled-SPC/MARTINI water with DPD thermostat

The Langevin thermostat does not reproduce the correct hydrodynamics, i.e., the hydrodynamic interactions are unphysically screened. To correctly describe hydrodynamic interactions, we have to use the DPD thermostat<sup>1,2</sup> instead. The DPD thermostat satisfies Newton's third law by construction and owing to mass, momentum and temperature conservation, hydrodynamics is also properly reproduced.<sup>3</sup> We report here the results for multiscale simulation of hybrid bundled-SPC/MARTINI water with dissipative particle dynamics (DPD) thermostat.<sup>2</sup> The coupling constant is 0.025 a.u./ps, while the cutoff radius is 1.4 nm. The simulation setup is the same as described in the main paper. Simulations were performed by ESPResSo++ software package.<sup>4</sup>

To check the structural properties of the system we compute the radial distribution functions (RDFs) of oxygen atoms and bundle centers of mass (COMs) in the atomistic (AT) and coarse-grained (CG) regions of AdResS simulations. We compared these RDFs with those obtained from fully AT/CG simulations. All RDFs are identical to the ones obtained with Langevin thermostat (see main text) and are therefore not shown.

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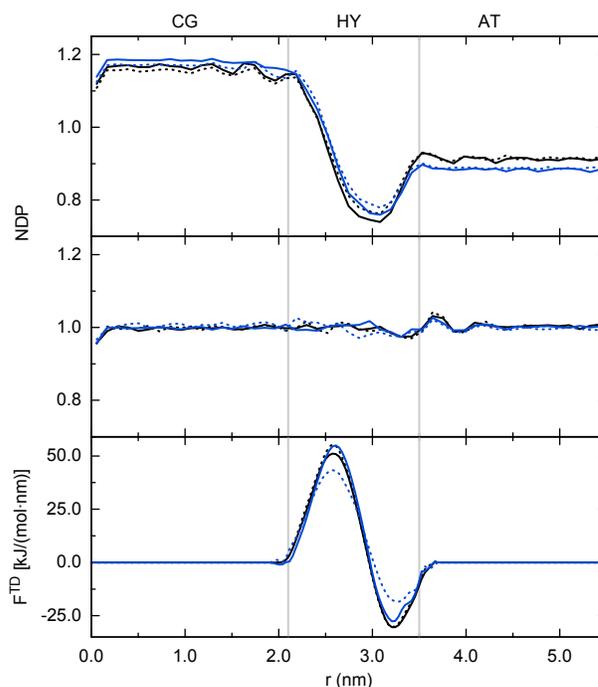


Figure S1: Normalized density profile of bundled water models 1 and 2 simulated at  $T = 300$  K and  $T = 323$  K with the DPD thermostat (black and blue lines indicate models 1 and 2, respectively; full and dotted lines indicate  $T = 300$  K and  $T = 323$  K, respectively). The top plot shows the case without TD force, while the middle plot shows the case with TD force. Error bars are approximately 1%. The bottom plot shows the applied TD force for each model and temperature. Vertical lines show the boundaries of the AT, HY, and CG regions.

The thermodynamic (TD) force acts on the COM of bundles in the hybrid (HY) region and ensures that the system is in thermodynamic equilibrium. The result of several iterations is shown in Figure S1. As with the Langevin thermostat, application of the TD force could successfully compensate any density imbalances, for all tested combinations of bundling model and temperature.

Figure S2 shows the average orientation of the dipole moment ( $\alpha$ ), the vector perpendicular to the plane of the molecule ( $\beta$ ), and the vector joining the two hydrogen atoms ( $\gamma$ ). As with the Langevin thermostat, the presence of interfaces in the system causes water molecules to become slightly anisotropically oriented in the HY region. The HY region, however, is large enough that we do not observe any preferential orientation of the molecules in the AT region.

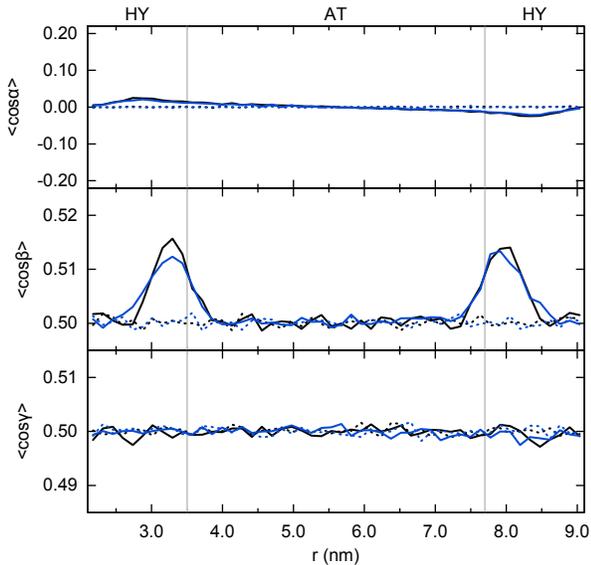


Figure S2: The average cosine value of the angle formed by the dipole moment vector (top panel), the vector joining the two hydrogen atoms (middle panel) and the vector perpendicular to the plane of the molecule (bottom panel) with the interface normal vector pointing toward the CG region. We compare the results for bundled water models 1 and 2 (black and blue, respectively) at 300 K obtained with AdResS (full line) and fully atomistic (dotted line) simulation.

The bundles' self diffusion coefficients are calculated from the mean square displacement with

finite size correction.<sup>5,6</sup> In Table S1 we report results for atomistic and CG simulation. The values are slightly higher but very similar to those for Langevin thermostat.

Table S1: Diffusion coefficients in units  $10^{-9}\text{m}^2\text{s}^{-1}$  for models 1 and 2 at temperatures  $T = 300$  K and  $T = 323$  K.

model	T [K]	D (AT)	D (CG)
1	300	1.9	1.8
2	300	1.9	1.9
1	323	2.1	2.0
2	323	2.1	2.3

The time evolution of bundles position in x is plotted in Figure S3 and shows that bundles can move from one region to another without experiencing any boundaries. Shown are diffusion profiles where the bundles are initially in the AT or CG region (left), or the HY region (right). As in the system with Langevin thermostat the observed dispersion of diffusion profile is almost symmetrical.

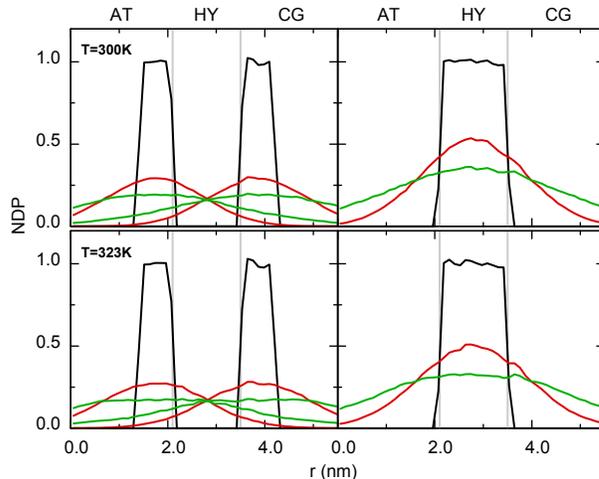


Figure S3: Diffusion of the COMs of bundled waters for model 1 at 300 (top) and 323 K (bottom). Left: The particles at time  $t = 0$  ps (black) in a slab 0.7 nm wide in either CG and AT region and at later times (red:  $t = 50$  ps; green:  $t = 100$  ps). Right: The same time evolution for particles initially in a slab corresponding to the entire HY region.

## 2 Bundled-SPC/MARTINI water simulated with GROMACS

### 2.1 Modified force truncation

In a hybrid simulation coupled with the AdResS scheme it is possible for AT particles to come close or even overlap when one of their COMs enters the HY region from the CG region. This is so because up until the moment the COM enters the HY region any AT interactions are scaled to zero. When the close contact between AT particle does occur, very high forces will result, rendering the system unstable. Granted, this interaction will still be scaled by a very low weight (since one of the COMs is still very close to the CG region); however, it is unavoidable that in some of these cases the AT particles are close enough that the interaction force greatly overpowers this down-scaling.

Due to this possibility, AT forces generated in the HY region must be limited.<sup>7</sup> Close contacts will still occur close to the HY–CG boundary, but the limited force is still strong enough to drive the separation of the particles. The ESPResSo++<sup>4</sup> approach to limiting the force is to soft-core the interactions by calculating them as though particles never get closer than a given limit  $r_c$ :

$$\|F(r)\| = \begin{cases} \|I(r)\|, & r > r_c \\ \|I(r_c)\|, & r \leq r_c \end{cases} \quad (\text{S1})$$

where  $r$  is the interparticle distance, and  $F(r)$  and  $I(r)$  the truncated and unmodified force functions, respectively. The GROMACS approach, conversely, is to set a maximum,  $f_{\max}$ , for the interparticle interactions:

$$\|F(r)\| = \begin{cases} \|I(r)\|, & \|I(r)\| \leq f_{\max} \\ \|I(r_c)\|, & \|I(r)\| > f_{\max} \end{cases} \quad (\text{S2})$$

In both cases  $F(r)$  will be a truncated interaction force profile. The GROMACS approach, however, has the subtle difference that the interparticle distance at which truncation occurs depends on the force profile itself (stronger interactions that generate higher forces will be truncated sooner—at larger interparticle distances—than weaker interactions). While this was not a problem for butane simulations, it severely imbalanced the SPC

oxygen-hydrogen interactions in our simulations to the point that significant particle overlaps occurred well into the AT region.

To circumvent this problem we implemented the same soft-core approach as in ESPResSo++ into GROMACS version 4.6.5. This implementation successfully kept SPC molecules from overlapping when an  $r_c$  of 0.14 nm was used.

### 2.2 Results

The modified GROMACS version was tested with SPC bundling model 2, at 323 K. As with the ESPResSo++ results, simulation in the absence of a TD force resulted in a density imbalance, most pronounced in the HY region (Figure S4). A TD force, which successfully compensated for this, could be obtained by an iterative procedure using the VOTCA package<sup>8</sup> as described for butane. (It should be noted that for this system, contrary to the default behavior of VOTCA, the iterative density correction must be done based on densities of COMs, not of AT particles).

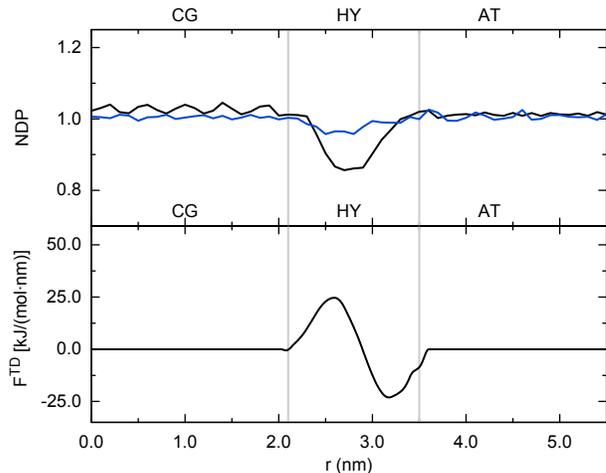


Figure S4: Top: normalized density profile of bundled SPC water COM in an AdResS simulation as a function of the x-distance to the center of the box. A density imbalance is visible in a free AdResS simulation (black), which is successfully compensated for when an appropriate TD force is used (blue). Bottom: the used TD force. Vertical lines show the boundaries of each resolution region.

To ensure that water structure was preserved also with the modified GROMACS method the RDFs

of the oxygen atoms and of the COMs was calculated and compared to reference AT or CG systems simulated without AdResS (Figure S5). The results, just as the ESPResSo++ ones, show excellent agreement between RDFs.

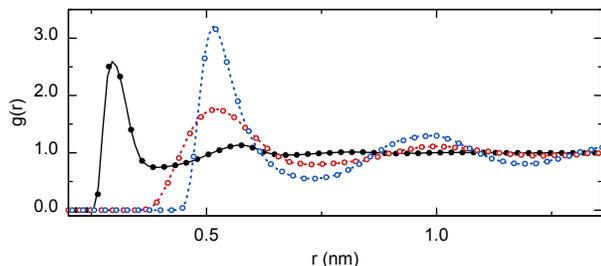


Figure S5: RDF of oxygen atoms (black), bundle COMs (dotted red), and CG beads (dotted blue) for bundled water model 2 at 323 K obtained from the AT region (oxygen and COM RDFs), or from the CG region (CG RDFs) of the AdResS simulation. The RDFs from the reference AT and CG simulations are overlaid as circles in the relevant plots (black and red, and blue, respectively), with very good agreement.

## References

- (1) Junghans, C.; Praprotnik, M.; Kremer, K. *Soft Matter* **2008**, *4*, 156–161.
- (2) Soddemann, T.; Dunweg, B.; Kremer, K. *Phys. Rev. E* **2003**, *68*, 046702.
- (3) Español, P. *Phys. Rev. E* **1995**, *52*, 1734–1742.
- (4) Halverson, J. D.; Brandes, T.; Lenz, O.; Arnold, A.; Bevc, S.; Starchenko, V.; Kremer, K.; Stuehn, T.; Reith, D. *Comput. Phys. Commun.* **2013**, *184*, 1129–1149.
- (5) Dunweg, B.; Kremer, K. *J. Chem. Phys.* **1993**, *99*, 6983–6997.
- (6) Yeh, I. C.; Hummer, G. *J. Phys. Chem. B* **2004**, *108*, 15873–15879.
- (7) Praprotnik, M.; Delle Site, L.; Kremer, K. *J. Chem. Phys.* **2005**, *123*, 224106.
- (8) Ruehle, V.; Junghans, C.; Lukyanov, A.; Kremer, K.; Andrienko, D. *J. Chem. Theory and Computation* **2009**, *5*, 3211–3223.