

9th Dutch Molecular Dynamics Day

Location: Room Number D1.111, HIMS,
University of Amsterdam, Science Park

May 24, 2019

9:30-10:00 - Registration and coffee/tea

10:00 - 10:10 - Welcome and Introduction

Session 1 chair:

10:10 - Weria Pezeshkian

University of Groningen

Shape transformations of biological membranes, from atomistic to macroscopic length scale

10:35 - Selim Sami

University of Groningen

Unravelling the nature and the timescale of the dielectric constant for organic semi-conductors

11:00 - Ioana M. Ilie

University of Zurich

From monomeric disorder to fibrillar order: A microscopic view

11:25 - Fabian Grunewald

University of Groningen

Titrateable MARTINI

11:50 - Vishal Metri

University of Twente

Brownian Dynamics Simulations of Orthogonal Superposition Rheology

12:15 to 13:35 - Lunch and Poster session 1

Session 2 chair:

13:40 - Josef Melcr

University of Groningen

Electronic polarization in MD simulations of lipid membranes

14:05 - Max Dopke

Technical University of Delft

Preferential adsorption on charged amorphous silica

14:30 - Henry de Vries

University of Groningen

Redesigning the Nuclear Pore Complex: Coarse-grained modeling of artificial FG-Nups and ionic conductance in biomimetic nanopores

14:55 - Máté Erdős

Technical University of Delft

Inclusion complexation of organic micropollutants with β -cyclodextrin

15:30 to 16:05 - Poster session 2

Session 3 chair:

16:10 - Ambuj Tiwari

University of Amsterdam

Can hydrogen bond network explain phase transitions?

16:35 - Thejas Hulikal Chakrapani

University of Twente

Mesosopic simulations of ink-imbibition into paper

17:10 Drinks / Beer at HIMS coffee corner with Poster session 3

Talks

Shape transformations of biological membranes, from atomistic to macroscopic length scale

Weria Pezeshkian, University of Groningen

Many biological processes involve large scale changes in lateral chemical organization and geometrical shapes of biological membranes. Modelling of these processes, by computer simulation, is a challenging task since they typically involve a wide range of length and time scales that cannot be captured in full by any single current simulation technique. To overcome this limitation, we combine distinct computer simulation techniques i.e. all atom molecular dynamics, coarse grained Martini model and dynamic triangulated surface, in a multi-scale simulation scheme.

The multi-scale simulation produce will be described and results of few examples will be shown.

Unravelling the nature and the timescale of the dielectric constant for organic semiconductors

Selim Sami, University of Groningen

The current generation of organic photovoltaic devices still lacks the required efficiency to be economically competitive. One way to improve their efficiency is the use of materials with a high dielectric constant, thereby decreasing the effective Coulombic attraction between the electron-hole pairs and therewith facilitating their transport to the respective electrodes without suffering from recombination. The most prominent strategy to this end is the use of ethylene glycol side chains which are known to increase the dielectric constant drastically. However, both the timescale and a clear molecular understanding of the origin of these contributions are still lacking.

In this communication, we present a multiscale computational scheme to calculate the different contributions (electronic, dipolar and induced) to the dielectric constant. We employ polarizable force fields for molecular dynamics simulations, for which we derive the parameters from quantum chemical calculations. Having access to detailed molecular information, we were able to dissect the dielectric contribution into molecular fragments, allowing us to clearly pinpoint the origin of these contributions.

Moreover, our results, for the first time, unravel the timescale of these contributions and shed light on their relevance for high efficiency organic photovoltaics.

From monomeric disorder to fibrillar order: A microscopic view

Ioana M. Ilie, University of Zurich

The accumulation of amyloid fibrils is the hallmark of neurodegenerative diseases, such as Parkinsons and Alzheimers disease. Here we use atomistic simulations to explore the intricate dynamics and aggregation of α -synuclein[1] amyloid- β (42)[2], the proteins associated with these disorders.

We start by simulating the amyloidogenic core of monomeric α -synuclein and find it has a preference towards attaining non- β conformations in solution. Additionally, results indicate that the fibrillar structure is stabilized by interactions with neighbouring strands. Furthermore, we combine the free energy profiles of individual fragments into the reaction free energy of a protein binding to a fibril and obtain values comparable to experimental measurements[1].

For the second part, we simulate an 18-meric A β 42 double-horseshoe fibril. We find that its core 14 peptides are structurally stable on a timescale of 8 s and that the tip peptides record a localized detachment from the fibril surface. The tip peptides can associate with the adjacent layers occasionally in an ordered fashion, contributing to the stop-and-go mechanism of amyloid growth by shielding the fibrillary template and hindering growth by monomer addition to the fibrillary end[2].

References

- [1] I.M.Ilie et.al., J.C.T.C., 14:32983310 (2018)
- [2] I.M.Ilie & A. Caffisch, J. Phys. Chem. B, 122:1107211082 (2018)

Titratable MARTINI

Fabian Grunewald, University of Groningen

Titratable functional groups such as carboxylic acids or amines are abundant in bio-chemistry and material science. The biological or technological function of certain lipids, drugs, or polymers critically depends on their response to pH. Yet studying these systems in a complex environment for instance close to a membrane or in a composite material is difficult. To improve the current tool set to study these systems, we present the progress on the extension of the coarse-grained MARTINI force-field to constant pH simulations. In the MARTINI force-field about four heavy atoms are grouped into one interaction center, called bead. The interactions between beads represent the nature of the underlying chemical groups; the strength of the interaction is selected from a discrete set of levels by reproducing the free energies of transfer between water and different organic solvents. In our model pH effects are mediated by explicit positive particles that act somewhat like protons. By combining the MARTINI like building block approach to coarse-graining with dynamic effects of protonation and pH, one is able to parametrize complex systems with many different components in an efficient manner.

Electronic polarization in MD simulations of lipid membranes

Josef Melcr, University of Groningen

In this presentation, I will discuss where and how accounting for the electronic polarization affects the accuracy of classical molecular dynamics simulations. While the effects of electronic polarization are highly pronounced for molecules with an opposite total charge, they are also non-negligible for interactions with overall neutral molecules. For instance, neglecting these effects in important biomolecules like amino acids and phospholipids affects the structure of proteins and membranes having a large impact on interpreting experimental data as well as building coarse grained models.

I will show, how the effects of electronic polarization can be included at zero additional computational cost compared to standard fixed-charge force fields using the electronic continuum correction on the interactions between ions and phospholipid membranes.

Redesigning the Nuclear Pore Complex: Coarse-grained modeling of artificial FG-Nups and ionic conductance in biomimetic nanopores

Henry de Vries, University of Groningen

Nuclear Pore Complexes (NPCs) govern transport from and into the cell nucleus in a size-selective manner. Whereas small molecules pass the NPC freely, large (macro-)molecules bind to a Nuclear Transport Receptor (NTR) in order to translocate through the NPC. The central channel of the NPC contains a meshwork of FG-Nups: intrinsically disordered proteins rich in the amino acids phenylalanine (F) and glycine (G). The disordered nature of the NPC's central channel renders it inaccessible for study via direct measurements, motivating the recent development of well-controlled experimental replicas[1,2]. These biomimetic nanopores contain a single type of FG-Nup, enabling a systematic study of the link between the FG-Nup amino acid sequence and the NPC's transport properties.

Here we present two aspects of coarse-grained simulations of FG-Nup meshworks in biomimetic nanopores: (i) the bottom-up design of artificial FG-Nups, and (ii) the development of a coarse-grained model for ionic conductance in biomimetic nanopores. More precisely, we designed a 311-residue artificial FG-Nup (NupX) and assessed experimentally obtained size-selective properties of NupX proteins grafted to nanopores and brushes. Using a one-bead-per-amino acid (1-BPA) model for intrinsically disordered proteins[3], we confirmed the size-selectivity of NupX-coated brushes using umbrella sampling simulations of the absorption of NTRs and equally-sized inert cargoes (tCherry). Finally, we discuss the development of a coarse-grained forcefield for hydrated ions and related (hydrodynamic) challenges in modeling ionic conductance in biomimetic nanopores.

References

[1] S.W. Kowalczyk, L. Kapinos, T.R. Blosser, T. Magalhes, P. van Nies, R.Y.H. Lim and C. Dekker, *Nat. Nanotech.* 6(7), 433 (2011)

[2] A.N. Ananth, A. Mishra, S. Frey, A. Dwarkasing, R. Versloot, E. van der Giessen, D. Grlich, P.R. Onck and C. Dekker, *eLife* 7, e31510 (2018)

[3] A. Ghavami, L. Veenhoff, E. van der Giessen and P.R. Onck, *Biophys. J.* 107(6), 1393 (2014)

Preferential adsorption on charged amorphous silica

Max Dopke, Technical University of Delft

Preferential ion adsorption in mixed electrolytes plays a crucial role in many practical applications, such as ion sensing and separation and in colloid science. Using all-atom Molecular Dynamics simulations of aqueous NaCl, CaCl₂ and NaCl–CaCl₂ solutions confined by charged amorphous silica, we show that Na⁺ ions can adsorb preferentially over Ca²⁺ ions, depending on the surface structure. We propose that this occurs when the local surface structure sterically hinders the first hydration shell of the Ca²⁺ ion. Introducing a protrusion metric as a function of protrusion and orientation of deprotonated silanols, ion-specificity is successfully predicted on isolated, vicinal and geminal silanols alike, provided that no other deprotonated silanols are found nearby. Furthermore, we introduce a new strategy to analyze the results as a function of distance to the surface. This approach effectively removes surface roughness effects allowing for direct comparison with classical Electric Double Layer theory and distinction of specifically adsorbed ions and electrostatically adsorbed ions.

Inclusion complexation of organic micropollutants with β -cyclodextrin

Máté Erdős, Technical University of Delft

Water contamination poses a serious threat to public health and the ecosystem. Natural and anthropogenic organic contaminants are present at significant concentration in water bodies all over the world. Most of the current wastewater treatment techniques are not specifically designed to remove organic compounds. Considering the ever-rising intensity of industrial, agricultural and domestic activities, the design of efficient materials for water decontamination is essential. Recent experiments showed that polymers based on β -cyclodextrin (β CD), a cyclic oligosaccharide, can rapidly capture a wide variety of organic micropollutants (OMPs) from water, exhibiting distinct advantages over activated carbons, the most widely utilized materials for such processes today. Although many experimental studies are reported on the adsorption of OMPs in β CD polymers, the understanding of the exact mechanisms via which the micropollutants are being captured is still unclear. Previous studies suggest that one of the main governing adsorption mechanisms is the inclusion complex formation of OMPs with the β CD units of the polymer. In this study, we investigated the inclusion complexation of several OMPs with β CD by performing molecular dynamics simulations. The binding free energy and binding enthalpy of the complexes were calculated and the governing interactions were studied. Our results are in agreement with the experimental data which indicates that the used force field and methodology has a great potential for the investigation of the inclusion complexation of OMPs with β CD.

Can hydrogen bond network explain phase transitions?

Ambuj Tiwari, University of Amsterdam

No other substance is as vital for the life on earth as liquid water. Thus, it is not surprising that the properties of water have always been, and still are, subject to intense experimental and theoretical studies. However, we are still challenged in understanding and explaining water with all its anomalies. Examples of these anomalies are the critical point in supercooled water and its long angular correlation lengths. There are indications [1] that these anomalies might be consequences of an extensive but fragile hydrogen bond network in the liquid water. Unfortunately, it is not possible to access the exact topology of the hydrogen bond network experimentally and theoretical models have been at the forefront of elucidating the network.

Due to recent advances in computational simulations[2], we are now able to obtain data sets on water and its hydrogen bond network for large systems while accounting for polarization effects. We study the topological properties of the hydrogen bond network as the percolation threshold, the giant component, clustering, cyclomatic number, etc., as a function of temperature. We find that some of the hydrogen

bond network properties, as for instance, the percolation threshold, are very close to the properties of the conventional configuration model [3] used for studying complex polymer networks. Interestingly, when studying percolation on networks that are attributed to different temperatures, we find the percolation parameter can be related to the temperature by an inversely proportional relationship.

References

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Brownian Dynamics Simulations of Orthogonal Superposition Rheology

Vishal Metri, University of Twente

We performed Brownian Dynamics simulations of Orthogonal Superposition Rheology (OSR) of a system of star polymers with functionality 13. The orthogonal superposition moduli were obtained for different steady shear rates by applying a small amplitude sinusoidal oscillatory strain perpendicular to the direction of shear with the gradient in the same direction, and then fitting the resulting stress by an in-phase and another out-of-phase sinusoid whose coefficients give the storage and loss moduli respectively for that particular steady shear rate. We show that the relaxation modulus obtained after inverse Fourier transforming the moduli to time-domain is different from the stress response after a unit impulse in the orthogonal direction, unlike in linear viscoelasticity, with the former developing a power law tail while the latter always decaying exponentially. The plateau value of both moduli are the same, only the tail becomes increasingly algebraic with shear rate. In addition, a plot of the power law exponents with shear rate reveals that the Maxwellian slope of 2 for the storage modulus at zero-shear seems to be a singular point. We also give an expression for the plateau value of the storage modulus with shear, which can be directly calculated from a simulation and we also link it to the perturbation in the pair distribution function.

Mesoscopic simulations of ink-imbibition into paper

Thejas Hulikal Chakrapani, University of Twente

Jetable ink is a mixture of water, co-solvent like glycerol, surfactants and pigment particles for color. The typical size of these pigment particles is between 20-200 nm. On the other hand, office paper consists of dried hollow natural fibres of 2 mm length, and pores which are tens of nanometer in size. Further, these fibres are compressed into a 100 micrometer layer, which generates a complex network of pores [1]. In addition, paper coatings are granular in nature and contain pores of width between 10-400 nm. Hence, ink-imbibition into paper is a highly complex process which encompasses the complexity of the fluid, complex geometry of paper, and the multi-scale nature of the problem.

We have started on this topic, using the particle-based mesoscopic simulation technique called MDPD [2]. The first topic to be presented is the surface-tension-driven flow of various fluids into cylindrical pores, to assess the impact of the fluid on the expected Lucas-Washburn imbibition rate. Next, results will be presented on the surface-tension-driven flow of a simple fluid into a variety of idealized arrays of (hollow) cylinders, representing our first step to a model for paper.

References

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