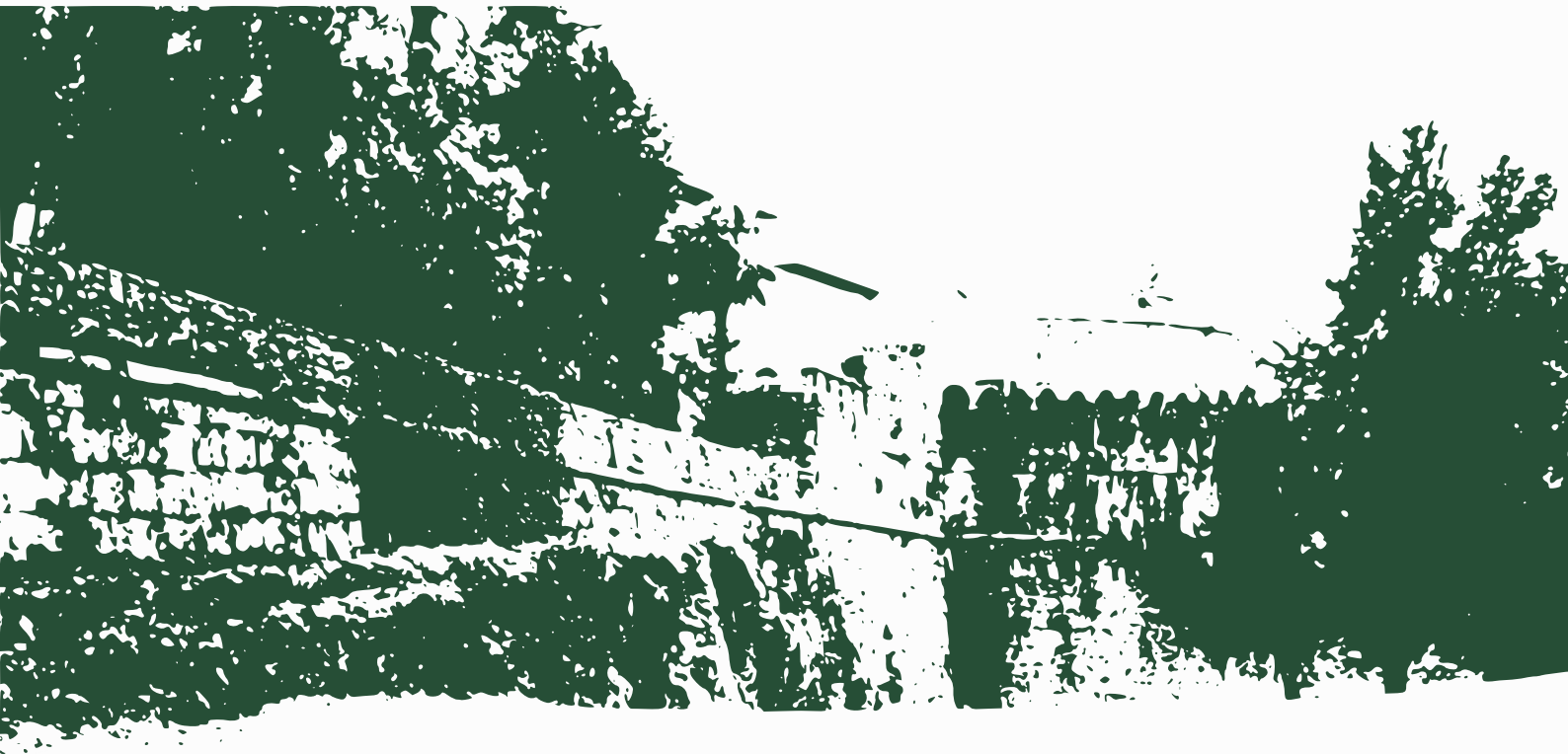
XMAS BIOPHYSICS WORKSHOP

Gradisca d'Isonzo, Italy

9-10 December 2019

Book of abstracts



Contents

Welcome

The Christmas Biophysics Workshops (XBW) consist of a series of regional meetings for research groups from Austria, Croatia, Italy and Slovenia in the fields of biophysics, soft matter physics and related fields.

The first Christmas Biophysics Workshop was organized by Rudolf Podgornik (Ljubljana, Slovenia) and Silvia Tomić (Zagreb, Croatia) in 2006 in Zagreb. Since then, every year in early December research groups from Austria, Croatia, Italy and Slovenia gather together in a small town of the region to share their research. The character of the meeting is rather informal and it aims to create a relaxed atmosphere in which recent results and ideas are discussed, scientific collaborations are established and friendships grow beyond borders.

This year the workshop will be held in Gradisca d'Isonzo, a small town of the Province of Gorizia in Friuli-Venezia Giulia region, located at north-eastern Italy. Participants will present their work in short talks throughout Monday 9 and the morning of Tuesday 10 of December. At the midpoint we all will enjoy a social dinner with a festive mood in the expectation of holidays.

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- Zankoc, Clément. *Jožef Stefan Institute* (Ljubljana).
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Program

Monday 09/12/19

09:50 - 10:00 **Welcome by Cristian Micheletti**

10:00 - 11:15 **Session 1: Cellular Systems – Chair: Irene Adroher-Benítez**

10:00 - 10:25 Bernat Corominas-Murtra
Criticality and phase transitions at the onset of morphogenesis.

10:25 - 10:50 Jan Rozman
3D Vertex Model of Ventral Furrow Formation in Fruit Fly.

10:50 - 11:15 Saša Svetina
The effect of a single Piezo1 trimer on shapes of phospholipid vesicles.

11:15 - 11:45 **Coffee break**

11:45 - 13:25 **Session 2: Biophysics – Chair: Antonio Šiber**

11:45 - 12:10 Ema Slejko
The influence of the poly(ethylene glycol) on the mean activity coefficients of NaCl aqueous solutions.

12:10 - 12:35 Tomislav Vuletić
FCS study of interaction of DNA and supramolecular systems with adamantyl guanidines.

12:35 - 13:00 Fabio Staniscia
Passive viscoelastic response of striated muscles.

13:00 - 13:25 Lucija Dončević
Protein self-association.

13:30 - 14:30 **Lunch**

14:30 - 15:00 **Check in**

15:00 - 16:40 **Session 3: Soft Matter** – **Chair: Primoz Ziherl**

15:00 - 15:25 Horacio A. V. Guzmán
Quantifying the disassembly of viral capsids from a multiscale molecular simulation approach.

15:25 - 15:50 Clément Zankoc
Nonlinear stochastic dynamics of adherens junctions.

15:50 - 16:15 Petra Papež
Hydration of lower alcohols using theoretical methods.

16:15 - 16:40 Antonio Šiber
Collapsing pollen grains.

16:40 - 17:10 **Coffee break**

17:10 - 19:15 **Session 4: Biomolecules, structure and function** – **Chair: Matej Kanduč**

17:10 - 17:35 Angelo Rosa
Untangled ring polymers in melts: The Physics of crumpling.

17:35 - 18:00 Stefano Franzini
hicRED: A spectral method for comparing HiC-maps.

18:00 - 18:25 Anze Bozic
Coupling electrostatics and elasticity of virus capsids.

18:25 - 18:50 Mattia Bernetti
Combining molecular dynamics simulations with SAXS experiments to characterize RNA conformational dynamics.

18:50 - 19:15 Nicola Calonaci
Machine-learning experimental data for RNA structure prediction.

20:15 - 22:00 **Social dinner**

22:00 - ? ***Grappa discussion***

Tuesday 10/12/19

07:00 - 09:15 **Breakfast**

09:15 - 10:30 **Session 5: Biophysics – Chair: Tomislav Vuletić**

09:15 - 09:40 Ina Erceg

The kinetics of bovine serum albumine adsorption on calcium ohosphate and TiO_2 nanoparticles or nanotubes nanocomposites.

09:40 - 10:05 Anja Sadžak

Protection of lipid membranes during oxidative stress using flavonoid embedded silica nanoparticles.

10:05 - 10:30 Adela Štimac

Measurement of the biomolecular interaction between plant lectin and peptidoglycan functionalized self-assembled hybrid bilayers by a quartz crystal microbalance.

10:30 - 11:20 **Coffee break and check out**

11:20 - 13:00 **Session 6: Soft Matter – Chair: Adela Štimac**

11:20 - 11:45 Matej Kanduč

Biological liquids under tension.

11:45 - 12:10 Andraž Gnidovec

Orientational ordering of point dipoles on a sphere.

12:10 - 12:35 Matej Krajnc

Active elastic networks as models of biological tissues.

12:35 - 13:00 Primoz Ziherl

Morphologies of vesicle doublets: Competition among surface tension, bending elasticity, and adhesion.

13:00 - 14:00 **Lunch**

14:00 **Departure**

Abstracts

Criticality and phase transitions at the onset of morphogenesis

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Tissue morphogenesis in multicellular organisms is one of the most fascinating phenomena of nature. From a small collection of apparently identical cells, an explosion of complexity leads to the formation of a new, fully developed organism. Despite the enormous number of variables the process relies upon, morphogenesis is a very robust process that occurs following a well ordered sequence of stages through apparently fragile metastable states. A crucial question is: what are the driving forces that enable and promote the transition from one state to the next? Recent findings reported abrupt changes in the material properties of the tissues, pointing to the hypothesis that such transitions can be actually conceptualized as structural phase transitions. However, no approach has been able to connect the assumptions of a microscopic theory –in the sense of statistical mechanics– to the observed, macroscopic observables. In this talk I will show how, in the first stages of the development of the zebrafish embryo, the network structure of the tissue suffers dramatic changes that are surprisingly well characterized as rigid-to-fluid phase transitions, a phenomenon intimately linked to percolation and that would act as a critical regulator of embryo morphogenesis. Interesting deviations are observed in the systems genetically modified where cell cycle gets desynchronized and, in consequence so does the ability of uniform loss/gain of cell contacts that leads to the phase transition. Crucially, those embryos show a non-uniform fluidization/transition and fail to undergo normal tissue morphogenesis. This negative observation acts as a counterfactual proof of our results, supporting the hypothesis that the observed transition plays a critical role in embryo development. Our results are able to bridge, for the first time, the theoretical approach based on the patterns of cell interactions with macroscopic observables and match them with real data coming from experiments. This opens a vast and intriguing scenario towards the theoretical understanding of this crucial biological phenomenon where criticality theory is called to occupy a prominent role.

3D vertex model of ventral furrow formation in fruit fly

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The formation of the ventral furrow - an invagination of the ventral side of the early embryo - is a key morphogenic event during the gastrulation of the fruit fly Drosophila Melanogaster, and one of the most studied morphogenetic processes from both biological and biophysical perspective. Previous studies have shown that a 2D surface tension based vertex model can reproduce the invaginated morphology, either as a consequence of collective mechanics of identical cells[1] or in a system with multiple mechanically distinct groups of cells[2]. We build on these results by devising a 3D vertex model of the invaginated tissue, reproducing the formation of the ventral furrow in a simplified, cylindrical geometry. We generalize the model by adding time-dependent tensions along the apical and basal edges of individual cells, analyzing the mechanical effects of the resulting T1 transitions on the shape of the tissue.

References

[1] A. Hočevar Brezavšček, M. Rauzi, M. Leptin, and P. Ziherl, A model of epithelial invagination driven by collective mechanics of identical cells, Biophys. J. 103 5, 1069 (2012).

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The effect of a single Piezo1 trimer on shapes of phospholipid vesicles

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Piezo1 trimer is a large (~ 0.9 MDa) mechanosensitive protein that converts mechanical forces on cellular membranes into electrochemical signals in physiological processes such as blood vessel formation and vascular structure, hearing, touch, notiception etc. It also plays a role in the regulation of red blood cell volume. The mechanism of Piezo1 mechanosensitivity is still a matter of research. Several recent cryo-electron microscope studies have revealed its dome-like structure characterized by three "propeller-like" extensions. It was also demonstrated that Piezo1 affects shapes of phospholipid vesicles. Here we shall present the results of a corresponding theoretical model. The shape of a vesicle with a single Piezo1 trimer embedded onto its membrane is predicted by minimizing the sum of membrane bending energy and the elastic energy of the protein. It is shown how the radius of curvature on Piezo1 side of vesicle depends on the radius of curvature on opposite vesicle pole.

The influence of the poly(ethylene glycol) on the mean activity coeffcients of NaCl aqueous solutions

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The influence of the poly(ethylene glycol) on the mean activity coefficients of NaCl aqueous solutions

In this work I have systematically researched the influence of different poly(ethylene glycol) (PEG) on mean activity coefficient of sodium chloride in water solutions.

By measuring the voltage of galvanic cell (as indicator electrode ISE of chloride and sodium were used) the mean activity coefficient of NaCl was determined as a function of salt concentration. From measurements it can be seen, that activity coefficient of NaCl decreases with concentration of salt, however at high concentrations it starts to increase. Also, the increase of activity coefficient when PEG is added is observed.

In second part of this work mean activity coefficient of NaCl in PEG aqueous solutions were calculated with theoretical methods. For calculations of mean activity coefficient of NaCl in PEG, Ornstein-Zernike integral equation with HNC approximation was used. Further relative permittivity at different conditions was calculated. It can be seen that relative permittivity of water solutions of salts is lower than of pure water. It can also be observed that by adding PEG in to solution relative permittivity is additionally lower.

FCS study of interaction of DNA and supramolecular systems with adamantyl guanidines

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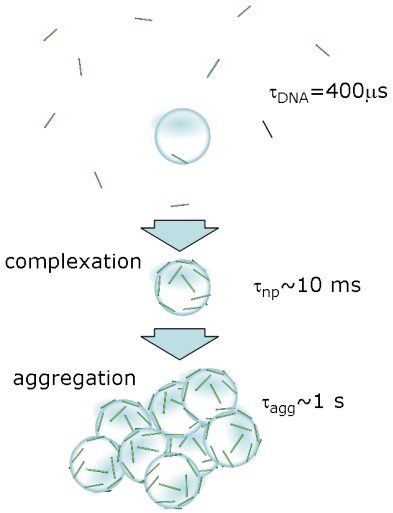
Fluorescence correlation spectroscopy (FCS) was applied to examine the interactions between ternary systems of fluorescently labeled DNA120* and nanoparticles functionalized with guanidinium group on the surface. The guanidinium group appeared particularly well suited for interaction with the phosphate residues of polynucleotides through establishing a characteristic pair of hydrogen bonds. FCS is a non-destructive and powerful technique that is based on fluctuations of fluorescence intensity over time within a small observation volume under equilibrium conditions.

In this work, FCS is used to detect the formation of complex between small and quickly diffusing fluorescently labeled DNA120* (Cy5-labeled double-stranded 120 base-pair DNA) and larger, slowly diffusing nanoparticles. We performed a series of FCS measurements of diffusion times for DNA120* in HEPES buffer in presence of a range of concentrations of various nanovesicles. FCS result for DNA120* only, without nanoparticles, serves as the baseline. In Supplementary material we present the prerequisite steps to take to ascertain that the FCS experiment measures the relevant features of the system under study.



Passive viscoelastic response of striated muscles

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Muscle cells with sarcomeric structure exhibit highly nontrivial passive mechanical response. The difficulty of its continuum modeling is due to the presence of long-range interactions transmitted by extended protein skeleton. To build a rheological model for muscle 'material' we use a stochastic micromodel and derive a linear response theory for a half-sarcomere. Instead of the first order rheological equation, anticipated by A.V. Hill on the phenomenological grounds, we obtain a novel second order equation. We use the values of the microscopic parameters for frog muscles to show that the proposed rheological model is in excellent quantitative agreement with physiological experiments.

Protein self-association

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Monomeric protein structure can form dimers, trimers and other aggregates induced by different types of stressors. During protein association process different types of bonding may occur, such as covalent, especially disulfide bonds, and non-covalent bonds: hydrogen bonds, electrostatic interactions, Van der Waals interactions and hydrophobic bonds. Protein structure complexity makes mechanism of aggregates emergence entirely unrevealed or poorly described.

Affected by these stressors, covalent and non-covalent bondage may occur and produce irreversible or reversible protein aggregates. Irreversible aggregates can be produced through heating, freezing-thawing, over-concentrating, isomerization, oxidation, etc. On the other hand, reversible aggregates or self-associates might be formed by the aforementioned processes but most likely by agitation[1].

We examined the formation of dimers, trimers, and tetramers on rHuG-CSG, also known as Granulocyte Colony Stimulating Factor, induced by agitation through a time period of 150 s. The analysis was performed immediately after agitation by liquid chromatography (gel permeation) at pH= 7.0 (50 mM NH4HCO3 mobile phase). Due to increased pressure caused by centripetal acceleration during agitation monomeric structures merges and makes dimers, trimers, tetramers, and other aggregates. Increased agitation power results in a significant increase of reversible self-associate quantity.

References

[1] R. Pavišić, I. Dodig, A. Horvatić, L. Mijić, M. Sedić, M. Rajić Linarić, I. Gruić Sovulj, T. Preočanin, M. Bukvić Krajačić, M. Cindrić, Differences between reversible (self-association) and irreversible aggregation of rHuG-CSF in carbohydrate and polyol formulation. European Journal of Pharmaceutics and Biopharmaceutics 76 (2010) 357-365.

Quantifying the disassembly of viral capsids from a multiscale molecular simulation approach

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Molecular simulation of large biological systems, such as viral capsids, remains a challenging task in soft matter research. On one hand, coarse-grained (CG) models attempt to make feasible the description of the entire viral capsids. On the other hand, novel development of molecular dynamics (MD) simulation approaches, like enhance sampling which attempt to overcome the time scales required in biophysics. Those methods have a potential for delivering molecular structures and properties of biological systems. Nonetheless, exploring the process on how a capsid disassembles by all-atom MD simulations has been rarely attempted. Here, we propose a methodology to analyze the disassembly process of viral capsids quantitatively. In particular, we look at the effect of pH and charge of the genetic material inside the capsid, and compute the free energy of a disassembly trajectory by combining CG simulations to a Poisson-Boltzmann solver. We employ such multiscale approach on the triatoma virus as a test case, and find that even though an alkaline environment enhances the stability of the capsid, the resulting deprotonation of the internal solvent generates an electrostatic repulsion that triggers disassembly.

Nonlinear stochastic dynamics of adherens junctions

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It is widely known that Myosin, a molecular motor, plays a fundamental role in epithelium dynamics. Through its action, the sliding of anti-parallel actin filaments, coupled to the adherens junction, it generates mechanical tension that leads to the shortening of the adherens junction, and, therefore plays a key role in local topological rearrangment (T1-transition). Indeed, it has been experimentally observed that periodic membrane contractions are accompanied by antiphasic myosin density oscillations. Inspired by these results and recent literature, we propose an extension of the vertex model where the interplay between membrane tension (i.e. myosin local density) and length is taken into account. We begin by introducing a simple dynamical system which allows us to understand the main features of such retroaction. We then extend our analysis on a larger scale system where such interplay seems to be responsible for global rearrangements. Other important factors, such as tension fluctuations, are also investigated.

Hydration of lower alcohols using theoretical methods

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Hydrophobic hydration is a hydration of small and large hydrophobic solutes and it is closely related to the hydrophobic effect. Hydrophobicity is an important driving force for biomolecular processes, e.g., self-assembly of amphiphiles into micelles and membranes, protein folding, ligand binding. It is established that it manifests itself differently on micro and macro length scales[1–3] .

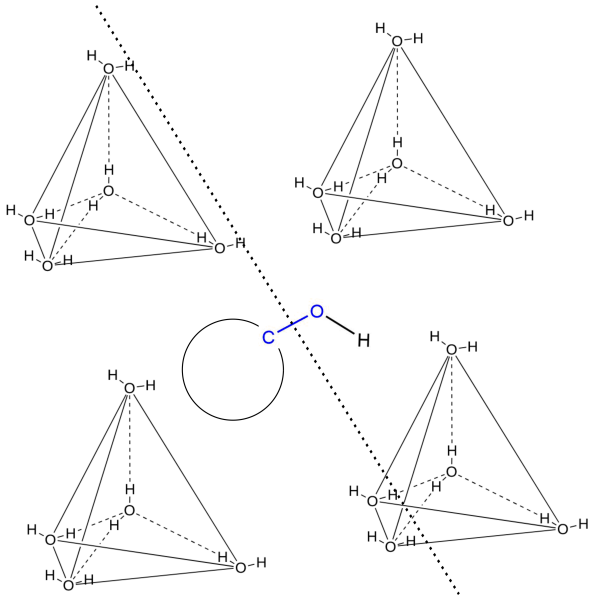

Figure 1: Structural ordering of water molecules around hydrophilic and hydrophobic parts of lower alcohols.

The traditional explanation of hydrophobicity, is that the ”ice-like” structures (i.e., ordering of water molecules) are formed near the hydrophobic solutes, arising from strengthened water hydrogen bonding[4,5].

The experimental evidence supported by the results extracted from the *ab initio* molecular dynamics simulations for the enhanced and more tetrahedrally oriented hydrogen bonds near small purely hydrophobic solutes (methane, ethane, krypton, and xenon) was given by Grdadolnik *et al.*[6]. There are structural changes in the arrangement of water molecules around the hydrophilic and hydrophobic parts of the alcohol, however, they are not very pronounced. In addition, structural changes are expected to be more pronounced in the

presence of larger hydrophobic surfaces of alcohols (e.g., *t*-butanol). In this work we tried to address the question regarding different structural ordering of water molecules around the hydrophilic and hydrophobic parts of lower alcohols (methanol, ethanol, propan-1-ol, and *t*-butanol) in very diluted solutions of alcohols and water (Figure 1). We found that water around hydrophobic parts of alcohols shows greater structural order compared to the water around hydrophilic parts.

References

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Collapsing pollen grains

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Pollen grains come in all sorts of shapes - they can be spherical, ellipsoidal, lobate, prismatic, polyhedral, and then, there are some which escape easy qualification in terms of geometry. The sizes also differ very much, from less than 10 micrometers (e.g. in Myosotis scorpioides or nontiscordardimè delle paludi, Vergissmeinnicht, močvirska spominčica, and močvarni nezaboravak, as we say in Italian, German, Slovenian and Croatian, respectively) to more than 100 micrometers (e.g. in Cucurbita pepo or zucchino, Gartenkürbis, buča, and tikva). Shapes and sizes of grains depend on the specie in question and they are often used to identify the plant, especially in the fossil records. Knowing that all life is related, it is tempting to search for evolutionary reasons for different shapes and sizes of pollen grains. It is also tempting to identify the elements of the "design" and relate them to the function which the pollen grain needs to fulfil. Pollen grains are reasonably elastic shells which contain and protect a sensitive interior - vegetative and generative cells, whose preservation is essential for fertilization. They need to function on a border of stability, i.e. need to be sufficiently strong to protect the interior, yet sufficiently labile to activate and release the interior once they reach a suitable environment. This happens once they land on a stigma of a flowering plant. In order to function properly, these shells need to conform to specific mechanical requirements. These include the resistance of shells to the effective pressure from the outside - the pollen grains crumple and deform upon desiccation. Yet, the crumpling (or buckling) is often not irregular and catastrophic, which is what the word usually suggests in the mechanical context. The inward buckling of the pollen grains proceeds often orderly and reversibly due to specific mechanical features of the grain design. A classical theory of shell elasticity can be profitably applied to learn more about such systems, as will be shown.

Untangled ring polymers in melts: The Physics of crumpling

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Unknotted and unconcatenated ring polymers in melt represent in many ways a puzzling subject in Polymer Science, as they challenge the theoretical schemes commonly accepted in the description of linear melts like screening of excluded volume effects and reptational dynamics. In this talk, I will describe the state-of-the-art of this fascinating topic: in particular, I will present recent results concerning an efficient numerical scheme to simulate large melts of rings, discuss its limitations and highlight possible generalizations for future work.

hicRED: A spectral method for comparing HiC-maps

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HiC assays provide genome-wide maps of chromatin interactions, allowing researchers to understand cell-type differentiation and disease emergence based on the 3D organization of the genome. An open issue is assessing the reproducibility of repeated experiments and finding significant differences between cell lines, a task made challenging by the presence of multiple length-scales patterns and by the noisiness of the matrices. Spectral methods exploit the innate hierarchy of the eigenspaces of HiC-maps to tackle the problem: here we show, by comparison with the spectral properties of random matrices, that only a subset of eigenspaces are robust, while the rest contain mainly noise. As a result we propose hicRED, the HiC Reduced Eigenspace Distance, a novel method in which data are compared after a single matrix spectral denoising procedure to classify experiments according to their cell lines and identify meaningful differences between them.

Coupling electrostatics and elasticity of virus capsids

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A major part of the interactions involved in the assembly and stability of small icosahedral viruses is electrostatic in nature, as can be inferred from the strong pH- and salt-dependence of their assembly phase diagrams. What is more, changes in environmental pH can induce morphological changes in empty shells of viruses that cannot be explained with a simple elastic model alone. I will present two models that combine the elasticity of thin icosahedral shells and the pH dependence of their protein charges. The first model couples the elastic parameters of the capsid to the electrostatic pressure acting on it. In this way, it is possible to develop a clear theoretical description of radial swelling in virus-like particles that delineates the importance of electrostatic contributions to swelling in the absence of any conformational changes. The second model takes explicitly into account the positions and magnitudes of protein charges and couples them with the thin-shell elastic model, predicting the equilibrium shapes of viral shells that depend on a single elastic parameter and the configuration of protein charges. I will show how the model can be applied to in vitro shell reconstructions of bacteriophage HK97 in order to elucidate how some reversible transitions between different procapsid states of HK97 are induced by pH changes.

Combining molecular dynamics simulations with SAXS experiments to characterize RNA conformational dynamics

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RNA molecules are highly dynamic systems. In order to exert their biological functions, they adopt a well-defined structural organization, which in turn allows establishing interactions with specific molecular partners.1 Characterizing the mechanistic rearrangements leading to peculiar tertiary structures is thus of central interest to understand RNA roles. Despite experimental techniques such as fluorescence spectroscopy and small-angle x-ray scattering (SAXS) are well suited to obtain structural insights, their outcome data are generated as time and ensemble averages and produce low resolution information. As such, interpreting them unambiguously is not always straightforward. Therefore, integrating the available data with an atomic-level outlook, as provided by molecular dynamics (MD) simulations, can be of striking support.

We explore such possibility for the GTPase-associated center (GAC), a 58-nucleotide RNA in the 23S ribosomal subunit, which must adopt a complex tertiary structure to associate with its ribosomal protein partner L11 and play its function in protein translation. Recent SAXS experiments reported on GAC structural flexibility in response to ions of different nature in the buffer solution,2 noticing in particular that Mg2+ can stabilize the folded state, while K+ favored less compact and more extended conformations. Using such experimental data as a reference, we performed MD simulations and predicted SAXS spectra from the sampled structures. Through this procedure, we thus aim at providing an atomic-level view of the conformations adopted by GAC along its folding pathway.

References

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Machine-learning experimental data for RNA structure prediction

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Chemical probing and co-evolutionary data potentially encode structural information for RNA molecules. We face the challenge of exploiting these data in the most efficient way for RNA structure prediction. As we look for models that best reproduce available experimental data without overfitting them, we consider machine-learning to be the most suitable framework for the required balance between optimality and transferability. In this framework we test two different approaches: discriminative and generative models. In both cases we find our way to improve the accuracy of RNA secondary structure predictions, ensuring transferability via a robust pipeline of model selection and validation procedures.

The kinetics of bovine serum albumine adsorption on calcium ohosphate and TiO_2 nanoparticles or nanotubes nanocomposites

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One of the largest health issue in modern society is increased frequency of hard tissues chronic diseases[1]. Often the only treatment of such diseases is implementation with the aim to regenerate damaged or diseased tissue. Considering that the main inorganic component of hard tissue is biological apatite[2], form of calcium phosphate (CaP), composite materials based on calcium phosphate and different inorganic nanomaterials attracts attentions as possible new and innovative implant materials. Among different nanomaterials, TiO_2 nanomaterials stand out because they can improve mechanical properties of CaP. Albumine is one of three soluble proteins which adsorbs on the surface of implant materials right after its implantation and affect their behavior in vivo[3]. But, its role in formation of calcium phosphates on titanium implants is still not clarified. Therefore, the aim of this study is to investigate the adsorption of bovine serum albumin (BSA) on nanocomposites of calcium phosphate (CaP) and TiO_2 nanoparticles (CaP/TiNP) or nanotubes (CaP/TiNT). In order to do that, the kinetics of BSA adsorption kinetics of BSA adsorption on TiO_2 nanoparticles (TiNP), titanate nanotubes (TiNT), calcium deficient hydoxiapatite (CaDHA) obtained in control system, CaP/TiNP and CaP/TiNT was measured on in situ in UV/VIS scanning spectrophotomer. Samples obtained after adsorption were filtered and given for further analysis which included Fourier-transform infrared apectroscopy (FTIR), powder x-ray diffraction (XRD) and scanning electron microscopy (SEM). The results of kinetics measurements were modeled using kinetics models of pseudo-first, pseudo-second rate and interparticle diffusion model. From the results of various kinetic models, the adsorption kinetics were found to follow pseudo-second-order rate kinetic model for CaP/TiNT nanocomposites, respectively pseudo-second-order rate and interparticle diffusion model for CaP/TiNP nanocomposites. Results obtained from FTIR, XRD and SEM analysis showed that albumin did not influence the composition and solid phase morphology.

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Protection of lipid membranes during oxidative stress using flavonoid embedded silica nanoparticles

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Mesoporous silica nanoparticles were synthesized and stabilized using polyethylene glycol. Characterization was carried out using various methods, including XRD, FE-SEM and AFM. Specific surface was determined using BET analysis and electrokinetic measurements were performed in order to elucidate properties of MSNs in liquid media. MSNs were loaded with structurally different flavonoids. It was shown that it is possible to efficiently load and release flavonoids with different physicochemical and structural properties.

Interaction with model membranes was investigated using AFM and the protective role of flavonoid was monitored before and after induced lipid peroxidation. Lipid peroxidation was induced by addition of hydrogen peroxide.

The nanomechanical properties of DOPC membranes after lipid peroxidation confirmed membrane damage, which was attenuated when using flavonoid loaded nanoparticles. By applying combination of experimental techniques, this work generated detailed knowledge about the effects of flavonoid loaded MSNs on the elasticity of model membranes, especially under oxidative stress conditions.

Measurement of the biomolecular interaction between plant lectin and peptidoglycan functionalized self-assembled hybrid bilayers by a quartz crystal microbalance

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Peptidoglycan is the major component of bacterial cell walls which is recognized by the innate immune system through a series of pattern recognition receptors (PRR), which play a key role in first-line defense of the body[1]. Lectins, naturally occurring carbohydrate-binding proteins, are involved in numerous biological processes and some of them act as PRR and bind significantly to PGN[2]. In this study we were primarily interested to test interaction of peptidoglycan monomer (PGM)[3], disaccharide pentapeptide isolated from B. divaricatum with model plant lectins, wheat germ agglutinin (WGA), by quartz crystal microbalance (QCM) method. In order to study interactions of PGM with lectins, lipophilic derivative, PGM-oleyl was synthesized and was used for preparation of the self-assembled hybrid bilayer membrane (HBM). It was demonstrated that PGM was effectively recognized by WGA and that strength of interactions depend on amount of PGM-oleil used for HBM preparation. The association konstant for the binding of WGA to PGM functionalized hybrid bilayers was determined.

The results showed that the established QCM method for measurement of molecular recognition between lectin and peptidoglycan functionalized HBM could be successfully employ in analyses of lectin-carbohydrate interactions, such as specificity, affinity and kinetics.

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Biological liquids under tension

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Numerous biological systems contain metastable liquids at considerable negative pressures. As a prominent example, plants use negative pressures to suck water from the soil into their leaves. A long-debated mystery is why the maximal negative pressures are approximately -100 bar. An ubiquitous ingredient of biological liquids are lipids. Combining atomistic simulations and kinetic modeling, we show that lipid bilayers lead to cavitation at negative pressures of about -100 bar over time scales of hours to days, whereas water with added salt or nonpolar gas stay stable over many years. Our findings show that the presence of lipid aggregates imposes an upper limit for the magnitude of negative pressure and with that restricts the height up to which trees can grow.

Orientational ordering of point dipoles on a sphere

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Distribution of interacting particles on a sphere is historically a well known problem, however, ordering of systems on a sphere with anisotropic interaction, such as the dipole dipole interaction, has remained unexplored. We solve orientational ordering of point dipoles on a sphere with fixed positional order by numerically minimizing the system energy and analyze stable configurations depending on their symmetry and degree of ordering. We find macrovortex ground states with various rotational symmetries for different system sizes while excited states also show other configurations. We explore system response in external field both for the fixed sphere as well as for the freely-rotating sphere and study the orientational phase transitions that emerge with increasing field amplitude. For the case of freely rotating sphere, we also observe the change of configuration symmetry for certain states at higher field amplitudes.

Active elastic networks as models of biological tissues

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Epithelial monolayers usually appear close to 100% confluency and yet their constituent cells are often able to exchange neighbors and travel across tissue-scale distances. This is enabled by active processes at the cell-cortex level, which act as local energy sources to drive cells over the energy barriers for rearrangement. Using a two-dimensional vertex model of polygonal cells, we study the transition from a solid-like to a fluid-like behavior of tissues with a stochastic turnover dynamics of molecular motors at cell-cell junctions. We show that the diffusion coefficient of cell movements becomes finite at a critical value of tension fluctuations. While this critical value depends on the persistence time of molecular motors, the diffusion coefficient surprisingly collapses when plotted against the average cell-shape index. This results suggests that the degree of cell movements can be measured from static images of tissues with no need for cell tracking. To better understand the cell-rearrangement dynamics under tension fluctuations, we also develop a simple Markov-chain model and discuss a new machine-learning-based approach. Here, the algorithm, previously trained on the vertex model, can efficiently mimic the vertex-model dynamics with no need of explicit force calculations and solving the system of differential equations.

Morphologies of vesicle doublets: Competition among surface tension, bending elasticity, and adhesion

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We experimentally investigate the morphology of doublets of giant unilamellar vesicles suspended in a salt solution which controls the strength of intermembrane adhesion. Using a hot stage, we explore the transformation of doublets from the spherical-cap shapes to either prolate doubles or to doublets with a spherical external shape and a sigmoidal contact zone seen in the weak- and strong-adhesion regime, respectively. The observations are interpreted using the standard theory of vesicle elasticity generalized so as to allow for two distinct surface tensions, and the shapes obtained numerically using the Surface Evolver package agree rather well with the experimental images. The best-fit adhesion strengths agree well with the theoretical predictions including the van der Waals attraction as well as the undulation and screened electrostatic repulsion.

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