November 13, 2026

Ruđer Bošković Institute
Zagreb



2nd MEETING OF YOUNG BIOPHYSICISTS

PROGRAMME AND BOOK OF ABSTRACTS

Croatian Biophysical Society

2nd Meeting of Young Biophysicists

November 13, 2026
Ruđer Bošković Institute
Zagreb, Croatia

PROGRAMME
&
BOOK OF ABSTRACTS

Croatian Biophysical Society

Organizing Committee

Anja Sadžak, Kristina Serec.

Scientific Committee

Ida Delač, Nadica Ivošević DeNardis, Piotr Nowakowski, Marija Raguž.

Editors

Anja Sadžak, Kristina Serec.

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Preface

It is our great pleasure to welcome all participants to the **2nd Meeting of Young Biophysicists**, held on November 13, 2026, at the Ruđer Bošković Institute in Zagreb, Croatia. The meeting continues the initiative launched in 2025 and provides a focused, one-day forum for young researchers to present and discuss their work in a friendly and encouraging scientific atmosphere.

This year's programme brings together research in molecular, membrane, cell, computational, and applied biophysics. It includes an invited lecture by Dunja Šimičić and 17 contributed oral presentations. The programme is organized into four sessions, with two equally sized Computational Biophysics sessions to support focused discussion.

We thank all young presenters and biophysicists featured in the programme, as well as the moderators, sponsors, and supporting institutions, for contributing to the success of the meeting and to the continued growth of the young biophysics community.

Editors

PROGRAMME

08:30	**Registration**
09:00-09:15	**Opening & Welcome Remarks** **Anja Sadžak & Kristina Serec, Organizing Committee** **David M Smith, Director of the Ruđer Bošković Institute** **Nadica Ivošević DeNardis, President of the Croatian Biophysical Society**
09:15	**Invited lecture** **Dunja Šimičić, University of Zagreb School of Medicine, Johns Hopkins University School of Medicine, Baltimore, MD, USA** Magnetic resonance spectroscopy and its applications in brain tumor research
Molecular, Membrane & Cell Biophysics **Chairs: Marija Raguž & Anja Sadžak**	
09:45	**Lucija Brtan, University of Zagreb, Faculty of Science** Complementary biophysical approaches to thermal characterisation of PLA-active polyesterases
10:00	**Andrej Nikolić, Faculty of Biotechnology and Drug Development, University of Rijeka** Porphyrins as intrinsic probes of structure and self-association in conjugates of antimicrobial peptides
10:15	**Mateo Šerić, University of Split School of Medicine** Investigating buffer effects on electroformation of giant unilamellar vesicles from damp lipid films
10:30	**Vedrana Krajnović, Ruđer Bošković Institute** Elucidation of macroscopic and molecular properties of model Gram-positive and Gram-negative bacterial membranes using biophysical techniques
10:45	**Filip Putak, Ruđer Bošković Institute** Salinity and growth phase-dependent morphology of microalgae probed by AFM
11:00	**Dorijan Vulić, Ruđer Bošković Institute** A unified mechanochemical framework for amoeboid cell locomotion
11:15	**Coffee break**

Computational Biophysics I Chair: Piotr Nowakowski	
11:45	**Eva Knežević, University of Split, Faculty of Science** Stochastic modeling of chromosome segregation in fission yeast
12:00	**Maja Milas, Ruđer Bošković Institute** Rethinking cancer therapy on a computer: the role of cell mechanics in adaptive therapy
12:15	**Petra Grubišić, Institute of Physics / University of Zagreb, Faculty of Science** Fitting experimental CW-EPR spectra using EasySpin
Computational Biophysics II Chair: Kristina Serec	
12:30	**Mario Jurada, University of Zagreb, Faculty of Science** CG modelling of the *E. coli* cell envelope: from membrane construction to electroporation
12:45	**Boris Gomaz, University of Zagreb, Faculty of Science** Atomistic modelling of the *E. coli* cell envelope and DNA interactions with the outer membrane
13:00	**Matej Kožić, University of Zagreb, Faculty of Science** Spontaneous formation of a DNA-bilayer complex stabilizes an electroporation-induced membrane pore
13:15	**Lunch Break + Group Photo**
Applied Biophysics Chair: Ida Delač & Kristina Serec	
14:15	**Katarina Carmen Tomašić, University of Zagreb School of Medicine** X-ray fluoroscopy in interventional cardiology: radiation exposure and potential biological effects
14:30	**Andrea Christina Odermatt & Neva Crnković Hahn, University of Zagreb School of Medicine** Investigating the biological effects of ionizing radiation in blood
14:45	**Lukas Levanić, University of Zagreb, Faculty of Science** Laser-induced graphene for bioelectronic applications
15:00	**Karla Filipović, University of Zagreb, Faculty of Science** Adhesive-free sealing of glass lab-on-chip devices for neuronal connectivity studies using femtosecond laser welding
15:15	**Rea Boban, University of Zagreb, Faculty of Science** Towards integration of biomolecular motors with 2D solid-state nanopores
15:30	**Best Talk Awards & Meeting Closure Anja Sadžak & Kristina Serec**

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ORAL PRESENTATIONS

Magnetic resonance spectroscopy and its applications in brain tumor research

Dunja Šimičić[1,2*]

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Wad Magnetic Resonance Spectroscopy (MRS) is a unique technique that combines the ability of nuclear magnetic resonance (NMR) to differentiate molecules and imaging features of localization characteristic for magnetic resonance imaging (MRI) [1]. This gives us a unique opportunity to gain molecular insight and study tissue metabolism in vivo in physiologic or disease processes. With MRS we can detect and quantify multiple metabolites in tissue, including up to 18 metabolites in the brain, such as neurotransmitters, antioxidants, and markers of cellular proliferation. Because MRS does not require contrast agents or involve ionizing radiation, it is particularly well suited for monitoring metabolism in disease. Therefore, MRS has long been used in brain tumor research to characterize tumor metabolism, help distinguish between tumor types and grades, and provide insights into tumor aggressiveness [1].

More recently, MRS has gained an increasingly important role in the characterization of diffuse gliomas, the most common primary brain tumors in adults. The latest WHO classification of brain tumors incorporates genetic features such as mutations in the isocitrate dehydrogenase (IDH) genes and 1p/19q codeletion. These genetic alterations are associated with distinct metabolic changes. In particular, IDH mutations lead to the accumulation of D-2-hydroxyglutarate (2HG), while elevated cystathionine has been reported in gliomas with 1p/19q codeletion. Both metabolites can be detected using MRS, providing a non-invasive way of assessment [2]. Furthermore, the identification of these genetic characteristics has opened new avenues for targeted therapies, making metabolic characterization and treatment monitoring with MRS increasingly relevant in clinical practice.

Keywords: Magnetic Resonance Imaging (MRI), Magnetic Resonance Spectroscopy (MRS), Glioma, Tumor, Therapy

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Invited lecture

Complementary biophysical approaches to thermal characterisation of PLA-active polyesterases

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Thermal stability is a key parameter in the characterisation of enzymes intended for polymer-degrading applications, yet the apparent melting temperature can depend strongly on the experimental method and the physical property being monitored. Here, we compared complementary approaches for characterising the thermal behaviour of a set of PLA-active polyesterases with distinct stability profiles. Preliminary dye-based differential scanning fluorimetry using SYPRO Orange was limited by elevated baseline fluorescence, which complicated assignment of unfolding transitions for several protein preparations. Intrinsic-fluorescence nanoDSF therefore provided the primary comparative readout and resolved pronounced differences between proteins, with selected high-temperature transitions ranging from approximately 68 °C to 86 °C. Importantly, several preparations displayed multiple thermal features, indicating that a single transition temperature does not fully describe their unfolding behaviour. Nano-differential scanning calorimetry provided complementary calorimetric information, whereas temperature-resolved dynamic light scattering revealed concurrent changes in hydrodynamic behaviour. Thermal pre-incubation followed by activity measurements further distinguished structural transitions from functional persistence. Together, these results demonstrate that thermal characterisation of polyesterases benefits from combining orthogonal biophysical and functional measurements and caution against interpreting a single method-derived transition as an absolute measure of protein thermal stability.

Keywords: protein thermal stability; nanoDSF; differential scanning fluorimetry; nanoDSC; dynamic light scattering

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This work was funded by the European Union – NextGenerationEU through the project "Enzyme Engineering for Sustainable Recycling of Bioplastics" (NPOO.C3.2.R2-I1.06.0041) and HrZZ project "A Modular Loop Grafting Strategy for Enzyme Engineering".

Porphyrins as intrinsic probes of structure and self-association in conjugates of antimicrobial peptides

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Conjugating porphyrins to peptides to form peptide–porphyrin conjugates (PPCs) offers an attractive way to combine peptide's bioactivity with the porphyrins' light-activated photodynamic activity, light-independent membrane partitioning and potential protection against proteolysis [1]. Given the importance of peptide's secondary structure on its function, the question is how attaching a bulky, hydrophobic macrocycle will affect peptide's structure and activity. Here, we conjugated four antimicrobial peptide sequences to two porphyrin derivatives and used the porphyrin itself as intrinsic reporter of conjugate structure.

In two-dimensional nuclear magnetic resonance (NMR) spectroscopy, porphyrin-induced ring-current effects produced distance-dependent proton chemical-shift perturbations that mapped peptide–macrocycle proximity [2]. In near-UV circular dichroism (CD), the Soret-region signal reported on the macrocycle's chiral environment and its supramolecular association. Complementing this, far-UV CD revealed environment-dependent conformational changes, with sodium dodecyl sulfate (SDS) micelles, an anionic membrane mimetic, promoting increased peptide α-helicity. All-atom molecular dynamics simulations and well-tempered metadynamics gave molecular-level insight into the conformational preferences, and into the porphyrin-driven self-association, underlying these observations.

Together, these results show a role for porphyrins beyond that of a functional appendage: their intrinsic optical and magnetic properties offer a possible window for better elucidation of the PPCs' structural organization and its relationships with their biological activity.

Keywords: peptide–porphyrin conjugates, CD, NMR ring-current effect, molecular dynamics

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Investigating buffer effects on electroformation of giant unilamellar vesicles from damp lipid films

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Giant unilamellar vesicles (GUVs) are widely used as model systems for studying biological membranes. Electroformation is a commonly used technique for GUV production; however, their formation under physiologically relevant conditions remains challenging due to the influence of buffer composition.[1] In addition, incorporating high cholesterol (Chol) concentrations into lipid bilayers can also be problematic with conventional dry-film electroformation. During film preparation, Chol can crystallize, potentially reducing its incorporation into the vesicles. This effect is known as the Chol demixing artefact.[2] These limitations highlight the need to optimize preparation protocols and better understand the factors affecting GUV formation.

In this study, we investigated the influence of buffer physicochemical properties on GUV electroformation using a modified protocol based on damp lipid films, which helps overcome the limitations associated with Chol demixing.[2] The Chol-to-1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (POPC) molar ratio in the lipid mixtures ranged from 0 to 2. We compared four buffers at pH 7, each supplemented with different salts, to assess their effects on vesicle yield and size distribution. Besides, we adjusted the buffer conductivity to a common value to further investigate the influence of buffer physicochemical properties on GUV electroformation. GUV yield and size were evaluated using fluorescence microscopy, providing insight into the suitability of different buffer systems for preparing Chol-containing GUVs under physiologically relevant conditions.

Keywords: electroformation, cholesterol, buffers, salts, physiological

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Elucidation of macroscopic and molecular properties of model Gram-positive and Gram-negative bacterial membranes using biophysical techniques

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Understanding the biophysical properties of bacterial membranes is an important step toward elucidating mechanisms of action and advancement of antimicrobial peptides with improved membrane-targeting activity [1]. In this study, model membranes representing Gram-positive *Streptococcus pneumoniae* and the outer membrane of Gram-negative *Escherichia coli* K-12 were prepared from 16:0 phosphatidylethanolamine (DPPE), 16:0 phosphatidylglycerol (DPPG) and 16:0 cardiolipin (CL) at ratios 50:50 for DPPG/CL and 75:20:5 for DPPE/DPPG/CL, respectively [2]. The prepared membranes were characterized by calorimetric and spectroscopic techniques (Figure 1), and the mosaic of their responses reflects the specific characteristics of each membrane model at the molecular and macroscopic levels.

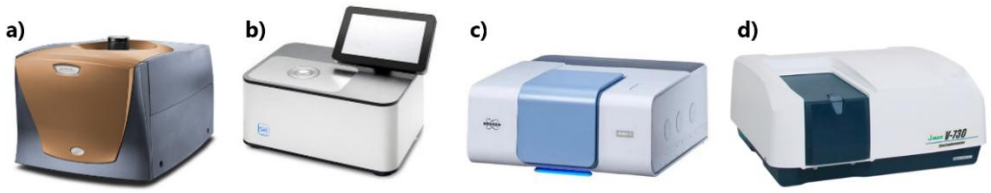


Figure 1. a) Differential scanning calorimeter; b) Refractometer; c) FTIR spectrometer; d) UV-Vis spectrophotometer

Keywords: Model bacterial membranes; Biophysical characterization

ACKNOWLEDGMENTS

This work was supported by HRZZ grant UIP-2020-02-7669 and NPOO.C3.2.R3-I1.05

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Salinity and growth phase-dependent morphology of microalgae probed by AFM

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Atomic force microscopy (AFM) is a scanning probe microscopy technique that images a surface by sensing the forces between a sharp tip and the sample. Not limited by light diffraction, AFM achieves nanometer lateral and sub-nanometer vertical resolution without requiring staining, coating or vacuum, and operates in air or liquid. Its three-dimensional topographic images allow quantification of single-cell morphological parameters. For flagellated microalgae, however, such imaging remained challenging because of their pronounced motility until cell immobilization protocols were developed about a decade ago.

This study aimed to characterize the nanoscale morphology of the halotolerant microalga *Dunaliella tertiolecta* acclimated to elevated salinities relevant to salt ponds. As D. tertiolecta lacks a rigid cell wall, its morphology is highly sensitive to osmotic conditions. Cells were cultivated at two salinities (40 and 80 ppt) and examined in two growth phases (exponential and stationary) in parallel by AFM in air and confocal microscopy. Confocal imaging showed that cells remained viable, retaining their shape, flagella and autofluorescence. AFM, however, showed that exponential-phase cells at 80 ppt, unlike those at 40 ppt, did not retain their shape, indicating the need for an adapted sample preparation protocol. In the stationary phase, cells at 80 ppt preserved their shape, consistent with osmoregulatory mechanisms that stabilize cells over time. The obtained morphological parameters will be discussed in the context of salinity acclimation, providing quantitative nanoscale insight into single microalgal cells.

Keywords: atomic force microscopy, microalgae, *Dunaliella tertiolecta*, sample preparation, osmotic stress

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The research study was supported by the project titled 'Risk Management and Improvement of Salt Production at Solana Pag', funded by the European Regional Development Fund; Competitiveness and Cohesion Programme 2021–2027, Call IRI-S3.

A unified mechanochemical framework for amoeboid cell locomotion

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Cell migration underlies the survival and function of unicellular and multicellular organisms. Eukaryotic crawling arises from cyclic cytoskeletal protrusion and retraction regulated by reaction-diffusion (RD) dynamics of Rho GTPases and GTPase-activating proteins (GAP) between cytosol and cortex. These dynamics generate membrane patterning and front-rear polarity through coupled biochemical signaling and mechanical feedback. Interacting across multiple time and length scales, these subsystems produce the broad phase space of motility modes, cell shapes, and membrane patterns that are observed experimentally. No theoretical model has captured this diversity within a single framework.

We develop a cross-scale mean-field model integrating RD signaling with cytosolic and cortical hydrodynamics to describe shape evolution and emergent locomotion. Small parameter variations reproduce diverse experimentally observed phenotypes. Phase-space analysis shows that coupling to cytosolic flow and spatially varying surface tension is required to recover the full spectrum of motility modes, providing a theoretical basis for amoeboid migration. We validate the model against experiments on starved *Dictyostelium discoideum*, with motility patterns, cell shapes, and membrane Rho activator distributions measured simultaneously. By tuning Rho and GAP concentrations, the model reproduces all observed motility classes: RD-dominated cells with minimal movement; persistent trajectories driven by cytosolic flow and contractility; asymmetry-induced circling; alternating runners with intermittent loss of polarity; and run-and-turn cells where noise drives polarity vector wagging. The formulation suits amoeboid motility dominated by actin polymerization and surface-tension mechanics.

Keywords: amoeboid motility; reaction-diffusion; Rho GTPase signalling; cell hydrodynamics

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Stochastic modeling of chromosome segregation in fission yeast

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The stochastic dynamics of chromosome segregation in the mitotic spindle of fission yeast were investigated using a quantitative model of kinetochore–microtubule interactions. A previously developed one-dimensional mechanical model coupling spindle forces with stochastic attachment and detachment kinetics [1,2] was implemented and analyzed through numerical simulations. Key model parameters, including the kinetochore biorientation parameter and the Aurora B-like error-correction mechanism, were systematically explored to identify parameter values that best reproduced experimental observations. The influence of different initial kinetochore–microtubule attachment configurations on error correction during mitosis was then investigated, including the response to Aurora B inhibition. The results showed that merotelic attachments were not generated in simulations starting from configurations in which they were absent. Furthermore, only initial configurations containing merotelic attachments reproduced the experimentally observed response to Aurora B inhibition, suggesting that additional mechanisms may be required to account for the generation of merotelic attachments during mitosis.

Keywords: mitosis, stochastic simulations, error correction, initial attachments

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This research was conducted within the Tournier–Gachet team at the Cell-cycle, cell dynamics and mechanics Unit of CBI, CNRS.

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Rethinking cancer therapy on a computer: the role of cell mechanics in adaptive therapy

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Cancer treatments targeting proliferation pathways often show excellent early responses. However, under continuous treatment pressure, cancer cells mutate and become drug-resistant, causing uncontrolled growth and therapy failure. Adaptive therapy modulates this pressure by reducing drug exposure and maintaining competition between drug-susceptible and resistant populations, yet resistance remains inevitable. We hypothesize that adaptive therapy can also control resistant growth by optimizing the mechanical pressure from drug-susceptible cells competing for shared resources. Cancer is then not eradicated, but its expansion is slowed or arrested. Yet the underlying biomechanics and suitable adaptive protocols remain insufficiently explored.

We establish a dissipative particle dynamics framework for large-scale exploration and quantitative evaluation of treatment schedules. Proliferation and death are regulated by cell area and local mechanical stress, capturing single-cell mechanics within a spatially resolved tissue. Our results identify crowding and stress-regulated proliferation as key determinants of resistant takeover.

We validate the framework against experiments on melanoma monolayers, combining long-term single-cell tracking with systematic testing of adaptive protocols. Resistant colonies remain growth-restricted under crowding but expand once therapy-induced cell loss creates low-density regions that relieve confinement.

We demonstrate that crowding by drug-susceptible cells regulates stress in the proliferative phase of resistant tissue, prolonging this phase, reducing single-cell proliferation rates and slowing tissue growth. This moves adaptive therapy beyond well-mixed models towards a mechanics-based framework coupling growth to local stress, enabling more reliable predictions of therapy outcomes. Extending the platform to mutations, nutrient gradients, or metastatic spread can enable more faithful modeling of in vivo melanoma evolution.

Keywords: adaptive therapy, melanoma, agent-based simulations, tissue mechanics

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Fitting experimental CW-EPR spectra using EasySpin

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This presentation focuses on fitting experimental electron paramagnetic resonance (EPR) spectra using EasySpin, a MATLAB toolbox for EPR spectroscopy. It begins with a brief introduction to the fundamentals of EPR, explaining the physical principles behind the technique and the information it provides. The basic operation of a continuous-wave EPR (CW-EPR) spectrometer will then be presented, along with key experimental parameters and an introduction to WinEPR SimFonia, a software tool for spectral simulation. The main part of the presentation focuses on EasySpin and its functions for simulating and fitting experimental EPR spectra. The experimental data and spin-system parameters required for simulations will be discussed, followed by an overview of three main simulation functions: garlic, used for isotropic systems undergoing fast molecular motion; chili, used for systems in the slow-motion regime; and pepper, used for solid-state and powder spectra. The influence of selected parameters on the simulated spectra will also be demonstrated. Finally, the fitting procedure will be explained step by step, illustrating how simulated spectra can be adjusted to reproduce experimental data and improve the understanding of the underlying spin system.

Keywords: Electron paramagnetic resonance (EPR), EasySpin, spectral fitting, spectral simulation

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CG modelling of the *E. coli* cell envelope: from membrane construction to electroporation

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The Gram-negative cell envelope is a complex, multilayered structure that mediates interactions between the cell and its environment. To complement existing atomistic simulations, we are developing a Coarse-grained (CG) model of the Escherichia coli cell envelope, comprising the inner membrane (IM), peptidoglycan layer (PG), and outer membrane (OM). Simulations were performed using GROMACS and the MARTINI 3.0 force field. The model integrates literature-based representations of individual envelope components (IM [1], PG [2], OM [2]). In addition to model development, electric-field-driven simulations were conducted to investigate the responses of the IM and OM to electrical stress. These findings will inform the further evaluation of individual membrane models and the selection of simulation conditions for subsequent studies. The resulting framework aims to enable the investigation of the structural and dynamical properties of the bacterial cell envelope over extended molecular dynamics timescales.

Keywords: E. coli; Electroporation; Molecular Dynamics, Coarse-grain

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Atomistic modelling of the *E. coli* cell envelope and DNA interactions with the outer membrane

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The Gram-negative bacterial cell envelope comprises the inner membrane, a peptidoglycan network, and an asymmetric outer membrane. Its heterogeneous composition and layered architecture present substantial challenges for atomistic modelling. [1] An atomistic molecular dynamics workflow is presented for constructing an *Escherichia coli* cell envelope model. The model combines a heterogeneous phospholipid inner membrane, an asymmetric outer membrane containing lipopolysaccharides, and a peptidoglycan network positioned between them. The outer membrane is subsequently used to investigate electroporation [2] and DNA–membrane interactions. Initial observations show DNA adsorption onto the membrane surface, followed by entry into an electrically induced pore and gradual movement towards the inner side of the membrane as the pore narrows. These models provide a basis for further investigation of bacterial membrane permeability and DNA–membrane interactions during electroporation.

Keywords: Molecular dynamics; Outer membrane; Electroporation; DNA

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Spontaneous formation of a DNA-bilayer complex stabilizes an electroporation-induced membrane pore

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Recent advances in realistic *E. coli* inner membrane models, such as an "Avanti" [1] membrane, combined with modern force fields [2], have enabled the investigation of DNA–membrane interactions at the molecular level using molecular dynamics simulations. This study focuses on the formation and stability of DNA–membrane complexes, examining the role of cations in modulating DNA adsorption and membrane organization. The results reveal differences between calcium and magnesium ions and their role in DNA-bilayer complexes, and molecular dynamics simulations of electroporation provide insights into the interaction between DNA and membrane pores. The results suggest that DNA can act as a plug within a pore, with the formed DNA-bilayer complex stabilizing the pore and interfering with its healing. The obtained results are discussed in the context of mechanisms proposed in the literature, providing further insight into the molecular interactions governing DNA–membrane complex formation and its potential role in bacterial transformation.

Keywords: Molecular dynamics; lipid bilayer; DNA-membrane complex; electroporation

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X-ray fluoroscopy in interventional cardiology: radiation exposure and potential biological effects

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Fluoroscopy is an X-ray imaging technique widely used in interventional cardiology to provide real-time visualization of catheters and other medical instruments during cardiac procedures. One of its important applications is pulmonary vein isolation (PVI), a catheter-based procedure used to treat atrial fibrillation. Although technological advances have significantly reduced radiation exposure during these interventions, patients may still receive varying doses of ionizing radiation depending on the procedure, imaging protocols, and ablation technique [1].

This presentation will introduce the basic physical principles of fluoroscopy, the typical X-ray energies used in clinical practice, and the main dosimetric quantities used to characterize radiation exposure. Particular attention will be given to differences in radiation exposure associated with various PVI techniques, including radiofrequency ablation, cryoablation, and pulsed-field ablation. The potential biological effects of low-dose ionizing radiation will also be discussed, emphasizing the importance of investigating molecular changes that may occur following clinical exposure.

Finally, the presentation will introduce an ongoing research project investigating radiation-associated molecular changes in blood and blood plasma collected from patients undergoing PVI procedures.

Keywords: Fluoroscopy, ionizing radiation, pulmonary vein isolation, radiation dose, biological effects

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Investigating the biological effects of ionizing radiation in blood

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Fourier-transform infrared (FTIR) spectroscopy is an analytical technique that provides information about the molecular composition and structure of biological samples through their characteristic vibrational spectra. Its sensitivity to changes in proteins, lipids, nucleic acids, and other biomolecules makes it a promising tool for investigating radiation-induced molecular alterations [1]. In recent years, vibrational spectroscopy has attracted increasing attention in radiobiological research, particularly for detecting molecular responses to ionizing radiation [1,2].

The presentation will introduce the application of FTIR spectroscopy in an ongoing clinical study investigating molecular changes in blood collected before and after fluoroscopy-guided cardiac interventions. Particular attention will be given to sample preparation, the identification of characteristic infrared absorption bands, and the interpretation of spectral features associated with major biomolecular components. The potential of vibrational spectroscopy to detect radiation-associated molecular changes will be discussed based on previous studies [1,2].

Keywords: Fluoroscopy, ionizing radiation, pulmonary vein isolation, radiation dose, biological effects

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Laser-induced graphene for bioelectronic applications

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Laser-induced graphene (LIG), a porous graphitic material formed by direct laser conversion of polyimide [1], is attractive for flexible bioelectronics because a single maskless step defines both electrode geometry and conductivity. We fabricated LIG electrodes on 25 µm Kapton film with a desktop nanosecond Q-switched UV laser (355 nm, galvanometric scanner, f-theta lens) and characterised them by resistance measurements, electrochemical impedance spectroscopy (EIS) in 0.1 M KCl and Raman spectroscopy. Scan-field position proved as important as writing parameters: with a focused beam, the sheet resistance of nominally identical electrodes varied with position from about 160 Ω/□ to 3.8 kΩ/□, whereas a 3.2 mm defocus gave lower and more uniform values (42–70 Ω/□). EIS showed nearly ideal capacitive behaviour; the series resistance dropped sharply between power settings of 33 % and 38 % and was lowest near 43 %. Raman D, G and 2D bands indicate a nanocrystalline graphitic material (crystallite size of order 12–26 nm). With increasing power, the G and 2D bands narrow and the 2D-to-G area ratio rises from 0.17 to 1.03; the most ordered sample (48 %) approaches values reported for high-quality UV-laser LIG [2]. Since maximum structural order and minimum series resistance do not coincide, Raman spectra alone cannot rank electrode quality. A widely available desktop UV laser can thus produce LIG electrodes suitable for bioelectronic research, provided the laser beam parameters are well known and the scan-field is position controlled.

Keywords: laser-induced graphene, polyimide, UV laser, electrochemical impedance spectroscopy, Raman spectroscopy, bioelectronics

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Adhesive-free sealing of glass lab-on-chip devices for neuronal connectivity studies using femtosecond laser welding

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Studying how neuronal networks form in vitro requires devices in which organoids can survive, mature and extend axons, while remaining compatible with high-resolution optical imaging [1]. We image using an inverted confocal microscope, which views samples through the device bottom and thus requires very thin transparent materials. Glass lab-on-chip (LOC) devices are well suited, but thin glass is difficult to process and seal: it is brittle and conventional bonding often relies on adhesives or chemicals that may compromise biocompatibility.

We fabricate glass LOC devices by femtosecond laser micromachining, with minimal chemical use and without photolithography or cleanroom facilities. Here we focus on femtosecond laser welding, the step that encapsulates the device [2]. Thin fused silica substrates (200–500 µm) are particularly susceptible to cracking, and welding of two fused silica slides of this thickness with crack-free seams has, to our knowledge, rarely been reported. By tuning pulse energy, repetition rate, numerical aperture, scanning speed and focus position relative to the glass interface, we identified a parameter window that produces adhesive-free, crack-free welding seams. The modification is confined to the bulk of the glass, leaving the surfaces unaltered which is important for imaging.

The result is a transparent device with two wells connected by microchannels that act as a size-selective sieve: axons grow through, while larger cell bodies stay in the wells. Next steps include organoid culture in the devices and integration of organic photocapacitors for wireless optical stimulation [3].

Keywords: femtosecond laser welding; lab-on-chip; neuronal organoids; glass micromachining

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Towards integration of biomolecular motors with 2D solid-state nanopores

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Development of hybrid nanomaterials for nano-bio interfaces is of great interest for applications ranging from (bio)sensors and molecular transport platforms to neural interfaces. Among the most promising solid-state materials are two-dimensional (2D) transition metal dichalcogenides (TMDs), for their exceptional optoelectronic and mechanical properties, as well as their atomic thickness. One particularly interesting application of TMDs is their use in solid-state nanopores for single-molecule sensing and sequencing of DNA [1]. A notable challenge in these experiments is the high speed of DNA translocation through the nanopore, which limits measurement resolution. One potential solution, which has been demonstrated to be successful for biological nanopores, is the integration of motor enzymes, such as helicases [2], to control the speed of translocation.

As an important step towards this goal, we aim to study the interaction of Hel308 helicase with the surface of a 2D material, specifically molybdenum disulfide, MoS_2. Here we show our preliminary results using two surface-sensitive techniques: atomic force microscopy (AFM) and quartz crystal microbalance with dissipation monitoring (QCM-D). QCM-D is a label-free technique that probes interfaces with shear acoustic waves, complementing the information obtained from other surface characterization techniques [3].

Understanding interactions between 2D materials and biological systems is a key step towards integration of biomolecular motors with 2D solid state nanopores and, ultimately, developing functional nano-bio hybrid interfaces.

Keywords: nano-bio interfaces, 2D materials, nanopores, helicase, QCM-D

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