BP 14: Poster IIa

Bacterial Biophysics, Tissue Mechanics.

Time: Tuesday 18:00–20:30 Location: Poster E

BP 14.1 Tue 18:00 Poster E

Microfluidic Separation of Viable and Non-viable *Legionella* Cells by a Quantifiable Dielectrophoresis Approach — •Madeline Altmann[1], Anders Henriksson[1], Peter Neubauer[1], and Mario Birkholz[2] — [1]Laboratory of Bioprocess Engineering, Department of Biotechnology, Technische Universität Berlin, Ackerstr. 76, ACK24, D-13355 Berlin, Germany — [2]IHP Leibniz-Institut für Innovative Mikroelektronik, Im Technologiepark 25, 15236 Frankfurt (Oder), Germany

Traditional pathogen detection methods, notably PCR, often fail to distinguish viable and non-viable cells. This distinction is crucial as non-viable cells hold limited pathogenic potential. To overcome this limitation, analytical methods must be able to separate between viable from non-viable cells. Dielectrophoresis (DEP) can non-invasively separate cells according to viability, allowing for increased accuracy in subsequent bioanalytic workflows. This study focuses on employing positive dielectrophoresis in a microfluidic system to separate viable *Legionella parisiensis* cells from non-viable cells rendered inactive via heat shock to refine the specificity of biosensors. Although separation in realistic inactivation conditions was difficult, discrimination of viable cells was achieved by a video-based, quantifiable DEP method, that evaluates the percentage of fluorescent cells in a region of interest around the electrodes. It was found that long heat shock inactivation times decrease the positive DEP-effect at higher frequencies, enabling a separation of viable *Legionella* above 25 MHz and 10 Vpp in both tap water and demineralized water.

BP 14.2 Tue 18:00 Poster E

Improving Sensitivity of Micro-Ring Resonators for Photonic Biosensors — •Philipp Schrenk[1], Anders Henriksson[1], Christopher Borgmeier[1], Peter Neubauer[1], and Mario Birkholz[2] — [1]Department of Bioprocess Engineering, Institute of Biotechnology, Technical University Berlin, Ackerstr. 76, ACK24, D-13355 Berlin, Germany — [2]IHP GmbH, Im Technologiepark 25, 15236 Frankfurt (Oder), Germany

Silicon-based photonic biosensors represent a promising approach for the detection of various pathogens. Utilizing micro-ring resonator chips, assisted by dielectrophoresis and specific antibody coatings, enables label-free detection of a sample, such as Legionella pneumophila, already at concentrations below the limit value of 100 CFU/100 ml. In contrast to conventional methods for detecting Legionella cells, photonic biosensors are cost-efficient, have a small footprint of a few mm2, and notably, possess the capability to deliver real-time results. The measuring principle of photonic biosensors relies on the evanescent field and variations of the refractive index n associated with the sample adjacent to the waveguide. In this study, the sensitivities of five different micro-ring resonators were analyzed by employing solutions with varying NaCl concentrations. These solutions induce differences in n measured in refractive index units (RIU) and consequently affect the evanescent field. By variation of the chip architecture, the sensitivities could be increased from 3.6 up to 23.5 nm/RIU. These findings are crucial for further quantitative investigations in detecting Legionella pneumophila cells.

BP 14.3 Tue 18:00 Poster E

Drug interactions between antibiotics targeting translation and transcription — •Natawan Gadjisade and Tobias Bollenbach — University of Cologne, Institute for Biological Physics, Germany

Combining antibiotics has the potential to improve treatment efficacy and slow the evolution of resistance. When two antibiotics are combined, their effect on bacterial growth may be stronger or weaker than expected (i.e., synergistic or antagonistic). Recent work has shown that it is often possible to predict such interactions between ribosome-targeting antibiotics using a biophysical model based on bacterial growth laws. Here, we focus on establishing a new model that resolves the interplay between translation and transcription inhibitors. We classify drug interactions by measuring E. coli growth in two-dimensional concentration gradients of the transcription inhibitor rifampicin and several translation inhibitors. Our data indicate different types of interactions. We systematically quantify proteome allocation and individual protein regulation using mass spectrometry-based proteomics measurements optimized for absolute quantification of protein levels. Our preliminary data from single drug treatment with translation inhibitors confirm the known increase in ribosome concentration, whereas rifampicin led to a decrease. Our current aim is to quantify how the cells resolve the conflict of ribosome regulation by performing proteomics measurements in a two-dimensional concentration gradient of both drugs. This work may lead to a deeper understanding of the interplay of transcription and translation.

BP 14.4 Tue 18:00 Poster E

Tracing noisy gradients: chemotactic motion in fluctuating environments — •Thomas Suchanek — Institut für Theoretische Physik, Universität Leipzig, Leipzig, Germany

We study the collective dynamics of chemotactically interacting agents in a system of two species coupled unilaterally via a chemical signaling field: a tracer species actively follows the paths of a target species, which itself moves purely randomly. We observe that fluctuations in the chemical field can have an important impact on the shape of the effective non-reciprocal interactions that determine the averaged dynamics of the two species. In particular, this results in interactions that deviate from the Predator-Prey scheme often considered in the literature [1]. We investigate the form of collective states that arise from interactions of this form and discuss the effects of additional self-interaction (autochemotaxis) of the tracer species.

[1] Liebchen, B., & Löwen, H. (2020). Modeling chemotaxis of microswimmers: From individual to collective behavior. In Chemical Kinetics: Beyond the Textbook (pp. 493-516).

BP 14.5 Tue 18:00 Poster E

Guiding Escherichia coli biofilm growth with textured surfaces — •Clémentine Ferrari[1], Marie-Ly Chapon[2], Laurent Pieuchot[2], Wei Wang[3,4,5], Weiwei Wang[3], Nan Ma[3,4], and Cécile M. Bidan[1] — [1]Max Planck Institute of Colloids and Interfaces, Potsdam — [2]Université de Haute-Alsace, Mulhouse — [3]Helmholtz-Zentrum Hereon, Teltow — [4]Freie Universität Berlin, Berlin — [5]Jilin University, Changchun

Biofilms are complex 3D biological materials created by bacteria producing a protective matrix against adverse environments. These bacteria adapt their matrix in response to various chemical, biological or physical stimuli. This implies that the materials properties of biofilms can be influenced by the properties of their substrate. This project aims at regulating the growth and organization of biofilms by manipulating the geometry of their environment through structured surfaces. Therefore, we culture E. coli bacteria on agar plates to obtain 3D biofilms. The surface of the agar plate is previously shaped with different PDMS stamps. The patterns on these stamps consist of parallel periodic sinusoidal waves or an array of concave half-spheres. In both cases, different dimensions are tested to determine if there is a critical length range where biofilms respond to these modifications, and how this affect their growth and properties. First results indicate that microtopography can influence biofilm spreading. Quantitative methods based are now being established to characterize and measure these changes. Ultimately, textured surfaces may help to develop oriented biofilm-based materials with anisotropic properties.

BP 14.6 Tue 18:00 Poster E

Swimming motility and chemotaxis strategy of *Pseudomonas putida* in porous media — •Sönke Beier, Veronika Pfeifer, Robert Grossmann, and Carsten Beta — Institute of Physics and Astronomy, University of Potsdam, Potsdam, Germany

The chemotaxis strategy of bacteria in liquids is well studied and can be explained in most cases by a run time bias. But how do they adapt their strategy in a porous environment, where there is only a small free path length?

By studying the population spreading and analyzing individual trajectories of the soil bacterium *Pseudomonas putida* in agar, we elucidate the effect of a porous medium on the swimming behavior of *P. putida*. For this purpose, we use a computer-automated event detec-

tion method to recognize the stop and turn events known from the movement pattern in liquid and characterize the trap events which occur in agar. By investigating the orientation of run phases, we found evidence that *P. putida* performs chemotaxis by adapting its swimming direction, similar to earlier report on the peritrichously flagellated intestinal bacterium *Escherichia coli*, suggesting that this could be a generally strategy in many bacterial species.

BP 14.7 Tue 18:00 Poster E

Antibiotic efflux-mediated interactions in a spatially structured bacterial population — •Silvia Vareschi[1], Valerie Jaut[2], Vijay Srinavisan[1], Marco Mauri[1], Frank Schreiber[2], and Rosalind J. Allen[1] — [1]Friedrich Schiller University Jena — [2]Federal Institute for Materials Research and Testing (BAM), Berlin

Multidrug efflux pumps are transmembrane protein complexes that use energy to pump antibiotic outside bacteria. Efflux pumps are among the most common mechanisms by which bacteria become antibiotic resistant. Moreover, mutations that increase efflux pump expression have been found within bacterial biofilms - dense, surface-attached communities that are notoriously difficult to treat with antibiotics. Therefore it is important to understand the role of efflux pumps in the development of antibiotic tolerance in spatially structured bacterial assemblies.

This is a complex problem: on the one hand the local antibiotic concentration alters the growth rate and, potentially, the effluxing capability of bacteria, on the other hand bacteria affect the local antibiotic concentration both by importing the antibiotic and pumping it out.

Our central hypothesis is that this interplay leads to the emergence of antibiotic-mediated interactions between bacteria. These interactions can impact the overall antibiotic response of the population and its spatial structure. We present preliminary experimental data and theoretical analysis, showing how efflux activity, together with antibiotic influx, has non-trivial implications for the structure of a bacterial colony, and its fate in the presence of antibiotic.

BP 14.8 Tue 18:00 Poster E

Modeling of antibiotic-induced perturbation in gut microbiome — •Rie Maskawa[1], Hideki Takayasu[1], Lena Takayasu[2], Wataru Suda[2], and Misako Takayasu[1] — [1]Tokyo Institute of Technology, Tokyo, Japan — [2]RIKEN, Yokohama, Japan

It is important to understand the fluctuation of microbiome due to external perturbations. However, detailed microbiome response to perturbations has not been quantitatively evaluated. We analyzed high-resolution time series of the gut microbiome of mice receiving different concentrations of the antibiotics using the extended Lotka-Volterra model. By modeling of the antibiotic change based on a pharmacokinetic model, detailed temporal changes of perturbation were incorporated into the model. As a result of identifying parameters that accurately describe the kinetics and extracting robustly estimated bacterial interactions between mice, we concluded that the interbacterial network may change depending on the antibiotic pharmacokinetics.

BP 14.9 Tue 18:00 Poster E

Traffic Slowdown by Antibiotics — •Johannes Keisers, Luca Ciandrini, and Phillippe Fuchs — Centre De Structurale Biologe (CBS), Montpellier, France

Bacteria adapt to environmental changes through significant protein expression changes. Despite the complexity of transcription and translation, quantitative growth laws link ribosome allocation and growth. Our focus is on sub-lethal antibiotic effects, reshaping cellular resources. Using a modified TASEP model, we study antibiotic-induced ribosome pausing states, reproducing the second growth law and quantifying active and inactive ribosomes. The approach interprets the ribosome allocation-growth rate relationship under sub-lethal antibiotic doses. It successfully predicts the acceleration of ribosomes under sub-lethal doses of antitbiotics, as observed in E. coli. Our model estimates active versus antibiotic-bound ribosomes and predicts antibiotic impact on charged tRNA concentration. This framework enhances understanding of sub-lethal antibiotic effects on bacterial dynamics, potentially informing future transcriptional perturbations.

BP 14.10 Tue 18:00 Poster E

Mechanical Properties of the Premature Lung — •Jonas Naumann[1], Nicklas Koppe[1], Ulrich Thome[2], Mandy Laube[2], and Mareike Zink[1] — [1]Research Group Biotechnology & Biomedicine, Peter Debye Institute for Soft Matter Physics, Leipzig University, 04103 Leipzig, Germany — [2]Center for Pediatric Research Leipzig, Department of Pediatrics, Division of Neonatology, Leipzig University, 04103 Leipzig, Germany

Premature infants are often reliant on mechanical ventilation to survive. However, prolonged ventilation and associated mechanical stress may cause subsequent pulmonary diseases of the immature lung. To study the mechanical properties of fetal rat lungs on macroscopic scale, we performed rheology experiments under compression and tension using different velocities. Fetal lung tissue showed a hyperelastic behavior and became significantly stiffer with increasing deformation velocities. In fact, fetal lung tissue under compression showed clear viscoelastic features even for small strains. A higher Young's modulus of fetal lungs compared to adult controls clearly pointed towards altered tissue characteristics. In addition, the influence of a hydrostatic pressure difference on the electrophysiology of primary fetal distal lung epithelial cells was investigated on microscopic scale. We observed a strong impact of hydrostatic pressure on the activity of the epithelial sodium channel and the sodium-potassium pump. Vectorial sodium transport, crucial for alveolar fluid clearance, was significantly impaired.

BP 14.11 Tue 18:00 Poster E

Mechanical stress patterns instruct the division plane orientation and tissue morphology during radial growth in *Arabidopsis thaliana* — •Mathias Höfler[1], Xiaomin Liu[2], Thomas Greb[2], and Karen Alim[1] — [1]School of Natural Sciences, Technical University of Munich, Germany — [2]Centre for Organismal Studies, Heidelberg University, Germany

Growing tissues requires coordination to morph functionally structured cell arrangements. Particularly, in plants, where cells cannot rearrrange spatially, coordination of cell division orientation is essential. Here, the radially growing tissue of the plant hypocotyl displays orchestrated cell divisions that pattern cell arrangements. In close comparison with experimental data we investigate how cell mechanics and emerging stress patterns may control cell division orientation and thereby emerging cell arrangement. Starting from reconstructed early hypocotyl cell pattern we model cell growth and follow the emerging mechanical stress pattern. Comparing mechanical stress guided cell division orientation with random cell division orientations we find that the well-ordered cell topologies of the hypocotyl only emerge when incorporating guidance by mechanical stress. Further, the instructive mechanical stress pattern is found to be robust against the cell division orientation. Finally, comparing changes to cell division patterns in experiment and model by mechanically pinching the hypocotyl confirm that mechanical stress instruct the cell division orientation, and thus organize radial growth and plant tissue arrangement.

BP 14.12 Tue 18:00 Poster E

Unraveling Morphogen Dynamics and Growth Mechanisms in Zebrafish Pectoral Fin through Mathematical Modeling — •Maximilian Kotz[1], Benjamin M. Friedrich[1], Lucas de Oliveira Petrocchi Ribas[2], and Rita Mateus[2] — [1]TU Dresden — [2]MPI-CBG, Dresden

During animal development and regeneration, morphogen gradients control tissue growth and patterning. Here, we study mechanisms of growth control using the pectoral fin of zebrafish as model system. A key open question is whether morphogen function similarly in development and regeneration. To address this question, we build data-driven mathematical models of morphogen dynamics coupled to growth. We quantitatively compare finite-element simulations of the models to time-lapse microscopy data provided by our experimental collaborators. For this, we use AI-based image analysis for nuclei segmentation, as well as curved coordinate systems to unwrap the curved 3D tissue geometry. Ultimately, we aim to delineate similarities and differences between development and regeneration, with respect to growth control by morphogens.

BP 14.13 Tue 18:00 Poster E

Small tissues, big opportunities: versatile applications of a new muscle tissue chamber — •Bruno Schmelz[1], Mattias Luber[1], Polina Malova[1], Till Münker[1], Arne Hofemeier[2], and Timo Betz[1] — [1]Third Institue of Physics, Göttingen, Germany — [2]University Medical Center, Göttingen, Germany

Tension and mechanical properties of skeletal muscle tissue are tightly related to its functionality, which makes experimental access to the biomechanics of muscle tissue a key requirement to advance our understanding of muscle function, development and diseases. Recently devised *in vitro* culture chambers allow for raising 3D muscle tissues

under controlled conditions and measuring the global tissue force generation. However, PDMS-based systems are inherently incompatible with high resolution microscopy used for fluorescence-based investigation methods for live and dynamic measurements and absorb small molecules, including many active substances that need to be applied in small yet specific amounts. A recently introduced chamber design blazed a trail for real-time high resolution 3D microscopy during muscle formation and, simultaneously, enabled non-invasive quantification of global contractile forces *via* post deflection analysis. Here we show the versatility of the chamber design by inhibiting the cellular contractility using Cytochalasin D and Blebbistatin. While this largely reduced the force generation, some electrical stimulation of the tissue remained in the Cytochalasin D situation. This suggests either partial protection of the actin from depolymerization or additional effects that lead to voltage-initiated post-deflection.

BP 14.14 Tue 18:00 Poster E

Understanding the stress generation and relaxation in model epithelium — •Madhura Ramani[1], Kevin Höllring[1], Maxime Hubert[1], Rudolf Merkel[2], and Ana Sunčana Smith[1,3] — [1]PULS, FAU Erlangen-Nürnberg, Erlangen, Germany — [2]IBI-2: Mechanobiology, Institute of Biological Information Processing, Forschungszentrum Jülich,Germany — [3]Group for Computational Life Sciences,Ruder Bošković Institute, Zagreb, Croatia

Mechanical forces influence cells via a process known as mechanotransduction, in which cells within a tissue receive and respond to physical stimuli. Epithelia are constantly exposed to external mechanical stimuli, and compromised tissue morphology and architecture from the stress are associated with numerous pathological conditions such as cancer. It is crucial to understand the effect of stretch deformation on the maintenance of tissue structure and its function. We investigate the response of tissue by growing Madin-Darby canine kidney cells on a stiff PDMS substrate, which is later subjected to uniaxial stretch stress using a motorized stretch device. By subjecting the homeostatic tissue to uniaxial stretch stress, we investigate the stress relaxation responses in different time and length scales, providing insight into tissue remodelling, growth, and death. We present our in-house MATLAB code, which quantitatively measures the tissue remodelling, connectivity and cell growth upon tissue stretch. Our approach provides valuable insights into the mechanical feedback of tissue subjected to uniaxial stretch deformations, playing a crucial role in understanding the biophysical aspects of tissue response and disease progression.

BP 14.15 Tue 18:00 Poster E

Noninvasive measurement of tissue tension using low magnification brightfield microscopy — •Mattias Luber, Arne Hofemeier, and Timo Betz — Third Institute of Physics - University of Göttingen, Göttingen, Germany

The interplay of numerous biomechanical features is fundamental for proper tissue function. Therefore, having experimental access to biomechanics is crucial for advancing our understanding of the development of muscle and connective tissue, facilitating the identification of abnormalities and contributing to our understanding of disease mechanisms. Engineered in vitro tissues have proven to function as well-established disease models, allowing mimicking phenotypic conditions in a controlled environment. However, precise measurements of the relevant biomechanical features are still tedious and require specialized equipment as well as manual handling of the sensitive samples. To ease this burden, we present a platform to raise biomimetic tissue models under controlled conditions and measure the tissue tension (among others) noninvasively and throughout the full developmental lifecycle with low magnification brightfield microscopy only. Using this approach, we were able to identify tissue tension as a highly relevant readout for muscular disease like Duchenne Dystrophy, demonstrate the tension-regulating effect of certain compounds or, in context of connective tissues, to investigate fibrotic conditions.

BP 14.16 Tue 18:00 Poster E

Dense optical flow analysis to quantify spatiotemporal fluctuations during tissue growth — •Kai Lennard Fastabend[1], Tassilo von Trotha[2], Mario Christian Benn[2], Viola Vogel[2], and Philip Kollmannsberger[1] — [1]Biomedical Physics, Heinrich-Heine-Universität Düsseldorf, Germany — [2]Laboratory of Applied Mechanobiology, ETH Zürich, Switzerland

The growth of fibroblast microtissues depends on the interplay between cell contractility, extracellular matrix and the geometry of the underlying substrate. Previous studies revealed gradients of cell phenotype and matrix stretch between growth front and tissue interior [1], but how these gradients emerge over time is not clear. We aim to better understand the dynamics of growth by quantifying spatiotemporal deformation patterns during growth. We first evaluated different strain mapping algorithms applied to phase contrast time lapse movies of growing tissues from [2] and found that the Farnebäck algorithm for dense optical flow showed the most robust results. Based on the resulting deformation fields, the time dependent divergence of motion was calculated to identify regions of stretching and compression. Spatial and temporal smoothing of the flow fields was employed to evaluate local tissue deformations at different scales. The presented framework is a promising approach to analyze the mechanical feedback regulation involved in the organization of tissue growth, enabling a more nuanced understanding of cellular responses to microenvironmental mechanical cues. [1] P Kollmannsberger et al., Science Advances 4(1) eaao4881 (2018) [2] MC Benn et al. Science Advances 9(13) eadd9275 (2023)

BP 14.17 Tue 18:00 Poster E

Dystrophin as a tension regulator in human skeletal muscles — •Mariam Ristau[1], Arne Hofemeier[1,2], Bart Vos[1], Till Münker[1], Mattias Luber[1], and Timo Betz[1] — [1]Third Institute of Physics - Biophysics, Georg-August-University Göttingen — [2]Institute of Pharmacology and Toxicology - University Medical Center Göttingen

Skeletal muscles are associated with contraction, movement and force generation. They are important for maintaining posture, bone and joint stability. Muscular dystrophies such as Duchenne muscular dystrophy (DMD) result in progressive weakening and wasting of skeletal muscles. DMD is caused by the loss of the protein dystrophin which is thought to stabilize and protect muscle fibres from injury.

We have studied the contractile potential of reconstituted tissues derived from healthy and DMD patients, and found that DMD derived tissues exhibited an overall weaker contractility compared to healthy derived tissues. In contrast, DMD derived tissues showed an overall higher homeostatic tissue tension, suggesting that dystrophin may function as a tension regulator in skeletal muscles.

In order to rule out the possibility that these findings are due to patient variability, we established a DMD knockout model from healthy myoblasts by using the CRISPR/Cas9 system. Comparing the healthy tissues to the isogenic DMD tissues we could reproduce the same phenotype of increased homeostatic tissue tension in the DMD tissues, providing further evidence that dystrophin may regulate homeostatic tissue tension.

BP 14.18 Tue 18:00 Poster E

Mechanobiological response of an epithelial tissue under shear stress — •Narmin Abasova[1], Annemarie Wirth[1], Kevin Hoellring[1], Rudolf Merkel[2], and Ana-Sunčana Smith[1,3] — [1]PULS Group, Institute for Theoretical Physics, FAU Erlangen- Nurnberg (IZNF) — [2]Institute for Biological Information Processes (IBI), Forschungszentrum, 52428 Jülich, Germany — [3]Group of Computational Life Sciences, Division of Physical Chemistry, Ruder Bošković Institute, 10000 Zagreb, Croatia

Epithelial cells endure a continuous array of mechanical stresses within the human body, from the rhythmic pulsations of blood circulation to the dynamic stresses induced by exercise. Understanding the mechanobiological aspects of stress generation in epithelial cells is crucial for unraveling the complex dynamics underlying cellular responses and tissue functionality. Hence, we employ stress-generating devices to investigate the effects of distinct stress types on the tissue.The influence of solid shear stress transmitted through the extracellular matrix (ECM) remains a less-explored frontier in tissue mechanics. This research employs a custom-made device capable of applying controlled shear stress to the substrate supporting epithelial cell cultures. Upon subjecting the studied cluster to solid shear stress, we systematically document the tissue's response to the applied stress under the microscope. Our investigation delves into the implications of solid shear stress on cellular behavior, encompassing analyses of cell elongation, proliferation, stress relaxation, and the T1 transitions at the cell membrane, where neighbor exchanges occur.

BP 14.19 Tue 18:00 Poster E

Thick elastic sheets and complex tissue shape: theory and modeling — •Wan Yee Yau[1,2,3] and Carl D. Modes[1,2,3] — [1]Max Planck Ins,tute for Molecular Cell Biology and Gene,cs (MPI-CBG), Dresden 01307, Germany — [2]Center for Systems Biology Dresden (CSBD), Dresden 01307, Germany — [3]Cluster of Excellence, Physics

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Folding formation in epithelial tissue can be driven by the deformation gradient, induced by cellular-scale or tissue-scale effects. In this study, we employ shape programmability in thick elastic sheets to investigate epithelial morphogenesis. This approach, with finite-thickness elastic sheets, allows the flexibility to select distinct deformation patterns on both surfaces, enabling the exploration of distinct apical and basal deformations in epithelia. Additionally, we examine the thickness effect of these competing patterns. Simulations within the spring-lattice model are conducted to predict shapes based on the initial deformation pattern. Subsequently, we analyze the relationships using the theory of elasticity.