

BP 10: Cell Adhesion and Multicellular Systems

Time: Tuesday 10:00–12:30

Location: H13

BP 10.1 Tue 10:00 H13

Physics of gut motility governs digestion and bacterial growth — ●AGNESE CODUTTI^{1,2}, JONAS CREMER³, and KAREN ALIM^{1,2} — ¹Physics Department and CPA, Technische Universität München — ²Max-Planck-Institut für Dynamik und Selbstorganisation, Göttingen — ³Stanford University

Malfunctioning of the small intestine contractility and the ensuing bacterial population therein are linked to a plethora of diseases. We, here, study how the small intestine's variety of contractility patterns impacts nutrient uptake and bacterial population. Our analytical derivations in agreement with simulations identify flow velocity as the key control parameter of the nutrients uptake efficiency and bacterial growth, independently of the specifics of contractility patterns. Self-regulating flow velocity in response to the number of nutrients and bacteria in the gut allows achieving 100% efficiency in nutrient uptake. Instead of the specifics of intestine contractility, our work points to the flow velocity and its variation in time within the intestine to prevent malfunctioning.

BP 10.2 Tue 10:15 H13

Blue-light photoreceptors regulating light-switchable adhesion in *Chlamydomonas reinhardtii* — ●RODRIGO CATALAN^{1,2}, ANTOINE GIROT^{1,2}, ALEXANDROS FRAGKOPOULOS^{1,2}, SIMON KELTERBORN³, DARIUS RAUCH³, PETER HEGEMANN³, and OLIVER BÄUMCHEN^{1,2} — ¹Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen, Germany — ²University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany — ³Humboldt University Berlin, Institute of Biology, 10115 Berlin, Germany

Photoactive organisms have evolved a variety of light-sensitive molecules, called photoreceptors, which regulate phenotypes such as phototaxis, circadian life cycle and sexual reproduction. Recently it was discovered that the unicellular, eukaryotic microalga *Chlamydomonas reinhardtii* exhibits light-switchable flagellar adhesion to surfaces [Kreis *et al.*, Nature Physics, 2018]; a phenotype triggered by a blue-light photoreceptor. Using single-cell micropipette force measurements, we show that the action spectrum of flagellar adhesion forces in wild-type (WT) cells resembles the adsorption spectrum of photoreceptors called cryptochromes. Furthermore, adsorption experiments show that the number of WT cells adsorbing to surfaces under blue light increases after the start of the cells' day-phase, which coincides with the light degradation of plant cryptochrome (pCRY). Adhesion force and adsorption experiments of WT and photoreceptor deletion mutants illuminate the role of photoreceptors in this adhesion phenotype.

BP 10.3 Tue 10:30 H13

Motility and collective behavior of gliding *Chlamydomonas* populations — ●ALEXANDROS FRAGKOPOULOS^{1,2}, SEBASTIAN TILL¹, FLORIAN EBMEIER¹, MARCO G. MAZZA^{1,3}, and OLIVER BÄUMCHEN^{1,2} — ¹Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen, Germany — ²University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany — ³Department of Mathematical Sciences, Loughborough University, Loughborough, Leicestershire LE11 3TU, UK

The model microbe *Chlamydomonas reinhardtii*, a unicellular biflagellated microalga, can adhere and colonize almost any surface under particular light conditions. Once the cells attach to a surface, an intraflagellar transport machinery translocates the cell body along the flagella, which are oriented in a 180° configuration. This motion is known as gliding motility. We find that gliding enables surface-associated *Chlamydomonas* cells to cluster and form compact, interconnected microbial communities [1]. We detect and analyze the movement of single cells and characterize the spatio-temporal evolution of the morphology of the colony. The motion of single cells exhibits rapid movements, followed by prolonged immobility. By analyzing the cell clustering, we observe the colony transitioning from local clusters to a single global network with increasing cell density. Simulations based on a purely mechanistic approach cannot capture the non-random cell positions. However, by including flagellar mechanosensing through a cognitive model, we quantitatively reproduce the experimental observations.

[1] Till *et al.*, arXiv:2108.03902v1

BP 10.4 Tue 10:45 H13

Spatiotemporally resolved single-cell growth in bacterial biofilms — ●ERIC JELLI^{1,2,3}, TAKUYA OHMURA^{2,4}, NIKLAS NETTER^{2,3,4}, MARTIN ABT^{2,3}, EVA JIMÉNEZ-SIEBERT^{2,3,4}, KONSTANTIN NEUHAUS^{2,3,4}, DANIEL KARL-HEINZ RODE^{2,3,4}, and KNUT DRESCHER^{2,3,4} — ¹Max Planck Institute for Neurobiology of Behavior - caesar, Bonn, Germany — ²Max Planck Institute for Terrestrial Microbiology, Marburg, Germany — ³Department of Physics, Philipps-Universität Marburg, Marburg, Germany — ⁴Biozentrum - University of Basel, Basel, Switzerland

Bacterial biofilms are dense multicellular communities that are embedded in a self-produced matrix. The high density of cells gives rise to nutrient, oxygen, and metabolite gradients in space and time. To understand the underlying spatio-temporal growth principles in biofilms, single-cell segmentation algorithms are required. Current Deep Learning algorithms provide the required accuracy for tracking-dependent investigations, yet depend on suitable large training datasets.

We used an iterative training pipeline to densely annotate complete biofilms with thousands of cells in 3D. The pipeline reduced the required manual labeling steps which would otherwise be prohibitive for a dataset of a similar size. The collected data enabled us to compare the single-cell segmentation accuracy of recent Deep Learning algorithms with the results of classical biofilm segmentation approaches. We used the trained algorithms for single-cell tracking in 3D time-lapse confocal microscopy data and identified regions with different division rates inside the microbial communities.

15 min. break

BP 10.5 Tue 11:15 H13

The advantage of network topology in avoidance reaction — ●SIYU CHEN¹, JEAN-DANIEL JULIEN¹, and KAREN ALIM^{1,2} — ¹Max-Planck-Institut für Dynamik und Selbstorganisation, Göttingen — ²Physics Department and CPA, Technische Universität München, München

The unicellular slime mould *Physarum polycephalum* stands out among other unicellular organisms for having a network-shaped body. Which advantage does a network structure provide when facing a challenging environment with adverse conditions? We, here, follow how network topology impacts *P. polycephalum*'s avoidance response to adverse blue light. We stimulate either an elongated amoeboid or a simple Y-shaped networked specimen and quantify the retraction velocity of the light-exposed body part. The result shows that Y-shaped specimen can complete the avoidance retraction without increasing the migration velocity, while an elongated amoeboid requires bursts of higher velocities - an energetically costly expense. Our theoretical predictions suggest that a light-triggered change in cytoplasm viscosity may account for the difference in response, as the more complex topology of a network allows *P. polycephalum* to maintain large flows that enable quick retraction out of the blue light. The difference in the retraction behaviour suggest the complexity of network topology provides a key advantage in dealing with adverse environments. Our findings could lead to the better understanding of the evolutionary transition from unicellular to multicellularity.

BP 10.6 Tue 11:30 H13

Model-Based Prediction of an Effective Adhesion Parameter Guiding Multi-Type Cell Segregation — ●PHILIPP ROSSBACH, HANS-JOACHIM BÖHME, STEFFEN LANGE, and ANJA VOSS-BÖHME — DataMedAssist, HTW - University of Applied Sciences, 01062 Dresden, Germany

The process of cell-sorting is essential for development and maintenance of tissues. With the Differential Adhesion Hypothesis, Steinberg proposed that cell sorting is determined by quantitative differences in cell-type-specific intercellular adhesion strengths. An implementation of the Differential Adhesion Hypothesis is the Differential Migration Model by Voss-Böhme and Deutsch. There, an effective adhesion parameter was derived analytically for systems with two cell types, which predicts the asymptotic sorting pattern. However, the existence and form of such a parameter for more than two cell types is unclear. Here, we generalize analytically the concept of an effective adhesion parameter to three and more cell types and demonstrate its existence nu-

merically for three cell types based on in silico time-series data that is produced by a cellular-automaton implementation of the Differential Migration Model. Additionally, we classify the segregation behavior using statistical learning methods and show that the estimated effective adhesion parameter for three cell types matches our analytical prediction. Finally, we demonstrate that the effective adhesion parameter can resolve a recent dispute about the impact of interfacial adhesion, cortical tension and heterotypic repulsion on cell segregation.

BP 10.7 Tue 11:45 H13

Is cell segregation like oil and water: asymptotic versus transitory regime — ●FLORIAN FRANKE^{1,2}, SEBASTIAN ALAND^{2,3}, HANS-JOACHIM BOEHME^{1,2}, ANJA VOSS-BOEHME^{1,2}, and STEFFEN LANGE^{1,2} — ¹DataMedAssist, HTW Dresden — ²Faculty of Informatics/Mathematics, HTW Dresden - University of Applied Sciences — ³Faculty of Mathematics and Computer Science, TU Freiberg

Segregation of different cell types is a crucial process for the pattern formation in tissues. Since the involved cell interactions are complex and difficult to measure individually in experiments, mathematical modelling plays an increasingly important role to unravel the mechanisms governing segregation. The analysis of these theoretical models focuses mainly on the asymptotic behavior at large times, in a steady regime and for large numbers of cells. Most famously, cell-segregation models based on the minimization of the total surface energy, a mechanism also driving the demixing of immiscible fluids, are known to exhibit asymptotically a particular algebraic scaling behavior. However, it is not clear, whether the asymptotic regime of the numerical models is relevant at the spatio-temporal scales of actual biological processes and in-vitro experiments. By developing a mapping between cell-based models and experimental settings, we are able to directly compare previous experimental data to numerical simulations of cell segregation quantitatively. We demonstrate that the experiments are reproduced by the transitory regime of the models rather than the asymptotic one. Our work puts a new perspective on previous model-driven conclusions on cell segregation mechanisms.

BP 10.8 Tue 12:00 H13

Self-Buckling of filamentous cyanobacteria reveals gliding forces — ●MAXIMILIAN KURJAHN¹, ANTARAN DEKA¹, ANTOINE GIROT^{1,2}, LEILA ABBASPOUR^{3,4}, STEFAN KLUMPP^{3,4}, MAIKE LORENZ⁵, OLIVER BÄUMCHEN^{1,2}, and STEFAN KARPITSCHKA¹ — ¹Max Planck Institute for Dynamics and Self-Organization (MPS), Göttingen — ²Experimental Physics V, University of Bayreuth

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Filamentous cyanobacteria are one of the oldest and today still most abundant lifeforms on earth, with manifold implications in ecology and economics. These phototrophic organisms form long and flexible filaments that do not actively swim in bulk liquid but exhibit gliding motility in contact with solid surfaces. The underlying force generating mechanism of their gliding apparatus is not yet understood. We measure their bending modulus with micropipette force sensors, and investigate how filaments buckle after gliding onto an obstacle. Comparing Kirchhoff theory to the experiments, we derive the active forces and the friction coefficients associated with gliding from the observed critical filament length for buckling. Remarkably, we find that these two quantities are strongly coupled, while dependencies on other observables are largely absent. The critical length also aligns with the peak of their natural length distribution, indicating the importance of buckling for their collective.

BP 10.9 Tue 12:15 H13

Structural and mechanical properties of filamentous cyanobacteria — ●MIXON FALUWEKI^{1,2} and LUCAS GOEHRING¹ — ¹Nottingham Trent University, Nottingham, UK. — ²Malawi University of Science and Technology, Limbe, Malawi.

Filamentous cyanobacteria, long strands of connected cells, are one of Earth's earliest forms of life. They are found in multiple environments playing different roles and forming large-scale patterns in structures like biomats and stromatolites. The mechanical properties of these structures contribute to cyanobacteria's success in inhabiting their environments and are useful in applications such as algae-based biofuel production. One of the most important mechanical properties of these active polymers is the bending modulus or flexural rigidity. Here, we quantify the flexural rigidity of three cyanobacteria species, of order *Oscillatoriales*, via bending tests in a microfluidic flow device, where single cyanobacteria filaments are introduced into the microfluidic channel and deflected by fluid flow. Our measurements are confirmed separately by measuring the Young's modulus and cell wall thickness using atomic force microscopy and transmission electron microscopy, respectively. These measurements can be used to model interactions between cyanobacteria, or with their environment, and how their collective behaviour emerges from such interactions.