Fysikermøtet 2023

Presentasjoner under biofysikk og medisinsk fysikk

Presentations at the strand for Biophysics and medical physics

Venue: VilVite

Thursday 10:20-12:00, Conference room CD

10:20 Deanna Wolfson, UiT: ***A view into fish skin – multimodal microscopy of salmon epithelial cells***

ISalmon is critical to the Norwegian economy, with >100 billion nok of exports each year. However, the industry suffers from a steady 15% fish mortality rate, and disease from fish farms has both economic and environmental impacts. Epithelial cells are the first line of defense for the fish, thus it is important to understand their mechanisms and responses to challenges and stimuli. Microscopy is an excellent tool to study single-cell and sub-cellular behavior, but each microscopy technique has its own advantages and drawbacks. Here I will present a sampling of our use of both traditional and new microscopy methods to investigate inter- and intracellular interactions of salmon epithelial cells. Our work ranges from producing a public dataset with dozens of hours of DIC video showing the migratory behavior of cells directly from a fish scale, to QPM showing the details of fluctuations in cellular lamellipodia, to TIRF investigations to determine motion and the forces involved, to holotomography to study nanoparticle uptake, and fluorescence imaging to look at potential cellular repair mechanisms and communication. This presentation will highlight the benefits of a multimodal approach to microscopy as well as show how the use of new techniques revealed unexpected findings, thus opening up new research avenues.

10:45 Harish Pruthviraj Jain, Njord Centre, Department of Physics, UiO: ***Energy profiles and statistics of spontaneous T1 transitions in confluent tissues***

T1 transitions (or cell intercalations) play an important role in several morphogenetic processes. They are observed during morphogenesis of developing embryos and in epithelial cell monolayers. We use a multiphase field model to study spontaneously generated T1 transitions for varying cell deformability and cell-cell interaction. We observe a universal profile of energy evolution at the site of T1 transitions that indicates a slow accumulation of energy and a fast decay, followed by a very slow relaxation. We also explore the effect of cell shape deformability and intercellular interactions on properties of T1 transitions such as the rate of T1 transitions, their time durations, and the total amount of energy accumulated during them. We also show that, in cell monolayers, large

deformations only occur when there are T1 transitions, provided there is no apoptosis or cell division. Lastly, we link large scale flow patterns in cell monolayers with a cascading process of T1 transitions.

11:10 Kristian S Ytre-Hauge, Department of physics and technology, UiB, *Biological dose in proton therapy*

Dose prescription in cancer treatment with radiotherapy has traditionally been based on the energy deposition of the radiation, i.e. the absorbed dose. Proton therapy is now emerging as a new treatment option in Norway and due to the variation in energy deposition pattern depending on the proton energy, the absorbed dose may be an insufficient measure of the expected radiation effect. We therefore propose the used of biological dose in treatment planning and dose prescriptions. The biological dose can be estimated based on the absorbed dose, the proton energy or linear energy transfer and tissue specific parameters.

11:35 Erlend Lyngholm, Department of physics and technology, UiB, *Towards a unified proton relative biological effectiveness model for clinical application*

In proton treatment planning today, a constant relative biological effectiveness (RBE) factor of 1.1 is used to account for the difference in biological effect between photons and protons. However, preclinical studies have shown that the RBE varies with several physical and biological factors. As this is not considered by applying a constant RBE in the planning process, we might underestimate the dose delivered to healthy tissue during treatment, especially compromising the sparing of organs at risk close to the target which can increase the normal tissue complication probability for the patient. Several models have been developed to account for the variations in RBE, based on different datasets with data from cell irradiation experiments with protons and photons. However, there are large variations between the model estimates, which makes it hard to choose one of them for clinical implementation. We collected a large database of in vitro RBE data to investigate the source of these inter-model variations and how they can be reduced, aiming to propose a new model based on this large and updated database. To obtain this goal, we tested previously used model assumptions on the database and investigated how the modelling outcome is affected by applying different database restrictions. Furthermore, previously published models were refitted in the updated database to explore the effects of using the same data to fit the models and separate variations due to data differences from variations due to the appliance of different model assumptions for the RBE dependencies.

12:00 – 13:00 Lunch

We resume in conference room C at 13:00

13:00 Erika Eiser, PoreLab, Dept. of Physics, NTNU, *Entropy-Driven, Whole Genome Detection*

The incorrect prescription of antibiotics drives the global increase in antibiotics resistance. One key reason for the over-prescription of antibiotics is that many developing countries lack the infra-structure needed for the rapid identification of the pathogens that cause an infection. Clearly, we need to be able to distinguish the DNA of particular, pathogenic bacteria from viral DNA, and from the DNA of other bacteria.

Current techniques such as Polymerase Chain Reaction (PCR) rely on amplification of a specific DNA segment of the target genome to get a reliable readout, a process that is typically carried out in a "high-tech" environment.

Computer simulations by Curk et al. [1], exploiting exploits ideas that have been developed in the context of Soft-Matter Physics, suggested that judiciously selected, shorter DNA-probes can bind to dozens of sites along the target DNA. The advantage of using multivalent DNA-probe binding is that it does not require the use of PCR. As this technique is based on the recognitions of dozens of sequences along the entire genome, it is robust against single-point mutations, and the strength of binding is entropically enhanced by the fact that huge numbers of permutations of the DNA target-probe bonds are possible.

I will report the first direct experimental validation of the approach proposed by Curk et al.[1] using colloids that have been functionalized with the DNA probes that follow from the theory of ref. [1]. Our results show that we can indeed recognize low concentrations of a target bacterium (a "safe" E-coli strain) without DNA amplification [2]. Moreover, the test is selective in the sense that it does not respond to other, closely related bacterial strains.

13:25 Richard Ho, UiO, *Minimal Model of Gastruloid Elongation*

During morphogenesis, a group of cells can change shape and orientation, including breaking previous global symmetry. Simulations of this process often impose this symmetry breaking on the system, whereas we would like to make these changes emergent from the evolution of the individual cells. We extend a previously developed discrete 3D cell model, which can capture cell morphological effects such as budding, gastrulation, and neurulation. This model couples the evolution equations of two polarities and position and its simplicity allows the simulation of thousands of interacting cells at reasonable computational cost. We now extend it to include the presence of polarity and add multiple cell types with differential adhesion. With a particular interest on how these results relate to organoids, we examine the presence of these effects on the morphological changes. We find strong similarities with experimental results.

13:50 Andreas Handeland, Department of physics and technology, UiB and Haukeland University Hospital, *Protonterapibehandling for barnekreft kan minske risiko for biverknadar*

Stråleterapi er ei viktig form for kreftbehandling som vanlegvis bruker fotonstråler, men protonstråler er eit alternativ til foton som kan vere meir skånsamt for kroppen. I dag sendes pasientar til Sverige eller Danmark for protonbehandling, men i 2025 skal protonsenteret i Bergen behandla sin fyrste pasient. Grunna den potensielle skånsemda til protonet blir mange barn behandla med proton for å unngå skadar til friskt vev i utvikling og for å minska risiko for helseplager frå strålinga seinare i livet. Likevel har me meir erfaring med foton og å kartleggja korleis protonet sin effekt på kroppen kan skiljes frå fotonet er derfor viktig. Målet med mitt doktorgradprosjekt er å sjå på korleis protonstråling påverkar friskt kroppsvev i behandling av barnekreft og korleis me kan optimere behandlinga for å minske risiko for stråle-induserte biverknadar.

14:15 Johannes Tjelta Department of physics and technology, UiB and Haukeland University Hospital Radiation, *Exposure to a parent-in-the-treatment-room during pencil beam scanning proton therapy*

Radiation protection regulations prohibit parents from remaining near patients or occupying the treatment room during radiotherapy. With modern radiotherapy methods such as intensity-modulated proton therapy, in-treatment room measurements have shown the dose to be well below the dose limit set for the general public. In this study, we examined the whole-body dose of a parent through Monte Carlo simulations and open a discussion on whether we should rethink the regulations set in the past.

14:40 End of session