Abstracts

Juliane Schröter (Columbia University, USA)

Building Immunity: Modelling Immune Development and Vaccine-Induced Protection

How does our immune system respond to infection or vaccination – and how can mathematics help us understand and improve those responses? Understanding how the immune system matures and develops memory remains a central question in immunology. My research focuses on paediatric immunology and viral infections, using mathematical models to unravel the complex dynamics of immune maturation and responses, particularly in early life.

In this talk, I will present recent work on SARS-CoV-2 that integrates computational modelling with high-dimensional immunological data from adult human organ donors. We analysed systemic and tissue-resident cellular immune responses to infection and vaccination across multiple tissues. Despite data sparsity, probabilistic imputation and ensemble modelling strategies enabled us to identify key correlates of serum antibody titers, including positive associations with memory B cells and $CD8^+$ T cells, and negative associations with T follicular helper cells in certain tissues. Our findings show that natural infection amplifies immune responses beyond vaccination alone, and that immune features from peripheral tissues provide valuable insight into long-term systemic protection. These results underscore the importance of tissue-based profiling and quantitative approaches to assess vaccine efficacy.

Beyond the SARS-CoV-2 context, these insights raise fundamental questions: How does the developing immune system fight infections? Are immune memory mechanisms in childhood distinct from those in adulthood – and could these differences explain the durability of many childhood vaccines?

By combining mathematical models with experimental data, we aim to better understand how immunity builds across the lifespan. I will briefly introduce the modelling techniques we use and discuss how they can inform (paediatric) vaccine strategies, especially when empirical data are limited. Through these examples, I hope to illustrate how interdisciplinary approaches can advance our understanding of immune development and protection.

Lena Collienne (Fred Hutchinson Cancer Center, USA)

Using Deep Learning to Guide Phylogenetic Tree Search

Phylogenetic tree inference is a challenging task. The number of phylogenetic trees grows super-exponentially with the number of sequences (leaves), making it impossible to exhaustively search for the best phylogeny for a given dataset. Additionally, the space of all phylogenetic trees is a complex, high dimensional structure, making searching for the best tree for a given dataset a difficult optimisation problem. Despite this, we are nowadays able to infer phylogenetic trees for thousands of sequences. This has been enabled by two concepts: local search (via tree rearrangements) and dynamic programming (e.g. the Fitch algorithm).

In this talk I will explain how we can combine these techniques with deep learning to guide tree search. As an application of our model we consider maximum parsimony inference, which has recently regained attention as it is able to produce high quality trees for densely sampled data sets like SARS-CoV2. I will show that our model is able to detect suboptimal regions in a tree under the maximum parsimony criterion and thereby has potential to improve tree search by directing tree proposals to modify trees in these regions.

Kieran Collienne (Fred Hutchinson Cancer Center, USA)

Faster Bayesian Tree Inference with Hamiltonian Monte Carlo

Inferring evolutionary parameters, including mutation rates, population sizes, and phylogenies, can currently be done thoroughly or quickly, but not both. A single best-guess can be found quickly, but more detailed Bayesian inference requires a much slower Markov chain Monte Carlo (MCMC) sampling approach. Sampling large evolutionary histories with MCMC is prohibitively expensive, making it an impractical approach in epidemiology, where an abundance of data can force us to use less informative methods.

With densely sampled viral data we often infer trees with few or no mutations on branches. This dense data allows us to be confident in the branches where mutations occur, and we propose fixing these regions of the tree. By representing the remainder of the tree using continuous parameters, we can differentiate the likelihood function and sample from the constrained distribution over tree-space using Hamiltonian Monte Carlo. This approach is orders of magnitude faster than classic MCMC using tree rearrangements.

Sophie Kersting (Greifswald University)

From Phylogenetic Balance to Plant Architecture: Investigating Tree-like Structures in Evolution, Ecology, and Agriculture

In my talk I will present three biomathematical projects on which I have worked. The first and main part of the talk focuses on /tree balance/ in mathematical phylogenetics: Phylogenetic trees capture the "shape" of evolutionary history and their structure can provide insights into processes such as fertility inheritance, selection, and diversification. Over the last few decades, a wide range of statistical measures that quantify the (a)symmetry of phylogenetic trees has been developed, known as /tree balance indices/. With over 30 (families of) balance indices existing in the literature, we wanted to address a central question: Which indices are most informative or powerful for which applications?

In pursuit of this question we conducted a comprehensive comparison study of the statistical power of nearly all known balance indices across a wide range of evolutionary tree models. Our investigation reveals distinct balance indices better suited for identifying different tree models, suggesting that decisions on balance index

selection can be enhanced with prior knowledge. Alongside this, I will also introduce our R package PoweRbal, which allows users to do their own simulations studies, and test new indices and tree models.

In the second part of the talk, I will briefly present two additional projects: one in plant ecology, using 3D imbalance indices to analyze the architecture of 3D tree models, and another in agricultural science, using root scans to quantify below-ground plant growth. These case studies highlight how diverse — yet related — biomathematical research projects can be.

The presented results are joint work with Mareike Fischer, Lina Herbst, Linda Knüver, Luise Kühn and Kristina Wicke.