

Tuesday, February 4, 2020

11:30 Registration opens (with small lunch)

12:45–13:00 Welcome

Session 1: Dynamical modeling

13:00–13:40 Keynote lecture: Fabien Crauste

Mathematical Immunology: How to account for individual heterogeneity in theoretical models of the immune response?

13:40–14:00 Congxin Li

Non-equilibrium Transcriptional Regulation: Theory and Experiment

14:00–14:20 Marco Blickensdorf

*Agent-based modelling of the impact of Pores of Kohn on infection dynamics of *A. fumigatus* in human alveoli*

14:20–14:40 Yuri Kheifetz

Shiny platform for the analysis of complex individualized biomathematical models of hematopoiesis as well as for their implementation in controlling hematopoietical side effects during guided dose adaptation in chemotherapy

14:40–15:00 Thomas Zerjatke

Divisional behaviour of haematopoietic stem cells revisited: a quantitative comparison of label dilution techniques

15:00–16:00 Coffee break & poster session I

Session 2: Statistical modeling, machine learning and open topics

16:00–16:40 Keynote lecture: Volker Roth

Interpretable Machine Learning for Personalized Medicine

16:40–17:00 Michael Huttner

Diagnosis of Lymphoma subtypes using deep neural nets

17:00–17:20 Thomas Linden

Predicting comorbidities of epilepsy patients using big data from Electronic Health Records combined with biomedical knowledge

17:20–17:40 Helena Zacharias

A multi-source data integration approach reveals novel associations between metabolites and renal outcomes in the German Chronic Kidney Disease study

17:40–18:00 Johannes Hertl

Translating microbiome abundance patterns into patterns of metabolic function by integrating constraint based modelling with population statistics

18:30 Conference dinner in the Restaurant zur Bühne Bonn
Kapuzinerstr. 13, 53111 Bonn

Wednesday, February 5, 2020

Session 3: Genomics, proteomics and imaging

8:30–9:10 Keynote lecture: Dagmar Iber
From Networks to Function – Computational Models of Organogenesis

9:10–9:30 Moritz Kohls
Resampling metagenomics findings to assess reproducibility

9:30–9:50 John Wiedenhoefl
Dynamically compressed Bayesian Hidden Markov models using Haar wavelets

9:50–10:10 Rudolf Schill
Modelling cancer progression using Mutual Hazard Networks

10:10–11:10 Coffee break & poster session II

Session 4: Single-cell data analysis

11:10–11:50 Keynote lecture: Malte Lücken
Making the most of your data: Building a single-cell RNA-seq pipeline

11:50–12:10 Vladislava Milchevskaya
Distance metrics for single cell data

12:10–12:30 Martin Treppner
Generating Synthetic Single-Cell RNA-Sequencing Data from Small Pilot Studies using Deep Learning

12:30–12:50 Marian Schön
DTD: an R package for Digital Tissue Deconvolution

12:50–13:00 Closing remarks & poster award

13:00 Small lunch