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 Wiedenhoeft
*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