

*Thursday, March 7, 2019*

*Session 1: Bioinformatics of NGS data (Chair: Klaus Jung)*

**12:00–12:40 Keynote lecture:** Ivo Grosse

*Phylotranscriptomic Hourglass Patterns of Animal and Plant Development and the Emergence of Biodiversity*

**12:40–13:00** Lea Schuh

*Simulation and characterization of rare correlated gene expression using stochastic network modeling*

**13:00–13:20** Martin Treppner

*Simulating Single-Cell RNA-Sequencing Data using Negative Binomial Deep Boltzmann Machines*

**13:20–13:40** Laura Jenniches

*Multilevel modeling of HTS data*

**13:40–14:00** Michael Seifert

*Survival differences and associated molecular signatures of DNMT3A-mutant acute myeloid leukemia patients*

**14:00–15:00 Coffee break & poster session**

*Session 2: Disease modelling (Chair: Ingmar Glauche)*

**15:00–15:40 Keynote lecture:** Benjamin Werner

*Quantitating somatic evolution in healthy and cancerous human tissues*

**15:40–16:00** Pietro Mascheroni

*Cancer cells under pressure: How do glioma cells respond to mechanical forces?*

**16:00–16:20** Gang Zhao

*The temporal pattern of insulin secretion influences liver function: explanation from a mathematical model*

**16:20–16:40** Michael Huttner

*Lyra - containerized microservices for browsing shared biomedical data*

**16:40–17:00 Coffee break & poster session**

*Session 3: Disease modelling (Chair: Markus Scholz)*

**17:00–17:20** Masoud Hoore

*Mathematical model of Amyloid beta fibrillization in Alzheimer's disease*

**17:20–17:40** Maria T. E. Prauße

*Verifying hypotheses on pathogenic immune evasion in human whole blood by state-based virtual infection models*

**17:40–18:00** Shabaz Sultan

*Modelling the Immune System's Interaction with the Tumour Microenvironment*

**18:00–18:20** Ingmar Glauche

*Mathematical modeling of therapy response in CML patients reveals the potential for substantial dose reductions in many patients*

**19:30 Social event at Anders, das Pfannenrestaurant**

Address: Am Magnitor 7, Braunschweig, <https://www.das-anders.de/>

*Friday, March 8, 2019*

*Session 3: Machine Learning / Optimization in Computational and Systems Biology (Chair: Michael Altenbuchinger)*

**8:30–10:00 Educational lecture: Jan Hasenauer** *Mechanistic models of large-scale biochemical reaction networks*

**10:00–10:30 Coffee break**

*Session 4: Machine Learning / Optimization in Computational and Systems Biology (Chair: Michael Altenbuchinger)*

**10:30–10:50** Zahra Nasrollah

*Learning the topology of latent signaling networks from high dimensional transcriptional intervention effects*

**10:50–11:10** Victor Greiff

*Mining immune repertoires using machine learning and high-dimensional statistics*

**11:10–11:30** Darius Schweinoch

*Temporal control of the RIG-I-dependent antiviral innate immune response*

**11:30–11:50** Hryhorii Chereda

*Utilizing molecular networks in Convolutional Neural Networks on Graphs to predict the appearance of a metastatic event*

**11:50–12:10** Ashar Ahmad

*Stratifying PD patients by disease progression using advanced machine learning techniques*

**12:10–12:30: Poster award and workshop closing**