

Thursday, Jun 15, 2023

11:30 Registration opens (with small lunch)

12:45–13:00 Welcome

Session 1: FAIR model and data principles

13:00–13:40 Keynote lecture: Matthias König

Advancing Liver Function Assessment: Personalized and Stratified Approaches with Standardized Computational Models and Data

13:40–13:55 Dagmar Waltemath

Having fun reusing computational biology models? - and why not?

13:55–14:10 Jürgen Pleiss

EnzymeML - Modelling challenges in enzymology and biocatalysis

14:10–14:25 Sebastian Höpfl

Journals in Systems Biology could improve their impact factor by enforcing reproducibility

14:25–15:30 Coffee break & poster session I

Session 2: Dynamical modeling in health and disease

15:30–16:10 Keynote lecture: Jana Wolf

Modeling signal transduction and gene expression in cancer: from information processing to patient specific-models

16:10–16:25 Bachelot Yann

Spatial distancing: Investigation of a defense mechanism for pathogen immune evasion

16:25–16:40 Ulrich Mansmann

Shape-specific characterization of colorectal adenoma growth and transition to cancer with stochastic cell-based models

16:40–17:10 Coffee break

17:10–17:25 Philipp Altmann

Stochastic dynamics of cancer relapse in hematologic malignancies

17:25–17:40 Gavin Fullstone

In silico-guided optimisation of CNS-targeted Therapeutic Antibodies

17:40–17:55 Felix Weidner

Leveraging quantum computing for dynamic analyses of gene regulatory networks

18:00 Dinner (Pizza with vegetarian and vegan options) & poster session II

Friday, Jun 16, 2023

8:30–9:00 Brezeln and coffee

Session 3: Statistical analysis and machine learning

9:00–9:40 Keynote lecture: Lars Kaderali
Mathematical Modeling of Infection and Immune Response

9:40–9:55 Hryhorii Chereda
Ensemble-GNN: federated ensemble learning with graph neural networks for disease module discovery and classification

9:55–10:10 Stefan Schrod
Individual treatment effect estimation for survival data

10:10–10:25 Konrad Grützmann
Network-based analysis of heterogeneous patient-matched brain and extra-cranial melanoma metastases pairs reveals three homogeneous subgroups

10:25–10:40 Elham Shamsara
A COVID-19 informed neural network with adaptive weighting during variants of concern in Germany

10:40–10:55 Poster award and group picture

10:55–11:30 Coffee break

Session 4: Open topics

11:30–12:10 Keynote lecture: Achim Tresch
Dimension reduction for spatial transcriptomics data

12:10–12:25 Ana Stolnicu
Establishing a trustworthy signalling entropy calculation for biological processes analysis

12:25–12:40 Franziska Görtler
ADTD - Adaptive Digital Tissue Deconvolution.

12:40–12:55 Laura Strohmaier
Gene-regulatory networks controlling cell fates downstream of TGF β -signaling in MCF10A cells

12:55–13:10 Sophia Krix
MultiGML: Multimodal Graph Machine Learning for Prediction of Adverse Drug Events

13:10–13:15 Closing remarks