Workshop on Computational Models in Biology and Medicine

Thursday, June 06, 2024

11:30 — Registration opens

13:00–13:10 — Welcome

Session 1: AI applications – Chair: Ingmar Glauche

13:10–13:50 — **Keynote lecture: Carsten Marr (*Helmholtz Munich*):**

Revolutionizing the diagnosis, therapy and understanding of severe blood disorders with AI

13:50–14:05 — Jan-Niklas Eckardt (*University Hospital Carl Gustav Carus; Else Kröner Fresenius Center for Digital Health, TUD Dresden University of Technology*):

Fight AML with AI - a clinical perspective

14:05–14:20 — Marie Steinacker (*Center for Scalable Data Analytics and Artificial Intelligence (ScaDS.AI) Dresden/Leipzig*):

´ — Combining biological knowledge and machine learning for predicting dynamics of haematotoxcity after chemotherapy: a comparative analysis

14:20–14:35 — Stefan Schrod (*Department of Medical Bioinformatics, University Medical Center Göttingen*):

Counterfactual Deep Learning for treatment combinations

14:35-14:50 — Dagmar Waltemath (*Medical Informatics Laboratory University Medicine Greifswald*):

Community survey on standards and resources for systems biology and systems medicine: results and next steps

14:50–16:30 — **Coffee break & poster session**

Session 2: Disease and treatment modelling – Chair: Nicole Radde

16:30–17:10 — **Keynote lecture: Kathrin Thedieck (*University of Innsbruck*):**

Systems Approaches to Metabolic Signaling

17:10–17:25 — Artur Fassoni (*Universidade Federal de Itajubá, Brazil*):

Modeling of cytokine release syndrome in CAR-T cell therapy reveals macrophage contact-dependent mechanism as target for toxicity reduction

17:25–17:40 — Markus Kreuz (*Fraunhofer Institute for Immunology and Cell Therapy, Leipzig*):

In-depth molecular characterization of patients undergoing CAR-T cell therapy reveals novel biomarkers for response and severe adverse events

17:40–17:55 — Pejman Shojaee (*TUD Dresden University of Technology*):

Predicting the time to relapse for individual patients with Glioblastoma for the second-line of intervention

17:55–18:10 — Viviane Steinberg (*Medizinische Hochschule Hannover*):

Delineating immune escape mechanisms in acute myeloid leukemia through single-cell analyses

18:10- 18:15 — **Group picture**

19:00 — **Conference dinner at the Paulaner Bräuhaus am Waldschlösschen**
(at your own expense)
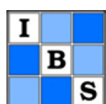
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Friday, June 07, 2024

8:30–9:00   Coffee

Session 3: From bioinformatics to AI – Chair: Tim Kacprowski

9:00–9:40   **Keynote lecture: Anne-Christin Hauschild (*Georg-August Universität Göttingen*):**

Advancing Clinical Research with Cross Species Knowledge Transfer and Explainable AI

9:40–9:55   Michael Seifert (*Institute for Medical Informatics and Biometry, Faculty of Medicine Carl-Gustav Carus, TUD Dresden University of Technology*):

HMM-based identification of gene expression differences between patient-matched melanoma metastasis pairs

9:55–10:10   Clemens Schächter (*Institute of Medical Biometry and Statistics (IMBI), Universitätsklinikum Freiburg*):

Enhancement of network architecture alignment in comparative single-cell studies.

10:10–10:25   Sophie Schmiegel (*Bielefeld University*):

Revealing the Effectiveness of Antibiotics in Patients with Sepsis or Septic Shock using Continuous-time Hidden Markov Models

10:25–10:40   Jonas Lippl (*University Medical Center Göttingen*):

FACT: Federated Adversarial Cross Training

10:40–10:45   **Poster award**

10:45–11:15   **Coffee break**

Session 4: Reproducibility and usability – Chair: Markus Wolfien

11:15–11:30   Ian-C. Jung (*Institute for Medical Informatics and Biometry, Faculty of Medicine Carl-Gustav Carus, TUD Dresden University of Technology*):

Usability and summary of the co-creation workshop

11:30–11:45   Florian Auer (*IT Infrastructure for Translational Medical Research, University of Augsburg*):

Enhancing Reproducibility: A Comprehensive Workflow for Integrating and Visualizing Biological Networks

11:45–12:00   Sebastian Höpfl (*Institute for Stochastics and Applications, University of Stuttgart*):

A reproducible Bayesian workflow to integrate discrete time series data into continuous models

12:00–12:15   Lisa-Marie Bente (*PLRI, Data Science in Biomedicine, TU Braunschweig*):

Semi-Automatic Dead-End and Gap Correction for Metabolic Models

12:15–12:30   Joao Marcelo Brazao Protazio (*IMISE, Leipzig*):

FluModell - A Hybrid Discrete Compartmental Model to Predicting the Impact of Seasonal Influenza on the German Healthcare System

12:30–12:45   **Closing remarks**