Workshop on Computational Models in Biology and Medicine (5/6 March 2026)

Location: Konrad-Zuse-Haus (Albert-Einstein-Straße 22, 18059 Rostock)
Funded by: GMDS & IBS-DR

Program Thursday, March 5

Time	Event	Speaker	Title
12:00 - 13:00	Registration		
12:50 - 13:00	Opening		
13:00 - 13:45	Keynote	Olaf Wolkenhauer	The beginning and end of systems medicine
13:45 - 14:15	Coffee Break		
14:15 - 15:00	Submitted Talks	Benjamin Castellaz	Bridging Model and Data: A Parametrization–Projection Method for Overdetermined Stochastic Inverse Problems
		Philipp Henning	A Multi-Level Model Highlights the Role of Asymmetric Mitochondrial Fission for Insulin Secretion
		Fiete Haack	Rule-based modeling unravels decisive role of receptor trafficking in signalosome formation and sustained long-term Wnt/β-catenin signaling
15:00 - 16:00	Poster Session + Coffee Break		
16:00 - 16:45	Submitted Talks	Malte Mensching-Buhr	Deconomix: A Python Package for Cell-Type Deconvolution of Bulk Omics Data
		Fazel Amirvahedi Bonab	Distributional Regression for Large-Scale Drug Perturbation Prediction
		Thomas Sterr	SpaCeNet2 – Cell-type-specific cell-cell interaction networks from spatial transcriptomics data
16:45 - 17:30	Poster Session + Coffee Break		
17:30 - 18:15	Keynote	Federico Marini	Exploring, managing and interpreting single-cell data
From 19:00	Restaurant "Klock 8"	https://www.klock8.de/	Optional (on a self-pay basis)

Program Friday, March 6

Time	Event	Speaker	Title
8:00 - 8:30	Registration		
8:30 - 9:15	Keynote	Olga Tsoy	Exploring alternative splicing across omics data types
9:15 - 9:30	Coffee Break		
9:30 - 10:15	Submitted Talks	Michael Seifert	Gene expression alterations associated with strong survival differences of DNMT3A and NPM1 co-mutated acute myeloid leukemia patients
		Matthias Overmann	Benchmarking precision matrix estimation methods for differential co-expression network analysis
		Manuel Nietert	Automated extraction of chemical structures from the images / plots in publications to create special topic compound databases
10:15 - 10:25	Group Photo		
10:25 - 10:45	Coffee Break		
10:45 - 11:30	Keynote	Nils Blüthgen	Latent variable models for pooled single cell screens unveils clinically relevant transcriptional modules induced by oncogenes
11:30 - 12:15	Submitted Talks	Marek Sztuka	Comparative Deep Learning Architectures for Exploring High-Dimensional, Small-Sample Data
		Emetis Niazmand	Privacy-Preserving Chronic Kidney Disease Prediction Using Federated Learning
		Markus Wolfien	Leveraging Synthetic Patient Data to Empower Clinical AI in Oncology
12:15 - 12:30	Closing		