FIAS Symposium - Friday, 25 Oct 2019

08:45 – 10:25	**Chair: Volker Lindenstruth**	**HPC Applications in Life Sciences**
08:45 – 09:15	**Bertil Schmidt**	***Next-Generation Sequencing: Big Data meets HPC***
09:25 – 09:40	Nicolas Behr	*Tracelets - a parallelizable algorithmic framework for the analysis of pathway dynamics in biochemical reaction systems*
09:45 – 10:00	Gerhard Koenig	*Quantitative physics-based predictions for life sciences*
10:05 – 10:20	Thomas Sokolowski	*Advancing spatial-stochastic simulation of biophysically realistic models at multiple scales*
10:25 - 10:45	coffee break	
10:45 - 12:45	**Chair: Franziska Matthäus**	**Simulation of Biological Systems**
10:45 - 11:15	**Edda Klipp**	***Systematic integration of models and data for yeast growth and division***
11:25 – 11:40	Ramachandra Bhaskara	*Mapping the architectural landscape of the endoplasmic reticulum*
11:45 – 12:00	Roberto Covino	*AI-Assisted Discovery of Molecular Mechanisms from Computer Simulations*
12:05 – 12:20	Pablo Sartori	*Physical principles of protein complex assembly*
12:25 - 12:40	Sebastian Thallmair	*A microscopic view on biological systems - from lipid-protein interactions to optical spectra*
12:45 - 13:45	lunch	
13:45 - 16:05	**Chair: Enrico Schleiff**	**Methods of Multiscale Modelling in Life Sciences**
13:45 - 14:15	**Reinhard Schneider**	***Systems BioMedicine - merging basic research with health care data***
14:25 – 14:40	Vittoria Barbarossa	*Mathematical modeling of multiscale phenomena in immunology and infectious diseases*
14:45 – 15:00	Erida Gjini	*Predicting coexistence of many strains from co-colonization interactions*
15:05 – 15:20	Ulrike Münzner	*From mechanistic signaling pathways to mechanistic gene regulatory networks*
15:25 - 15:40	Neetika Nath	*Machine learning approach from data to diagnosis*
15:45 - 16:00	Ali Salehzadeh-Yazi	*A comprehensive benchmark for assessment of metabolic pattern in cancers*
16:05 - 16:30	coffee break	
16:30 – 18:15	**Chair: Volker Dötsch**	**Pharmacological probe development and characterization by AI methods**
16:30 – 17:00	**Gisbert Schneider**	***Molecular design with chemistry-savvy machine intelligence***
17:10 – 17:25	Philipp Altrock	*Math vs Machine in predictive modeling of cancer dynamics*
17:30 – 17:45	Guillermo de Anda-Jáuregui	*Functional modularity in genomic networks - applications to breast cancer.*
17:50 – 18:05	Ahmadreza Mehdipour	*Lipid-binding domains in membrane transport proteins as potential drug targets*
18:15	end	