

ii. Conference Schedule


All events take place in Seminaris Campus Hotel, Domus Conference Room, 2nd floor, unless announced otherwise.



Tuesday, 13. 9. 2016 - Day 2

8.00	Registration opens	
9.00	Opening by Prof Knut Reinert, Organizer of GCB2016 and Professor Peter-André Alt, President of FU Berlin	
9.30	Rare genetic variants and the onset of multiple tumours Francesca Ciccarelli, King's College London, UK, Keynote 1	Chair: Knut Reinert
10.10	MARCARviz: Interactive web-platform for exploratory analysis of toxicogenomics data for nongenotoxic hepatocarcinogenesis Michael Römer, Talk 1	
10.30	An Integrative Computational Framework for Personalized Detection of Tumor Epitopes in Melanoma Immunotherapy Tanushree Jaitly, Talk 2	
10.50	Coffee Break	
11.30	Prediction of amyloidogenicity based on the n-gram analysis Synthetases Michal Burdukiewicz, Talk 3	Chair: Bernhard Renard
11.50	Binding Mode Characterization of Class II Aminoacyl tRNA Synthetases Florian Kaiser, Talk 4 (Highlight)	
12.10	Computational molecular design with focus on protein-protein interactions, privileged scaffolds and recurring folding patterns in proteins. Synthetases Oliver Koch, Talk 5 (Junior Research)	
12.30	Lunch break at Mensa	
14.00	AlITV – interactive visualization of whole genome comparisons Sonja Hohlfeld, Talk 6	Chair: Marcel Schmitt
14.20	BIH Award for Women in Bioinformatics: Award ceremony Laudatio and talk by the winner	

at Seminaris lobby, ground floor

12.20	R&D Session Impulse Talks	
13.00	Open R&D Session with finger food lunch, supported by 	13.00 Scientific Posters are still on display in parallel in the lobby of Seminaris Campus Hotel, 1st floor

at Domus Conference Room, 2nd floor


15.00	Open FaBI meeting	
15.30	Social event: Wannsee boat cruise w/ coffee A bus shuttle is organized and leaves at 15.30 sharp in front of Seminaris, Takustr 39	
19.00	Program Committee Dinner (invited guests only) at Loretta am Wannsee	19.00 alternatively: Berlin Night out (plan individually!)

Thursday, 15. 9. 2016 - Day 4

8.00	Registration	
9.00	Computational Biology to understand RNA regulatory mechanisms Uwe Ohler, MDC, Berlin, Keynote 5	Chair: Ulf Leser
9.40	Predicting enhancers using a small subset of high confidence examples and co-training Matthew Huska, Talk 8	
10.00	FUCHS - Full circle characterization using RNaseq Franziska Metge, Talk 9	
10.20	A statistical model for epigenetic control of miRNAs Lisa Barros de Andrade e Sousa, Talk 10	
10.40	Coffee Break	

15.00	How gene regulation networks change during development: network inference from single cell data Michael Stumpf, Imperial College London, UK, Keynote 2	Chair: Marcel Schulz
15.40	Coffee Break	
16.00	tmod: an R package for general and multivariate enrichment analysis January Weiner, Talk 7	
16.20	Poster Pitch	
16.40	Poster Session in the lobby of Seminaris Campus Hotel, ground floor	
19.00	BIH Award for Women in Bioinformatics: Celebration get-together in the lobby of Seminaris Campus Hotel, ground floor	

Wednesday, 14. 9. 2016 - Day 3

8.00	Registration	
9.00	Modeling cancer evolution from genomic data Niko Beerenwinkel, ETH, Switzerland, Keynote 3	Chair: M. Vingron & I. Koch
9.40	Exploring and exploiting interspecific interactions Marie-France Sagot, Université Claude Bernard Lyon, France, Keynote 4	
	Coffee Break	
10.40	Intel R&D Session Opening and chair by Lena Prochnow from Berlin Partner	sponsored by 
10.50	Intel's activities in software for life sciences Pascal Costanza, Intel, R&D Talk 1	
11.20	Science for a Better Life: what is the purpose of my research? Bertram Weiss, Bayer, R&D Talk 2	
11.50	Distilling experimental data into actionable drug discovery Daniel Ziemek, Pfizer, R&D Talk 3	

11.00	AnnoTALE: bioinformatics tools for identification, annotation, and nomenclature of TALEs from Xanthomonas genomic sequences Jan Grau, Talk 11 (Highlight)	Chair: Oliver Kolibacher
11.20	Computational Biology and Evolutionary Genomics Michael Hiller, Talk 12 (Junior Research)	
11.40	Multitask regression for context-specific prioritization of miRNA targets in transcripts Azim Dehghani Amirabad, Talk 13	
12.00	PaPrBaG: A random forest approach for the detection of novel pathogens from NGS data Carlus Deneke, Talk 14	

12.30 Lunch break at Mensa

13.30	Systems BioMedicine using high-throughput screening – From RNAi, CRISPER/cas9, miRNA and drug screens to targeting signaling pathways Jan Baumbach, Talk 15 (Highlight)	Chair: Daniel Huson & Knut Reinert
13.50	de.NBI - German Network for Bioinformatics Infrastructure Alfred Pühler, Talk 16, Report	
14.30	Bioinformatics support for the Tübiom community gut microbiome project Sina Beierl, Talk 17	
14.50	SLIMM: Species Level Identification of Microorganisms from Metagenomes Temesgen Dadi, Talk 18	

15.10 Coffee Break

15.20	Monolithic Multiparameter Diagnostics, from Molecules to Applied Statistical Bioinformatics Stefan Rödiger, Talk 19 (Junior Research)	Chair: Jan Baumbach
15.40	RGFA: powerful and convenient handling of assembly graphs Giorgio Gonnella, Talk 20	
16.10	Improving ancient DNA genome assembly Alexander Seitz, Talk 21	
16.30	GCB 2016 Poster Award by Tim Conrad	
16.50	Closing words by Prof Knut Reinert	