

Workshop Program

Wednesday, March 7th

14:15-14:30	Opening	
14:30-15:10	Ralf Hofstaedt	Gene regulation: Databases and Integration
15:10-15:50	Julio Collado Vides	RegulonDB: Accelerating access to genomic knowledge in Escherichia coli K-12
15:50-16:30	Dieter Jahn	Gene regulatory networks in bacteria
16:30-17:00	Coffee Break	
17:00-17:40	Tim Beissbarth	Methods to analyse transcriptome data in view of gene regulation and signaling pathways
17:40-17:55	Sebastian Zeidler	Variability in Gene Regulation during Cardiomyogenesis
17:55-18:10	Mehmet Gültas	Identification of cooperative transcription factors
18:30	Welcome Reception	

Thursday, March 8th

09:00-09:40	Vsevolod Makeev	From TRANSFAC to HOCOMOCO: using cross-validation and human curation to take most from the high throughput data compiling a complete collection of transcription factor binding motifs
09:40-10:20	Fedor Kolpakov	GTRD - a database on gene transcription regulation
10:20-10:50	Coffee Break	
10:50-11:30	Philipp Bucher	Biophysical modeling of transcription factor binding specificity using large SELEX libraries and computational simulations
11:30-12:10	Johannes Soeding	Bayesian Markov models consistently improve accuracy of DNA binding site predictions by learning inter-nucleotide dependencies
12:10-12:25	Martin Haubrock	Lessons to be learned from transcription factor co-association analysis
12:30-14:00	Lunch Break & Information about the MPI	
14:00-14:40	Martin Vingron	Computational methods in epigenetic regulation
14:40-15:20	Alvaro Perdomo Sabogal	Soft selective sweeps on clusters of gene regulatory factors, a source of population-specific regulatory diversity in human
15:20-15:50	Coffee Break	
15:50-16:30	Reinhard Hehl	Cross-kingdom transcriptional regulation in innate immunity
16:30-17:10	Takako Takai	Tohoku Medical Megabank Project: a project for personalized preventive medicine based on a biobank and prospective genome cohort studies
17:10-17:25	Cornelia Meckbach	Identification of associated TFs in promoters and their related enhancer regions
17:25-17:40	Darius Wlochowitz	A novel information theory-based method for detecting candidate transcription factors predicts drivers of altered gene expression in cancer
18:30	Conference Dinner	

Friday, March 9th

09:00-09:40	Thomas Werner	From transcription factor binding sites to metabolic phenotype: A tale of MORE gene regulation
09:40-10:20	Alexander Kel	TRANSFAC versus Cancer
10:20-10:35	Jürgen Dönitz	TFClass - a classification of transcription factors
10:35-11:05	Coffee Break	
11:05-11:45	Ekaterina Shelest	Promoter-based prediction of gene clusters in eukaryotic genomes
11:45-12:25	Ivo Grosse	Phylotranscriptomic hourglass patterns and the emergence of biodiversity
12:25-12:45	Conclusions & Farewell	