

Ascona Workshop 2015

Statistical Learning of Biological Systems from Perturbations

Conference Center Monte Verità, Ascona, Switzerland, May 31 – June 5, 2015

PROGRAM (last update 2015-05-29)

Sunday, May 31	15:00 – 19:00	ARRIVAL and CHECK-IN	
	18:00 – 19:00	<i>Welcome drinks</i>	
	19:00	<i>Dinner</i>	

Monday, June 1	8:45 – 9:00	<i>Welcome</i>	
	9:00 – 10:00	Michael Boutros	Mapping genetic interactions across multiple phenotypes and signaling states
	10:00 – 10:30	<i>Coffee break</i>	
	10:30 – 11:00	Fabian Schmach	Deconvoluting off-target confounded RNA interference screens
	11:00 – 11:30	Martin Pirkl	Modeling protein signaling pathways with Boolean Nested Effect Models
	11:30 – 12:00	Ke Yuan	Capturing rewiring events during network evolution underlying dynamic biological processes
	12:15	<i>Lunch</i> <i>Unstructured time</i>	
	15:30 – 16:30	Bernd Fischer	Inferring directional genetic interactions from combinatorial, multi-parametric data
	16:30 – 17:00	<i>Coffee break</i>	
	17:00 - 17:30	Jean Yee Hwa Yang	A multi-step classifier identifies cohort heterogeneity in cancers leading to improved accuracy of prognostic biomarkers
	17:30 - 18:00	Jack Kuipers	Cancer progression with Bayesian inference for acyclic digraphs
18:00 – 18:30	Simon Anders	Genomics of ex-vivo drug sensitivity in primary tumour cells	
19:00	<i>Dinner</i>		

Tuesday, June 2	9:00 – 10:00	Brenda Andrews	Genetic networks: general properties and complex phenotypes
	10:00 – 10:30	<i>Coffee break</i>	
	10:30 – 11:00	Alena van Bömmel	Inferring the underlying null model in three-way contingency tables with application to transcription factor co-occurrence
	11:00 – 11:30	Mohammad Sadeh	Estimating causal effect strength between chromatin modifiers and histone modifications
	11:30 – 12:00	Chenchen Zhu	Multi-omics data Integration identifies causal mediators of global phenotypes
	12:15	<i>Lunch</i> <i>Unstructured time</i>	
	15:00 – 16:00	Anne Carpenter	Morphological profiling for targeting diseases and characterizing compounds
	16:00 – 16:30	<i>Coffee break</i>	
	16:30 – 18:30	POSTER SESSION	
	19:00	<i>Dinner</i>	

Wednesday, June 3	9:00 – 10:00	Roderick Beijersbergen	Pooled shRNA screening: from large scale perturbation to single genes as hits
	10:00 – 10:30	<i>Coffee break</i>	
	10:30 – 11:00	Ivo Kwee	Removing batch effects and unwanted variation in gene expression data using nearest-neighbour matched sampling
	11:00 – 12:00	Susan Holmes	Statistical challenges in the study of stability in the human microbiome
	12:15	<i>Lunch</i>	
	13:45	EXCURSION	<i>Hike in the Verzasca Valley</i>
	19:00	<i>Dinner</i>	<i>Ristorante Grotto Broggini, Via S. Materno, 6616 Losone</i>

Thursday, June 4	9:00 – 10:00	Achim Tresch	Factor graphs for the modeling of single cell time lapse movies
	10:00 – 10:30	<i>Coffee break</i>	
	10:30 – 11:00	Sven Bergmann	Fast and rigorous computation of gene and pathway scores from SNP-based summary statistics
	11:00 – 11:30	Daniel Marbach	Cell type-specific regulatory circuits reveal modules disrupted in complex diseases
	11:30 – 12:00	Judith Zaugg	Multi-omics integration reveals local and distal genetic control of chromatin states and gene expression
	12:15	<i>Lunch</i> <i>Unstructured time</i>	
	16:00 – 16:30	<i>Coffee break</i>	
	16:30 – 17:30	George Michailidis	Reconstructing regulatory networks by combining perturbation screens and steady state
	17:30 – 18:00	Matthew McCall	The epigenetic code: experimental and computational approaches to unravel the interplay between multiple epigenetic and regulatory layers
	18:00 – 18:30	Mattia Pelizzola	
19:00	<i>Dinner</i>		

Friday, June 5	9:00 – 10:00	Marloes Maathuis	Advances in causal inference with applications to systems biology
	10:00 – 10:30	Dorothee Childs	Analysis of thermal proteome profiling experiments
	10:30 – 11:00	<i>Coffee break</i>	
	11:00 – 12:00	Lars Steinmetz	Systems genetics approaches to health and disease
	12:00 – 12:15	<i>CSF Award</i>	
	12:15	<i>Lunch</i>	
		DEPARTURE	