Ascona Workshop 2011
Statistical Challenges and Biomedical Applications of Deep Sequencing Data
Centro Stefano Franscini, Monte Verità, Ascona, Switzerland, June 5 – 10, 2011

PROGRAM

Sunday, June 5	15:00 – 19:00	ARRIVAL and CHECK-IN	
	18:00 – 19:00	*Welcome drinks*	
	19:00	*Dinner*	

Monday, June 6	9:15 – 9.30	*Welcome*	
	9:30 – 10.30	**Michael Brudno**	Discovering INDEL and Copy Number Genomic Variation from Paired-end Sequencing
	10:30 – 11:00	*Coffee break*	
	11:00 – 11:30	Margaret Taub	The Effects of Low-Level Choices on Detecting Genetic Variants with High-Throughput Se quencing
	11:30 – 12:00	Moritz Gerstung	A Test for Low-frequency Mutations in Ultra-deep Sequencing Data of Heterogeneous Tumors
	12:15	*Lunch* *Unstructured time*	
	15:45 – 16:30	*Coffee break*	
	16:30 – 17.30	**Ben Raphael**	Characterization of Somatic Mutations in Cancer
	17:30 – 18:00	Daniel Stekhoven	Causal Gene Ranking
	18:00 – 18:30	Daniela Beisser	Robust Subnetworks: Computing Confidence Values for Functional Modules
	19:00	*Dinner*	

Tuesday, June 7	9:00 – 10:00	**Chris Greenman**	Inferring the Evolution of Cancer Genomes
	10:00 – 10:30	*Coffee break*	
	10:30 – 11.00	Irina Ostrovnaya	Statistical Challenges in Testing Clonal Relatedness of Tumors Using their Genomic Profiles
	11:00 – 11:30	Kaspar Hansen	Analysis of Shotgun Bisulfite Sequencing of Cancer Samples
	11:30 – 12:00	Volker Roth	HIV Haplotype Inference using a Constraint-based Dirichlet Process Mixture Model
	12:15	*Lunch* *Unstructured time*	
	15:00 – 16:00	**Willi Gruissem**	Integrating Leaf Growth and Circadian Regulation – A Systems Approach
	16:00 – 16:30	*Coffee break*	
	16:30 – 18.30	POSTER SESSION	
	19:00	*Dinner*	

Wednesday, June 8	9:00 – 10:00	**John Marioni**	The Regulation of Gene Expression Levels in Mammals
	10:00 – 10:30	*Coffee break*	
	10:30 – 11:00	Simon Anders	Statistical Methods for Comparative RNA-Seq Studies
	11:00 – 12:00	**Wolfgang Huber**	Applications to Transcriptomics – Characterisation and Functions of Non-coding RNAs
	12:15	*Lunch*	
	14:45	EXCURSION	
		DINNER	

Thursday, June 9	9:00 – 10:00	**Amalio Telenti**	Issues on the Joint Analysis of Two Genomes: the Viral Infection of the Cell
	10:00 – 10:30	*Coffee break*	
	10:30 – 11.00	Ingo Ruczinski	Some Study Designs to Improve Statistical Power in Association Tests for Rare Variants
	11:00 – 11:30	Brooke L. Fridley	Association Testing in Sequencing Studies: A Novel Framework
	11:30 – 12:00	Iuliana Ionita-Laza	A Unified Framework for the Statistical Analysis of Rare Variant Sequence Data, with Applications to Autism and Study Design
	12:15	*Lunch*	
		Unstructured time	
	16:00 – 16:30	*Coffee break*	
	16:30 – 17.30	**Mark Robinson**	Integrative Analyses of Epigenome Sequencing Data
	17:30 – 18:00	Erik Van Zwet	The Effect of Prenatal Famine Exposure on DNA Methylation
	18:00 – 18:30	Discussion	
	19:00	*Dinner*	

Friday, June 10	9:00 – 9:30	Edoardo Missiaglia	Measuring MicroRNA Expression by NGS
	9:30 – 10:00	Hubert Rehrauer	Normalization and Analysis of ChIP-seq of Histone Modifications that Cover Long Stretches and are Prevalent in the Genome
	10:00 – 10.30	*Coffee break*	
	10:30 – 11:30	**Philipp Bucher**	What ChIP-Seq Data Tell Us About Gene Regulation
	11:30 – 12:00	*CSF Award*	
	12:00	*Lunch*	
		DEPARTURE	

www.cbg.ethz.ch/news/ascona2011