

Ascona Workshop 2019

Statistical Challenges in Medical Data Science

Centro Congressi Stefano Franscini, Ascona, Switzerland, 16-21 June 2019

Programme

Sunday 16 June

15:00 – 19:00	<i>Arrival and check-in</i>
18:00 – 19:00	<i>Welcome drinks</i>
19:00	<i>Dinner</i>

Monday 17 June

08:45 – 09:00	<i>Welcome</i>	
09:00 – 10:00	Tianxi Cai	<i>Towards A Self-Learning EHR System</i>
10:00 – 10:30	Gunnar Rätsch	<i>Representation Learning of Patient Health States</i>
10:30 – 11:00	<i>Coffee break</i>	
11:00 – 11:30	Tim van de Brug	<i>Stable prediction with radiomics data</i>
11:30 – 12:00	Jean Yee Hwa Yang	<i>Evaluation strategies to examine impact of a risk-based allocation algorithm for transplantation</i>
12:00	<i>Lunch</i>	
	<i>Unstructured time</i>	
15:00 – 15:30	<i>Coffee break</i>	
15:30 – 16:30	Marylyn Ritchie	<i>Embracing the complexity of complex traits</i>
16:30 – 17:00	Kasper Hansen	<i>Using network analysis to illuminate neurological dysfunction</i>
17:00 – 19:00	Poster session	
19:00	<i>Dinner</i>	

Tuesday 18 June

09:00 – 10:00	Christina Curtis	<i>Delineating the rates and routes of metastasis</i>
10:00 – 10:30	Simona Cristea	<i>Unravelling subclonal heterogeneity and aggressive disease states in TNBC through single-cell RNA-seq</i>
10:30 – 11:00	<i>Coffee break</i>	
11:00 – 11:30	Marek Kimmel	<i>Estimation of Mutation, Drift and Selection in Single-Driver Hematologic Malignancy</i>
11:30 – 12:00	Stephen Cristiano	<i>Genome-wide cell-free DNA fragmentation as a biomarker for early detection of cancer</i>
12:00	<i>Lunch</i>	
	<i>Unstructured time</i>	
15:00 – 15:30	<i>Coffee break</i>	
15:30 – 16:30	Yinyin Yuan	<i>Deciphering geographical complexity of the tumour ecosystem</i>
16:30 – 17:00	Quaid Morris	<i>Pairtree: constructing mutation trees from multi-sample sequencing data using pairwise interactions between mutations</i>

17:00 – 19:00 Poster session
19:00 Dinner

Wednesday 19 June

09:00 – 10:00 **Chris Holmes** *Challenges in Bayesian analysis with complex models arising in modern health applications*

10:00 – 10:30 H  l  ne Ruffieux *Large-scale variational inference for hierarchical multiple-response regression modelling of high-dimensional genetic data*

10:30 – 11:00 *Coffee break*

11:00 – 12:00 **Anna Goldenberg** *Brief excursion into the problem of drug response prediction*

12:00 *Lunch*

14:00 *Excursion*

19:00 *Conference dinner*

Thursday 20 June

09:30 – 10:30 **Michael Snyder** *Big Data and Health*

10:30 – 11:00 *Coffee break*

11:00 – 11:30 Johann Gagnon-Bartsch *Parsing latent factors in high dimensional classification*

11:30 – 12:00 Beate Sick *Know when you don't know: Quantifying the uncertainty of deep learning based image classifications*

12:00 *Lunch*
Unstructured time

16:00 – 16:30 *Coffee break*

16:30 – 17:30 **Jennifer Listgarten** *Machine Learning for Protein Engineering*

17:30 – 18:00 Francesco Marass *Inference of single-cell copy number profiles from parallel DNA and RNA sequencing*

18:00 – 18:30 Junyan Lu *Latent factor modelling applied to multi-omics data integration and to precision oncology in chronic lymphocytic leukaemia*

19:00 *Dinner*

Friday 21 June

09:00 – 10:00 **Matthew Stephens** *A simple new approach to variable selection in regression, with application to genetic fine-mapping*

10:30 – 11:00 Svetlana Ovchinnikova *Sleepwalk: a tool to interactive explore dimension-reduced embeddings*

10:30 – 11:00 *Coffee break*

11:00 – 12:00 **Karsten Borgwardt** *Machine Learning for Biomarker Discovery: Combinatorial Association Mapping*

12:00 – 12:30 *CSF award*

12:30 *Lunch*
Departure