

PROGRAMME

Day 1

Thursday	Session	Chair
9:30 – 10:00	<i>Registration</i>	
10:00 – 10:30	Welcome <ul style="list-style-type: none"> • <i>View on Danish Bioinformatics.</i> Søren Brunak, UCPH, DTU, RegionH; Anders Krogh, UCPH 	
10:30 – 12:00	Network Biology in Disease <ul style="list-style-type: none"> • TBA. Jürgen Cox, MPG, DE • TBA. Anaïs Baudot, CNRS, FR • <i>Systems BioMedicine using high-throughput screening - From RNAi, miRNA and drug screens to targeting signaling pathways.</i> Jan Baumbach, SDU, DK • <i>Unsupervised learning of complex and time-series OMICS data together with biological networks.</i> Richard Röttger, SDU, DK 	Kirstine Belling Bent Petersen
12:00 – 12:45	<i>Lunch</i>	
12:45 – 14:15	Transcriptomics and Transcriptional Regulation <ul style="list-style-type: none"> • TBA. Robert Young, UoE, UK • <i>Principles for RNA metabolism and alternative transcription initiation within closely spaced promoters.</i> Yun Chen, UCPH, DK • <i>The Landscape of Isoform Switching in human cancer.</i> Kristoffer Vitting Seerup, UCPH, DK • <i>Characterizing age-dependent regulatory variation in the human frontal lobe region.</i> Maria Dalby, UCPH, DK • <i>A promoter atlas of Schizosaccharomyces pombe reveals stress-induced usage of alternative promoters.</i> Malte Thodberg, UCPH, DK 	Robin Andersson Ida Moltke
14:15 – 14:30	<i>Break</i>	

PROGRAMME

Day 1 - continued

14:30 – 16:00	Population genetics and evolution	
14:30-15:00	<ul style="list-style-type: none"> • Hummingbird diversification: a tale of introgression. Rute R. da Fonseca, UCPH, DK 	
15:00-15:15	<ul style="list-style-type: none"> • Nationwide genomic study in Denmark reveals remarkable population homogeneity. Georgios Athanasiadis, AU, DK 	Søren Besenbacher
15:15-15:30	<ul style="list-style-type: none"> • Reconstructing ancient pathogens - discovery of <i>Yersinia pestis</i> in Eurasia 5,000 years ago. Simon Rasmussen, CBS, DTU, DK 	Kasper Munch
15:30-15:45	<ul style="list-style-type: none"> • Improved D-statistic for low-coverage data. Samuele Soraggi, UCPH, DK 	
15:45-16:00	<ul style="list-style-type: none"> • Inference of distribution of fitness effects: impact of beneficial mutations. Paula Tataru, AU, DK 	
16:00 – 16:15	<i>Break</i>	
16:15 - 17:15	POSTER SESSION	
17:15 – 18:45	Non-coding RNA Bioinformatics	
17:15-17:45	<ul style="list-style-type: none"> • RNAcentral and Rfam: Tools for understanding the RNA universe. Anton Petrov, EMBL-EBI, UK 	Stefan Seemann
17:45-18:00	<ul style="list-style-type: none"> • Large-scale prediction of RNA-RNA interactions and siRNA off-targets. Ferhat Alkan. UCPH, DK 	
18:00-18:45	<ul style="list-style-type: none"> • TBA. Bruce Shapiro, NIH/NCI, USA 	
19:30	<i>Dinner</i> at Musikhuset Posten, Østre Stationsvej 35, 5000 Odense C	

Annual Danish Bioinformatics Conference 2016

August 25-26, Odense, Denmark

Day 2

Friday	Session	Chair
9:00 – 10:30	Machine Learning in Bioinformatics	
9:00-9:30	<ul style="list-style-type: none"> • Multi-layered latent variable models for learning genome-to-phenome maps. Luc Janss, AU, DK 	
9:30-9:45	<ul style="list-style-type: none"> • Identification of known and novel recurrent viral sequences in data from multiple patients and multiple cancers. Jose MG Izarzugaza, DTU, DK 	
9:45-10:00	<ul style="list-style-type: none"> • Tandem mass spectrometry peptide fragment ion prediction by Hidden Markov Models. Jan Christian Refsgaard, UCPC, DK 	Vivi Gregersen
10:00-10:15	<ul style="list-style-type: none"> • Chromosomal transcriptional initiation walks reflect three dimensional chromatin organization. Sarah Rennie, UCPH, DK 	
10:15-10:30	<ul style="list-style-type: none"> • Cataloging the landscape of RNA bioinformatics tools. Anne Wenzel. UCPH, DK 	
10:30 - 10:45	<i>Break</i>	
10:45 - 11:45	Industrial View on Danish Bioinformatics	
10:45-11:05	<ul style="list-style-type: none"> • Rapid detection of drug-resistance – a successful industry-academic cooperation. Martin Simonsen, QIAGEN, DK 	
11:05-11:25	<ul style="list-style-type: none"> • Bioinformatics in oligonucleotide drug discovery. Morten Lindow, Roche Innovation Center Copenhagen, DK 	Peter Løngreen
11:25-11:45	<ul style="list-style-type: none"> • Providing NGS data analysis as a service – XploreRNA. Jesper Culmsee Tholstrup, Exiqon 	
11:45 – 12:30	POSTER SESSION	
12:30 – 13:15	<i>Lunch</i>	

Day 2 - continued

13:15 – 14:15	Computerome and ELIXIR Denmark	
13:15-13:35	<ul style="list-style-type: none"> • Computerome, big data, and cloud computing. Peter Løngreen, DTU, DK 	Peter Løngreen
13:35-13:55	<ul style="list-style-type: none"> • TBA. Jon Ison, DTU, DK 	
13:55-14:15	<ul style="list-style-type: none"> • TBA. Mikkel H. Schierup, AU, DK 	
14:15 – 14:30	<i>Break</i>	
14:30 – 15:45	Computational Proteomics	
14:30-15:00	<ul style="list-style-type: none"> • TBA. Lennart Martens, UGent, BE 	Veit Schwämmle
15:00-15:15	<ul style="list-style-type: none"> • Proteogenomic analyses for discovery of bi-specific chimeric antigen receptor targets. Lars Rønn Olsen, CBS, DTU, DK 	
15:15-15:30	<ul style="list-style-type: none"> • Employing complementary ions for deconvolution of mixture tandem mass spectra. Vladimir Gorshkov, SDU, DK 	
15:30-15:45	<ul style="list-style-type: none"> • Scientific workflows for combining MS and MS/MS data and improving mass measurement accuracy in proteomics. Arzu Tugce Guler, LUMC, NL 	
15:45 – 16:00	<i>Meeting closure & Announcement of best poster</i>	Peter Løngreen