

PROGRAMME

Day 1

Thursday	Session	Chair
9:30 – 10:00	<i>Registration</i>	
10:00 – 10:15	Welcome <ul style="list-style-type: none"> • <i>View on Danish Bioinformatics.</i> Søren Brunak, UCPH, DTU, RegionH; Anders Krogh, UCPH 	
10:15 – 10:35	<ul style="list-style-type: none"> • <i>On the Genomics of Rainforests.</i> Thomas Sicheritz-Pontén, DTU, DK 	
10:35 – 12:05	Non-coding RNA Bioinformatics <ul style="list-style-type: none"> • <i>New computational and single-cell transcriptomic approaches in microRNA biology.</i> Marc Friedländer, SU, S (keynote speaker) • <i>CRISPR specificity and off-target assesment with RNA-DNA duplex energy model.</i> Ferhat Alkan, UCPH, DK 	Stefan Seemann
10:35 – 11:20		
11:20 – 12:05		
12:05 – 12:15	CBioVikings <ul style="list-style-type: none"> • <i>CBioVikings - Bringing the next generation of Bioinformaticians together!</i> Georgi Dimitrov, President of CBioVikings, DK 	
12:15 – 12:45	<i>Lunch</i>	
12:45 – 14:15	Systems Toxicology and Adverse Drug Reactions <ul style="list-style-type: none"> • <i>Applying Bioinformatics to Chemical Risk Assessment: Assays, Databases, Models.</i> Richard Judson, US EPA, US (keynote speaker) • <i>From chemical-target to systems toxicology: An integrative computational approach to gain insight into disease etiology.</i> Olivier Taboureau, UCPH, DK 	Lasse Folkersen Alejandro Aguayo Orozco
12:45 – 13:30		
13:30 – 13:45		

PROGRAMME

Day 1 - continued

Thursday	Session	Chair
14:15 – 14:30	<i>Break</i>	
14:30 – 16:00	Data integration	Vivi Gregersen
14:30 – 15:15	<ul style="list-style-type: none"> • <i>Integration of Biological Data: The whole is greater than the sum of its parts.</i> Danielle Lemay, USDA, US (keynote speaker) 	
15:15 – 15:45	<ul style="list-style-type: none"> • <i>Prediction of genetic predisposition using prior biological information.</i> Peter Sørensen, AU 	
15:45 – 16:00	<ul style="list-style-type: none"> • <i>Elucidation of time-dependent systems biology cell response patterns with time course network enrichment.</i> Christian Wiwie, SDU, DK 	
16:00 – 16:15	<i>Break</i>	
16:15 - 17:15	POSTER SESSION	
17:15 – 18:45	Bioinformatics in precision medicine	Kenneth Kastaniegaard
17:15 – 18:00	<ul style="list-style-type: none"> • <i>Bioinformatics for Precision Oncology.</i> Rasmus Froberg Brøndum, AAU, DK (keynote speaker) 	
18:00 – 18:15	<ul style="list-style-type: none"> • <i>Approaches to Personalized Rheumatic Medicine using Mass Spectrometry.</i> Michael Kruse Meyer, RN/AAU, DK 	
18:15 – 18:30	<ul style="list-style-type: none"> • <i>Identification of underdiagnosed patients in the context of time-ordered comorbidities.</i> Isabella Friis Jørgensen, UCPH, DK 	
18:30 – 18:45	<ul style="list-style-type: none"> • <i>Conflicting associations of dietary patterns with changes of anthropometric traits in different subgroups of middle-aged women and men.</i> Jose Alejandro Romero Herrera, UCPH, DK 	
19:30	<i>Dinner at Restaurant Nordatlanten, Nordatlantisk Promenade 1, 5000 Odense C</i>	

PROGRAMME

Day 2

Friday	Session	Chair
9:00 – 10:30	Machine and deep learning, and probabilistic programming	
09:00 – 09:45	<ul style="list-style-type: none"> • Advances in Probabilistic Programming using Python. Christopher Fonnesbeck, VUMC, USA (keynote speaker) 	Thomas Hamelryck
09:45 – 10:00	<ul style="list-style-type: none"> • DeepLoc: Prediction of protein subcellular localization using deep learning. Henrik Nielsen, DTU, DK 	
10:30 – 10:45	<i>Break</i>	
10:45 – 11:05	ELIXIR Denmark	
	<ul style="list-style-type: none"> • bio.tools update: status and plans. 	
11:05 – 11:45	Industry session	
11:45 – 12:15	POSTER SESSION	
12:15 – 12:45	<i>Lunch</i>	
12:45 – 14:15	Proteogenomics and Computational Proteomics	
12:45 – 13:30	<ul style="list-style-type: none"> • Public proteomics data: a (mostly unexploited) gold mine for computational researchers. Juan Antonio Vizcaino, EMBL-EBI, UK (keynote speaker) 	Veit Schwämmle Thomas Doktor
13:30 – 14:00	<ul style="list-style-type: none"> • Meta-analysis and generation of proteomics data analysis workflows combining text mining, ontologies and the bio.tools registry. Magnus Palmblad, LUMC, NL 	

PROGRAMME

Day 2 - continued

Friday	Session	Chair
14:00 – 14:15	<ul style="list-style-type: none"> • <i>CompSig (Complex Significance): A Computational Approaches to Decipher Composition and Regulation of Protein Complexes by Large-Scale Analysis of Mass Spectrometry Data.</i> Morteza Chalabi Hajkarim, SDU, DK 	Veit Schwämmle Thomas Doktor
14:15 – 14:30	<i>Break</i>	
14:30 – 16:00	Population genomics and evolution	
14:30 – 15:15	<ul style="list-style-type: none"> • <i>Deconstructing evolutionary processes through the population palaeogenomic window.</i> Tom Gilbert, UCPH, DK (keynote speaker) 	Kasper Munch Jonas Berglund
15:15 – 15:30	<ul style="list-style-type: none"> • <i>A probabilistic approach to whole genome based phylogeny.</i> Johanne Arhenfeldt, DTU, DK 	
15:30 – 15:45	<ul style="list-style-type: none"> • <i>Hidden Markov Model Based on Genotype Likelihood and Sequencing Depth to Detect Ploidy Levels.</i> Samuele Soraggi, UCPH, DK 	
16:00 – 16:10	<i>Meeting closure & Announcement of best poster</i>	

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15:15 – 15:30	<ul style="list-style-type: none"> • <i>FarGen: The Faroese Reference Genome and Demographic Inference of the Faroese Population.</i> Leivur N. Lydersen, FarGen, FO 	
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