

FRIDAY August 30th

12:00 Registration opens

15:00 Opening Remarks [TIVOLI HALL]

15:05 Keynotes [TIVOLI HALL]

Chair: N-H Holstein-Rathlou, DK

15:05 Stuart Kauffmann, USA: *Transformations We Must Explore in Systems Biology, Medical Science, Medical Practice and Medical Regulation*

15:35 Kim Sneppen, DK: *Epigenetics in cis and olfactoric differentiation*

16:05 Marc Vidal, USA: *Interactome networks and human disease*

16:35 Pause

16:45 Industry keynotes [TIVOLI HALL]

Chair: Rune Linding, DK

16:45 Eng Lim Goh: *High dynamic range systems for next generation data-intensive biology and beyond (Silicon Graphics Int.)*

17:30 Dan Marshak: *Dynamic Cellular Analysis in High Content Screening (Perkin Elmer Inc.)*

18:00 Klaus Lindpainter: *Innovation and Science (Thermo Fisher Scientific)*

18:30 Opening Reception

SATURDAY August 31st

08:30 Keynotes [TIVOLI HALL]

Chair: Søren Brunak, DK

08:30	Gene Myers, GER:	<i>Light-Based Systems Biology</i>
09:00	Wendell Lim, USA:	<i>The design principles of cell signaling networks</i>
09:30	Philippe Bastiaens, DE:	<i>Safeguards against autocatalytic activation of RTKs</i>

10:00 Coffee

10:30 Parallel Session I: Metagenomics [TIVOLI HALL]

Chair: Henrik Bjørn Nielsen, DK

10:30	Henrik Bjørn Nielsen	Microbial adaptation to (social) life in the human gut microbiome
11:00	Jacob Bælum	The Microbiome of Vultures
11:20	Damian Rafal Plichta	Transcriptional interference among microbial species in the human gut
11:40	Yuri Kosinsky	Modeling of short-chain fatty acids metabolism in human gut: reconstruction of possible relations between microbiota composition and type 2 diabetes
12:00	M. Arumugam	Richness of human gut microbiome correlates with metabolic markers

10:30 Parallel Session II: Systems biology - industrial applications [CARSTENSEN HALL]

Chair: Greg Stephanopoulos, USA, and Mikkel W. Pedersen, DK

10:30	Greg Stephanopoulos	Linking cancer and metabolism via isotopic labeling and network analysis
11:00	Adam Feist	An integrated multi-omics and computational characterization of Escherichia coli species used in industrial biotechnology
11:20	Joseph French	Metabolic burden of recombinant protein production: a Flux Balance Analysis approach
11:40	Philipp Jaeger	Super-high-density screens: Whole-genome yeast mutant libraries on a single plate
12:00	Mikkel W. Pedersen	Receptor Tyrosine Kinase Plasticity as a Mechanism of Resistance to mAb Therapy- Potential for Co-Targeting with Antibody Mixtures

10:30 Parallel Session III: Temporal phenomena across biological timescales [HARLEKIN HALL]

Chair: Felix Naef, CH

10:30	Felix Naef	Systems biology of temporal gene expression linked to circadian clocks
11:00	Philipp Jaeger	Mapping telomerase network changes caused by telomere shortening
11:18	David Rand	Circadian control of the cell cycle
11:36	Thirimo Rohlf	A computational model of stem cell differentiation and ageing based on dynamic interactions between Histone modifications and DNA

		methylation
11:54	Soren Vedel	Population-level benefits of aging in bacteria
12:12	Hanspeter Herzel	Combinatorial Regulation of Circadian Gene Expression
12:30	Lunch	
12:30	LUNCHEON I: (Perkin Elmer Inc.) [TIVOLI HALL]	
	Ismail Ijjaali	<i>Turning Data into Insights: Application in Systems Biology</i>
12:30	LUNCHEON II: (sbvIMPROVER) [CARSTENSEN HALL]	
		<i>Presenting the sbvIMPROVER Network Verification Challenge: Crowdsourcing Platform For Network Building and Verification</i>
13:30	Parallel Session IV: Cancer and Stem Cell Systems Biology [TIVOLI HALL]	
	Chair: Ben Neel, USA	
13:30	Ben Neel	Unexpected role of PTPN11 as a tumor suppressor gene
14:00	Laurent Vallat	Predicted intervention in a cancer genetic program
14:18	Gentian Buzi	Structural properties of feedback control in cell lineages
14:36	David Cohen	Mathematical modeling of synthetic-dosage gene interactions leading to EMT-like phenotype in colon cancer mouse model
14:54	Kate Byrne	Bistability in the Rac1, PAK and RhoA network which governs cancer cell motility
15:12	Erik Andreas Martens	Spatial structure increases the waiting time for cancer
13:30	Parallel Session V: Physiology based modeling of disease states [CARSTENSEN HALL]	
	Chair: Hans Westerhoff, NL and James Faeder, USA	
13:30	James Faeder	Combining Rule-Based Modeling and Bayesian Parameter Estimation to Infer Biochemical Mechanisms
14:00	Karen van Eunen	Competition in fatty-acid beta-oxidation leads to robustness against enzyme deficiency and sensitivity to substrate overload
14:20	Robert Palmér	A Quantitative Systems Pharmacology Modelling Approach to Understand the Effect of IL-1 Blocking Therapies in Type 2 Diabetes Mellitus
14:40	Gijs den Besten	In vivo fluxes rather than concentrations of short-chain fatty acids correlate with metabolic syndrome markers
15:00	Hans Westerhoff	The systems biologies of drug detoxification and vacation
13:30	Parallel Session VI: Metabolomics [HARLEKIN HALL]	
	Chair: Chris Newgard, USA and Jens Nielsen, SE	
13:30	Chris Newgaard	Mechanisms of cardiometabolic diseases revealed by metabolomics
14:00	Kirill Tarasov	High-content screening of yeast mutant libraries by shotgun lipidomics
14:20	Thomas Nägele	Linking high-throughput experiments to complex biochemical regulation
14:40	Markus Rehberg	The regulation of central carbon metabolism during adherent MDCK cell cultivation

15:00 Jens B Nielsen Regulating the yeast metabolome

15:30 Coffee

16:00 Keynotes [TIVOLI HALL]
Chair: Lars Juhl Jensen, DK

16:00 Peer Bork, DE: *Systemic analysis of the human gut microbiome: Variation, Stratification and association with diseases*

16:30 A van Oudenaarden, NL: *Controlling gene expression fluctuations during development*

17:00 Poster session I

- o *Bridging modeling and genome scale data sets*
- o *Complete cell modeling*
- o *Complex genetic traits*
- o *Drug discovery*
- o *From cells to tissues*
- o *Genetic networks*
- o *Host - pathogen interactions*
- o *Metabolomics*
- o *Metagenomics*
- o *Network Engineering for Biotechnology*
- o *Personalized medicine*
- o *Physiology based modeling of disease states*
- o *Protein Interaction networks*
- o *Synthetic biology*
- o *Temporal phenomena across biological timescales*
- o *Very large scale data visualization*

SUNDAY September 1st

08:30 Keynotes [TIVOLI HALL]

Chair: Jørgen Kanters, DK

- 08:30 Giulio Superti-Furga, AU: *Systems pharmacology and the mechanism of action of clinically approved cancer drugs*
- 09:00 Ruedi Aebersold, CH: *Dynamic protein networks: Analysis and significance*
- 09:30 Anne-Claude Gavin, DE: *Expanding the interaction space: protein-lipids networks*

10:00 Coffee

10:30 Parallel Session I: Precision Medicine [TIVOLI HALL]

Chair: Michael Lee, USA and Janine Erler, DK

- 10:30 Michael Lee Dynamic Rewiring of Apoptotic Signaling: A network-centric study of combination therapies for triple-negative breast cancer
- 11:00 Nicolas Chia Evidence-based gap filling and assignment of genes to gap-filled reactions
- 11:20 Gunnar Cedersund The information contained in a mechanistic model improves existing methods for data analysis when diagnosing diffuse liver disease
- 11:40 Eric Batchelor p53 signaling dynamics in single cells
- 12:00 Janine Erler Network medicine tackles cancer metastasis

10:30 Parallel Session II: Systems biology for health care data [CARSTENSEN HALL]

Chair: Søren Brunak, DK

- 10:30 Søren Brunak Population-wide high-throughput phenotyping from electronic patient record data mining
- 11:00 James Timmons Using molecular classification to produce a diagnostic of healthy ageing in humans
- 11:18 Anja Thormann Ensemble Variation – A comprehensive resource for genomic variation data
- 11:36 Fabian Theis Characterizing transcriptional cell-to-cell heterogeneities during differentiation
- 11:54 Jason Shoemaker From Omics to Medically-Relevant Disease Models
- 12:12 Francesca Sacco Establishing the logic network underlying the anti-cancer activity of metformin: a systems biology approach

10:30 Parallel Session III: Network engineering for biotechnology [HARLEKIN]

Chair: Morten Sommer, DK

- 10:30 Morten Sommer Cycling antibiotics based on drug interaction networks
- 11:00 J Krishnan Elucidating design principles underlying attractive and repulsive gradient sensing
- 11:18 Bence Mélykúti A mathematical comparison of transcription factor-facilitated mechanisms of gene regulation
- 11:36 Irene Otero Muras Multicriteria global optimization for biological circuit design
- 11:54 Shodhan Rao Model reduction of biochemical reaction networks

12:12	Wendell Lim	
12:30	Lunch	
12:30	LUNCHEON: (Perkin Elmer Inc.) [TIVOLI HALL]	
	M. Daffertshofer	<i>Observing and Describing Cellular Phenotypes - High Content Imaging Tools for Systems Biology</i>
13:30	Parallel Session IV: Strategies for Modeling Biological Systems [TIVOLI HALL]	
	Chair: Julio Saez-Rodriguez, UK and Jasmin Fisher, UK	
13:30	Jasmin Fisher	Prospects and challenges of executable cell fate determination models
14:00	Pau Creixell	Kinome-wide discovery of network-attacking mutations in cancer
14:20	Pierre Millard	ThEcoli: a kinetic model of Escherichia coli central metabolism
14:40	Andreas Raue	Lessons Learned from Quantitative Dynamical Modeling in Systems Biology
15:00	Julio Saez-Rodriguez	Logic models of signalling networks in disease
13:30	Parallel Session V: Protein interaction networks [CARSTENSEN HALL]	
	Chair: Bernd Bodenmiller, CH and Luis Serrano, ES	
13:30	Bernd Bodenmiller	Analysis of Single Cell Signaling Through Time and Space by Mass Cytometry
14:00	Marco Hein	Combined proteome-interactome study of human cells by proteomics in three quantitative dimensions
14:20	Michael Kuhn	Scaffold proteins shaped the evolution of the centrosome
14:40	Andrew Jarnuczak	Linking quantitative changes in the Saccharomyces cerevisiae proteome to system-wide perturbations of the underlying protein-protein interaction network
15:00	Luis Serrano	Integrative systems biology analysis of a small bacterium
13:30	Parallel Session VI: Drug discovery [HARLEKIN HALL]	
	Chair: Giulio Superti-Furga, AU	
13:30	Giulio Superti-Furga	Anti-viral molecular networks
14:00	Robert Tonge	Qualitative and quantitative characterization of the metabolome, lipidome and proteome of human hepatocytes stably transfected with cyp 2E1
14:18	Avijit Ghosh	The Physiochemical Determinants of Therapeutic Index: On the Quantitative Prediction of Tissue Distribution and its Implication for Drug Design
14:36	Ulrike Korf	Using reverse phase protein arrays to elucidate impact of ERBB-targeting drugs on signaling networks
14:54	Nirmala Paudel	A novel computational approach for drug target identification in a biochemical network
15:12	Frank Stefan Heldt	Multiscale modeling of influenza virus infection supports the development of antiviral drug
15:30	Coffee	

16:00 Keynotes [TIVOLI HALL]

Chair: Olga Sosnovtseva, DK

16:00 Chris Voigt, USA *TBA*

16:30 Norbert Perrimon, USA: *Spatial and temporal organization of signaling pathways*

17:00 Excursion

19:30 Conference Dinner

MONDAY September 2nd

08:30 Keynotes [TIVOLI HALL]

Chair: Jens Christian Brings Jacobsen, DK

- | | | |
|-------|--------------------|--|
| 08:30 | Mikael Benson, SE: | <i>CASyM: A roadmap for the clinical implementation of Systems Medicine</i> |
| 09:00 | Matthias Mann, DK: | <i>Very deep and accurate proteome mapping and its use in disease classification</i> |
| 09:30 | Ben Neel, USA: | <i>Integrative Functional Genomics of Breast Cancer</i> |

10:00 Coffee

10:30 Parallel Session I: Genetic networks [TIVOLI HALL]

Chair: Norbert Perrimon, USA

- | | | |
|-------|------------------|---|
| 10:30 | Norbert Perrimon | Mapping Kinase pathways in Drosophila |
| 11:00 | Luca Albergante | Robustness and evolvability determine the organization of transcriptional networks |
| 11:18 | Laura Astola | Enhancing Time Series Expression Data for Network Inference |
| 11:36 | Patrick Kemmeren | A Mosaic of Transcriptional Fingerprints |
| 11:54 | Elizabeth Koch | Discovering multifunctional genes from genetic interactions |
| 12:12 | Andrei Zinovyev | Computational analysis of synthetic lethality in DNA repair pathways with application to cancer treatment |

10:30 Parallel Session II: Complete cell modeling [CARSTENSEN HALL]

Chair: Jonathan Karr, USA

- | | | |
|-------|------------------|---|
| 10:30 | Jonathan Karr | Whole-cell models for science and engineering |
| 11:00 | Evert Bosdriesz | Escherichia coli implements a robust regulatory network motif that maximizes growth-rate |
| 11:18 | Lilia Alberghina | Towards a complete yeast cell model: development of a multi-level model of cell growth and cell cycle in the budding yeast Saccharomyces cerevisiae |
| 11:36 | Charlotte Sonck | Equilibria of structured cell population models with internal cell cycle |
| 11:54 | Ottar Rolfsson | Metabolic network model driven discovery of human metabolic reactions |
| 12:12 | Tomas Helikar | Toward whole-cell models via open science and crowd-sourcing |

10:30 Parallel Session III: Host-pathogen interactions [HARLEKIN HALL]

Chair: Wendell Lim, USA

- | | | |
|-------|------------------|---|
| 10:30 | Nevan Krogan | Using Systems Approaches to Study the Host-Pathogen Interface |
| 11:00 | K Chandrasekaran | Candida Albicans Response to Phagosomic Stresses – Implications for Pathogenesis and Host-Pathogen Interactions |
| 11:18 | Lars Kaderali | Quantitative modelling of the innate immunity induction via RigI |

11:36	Neda Nasheri	Tracking down hepatitis C virus hijacking of host enzymes, using activity-based protein profiling
11:54	Max Schelker	Modeling the intracellular dynamics of the influenza A infection
12:12	Reiko Tanaka	Mathematical modelling of Aspergillus host-pathogen Interaction
12:30	Lunch	
12:30	LUNCHEON I: (Thermo Fisher Scientific) [TIVOLI HALL]	
	Matthias Mann	<i>Quantitative, high resolution mass spectrometry as a basis for systems biology</i>
	Rune Linding	<i>Multi-scale proteomics in Network Medicine</i>
	Martin Miller	<i>Cell-selective labeling using amino acid precursors for proteomic studies of multicellular environments</i>
12:30	LUNCHEON II: (ISBE) [CARSTENSEN HALL]	
	<i>Infrastructure for Systems Biology Europe</i>	
13:30	Parallel Session IV: Signaling networks [TIVOLI HALL]	
	Chair: Gerard Manning, USA	
13:30	Gerard Manning	Billions of Years and Trillions of Bases: How genome sequences and evolution are starting to unearth biological history and the functional logic of life
14:00	Ozlem Yavas	Heritability of NF-kappaB dynamics and state-switching revealed by single-cell genealogy
14:18	Erwin M. Schoof	Targeting cancer metastasis using global, quantitative and integrative network biology
14:36	Kirti Sharma	Deep phosphoproteome: Towards systems biology of signaling events
14:54	Minsoo Choi	Optimal combined anti-cancer therapy overcoming cell-type specific drug resistance based on attractor landscape analysis of p53 network
15:12	Jennifer Ewald	Cyclin-dependent kinase routes carbon fluxes to fuel cell cycle progression
13:30	Parallel Session V: From cells to tissues [CARSTENSEN HALL]	
	Chair: Rune Linding, DK	
13:30	Rune Linding	Biological Forecasting - From Cells to Tumors
14:00	Thomas Cox	Deep proteomic analysis of the hypoxic secretome reveals lysyl oxidase as a critical mediator of pre-metastatic bone lesions in breast cancer
14:18	Ulrik Nielsen	Computational modeling to predict in vivo responses of drug combinations for HER2-amplified tumors
14:36	Craig Jolley	From cell-autonomous circadian clocks to tissue-level timekeeping
14:54	Chris Madsen	STRIPAK components determine mode of cancer cell migration and metastasis
15:12	Safia Thaminy	Integrated -omic analysis uncovers a fundamental hypoxia-driven mechanism of breast cancer progression

13:30 Parallel Session VI: Very large scale data visualization [HARLEKIN HALL]

Chair: Sean O'Donoghue, Australia

13:30	Sean O'Donoghue	Visual Analytics: A New Approach for Systems Biology
14:00	Glyn Bradley	Applied network analysis in drug discovery: strategies and future directions
14:18	Tobias Sargeant	Visualizing Correlation Patterns in Gene Expression
14:36	Falk Schreiber	Visualisation of Biological Networks and Data
14:54	Martina Kutmon	Building biological regulatory networks in Cytoscape using CyTargetLinker
15:12	Martin Falk	Visualizing Results of Mesoscopic Whole-Cell Simulations

15:30 Coffee

16:00 Keynotes [TIVOLI HALL]

Chair: Jens Christian Brasen, DK

16:00	Bernhard Palsson, DK:	<i>Predictive use of metabolic reconstructions</i>
16:30	Lars Steinmetz, DE:	<i>Integrating and characterizing transcriptional networks</i>

17:00 Poster Session 2

- o *Cancer and stem cell systems biology*
- o *Signaling networks*
- o *Strategies for modeling biological systems*
- o *System genetics and imaging*
- o *Systems biology - industrial applications*

TUESDAY September 3rd

08:30 Keynotes [TIVOLI HALL]
Chair: Morten Sommer, DK

08:30 Rama Ranganathan, USA: *The Evolutionary 'Design' of Proteins*
09:00 Dana Pe'er, USA: *What can you do with 40 dimensions in single cells, mapping development, signal processing and disease*

09:30 Coffee

10:00 Parallel Session I: System genetics and imaging [TIVOLI HALL]
Chair: Bob Murphy, USA

10:00 Prisca Liberali Inferring functional genetic interactions between signalling and membrane trafficking from parallel image-based screens in thousands of single cells
10:30 Frederic Bard Deep phenotyping and phenotypic networks allows functional analysis of regulatory networks
10:50 John Lock A coarse-grained, imaging-based analysis of Granger causality during single cell migration
11:10 Erin Styles A phenomic assessment of sub-cellular morphology in *S. cerevisiae*
Using synthetic genetic array and high-content screening
11:30 Robert F. Murphy Image-derived Spatiotemporal Models of Cell Organization, Differentiation and Perturbation

10:00 Parallel Session II: Complex genetic traits [CARSTENSEN HALL]
Chair: Haja Kadarmideen, DK and Elaine Mardis, USA

10:00 Hadja Kadarmideen From genomics to systems biology of complex phenotypes and diseases in animals
10:30 Taru Muranen Genetic modifiers of breast cancer risk associated with CHEK2 mutations
10:48 Sean Hackett Genetic basis of metabolome variation in yeast
11:06 Lisette Kogelman A systems genetics analysis of obesity using the Weighted Interaction SNP Hub (WISH) network method
11:24 Chikara Furusawa Phenotypic convergence in experimental evolution of antibiotic resistant bacteria
11:42 Li Jiang Exploring the influence of diet and lifestyle in body weight changes from large questionnaire data sets

10:00 Parallel Session III: Synthetic biology [HARLEKIN HALL]
Chair: Jay Keasling, USA

10:00 Jay Keasling Engineering Microorganisms for Production of Hydrocarbons
10:30 Jean Peccoud Estimation of reference-free gene expression rate parameters from imaging cytometry data
10:48 Domitilla Del Vecchio Combating context-dependence in biological circuits with a load driver

11:06	Joel Wilsson	A probabilistic model for genetic regulation of metabolic networks
11:24	Florian David	Novel biosensors for optimizing sustainable biodiesel production in yeast cell factories
11:42	J Raquel Pinto Vieira	Computational analysis of the interplay between tRNA competitive behavior and decoding type on the modulation of translation elongation rate

12:00 Keynotes [TIVOLI HALL]

Chair: Niels-Henrik Holstein-Rathlou, DK

12:00	Elaine Mardis, USA:	<i>The Genomics of Cancer's Evolution</i>
-------	---------------------	---

12:30 Closing ceremony & Introduction of ICSB 2014 [TIVOLI HALL]