
SATURDAY, 15 NOVEMBER 2008

- 13:00 - 15:00 Registration (Operon Foyer)
- 15:00 – 15:05 Welcome address
- Session I: Genome control I**
Chair: Frank Holstege
- 15:05 – 15:35 Eran Segal
Weizmann Institute, REHOVOT, Israel
Distinct modes of regulation by chromatin encoded through nucleosome positioning signals
- 15:35 – 16:05 Tim Hughes
University of Toronto, TORONTO, Canada
Protein-nucleic acid interactome mapping
- 16:05 – 16:35 Eileen Furlong
EMBL Heidelberg, HEIDELBERG, Germany
Developmental networks in cis: Can we decipher the code?
- 16:35 – 16:50 Caroline Friedel
LMU Munich, MUNICH, Germany
A conserved role of RNA half-life in mice and men
- 16:50 – 17:20 Coffee break
- 17:20 – 17:50 Martha Bulyk
Harvard Medical School, Boston, MA, United States of America
High-resolution DNA binding specificity profiles of transcription factors and cis regulatory codes in DNA
- 17:50 – 18:05 Nick Luscombe
EMBL-EBI Hinxton, HINXTON, CAMBRIDGE, United Kingdom
Genomic analysis of a ubiquitous small-molecule second messenger signalling system in Bacteria
- 18:05 – 18:35 Richard Young
Whitehead Institute for Biomedical Research, CAMBRIDGE, United States of America
Transcriptional circuitry and epigenetic reprogramming in stem cells
- 19:00 – 22:00 Dinner & Drinks (Canteen)

SUNDAY, 16 NOVEMBER 2008

Session II: Genome control II**Chair: Eileen Furlong**

- 09:00 – 09:30 Ewan Birney
EMBL-EBI Hinxton, HINXTON, CAMBRIDGE, United Kingdom
Ensembl and ENCODE, understanding our genome
- 09:30 – 09:45 Michael Wilson
Cambridge Research Institute, CAMBRIDGE, United Kingdom
Tissue-specific transcription is directed by genome sequence in mice carrying human chromosome 21
- 09:45 – 10:15 Marian Walhout
University of Massachusetts, WORCESTER, MA, United States of America
Gene-centered transcription regulatory networks
- 10:15 – 10:30 Esti Yeger-Lotem
Whitehead, MIT, BROOKLINE, MA, United States of America
Bridging the gap between high-throughput genetic and transcriptional data reveals cellular pathways responding to alpha-synuclein toxicity
- 10:30 – 11:00 Coffee break
- 11:00 – 11:30 Patrick Lemaire
IBDML, MARSEILLE, France
Of gene regulatory networks and the control of cell shape in early ascidian embryos
- 11:30 – 11:45 Eric Bonnet
Ghent University / VIB, GENT, Belgium
MicroRNA module network inference from expression data
- 11:45 – 12:15 Frank Holstege
University Medical Centre Utrecht, UTRECHT, Netherlands
Understanding regulatory circuitry through expression-profile phenotypes
- 12:30 – 14:00 Lunch (Canteen)
- 14:00 – 15:30 **Poster Session I: A – L (Poster Tent)**

Session III: Variation, phenotype and disease

Chair: Judith Boer

- 15:30 – 16:00 Lars Steinmetz
EMBL, HEIDELBERG, Germany
A high-resolution map of crossovers and gene conversion across the yeast genome
- 16:00 – 16:30 Edwin Cuppen
Hubrecht Institute and University Medical Center Utrecht, UTRECHT, Netherlands
Exploring the effect of structural variation in genomes on phenotypic diversity
- 16:30 – 16:45 Stig Omholt
CIGENE (Centre for Integrative Genetics), AAS, Norway
Allele interaction motifs reveal gene regulatory architecture
- 16:45 – 17:15 Ritsert Jansen
University of Groningen, HAREN, Netherlands
Genetical genomics: a combination of genetic variation with genomic profiling to reconstruct molecular networks
- 17:15 – 17:45 Coffee break
- 17:45 – 18:15 Emmanouil Dermitzakis
The Wellcome Trust Sanger Institute, HINXTON, CAMBRIDGE, United Kingdom
Population genetics and genomics of human gene expression
- 18:15 – 18:30 Boris Lenhard
University of Bergen, BERGEN, Norway
Disease susceptibility variants mapping within long-range regulatory domains of transcription factor genes
- 18:30 – 19:00 Peer Bork
EMBL Heidelberg, HEIDELBERG, Germany
Integrating molecular and metadata in two diverse biological systems: The human body and the ocean
- 19:00 – 20:30 Dinner (Canteen)
- 20:30 – 22:00 Cheese and wine reception (Operon Foyer)

MONDAY, 17 NOVEMBER 2008

Session IV: Protein function & regulatory networks I**Chair: Michel Werner**

- 09:00 – 09:30 Marc Vidal
Dana-Farber Cancer Institute, BOSTON, United States of America
Interactome networks and human disease
- 09:30 – 09:45 Patrick Cramer
University of Munich - Gene Center Munich, MÜNCHEN, Germany
Structure-system correlations identify gene regulatory modules
- 09:45 – 10:15 Brenda Andrews
University of Toronto, TORONTO, Canada
Deciphering cellular networks and pathways using yeast functional genomics
- 10:15 – 10:30 Roded Sharan
Tel Aviv University, TEL AVIV, Israel
Using protein networks to elucidate cellular phenotypes
- 10:30 – 11:00 Coffee break
- 11:00 – 11:30 Michael Boutros
German Cancer Research, HEIDELBERG, Germany
Dissection of synthetic interaction networks by RNAi
- 11:30 – 11:45 Rune Linding
Institute of Cancer Research, LONDON, United Kingdom
Molecular logic gates and network medicine
- 11:45 – 12:15 Roger Brent
University of California at Berkeley, BERKELEY, CA, United States of America
Quantitative single cell physiological and genetic study of signal control in yeast pheromone response system reveals conserved systems level cell signaling behaviors and general regulatory mechanisms
- 12:30 – 14:00 Lunch (Operon Foyer)
- 14:00 – 15:30 **Poster Session II: M – Z (Poster Tent)**

Sessions V: Protein function & regulatory networks II

Chair: Anne-Claude Gavin

- 15:30 – 16:00 Ruedi Aebersold
ETH Zurich, ZURICH, Switzerland
Proteome biology
- 16:00 – 16:30 Sarah Teichmann
MRC, CAMBRIDGE, United Kingdom
Evolution of protein complexes and protein interaction networks
- 16:30 – 16:45 Finn Kirpekar
University of Southern Denmark, ODENSE, Denmark
Identification of RNA by RNA mass mapping
- 16:45 – 17:15 Nevan Krogan
University of California, San Francisco, SAN FRANCISCO, CA, United States of America
Functional insights from genetic and protein-protein interaction map
- 17:15 – 17:45 Coffee break
- 17:45 – 18:15 Giulio Superti-Furga
CeMM Center for Molecular Medicine of the Austrian Academy of Sciences, VIENNA, Austria
Molecular machines, molecular networks and the mechanism of action of drugs
- 18:15 – 18:30 Inna Lavrik
German Cancer Research Center, HEIDELBERG, Germany
Dynamics within the CD95 death-inducing signaling complex decide life and death of cells
- 18:30 – 19:00 Edison Liu
Genome Institute of Singapore, SINGAPORE
To be confirmed
- 19:30 – 23:00 **Gala Dinner and Party (Castle of Schwetzingen)**

TUESDAY, 18 NOVEMBER, 2008

Sessions VI: Systems**Chair: Marc Vidal**

- 09:30 – 10:00 Luis Serrano
CRG, BARCELONA, Spain
***In vivo* analysis and computer simulations of Ras-Raf structure-based design mutant complexes with changed kinetic properties and affinities**
- 10:00 – 10:30 Steve Oliver
University of Cambridge, CAMBRIDGE, United Kingdom
Functional genomic and genetic approaches to the systems biology of the eukaryotic cell
- 10:30 – 10:45 Stein Aerts
VIB, University of Leuven, LEUVEN, Belgium
Functional identification of regulatory interactions through a pipeline of genetic perturbations, microarray experiments, motif predictions, and *in vivo* reporter assays in *Drosophila*
- 10:45 – 11:15 Coffee break
- 11:15 – 11:45 Michael Snyder
Yale University, NEW HAVEN, CT, United States of America
Analysis of genomes and regulatory networks in eucaryotes
- 11:45 – 12:00 Marcelo Rivas Astroza
Pontificia Universidad Católica de Valparaíso, VALPARAÍSO, Chile
Minimization of the regulatory adjustment for the prediction of cellular metabolic flux distribution after gene knockout
- 12:00 – 12:30 Jussi Taipale
University of Helsinki, HELSINKI, Finland
Systems biology of cancer
- 12:30 Boxed lunch (Operon Foyer)
- 13:00 Bus to Frankfurt Airport (from EMBL Operon)

EMERALD Workshop: “Microarray Data Quality And Systems Biology”

- 13:00 – 13:45 John Quackenbush Dana-Farber, Harvard, US
Keynote lecture
- 13:45 – 13:55 Martin Kuiper, NTNU, Norway
The Emerald project
- 13:55 – 14:25 Chris F. Taylor, EBI, UK
MIBBI: Minimum Information for Biological and Biomedical Investigations
- 14:25 – 14:55 Marc Salit, NIST, USA
Standards
- 14:55 – 15:15 Coffee break
- 15:15 – 16:00 Misha Kapushesky, EBI, UK
Data quality and network inference
- 16:00 – 16:30 Audrey Kauffmann, EBI, UK
The Bioconductor package "arrayQualityMetrics" for producing quality metrics, diagnostic plots and reports – application to the ArrayExpress database
- 16:30 – 17:00 Wolfgang Huber, EBI, UK
Metrics: use cases, case studies, and new directions