



Systems Genetics: From Genomes to Complex Traits

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- Seeing is Believing
- Non-Coding Genome
- Metabolism Meets Epigenetics

Location & dates

EMBL Heidelberg, Germany 29 Sep - 2 Oct 2019

Deadlines

Registration closed Abstract submission closed



Programme

Got something to say? Tweet it! #EESSysGen

Day 1 - Sunday 29 September 2019

Time	Speaker
11:30 - 13:00	Arrival and Registration with light lunch
13:00 - 13:15	Opening Remarks
13:15 - 14:15	Keynote Lecture: Systematic genetic perturbation screens to map biological networks Brenda Andrews - University of Toronto, Canada

Time	Speaker
14:15 - 17:15	Session 1 Chair: Patricia Wittkopp
14:15 - 14:45	Analysis of context-specific genetic effects using single-cell RNA-sequencing of differentiation iPSC cells Oliver Stegle - EMBL Heidelberg and German Cancer Research Center, Germany
14:45 - 15:00	Cross-species analysis of melanoma enhancer logic Liesbeth Minnoye - KU Leuven - VIB, Belgium
15:00 - 15:30	Coffee Break and Meet the Speakers in ATC Foyer with: Brenda Andrews - University of Toronto, Canada Oliver Stegle - EMBL Heidelberg and German Cancer Research Center, Germany Lars Steinmetz - EMBL Heidelberg, Germany Maitreya Dunham - University of Washington, USA
15:30 - 16:00	New technologies to read, write, edit (and heal) genomes Lars Steinmetz - EMBL Heidelberg, Germany
16:00 - 16:15	Comparative analysis of yeast species reveals transcriptional rewiring in cis and in trans Gat Krieger - Weizmann Institute of Science, Israel
16:15 - 16:30	Cell-to-cell protein expression variability in the human immune system is a heritable and polygenic trait Michael Morgan - Wellcome Sanger Institute, UK
16:30 - 16:45	Identifying signs of polygenic adaptation using polygenic scores Olivier Bakker - University Medical Centre Groningen, The Netherlands

Time	Speaker
16:45 - 17:15	High throughput functional characterization of natural alleles in <i>S. cerevisiae</i> Maitreya Dunham - University of Washington, USA
17:15 - 18:30	Speed Networking Session in ATC Foyer
18:30 - 20:00	Dinner in EMBL Canteen
20:00 - 22:00	Welcome Reception with Live Music in the ATC Rooftop Lounge

Day 2 - Monday 30 September 2019

Time	Speaker
09:00 - 12:00	Session 2 Chair: Marcelo Nobrega
09:00 - 09:30	Towards predicting gene expression from DNA sequence Jussi Taipale - University of Cambridge, UK
09:30 - 09:45	Defining the architecture of complex traits to understand the emergent properties of genomes Chris Jakobson - Stanford University School of Medicine, USA
09:45 - 10:15	The genomic aetiology of osteoarthritis Eleftheria Zeggini - Helmholtz Zentrum München, Germany
10:15 - 10:45	Coffee Break and Meet the Speakers in ATC Foyer with: Jussi Taipale - University of Cambridge, UK Eleftheria Zeggini - Helmholtz Zentrum München, Germany Marylyn Ritchie - University of Pennsylvania, USA

Time	Speaker
10:45 - 11:00	The genetic interaction landscape of human membrane transporters Enrico Girardi - CeMM Research Center for Molecular Medicine, Austria
11:00 - 11:30	Exploring genomics and phenomics with machine learning toward an improved understanding of complex traits Marylyn Ritchie - University of Pennsylvania, USA
11:30 - 11:45	Integration of transcriptome, proteome and phosphoproteome data elucidates the genetic control of molecular networks Andreas Beyer - University of Cologne, Germany
11:45 - 12:00	Context-sensitive analysis of genomic insulator function Matt Maurano - New York University School of Medicine, USA
12:00 - 13:30	Lunch in ATC Foyer
13:30 - 17:00	Session 3 Chair: Leopold Parts
13:30 - 14:00	From epigenetic variation across individuals to insights into disease and ageing Judith Zaugg - EMBL Heidelberg, Germany
14:00 - 14:15	Single and combinatorial CRISPR gene perturbations with 3Cs gRNAs Manuel Kaulich - Goethe University Frankfurt, Germany

Time	Speaker
14:15 - 14:30	Exploring the omnigenic model Neel Prabh - Max Planck Institute for Evolutionary Biology, Germany
14:30 - 15:00	Single cells collectively reveal non-deterministic effects of genetic variants Gaël Yvert - CNRS and École Normale Supérieure de Lyon, France
15:00 - 15:30	Coffee Break and Meet the Speakers in ATC Foyer with: Judith Zaugg - EMBL Heidelberg, Germany Gaël Yvert - CNRS and École Normale Supérieure de Lyon, France
15:30 - 16:30	Panel Discussion Session: Open science and opportunities in systems genetics Moderator: Thomas Lemberger Panel members: Bart Deplancke - École Polytechnique Fédérale de Lausanne, Switzerland Tuuli Lappalainen - New York Genome Center and Columbia University, USA Michael Snyder - Stanford University, USA Oliver Stegle - EMBL Heidelberg and German Cancer Research Center, Germany Alexandra Zhernakova - University Medical Center Groningen, The Netherlands

Time	Speaker
16:30 - 17:00	<p>Flash Talks Session 1</p> <p>Pablo Baeza-Centurion (abstract #47) - Centre for Genomic Regulation, Spain</p> <p>Marc Jan Bonder (abstract #53) - EMBL Heidelberg, Germany</p> <p>Roeland Broekema (abstract #56) - University Medical Center Groningen, The Netherlands</p> <p>Anneke Brümmer (abstract #57) - University of Lausanne, Switzerland</p> <p>Bede Busby (abstract #59) - EMBL Heidelberg, Germany</p> <p>Robert Linder (abstract #83) - University of California Irvine, USA</p> <p>Alicia Zamudio (abstract #115) - Massachusetts Institute of Technology, USA</p>
17:00 - 19:00	<p>Poster Session 1 (odd numbers)</p> <p>with beer, wine and snacks</p>
19:00 - 20:30	<p>Dinner in EMBL Canteen</p>
20:30 - 22:30	<p>After Dinner Drinks in the ATC Rooftop Lounge</p>

Day 3 - Tuesday 1 October 2019

Time	Speaker
09:00 - 12:00	<p>Session 4</p> <p>Chair: Brenda Andrews</p>
09:00 - 09:30	<p>Using single-cell genomics to investigate transcriptional dynamics</p> <p>Rickard Sandberg - Karolinska Institutet, Sweden</p>

Time	Speaker
09:30 - 09:45	Dynamic control of transcription at different chromosome positions Siqi Zhao - Washington University in St. Louis, USA
09:45 - 10:00	Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming Mirko Francesconi - LBMC and École Normale Supérieure de Lyon, France
10:00 - 10:15	Quantitative phenotyping of <i>C. elegans</i> drug responses Andy Fraser - University of Toronto, Canada
10:15 - 11:00	Coffee Break and Meet the Speakers in ATC Foyer with: Rickard Sandberg - Karolinska Institutet, Sweden Patricia Wittkopp - University of Michigan, USA
11:00 - 11:15	An integrated deep mutational scanning approach to defining the PTEN genotype-phenotype map Taylor Mighell - Oregon Health & Science University, USA
11:15 - 11:30	Curating an atlas of human gene function from CRISPR-Cas9 fitness screens Joshua Pan - Broad Institute, USA
11:30 - 12:00	Impacts of mutations on regulatory networks Patricia Wittkopp - University of Michigan, USA
12:00 - 13:30	Lunch in ATC Foyer
13:30 - 17:00	Session 5 Chair: Gaël Yvert

Time	Speaker
13:30 - 14:00	Solving protein structures and understanding genetic interactions using deep mutagenesis Ben Lehner - Centre for Genomic Regulation, Spain
14:00 - 14:15	Sequencing the BXD family, a cohort for experimental systems genetics and precision medicine David Ashbrook - The University of Tennessee Health Science Center, USA
14:15 - 14:30	Characterizing cell type specificity of eQTLs from estimated cell type abundances across GTEx tissues Sarah Kim-Hellmuth - New York Genome Center, USA
14:30 - 15:00	Humans and their bugs: the role of host-microbiome interactions in health and diseases Alexandra Zhernakova - University Medical Center Groningen, The Netherlands
15:00 - 15:30	Coffee Break and Meet the Speakers in ATC Foyer with: Ben Lehner - Centre for Genomic Regulation, Spain Alexandra Zhernakova - University Medical Center Groningen, The Netherlands Bart Deplancke - École Polytechnique Fédérale de Lausanne, Switzerland
15:30 - 16:00	Dissecting the genetic and molecular basis of organismal phenotypes in the Drosophila Genetic Reference Panel Bart Deplancke - École Polytechnique Fédérale de Lausanne, Switzerland
16:00 - 16:15	Disentangling genetic and environmental effects on the proteotypes of individuals Natalie Romanov - EMBL Heidelberg, Germany

Time	Speaker
16:15 - 16:30	<p>Fission yeast transcriptional heterogeneity surveyed by single cell RNA sequencing</p> <p>Samuel Marguerat - MRC London Institute of Medical Sciences and Imperial College London, UK</p>
16:30 - 17:00	<p>Flash Talks Session 2</p> <p>Jacob Bergstedt (abstract #50) - Institute Pasteur, France Michal Chapal (abstract #62) - Weizmann Institute of Science, Israel Pieter Clauw (abstract #64) - Gregor Mendel Institute, Austria Julie Demars (abstract #68) - INRA, France Nelly Frenkel (abstract #70) - Weizmann Institute of Science, Israel Wei Shern Lee (abstract #82) - Murdoch Children's Research Institute, Australia Josine Min (abstract #88) - University of Bristol, UK Balázs Szappanos (abstract #106) - Biological Research Centre, Hungary</p>
17:00 - 19:00	<p>Poster Session 2 (even numbers) with beer, wine and snacks</p>
19:00 - 21:00	<p>Conference Dinner in EMBL Canteen</p>
21:00 - 00:00	<p>Conference Party with DJ in the ATC Foyer</p>

Day 4 - Wednesday 2 October 2019

Time	Speaker
09:00 - 12:45	<p>Session 6 Chair: Rickard Sandberg</p>

Time	Speaker
09:00 - 09:30	The GTEx Consortium atlas of genetic regulatory effects across human tissues Tuuli Lappalainen - New York Genome Center and Columbia University, USA
09:30 - 09:45	A high-resolution genetic map of the metazoan cell generated by image-based profiling of co-perturbations Florian Heigwer - German Cancer Research Center and Heidelberg University, Germany
09:45 - 10:00	Adaptation is shaped by genetic architecture and genotype Rob Jelier - KU Leuven, Belgium
10:00 - 10:30	Functionally dissecting the genetic landscape of complex human traits Marcelo Nobrega - The University of Chicago, USA
10:30 - 11:00	Coffee Break and Meet the Speakers in ATC Foyer with: Tuuli Lappalainen - New York Genome Center and Columbia University, USA Marcelo Nobrega - The University of Chicago, USA Leopold Parts - Wellcome Sanger Institute, UK Michael Snyder - Stanford University, USA
11:00 - 11:30	Variation of gene essentiality in yeast and human Leopold Parts - Wellcome Sanger Institute, UK
11:30 - 11:45	Simultaneous quantification of mRNA and protein in single cells reveals trans-acting genetic variation Frank Albert - University of Minnesota, USA
11:45 - 12:45	Keynote Lecture: Big data and health Michael Snyder - Stanford University, USA

Time

Speaker

12:45 -
13:00

Closing Remarks and Poster Prize

13:00

Packed Lunch and Departure