Single Cell Omics

May 26–30, 2017 | Clarion Hotel Sign | Stockholm | Sweden

Scientific Organizers:
Sarah Teichmann, Wellcome Trust Sanger Institute, UK
Evan W. Newell, Singapore Immunology Network, SigN, Singapore
William J. Greenleaf, Stanford University, USA

Single cell omics is a new frontier in biology, where genome-wide data is captured at the resolution of individual cells. Single cell high-throughput technologies are being developed in the areas of imaging, mass spectrometry and DNA- and RNA-sequencing, and combinations thereof. The corresponding software and visualization tools are also a large active field of research. Single cell omics has important implications for all areas of development, differentiation and cellular decision-making, because these can now be studied at unprecedented resolution. Equally, single cell omics methods are shedding new light on immunity and cancer, due to the heterogeneous cell populations involved in both areas of biology. Therefore, these approaches are revolutionizing both basic biology as well as our understanding of disease, and technologies involved in translation to medicine. Since the field is in its infancy, and there are few meetings dedicated to this topic, there is a huge unmet need in the community to congregate and exchange ideas and information about new methods and the biological insights gained. A meeting such as this will be of continuing importance until single cell omics technologies become commonplace and established, and integrated into all areas of biology.

Session Topics:
- Single Cell DNA-Sequencing and Cancer
- Workshop 1: Making Sense of Single Cell Data (Visualization, Analysis)
- High-Throughput Imaging for Single Cell Analysis
- Single Cell Epigenomes
- Single Cell Transcriptomes
- Single Cell Nuclear Architecture
- Spatial Omics
- Single Cell Proteomics
- Workshop 2: Technology
- Single Cell Immunology

Scholarship Application & Discounted Abstract Deadline: January 26, 2017
Abstract Deadline: February 28, 2017
Discounted Registration Deadline: March 28, 2017

Note: Scholarships are available for graduate students and postdoctoral fellows and are awarded based on the abstract submitted.

Meeting Hashtag: #KSomics
www.keystonesymposia.org/17E3
FRIDAY, MAY 26
Arrival and Registration

SATURDAY, MAY 27
Welcome and Keynote Address
*Sarah Teichmann, Wellcome Sanger Institute, UK
Alexander van Oudenaarden, Hubrecht Institute, Netherlands
Revealing New Cell Types and Interactions Using Single Cell Omics

Single Cell DNA Sequencing and Cancer
*Evans W. Newell, Fred Hutchinson Cancer Research Center, USA
Anna Marciniak-Czochra, University of Heidelberg, Germany
Mathematical Modeling of Heterogeneity, Clonal Selection and Emergence of Resistance in Acute Leukemias
Michael Stratton, Wellcome Trust Sanger Institute, UK
Clonal Evolution of Cancers
Samuel Aparicio, University of British Columbia, Canada
Clonal Dynamics in Cancer at Single Cell Resolution
Massimiliano Pagani, Fondazione INGM, Italy
Short Talk: Single Cell Transcriptome Analysis of Human Tumor-Infiltrating T Regulatory Cells
Joanna Hård, Karolinska Institutet, Sweden
Short Talk: Identification of Clonal Somatic Mutations in DNA Sequencing Data from Single Cells

Path to Publication
*Barbara Cheifet, Springer Nature, USA

Workshop 1: Making Sense of Single Cell Data (Visualization, Analysis)
*Alexander van Oudenaarden, Hubrecht Institute, Netherlands
Joshua D. Campbell, Boston University, USA
Don't Fear the Zeros: Identifying Transcriptional States and Cellular Populations in Sparse Single-Cell RNA-Seq Data with Bayesian Hierarchical Modeling
Dominic Grün, Max Planck Institute of Immunobiology and Epigenetics, Germany
Single Cell RNA-Seq Reveals Cell Fate Bias of Multipotent Lymphoid Progenitors
Sue Hammad, University of Michigan, USA
Functional Heterogeneity of Spermatogenesis Revealed by >27,000 Single Cells of Mouse Testis
Martin Hemberg, Wellcome Trust Sanger Institute, UK
VR Genome Browser - Using Virtual Reality to Visualize Complex Genomic Data
Bojan Losic, Icahn School of Medicine at Sinai, USA
Predicting Peanut Allergic Reaction with Integrative Single Cell Models of T Cell Immuno-Synapse
Santiago J. Carmona, University of Lausanne, Switzerland
Single-Cell Transcriptomics of Zebrafish Immune Cells Provides Insight into the Evolution of Vertebrate Immune Cell Types

High-Throughput Imaging for Single Cell Analysis
*A. Pombo, Max-Delbrück-Centrum für Molekulare Medizin, Germany
Rahul Satija, New York Genome Center, USA
Learning the "Metadata" of a Cell with Single Cell Genomics
Long Cai, Institute of Technology, USA
Single Cell Expression Profiling and Lineage Dynamics by seqFISH and MEMOIR
Xiaowei Zhuang, Harvard University, USA
In situ Transcriptome and Genome Imaging in Single Cells
Johan Elf, Uppsala University, Sweden
Short Talk: Characterizing a library of cells at single molecule sensitivity

Poster Session 1

SUNDAY, MAY 28
Single Cell Epigenomes
*X. Sunney Xie, Peking University, China
Edith Heard, Institut Curie, France
X Inactivation
William J. Greenleaf, Stanford University, USA
Methods for Single Cell Epigenome Analysis
Arjun Raj, University of Pennsylvania, USA
Single Cell Gene Expression
Oliver Stegle, European Bioinformatics Institute, UK
Methods and Applications for Single Cell Epigenetics
Steffen Rulands, Max Planck Institute for the Physics of Complex Systems, Germany
Short Talk: Genome Scale Oscillations of DNA Methylation during Exit from Pluripotency
Yasuyuki Ohkawa, Kyushu University, Japan
Short Talk: ChiLT - an Immunoprecipitation-Free Epigenome Profiling Technology

Single Cell Transcriptomes
*Dana Pe'er, Memorial Sloan Kettering Cancer Center, USA
Sarah Teichmann, Wellcome Sanger Institute, UK
Understanding Cellular Heterogeneity
Alexandra-Chloé Villani, Broad Institute of MIT and Harvard, USA
Discovery of Human Immune Cell Populations by Single Cell Profiling
Rickard Sandberg, Karolinska Institutet, Sweden
Single Cell Gene Expression Analyses with Allelic Resolution
Sten Linnarsson, Karolinska Institutet, Sweden
An Atlas of Mouse Brain Cell Types

Poster Session 2

MONDAY, MAY 29
Single Cell Nuclear Architecture
*William J. Greenleaf, Stanford University, USA

* Session Chair † Invited but not yet accepted
Program current as of May 24, 2019. Program subject to change. Meal formats are based on meeting venue.
For the most up-to-date details, visit www.keystonesymposia.org/17E3.
**Spatial Omics**

**Ana Pombo**, Max-Delbrück-Centrum für Molekulare Medizin, Germany

*Genome Architecture Mapping, a New Single Cell Approach to Map Chromatin Contacts*

**X. Sunney Xie**, Peking University, China

*Single Cell Genomics: When Stochasticity Meets Precision*

**Ulrike Litzenger**, Stanford University, USA

*Short Talk: Single-Cell Epigenomic Variability Reveals Functional Cancer Heterogeneity*

**Christoph Bock**, Austrian Academy of Sciences, Austria

*Short Talk: CRISPR Screening with Single Cell Transcriptome Readout Establishes a High-Throughput Method for Dissecting Gene-Regulatory Mechanisms*

**Suman Bose**, Massachusetts Institute of Technology, USA

*Short Talk: A Microfluidic Platform for High-Throughput Micro-RNA Profiling of Single Cells*

**Anita Göndör**, Karolinska Institute, Sweden

*Short Talk: Novel Feedback Loops between 3D Genome Organizers and the Circadian Clock Regulate Rhythmic Chromatin Transitions in the Nuclear Architecture*

**Thomas Norman**, University of California, San Francisco, USA

*Short Talk: Interpreting Genetic Screens using Perturb-seq*

**Jeanette Baran-Gale**, University of Edinburgh, UK

*Short Talk: The Complexity of Promiscuous Gene Expression in Medullary Thymic Epithelial Cells*

**Emma K. Lundberg**, SciLifeLab Stockholm and School of Biotechnology, KTH, Sweden

*Short Talk: The Cell Atlas of the Human Protein Atlas*

**Poster Session 4**

**Workshop 2: Technology**

*Emma K. Lundberg*, SciLifeLab Stockholm and School of Biotechnology, KTH, Sweden

**Kylie R. James**, Wellcome Trust Sanger Institute, UK

*Resolving CD4+ T Helper Fate Bifurcation during Malaria*

**Nemanja Despot Marjanovic**, Massachusetts Institute of Technology, USA

*Longitudinal Profiling of Tumor Evolution in Autochthonous Mouse Models of Kras-Driven Human Lung Adenocarcinoma*

**Wissam H. Hamou**, Icahn School of Medicine at Mount Sinai, USA

*Flexible Single Cell Isolation Technologies Combined with High-Throughput Targeted Sequencing Enable the Characterization of Intratumor Heterogeneity*

**Linda Kvastad**, Royal Institute of Technology, Sweden

*In Situ Quality Control Assay Generates a Spatial Heat Map of RNA Integrity with Single Cell Resolution*

**Leeat Keren**, Stanford University, USA

*Characterization of Tumor Immune Microenvironment in Breast Cancer using Multiplexed Imaging*

**Amina Ann Qutub**, University of Texas, USA

*Communication between Developing Neural Cells*

**Single Cell Immunology**

*Garry P. Nolan*, Stanford University, USA

**Richard Conroy**, NIH Common Fund, USA

*HuBMap*

**Nir Friedman**, Weizmann Institute of Science, Israel

*Clonal Expansion under the Microscope: Imaging Collective T Cell Responses with Single Cell Resolution*

**Shalin H. Naik**, Walter & Eliza Hall Institute, Australia

*Clonal Multi-Omics*

**Meeting Wrap-Up: Outcomes and Future Directions (Organizers)**

**WEDNESDAY, MAY 31**

**Departure**

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