



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

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Organized in collaboration with Knut and Alice Wallenberg Foundation and Science for Life Laboratory. Sponsored by Janssen R&D: Pharmaceutical Companies of Johnson & Johnson, Regeneron Pharmaceuticals, Inc. and Vertex Pharmaceuticals Incorporated.

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

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

***Evan 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 Hammoud, 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

***Ana 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, California 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

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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 Litzenerger, 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

Spatial Omics

Mark D. Lynch, Fluidigm Corporation, USA
Single Cell Omics and Functional Analysis

***John Marioni**, European Bioinformatics Institute, EMBL-EBI, UK
Modeling Cell Fate Decisions during Early Development

Je H. Lee, Cold Spring Harbor Laboratory, USA
In situ Sequencing Platforms for Investigating Cellular Variations and Lineage

Mats Nilsson, Science for Life Laboratory, Sweden
Short Talk: Spatial Neuron Cell-Type Mapping in Mouse Brain by in situ Sequencing

Poster Session 3

TUESDAY, MAY 30

Single Cell Proteomics

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

Evan W. Newell, Fred Hutchinson Cancer Research Center, USA
High-Dimensional Cellular Immune Profiling in Health and Disease

Garry P. Nolan, Stanford University, USA
System-Wide Order, from Disorder, at the Cancer-Immune Interface

Dana Pe'er, Memorial Sloan Kettering Cancer Center, USA
Machine Learning for Data Analysis and Visualization

J. Christopher Love, Massachusetts Institute of Technology, USA
Integrated Single Cell Analysis for Discovery and Development

Bogdan Budnik, Harvard University, USA
Short Talk: Single Cell Proteomics by Mass Spectrometry (SCoPE-MS) New Technique for Quantification of Proteomes of Single Mammalian 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