Individual cells are the building blocks of all metazoan organisms, and the importance of analyzing biology at the single cell level has long been recognized. However, only recently have technological developments allowed quantitative single cell analyses on a broad scale, leading to an explosion of international single-cell research. This is an interdisciplinary field with fast-developing data acquisition modalities together with bespoke computational approaches, and now is a major driver of progress across many areas of biology, diagnostics and therapy. Dedicated conferences bringing together scientists with different technological, computational and bi-medical focus are therefore crucial to ensure mutual communication and to shape future developments. Current single cell meetings focus on high-throughput molecular snapshot measurements and their computational analysis. This conference will go beyond by emphasizing biological and biomedical applications of single cell approaches, including dynamic live cell measurements, to better understand the molecular control of cell fates and multicellular tissue generation in health and disease.

Plenary Session Topics:
• Single Cell Computational Biology
• Development at Single Cell Resolution
• From Single Cell Measurements to Molecular Mechanisms
• Imaging in 3D and in vivo
• New Technology for New Biology
• Extracting Information from High-Dimensional Measurements
• Reconstructing Cell Lineages
• Neuroscience at Single Cell Resolution

plus two workshops

Scholarship/Discounted Abstract Deadline: Oct 10, 2018; Abstract Deadline: Oct 18, 2018; Discounted Registration Deadline: Nov 15, 2018
Visit www.keystonesymposia.org/19L1 for more details.
SUNDAY, JANUARY 13
Arrival and Registration

MONDAY, JANUARY 14
Welcome and Keynote Address
*Berthold Göttingens, Cambridge Institute for Medical Research, UK
*Timm Schroeder, ETH Zürich, Switzerland
Scott E. Fraser, University of Southern California, USA
Multimodal Single Cell Imaging

Single Cell Computational Biology
*Timm Schroeder, ETH Zürich, Switzerland
Fabian Theis, Helmholtz Zentrum München, Germany
Rahul Satija, New York Genome Center, USA
Dana Pe’er, Memorial Sloan Kettering Cancer Center, USA
Chuangqi Wang, Worcester Polytechnic Institute, USA
Hanchuan Peng, Allen Institute for Brain Science, USA

Workshop 1: Driving Innovation in Single Cell Sequencing Data Analysis
*Dana Pe’er, Memorial Sloan Kettering Cancer Center, USA
*Rahul Satija, New York Genome Center, USA
Robin Browaeys, VIB-UGent Center for Inflammation Research, Belgium

Panel: Future Directions for Single Cell Computational Biology
*Berthold Göttingens, Cambridge Institute for Medical Research, UK
Dana Pe’er, Memorial Sloan Kettering Cancer Center, USA
Rahul Satija, New York Genome Center, USA
Fabian Theis, Helmholtz Zentrum München, Germany

Gregory W. Schwartz, University of Pennsylvania, USA
Too Many Cells Identifies and Visualizes Relationships of Single-Cell Clades
Rongxin Fang, University of California, San Diego & Salk Institute, USA
Single-Cell Regulomes Reveal Cell Taxonomy, Architectonic Heterogeneity and Regulatory Elements in Mammalian Cortex
Junil Kim, University of Copenhagen, Denmark
Reconstruction of Gene Regulatory Network from Pseudo-Time Ordered Single-Cell RNA Sequencing Data Using Conditional Mutual Information
Corey M. Williams, University of Virginia, USA
Trajectory Mapping in Single Cell Time Course Datasets using FLOW-MAP: A Graph-Based, Force-Directed Layout Algorithm
Robrecht Cannoodt, Ghent University, Belgium
Dynbenchmarks: Assessing Accuracy, Scalability, Robustness and Usability of Single-Cell Trajectory Inference Methods
Wouter Saelens, Ghent University, Belgium
Dyno: Inferring, Visualizing and Interpreting Single-Cell Trajectories

Development at Single Cell Resolution
*Ellen V. Rothenberg, California Institute of Technology, USA
Berthold Göttingens, Cambridge Institute for Medical Research, UK
Amos Tanay, Weizmann Institute, Israel
Dana Pe’er, Memorial Sloan Kettering Cancer Center, USA
Rahul Satija, New York Genome Center, USA
Allon Klein, Harvard University, USA

Panel: From Single Cell Measurements to Molecular Mechanisms
*Patricia Ernst, University of Colorado Anschutz Medical Center, USA
Lucas Peikmans, University of Zürich, Switzerland

TUESDAY, JANUARY 15
From Single Cell Measurements to Molecular Mechanisms
*Patricia Ernst, University of Colorado Anschutz Medical Center, USA
Lucas Peikmans, University of Zürich, Switzerland

Crossing Scales in Single-Cell Biology

* Session Chair † Invited but not yet accepted  
Program current as of October 15, 2019. Program subject to change. Meal formats are based on meeting venue. 
For the most up-to-date details, visit www.keystonesymposia.org/19L1.
Ellen V. Rothenberg, California Institute of Technology, USA
Single-Cell Insights into Molecular Mechanisms Controlling Lymphoid Cell Fates

Caroline Uhler, Massachusetts Institute of Technology, USA
From Single Cell Measurements to Computational Models of Gene Networks and 3D DNA Organization

Timm Schroeder, ETH Zürich, Switzerland
Analyzing Cell Fate Control Dynamics by Long-Term Single-Cell Quantification

Rene Maehr, University of Massachusetts Medical School, USA
Short Talk: Single-Cell RNA Sequencing-Based CRISPRi Screening Resolves Molecular Drivers of Human Endoderm Development

Min Xue, University of California, Riverside, USA
Short Talk: Dynamic Profiling of Intracellular Signaling Activities in Single Cells

Masahiro Ueda, RIKEN, Japan

Imaging in 3D and In Vivo

*Scott E. Fraser, University of Southern California, USA
Cristina Lo Celso, Imperial College London, UK
Healthy and Malignant Haematopoiesis in the Bone Marrow: Dynamic Cells in a Plastic Environment

Prisca Liberali, Friedrich Miescher Institute for Biomedical Research, Switzerland
Self-Organization and Symmetry Breaking in Intestinal Organoid Development

Sinem K. Saka, Harvard University, USA
Short Talk: Immuno-SABER for Highly Multiplexed and Sensitive in situ Protein Imaging with Signal Amplification

Leo Kunz, ETH Zurich, Switzerland
Short Talk: Visualization and Quantification of Cytokines at the Single Molecule Level in situ

Poster Session 2

WEDNESDAY, JANUARY 16

New Technology for New Biology

*Xiaowei Zhuang, Harvard University, USA
Stephen Quake, Stanford University, USA
Fluidics Devices for Single Cell Quantification and Manipulation

Bart Deplancke, Swiss Federal Institute of Technology Lausanne, Switzerland
Low-Input Single- and Intra-Cell RNA-Seq Technologies

Georg Seelig, University of Washington, USA
Single-Cell Profiling of the Developing Mouse Brain and Spinal Cord with Split-Pool Barcoding

Alex K. Shalek, Massachusetts Institute of Technology, USA
New Technologies for Complex Single Cell Profiling

Gary Hon, University of Texas Southwestern Medical Center, USA
Short Talk: Rational Reprogramming of Cellular States by Single-Cell Combinatorial Perturbation

Breanna DiAndret, Massachusetts Institute of Technology, USA
Short Talk: One-Pot Transfection Method for Rapid Characterization and Optimization of Genetic Systems

Luca Rappez, European Molecular Biology Laboratory, Germany
Short Talk: Spatial Single-Cell Profiling of Intracellular Metabolomes in situ

Extracting Information from High-dimensional Measurements

*Lucas Pelkmans, University of Zürich, Switzerland
Xiaowei Zhuang, Harvard University, USA
Single-Cell Transcriptome and Genome Imaging

Rick F. Horwitz, Allen Institute for Cell Science, USA
Conjoining Single Cell Imaging, Genomics and Computation to Create a Stem Cell State Space

Remco Loos, Celgene Institute for Translational Research Europe, Spain
Understanding Heterogeneity in Acute Myeloid Leukemia through Bulk and Single-Cell Gene Expression Profiling

Fan Zhang, Harvard Medical School, USA
Short Talk: Integrating Bulk and Single-Cell Transcriptomics with Mass Cytometry Data to Define Inflammatory Cell States in Rheumatoid Arthritis

Poster Session 3

THURSDAY, JANUARY 17

Reconstructing Cell Lineages

*Allon Klein, Harvard University, USA
Thomas Hofer, Deutsches Krebsforschungszentrum, Germany
Modeling Population Dynamics of Lineage Pathways through Barcoding Analysis

Barbara Wold, California Institute of Technology, USA
Following Cellular Reprogramming at the Single Cell Level

Wolf Reik, Babraham Institute, UK
Single Cell Epigenome Landscape of Development and Aging

Fernando D. Camargo, Boston Children's Hospital, USA
Cellular Barcoding in Mammalian Systems

Aziz Al'Khafaji, University of Texas, USA
Short Talk: Studying Therapeutic Resistance in Chronic Lymphocytic Leukemia using Functionalized Lineage Tracing

Bushra Raj, Harvard University, USA
Short Talk: Reconstruction of Brain Specification and Lineage Trees with Single-Cell Profiling and CRISPR Recorders

Poster Session 4

Workshop 2: Novel Single Cell Technologies

*Bart Deplancke, Swiss Federal Institute of Technology Lausanne, Switzerland

Keyue Ma, University of Texas at Austin, USA
High-Throughput Single-Cell Linking of Antigen Specificity to T Cell Receptor Sequences

* Session Chair † Invited but not yet accepted Program current as of October 15, 2019. Program subject to change. Meal formats are based on meeting venue. For the most up-to-date details, visit www.keystonesymposia.org/19L1.
Christopher S. McGinnis, University of California, San Francisco, USA
MULTI-seq: Scalable Sample Multiplexing for Single-Cell RNA Sequencing using Lipid-Tagged Indices

Arnav Moudgil, Washington University in St. Louis, USA
Joint Assay of Single Cell RNA-Seq and Transcription Factor Binding

Mandeep Singh, Garvan Institute of Medical Research, Australia
Linking High-Throughput Single-Cell RNA Sequencing with Targeted Long-Read Sequencing

Chengzhe Tian, University of Colorado Boulder, USA
A “Global Tracker” for Hard-to-Track Cancer Cells Reveals Substantial Heterogeneity in the Dynamics of Single-Cell Drug Responses

David M. Suter, École Polytechnique Fédérale de Lausanne, Switzerland
Single Live Cell Monitoring of Protein Turnover Reveals Intercellular Variability and Cell Cycle Dependence of Degradation Rates

Emily B. Fabyanic, University of Pennsylvania, USA
Probing the Mammalian Hydroxymethylome at Single-Cell Resolution Using a DNA Deaminase

Neuroscience at Single Cell Resolution
*Prisca Liberali, Friedrich Miescher Institute for Biomedical Research, Switzerland

Hongkui Zeng, Allen Institute for Brain Science, USA
Cell Type Classification in the Mouse Brain

Barbara Treutlein, ETH Zürich, Switzerland
Single-Cell Transcriptomics Uncovers Convergence of Cell Identities during Axolotl Limb Regeneration

Farimah Mapar, Massachusetts Institute of Technology, USA
Short Talk: Design and Analysis of Staged Mutual Inhibition: Using Single Neuron Computation to Implement Bi-Stable Neuronal Toggle Switch

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

FRIDAY, JANUARY 18

Departure