



NIH Common Fund
3rd Annual Single Cell Analysis Investigators Meeting
Natcher Conference Center, NIH Campus, Bethesda, MD

Meeting materials and further details are available online:

<http://commonfund.nih.gov/singlecell/meetings>

MONDAY, APRIL 20, 2015

7:30 a.m. Registration and Check-In

8:00 a.m. Welcome & Opening Remarks

- Thomas Insel, M.D., Director of the National Institute of Mental Health (NIMH)
- Roderic Pettigrew, Ph.D., M.D., Director of the National Institute of Biomedical Imaging and Bioengineering (NIBIB)

8:15 a.m. Presentation of Awards for the NIH “Follow that Cell” Challenge

8:30 a.m. Keynote Address

“A new focus on the cell: The Allen Institute for Cell Science”

Alan “Rick” Horwitz, Ph.D., Allen Institute for Cell Science

9:00 a.m. “Expansion microscopy: Towards imaging at arbitrary resolution, scale, and multiplexing”

Edward Boyden, Ph.D., MIT Media Lab and McGovern Institute, MIT

9:20 a.m. “Towards the living connectome: Imaging of individual neurons in intact, developing embryos”

Daniel Colón-Ramos, Ph.D., Department of Cell Biology, Yale University School of Medicine

9:40 a.m. Break

10:00 a.m. Lightning Talks

11:00 a.m. Break

11:20 a.m. Keynote Address

“Probing stem cell biology with single-cell gene expression”

Stuart Orkin, M.D., Dana Farber Cancer Institute, Boston Children's Hospital, Harvard Medical School

11:50 a.m. “Single-cell dissection of transcription factor expression heterogeneity in a lymphocyte developmental gene network”

Ellen Rothenberg, Ph.D., Division of Biology & Biological Engineering, California Institute of Technology

12:10 p.m.	“Detection of cell-type specific effects of pathway manipulation in neural cells” Tracy Young-Pearse, Ph.D., Brigham and Women's Hospital; Harvard Medical School
12:30 p.m.	Lunch on Your Own
1:15 p.m.	Poster Session
3:15 p.m.	<i>Keynote Address</i> “Dynamic functional heterogeneity of primary immune cells revealed by single-cell transcriptomics” Hongkun Park, Ph.D., Department of Chemistry and Chemical Biology, Harvard University
3:45 p.m.	“Single cell transcriptomics analysis of neurons and cardiomyocytes from live human tissue” Mugdha Khaladkar, Ph.D., and Jennifer Singh, Ph.D., Perelman School of Medicine, University of Pennsylvania
4:05 p.m.	“Dynamic single-cell analysis and interactions in cancer, allergy and senescence” Tania Konry, Ph.D., Department of Pharmaceutical Sciences, Northeastern University
4:25 p.m.	“Cross-scale integrin regulation organizes ECM and tissue topology” Scott Holley, Ph.D., Department of Molecular, Cellular and Developmental Biology, Yale University
4:45 p.m.	Break
5:00 p.m.	Breakout Sessions
7:00 p.m.	Day 1 General Meeting Adjourns

TUESDAY, APRIL 21, 2015

7:30 a.m.	Registration and Check-In
8:00 a.m.	Keynote Address “Targeted proteomics with single-cell and sub-cellular resolution” Amy Herr, Ph.D., Department of Bioengineering, University of California, Berkeley
8:30 a.m.	“Single-cell metabolic imaging using molecular fingerprinting” Ji-Xin Cheng, Ph.D., Weldon School of Biomedical Engineering, Purdue University
8:50 a.m.	“Single-cell microsampling mass spectrometry for elucidating cell heterogeneity in the developing embryo” Peter Nemes, Ph.D., Department of Chemistry, George Washington University
9:10 a.m.	Break
9:30 a.m.	Keynote Address “Towards a human cell atlas” Aviv Regev, Ph.D., Department of Biology, MIT; Broad Institute of MIT & Harvard
10:00 a.m.	“Single-cell SNP FISH reveals epigenetic mosaicism in genomic imprinting mutants” Arjun Raj, Ph.D., Department of Bioengineering, University of Pennsylvania
10:20 a.m.	“Characterizing neuronal subtypes in human adult cortex with single-nucleus transcriptome sequencing” Kun Zhang, Ph.D., Bioengineering Department, University of California, San Diego
10:40 a.m.	“Transcription profiling in situ by seqFISH” Long Cai, Ph.D., Division of Biology and Biological Engineering, California Institute of Technology
11:00 a.m.	Breakout Session Reports
11:55 a.m.	Wrap-Up and Summary
12:00 p.m.	Meeting Adjourns

Breakout Sessions

Monday, April 20, 2015 - 5:00-7:00 p.m.

The breakout sessions serve two purposes:

- Stimulate discussion leading to future collaborations / supplement requests
- Collect useful information for future development of the Single Cell Analysis Program (current program ends September 2016)

You are welcome to attend any session and move between them. Please contribute to the discussion by highlighting (1) how single cell analysis is having / can have an impact, (2) common challenges, (3) opportunities for new technologies, and (4) gaps in the field. Each breakout group should identify a note-taker and a representative. Representatives from each breakout session will give a 10-minute report during the meeting on April 21. Below are some suggested questions to facilitate discussion in the breakout sessions.

<p>Complete Single Cell 'omics (Room E1/E2)</p> <ul style="list-style-type: none"> • What biological insight would we gain from a single cell epigenome / proteome / metabolome / lipidome / interactome? What advances in technology would we need to see past the most abundant molecules in each class? • Where are potential dividends for a better understanding cell biology? Are they in carrying out a detailed inventory of biomolecules present, understanding the interaction of different classes of biomolecules within a cell, tracking the spatiotemporal dynamics of a subset of biomolecules? • The focus of the program has been on multicellular eukaryotic cells in a complex environment. How important is context (spatial and temporal), and how can it be better accounted for in reporting results? 	<p>Intracellular, Intercellular and Multi-scale Correlations (Room A)</p> <ul style="list-style-type: none"> • Can we fractionate the components of a single cell with high efficiency? • Is a single cell transcriptome representative of the proteome? Over what time scales? • How well does an analysis of the epigenome predict the phenotype of an individual cell? • Do correlations exist within populations of cells? Over what length and time scales do correlations exist? • How can we better link molecular / physical analysis at the single cell level with tissue and organ function? 	<p>Stochasticity at the Single Cell Level (Room G1/G2)</p> <ul style="list-style-type: none"> • What are the design principles that allow cells to function and evolve in a stochastic environment? • What role does stochasticity play in cell fate, disease progression, and development processes? • How do you measure and model technical, intrinsic, and extrinsic sources of noise in single cell analysis? • How does stochasticity vary among prokaryotic cells, unicellular eukaryotic organisms, and multicellular organisms? What insights can we gain from comparing across different cell types and environments?
<p>Is there a Periodic Table of Cell Types? (Room F1/F2)</p> <ul style="list-style-type: none"> • What kind of framework (standards, ontology, processes etc.) do we need to promote validation of cell types in research to promote reproducibility of results? • Can we readily identify the original and type of a single cell of unknown origin? • Can cell types be uniquely and robustly described solely by molecular characteristics? • What tools or techniques are required to reliably engineer a population of cells into any arbitrary pattern of known cell types? • What new insights would a systematic survey of cells at the level of level of an organ or mammal provide? • How do we map out and extract basic organizing principles of cells in complex environments? 	<p>The Future of the Single Cell Analysis Community (Room C1/C2)</p> <ul style="list-style-type: none"> • What indicators are there of the impact of single cell analysis on the research community? • What research (supported by private foundations, other government agencies, and across the world) is having a dramatic impact on the field of single cell analysis? • Is wider access to community resources a significant barrier to the development or adoption of single cell analysis techniques? If so, what resources are needed and why would they make a difference? • What level of technology performance and understanding of heterogeneity at the single cell level could be reasonably expected by 2020? What new insights will come from comprehensive tracking of cell phenotypes? For example, could we engineer synthetic multicellular organisms or re-engineer cells in vivo to halt or reverse disease progression? 	

More information available at <http://commonfund.nih.gov/singlecell/meetings>

Poster Abstracts

Poster Number	Single Cell Analysis Program Initiative	Poster Presenter	Poster Title
1	"Follow that Cell" Challenge Phase I Finalist	James Ankrum	Self-destructing cellular barcode: A versatile tool for single cell analysis
2	"Follow that Cell" Challenge Phase I Finalist	Paul Blainey	Single-cell time-lapse gene expression profiling via an engineered self reporting pathway
3	"Follow that Cell" Challenge Phase I Finalist	James Eberwine	BLINKER assessed live cell transcriptomics
4	"Follow that Cell" Challenge Phase I Finalist	Tania Konry	Microfluidic droplet based platform for dynamic single cell phenotype, secretion and interaction analysis
5	"Follow that Cell" Challenge Phase I Finalist	Markita Landry	Synthetic nano-antibodies for real-time monitoring of cellular biomarkers
6	"Follow that Cell" Challenge Phase I Finalist	Xin Lu	Single cell oncogenesis
69	"Follow that Cell" Challenge Phase I Finalist	Klas Magnusson	Next generation automated cell tracking software to Follow That Cell and its progeny accurately in complex multicellular environments
7	"Follow that Cell" Challenge Phase I Finalist	Nader Pourmand	Study the longitudinal expression of the genome of a single cell
8	"Follow that Cell" Challenge Phase I Finalist	Frederick Sachs	Tracing cells by their mechanics
9	"Follow that Cell" Challenge Phase I Finalist	Alexis Wong	Development, optimization, and enhancement of fluorescent DNA-hairpin functionalized gold nanoparticles as imaging tools
10	"Follow that Cell" Challenge Phase I Finalist	Nancy Xu	Photostable multiplexing nanoassays for real-time molecular imaging of single live cells
11	"Follow that Cell" Challenge Phase I Finalist	Eli Zunder	Tracking the phenotype of single cells using multicolor flow cytometry combined with cell-specific barcodes
12	FY 2012 RFA-RM-11-013	Matthew Cai	Highly multiplexed in situ digital quantification of targeted RNA transcripts

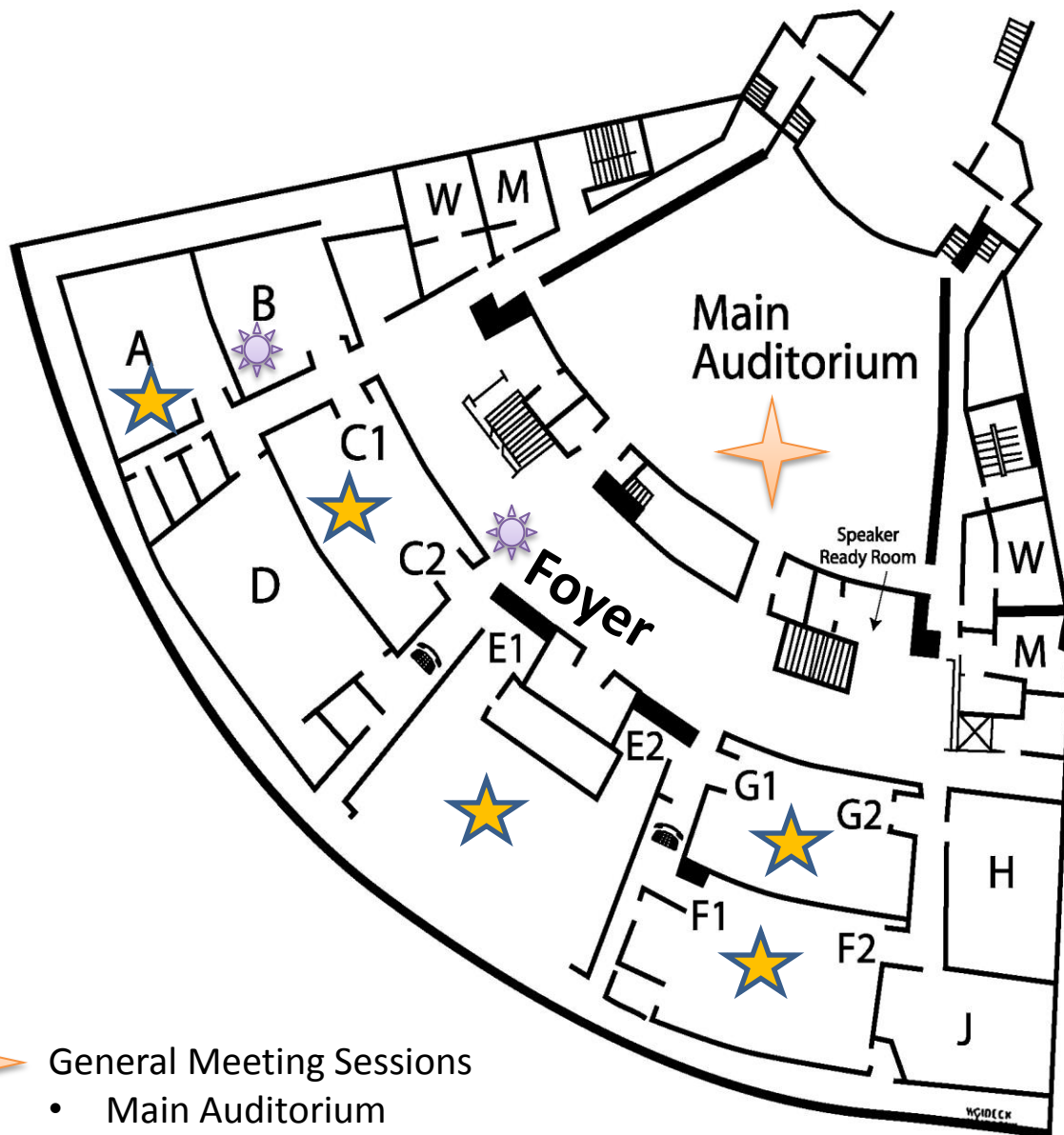
Poster Number	Single Cell Analysis Program Initiative	Poster Presenter	Poster Title
13	FY 2012 RFA-RM-11-013	Ming-Yi Lin	Use of single-cell RNA-seq to molecularly define human Cajal-Retzius neurons
14	FY 2012 RFA-RM-11-014	Suman Ghorai	Near field laser ablation sample transfer mass spectrometry and application to single cell and tissue analysis
15	FY 2012 RFA-RM-11-014	Todd Gierahn	Correlating form and function: Integrating single cell transcriptome analysis into massively parallel single cell functional assays
16	FY 2012 RFA-RM-11-014	Deirdre Meldrum	Multi-parameter single-cell analysis for comprehensive biosignature discovery
17	FY 2012 RFA-RM-11-014	Qin Peng	Single cell imaging of epigenetic dynamics
18	FY 2012 RFA-RM-11-015	Yuri Bushkin	RNA temporal expression profiles in monitoring T cell activation using single-molecule fluorescence in situ hybridization and flow cytometry (FISH-Flow)
19	FY 2012 RFA-RM-11-015	Long Cai	Single cell in situ RNA profiling by sequential FISH (seqFISH)
20	FY 2012 RFA-RM-11-015	Daniel Colón Ramos	Towards the living connectome: Imaging of individual neurons in intact, developing embryos
21	FY 2012 RFA-RM-11-015	Craig Forest	High-throughput robotic analysis of integrated neuronal phenotypes
22	FY 2012 RFA-RM-11-015	Eliot McKinley & Michael Gerdes	Characterization of the intestinal stem cell landscape with MultiOmyx™ Single Cell Analysis
23	FY 2012 RFA-RM-11-015	George McNamara	Tattletales and T-Bow: Multiplex fluorescent protein biosensors to measure and make better serial killers
24	FY 2012 RFA-RM-11-015	Navin Varadarajan	Individual motile CD4+ T cells can participate in efficient multi-killing through conjugation to multiple tumor cells
25	FY 2014 RFA-RM-13-020	Dipjyoti Das	Regulated transitions in levels of cell movement velocity and directional heterogeneity underlie vertebrate body elongation
26	FY 2014 RFA-RM-13-020	Bo Huang	Analyzing genomic elements in live animals by CRISPR imaging

Poster Number	Single Cell Analysis Program Initiative	Poster Presenter	Poster Title
27	FY 2014 RFA-RM-13-020	Tony Jun Huang	Validation of acoustic tweezers for single-cell analyses of purine metabolism
28	FY 2014 RFA-RM-13-020	Jeremy Norris	Single cell analysis using high spatial resolution and high sensitivity imaging mass spectrometry
29	FY 2014 RFA-RM-13-020	Arjun Raj	Validation and development of single nucleotide variant RNA FISH in single cells in culture and tissue
30	FY 2014 RFA-RM-13-020	Rui Sousa-Neves & Claudia Mizutani	Light-induced genetic alterations within single cell of a live vertebrate animal
31	FY 2014 RFA-RM-13-020	Jai-Yoon Sul	Nuclear pre-mRNA analysis of single cells in brain slice
32	FY 2014 RFA-RM-13-020	Tracy Young-Pearse	Single-cell detection of A β and sAPP α secreted from human iPSC-derived neurons and glia
33	FY 2014 RFA-RM-13-021	Ji-Xin Cheng	Microsecond Raman spectroscopy: Assessing single cell metabolism in a vital organism
34	FY 2014 RFA-RM-13-021	Zev Gartner	Identifying the intercellular networks regulating estrogen receptor expression with a high definition single cell printer
35	FY 2014 RFA-RM-13-021	Li He	Innovative reporters to characterize heterogeneous states among cells
70	FY 2014 RFA-RM-13-021	Jae Kyoo Lee	High spatiotemporal resolution mass spectrometry for single cell analysis
36	FY 2014 RFA-RM-13-021	Peter Nemes	Single-cell microsampling mass spectrometry for elucidating cell heterogeneity in the developing embryo
37	FY 2014 RFA-RM-13-021	John Parant	Light-induced genetic alterations within single cell of a live vertebrate animal
38	FY 2014 RFA-RM-13-021	Guillem Pratx	Whole-body tracking of single cells by positron emission localization
39	FY 2014 RFA-RM-13-022	Olga Botvinnik	Novel computational metrics and approaches for evaluating population-wide differences in alternative splicing at the single-cell level
40	FY 2014 RFA-RM-13-022	Oleg Denisenko	Visualizing epigenetic mechanisms of megakaryocyte maturation at the single cell level

Poster Number	Single Cell Analysis Program Initiative	Poster Presenter	Poster Title
41	FY 2014 RFA-RM-13-022	Boyko Kakaradov & Janilyn Arsenio	Transcriptome-wide expression analysis of single cells during T-cell specification reveals distinct drivers of early differentiation states and final lineage fates
42	FY 2014 RFA-RM-13-022	Dinesh Rao	Characterizing tumor suppressive functions of microRNAs in B-cell neoplasia
43	FY 2014 RFA-RM-13-022	Ellen Rothenberg	Genomic site binding rules and regulatory factor function in developing T cells
44	FY 2014 RFA-RM-13-022	Assieh Saadatpour	Single-cell transcript profiles reveal multilineage priming in early progenitors derived from Lgr5+ intestinal stem cells
45	FY 2014 RFA-RM-13-022	Yan Song	Dynamic of splicing modality is uncovered from single cell transcriptomics during neuronal differentiation
46	FY 2014 RFA-RM-13-022	Daniel Tenen	Molecular biology of myeloid differentiation
47	FY 2014 RFA-RM-13-022	Guo-Cheng Yuan	Robust lineage reconstruction from high-dimensional single-cell data
48	FY 2014 RFA-RM-13-023	Jonathan Grinstein	The cellular landscape of cardiac development
49	Independent	Eric Batchelor	p53 pulses diversify and coordinate target gene expression
50	Independent	Omar De la Cruz Cabrera	Cycle-regulated genes via single cell RNA sequencing
51	Independent	Jean Fan	Bayesian hierarchical approach for CNV detection in single cells from RNA-seq data
52	Independent	Silvia Gravina	Aging, single-cell methylomes
53	Independent	Kyungheon Lee	On chip analysis of CNS lymphoma in cerebrospinal fluid
54	Independent	Dylan Malayter	Correlation and kinetics of IFN γ and TNF α mRNA and protein in lymphocyte subsets at the single-cell level by flow cytometry
55	Independent	Rebecca McNaughton	High-throughput microdevice for temporal single-cell analysis
56	Independent	James Michaelson	The single cell basis for plasma protein synthesis by the liver

Poster Number	Single Cell Analysis Program Initiative	Poster Presenter	Poster Title
57	Independent	Gregor Neuert	Non-invasive perturbation and control of signaling activated gene regulation
58	Independent	Xinghua Pan	Single-cell genome-wide CpG methylation pattern analysis based on enzymatic discrimination and selective amplification promise a substantial coverage
59	Independent	Diego Presman & Ville Paakinaho	Analysis of glucocorticoid receptor dynamics by number and brightness and single-molecule tracking methods
60	Independent	Manisha Ray	The Polaris System: Integrating cell and molecular analysis at the single-cell level
61	Independent	Masahiko Sato	Characterization of cultured cells treated with low doses of formaldehyde by exhaustive single-cell lineage tracking analysis
62	Independent	Hirofumi Shintaku	On-chip preparation system for simultaneous cytoplasmic RNA and genomic DNA analyses of single cells
63	Independent	Vaishnavi Srinivasaraghavan & Jeannine Strobl	Content-rich measurements of single-cell biophysical properties via microfluidics
64	Independent	Jerilyn Timlin	TLR 4 distribution and dynamics in individual macrophage cells during immune response
65	Independent	Mohammed Uddin	Somatic variation in neurons in autism spectrum disorder
66	Independent	Linwen Zhang	Metabolites and lipids in single human cells explored by capillary microsampling electrospray ionization mass spectrometry with ion mobility separation and stable isotope labeling
67	Independent	Shuqi Zhang	iTAST: Technology platform for high-throughput in situ TCR affinity and sequence test on human primary polyclonal CD8+ T cells
68	Independent	Weian Zhao	Rapid single bacterial detection from blood using Integrated Comprehensive Droplet Digital Detection

Map of Natcher Conference Center, Lower Level (P2)



General Meeting Sessions

- Main Auditorium



Poster Session (April 20th - 1:15-3:15 p.m.)

- Foyer – Posters #1-48
- Room B – Posters #49-69



Breakout Session (April 20th - 5:00-7:00 p.m.)

- Room E1/E2 – Complete Single Cell 'omics
- Room A – Intracellular, Intercellular and Multi-scale Correlations
- Room G1/G2 – Stochasticity at the Single Cell Level
- Room F1/F2 – Is There a Periodic Table of Cell Types?
- Room C1/C2 – The Future of the Single Cell Analysis Community