

Boston Single-Cell Network

SINGLE-CELL GENOMICS WORKSHOP

Day One | 11.29.2016

Current methods of single cell analysis

Day Two | 11.30.2016

Single cell bioinformatics

TUESDAY, NOVEMBER 29, 2016

Current methods of single cell analysis

Harvard University | Sherman-Fairchild, Room 268 | 7 Divinity Avenue | Cambridge, MA

8:15-8:45 Registration and *light breakfast (provided)*

8:45-9:00 Introduction and welcome | LEV SILBERSTEIN AND PETER KHARCHENKO

Suspension-based single cell analysis

9:00-9:30 *Discovery of new human cell population by scRNA seq: From observation to validation* | ALEXANDRA CHLOE VILLANI [MIT]

9:30-10:00 *Single nuclei RNA-seq in the adult mammalian brain* | NAOMI HABIB [Broad Institute of MIT and Harvard]

10:00-10:30 Mapping cell differentiation hierarchies with high-throughput single-cell transcriptomics | DAN WAGNER [HMS]

10:30-10:45 BREAK

10:45-11:15 *Seq-Well: A Portable, Low-cost Platform for Single-cell RNA-sequencing of Low-impact Samples* | TRAVIS HUGHES [MIT-Shalek Lab]

11:15-11:45 *Not all the cells are the same—fine-tuning of single cell analysis methods* | MD SAIFUL ISLAM [Stanford]

11:45-12:15 *Lessons from the single cell core* | SARAH BOSWELL [HMS]

12:15-1:00 LUNCH (provided)

Spatially-defined single cell analysis

1:00-2:00 PLENARY: *In situ transcriptome & genome imaging in single cells* | XIAOWEI ZHUANG [Harvard-Dept. of Chemistry]

2:00-2:30 *Spatial organization of chromatin domains and compartments in single chromosomes* | STEVEN WANG [Harvard - Dept. of Chemistry-Zhuang Lab]

2:30-2:45 BREAK

2:45-3:15 *From Single-cell Perturbation to Subcellular Analysis by Fluidic Force Microscopy* | ORANE GUILLAUME-GENTIL [ETH Zurich]

3:15-3:45 *Phenotype-driven single cell analysis* | LEV SILBERSTEIN [MGH]

3:45-5:00 Panel discussion (all faculty): Q&A on practical application/experimental design of single cell analysis experiment (topics Suggested by participants)

WEDNESDAY, NOVEMBER 30, 2016

Single cell bioinformatics

Harvard Medical School | Countway Library Lahey Rm, 5th Fl | 10 Shattuck Street | Boston, MA

8:00-8:50 Registration and *light breakfast (provided)*

8:50-9:00 Introduction | PETER KHARCHENKO [HMS]

9:00-10:40 *Learning the 'metadata' of the cell with single cell genomics* | RAHUL SATIJA [NY Genome Institute—<http://satijalab.org>]

10:45-11:40 *Towards progress in batch effects and technical biases in single-cell RNA-Seq data* | STEPHANIE HICKS [<http://www.stephaniehicks.com>]

11:40-12:00 *Overview of computational methods for single-cell analysis* | PETER KHARCHENKO [<http://pklab.med.harvard.edu>]

12:00-1:00 LUNCH (provided)

1:00-2:00 *Quality control and alignment* | RADHIKA KHETANI [<https://www.edx.org/bio/radhika-khetani>]

2:00-3:50 *Heterogeneity analysis using PAGODA* | JEAN FAN [<http://scholar.harvard.edu/jeanfan/home>]

3:50-4:00 BREAK

4:00-5:00 *Gene correlation network analysis* | ASSIEH SAADATPOUR [<http://bcb.dfci.harvard.edu/~gcyuan/people.html>]

Event co-sponsors:

