

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 Medical School | NRB, Room 350 | 77 Avenue Louis Pasteur | Boston, 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 Floor | 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](#)
[\[http://www.stephaniehicks.com\]](http://www.stephaniehicks.com)

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

12:00-1:00 **LUNCH** (*provided*)

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

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

3:50-4:00 **BREAK**

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

Event co-sponsors:

