

Single-Cell RNA-Sequencing Workshop

Thursday & Friday,
October 2 & 3, 2014

Harvard University
Sherman Fairchild, Rm 268
7 Divinity Avenue
Cambridge, MA

The two-day workshop will provide attendees with an opportunity to gain detailed information on several current methods for single-cell transcriptome analysis.

The speakers have either developed a particular method or extensively used it in their own research. The workshop will focus on the theory and key technical elements of each method (including practical demonstrations) and discuss their pros and cons depending on experimental design. The data analysis part will include a hands-on session on data quality assurance, differential expression analysis and subpopulation analysis steps.

REGISTRATION

Registration is required for this free event, and space is limited to the first 40 registrants. Attendance on both days is required!

Program includes a light breakfast and lunch on both days.

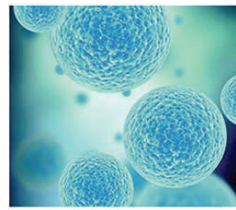
Faculty organizers:

Lev Silberstein

(lsilberstein1@mgh.harvard.edu)

Peter Kharchenko

(peter.kharchenko@post.harvard.edu)



PROGRAM: DAY ONE | OCTOBER 2

AM: Lectures (breakfast provided at 8:30 a.m.)

9:00-9:10 | Lev Silberstein and Peter Kharchenko
Introduction and overview of the workshop

9:10-9:50 | Sunney Xie (Harvard)
Single-cell RNA-Seq using multiple annealing and looping-based amplification cycles (MALBAC)

9:50-10:00 BREAK

10:00-10:40 | Saiful Islam (Stanford)
Single-cell RNA-Seq using unique molecular identifiers

10:40-11:20 | John Trombetta and Chloe Villani (Broad Institute/Regev & Hacohen Labs)
Single-cell RNA-Seq with Smart-Seq

11:20-11:30 BREAK

11:30-12:10 | Evan Daugharthy (Harvard)
FISSEQ for in situ transcriptional profiling

12:10-12:50 | Jim Eberwine (UPenn)
Single-cell transcriptomics—in fixed cells, live cell culture and live slices

LUNCH (12:50—2:00 / provided)

PM: Practical Demonstrations (group rotations)

2:00-2:40 | 2:50 -3:30 | 3:40-4:20 | 4:30—5:10

Jim Eberwine (UPenn)

Interpretation of the bioanalyzer data following single-cell cDNA amplification

Evan Daugharthy (Harvard)

FISSEQ demonstration

Saiful Islam (Stanford)

Cell isolation for single-cell RNA-Seq and UMI protocol overview

John Trombetta and Chloe Villani (Broad/Regev & Hacohen Labs)

Smart-Seq: Key experimental steps

PROGRAM: DAY TWO | OCTOBER 3

AM: Presentations & Discussion (breakfast at 8:30 a.m.)

9:00-9:40 | Manisha Ray (Fluidigm)

Using the C1 System to automate mRNA-Seq of single-cells: Introduction and implementation

9:40-10:20 | Ken Livak (Fluidigm)

Driving genomics to the single-cell level: Data analysis and implementing multiple RNA-Seq protocols on the C1 System

10:20-10:30 BREAK

10:30-11:30 | Roundtable Discussion:

Which single-cell RNA-Seq method should I choose for my experiment?

Lunch (11:30-12:30 / provided)

PM: Computational Analysis of Single-Cell Data*

12:45-1:45 | Peter Kharchenko (Harvard)

Overview of single-cell RNA-Seq analysis methods

1:30-2:30 | Guo Chen Yuan (DFCI)

Mapping cellular hierarchy by single-cell gene expression analysis

2:30—2:40 BREAK

2:45-4:00 | Data Analysis Practicum

Alignment/QC/Normalization/Differential Expression/Cell and Gene Networks/Subpopulation Analysis

* at Northwest B129 computer lab

Certificates of Attendance will be distributed at the conclusion of the program.

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AND TRANSLATIONAL
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