

Boston Single-Cell Network

SINGLE-CELL GENOMICS WORKSHOP

Day One | 11.03.2015

Current methods for genome and transcriptome analysis in single cells

Day Two | 11.04.2015

Computational analysis of the single-cell RNA-seq data

TUESDAY, NOVEMBER 3, 2015

Current methods for genome and transcriptome analysis in single cells

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

- 8:15-8:45 Registration and light breakfast
- 8:45-9:00 Introduction and welcome | **Lev Silberstein & Peter Kharchenko**
- 9:00-9:45 Keynote— **Xiaoliang Sunney Xie** [Harvard]
Single cell genome: Amplification, Characterization and Application
- 9:45-10:15 Smart-Seq | **Alexandra-Chloé Villani** [Broad Institute of MIT and Harvard]
- 10:15-10:45 **BREAK**
- 10:45-11:15 FISSEQ | **Evan Daugharthy** [Wyss Institute]
- 11:15-11:45 *Droplet barcoding for single-cell transcriptomes* | **Allon Klein** [Harvard Medical School]
- 11:45-12:15 Comparison of different single cell RNA-Seq methods | **Md Saiful Islam** [Stanford]
- 12:15-1:15 **LUNCH** (*provided*)
- 1:15-1:45 *The C1 and beyond: New methods for single-cells using Fluidigm* | **Manisha Ray** [Fluidigm]
- 1:45-2:15 Bench secrets (practical aspects of working with single cells) | **Md Saiful Islam**
- 2:15-2:45 Quality control in single cell RNA-Seq | **Alexandra-Chloé Villani**
- 2:45-3:00 **BREAK**
- 3:00-4:30 Round table discussion

WEDNESDAY, NOVEMBER 4, 2015

Computational analysis of the single-cell RNA-seq data

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

- 8:00-8:45 Registration and light breakfast
- 8:45-9:00 Introduction | **Peter Kharchenko** [HMS]
- 9:00-10:15 *Computational approaches for processing and analyzing single-cell RNA-sequencing data* | **John Marioni** [EBI UK]
- 10:15-11:30 *Mapping cellular hierarchy from single-cell gene expression data* | **Guo-Cheng Yuan** [DFCI]
- 11:30-12:15 Statistical challenges in scRNA-seq analysis | **Peter Kharchenko** [HMS]
- 12:15-1:15 **LUNCH** (*provided*)
- 1:15-2:15 Sequence processing for scRNA-seq data | **Radhika Khetani** [HSPH]
- 2:15-3:05 Quality checks and differential expression | **Joseph Herman** [HMS]
- 3:05– 3:20 **BREAK**
- 3:20– 4:20 Analysis of heterogeneity and subpopulations | **Jean Fan** [Harvard]
- 4:20– 5:00 Weighted gene correlation networks | **Assieh Saadatpour** [DFCI]