

# Boston Single-Cell Network

## SINGLE-CELL GENOMICS WORKSHOP

Day Two | 11.04.2015

*Computational analysis of the single-cell RNA-seq data*

**WEDNESDAY, NOVEMBER 4, 2015**

### Computational analysis of the single-cell RNA-seq data

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

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