

# Harvard Chan Bioinformatics Core

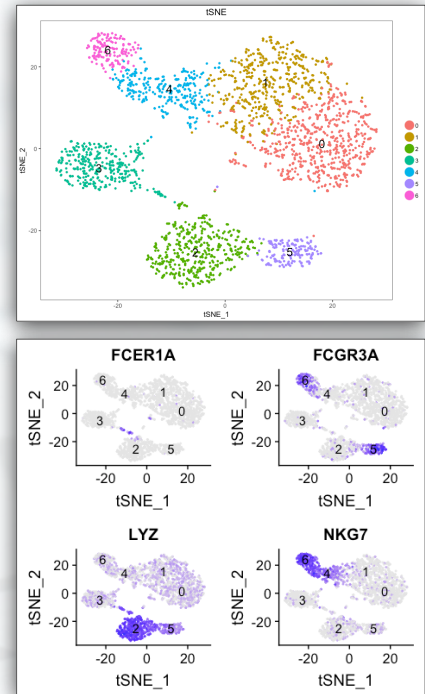
presents:

## Introduction to single-cell RNA-seq

For researchers on the Harvard Medical School Quad & those affiliated with the Harvard Stem Cell Institute (HSCI)

During this **online hands-on workshop**, participants will learn:

- how to **design a single-cell RNA-seq (scRNA-seq) experiment**
- the **steps involved** in taking raw scRNA-seq data and generating a count (gene expression) matrix
- how to use **Seurat** to analyze single-cell data, starting **from count matrices**
- how to compute and **assess QC metrics** at every step in the workflow
- how to cluster cells and **derive the identity** of the different cell types present



**This workshop has a pre-requisite:**  
**HBC's Introduction to R workshop**

OR

**Fluency with R**

**July 16<sup>th</sup>, 21<sup>st</sup> & 23<sup>rd</sup>, 2020**

**(9:30 AM - 12 PM all days)**

More information & registration link at <https://tinyurl.com/hbc-scrnaseq-workshop>

**Registration fee: \$20**

Workshop Location: **Online**

Sponsored by Harvard Medical School Foundry & the **Harvard Stem Cell Institute (HSCI)**