

Harvard Chan Bioinformatics Core

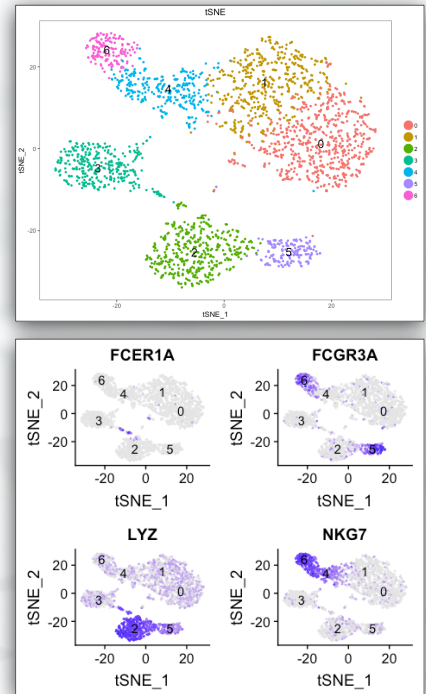
presents:

Introduction to single-cell RNA-seq

For researchers on the Harvard Medical School Quad & those affiliated with the Harvard Stem Cell Institute (HSCI) or Dana-Farber/Harvard Cancer Center

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

October 20th, 23rd & 27th 2020

(9:30 AM - 12 PM all days)

More information & registration link at: <https://tinyurl.com/HBC-scRNAseq>

Registration fee: \$40

Workshop Location: **Online**

*Sponsored by Harvard Medical School Foundry, Dana-Farber/Harvard Cancer Center
& the Harvard Stem Cell Institute (HSCI)*