[All Funders] Introduction to single-cell RNA-seq data analysis (online advanced workshop)

Introduction to single-cell RNA-seq data analysis (2020)

**Note:** This workshop is an online format using Zoom.

**Next workshop dates and times:**

- **Tuesday, October 20th:** 9:30 AM - 12 PM
- **Friday, October 23rd:** 9:30 AM - 12 PM
- **Tuesday, October 27th:** 9:30 AM - 12 PM

*Note:* Registration will open about 2 weeks prior to the workshop dates, and the dates/times above may be updated at that time.

The format of this workshop is as follows: Instruction will be mostly learner-centric requiring workshop participants to spend between 3-5 hours on reading and exercises from selected lessons before the workshop sessions. Online classes will be focused on exercises and discussion. Please make sure you take this into account when you sign up for the workshop!

**Description:**

This online hands-on workshop will instruct participants on how to design a single-cell RNA-seq experiment, and how to efficiently manage and analyze the data starting from count matrices. This will be a hands-on workshop in which we will focus on using the Seurat package in R.

**Prerequisites?**

This is one of our advanced workshops, and requires registrants to have attended the following Basic workshop offered by our training team within the last 6-8 months:

- **Introduction to R**

I am fluent in R but have not attended the HBC prerequisite workshop, can I still register?

Yes, you can register but please do the following:

- Complete the registration first
- Then email us directly at hbctraining@hsph.harvard.edu with a description of your knowledge/experience. **Failure to do this step may prevent you from being accepted into this advanced workshop.**

**Who should attend?**

Eligible Harvard researchers who want to learn:

1. How to design a single-cell RNA-seq experiment
2. How to use the Seurat package to analyze single-cell RNA-seq count matrices
3. How to compute and assess QC metrics at every step in the workflow
4. How to cluster cells based on expression data and derive the identity of the different cell types present
5. How to combine samples within a dataset, and across datasets using Integration

**Cost and Registration:**

There is a non-refundable and non-transferable $40 registration fee for this advanced workshop.

We will be accepting 20-30 participants on a first-come, first-served basis:

- If you are one of the first 20-30 eligible registrants, you will receive an email with a link to pay the (non-refundable & non-transferable) $40 registration fee.
- If you are not among the first 20-30 eligible registrants, you will be added to the waitlist and notified when we open registration for the next iteration of this workshop.
NOTE: You will not have a reserved seat for this workshop until you pay the registration fee. Please make sure you pay within the time stated in that email, else you will lose your spot to someone on the waitlist.

Eligibility requirements:

* To be eligible to attend this workshop you should fulfill at least one of the following criteria:
  
  * Harvard Medical School researcher in a lab on the Quad, with grants administered by HMS
  * Graduate student at the Harvard Medical School
  * Researcher affiliated with the Dana-Farber / Harvard Cancer Center (DF/HCC).
  * Harvard researchers whose PIs are associated with the HSCI as Principal or Affiliated faculty

  If you are unsure of your eligibility, please register anyway and we will get back to you.

Registration is closed.

(Please check the eligibility requirements above prior to registering)

Questions:

Please contact us at hbctraining@hsph.harvard.edu with any questions.