Note: Until further notice, workshops will be taught online via Zoom. However, we anticipate returning to in-person teaching in 2022.

Next workshop dates and times:

- Thursday, May 19th: 1:30 PM - 4 PM
- Monday, May 23rd: 1:30 AM - 4 PM
- Thursday, May 26th: 1:30 AM - 4 PM

Note: Registration will open about 3 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 and in-person classes will be focused on exercises and discussion, and participants are expected to attend all three sessions. Please make sure you take this into account when you sign up for the workshop!

Description:

This 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 $50 registration fee for this advanced workshop.

We will accept participants on a first-come, first-served basis:

- If you are one of the first eligible* registrants, you will receive an email with a link to pay the (non-refundable & non-transferable) $50 registration fee.
* If you are not among the first 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 must be an HSPH researcher in the lab/group of an HSPH primary faculty.

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

Registration is closed

(Registration will open approximately 3 weeks prior to first day of the workshop)

NOTE: We do not record our training sessions.

Questions?

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