Due to the COVID-19 outbreak, we are moving this workshop to an online format using Zoom.

Next workshop dates:

Tuesday April 14th : 9 AM - 12:30 PM

Wednesday April 15th : 9 AM - 12:30 PM

Thursday April 16th : 9 AM - 12:30 PM

Note: Registration will open about 3 weeks prior to the workshop dates, and the dates/times above may be updated at that time.

Description:

This online hands-on workshop will introduce participants to using R and RStudio. R is a simple programming environment that enables the effective handling of data, while providing excellent graphical support. RStudio is a tool that provides a user-friendly environment for working with R.

This workshop is intended to provide basic R programming knowledge. Participants should be interested in:

- learning the basics of R for reproducible data wrangling and visualizations (ggplot2)
- performing data analyses requiring a basic knowledge of R
- learning R to take an advanced workshop with us on the analysis of sequencing data in the next 6-8 months

Workshop segments will address the following:

- R syntax: Understanding the different ‘parts of speech’ in R; introducing variables and functions, demonstrating how functions work, and modifying arguments for specific use cases.
- Data structures in R: Getting a handle on the classes of data structures and the types of data used by R.
- Data inspection and wrangling: Reading in data from files. Using indices and various functions to subset and create datasets, including the tidyverse suite of packages.
- Visualizing data: Visualizing data using plotting functions from the external package ggplot2.
- Exporting data and graphics: Generating new data tables and plots for use outside of the R environment.

In addition to the above, we will focus on good data management practices, installing and working with data wrangling and visualization packages, and the different ways to get help when coding in R. After this workshop participants can expect to be comfortable with the basics of data wrangling and plotting using R.

Prerequisites?

This is one of our basic workshops, and has NO prerequisites and no prior programming experience is required.

This workshop (or fluency in R) is a prerequisite for advanced workshops introducing the analysis of bulk RNA-seq, scRNA-seq, and ChIP-seq data.

Who should attend?

Eligible* Harvard researchers who:

1. want to learn how to use R and RStudio for data wrangling and visualizations
2. desire to perform data analysis methods where basic knowledge of R is a requirement
3. are interested in taking an advanced workshop with us on analysis of sequencing data within the next 6 - 8 months

Cost and Registration:

There is a non-refundable and non-transferable $10 registration fee for this online workshop.

We will be accepting 25-30 participants on a first-come, first-served basis:

- If you are one of the first 25-30 eligible* registrants, you will receive an email within 1 week with a link to pay the (non-refundable & non-transferable) $10 registration fee.
- If you are not among the first 25-30 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 students at the Harvard Medical School
  - 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.

The workshop is now full!

(Please check the eligibility requirements prior to registering)

Questions?

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