[HSCI/HMS] Introduction to Differential Gene Expression Analysis workshop (2-day advanced workshop)

Introduction to Differential Gene Expression Analysis workshop (bulk RNA-seq)

**Note:** Due to the COVID-19 outbreak, we are cancelling the current workshop scheduled for May 19th and 20th. Please email us if you have any questions.

Next workshop dates:

*TBD* (updated dates will be added when they become available.)

*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 2-day hands-on workshop will introduce participants to statistical methods and considerations utilized to perform differential gene expression analysis on bulk RNA-seq data. Participants will learn about best practices in quality control, how to perform statistical analysis to obtain lists of differentially expressed (DE) genes using DESeq2. The workshop will also give participants an overview of tools for functional analysis of DE genes and how to extract some biological meaning from large gene lists.

**Please note that this workshop does **NOT** cover single-cell RNA-seq analysis.**

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

If you have **not taken the above workshop with us**, but **are already fluent** with R, please do the following:

- Complete the registration first
- Then email us directly at hbctraining@hsph.harvard.edu with a description of your knowledge/experience.

Who should attend?

Eligible* Harvard researchers who have attended an Introduction to R workshop recently, and want to learn:

1. How to perform a differential expression analysis at the gene-level
2. How to effectively use R to get your data in the appropriate format for DE analysis
3. The steps and statistical approaches used in assessing the quality of your abundance estimates (count data)
4. How to visualize expression patterns for differentially expressed genes
5. How to perform functional analysis on gene lists with R-based tools

Cost and Registration:

There is a non-refundable and non-transferable $65 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) $65 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
• Harvard researchers whose PIs are associated with the HSCI as Principal or Affiliated faculty

If you are unsure of your eligibility, please register anyways 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.