[DF/HCC] Introduction to Differential Gene Expression Analysis workshop

Introduction to bulk RNA-seq (Part II)

*(Differential Gene Expression and Functional analysis)*

**Note:** Due to the COVID-19 pandemic, we are moving this workshop to an online format using Zoom.

**Next workshop dates and times:**

- **Tuesday, August 4th:** 10 AM - 12 PM
- **Thursday, August 6th:** 10 AM - 12 PM
- **Tuesday, August 11th:** 10 AM - 12 PM
- **Thursday, August 13th:** 10 AM - 12 PM

!!NEW!! Instruction for this workshop 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 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 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 eligible to our advanced workshop.**

**Who should attend?**

Eligible* Harvard researchers who have attended our Introduction to R workshop (or have working knowledge of R), 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** $40 registration fee for this online workshop.

We will be accepting 25-35 participants on a first-come, first-served basis:
If you are one of the first 25-35 eligible registrants, you will receive an email within 1 week with a link to pay the (non-refundable & non-transferable) $40 registration fee.

If you are not among the first 25-35 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 be affiliated with the Dana-Farber / Harvard Cancer Center (DF/HCC).

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

Registration is now closed

(Please check the eligibility requirements above prior to registering)

Questions?

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