

Harvard Chan Bioinformatics Core

presents:

Introduction to bulk RNA-seq data analysis

(Experimental design -> Raw data -> Count matrices)

During this **online hands-on workshop**, participants will learn:

- how to **design a bulk RNA-seq experiment**
- the **steps involved** in taking raw RNA-sequencing data (Illumina) and generating a count (gene expression) matrix
- how to compute and **assess QC metrics** at every step in the workflow
- how to **automate a simple workflow** on the cluster using shell scripting
- how to effectively use HMS-RC's high performance **compute cluster (O2) for data management and analysis**

**The Introduction to command-line interface (shell) workshop
is a pre-requisite!**

Please check link below for eligibility requirements.

November 17th, 20th & 24th, 2020

(9:30 AM - 12 PM, all days)

More information & registration link at <https://tinyurl.com/hbc-rnaseq-online>

Registration fee: \$40

Workshop Location: **Online (Zoom)**

Sponsored by *HMS Foundry*, *DFHCC* & the *Harvard Stem Cell Institute (HSCI)*