

# Harvard Chan Bioinformatics Core

presents:

## Introduction to RNA-seq

During this **2-day 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.

**March 16<sup>th</sup> and 17<sup>th</sup>, 2020**

(9am - 5pm, both days)

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

**Registration fee: \$65**

Workshop Location: **Longwood Medical Area**

*Sponsored by Harvard Medical School's **Tools and Technology Committee (TnT)** &  
the **Harvard Stem Cell Institute (HSCI)***