Harvard Chan Bioinformatics Core
presents:

Introduction to High-Performance Computing for RNA-seq Data Analysis

*For **Harvard researchers affiliated** with*
Harvard Medical School labs on the Quad,** or the **Harvard Stem Cell Institute

**Are you planning to generate and/or analyze RNA-seq data?**

Do you want to use local clusters/high-performance computing environments for analysis?

This **2-day hands-on** workshop will instruct participants on how to efficiently manage and analyze data using the command line interface and high-performance computing (HPC), with a focus on the RNA-seq workflow.

Introduction to:

- *Unix/Linux shell*
- *O2 compute cluster (HMS-RC)*
- *RNA-seq data analysis workflow (from FASTQ to counts)*

Prior sequence analysis or command line experience not required
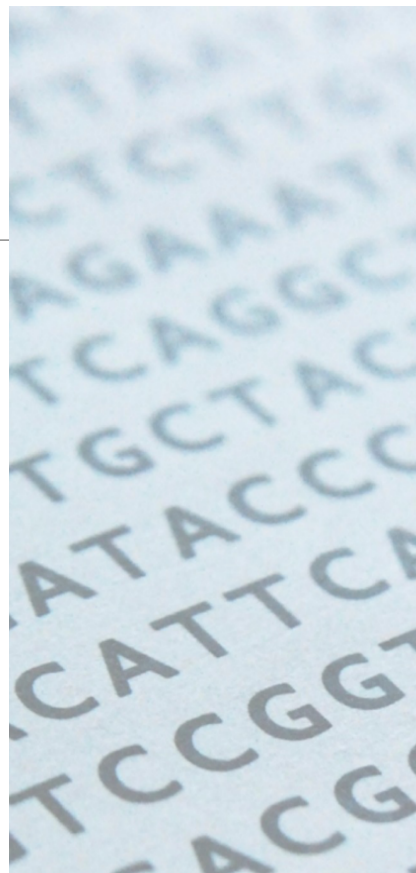
May 30th & 31st, 2018
(9am - 5pm)

More information & registration link at **http://tinyurl.com/rnaseq-hpc-may2018**

Registration fee: $70

Workshop Location: **Harvard University, Cambridge, MA**

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