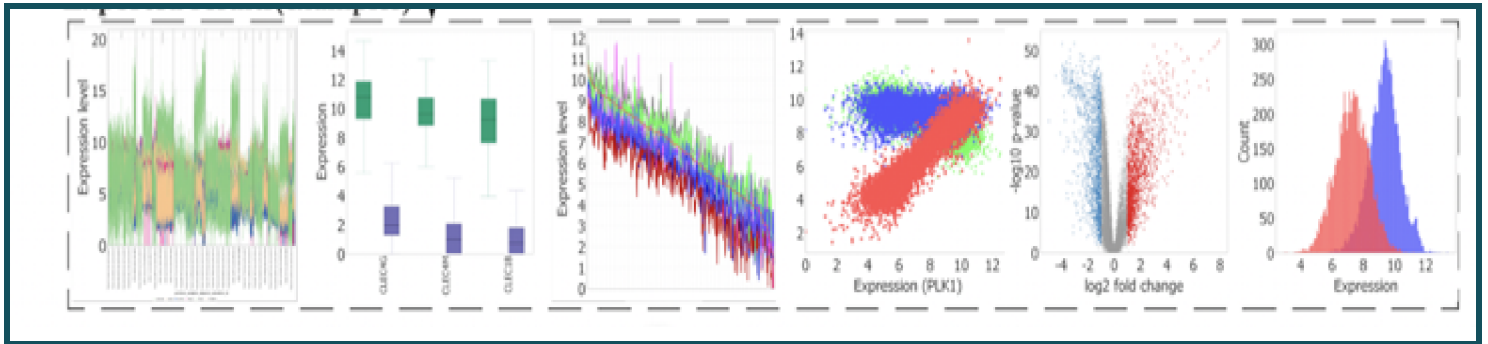


A hands-on workshop in COVID-19 RNA-Seq data analysis in an HPC environment



The goal of this workshop is to train people in *reproducible, high throughput* bioinformatics analysis of RNA-Seq datasets, as crucial to biological discovery.

March 29, 10 am-1 pm CST (4-7 pm UTC)

Session 1 Refresher in python.

Optional pre-workshop session. Refresher in python. Leader, Jeff Haltom.

March 29, 1:30 pm-3 pm CST (7:30-9 pm UTC)

Session 2. pyrpipe. Introduce best-practices for RNA-Seq analysis pipelines and detail popular

RNA-Seq processing tools like SRA Tools, Trimgalore, STAR, and stringtie. Describe anaconda environment manager, a popular package manager for maximizing reproducibility of RNA-Seq results. Hands-on analysis with **pyrpipe** (Singh et al., 2021), an efficient, flexible python package for writing RNA-Seq pipelines. We will describe pyrpipe, and detail how to customize it to process RNA-Seq data from COVID-19 studies. Leader, Urminder Singh.

March 29, 3 pm-4 pm CST (9-10 pm UTC)

Session 3. Integrating pyrpipe with the Snakemake workflow manager We will focus on

integrating pyrpipe with Snakemake workflow manager to write scalable pipelines. Leader, Urminder Singh.

March 30, 10-12 CST (4-6 pm UTC)

Session 4. MetaOmGraph (MOG). Downstream user-friendly exploratory analysis and visualization of RNA-Seq data. MOG (Singh et al, 2020) is a Java platform tool to enable analysis and visualization of large datasets. MetaOmGraph seamlessly integrates with R and with pyrpipe. Leader, Priyanka Bhandari

No coding required for Session 4

For each session, users will run programming exercises on real RNA-Seq data from COVID-19 studies.

Workshop is open to 30 participants.

Register at <https://forms.gle/MgP3DjtMj5ddBdBx9>

In conjunction with the 3rd COV-IRT Symposium <https://www.cov-irt.org/symposium-3/>

