
INTRO RNASEQ INFORMATICS WORKSHOP

INTRODUCTION

▶ Who

- ▶ Instructors: Vanessa L. González, Katie Murphy
- ▶ Helpers: Rebecca Dikow, Matt Kweskin, Mike Trizna
- ▶ Participants: You!

▶ What

- ▶ Training on how to run RNAseq pipeline on SI-HPC, “Hydra -5”

▶ Why

TIPS

- ▶ All materials are posted to the Smithsonian Workshops
GitHub: <https://github.com/SmithsonianWorkshops/2020-01-28-NMNH-RNAseq>
- ▶ If you have questions, raise your hand or put up a sticky note. If you are stuck, chances are someone else is too!

ROUGH SCHEDULE

- 9:00am - Introduction to Workshop
- 9:15am - Wet Lab discussion/LAB Resources
- 10:00am - Informatics Introduction
- 10:15am - BREAK
- 10:30am - Evaluate Read Quality (FASTQC)
- 11:00am - Trimming & Data refinement (Trimgalore)
- 11:30am - De Novo Transcriptome Assembly (Trinity)
- 12:00pm - Lunch
- 1:00pm - QA/QC of Assembly
- 1:30pm - Transcript Quantification
- 2:15pm - Differential Expression Analysis
- 3:00pm - BREAK
- 3:15pm - Differential Expression Analysis (Continued)

PRE-COURSE SURVEY

- ▶ Please fill out the pre-course survey:

<https://forms.gle/cGz68tMjbtz5ZVA67>

