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# INTRO RNASEQ INFORMATICS

## INTRODUCTION

### ▶ Who

- ▶ Instructors: Vanessa L. González (GGI)
- ▶ Participants: You!

### ▶ What

- ▶ Training on how to run RNAseq pipeline on SI-HPC, "Hydra"

### ▶ Why

### TIPS

- ▶ All materials are posted to the Smithsonian Workshops GitHub: [https://github.com/SmithsonianWorkshops/SMSC\\_Conservation\\_Genomics/tree/master/Day%2007](https://github.com/SmithsonianWorkshops/SMSC_Conservation_Genomics/tree/master/Day%2007)
- ▶ If you have questions, raise your hand. Don't be shy. If you are stuck, chances are someone else is too!

## ROUGH SCHEDULE

- 10:00am - Introduction to Workshop & RNAseq
- 10:45am - Evaluate Read Quality (FASTQC)
- 11:00am - Trimming & Data refinement (Trimgalore)
- 11:30am - Lunch
- 1:00pm - De Novo Transcriptome Assembly (Trinity)
- 2:15pm - QA/QC of Assembly
- 2:45pm - Transcript Quantification
- 3:00pm - Break
- 3:30pm - Differential Expression Analysis
- 5:30pm - Done!

# PRE-COURSE SURVEY

- ▶ Please fill out the pre-course survey:

<https://goo.gl/forms/iNbrEwqWGFdefsAt1>

### HANDS-ON

- ▶ Later analyses will require setting up our environment on Hydra. Because this may take a bit of time please go to [https://github.com/SmithsonianWorkshops/SMSC\\_Conservation\\_Genomics/tree/master/Day%2007](https://github.com/SmithsonianWorkshops/SMSC_Conservation_Genomics/tree/master/Day%2007) and follow the "1a\_Environment\_setup.md" tutorial.