INTRO RNASEQ INFORMATICS WORKSHOP

INTRODUCTION

▸ Who

    ▸ Instructors: Vanessa Gonzalez (GGI), Matt Kweskin (LAB), Paul Frandsen & Rebecca Dikow (Data Scientists from OCIO/SIBG)

    ▸ 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/RNA-seq

▸ 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
11:00am – Evaluate Read Quality (FASTQC)
11:30am – Trimming & Data refinement (Trimgalore)
12:15pm – Lunch
1:15pm   – De Novo Transcriptome Assembly (Trinity)
2:15pm   – QA/QC of Assembly
2:45pm   – Transcript Quantification
3:30pm   – Differential Expression Analysis

PRE-COURSE SURVEY

▸ Please fill out the pre-course survey:

https://goo.gl/forms/h9lHm6Yj29uo6mPn2

HANDS-ON

▸ Later analyses will require setting up our environment on Hydra. Because this may take a bit of time please go to http://github.com/SmithsonianWorkshops/RNA-seq and follow the "1a_Environment_setup.md" tutorial.