Welcome to the RNASeq Workshop/Course

Instructors

- Meg Staton
- Abdullah Almsaeed, mobile and web developer
- Matt Huff, researcher
- Fang Liu, PhD student in EPP
- Jiali Yu, PhD student in GST

- Bobby Whitten, Group Leader of the User Assistance Group, National Institute for Computational Sciences (NICS)

Learning Objectives

- Students will be able to apply basic bioinformatic theory and tools to analyze transcriptome datasets
- Students will be able to effectively communicate and critically assess the application of bioinformatic tools to transcriptome data
- Students will have basic competence in the UNIX shell and usage of bioinformatic tools from the command line

Syllabus Review

- Office hours 1:30 - 2:30
- Additional Linux command line practice today, if anyone requests it

Other Stuff

- Help is available!
- Ask questions, have discussion with your neighbors
- Use your stickies

Course Website

https://github.com/statonlab/rnaseq_workshop/wiki