Welcome to the RNASeq Workshop/Course

Instructors

ENTOMOLOGY & PLANT PATHOLOGY
UTIA INSTITUTE OF AGRICULTURE
THE UNIVERSITY OF TENNESSEE

A UT/ORNL PARTNERSHIP
NATIONAL INSTITUTE FOR COMPUTATIONAL SCIENCES
NICS

- Meg Staton
- Miriam Payá Milans, Postdoc
- Abdullah Almsaeed, researcher and web developer
- Ming Chen, PhD student in GST
- 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)

GENOME SCIENCE AND TECHNOLOGY

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, R scripting, and usage of bioinformatic tools from the command line

Syllabus Review

- UT Honor Code and Code of Conduct
- Email us with any problems
- We'll stay after class to help anyone who needs it!
- Additional Linux command line practice today, 2pm

Grading - the first 50%

- Attendance Grading – Each day of attendance will accrue 5 points.

- Output files - At the end of each day, you will need to send a file via email to mstaton1 at utk dot edu to get credit for completing the lab exercises. That file will be something you generated during the lab exercises and will be specified through the course website.

Grading – the second 50%

Journal Article Writing Assignment – Select a peer-reviewed journal article about RNASeq analysis.

Two page summary and review, single spaced. The goal is to think deeply about RNASeq as an experimental technique and to understand the methods used, from experimental design to software pipeline.

Send me an article by end of week if you want an ok on the scope.

Due Friday, June 23rd

Grading – the second 50%

Summary and review:

- What is the study's hypothesis?

- Why was RNASeq selected as an experimental method? (ie how does it relate to the biology of the hypothesis?) Is this technology appropriate for addressing the hypothesis?

- What is the experimental design? Is it statistically robust? What software was used?

- What are the results? How were the data interpreted?

- What do you think are the strengths and weaknesses of the paper? What sort of follow up studies could be conducted to further this work?

Due Friday, June 23rd

Other Stuff

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

Monday Schedule

9am Intro

9:20 NICS account set up

9:50 NICS introduction

10:20 Linux review