General introduction

Overall Course Learning Objectives

- Be capable of navigating a Linux operating system and TACC's Lonestar system in particular
- Understand common workflows and tools for NGS analysis:
  - "Re-sequencing" - comparing raw sequence data to a reference genome, calling variants, and annotating variants DNA sequencing data
  - RNA-seq - quantifying gene expression and determining splice variation from RNA-seq data
  - *de novo* genome assembly and annotation

Learning Objectives: Day 1, Part 1: Linux/TACC Introduction

- Understand the broadest definition of "biomedical/biological informatics" and where this course fits in
- Learn and practice essential Linux concepts and commands, including where to get more help & information
- Learn and practice working with TACC systems (Lonestar in particular)