

Core NGS Tools Home

This is the home of the Core NGS Tools course, June 2022, at <https://wikis.utexas.edu/display/CoreNGSTools>

This workshop provides an introduction to common analysis tools and file formats currently used in NGS, with emphasis on quality assessment and manipulation of raw NGS sequences ([FastQC](#), [cutadapt](#)), read mapping ([bwa](#), [bowtie2](#)), the Sequence Alignment Map (**SAM**) format, and tools for manipulating **BAM** files ([samtools](#), [bedtools](#)). Participants will gain hands-on experience using these and other NGS tools in the Linux command line environment at TACC, as well as exposure to the many bioinformatics resources TACC makes available.



For online attendees, the Zoom URL is: <https://utexas.zoom.us/j/98995501041>

There will be a short break each day around 10:30am.

Your TACC account will remain on our class TACC project allocation through June 30, 2022

We will provide access to recordings of each day's materials after the course is over.

Day 1: Intro to NGS, Linux and TACC

- [Introduction](#)
- [Getting started at TACC](#) – logging in
- lecture: NGS overview & technology ([2022_06-NGSintro.pdf](#) part 1)
- [Setting up your TACC environment](#)
- [File systems and transferring files](#)
- [Catch up](#) day 1 TACC setup

Day 2: TACC batch system and FASTQ files

- [Catch up](#) day 1 TACC setup
- lecture: NGS Terminology ([2022_06-NGSintro.pdf](#), part 2)
- [TACC batch jobs](#)
- lecture: the **FASTQ** format ([2022_06-NGSintro.pdf](#), part 3)
- [Working with FASTQ files](#)

Day 3: Working with raw sequences

- lecture: Sequence QC & preparation ([2022_06-NGSintro.pdf](#), part 3)
- [Sequence quality control](#)
- [Trimming](#)

Day 4: Alignment and BAM file manipulation

- lecture: Alignment to a reference ([2022_06-NGSintro.pdf](#), part 4)
- [The Basic Alignment Workflow](#)
- lecture: Alignment to a reference ([2022_06-NGSintro.pdf](#), part 4)
- [More Alignment exercises](#)

Day 5: Post-Alignment Analysis

- [Filtering with SAMTools](#)
- [Analysis using BEDTools](#)

Resources

- [Linux fundamentals](#)
- [Core NGS Resources](#)
- [Decimal and Hexadecimal](#)
- [Data wrangling best practices](#)