

Core NGS Tools Home

This is the home of the Core NGS Tools course, June 2023, 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/92348799002>
- There will be a short break each day around 10:30am
- We will provide access to recordings of each day's materials after the course is over
- Your TACC account will remain on our class TACC project allocation through June 30, 2023

Day 1: Intro to NGS, Linux and TACC

- [Introduction](#)
- [Getting started at TACC](#) – logging in
- lecture: NGS overview & technology ([2023_06-NGSintro.pdf](#) part 1)
- [Setting up your TACC environment](#)
- [File systems and transferring files](#)

Day 2: TACC batch system and FASTQ files

- [Catch up](#) day 1 TACC setup
- lecture: NGS Terminology ([2023_06-NGSintro.pdf](#), part 2)
- [TACC batch jobs](#)
- lecture: the **FASTQ** format ([2023_06-NGSintro.pdf](#), part 3)
- [Working with FASTQ files](#)

Day 3: Working with raw sequences

- lecture: Sequence QC & preparation ([2023_06-NGSintro.pdf](#), part 3)
- [Sequence quality control](#)
- [Trimming](#)

Day 4: Alignment and BAM file manipulation

- lecture: Alignment to a reference ([2023_06-NGSintro.pdf](#), part 4)
- [The Basic Alignment Workflow](#)
- lecture: Alignment to a reference ([2023_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](#)

Navigate space