

Core NGS Tools Home

This is the home of the Core NGS Tools course, June 2020, 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.



This workshop will be held via Zoom, URL: <https://utexas.zoom.us/j/91282159612>. Please make sure your version of Zoom is at least 5.0 (see <https://zoom.its.utexas.edu/zoom-upgrade>).

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



[Contact us](#) for access to recordings of each day's materials.

Day 1: Intro to NGS, Linux and TACC

- [Introduction](#)
- [Getting started at TACC](#) – logging in
- lecture: NGS overview & technology ([2020_06-NGSintro.pdf](#), part 1)
- [Setting up your TACC environment](#)

Day 2: Transferring files and TACC

- [File systems and transferring files](#)
- lecture: NGS Terminology ([2020_06-NGSintro.pdf](#), part 2)
- [TACC batch jobs](#)

Day 3: Working with raw sequences

- lecture: the **FASTQ** format ([2020_06-NGSintro.pdf](#), part 3)
- [Working with FASTQ files](#)
- lecture: Sequence QC & preparation ([2020_06-NGSintro.pdf](#), part 3)
- [Sequence quality control](#)
- [Trimming](#)

Day 4: Alignment and BAM file manipulation

- lecture: Alignment to a reference ([2020_06-NGSintro.pdf](#), part 4)
- The [Alignment workflow](#) – references
- lecture: Alignment to a reference ([2020_06-NGSintro.pdf](#), part 4)
- The [Alignment workflow](#) – performing an alignment

Day 5: Post-Alignment Analysis

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

Resources

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

Navigate space