

# 2020 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>.

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

- [2020 Introduction](#)
- [2020 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

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

## Day 5: Post-Alignment Analysis

- [2020 Filtering with SAMTools](#)
- [2020 Analysis using BEDTools](#)

## Resources

- [2020 Linux fundamentals](#)
- [2020 Core NGS Resources](#)
- [2020 Data wrangling best practices](#)