Handling Sequences Overview

The goal of this section is to familiarize you with the two main sequence file formats: FASTQ for raw reads and SAM/BAM for aligned reads.

We will cover Evaluating your raw sequencing data, including quality assurance steps and tools as well as tools to manipulate FASTQ files before alignment. Useful FASTQ resources are summarized on our Resources tool list, FASTQ section.

We'll also cover Mapped read data evaluation using SAMtools. Useful SAM/BAM manipulation resources are also summarized on our Resources tool list, Alignment section.