Biological Samples/Library Preparation

↓

Sequence Reads

.fastq

Read QC: *FASTQC*

.fastq

Adaptor Trimming: *Trimmomatic, FASTX-Toolkit, etc.*

.fastq

Splice-aware Mapping to Genome: *STAR*

.bam

Quantify Mapping: *HTSeq*

↓ counts matrix

Differential Expression Analysis: *DESeq2*