METAGENOMICS

* fastqc fastq.file -o output.directory
  + run quality control on a fastq file
* multiqc directory
  + searches for fastqc outputs within directory, compares them
* kraken2 -db database fastqfile
  + run kraken2for classifying kmers
  + –confidence #set confidence level between 0 and 1
  + --report #gives a nice report format
* bbduk.sh in= out= ref=adapters ktrim=
  + for trimming sequences (removing adapters, etc)
  + see help
* krona
  + can be installed using conda
  + useful for visualizing kraken2 outputs
* trimmomatic
  + for trimming sequences for quality
  + use help