

Fastqc: quality analysis

```
# first load the fastqc module
module load fastqc
# create a directory for outputs
mkdir DIRECTORY NAME
# run fastqc program
# be conscious on where you're at in your directory
# make sure you know your file paths
# make sure to continue using ctrl+tab to complete file/directory names
fastqc -o DIRECTORY NAME path/to/files/*.fastqc
# fastqc: command
# -o: this represents output, which is the directory you created
# add space, then the path to input files
# *.fastqc is useful when there are multiple .fastqc in a directory
# this way, fastqc automatically analyzes all .fastqc files, without needing multiple lines of code
# this works with other file extensions, such as .fastq.gz and .fq, simply edit as needed

# Linux will notify you when the program has finished running & periodically update
# i.e. Started analysis of [file1.fastqc]
#   Approx 35% complete for [file1.fastqc]
#   Approx 70% complete for [file1.fastqc]
#   Analysis complete for [file1.fastqc]
# back up output files (entire folder) to personal computer
# navigate to files in computer system
# open html files (in chrome or other web browser)
# analyze results

# move onto trimming steps
# perform fastqc on trimmed files
# compare fastqc files for pre and post trimmed files
# biggest difference is that trimming software will have improved quality
# especially at the end of reads
```