

[Docs](#) » sequence QC

FASTQ Quality controls

Using [FastQC](#) you can perform the necessary controls over fastq files.

```
fastqc C51C3ACXX_TC1-H3K4-A-D3_14s006647-1-1_Sinkkonen_lane514s006647_sequence.txt.gz
```

running serial

A tidy bit of `bash` programming to do it for all files

```
for f in *.gz
do fastqc $f
done
```

running in parallel

If you have booked **2** nodes, otherwise update the `-j` option:

```
parallel -j 2 "fastqc {}" ::: *.gz
```

the `{}` instruction will be replaced by all occurrences of the pattern `*.gz`, everything that ends by `.gz`. `parallel` takes care of submitting a new job so the number of parallel remains the same.

visualize the results

collect the `html` files using either `rsync`, `scp` for command lines or [FileZilla](#) for GUI tool.

You should observe some issues that needs to be solve.

[⏮ Previous](#)[Next ⏭](#)