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Workshop: <https://otagocarpentries.github.io/2019-09-25-otago/>

Pre: https://www.surveymonkey.com/r/dcpworkshopassessment?workshop_id=2019-09-25-otago

Post: https://www.surveymonkey.com/r/dcpworkshopassessment?workshop_id=2019-09-25-otago

Sign in: Name, Institution, Email, Twitter (optional)

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Collaborative notes

Here is a space we can take notes together about the stuff we cover today!

illumina sequencing video: <https://www.youtube.com/watch?v=fCd6B5HRaZ8>

Introduction to commandline

ASCII table: <http://www.asciitable.com>

Find bad reads and have it be a multiple of 4 (removes the group separator that -A and -B add in for non-contiguous results)

```
grep -B1 -A2 --no-group-separator NNNNNNNNNN SRR098026.fastq > bad_reads.txt
```

wget <ftp://ftp.ensemblgenomes.org/pub/release-37/bacteria/species> EnsemblBacteria.txt

Data Wrangling Section

Raw data

```
curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR258/004/SRR2589044/SRR2589044\_1.fastq.gz
curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR258/004/SRR2589044/SRR2589044\_2.fastq.gz
curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR258/003/SRR2584863/SRR2584863\_1.fastq.gz
curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR258/003/SRR2584863/SRR2584863\_2.fastq.gz
curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR258/006/SRR2584866/SRR2584866\_1.fastq.gz
curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR258/006/SRR2584866/SRR2584866\_2.fastq.gz
```

Adapter file

```
cp /home/dcuser/.backup/untrimmed_fastq/NexteraPE-PE.fa ./
```

```
curl -L -o sub.tar.gz https://ndownloader.figshare.com/files/14418248
```

```
set -e
```

```
cd ~/dc_workshop/data/untrimmed_fastq/
```

```
echo "Running FastQC ..."
```

```
fastqc *.fastq*
```

```
mkdir -p ~/dc_workshop/results/fastqc_untrimmed_reads
```

```
echo "Saving FastQC results..."
mv *.zip ~/dc_workshop/results/fastqc_untrimmed_reads/
mv *.html ~/dc_workshop/results/fastqc_untrimmed_reads/

cd ~/dc_workshop/results/fastqc_untrimmed_reads/

echo "Unzipping..."
for filename in *.zip
do
    unzip $filename
done

echo "Saving summary..."
cat */summary.txt > ~/dc_workshop/docs/fastqc_summaries.txt

curl -O https://raw.githubusercontent.com/datacarpentry/wrangling-genomics/gh-pages/files/run\_variant\_calling.sh
```