

Untitled

1. Getting the Data

1.1. Downloading the Reads

The reads were obtained from SRA in the form of a set of FASTQ files. The FASTQ files were downloaded using **sratoolkit.2.9.6**. The following Bash script was employed:

After saving the above script as *download-sra-reads.sh* in *bash-scripts* directory, the following Bash command was used for running it.

```
nohup sh bash-scripts/download-sra-reads.sh > download-sra-reads.out &
```

1.2. Reads Quality Control

The quality of the reads was checked using **FastQC-v0.11.8**. The following Bash script was employed.

```
#!/bin/bash
# ALL SAMPLES
fastqc -o fastqc /data/sra/*fastq.gz
```

1.3. Retrieving the Phenotype Data

1.4. Retrieving the Phen