Read simulation Using ART

Ubuntu Installation

cd ..
wget https://github.com/samtools/samtools/releases/download/1.9/samtools-1.9.tar.bz2
tar -vxjf samtools-1.9.tar.bz2
cd samtools-1.9
make

sudo apt install art-nextgen-simulation-tools

Isolate a chromosome sequence in a new fasta file

```
samtools faidx reference.fa chr1 > chr1.fa
```

Art_illumina -ss HS20 -sam -i
/home/lajoyce/Documents/sequence_alignment/chromosome_2.fasta -l 100 -c 1 -0 chr2_read

CL:art_illumina -ss HS20 -sam -i
/home/lajoyce/Documents/sequence_alignment/chromosome_2.fasta -l 100 -c 1 -o chr2_read
-rs 1686537059

How to download bwa-mem2 binaries

Use precompiled binaries (recommended)
curl -L
https://github.com/bwa-mem2/bwa-mem2/releases/download/v2.2.1/bwa-mem2-2.2.1_x64-linux
.tar.bz2 \
  | tar jxf -

bwa-mem2-2.2.1_x64-linux/bwa-mem2 index ref.fa
bwa-mem2-2.2.1_x64-linux/bwa-mem2 mem ref.fa read1.fq read2.fq > out.sam

Alignment Using bwa-mem2

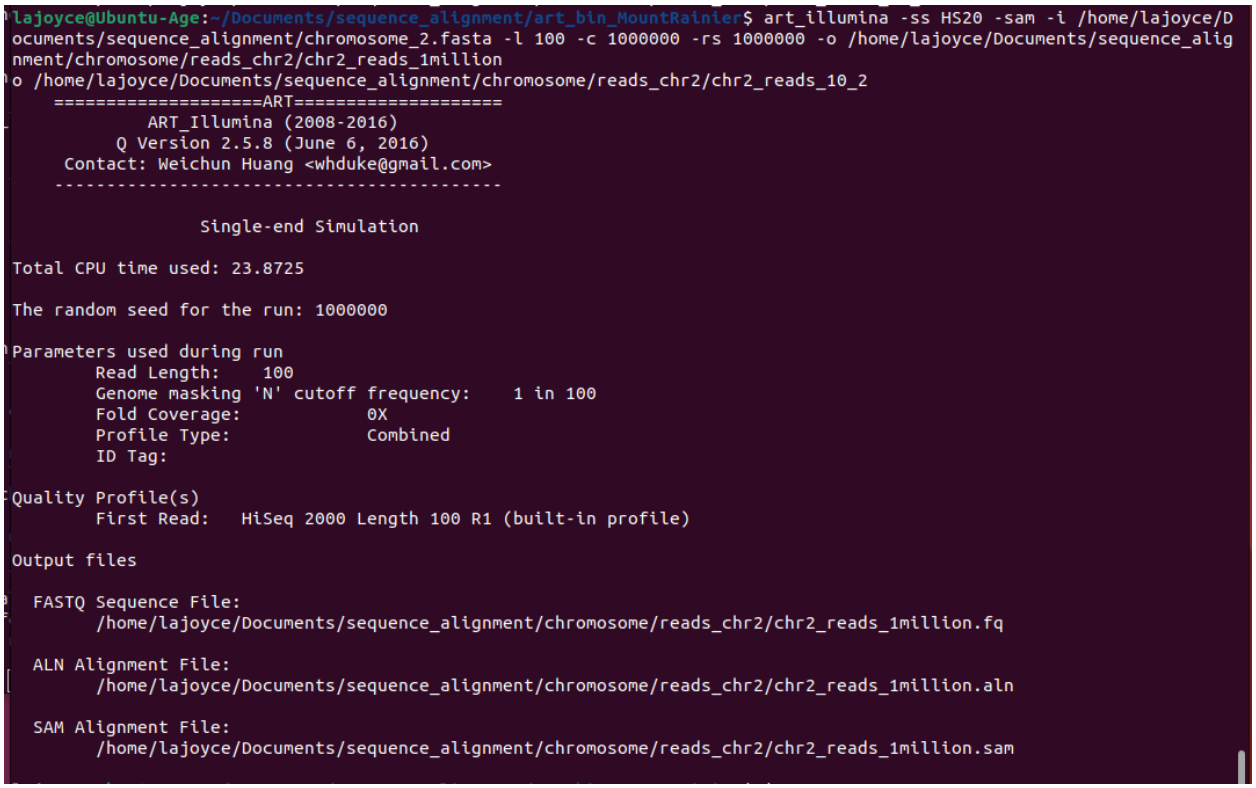
CL:bwa-mem2-2.2.1_x64-linux/bwa-mem2 mem chromosome_2.fasta chr2_read.fq

Run for 1 million coverage

-c --rcount number of reads/read pairs to be generated per sequence(not be used together with -f/--fcov) - **1 million**
-l --len the length of reads to be simulated - **100**
-rs --rndSeed the seed for random number generator (default: system time in second) - **1000000**

HS20 - HiSeq 2000 (100bp)

Screenshot of run



Overview of 1million coverage fastq file