## Mapping reads via STAR

#!/bin/bash

# Building genome index for mapping reads on genome

STAR --runThreadN 16 --runMode genomeGenerate --genomeDir /groups/songli\_lab/RegNetRNAseq/data/Gnmdir --genomeFastaFiles /groups/songli\_lab/RegNetRNAseq/data/TAIR10\_Chr.all.fasta --sjdbGTFfile /groups/songli\_lab/RegNetRNAseq/data/Araport11\_GFF3\_genes\_transposons.201606.gtf

# mapping reads via STAR

GNM=/groups/songli\_lab/RegNetRNAseq/data/TAIR10\_Chr.all.fasta;

GTF=/groups/songli\_lab/RegNetRNAseq/data/Araport11\_GFF3\_genes\_transposons.201606.gtf

GnmDir=/groups/songli\_lab/RegNetRNAseq/data/Gnmdir;

# setting out the directories;

dir1=/groups/songli\_lab/RegNetRNAseq/

echo "$dir1"

cd $dir1/data/SRA;

for f1 in \*.sra;

do

f2=${f1%.sra}

echo "$f1"

echo "$f2"

cd $dir1/data/fastq

if [ -f $f2"\_2.fastq" ]

then

f3=$f2"\_1.fastq"

f4=$f2"\_2.fastq"

echo "$f3"

echo "$f4"

# cutadapt -q 20 -a AGATCGGAAGAGC -A AGATCGGAAGAGC --minimum-length 30 -o home/shamima/data/prepro/$f2"\_1.p.fastq" -p home/shamima/data/prepro/$f2"\_1.fastq.p.fastq" $f3 $f4

#Quality checking with FastQc tools

#/home/shamima/scratch/FastQC/fastqc $dir2/$f1 $f2 --outdir $dir6

#Quality assessed files can be viewed as

#firefox $dir6/$f1\_fastqc.html $f2\_fastqc.html

cd /$dir1/data/bam

mkdir $f2

echo "---------------------------------------------"

STAR --runThreadN 16 \

--genomeDir $GnmDir \

--readFilesIn /$dir1/data/fastq/$f3 /$dir1/data/fastq/$f4 \

--outSAMstrandField intronMotif \

--outFileNamePrefix /$dir1/data/bam/$f2/$f2 \

--outSAMtype BAM SortedByCoordinate;

else

#cd /home/shamima/data/fastq

# for f1 in \*.fastq;do

# f2=${f1%.fastq}

# done

# echo "$f1"

#cutadapt -q 20 -a AGATCGGAAGAGC --minimum-length 30 -o /home/shamima/data/fastq/f2.p.fastq $f1.fastq

#Mapping via STAR

cd /$dir1/data/bam

mkdir $f2

echo "########################################"

STAR --runThreadN 16 \

--genomeDir $GnmDir \

--readFilesIn /$dir1/data/fastq/$f2.fastq \

--outSAMstrandField intronMotif \

--outFileNamePrefix /$dir1/data/bam/$f2/$f2 \

--outSAMtype BAM SortedByCoordinate;

fi

done