





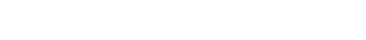




```
INDEX=$2
OUTPUT=$3
STAR --genomeDir $INDEX --genomeLoad Remove
  $INPUT | grep "[.]fq[.]gz$" | while read FILE; do
   SAMPLE=`basename "$FILE" trimmed.fq.gz`
    STAR
        --runThreadN 8 \
        --genomeDir $INDEX \
        --genomeLoad LoadAndKeep
        --readFilesIn $INPUT/$FILE \
        --readFilesCommand zcat \
        --outFileNamePrefix $0UTPUT/$SAMPLE. \
        --outSAMtype BAM Unsorted \
        --outSAMstrandField intronMotif
done
```

STAR --genomeDir \$INDEX --genomeLoad Remove

INPUT=\$1





```
STAR-alignReads.sh
```

```
Map reads
```

```
INPUT=$1
INDEX=$2
OUTPUT=$3
STAR ——genomeDir $INDEX ——genomeLoad Remove
                                                       Load the index into "mapped memory"
ls $INPUT | grep "[.]fq[.]gz$" | while read FILE; do
    SAMPLE=`basename "$FILE" _trimmed.fq.gz`
    STAR \
        --runThreadN 8 \
        --genomeDir $INDEX \
        --genomeLoad LoadAndKeep \
        --readFilesIn $INPUT/$FILE \
                                                         Map all the chunks of reads
        --readFilesCommand zcat \
        --outFileNamePrefix $0UTPUT/$SAMPLE. \
        --outSAMtype BAM Unsorted \
        --outSAMstrandField intronMotif
done
                                                         Unload the index
STAR ——genomeDir $INDEX ——genomeLoad Remove
```

Sample problem 1

Download "small_reads.fastq"