Map reads

```
INPUT=$1
INDEX=$2
OUTPUT=$3

STAR --genomeDir $INDEX --genomeLoad Remove

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 \
        --readFilesCommand zcat \
        --outFileNamePrefix $OUTPUT/$SAMPLE. \
        --outSAMtype BAM Unsorted \
        --outSAMstrandField intronMotif
done

STAR --genomeDir $INDEX --genomeLoad Remove
```

STAR-alignReads.sh

Map reads

```
INPUT=$1
INDEX=$2
OUTPUT=$3

STAR --genomeDir $INDEX --genomeLoad Remove

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 \
        --readFilesCommand zcat \
        --outFileNamePrefix $OUTPUT/$SAMPLE. \
        --outSAMtype BAM Unsorted \
        --outSAMstrandField intronMotif
done

STAR --genomeDir $INDEX --genomeLoad Remove
```

Load the index into “mapped memory”

Map all the chunks of reads

Unload the index

Sample problem 1

Download “small_reads.fastq”