

Problem: map NGS reads to a genome

Solution:

```
STAR \
  --runThreadN 8 \
  --genomeDir $INDEX \
  --genomeLoad LoadAndKeep \
  --readFilesIn $INPUT/$FILE \
  --readFilesCommand zcat \
  --outFileNamePrefix $OUTPUT/$SAMPLE. \
  --outSAMtype BAM Unsorted \
  --outSAMstrandField intronMotif
```

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

```
done
```

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

 ← Unload the index