

**STAR**

# 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
```