```
samtools sort example/Aligned.out.bam > example/sorted.bam

bedtools intersect -a genes.bed -b example/sorted.bam -wa -c
```

Sample problem 2

Download “genes.bed”

Use bedtools to count the number of reads you just mapped that hit each gene.

```
samtools sort example/Aligned.out.bam > example/sorted.bam

bedtools intersect -a genes.bed -b example/sorted.bam -wa -c
```

Sample problem 2

```
I       11947001        11953126        WBGene00011060  255     +       1
I       11953512        11961984        WBGene00002004  255     -       15
I       11971179        11971797        WBGene00044805  255     -       0
I       11979401        11985612        WBGene00013135  255     +       1
```

Note that the output is a BED file! The “score” field I told you to ignore earlier has the results.