

# Exercise 1

Find mean/median/min/max values for columns 5 and 6 from “fimo.bed” for the following regions of interest:

chr7	10000	11000
chr7	25000	30000

# Exercise 1 Answers

```
$ bedtools map -a fimo.regions_of_interest.bed  
               -b fimo.bed  
               -c 5  
               -o mean
```

```
chr7 10000 11000 -33.23  
chr7 25000 30000 -35.16
```

```
$ bedtools map -a fimo.regions_of_interest.bed  
               -b fimo.bed  
               -c 6  
               -o mean
```

```
chr7 10000 11000 0.48  
chr7 25000 30000 0.54
```

# Exercise 1 Answers

```
$ bedtools map -a fimo.regions_of_interest.bed  
               -b fimo.bed  
               -c 5  
               -o mean,median,min,max
```

```
chr7 10000 11000 -33.23 -33.43 -62.96 2.22e-308  
chr7 25000 30000 -35.16 -35.66 -64.90 4.46
```

# Exercise 1 Answers

```
$ bedtools map -a fimo.regions_of_interest.bed  
               -b fimo.bed  
               -c 5,6  
               -o min
```

```
chr7 10000 11000 -62.96 0.0032  
chr7 25000 30000 -64.90 0.00051
```

## Exercise 2

The strongest DNase-seq peaks across 80 different cell types and developmental stages were selected and placed in a file “master\_peaks.bed”.

For each master peak, list which other peaks (from the “all\_peaks.bed” file) are present at the peak.

# Exercise 2

## Master peaks:

```
chr1 3002720 3002870 4.37932 ENCFF001YVC  
chr1 3025600 3025750 8.0632 ENCFF001YLB
```

## All peaks:

```
chr1      3002720 3002870 1921300-ENCFF001YVC-4.37932  
chr1      3002740 3002890 4406931-ENCFF001YNU-6.60995  
chr1      3002740 3002890 562121-ENCFF001YPN-19.466
```

## Exercise 2 Answer

```
$ bedtools map -a master_peaks.bed -b  
all_peaks.bed -c 4 -o collapse | head -n 1
```

```
chr1 3002720 3002870  
4.37932 ENCFF001YVC  
1921300-ENCFF001YVC-4.37932,  
4406931-ENCFF001YNU-6.60995,  
562121-ENCFF001YPN-19.466,  
1641841-ENCFF001YMD-19.4139,  
739253-ENCFF001YLB-92.3323
```