

## Session 2

### ***Exercise Set #3***

Navigate yourself to the `Bootstrappers_Unix_Workshop` folder that you downloaded for the course. Change directories to the `Session_2` folder. Here we have a roster for a particular age group of summer camp (`Camp_Roster.txt`).

How many campers are registered?

How many girls are registered?

How many boys are registered?

How many six year olds are registered?

Sort the campers by their age (youngest to oldest).

Who is the oldest camper?

Who is the youngest camper?

Now let's look at a much larger file (`TF_Peaks.bed`). This is a list of peaks from ENCODE CHIP-seq experiments.

How many peaks are there in the bed file?

How many peaks on chromosome 1 are there?

How many peaks from CTCF are there?

What is the first peak on chromosome 2?

What is the last peak on chromosome 7?

Create a new file with all IRF4 peaks titled `IRF4_Peaks.bed`

### ***Exercise Set #4***

Navigate yourself to the `Bootstrappers_Unix_Workshop` folder that you downloaded for the course. Change directories to the `Session_2` folder. Here we have a roster for a particular age group of summer camp (`Camp_Roster.txt`).

Change the age of Hannah to 7.

Add a new camper at the end of the list: Michael, age 5, Male

Save these changes and exit.

Now let's look at a much larger file (`TF_Peaks.bed`). This is a list of peaks from ENCODE CHIP-seq experiments.

Jump to line 400.

What transcription factor does this peak correspond to?

Now change all of the "chr23" to "chrX".

How many instances were changed?

Save these changes and exit.

Open the file `IRF4_Peaks.bed` which you created in the last exercise. Remove "sc6059Pcr1xAlnRep0" in the fourth column and change "Irf4" to "IRF4" for each line.

Now delete the peak on chromosome 18.

Save these changes and exit.