

Homework Day 9:

1. In class we used Macs2 to peak call on two H3K27ac ChIP-seq samples, however, we also learned that the settings for this peak caller should be tweaked for different data types. Make a script to use Macs2 to peak call the P53 ChIP-seq data set (p53 is a transcription factor), sample SRR4090090. The background ChIP-seq control sample that is most relevant will be SRR4090089.
2. Again, produce another Macs2 peak calling script for the ATAC-seq data SRR5876158. In this case, we don't have a perfect control sample but the SRR5855054 should suffice.
3. Use X2go to view the raw data for these two samples as well as the H3K27ac samples used in class all in one viewer, as these are all from matched cell lines.
4. Also load the macs output bed files for the different data types and look around the genome to see if you think your peak calling scripts did a good job calling peaks for their respective data sets.