

Applied Genomics Assignment: ChIP-seq

Due Friday 20 April, 2018

Introduction:

An (unspecified) transcription factor ChIP-seq was performed in *Drosophila*.
For this assignment, perform a meme-chip analysis and report the most significant motif found.

Data:

The datasets required are on prince at `/scratch/courses/AppliedGenomics2018/HomeworkChIPseq/`.

This includes:

- (i) bam files (mapped by Bowtie2) for a single replicate of the ChIP-seq sample and associated input control are provided in files **TFxx_wt.bam** and **input.bam** respectively.
- (ii) *Drosophila* dm3 reference genome and chromosome sizes are provided in files `dm3.fa` and `dm3.chrom.sizes`.

Use the fly-specific known TF motif set at `/scratch/courses/AppliedGenomics2018/chip_seq1/peakfinding_lab/motif_db/motif_databases/FLY/fly_factor_survey.meme` in your analysis.

Final report:

In your report, show the motif, e-value and central enrichment statistics of the most significant motif that shows central enrichment. Identify the motif and give details of its function from FlyBase (<http://flybase.org>).