

ChIP-Seq peaks + scores
(.bed)

Select top 500 peaks

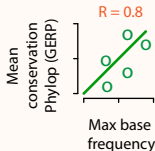
Discover motifs (MEME, +/- 100 bp)

Get motif coordinates within peaks (FIMO)

Obtain conservation scores
@ motif sites (PhyloP, GERP)

Average conservation
scores across motif sites

Calculate correlation between
the mean conservation score
(PhyloP, GERP) of a motif base
and the maximum frequency
of a nt (A, T, C or G) for the
same motif base.



Calculate:

1. p-value for correlation
between motif and conservation
2. p-value for increased conservation
of motif bases (vs. flanking)

Display the results

