Peak calling for Sutton Assay

Anurag Sethi May 2015 Pipeline for analyzing each pool



Peak calling might change based on simulations

Comparison of peaks (MACS)



At least 20% overlap of peaks

Comparison of peaks (HOMER)



At least 20% overlap of peaks

Comparison of peaks (HOMER)



At least 20% overlap of peaks

Comparison of peaks (HOMER vs MACS)

>90% peaks overlap in pools 1 and 2. 67% of peaks overlap in pool 3.

14648/19643 peaks overlap between shared peaks.

Comparison of peaks (new vs old)

10696/20572 HOMER peaks overlap with old peaks. 8683/19643 MACS peaks overlap with old peaks.

Length distribution of peaks



MACS peaks

HOMER peaks

Mean size close to 900-1200 bp width. HOMER peaks are larger on average (1 peak of 30 kb width)

Overlap of shared peaks with histone marks

New versus old











72K cells positive in each pool (28.6 enhancers each)













Improvements in pipeline



Improvements in pipeline







Future Work

Most of the work is related to the simulation method. This can probably help decide threshold (5% FDR currently) for peak calling.

Postprocessing Analysis:

TF binding peaks on enhancers/promoters to better define enhancer elements. TF motifs on enhancers/promoters.

Does this assay work better with certain kinds of promoters/enhancers?

A few slides about our method for predicting enhancers