Machine learning algorithms for simultaneous supervised detection of peaks in multiple samples and cell types

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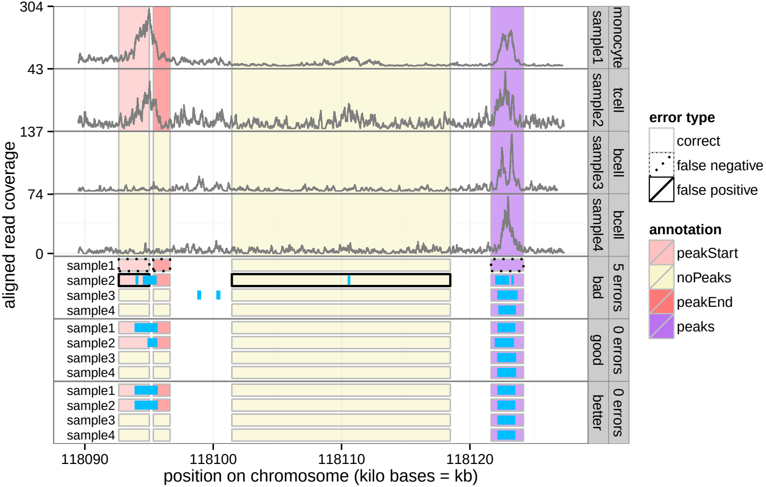
Peak detectors should predict differences between samples

Context: detecting presence/absence of peaks (active regions) in epigenomic data profiles such as ChIP-seq, ATAC-seq, ...

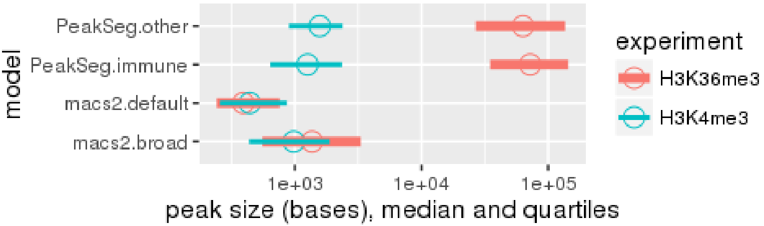


Algorithm and pipeline with two main novel ideas

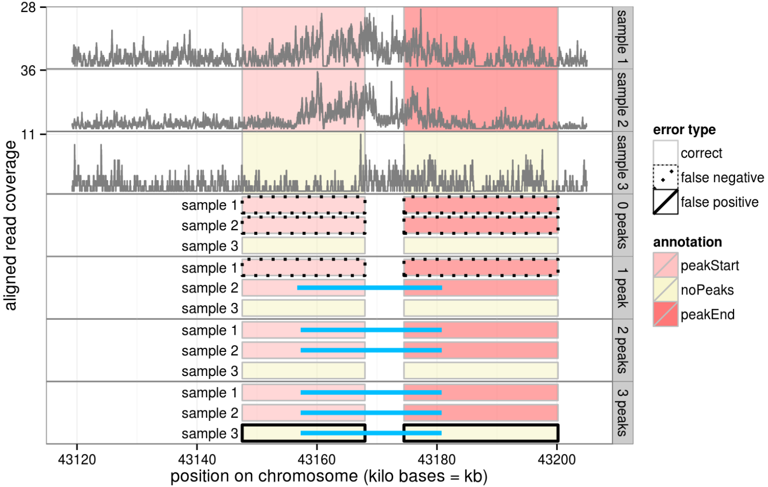
Supervised machine learning. Labels that indicate presence/absence of peaks in specific samples/regions are used to train model parameters (users do not need to know how to tune p-value thresholds, bin size parameters, etc).

Joint model predicts differences between any number of samples/groups. Unlike previous methods, not limited to one or two groups with replicates.

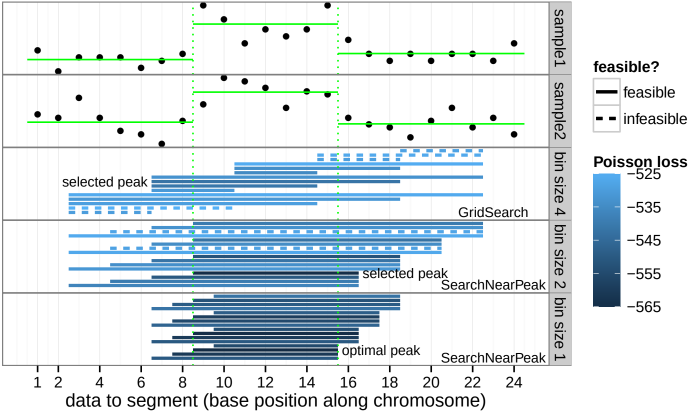
Results: state-of-the-art peak models with predicted sizes that are consistent with biological expectation.



Joint peak model for 3 labeled samples



Approximate algorithm for computing optimal peak boundaries for piecewise constant Poisson mean model

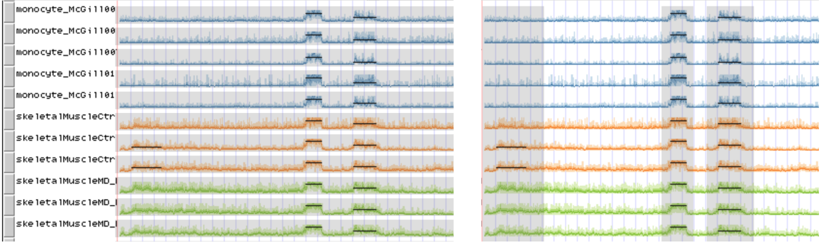


R package **PeakSegJoint**.

Two steps of the proposed peak prediction pipeline

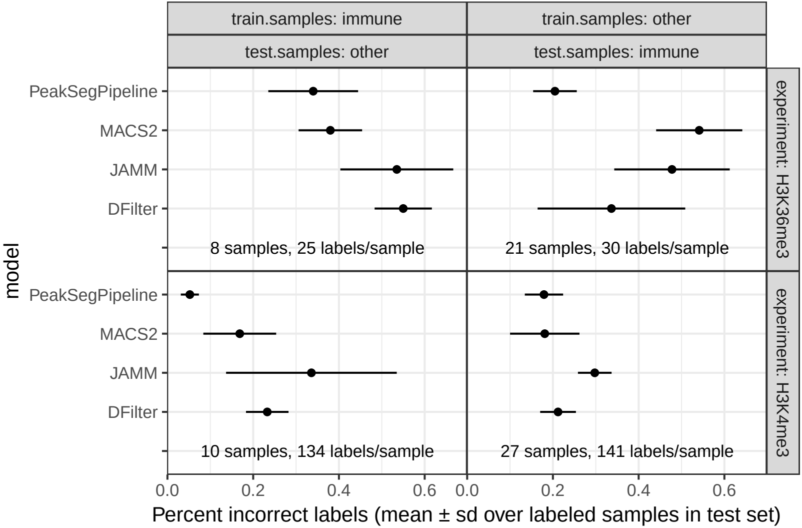
Preliminary peak predictions for each sample/contig

Joint prediction of presence/absence of a peak
with common boundaries in each sample/group,
for every genomic region with preliminary peaks



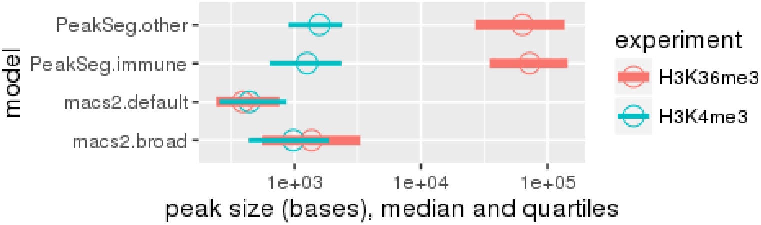
R package **PeakSegPipeline**.

Test error comparable to or better than baselines

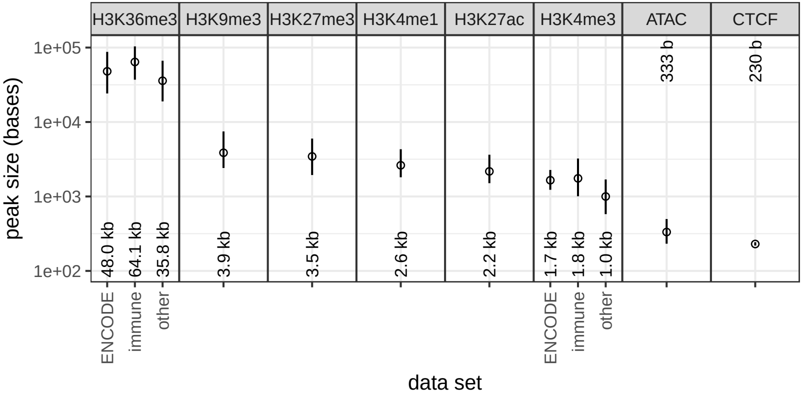


PeakSeg predicted sizes depend on experiment, macs2 baseline sizes depends on parameter settings

- Train PeakSeg models on either labeled samples of immune cell types (B cells, T cells, monocytes) or other cell types.
- Use macs2 baseline with either default parameter settings or broad command line argument.
- PeakSeg model has learned that H3K4me3 has smaller peaks than H3K36me3.



Predicted peak sizes vary by experiment type



Conclusions

- New algorithm for joint peak detection, R package **PeakSegJoint**.
- New pipeline for supervised joint analysis, R package **PeakSegPipeline**.
- State-of-the-art peak prediction accuracy and interpretable peak sizes.
- Recruiting graduate students for research projects! **toby.hocking@nau.edu**