Supervised detection of the same peaks jointly across several ChIP-seq samples

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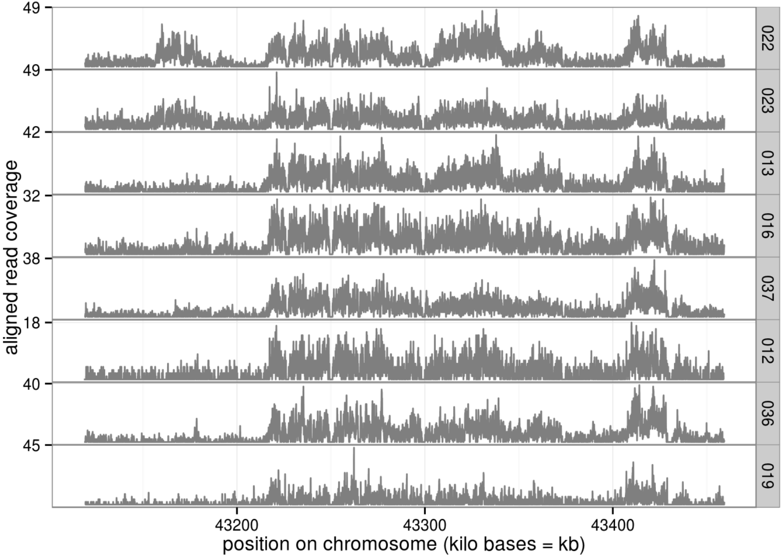
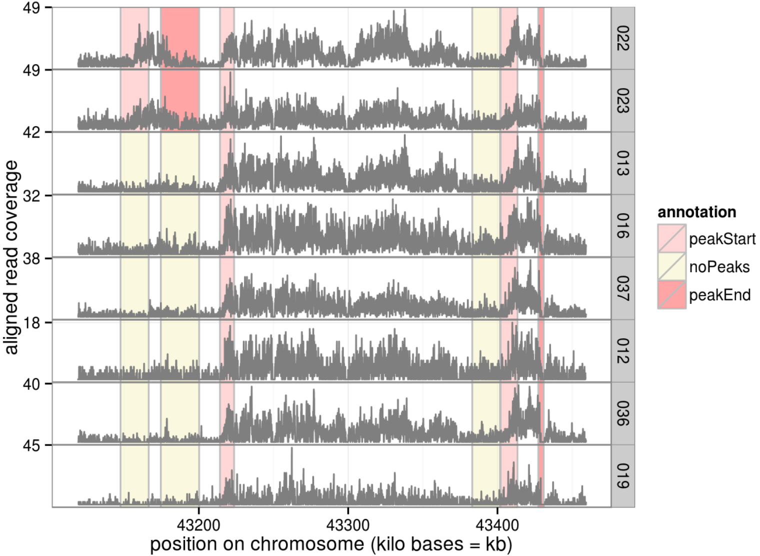
joint work with Guillem Rigaill and Guillaume Bourque

May 6, 2015

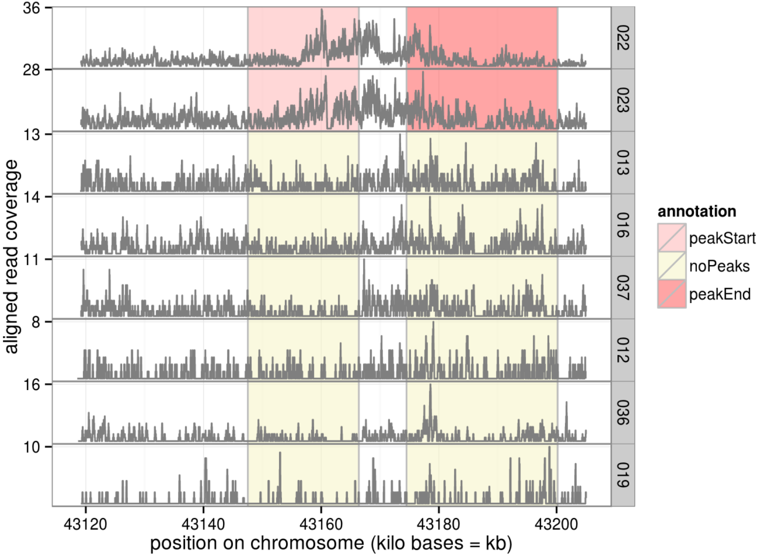
Peaks visually obvious in H3K36me3 data



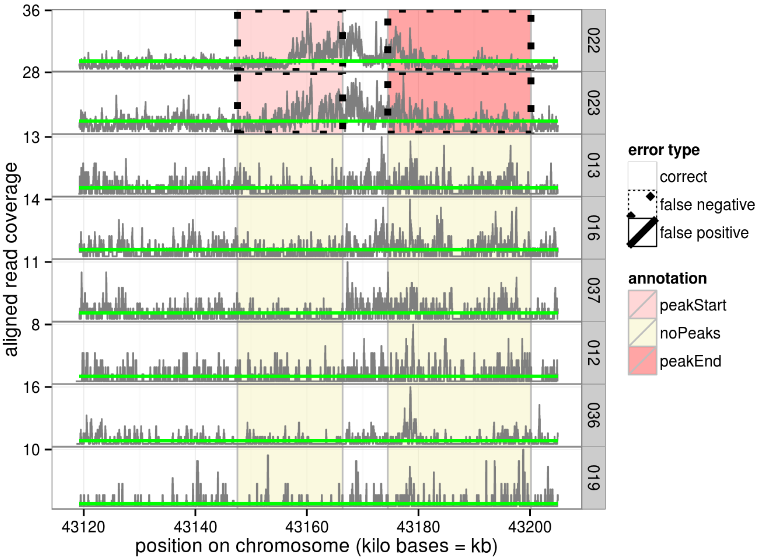
H3K36me3 data and visually determined labels



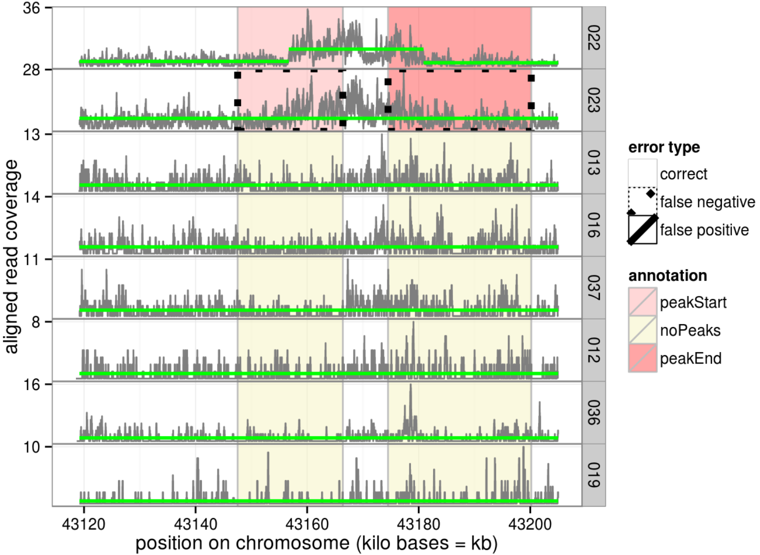
H3K36me3 data and labels (zoom to one peak)



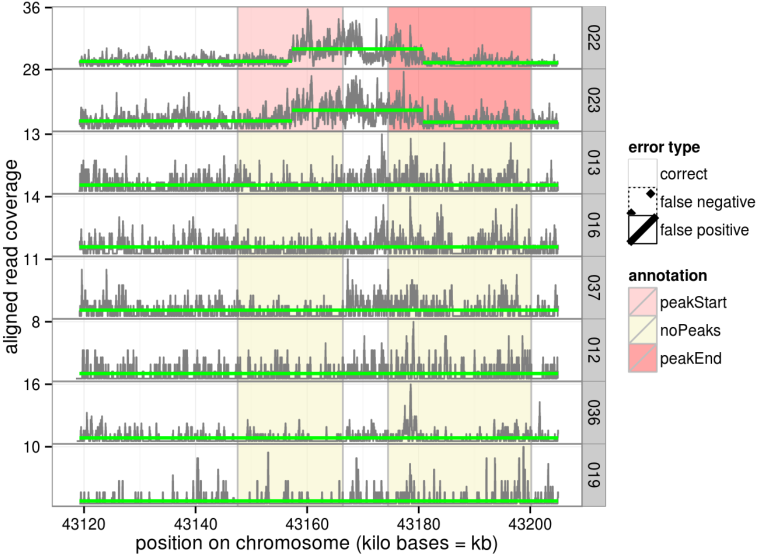
PeakSegJoint model with 0 peaks



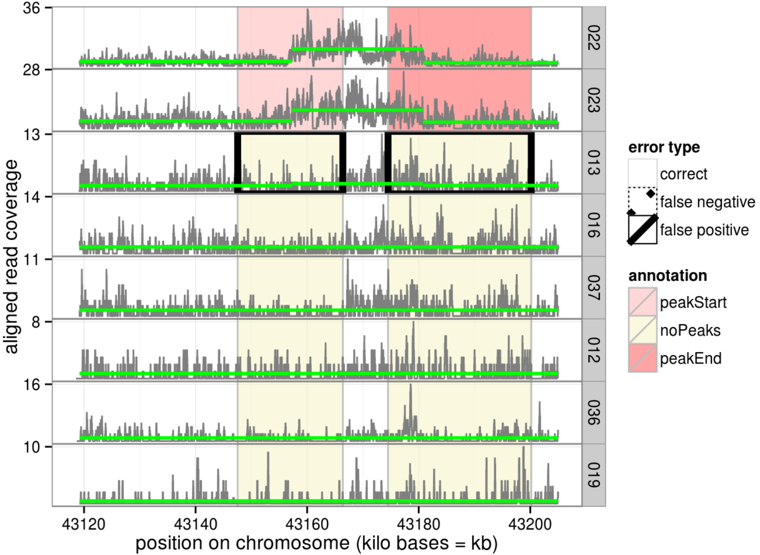
PeakSegJoint model with 1 peak



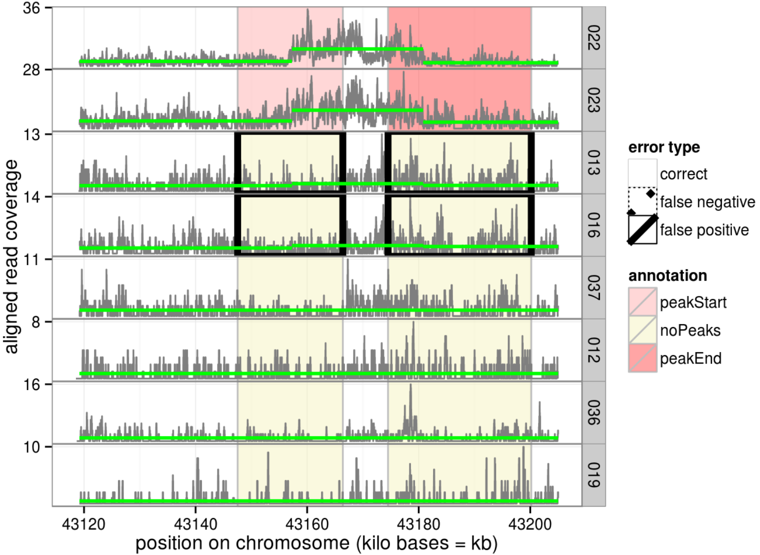
PeakSegJoint model with 2 peaks



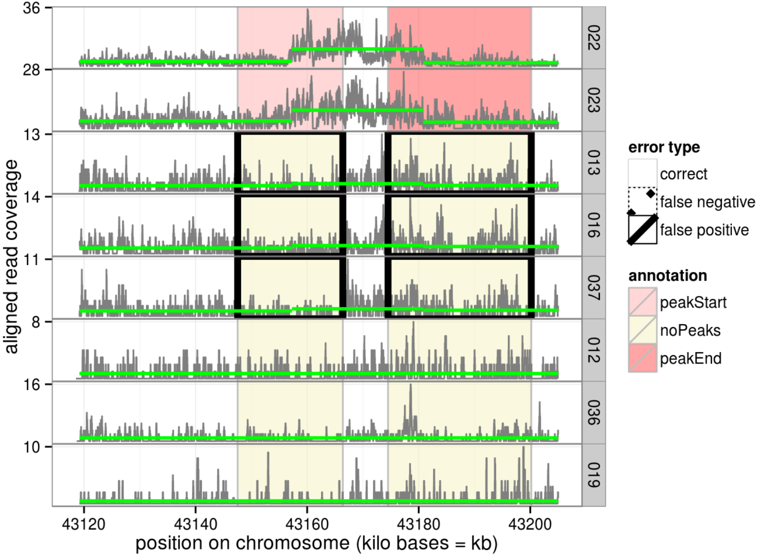
PeakSegJoint model with 3 peaks



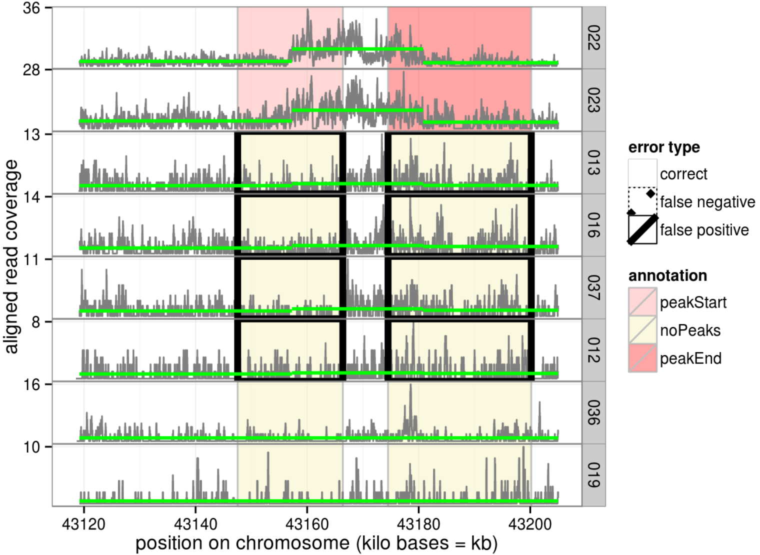
PeakSegJoint model with 4 peaks



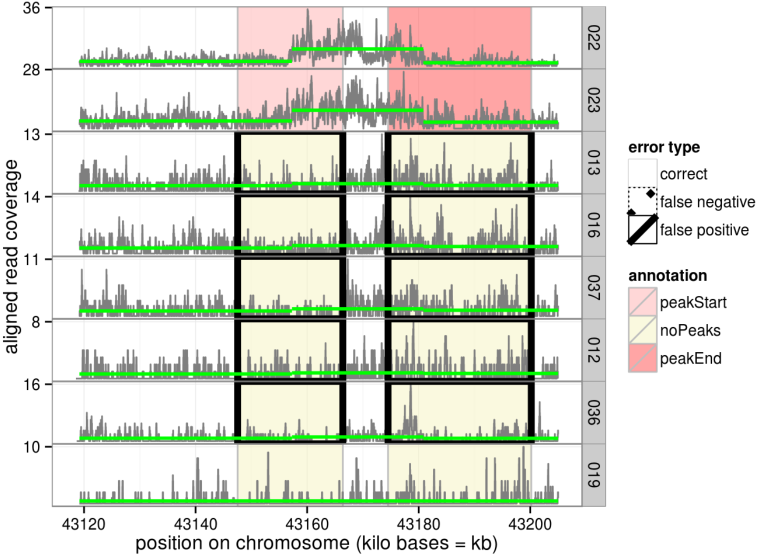
PeakSegJoint model with 5 peaks



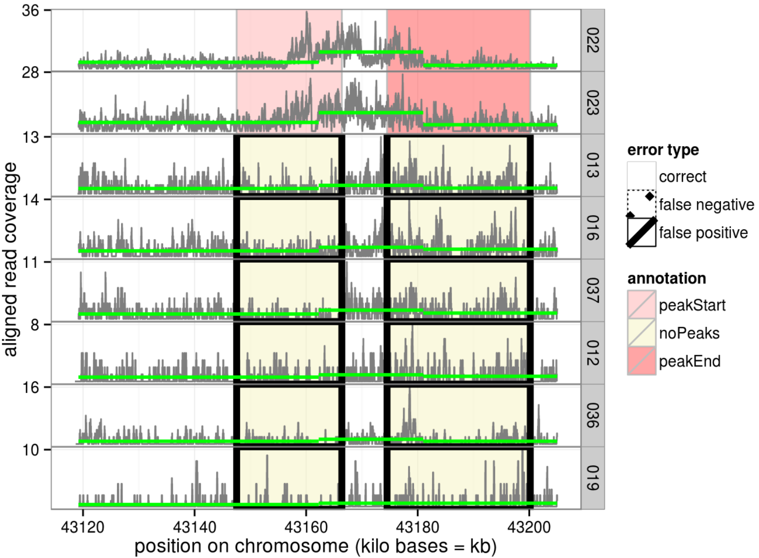
PeakSegJoint model with 6 peaks



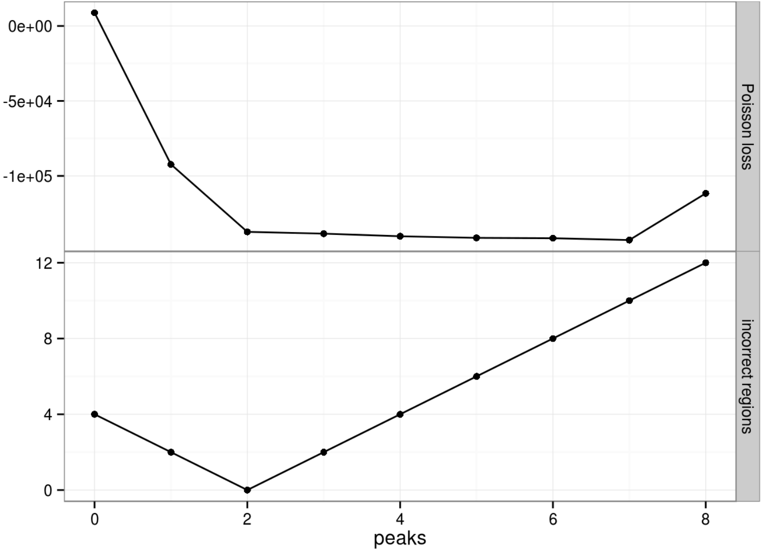
PeakSegJoint model with 7 peaks



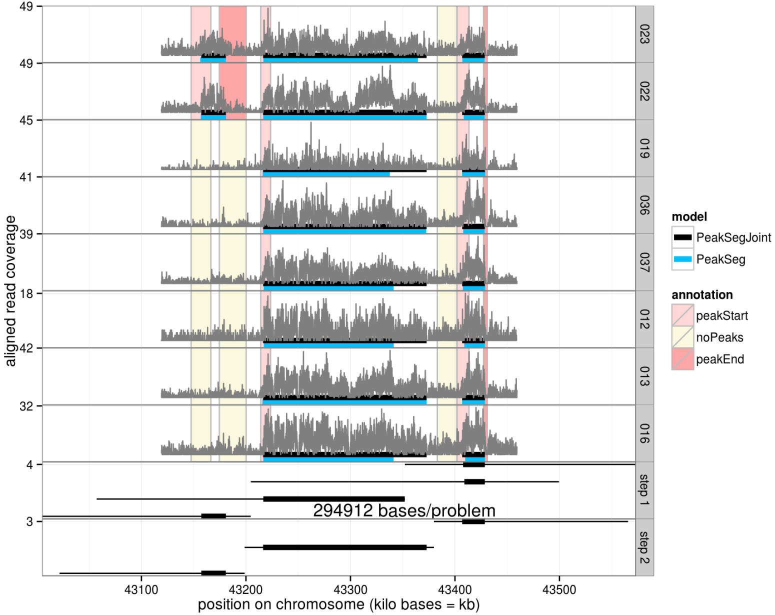
PeakSegJoint model with 8 peaks



Select model with minimal number of incorrect regions



H3K36me3 data, PeakSeg and Joint model



Timings on example H3K36me3 data

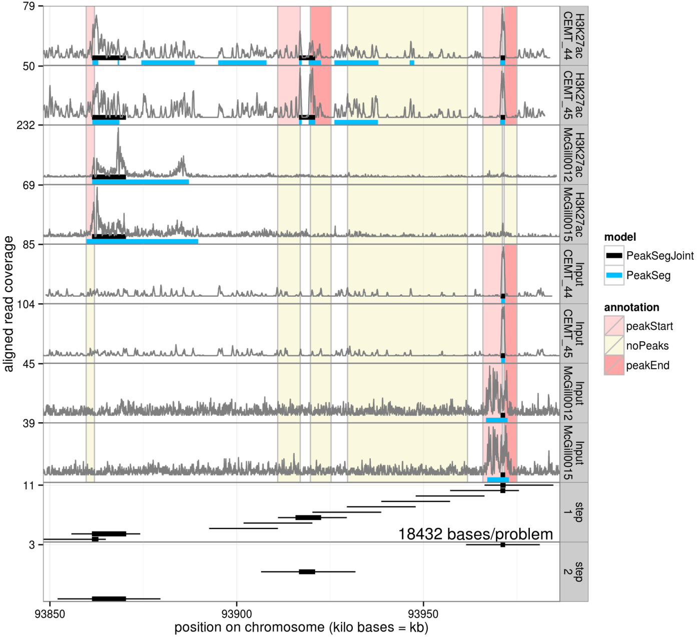
Find best 0,...,9 peaks in each of 8 samples (80 PeakSeg models):

seconds	sample.id
0.75	McGill0023
0.77	McGill0022
0.75	McGill0019
0.79	McGill0036
0.77	McGill0037
0.77	McGill0012
0.77	McGill0013
0.76	McGill0016
6.14	total

Find best common peak in 0,...,8 samples in each of 4 genomic regions (36 PeakSegJoint models):

	data	seconds
chr21:42909696-43204608	23595	0.04
chr21:43057152-43352064	162129	0.11
chr21:43204608-43499520	206437	0.12
chr21:43352064-43646976	67903	0.06
total		0.33

H3K27ac and Input data, PeakSeg and Joint model



Timings on example H3K27ac data

Find best
0,...,9 peaks
in each of 8 samples
(80 PeakSeg models)

seconds	sample.id
0.99	H3K27ac CEMT_44
0.96	H3K27ac CEMT_45
1.00	H3K27ac McGill0012
1.00	H3K27ac McGill0015
0.99	Input CEMT_44
1.00	Input CEMT_45
1.01	Input McGill0012
1.00	Input McGill0015
7.94	total

Find best common peak
in 0,...,8 samples
in each of 11 genomic regions
(99 PeakSegJoint models)

	data	seconds
chr11:93846528-93864960	7510	0.03
chr11:93855744-93874176	11675	0.03
chr11:93892608-93911040	5619	0.03
chr11:93901824-93920256	6236	0.03
chr11:93911040-93929472	5559	0.03
chr11:93920256-93938688	5149	0.04
chr11:93929472-93947904	4359	0.01
chr11:93938688-93957120	3071	0.03
chr11:93947904-93966336	3030	0.02
chr11:93957120-93975552	7184	0.04
chr11:93966336-93984768	7446	0.04
total		0.32

Conclusions

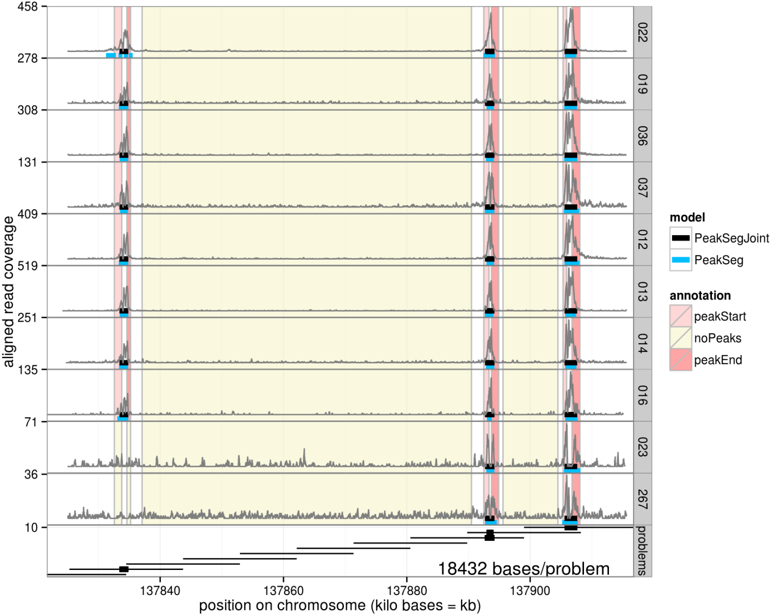
Thanks for your attention!

Write me at toby.hocking@mail.mcgill.ca to collaborate!

Source code for slides, figures, paper online!
https://github.com/tdhock/PeakSegJoint-paper

Supplementary slides appear after this one.

H3K4me3 data, PeakSeg and Joint model



Timings on example H3K4me3 data

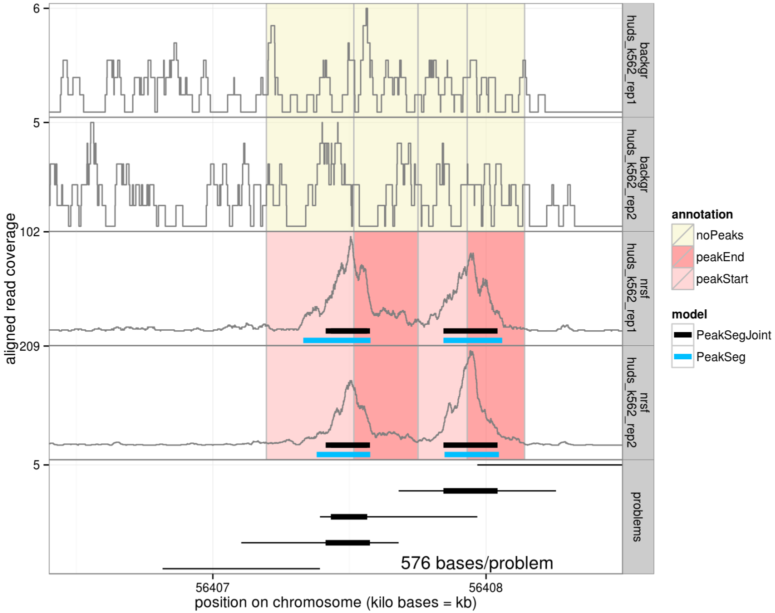
Find best
0,...,9 peaks
in each of 10 samples
(100 PeakSeg models)

seconds	sample.id
0.72	McGill0022
0.71	McGill0019
0.72	McGill0036
0.72	McGill0037
0.74	McGill0012
0.76	McGill0013
0.72	McGill0014
0.72	McGill0016
0.73	McGill0023
0.75	McGill0267
7.30	total

Find best common peak
in 0,...,10 samples
in each of 10 genomic regions
(110 PeakSegJoint models)

	data	seconds
chr21:137816064-137834496	7603	0.01
chr21:137825280-137843712	12420	0.05
chr21:137834496-137852928	7023	0.01
chr21:137843712-137862144	3915	0.04
chr21:137852928-137871360	3597	0.03
chr21:137862144-137880576	3588	0.03
chr21:137871360-137889792	4255	0.05
chr21:137880576-137899008	13317	0.05
chr21:137889792-137908224	26436	0.05
chr21:137899008-137917440	19644	0.05
total		0.36

NRSF transcription factor data, PeakSeg and Joint model



Timings on example transcription factor data

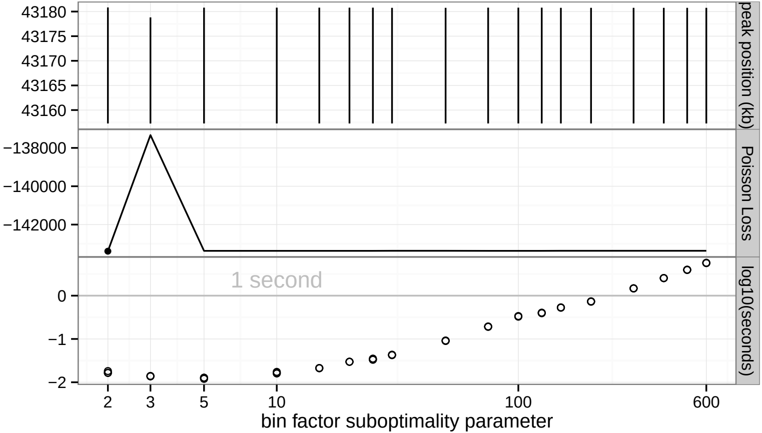
Find best
0,...,9 peaks
in each of 4 samples
(40 PeakSeg models)

seconds	sample.id
0.26	backgr huds_k562_rep1
0.24	backgr huds_k562_rep2
0.30	nrsf huds_k562_rep1
0.31	nrsf huds_k562_rep2
1.10	total

Find best common peak
in 0,...,4 samples
in each of 5 genomic regions
(25 PeakSegJoint models)

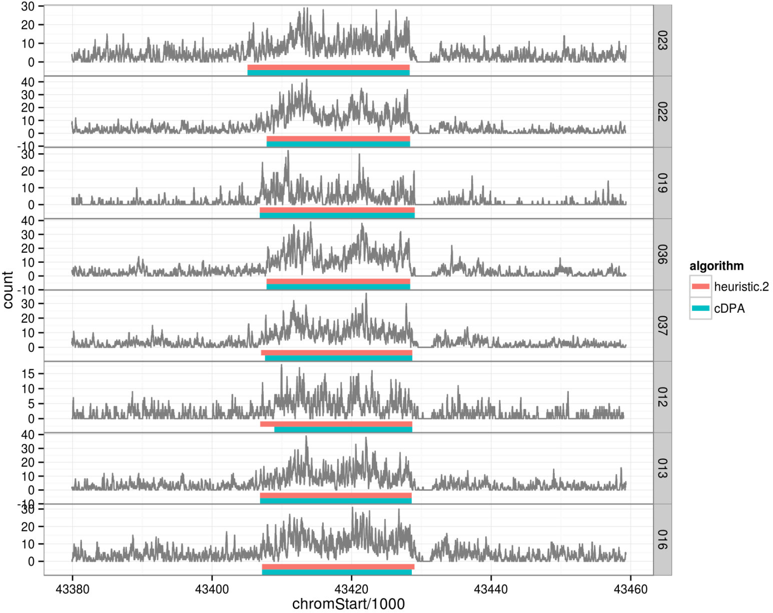
	data	seconds
chr21:56406816-56407392	345	0.01
chr21:56407104-56407680	761	0.02
chr21:56407392-56407968	975	0.01
chr21:56407680-56408256	709	0.02
chr21:56407968-56408544	298	0.01
total		0.07

Bin factor parameter controls optimality and speed

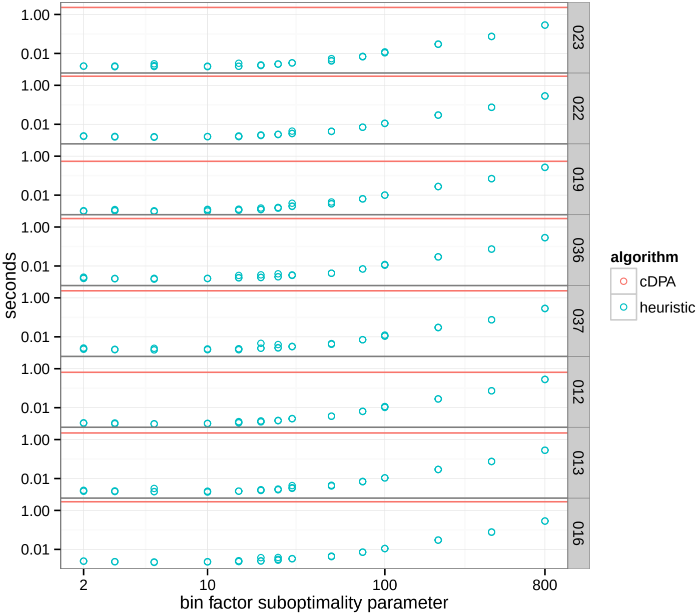


H3K36me3 example data set, PeakSegJoint model with 2 peaks.

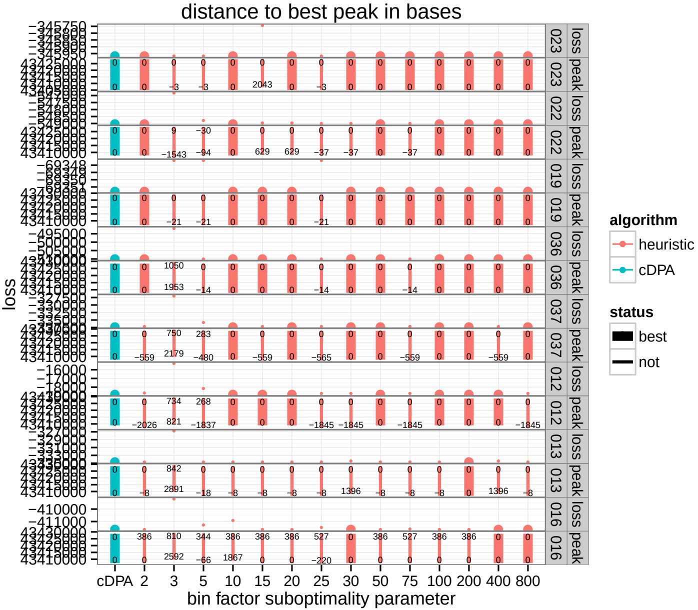
H3K36me3 data, cDPA and heuristic algorithms



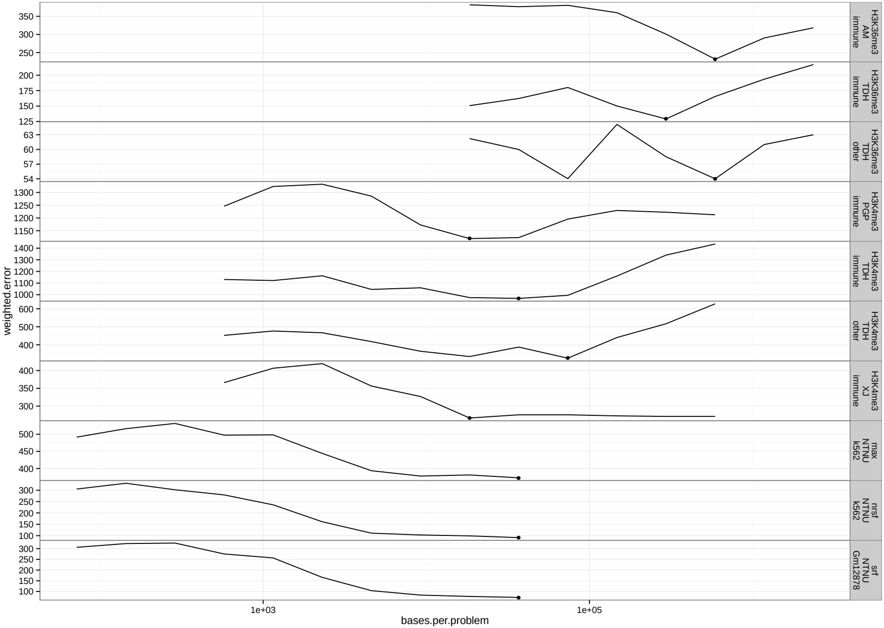
Heuristic is much faster than cDPA



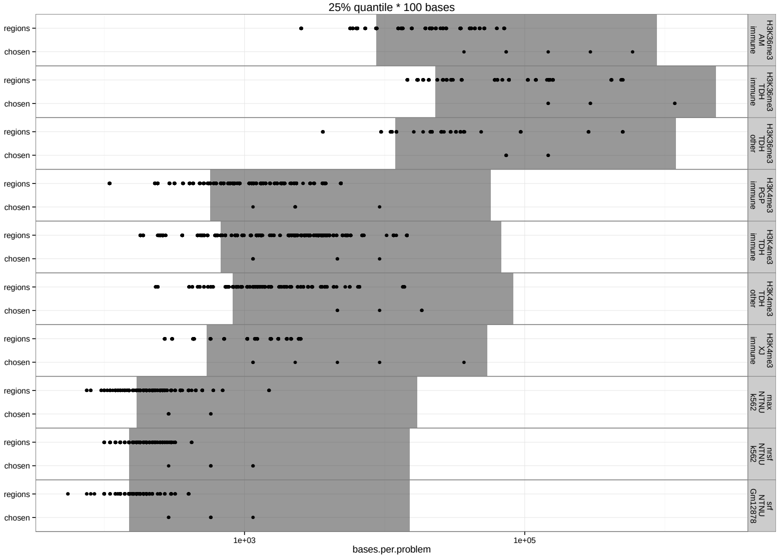
Heuristic often as good as cDPA



Weighted train error not good for model selection

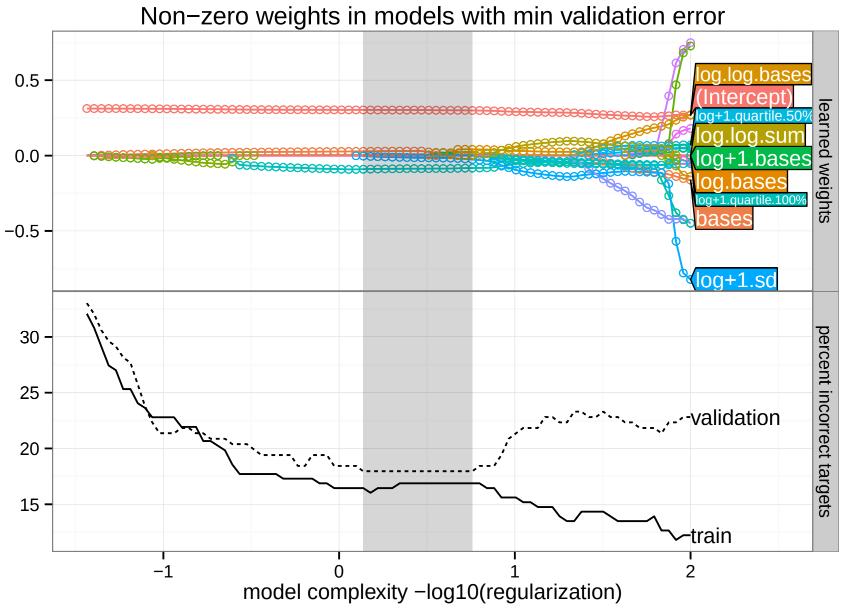


Size of positive regions good heuristic for initial grid search



6 train/test splits per data set.

Select L1-regularized model with minimal validation error


Non−zero weights in models with min validation error
log.log.bases
(Intercept)
log+1.quartile.50%
log.log.sum
log+1.bases
log.bases
log+1.quartile.100%
bases
log+1.sd
learned weights
validation
train
percent incorrect targets
model complexity −log10(regularization)