

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

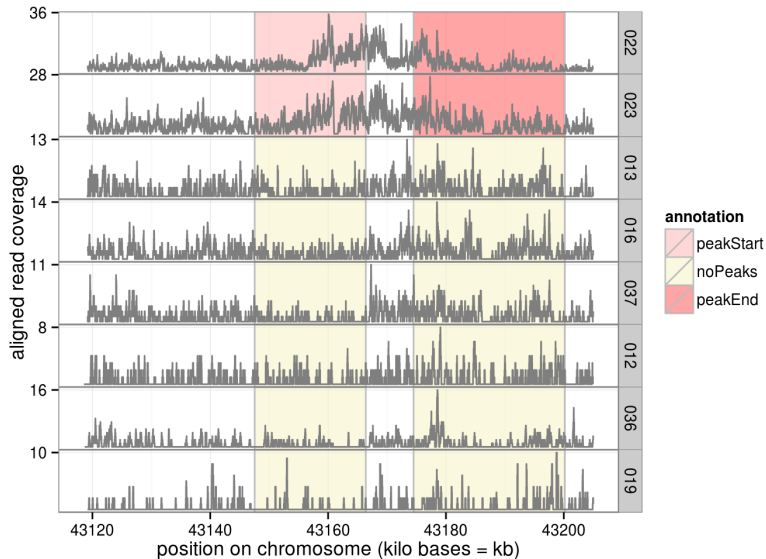
Toby Dylan Hocking

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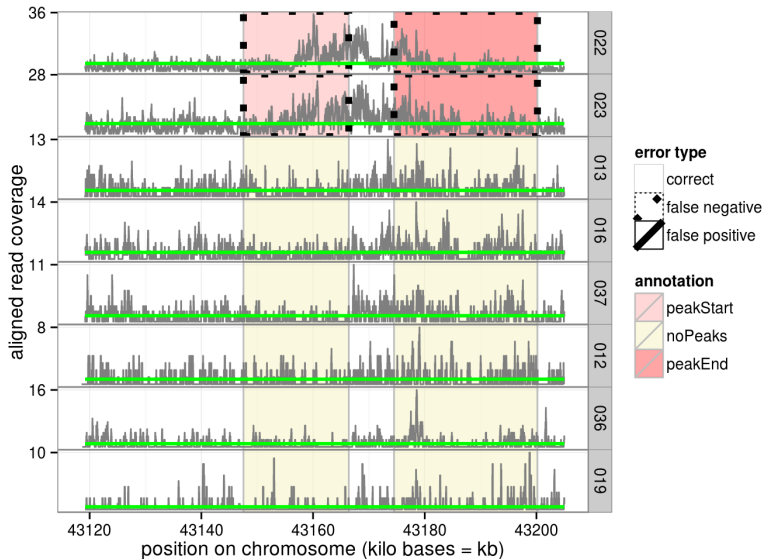
joint work with Guillem Rigau and Guillaume Bourque

2 April 2015

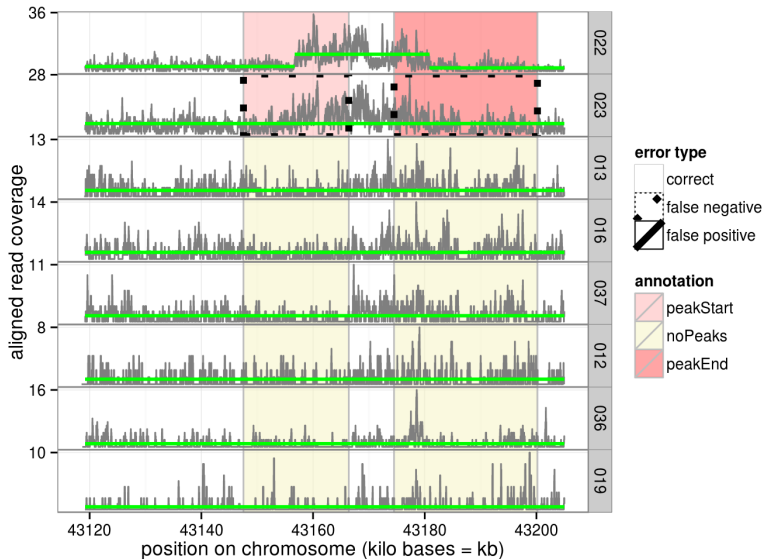
# H3K36me3 data and labels



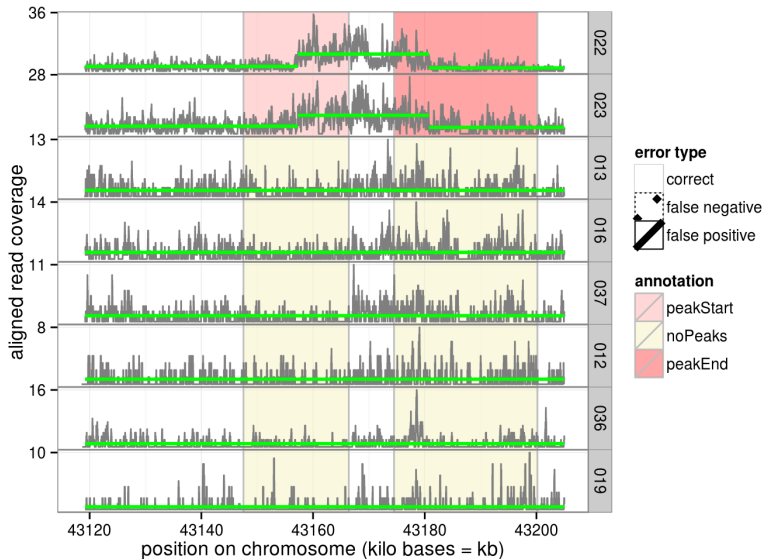
# PeakSegJoint model with 0 peaks



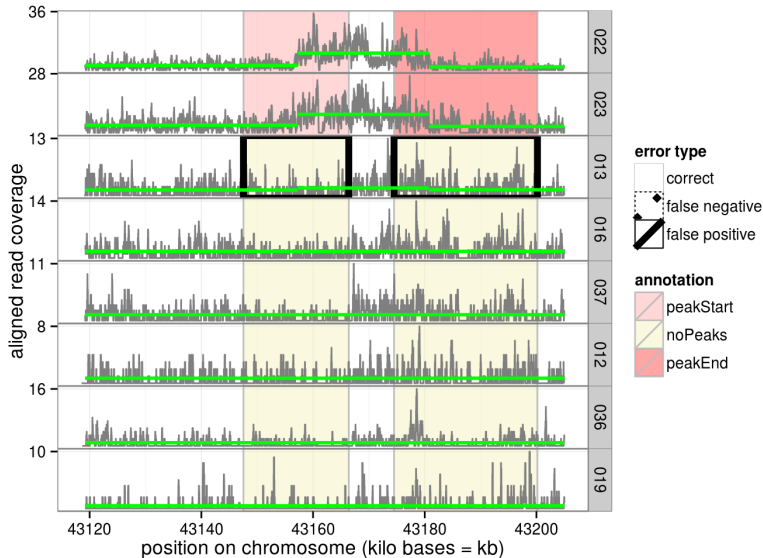
# PeakSegJoint model with 1 peak



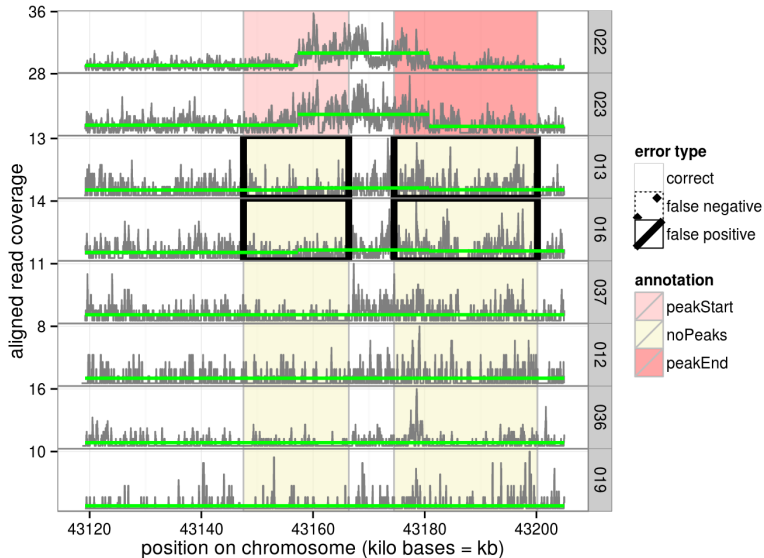
# PeakSegJoint model with 2 peaks



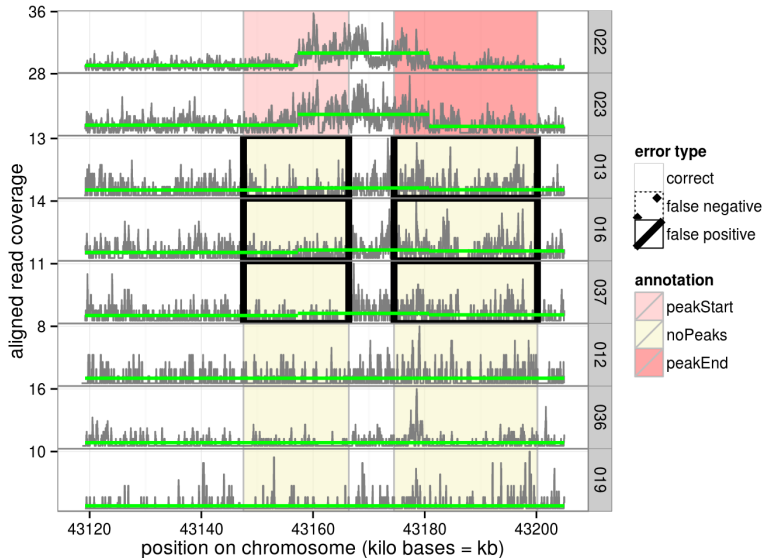
# PeakSegJoint model with 3 peaks



# PeakSegJoint model with 4 peaks

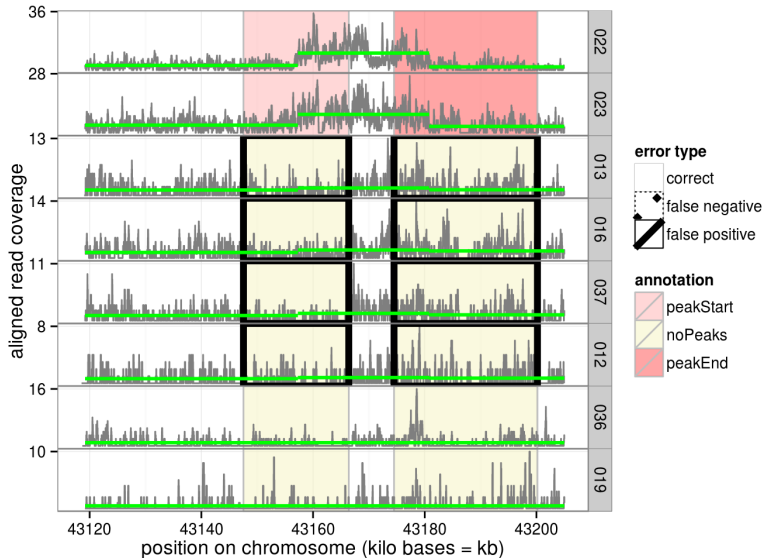


# PeakSegJoint model with 5 peaks

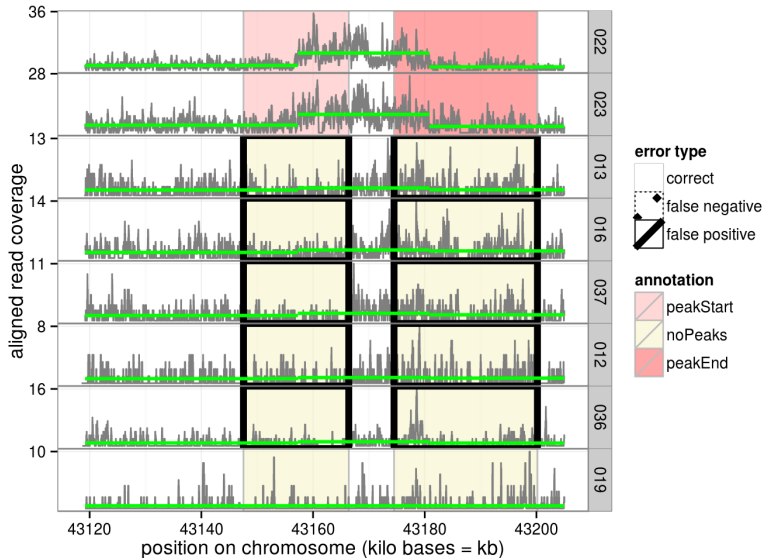




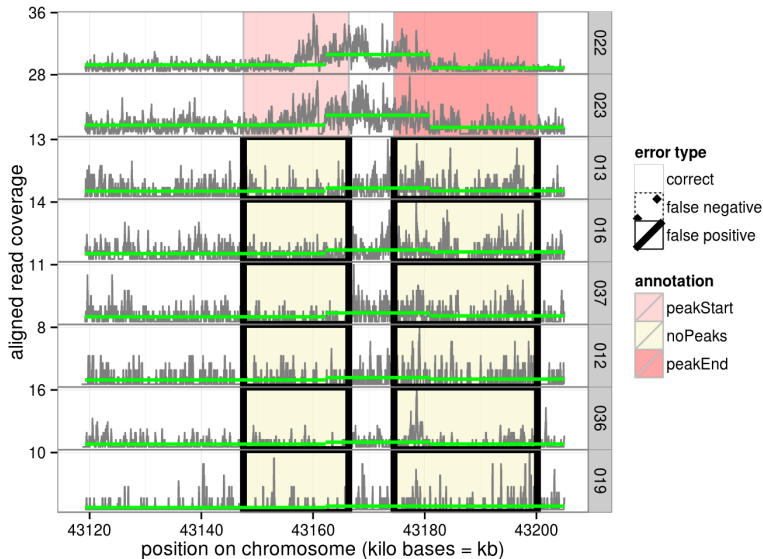
# PeakSegJoint model with 6 peaks



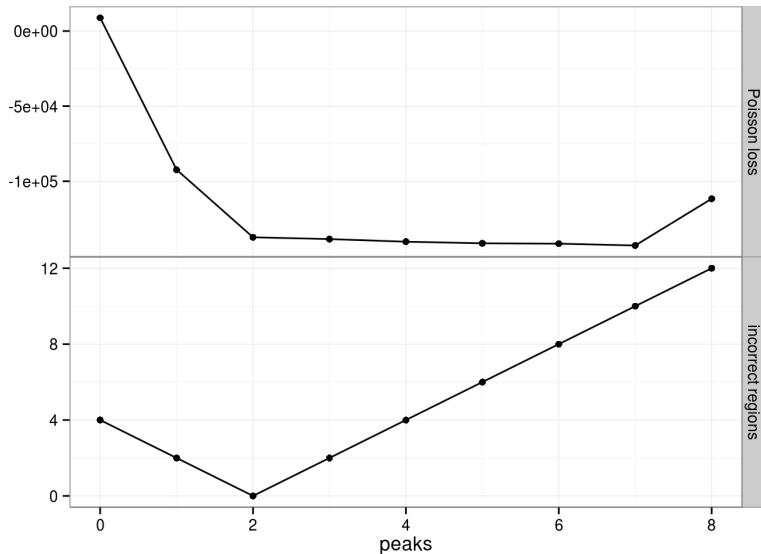
# PeakSegJoint model with 7 peaks



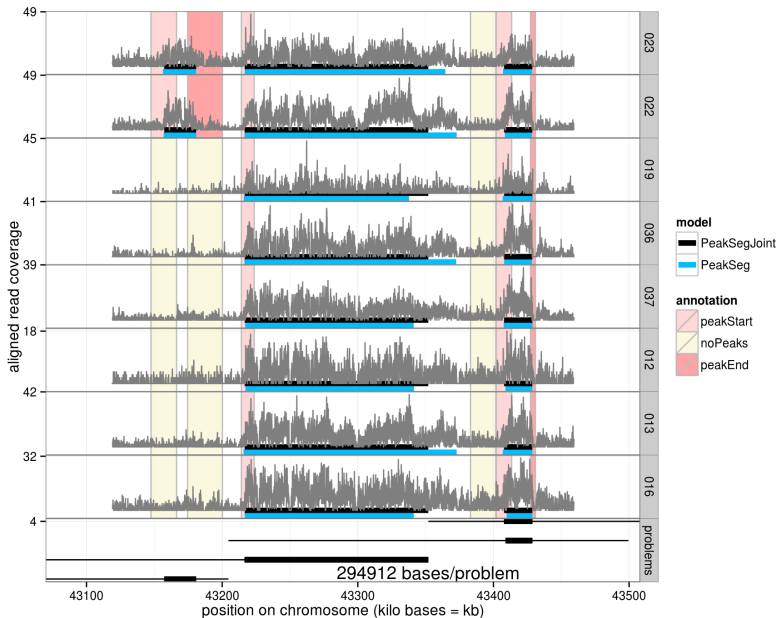
# PeakSegJoint model with 8 peaks



# Select model with minimal number of incorrect regions



# H3K36me3 data, PeakSeg and Joint model



## Timings on example H3K36me3 data

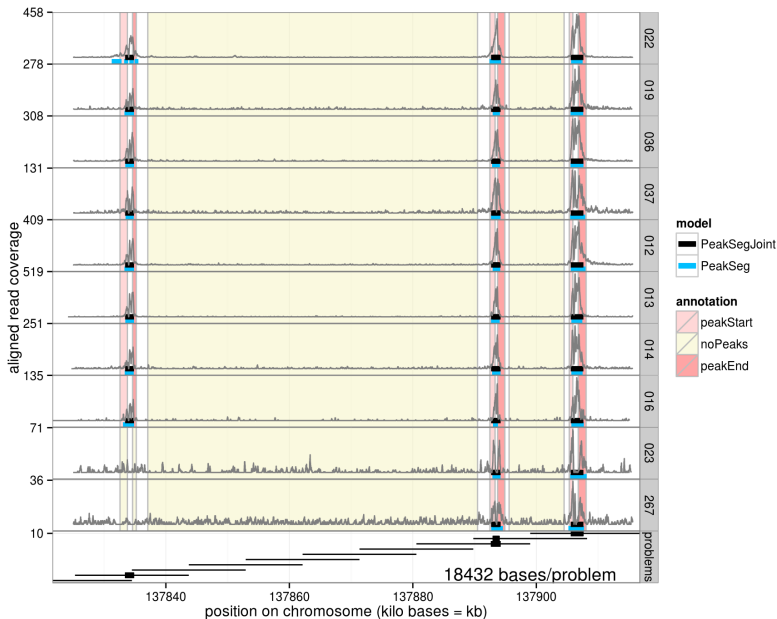
Find best 0,...,9 peaks in each of 8 samples (80 PeakSeg models):

seconds	sample.id
1.07	McGill0023
1.06	McGill0022
1.05	McGill0019
1.07	McGill0036
1.09	McGill0037
1.06	McGill0012
1.08	McGill0013
1.06	McGill0016
8.54	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	0.09
chr21:43204608-43499520	206437	0.11
chr21:43352064-43646976	67903	0.06
total		0.30

# 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
0.76	McGill0022
0.74	McGill0019
0.74	McGill0036
0.75	McGill0037
0.75	McGill0012
0.73	McGill0013
0.74	McGill0014
0.74	McGill0016
0.74	McGill0023
0.75	McGill0267
7.44	total

Find best common peak  
in 0,...,10 samples  
in each of 10 genomic regions  
(100 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	0.06
chr21:137899008-137917440	19644	0.06
total		0.39