

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

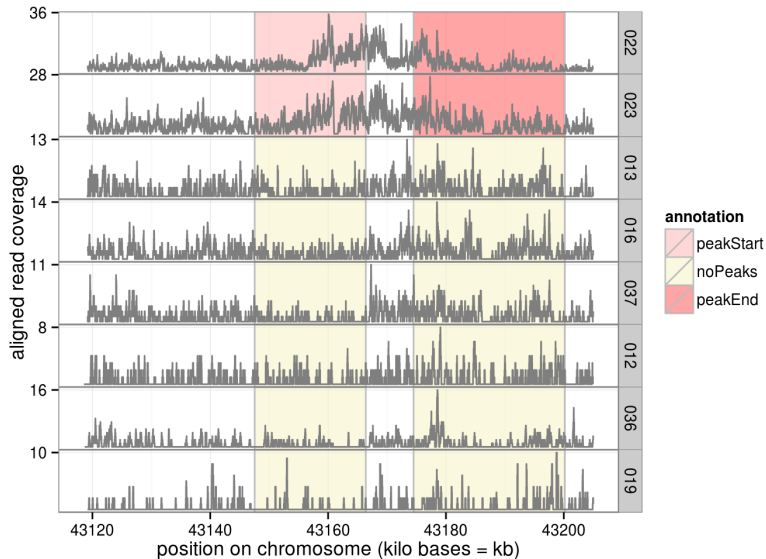
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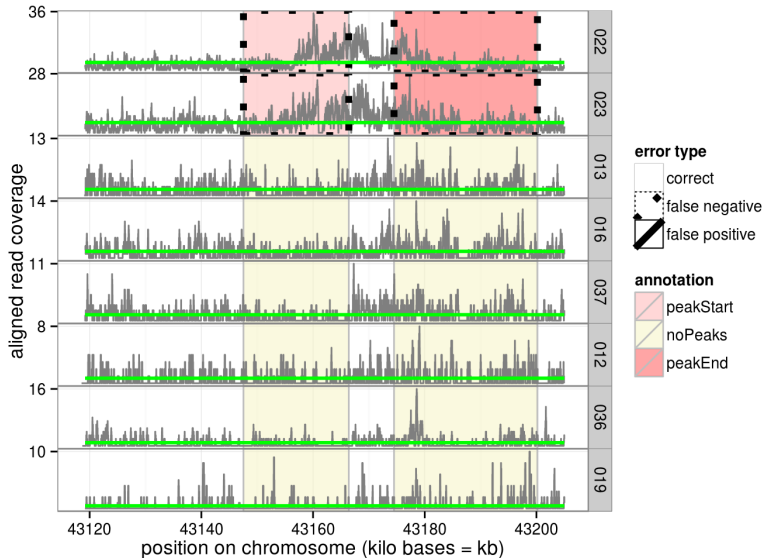
joint work with Guillem Rigau and Guillaume Bourque

2 April 2015

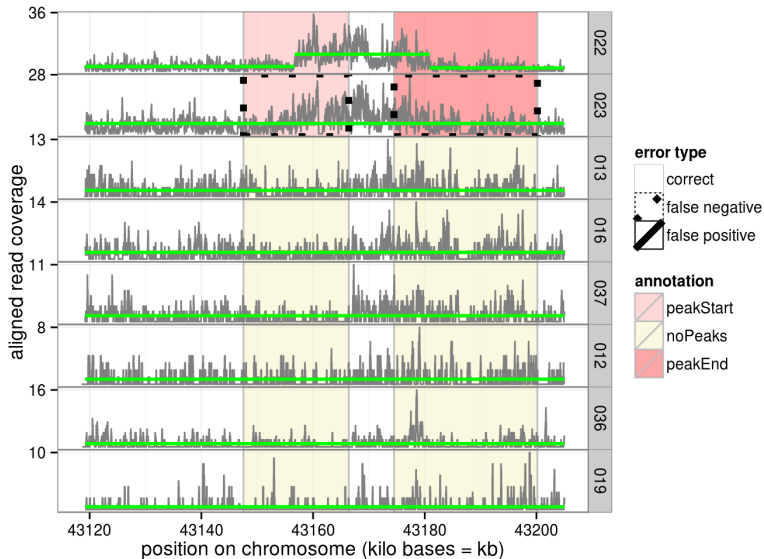
H3K36me3 data and labels



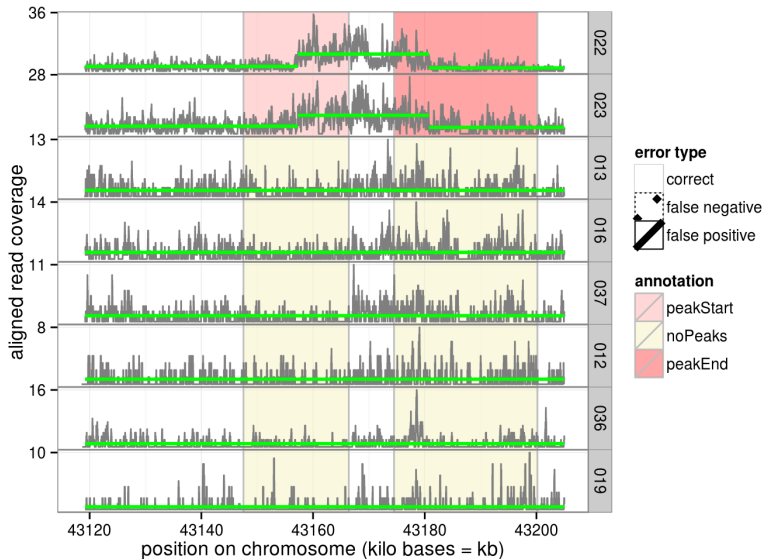
PeakSegJoint model with 0 peaks



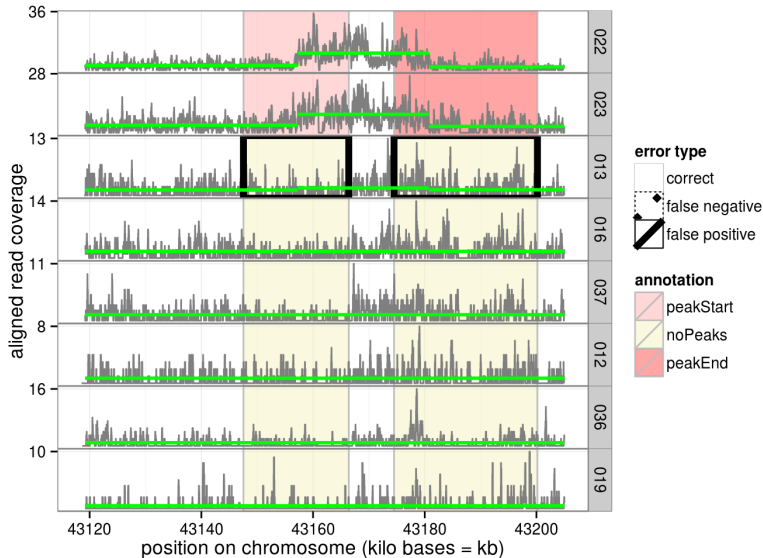
PeakSegJoint model with 1 peak



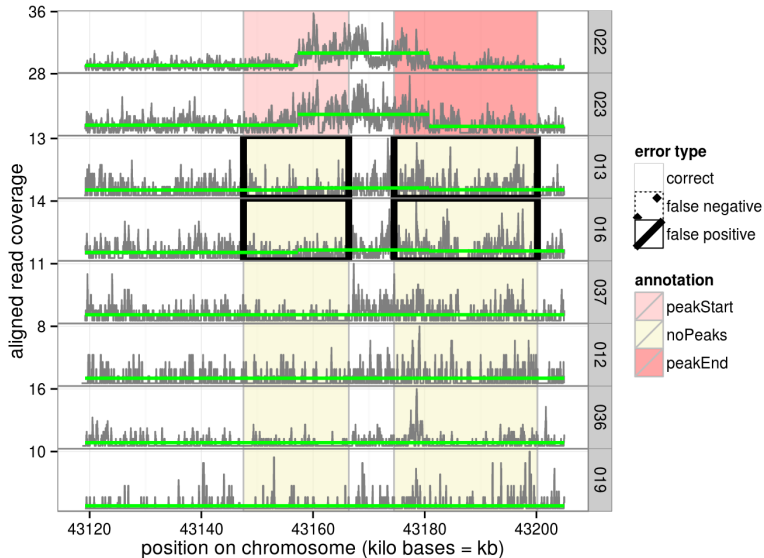
PeakSegJoint model with 2 peaks



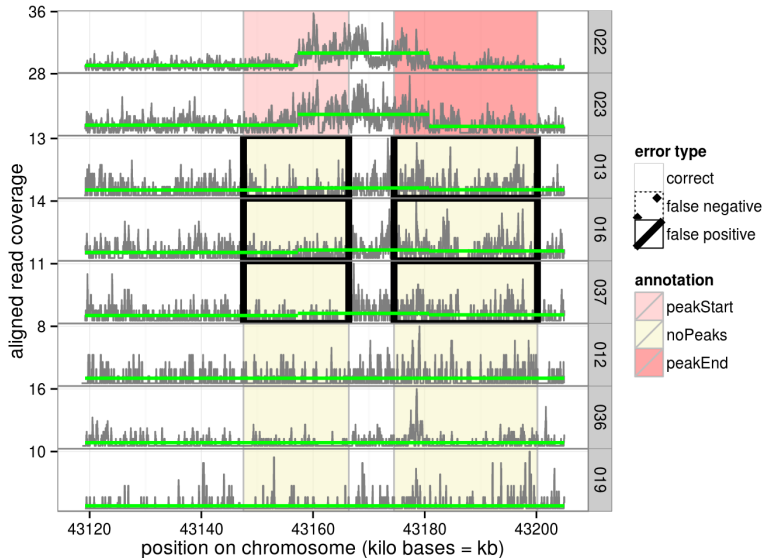
PeakSegJoint model with 3 peaks



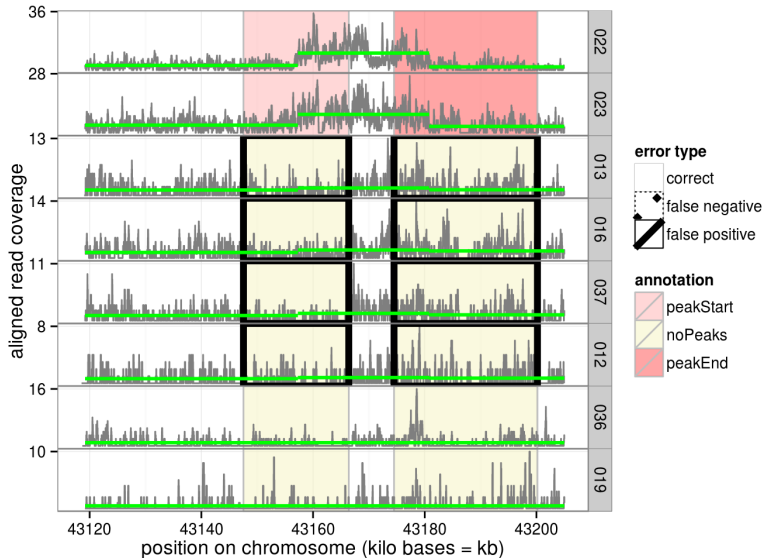
PeakSegJoint model with 4 peaks



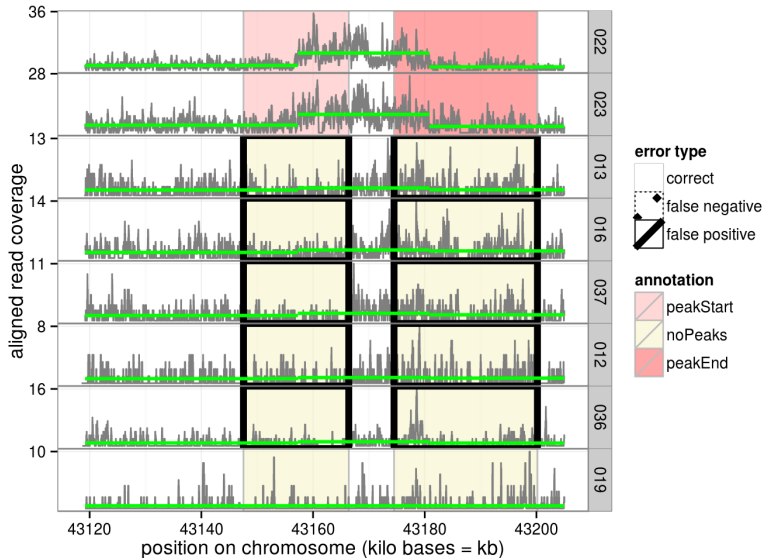
PeakSegJoint model with 5 peaks



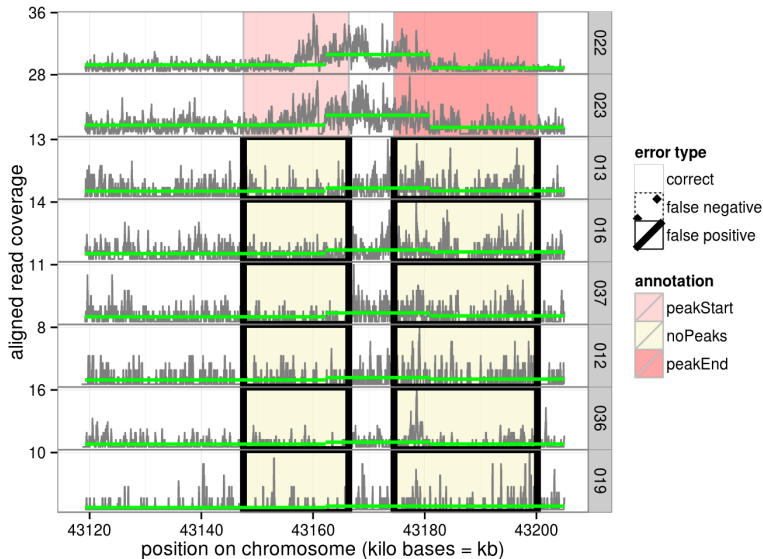
PeakSegJoint model with 6 peaks



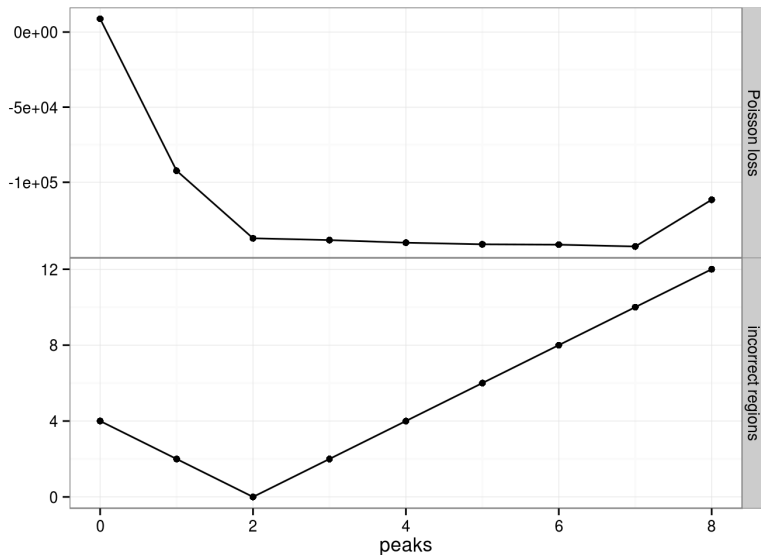
PeakSegJoint model with 7 peaks



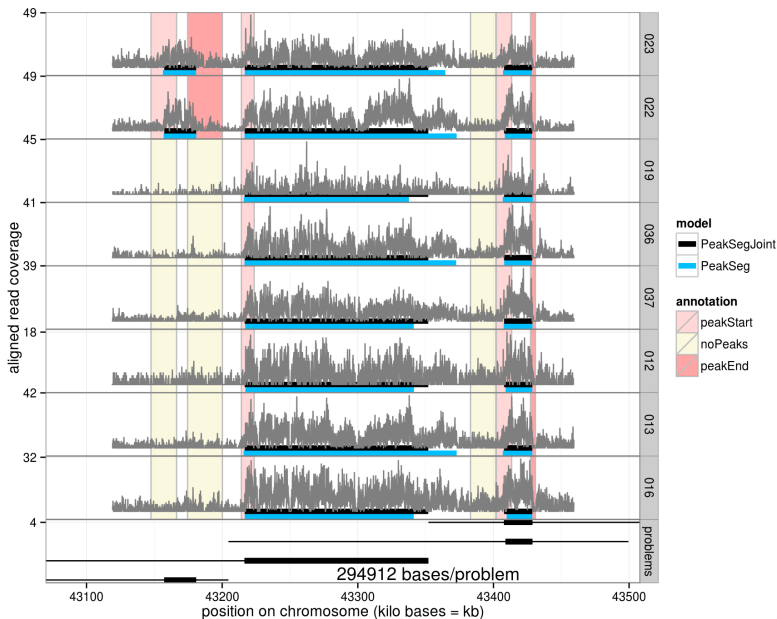
PeakSegJoint model with 8 peaks



Select model with minimal number of incorrect regions



H3K36me3 data, PeakSeg and Joint model



Timings on example H3K36me3 data

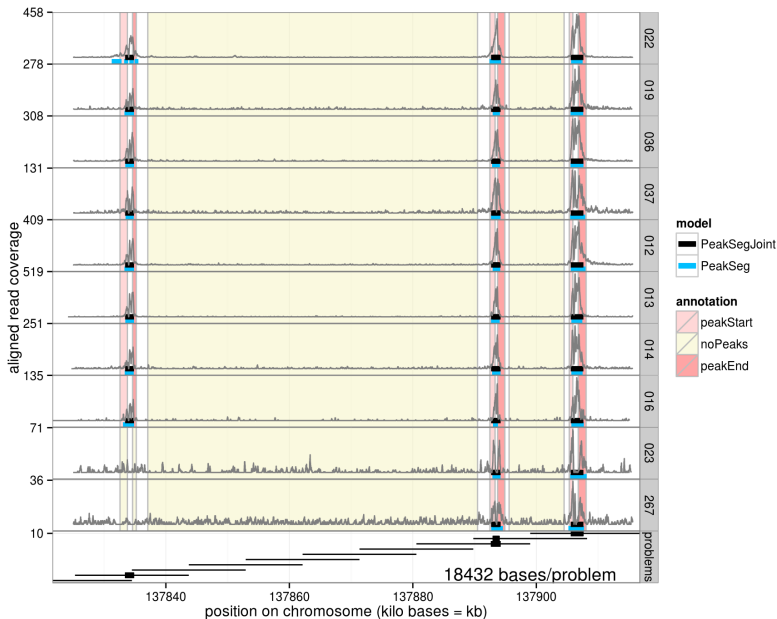
Segment each of 8 samples (PeakSeg):

seconds	sample.id
0.72	McGill0023
0.75	McGill0022
0.73	McGill0019
0.74	McGill0036
0.74	McGill0037
0.74	McGill0012
0.74	McGill0013
0.75	McGill0016
5.90	total

Segment each of 4 genomic regions (PeakSegJoint):

	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

Segment each of 10 samples (PeakSeg)		Segment each of 10 genomic regions (PeakSegJoint)		
seconds	sample.id		data	seconds
0.76	McGill0022	chr21:137816064-137834496	7603	0.01
0.74	McGill0019	chr21:137825280-137843712	12420	0.05
0.74	McGill0036	chr21:137834496-137852928	7023	0.01
0.75	McGill0037	chr21:137843712-137862144	3915	0.04
0.75	McGill0012	chr21:137852928-137871360	3597	0.03
0.73	McGill0013	chr21:137862144-137880576	3588	0.03
0.74	McGill0014	chr21:137871360-137889792	4255	0.05
0.74	McGill0016	chr21:137880576-137899008	13317	0.05
0.74	McGill0023	chr21:137889792-137908224	26436	0.06
0.75	McGill0267	chr21:137899008-137917440	19644	0.06
7.44	total	total		0.39