

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

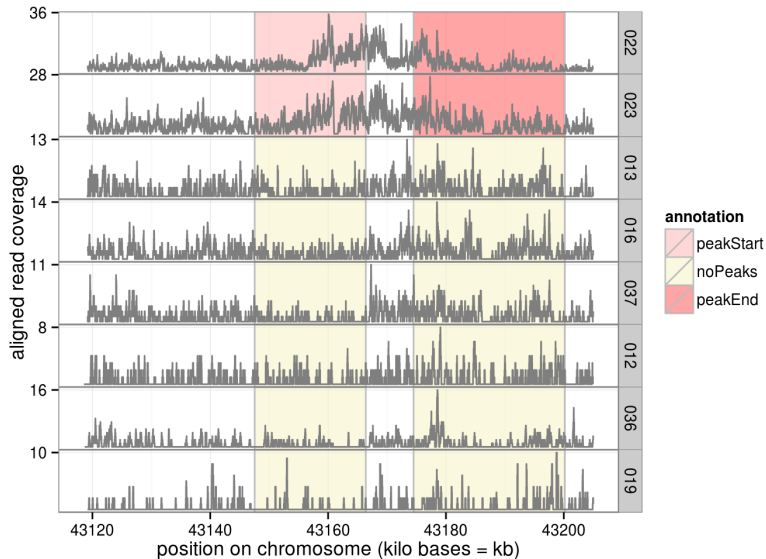
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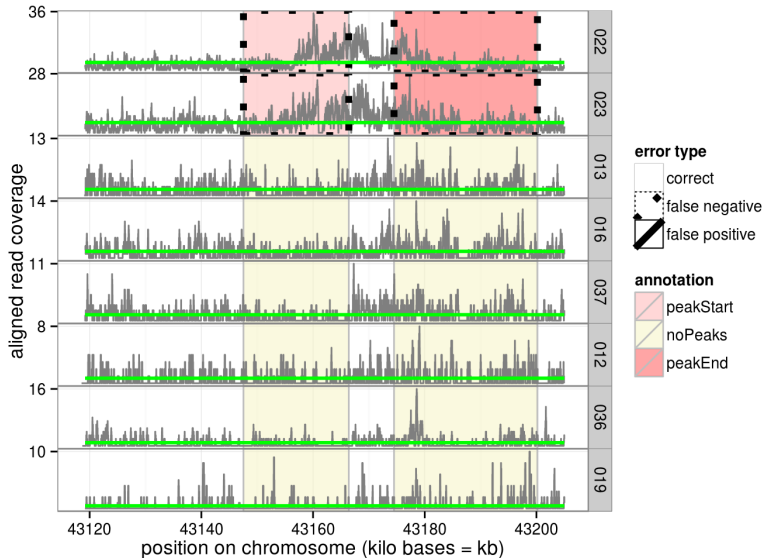
joint work with Guillem Rigau and Guillaume Bourque

2 April 2015

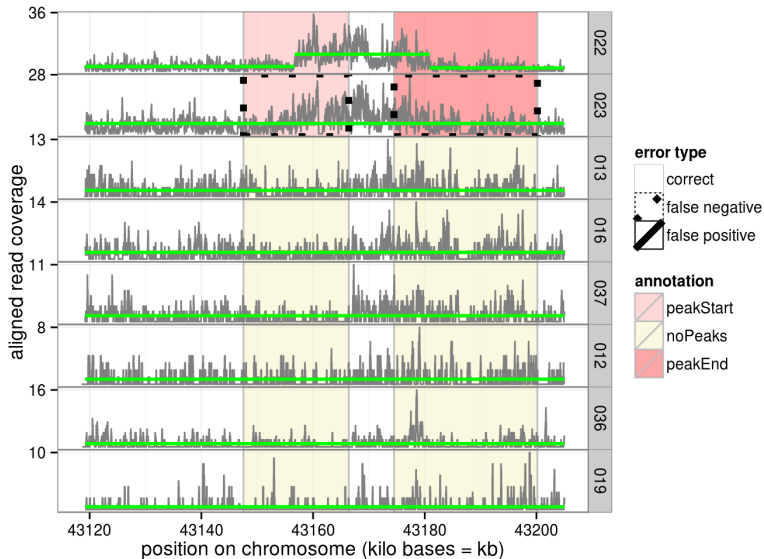
H3K36me3 data and labels



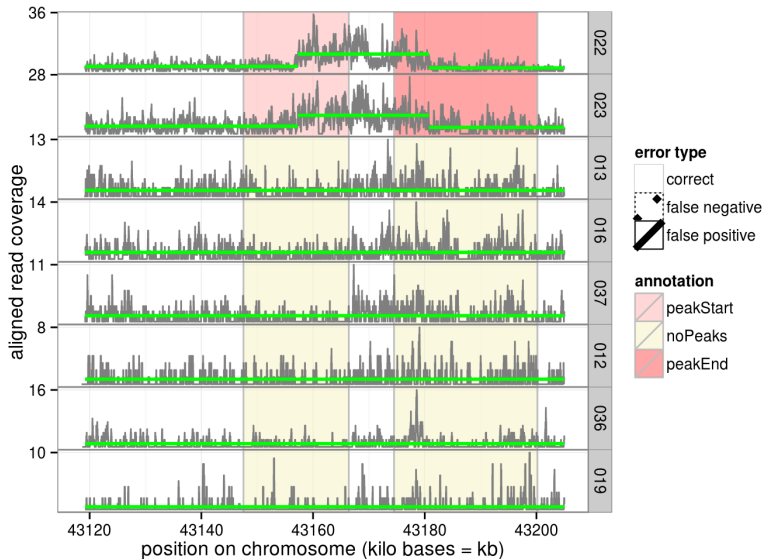
PeakSegJoint model with 0 peaks



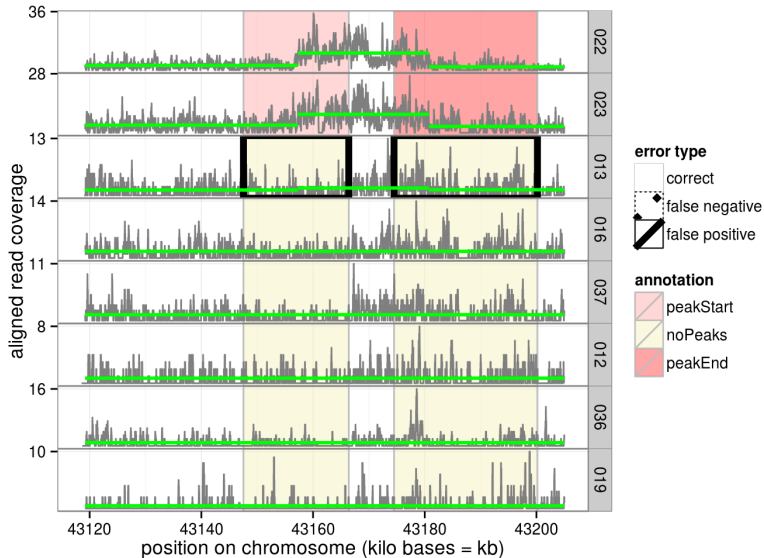
PeakSegJoint model with 1 peak



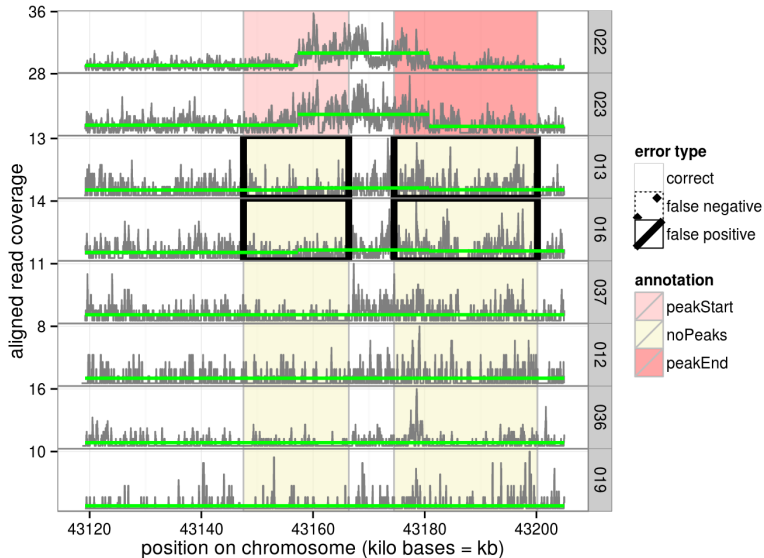
PeakSegJoint model with 2 peaks



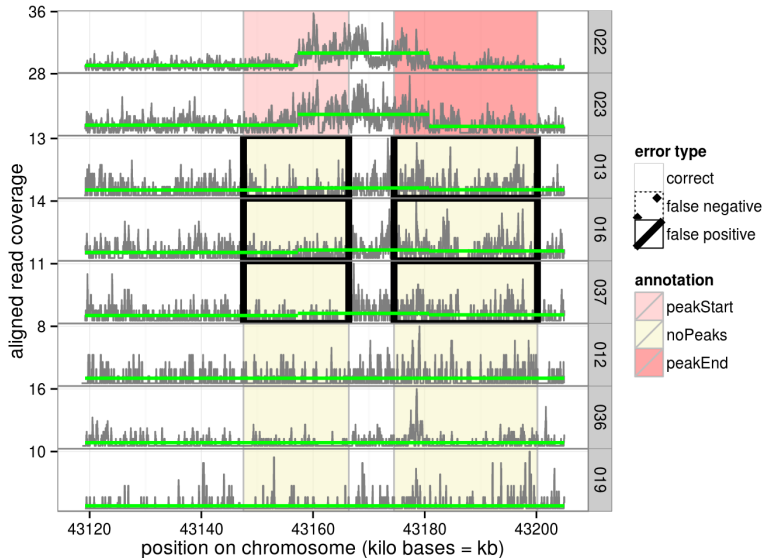
PeakSegJoint model with 3 peaks



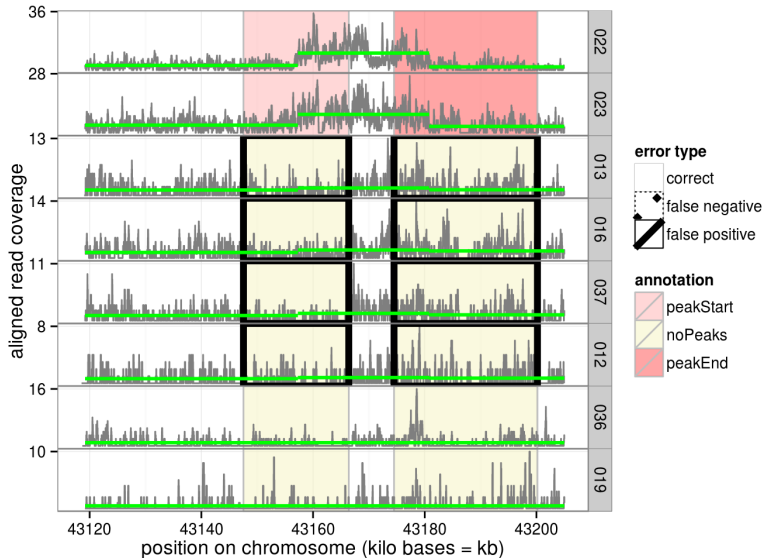
PeakSegJoint model with 4 peaks



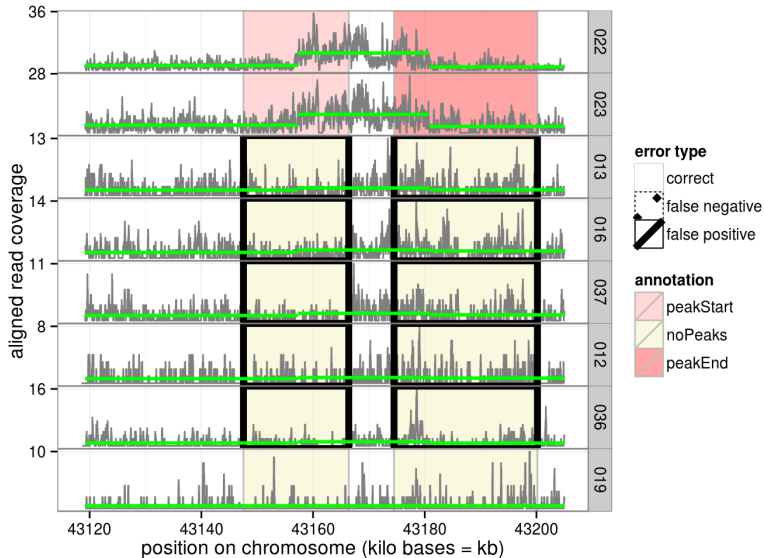
PeakSegJoint model with 5 peaks



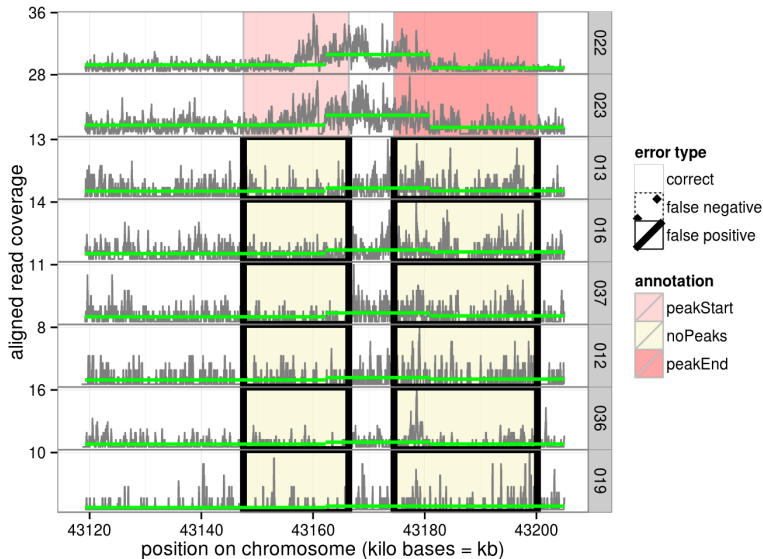
PeakSegJoint model with 6 peaks



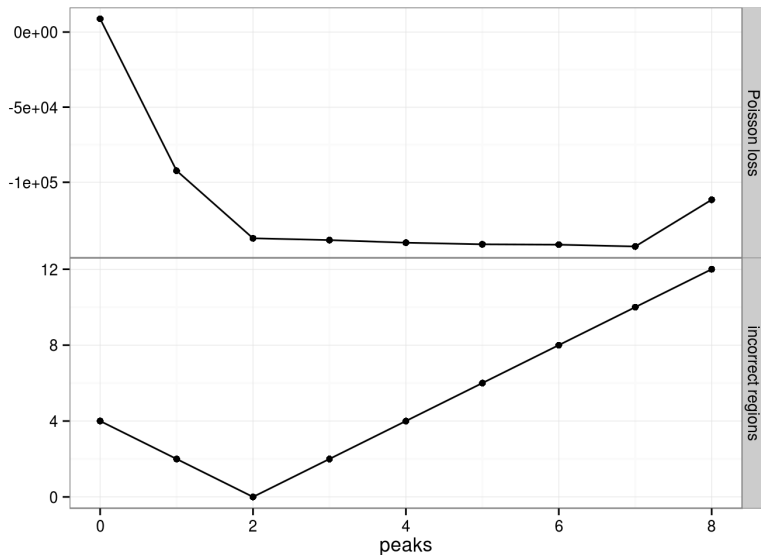
PeakSegJoint model with 7 peaks



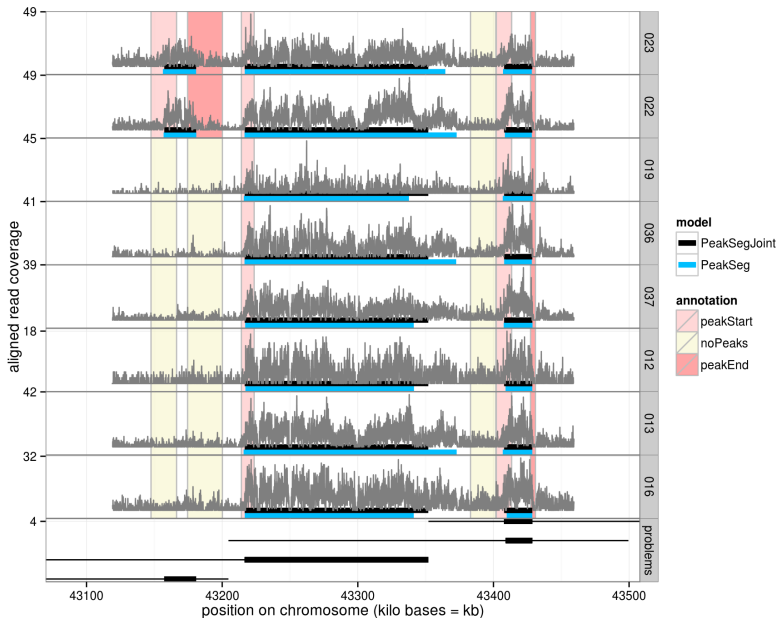
PeakSegJoint model with 8 peaks



Select model with minimal number of incorrect regions



Comparison of PeakSeg and Joint model



Comparing timings to segment 8 samples

Segment each sample (PeakSeg):

seconds	sample.id
0.91	McGill0023
0.89	McGill0022
0.90	McGill0019
0.89	McGill0036
0.90	McGill0037
0.89	McGill0012
0.91	McGill0013
0.87	McGill0016
7.15	total

Segment each genomic region (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