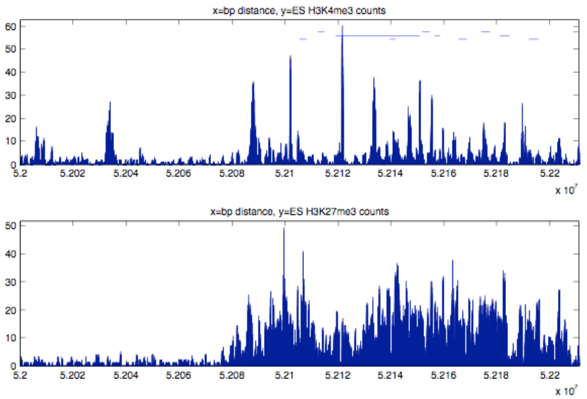


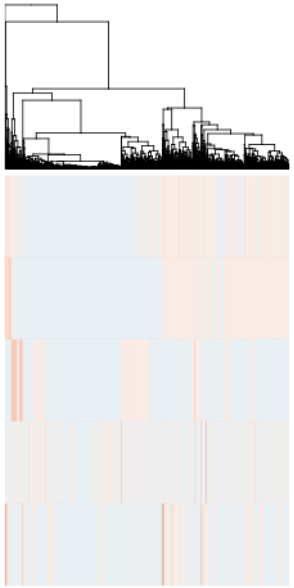
Raw ChIP-seq data

Step 1: Generate a 5-d score for each gene

	Gene A	Gene B	Gene C	…
H3K4me2	1.4608	2.148	3.6203	…
H3K4me3	7.4275	12.786	11.797	…
H3K27me3	0.1529	0.2705	4.9406	…
H3K9me3	0.2323	0.2529	0.5062	…
H3K36me3	0.05	4.0833	1.5883	…

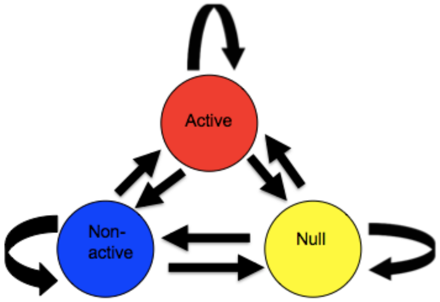
Score matrix of pre-processed ChIP-seq data

Step 2: Cluster the genes to obtain prior modification specific means and variances



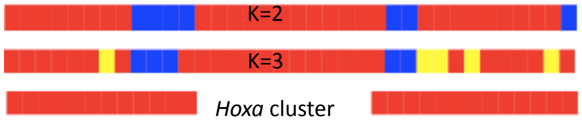
Heatmap cluster of score matrix data

Step 3: Assume a hidden Markov model where the observed scores are multivariate normal with prior parameters taken from cluster results



HMM true hidden states and possible transitions

Step 4: Find significant domains via permutation tests



Examine biological validity of domains