align genomes 
filter (optional) 
align genomes

score each site against each cactus
segment genome/optimise global score
assign cactus to each segment
re-compute cacti based on their sites

repeat? yes no

train network from segmented sites
find most representative neurons ("best")
find farthest neurons from best ("worst")
estimate cactus from global worst

SOM

Positions converted to vectors

SOM training

Worst Neuron expanded into cactus

Positions converted to binary cacti

Segments determined by HMM

Cacti retrained from segmentation

Biological interpretation

segmentation and cacti