

INPUT

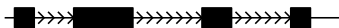
Bed file with genomic regions



Genomic sequence

...CTGATGGTCATTACTAG...

Genome annotation



Bed files with biological features

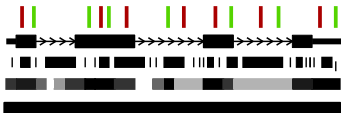


bigWig phastCons scores

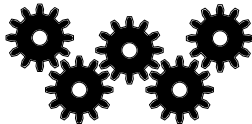


ANALYSIS

Background generation, feature extraction and datamatrix build



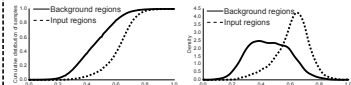
Statistical analysis, classification and feature importance scoring



OUTPUT

Tables with statistical p-value and classification scores

Cumulative distribution function and kernel density estimation



Classifier performance metrics

