

Input

Genome size
Gene family size
g value(s)

Input data

GFF3 or BED
data file

Protein
data file

GALEON's clusterfinder mode

g value
determination

Physical distance
matrix

Cluster finding
algorithm

Cluster
identification

Multiple sequence
alignment
mafft

Tree inference
FastTree or *iqtree*
Newick utils

Evolutionary distance
matrix

C_{ST} statistic
estimation

Output

