

https://github.com/vinuesa/get_phylomarkers

Flowchart showing how the GET_PHYLOMARKERS package integrates with
GET_HOMOLOGUES

Vinuesa et al., 2018

Benchmark analyses of the phylogenetic performance of FT vs IQ-TREE

Consensus core-genome
(n=239) computed with
GET_HOMOLOGUES

**Distribution of
SH-akt branch support
values** of gene-trees found
by the FThigh and IQThigh
Searches.

Wilcoxon signed-rank test
 $p < 2.2e-16$

Distribution of **consensus
values from majority-rule
consensus trees** computed
from the gene trees passing
all the filters, as a function
Of search-type.

Kruskal-Wallis $p < 0.027$

Computation time required
FT and IQT when run under
"default" (FTdef, IQTdef) and
thorough (FThigh, IQThigh)
search modes (s_type)
on the 239 consensus
Clusters

Kruskal-Wallis $p < 2.2e-16$

Association plot
summarizing the results of
**multi-way Chi-Square
analyses of the InL
score ranks** (1-4, meaning
best to worst) **of the
105 top-scoring ML
gene-trees** passing the
kdetrees filter in the
IQThigh run (Table 2)
for each search-type

$p < 2.2e-16$

Distribution of the
**edge-lengths of
species-trees** computed
from the concatenated
top-scoring markers,
as a function of
Search-type

Kruskal-Wallis $p < 1e-7$

ML species tree

- 118 genomes
- Top 52/(231) markers
- GTR+ASC+F+R7

→ ~8% misclassified genomes 13/169
→ ~8% unclassified genomes
14/169

- reclassified 27 RefSeq
genome sequences!

- The Smc is split into 5 major lineages
including *S. maltophilia* s. lato

- 13 clades (species?) are recognized
within the latter, which are consistent
with a 95.9% cgANiB cutoff

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