

**GET\_PHYLOMARKERS: open-source tools for phylogenomics**

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**GET\_PHYLOMARKERS: open-source tools for phylogenomics**

## Introduction

- What is GET\_PHYLOMARKERS supposed to do?

GET\_PHYLOMARKERS, a software package primarily designed to **select “well-behaved” phylogenetic markers to estimate a maximum likelihood (ML) species tree** from the supermatrix of concatenated, top-scoring alignments.

These are identified through a series of sequential filters that operate on orthologous gene/protein clusters computed by GET\_HOMOLOGUES to exclude:

- alignments with evidence for **recombinant sequences**
- sequences that yield **“outlier gene trees”** in the context of the distributions of topologies and tree-lengths expected under the multispecies coalescent
- poorly resolved gene trees**

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## Introduction

- What do I need to run GET\_PHYLOMARKERS?

### 1. To estimate a core-genome species tree

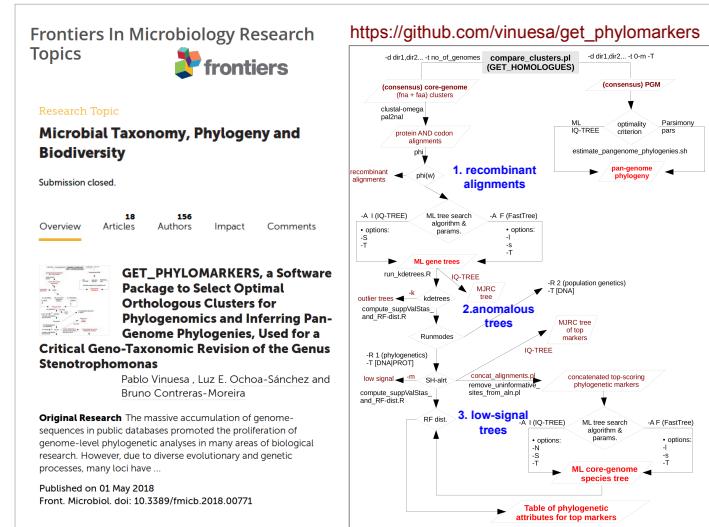
Assuming that you have GET\_PHYLOMARKERS installed, in order to it requires the clusters of orthologous clusters computed by GET\_HOMOLOGUES, that is:

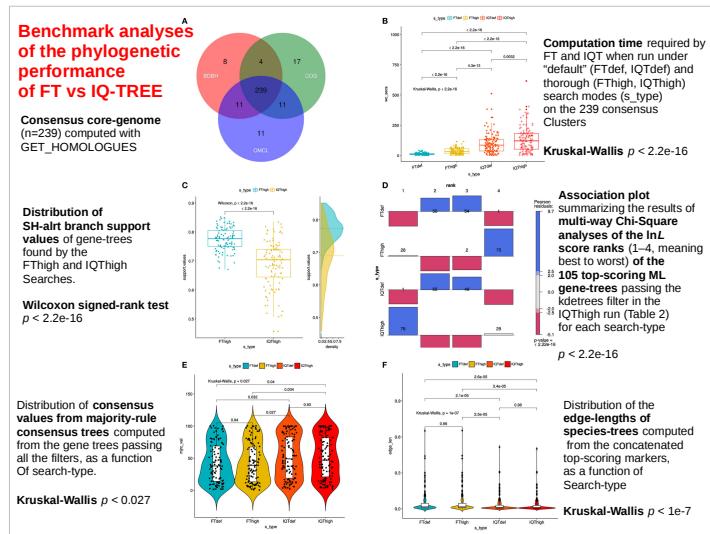
- clusters of homologues at the protein level (\*.faa files)
- the corresponding clusters at the DNA level (\*.fna files)
- call the main script `run_get_phylomarkers_pipeline.sh`

### 2. To estimate a pan-genome phylogeny

GET\_PHYLOMARKERS can also work on the pan-genome matrix computed by the `compare_clusters.pl` auxiliary script provided with the GET\_HOMOLOGUES suite to estimate maximum-likelihood or parsimony pan-genome trees.

- pan-genome matrix computed by `compare_clusters.pl` with -m
- call the auxiliary script `estimate_pangenome_phylogenies.sh`



**ML species tree**

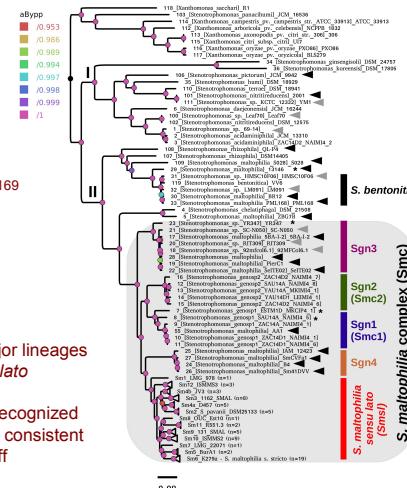
- 118 genomes
- Top 52(231) markers
- GTR+ASC+F+R7

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

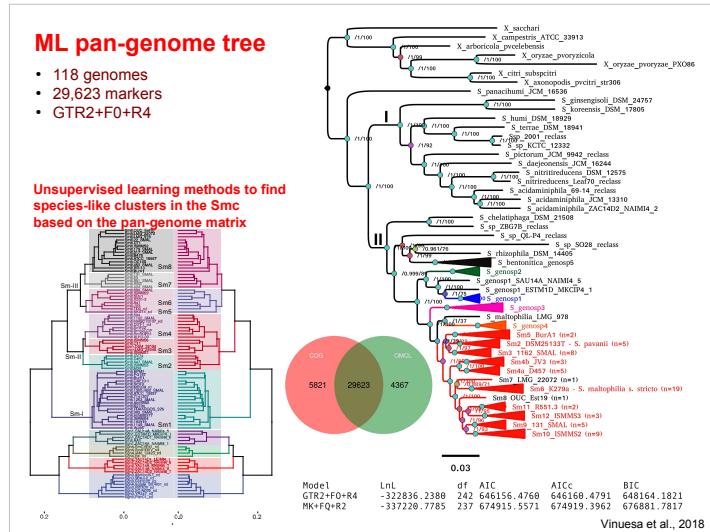
- reclassified 27 RefSeq genome sequences!

- 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



Vinuesa et al., 2018

**Unsupervised learning methods to find groups within the Smc and *S. maltophilia* s. lato lineages based on cgANDb (= 100 - cgANib)**

<img alt="A complex phylogenetic tree showing relationships between 118 genomes. The tree is rooted and shows several distinct lineages. Some lineages are color-coded and labeled with clade names: Sgn1, Sgn2, Sgn3, Sgn4, Sm1, Sm2, Sm3, Sm4, Sm5, Sm6, Sm7, Sm8, Sm9, Sm10, Sm11, Sm12, Sm13, Sm14, Sm15, Sm16, Sm17, Sm18, Sm19, Sm20, Sm21, Sm22, Sm23, Sm24, Sm25, Sm26, Sm27, Sm28, Sm29, Sm30, Sm31, Sm32, Sm33, Sm34, Sm35, Sm36, Sm37, Sm38, Sm39, Sm40, Sm41, Sm42, Sm43, Sm44, Sm45, Sm46, Sm47, Sm48, Sm49, Sm50, Sm51, Sm52, Sm53, Sm54, Sm55, Sm56, Sm57, Sm58, Sm59, Sm60, Sm61, Sm62, Sm63, Sm64, Sm65, Sm66, Sm67, Sm68, Sm69, Sm70, Sm71, Sm72, Sm73, Sm74, Sm75, Sm76, Sm77, Sm78, Sm79, Sm80, Sm81, Sm82, Sm83, Sm84, Sm85, Sm86, Sm87, Sm88, Sm89, Sm90, Sm91, Sm92, Sm93, Sm94, Sm95, Sm96, Sm97, Sm98, Sm99, Sm100, Sm101, Sm102, Sm103, Sm104, Sm105, Sm106, Sm107, Sm108, Sm109, Sm110, Sm111, Sm112, Sm113, Sm114, Sm115, Sm116, Sm117, Sm118, Sm119, Sm120, Sm121, Sm122, Sm123, Sm124, Sm125, Sm126, Sm127, Sm128, Sm129, Sm130, Sm131, Sm132, Sm133, Sm134, Sm135, Sm136, Sm137, Sm138, Sm139, Sm140, Sm141, Sm142, Sm143, Sm144, Sm145, Sm146, 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