

## Introducción a la filogenómica microbiana – GET\_PHYLOMARKERS

Frontiers in Microbiology Research Topics

**Microbial Taxonomy, Phylogeny and Biodiversity**

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**GET\_PHYLOMARKERS, a Software Package to Select Optimal Orthologous Clusters for Phylogenomics and Inferring Pan-Genome Phylogenies, Used for a Critical Geno-Taxonomic Revision of the Genus Stenotrophomonas**

Pablo Vinuesa, Luz E. Ochoa-Sánchez and Bruno Contreras-Moreira

**Original Research** The massive accumulation of genome-sequences in public databases promoted the proliferation of genome-level phylogenetic analyses in many areas of biological research. However, due to diverse evolutionary and genetic processes, many loci have ...

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[https://github.com/vinuesa/get\\_phylomark](https://github.com/vinuesa/get_phylomark)

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**get\_phylomarkers**

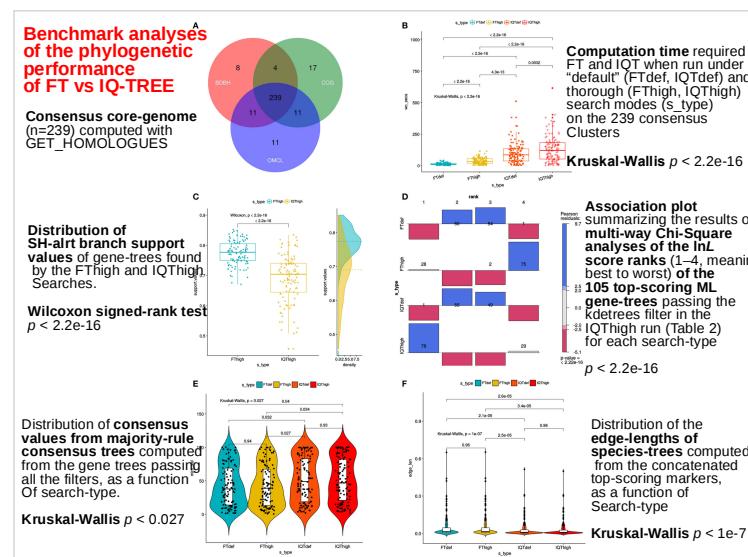
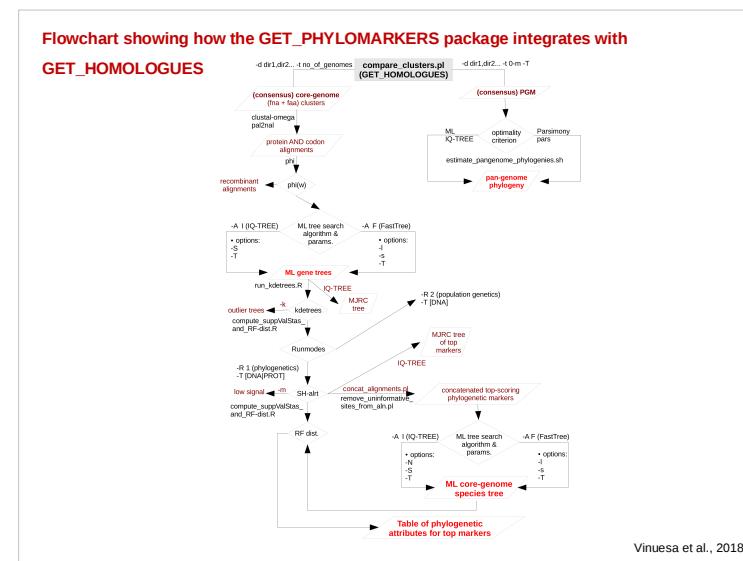
A Expert is to select optimal markers for microbial phylogenomics, population genetics and genomic taxonomy

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**Figure A**: Phylogenetic tree of Stenotrophomonas spp. based on pan-genome phylogenies. The tree is rooted at the bottom and shows relationships between various species and strains. Nodes are color-coded by species: S. maltophilia (red), S. bentonitica (green), S. marincola complex (blue), S. cibaria (yellow), and S. xylophilus (purple). Bootstrap support values are indicated at the nodes. The tree is rooted at the bottom.

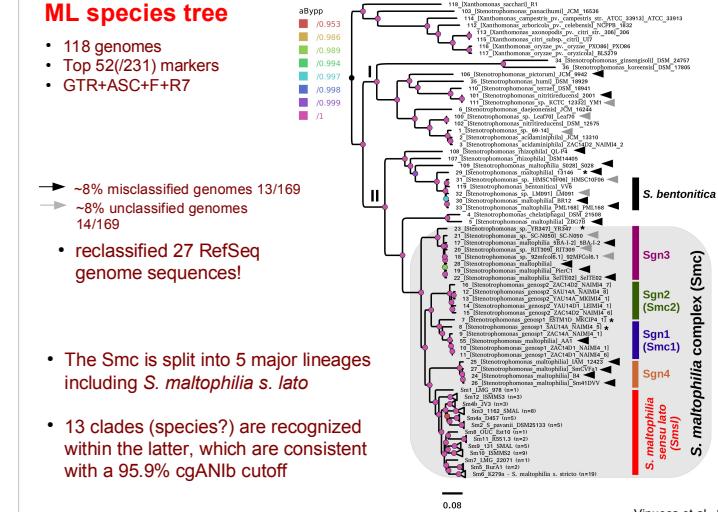
**Figure B**: Another phylogenetic tree showing similar relationships but with different node colors and bootstrap support values.

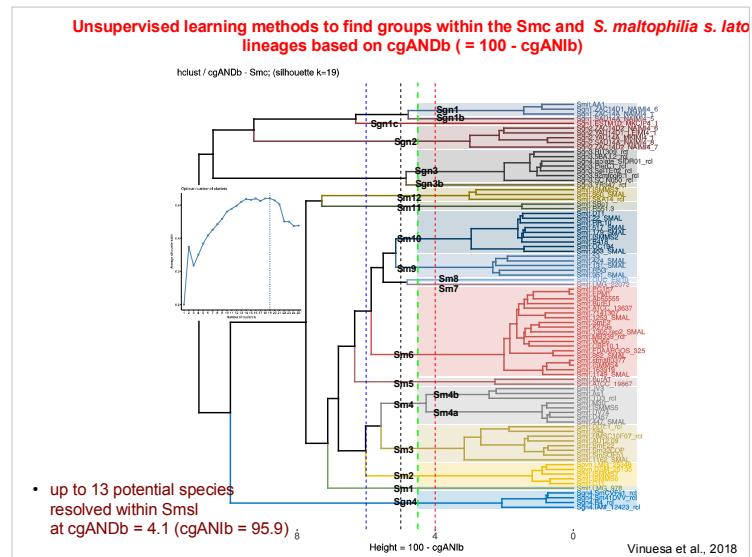
## Introducción a la filoinformática – pan-genómica y filogenómica. IBBM-CONYCET, UNLP Argentina. Julio 2018



### ML species tree

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





### ML pan-genome tree

- 118 genomes
- 29,623 markers
- GTR2+F0+R4

### Unsupervised learning methods to find species-like clusters in the Smc based on the pan-genome matrix

