

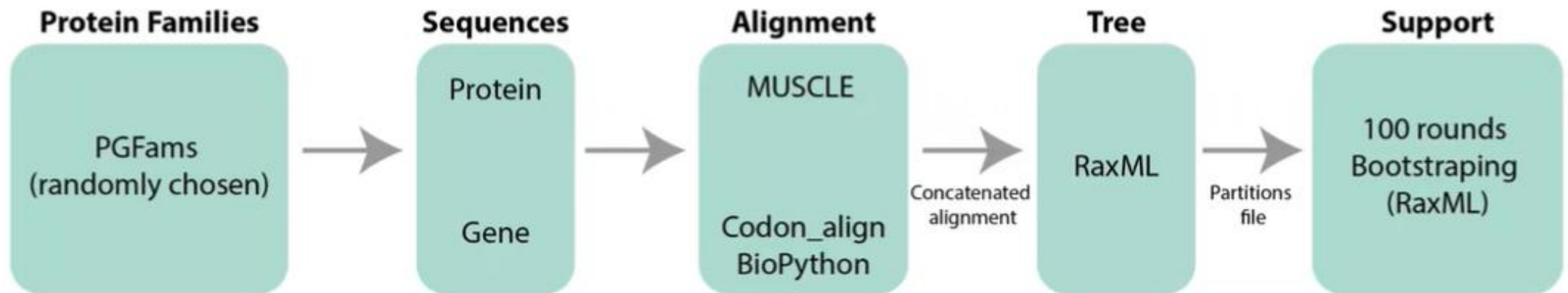
Building Phylogenetic Trees

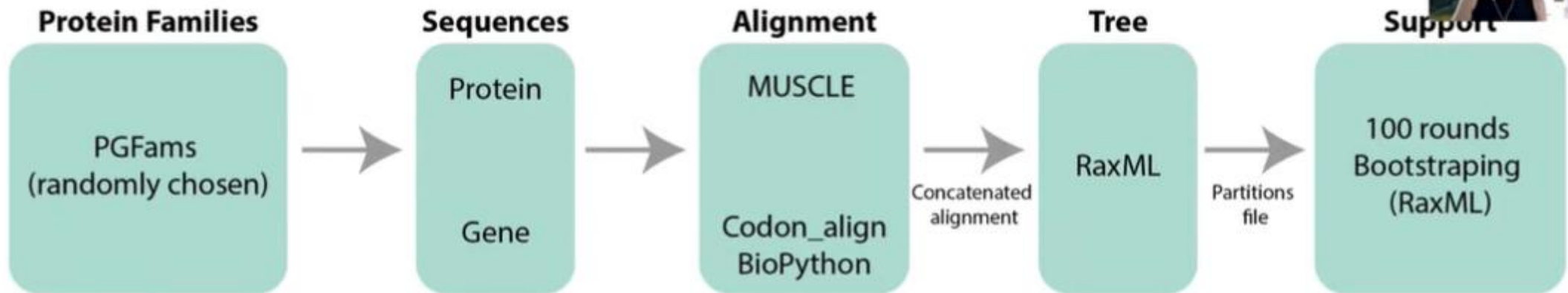
Codon Tree pipeline in PATRIC

Summary

- Time – Canu
- Coverage - Unicycler
- Contigs
 - Unicycler for total number
 - Canu for largest size of contigs
- Total length – Canu
- Annotation Fine Consistency – Canu
 - Pilon iterations influences this
- Annotation Contamination
 - Racon iterations influences this
- Protein encoding genes with functional assignment - Canu

Codon trees pipeline





[Front Microbiol.](#) 2016; 7: 118.
Published online 2016 Feb 8. doi:

PATtyFams: Protein F
Database

[James J. Davis](#),^{1,2,*} [Svetlana Ge](#)
[Veronika Vonstein](#),^{2,3} [Alice R. W](#)

MUSCLE: multi
accuracy and

[Robert C. Edgar](#) ✉

Nucleic Acids Research
<https://doi.org/10.1093/nar/nkt001>

Published: 01 March

RAXML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies 🐼

[Alexandros Stamatakis](#) [Author Notes](#)

Bioinformatics, Volume 30, Issue 9, 1 May 2014, Pages 1312–1313,
<https://doi.org/10.1093/bioinformatics/btu033>

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Computational
Molecular Biology

Submitting tree job

Input Genomes

Add at least 4 (up to 100) genomes.

SELECT GENOME

 e.g. *Mycobacterium tuberculosis* H37Rv

+ Add

AND/OR SELECT GENOME GROUP

 Optional

+ Add

SELECTED INPUT GENOME TABLE

Parameters

OUTPUT FOLDER





OUTPUT NAME

Output Name

NUMBER OF GENES:

100

MAX ALLOWED DELETIONS (0-10):

0

MAX ALLOWED DUPLICATIONS (0-10):

0

Reset

Submit