

Infering microbial growth in communities—Opportunities for model-data synthesis with genomics and metagenomics

JL Weissman, Liang Xu, Emily J. Zakem, Jesse McNichol, Yubin Raut, Shengwei Hou, Elisa R. Halewood, Craig A. Carlson, Stephanie Dutkiewicz, Jed A. Fuhrman, Naomi M. Levine



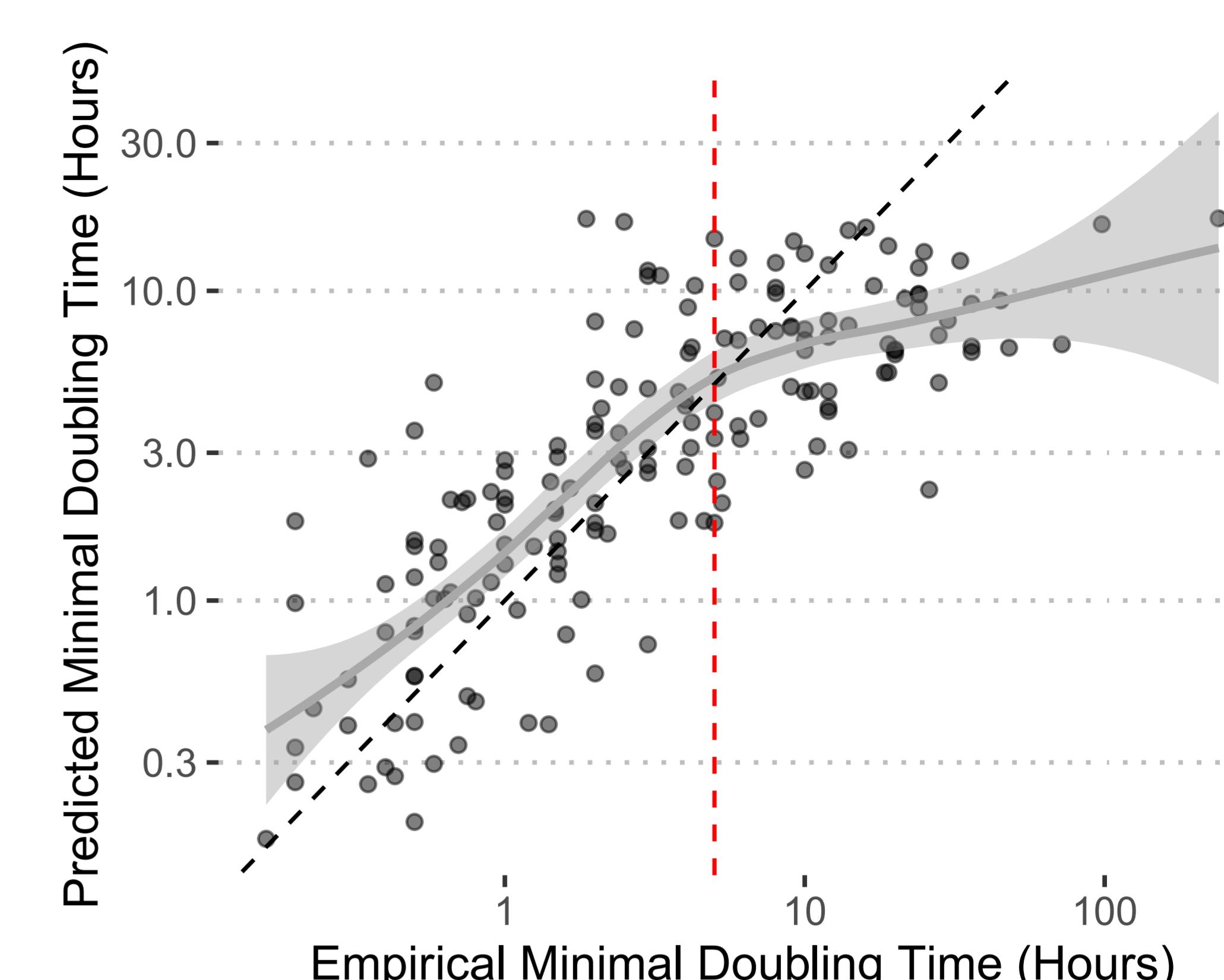
Motivation

- Despite the wide perception that microbes have rapid growth rates, many environments like seawater and soil are often dominated by microorganisms that can only grow very slowly.
- Our knowledge about growth is necessarily biased towards easily culturable organisms, which turn out to be those that tend to grow fast, because microbial growth rates have traditionally been measured using lab growth experiments.
- But how are potential growth rates distributed in nature? We develop a genomic predictor of maximal growth rate to find out.

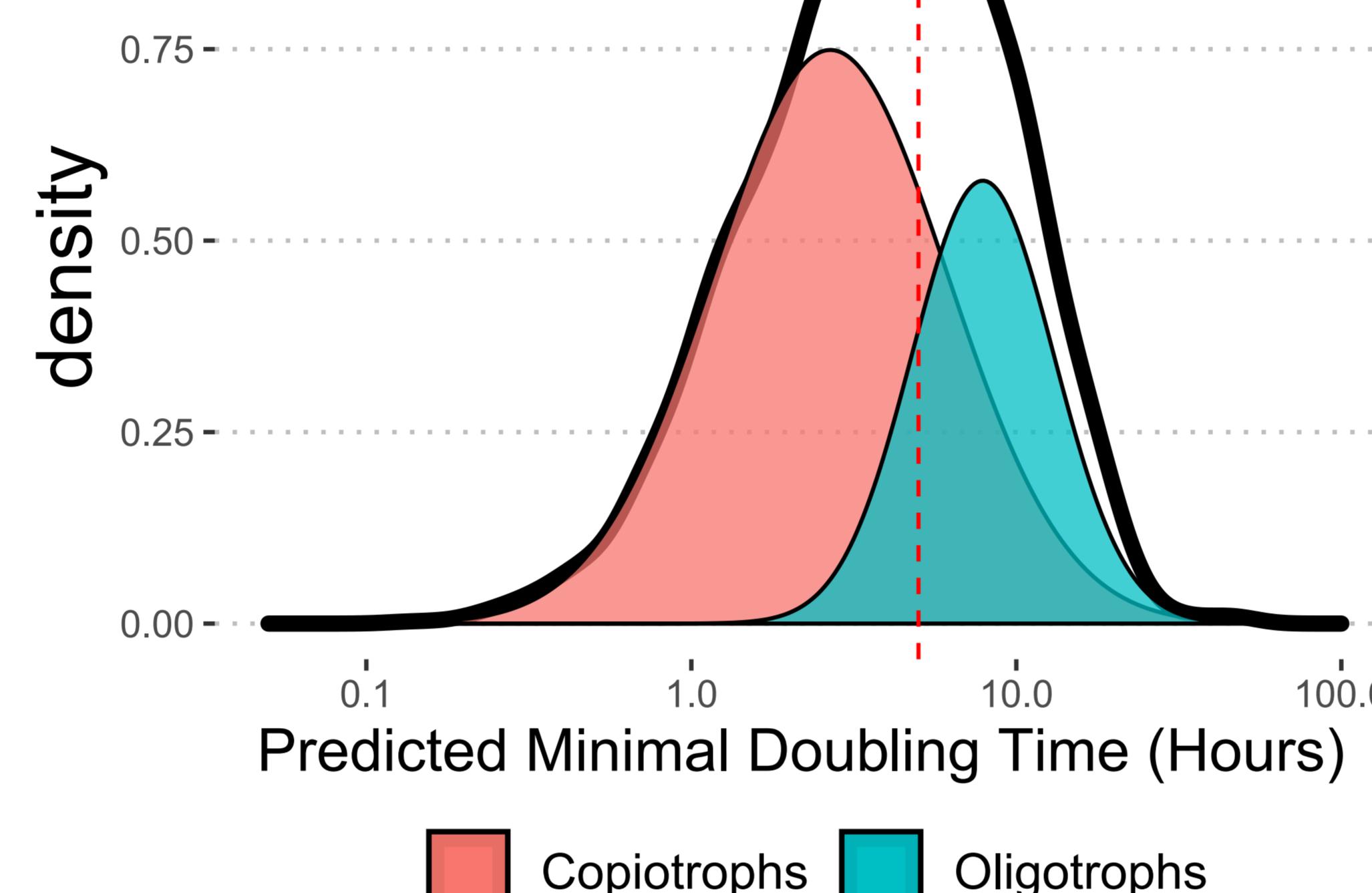
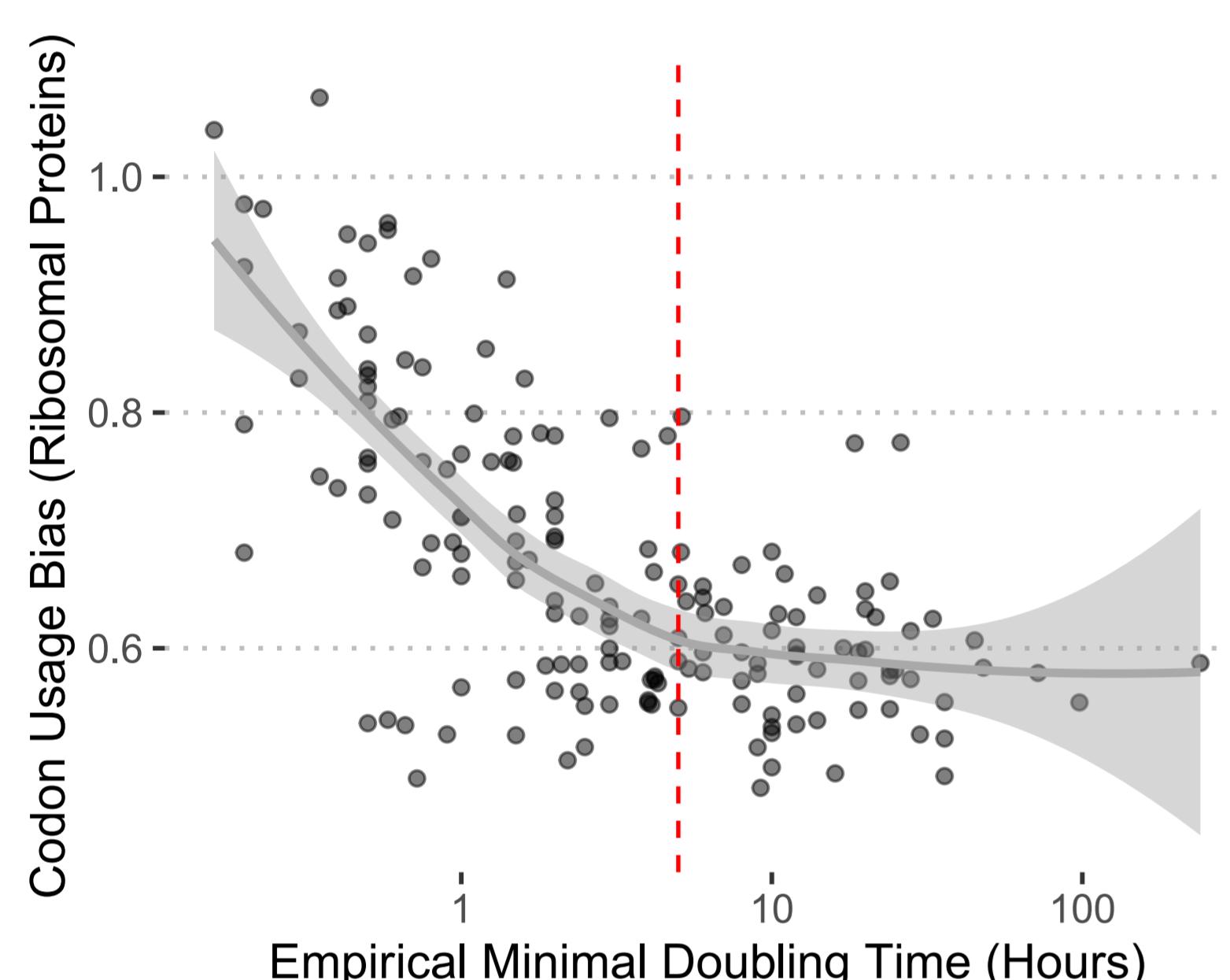
Codon Usage

Highly expressed genes demonstrate a biased usage of alternative codons, optimized to cellular t-RNA pools. In fast-growing organisms the degree of codon optimization is higher than in slow growing organisms, and this pattern can be used to predict maximum growth rate [1].

We assessed additional dimensions of codon usage to improve our predictive performance, implemented our predictor an **easy-to-use R package (gRodon)**, and built a **database of over 200,000 predicted maximal growth rates**



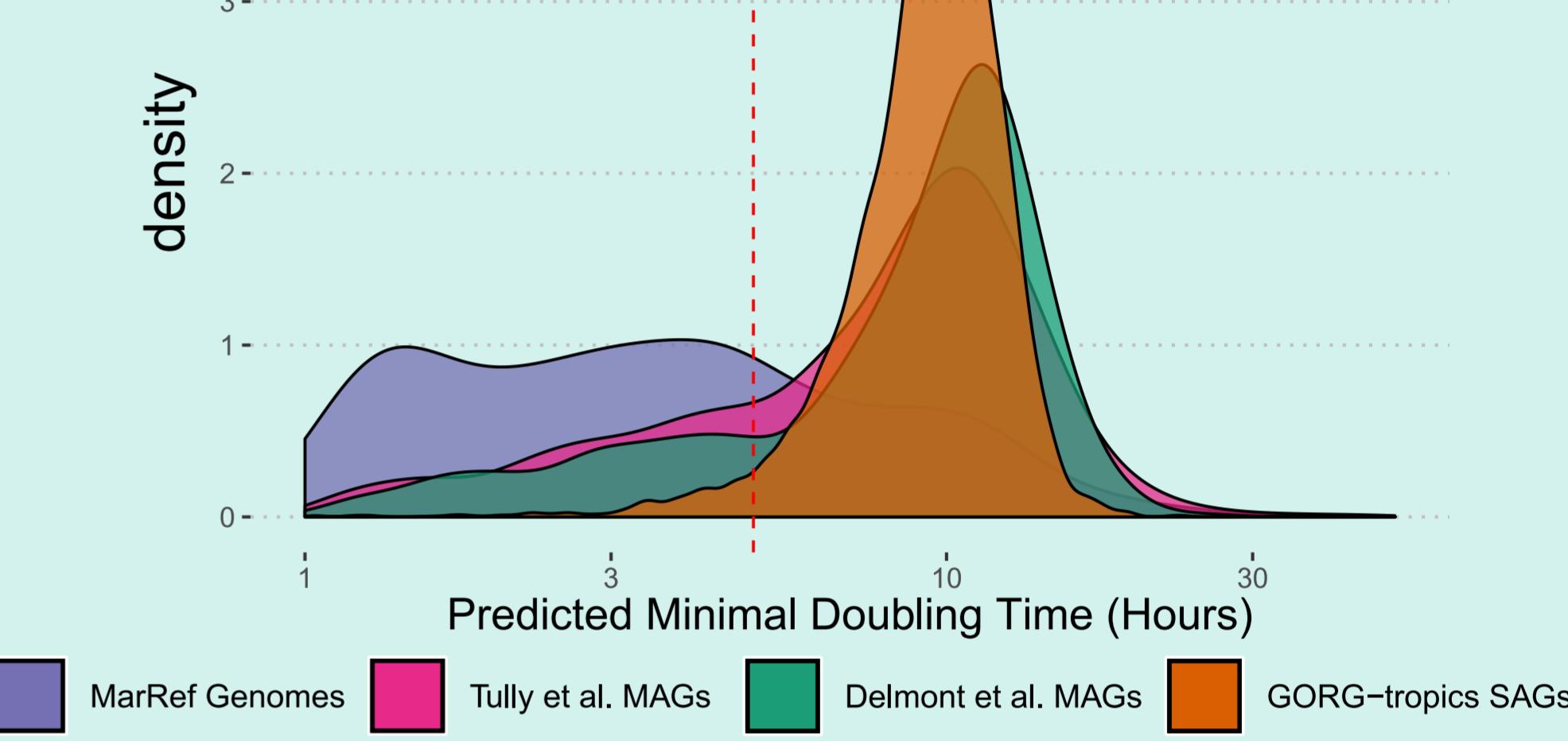
For Slow-Growers, Drift Overwhelms Selection (a natural divide between copiotrophs and oligotrophs)



Check out the papers and R package!

<https://doi.org/10.1073/pnas.2016810118>
<https://doi.org/10.1101/2020.07.25.221176>
<https://doi.org/10.1101/2022.04.12.488109>
<https://github.com/jlw-ecoenv/gRodon2>

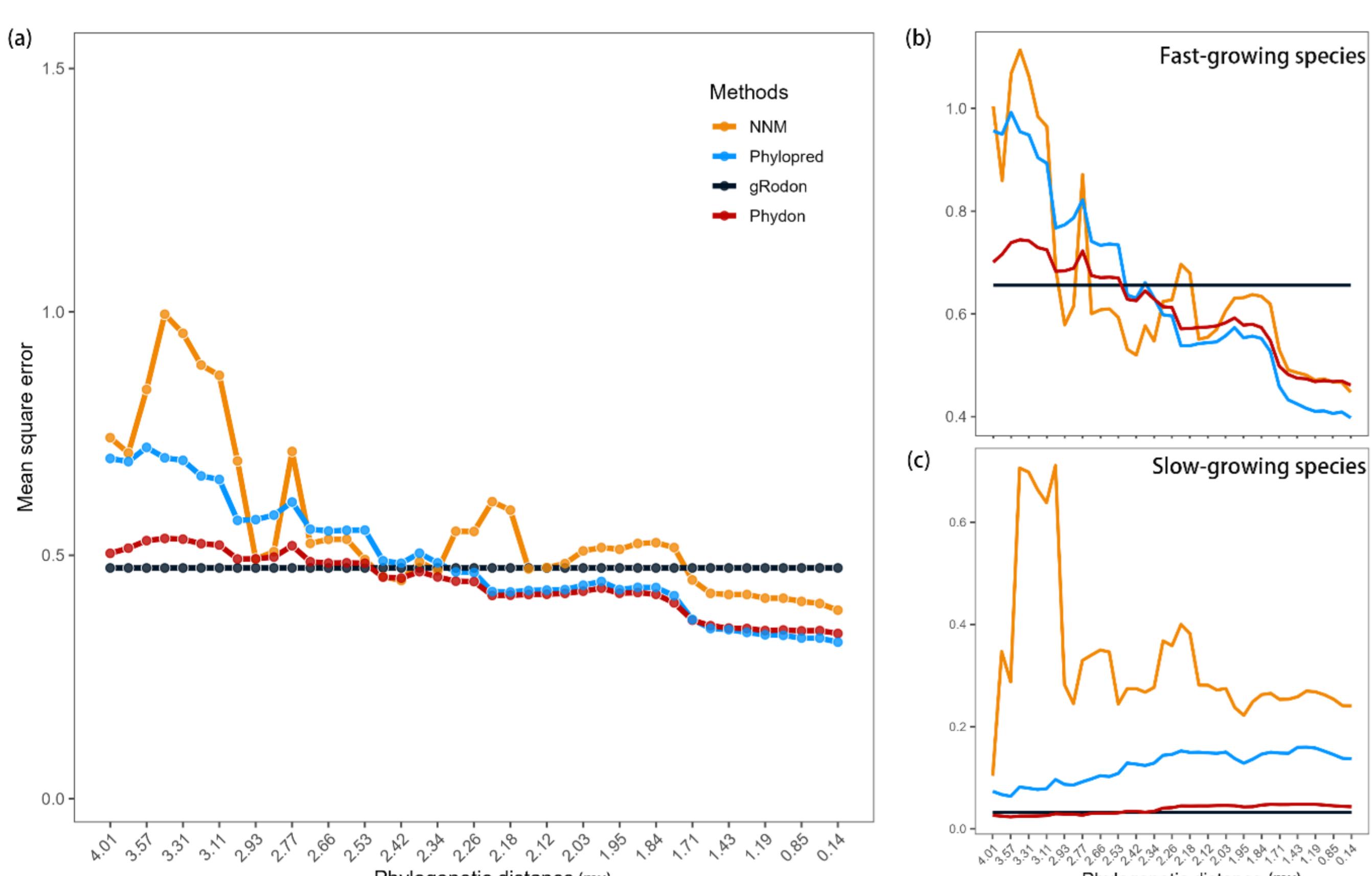
Culture Collections Are Biased Towards Fast Growers



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[1] Vieira-Silva, Sara, and Eduardo PC Rocha. "The systemic imprint of growth and its uses in ecological (meta) genomics." *PLoS Genet* 6.1 (2010): e1000808.

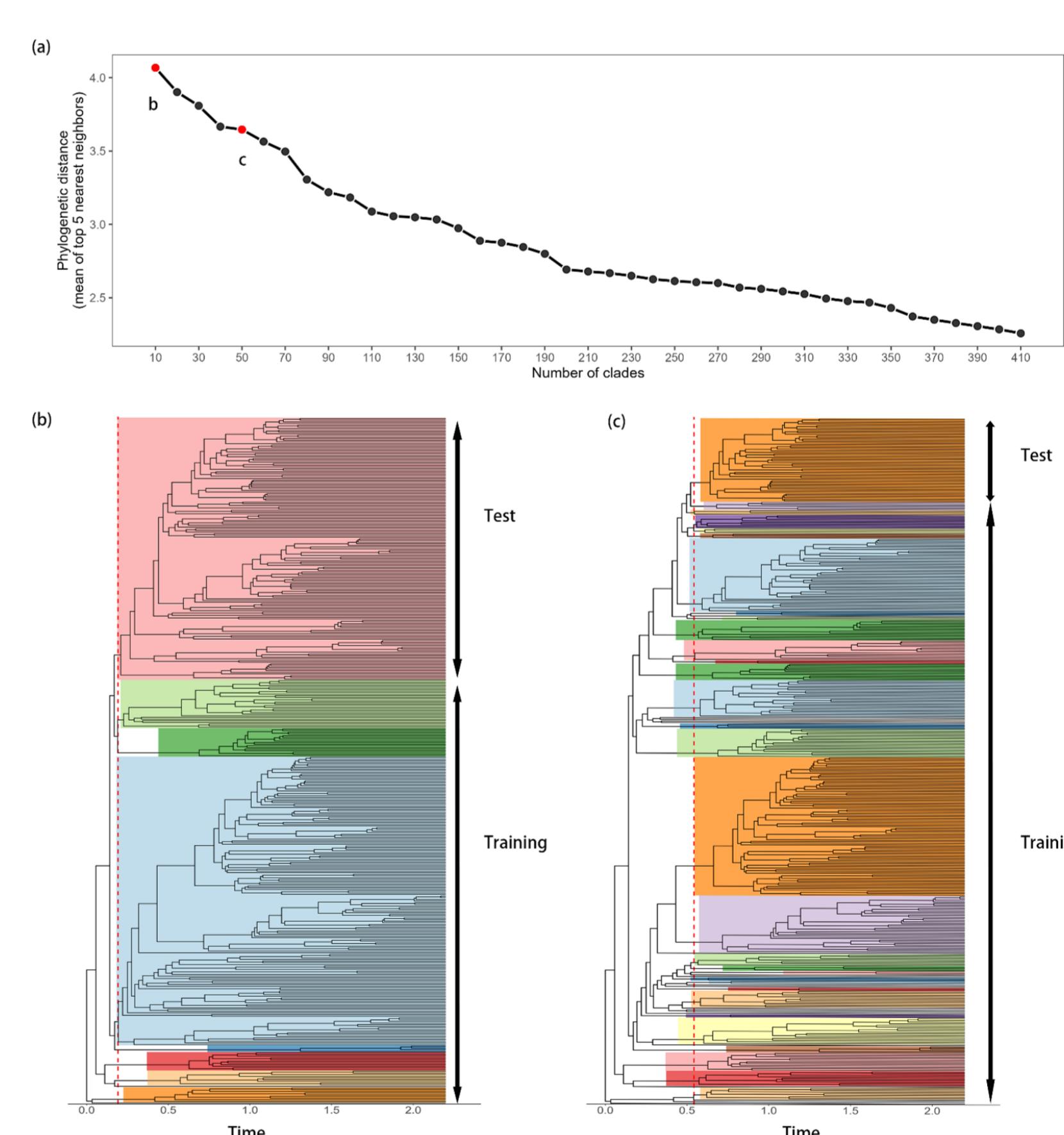
New: Improved Maximum Growth Rate Prediction by Integrating Phylogenetic Information



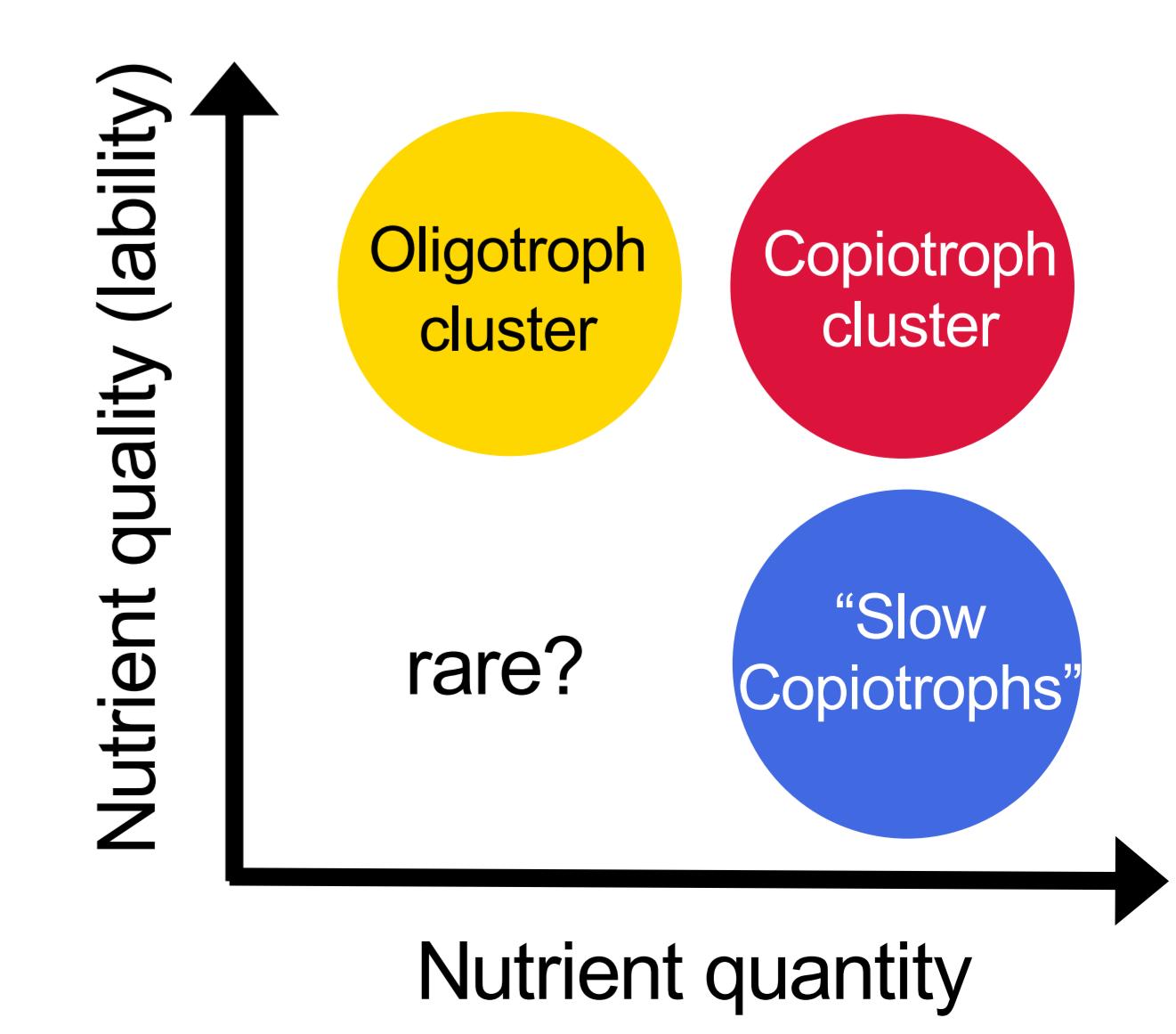
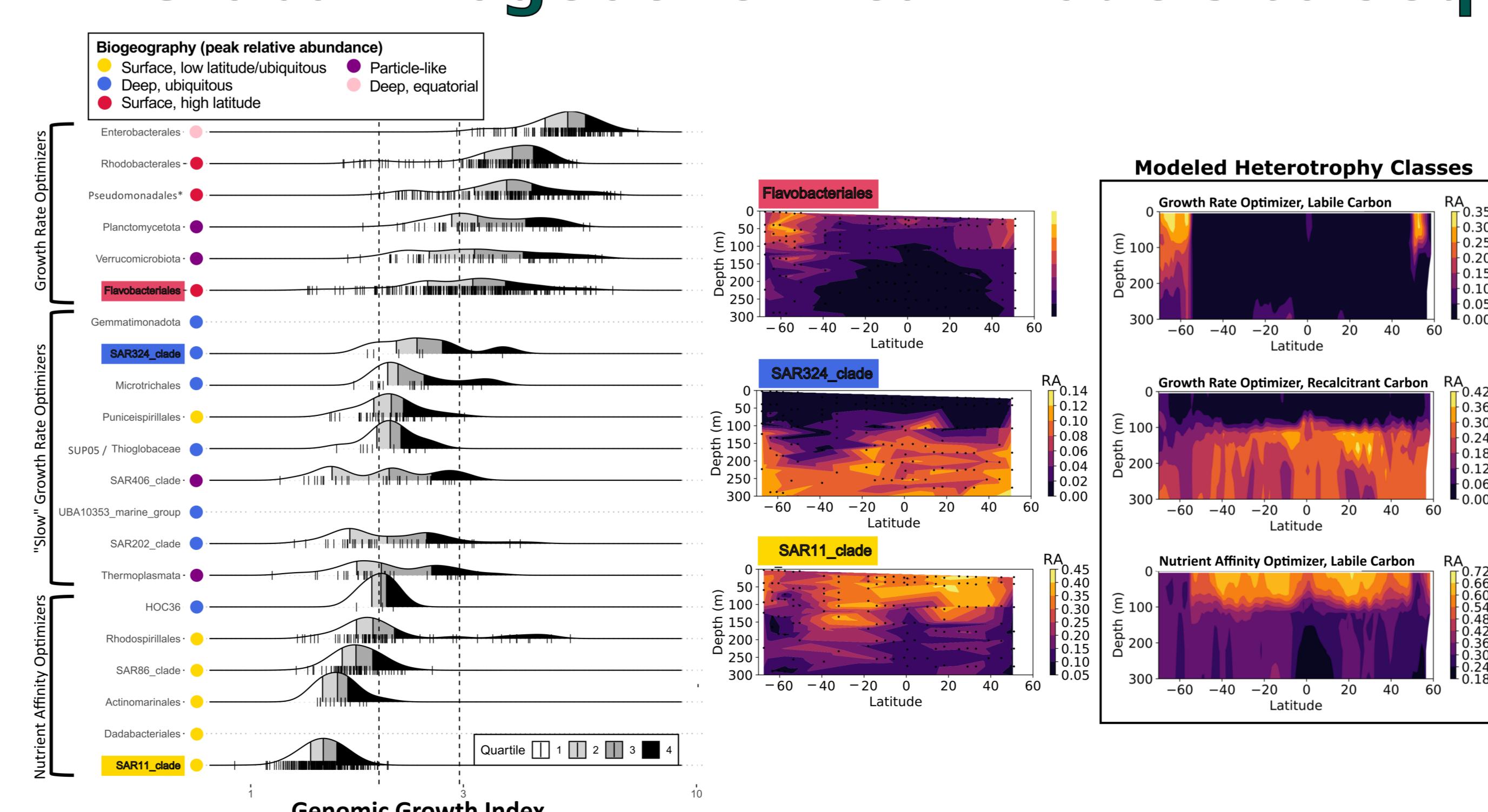
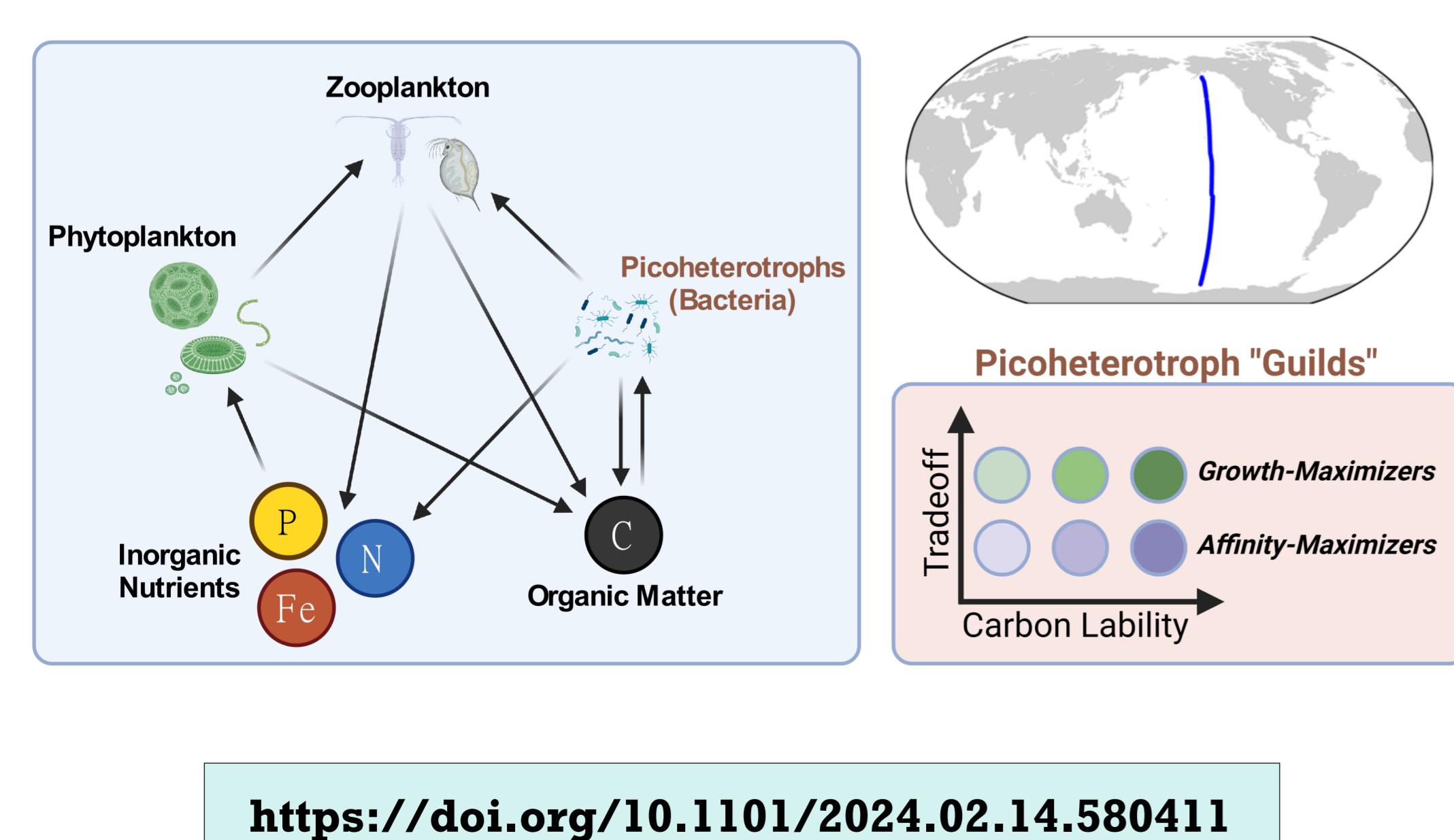
Phydon

Genomic features like codon usage statistics provide useful signals for predicting growth rates for as-yet uncultivated organisms, though current predictors often show high variance. To improve accuracy, we integrate phylogenetic signals, leveraging the evolutionary relationships among species to refine trait predictions.

<https://doi.org/10.1101/2024.10.03.616540>
<https://github.com/xl0418/Phydon>



Next: Using Growth Prediction to Link Global Biogeochemical Models to Sequencing Data



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