Predicting maximum growth rates from genomes and metagenomes for prokaryotes and eukaryotes

JL Weissman, Edward-Robert O. Dimbo, Arianna I. Krinos, Christopher Neely, Yuniba Yagües, Delaney Nolin, Shengwei Hou, Sarah Laperriere, David A. Caron, Benjamin Tully, Harriet Alexander, Marie Peras, Tyler Barnum, Jed A. Fuhrman

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.
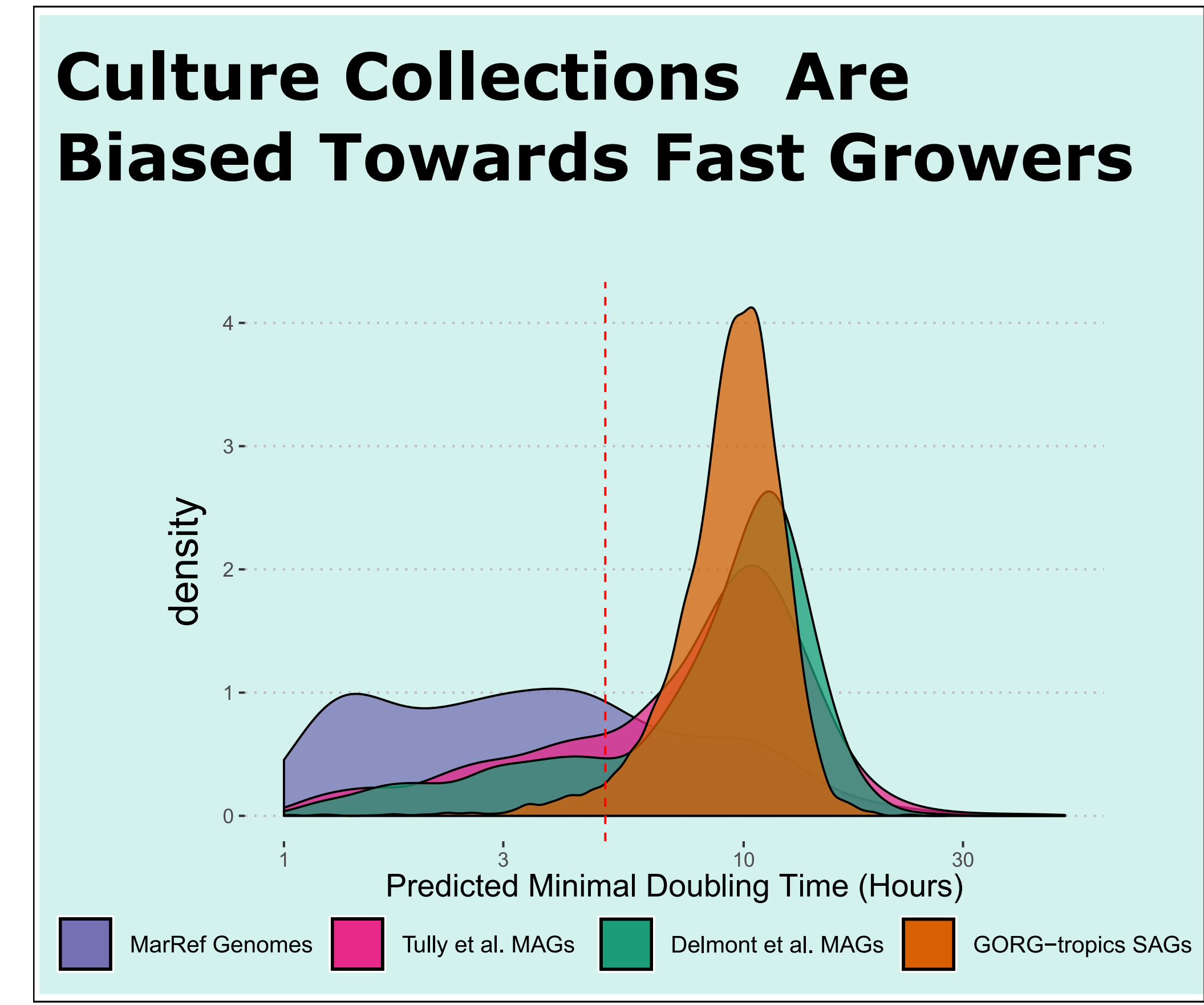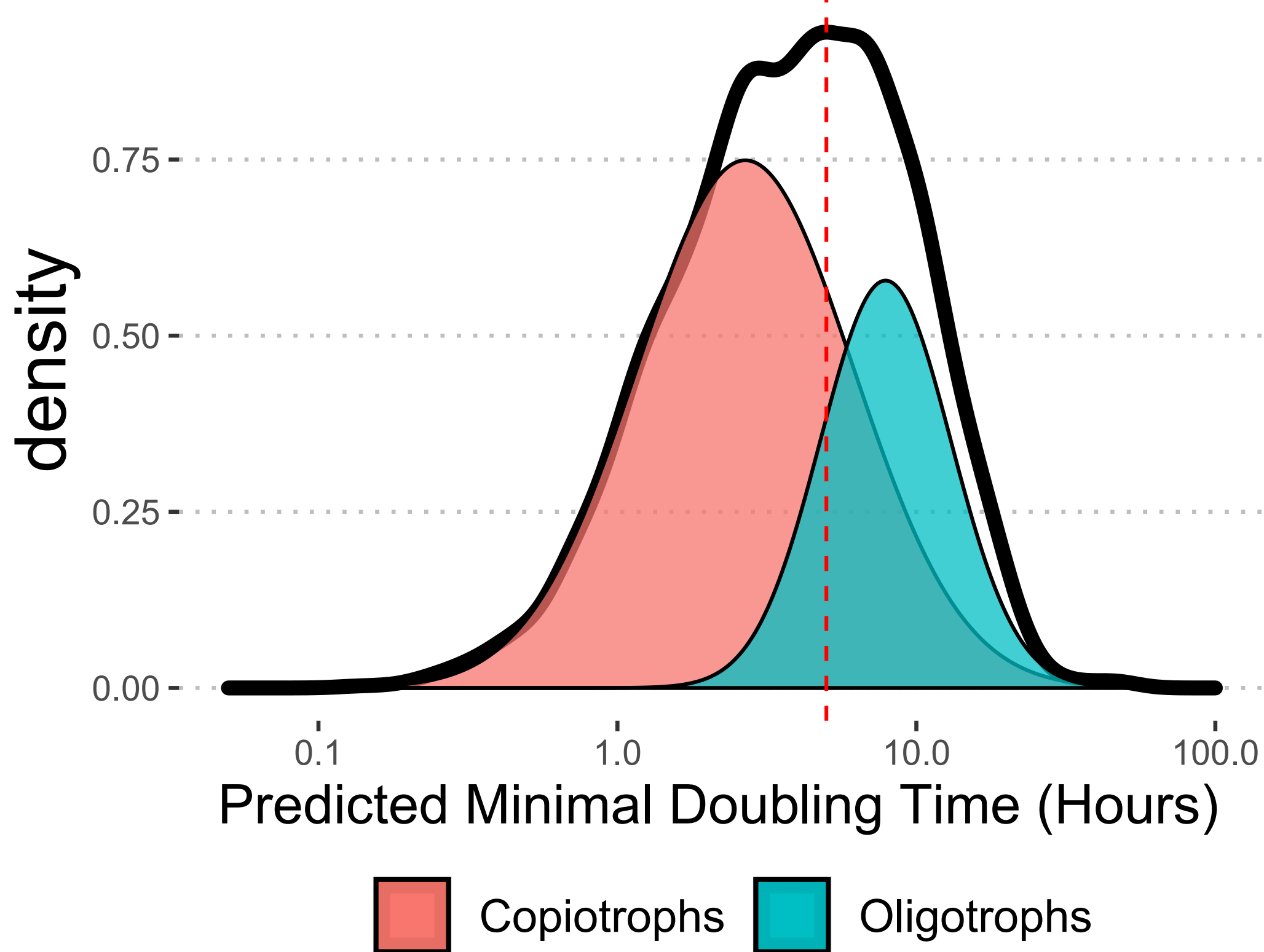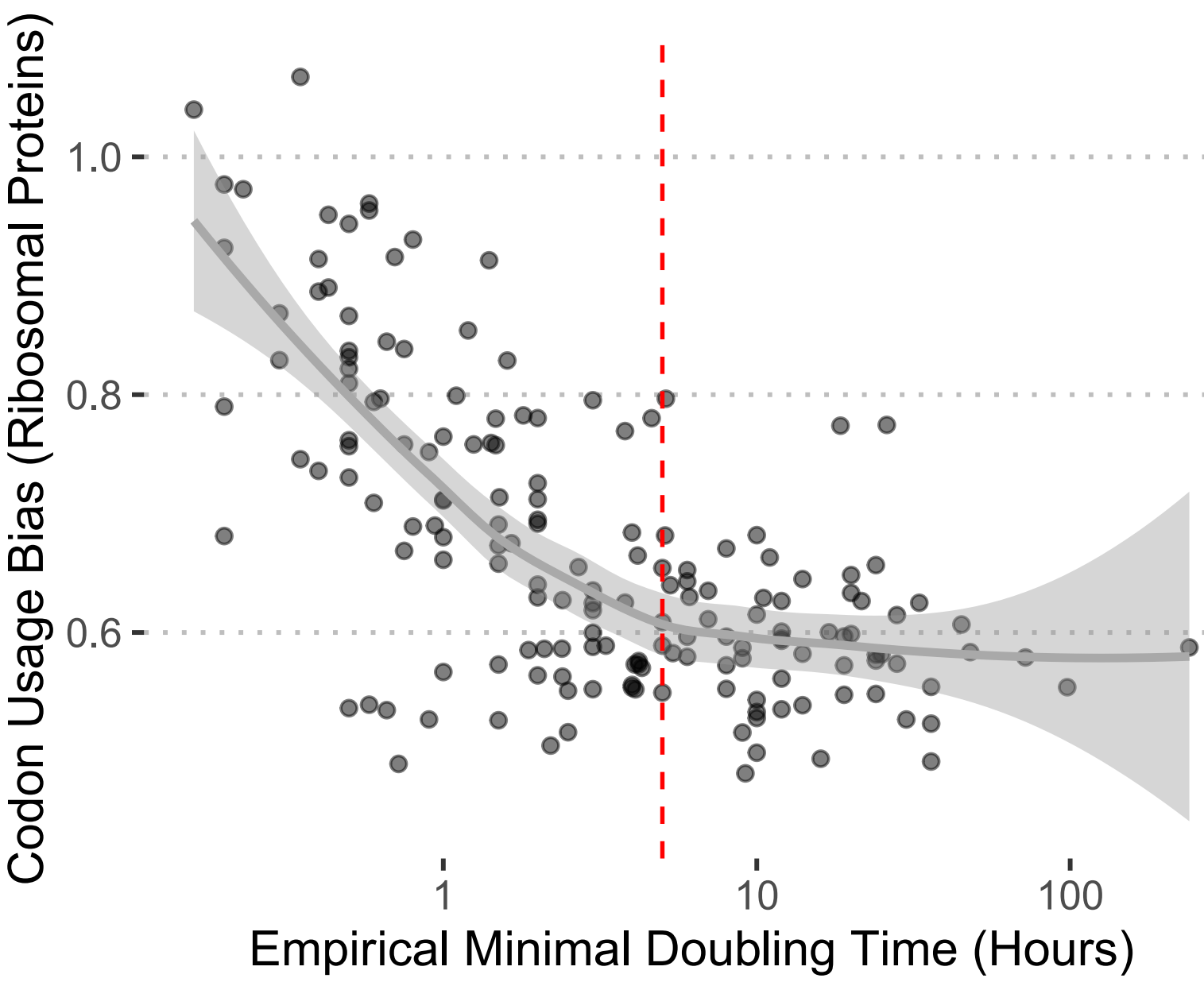
Codon Usage

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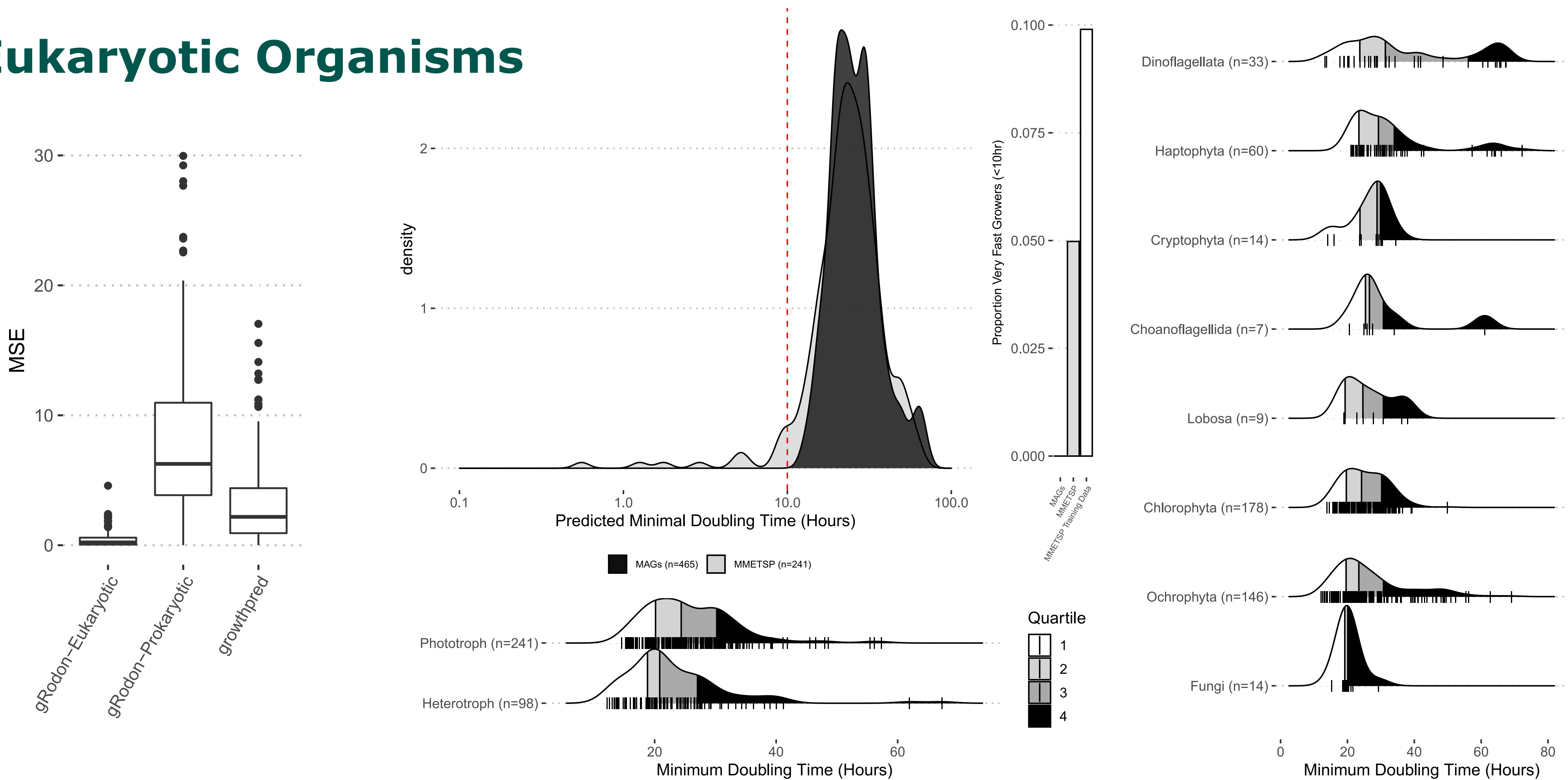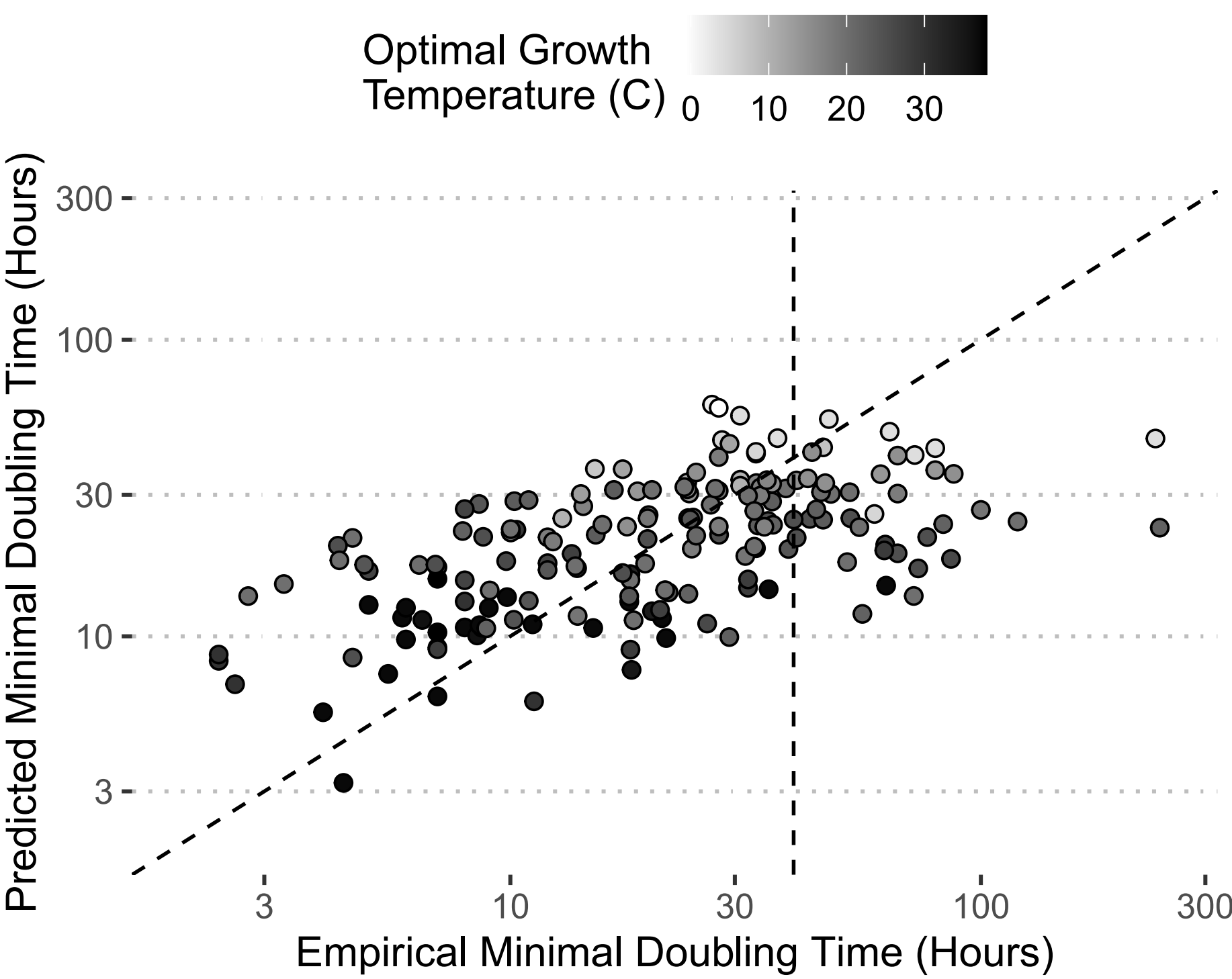
We assessed additional dimensions of codon usage to improve our predictive performance, implemented our predictor an **easy-to-use R package (gRodon)**, and built a **database of over 200,000 predicted maximal growth rates**
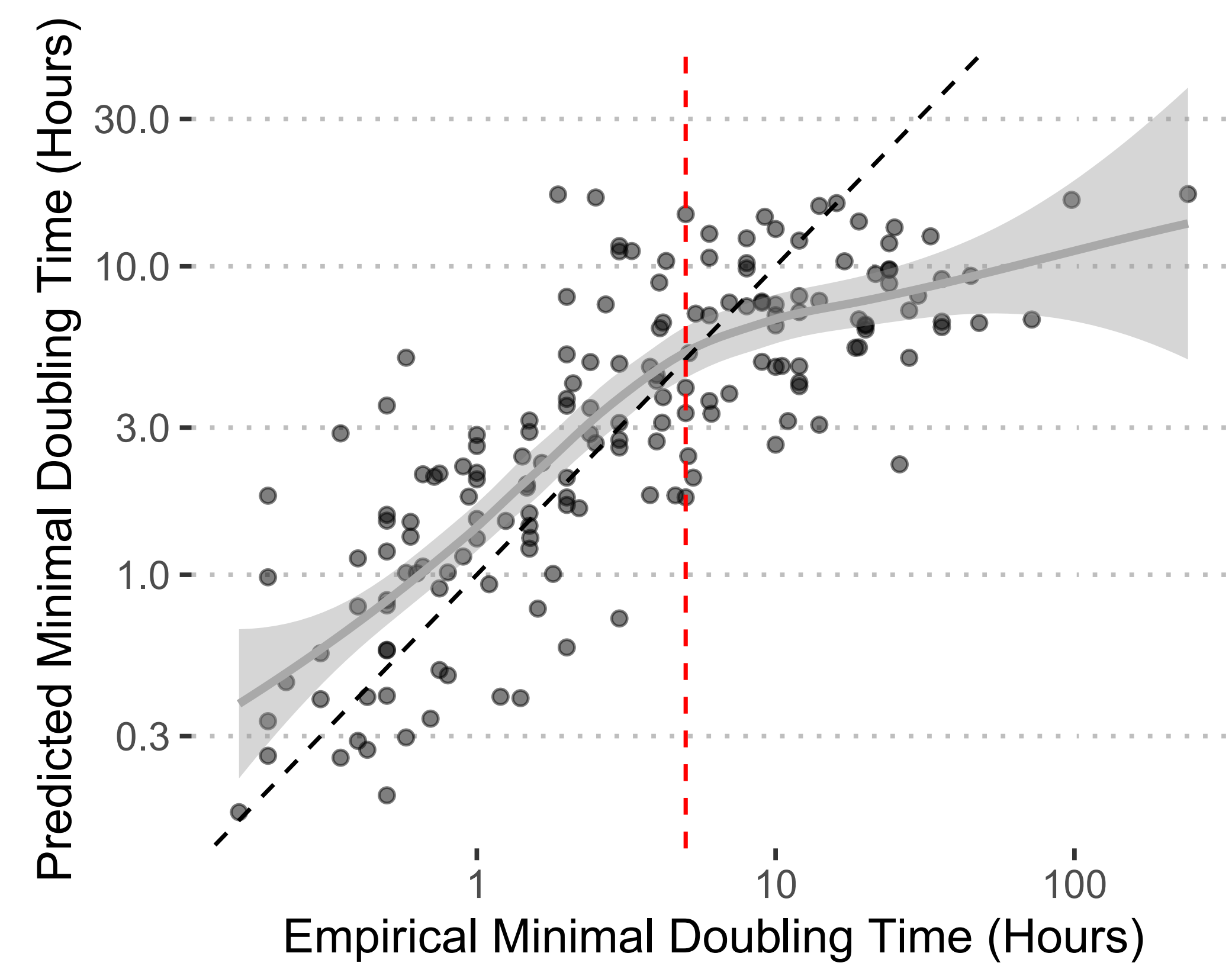

For Slow-Growers, Drift Overwhelms Selection
(a natural divide between copiotrophs and oligotrophs)

Copiotrophs   Oligotrophs

Culture Collections Are Biased Towards Fast Growers

MarRef Genomes   Tully et al. MAGs   Delmont et al. MAGs   GORG-tropics SAGs

Predicting the Growth Rates of Eukaryotic Organisms

Improved Metagenomic Prediction & Benchmarking with MMv2
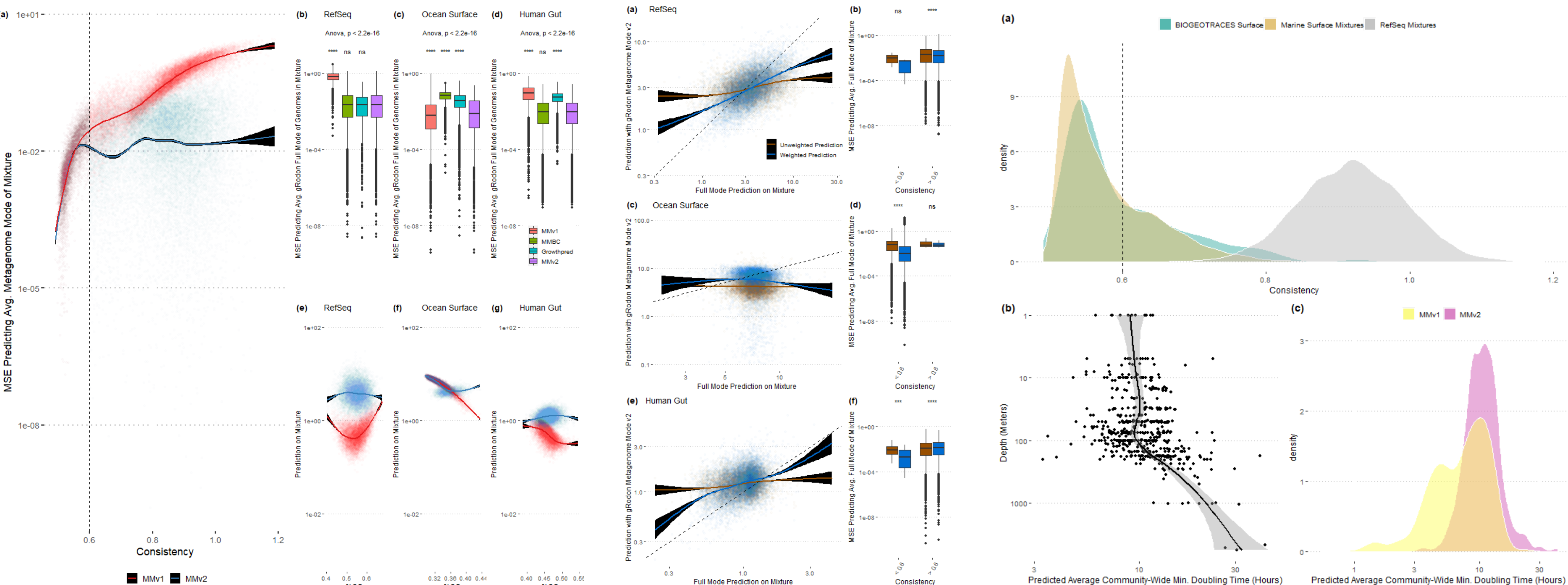
[1] Vieira-Silva, Sara, and Eduardo PC Rocha. "The systemic imprint of growth and its uses in ecological (meta) genomics." PLoS Genet 6.1 (2010): e1000808.

Check out the papers and R package!
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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-ecoevo/gRodon2
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jakeweis@usc.edu - https://jlw-ecoevo.github.io/ - @jlw_ecoevo