Microbial carbon use efficiency predicted from genome-scale metabolic models

The Science

The balance between respiration and biomass production of soil bacteria and fungi plays a large role in the global carbon cycle but the exact rates are not well defined to a high degree of specificity across taxa. Current models for carbon-use efficiency (CUE) of these species are not well parameterized and often weight environment conditions much greater than the physiology of the organisms. This study aims to use genome-scale metabolic models to predict the CUE in greater detail for different organisms.

The Impact

The global carbon balance represents one of the most pressing issues facing society. Greater understanding of microbial CUE not only allows researchers to make better predictions and models about the global carbon cycle, but also provides feedback on the carbon cycle that can be used to analyze microbial consortia for impacts on agriculture or biotechnology.

Summary

The researchers selected existing, manually curated genome-scale metabolic models from the Biochemically, Genetically, and Genomically structured knowledgebase of metabolic reconstructions (BiGG). Additional models were generated from automated pipelines to expand the sample size using KBase. These additional genomes were selected based on their known presence in forest soil bacterial communities.

By building models for 231 selected genomes using the Build Metabolic Model App, followed by gapfilling using the Gapfill Metabolic Model App on complete media, researchers were able to do flux balance analyses and calculate CUE based on carbon uptake and secretion.

The researchers also built phylogenetic trees for the genomes based on clusters of orthologous group families using the FastTree maximum likelihood method.

These relationships were then compared to the calculated CUE in order to determine the taxonomic level that best correlated to CUE values, resulting in Class and Order explaining the greatest variation in CUE.

Overall, CUE ranged from 0.22 to 0.98. Additionally, larger genomes are negatively correlated with CUE but were able to utilize a greater number of carbon sources because they tended to be found in environments with a high diversity of substrates in low concentrations.
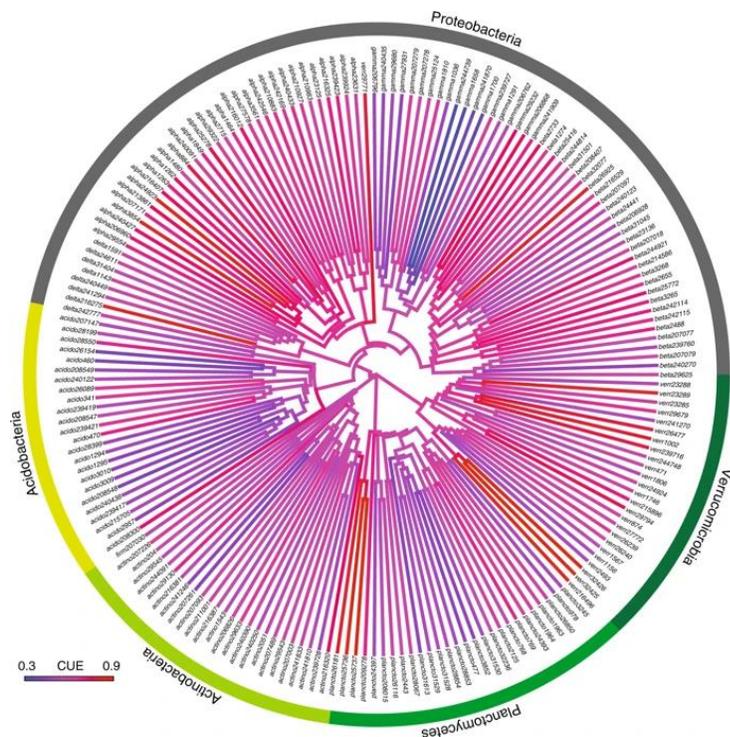
Phylogenetic heatmap of metabolic models of KBase genomes based on CUE.

Read the publication here: https://www.nature.com/articles/s41467-019-11488-z