Goldschmidt 2024 Abstract
https://doi.org/10.46247/gold2024.22558

Investigating carbon cycling microbial communities through Probabilistic Flux Balance Analysis: PrFBA

ANDREW FREIBURGER[1], FILIPE LIU[2], KEITH TYO[1] AND CHRISTOPHER HENRY[2]

[1]Northwestern University
[2]Argonne National Laboratory
Presenting Author: andrewfreiburger@gmail.com

Microorganisms are the most significant biogeochemical agents in most ecosystems, and naturally assemble into communities of metabolically complementary organisms. The Methanogenic Archaeal (ANME) and Sulphate-reducing bacteria (SRB) communities of the ocean floor, and the complex communities of surface wetlands, for example, are the largest sinks for methane and carbon, respectively. Understanding carbon flux to the atmosphere, and resultant consequences on global warming, therefore requires an intimate understanding of these microbial systems that can ultimately translate into engineering or better stewardship of these communities for more desirable climate outcomes. Microbial communities, however, are notoriously difficult to study because many members cannot be cultured and thus sequenced in vitro, which necessitates the use of imprecise and sometimes inaccurate metagenome assembled genomes (MAGs) that approximate member sequences. The problems with MAGs are further compounded by poor biological annotations of the functions of these unique community members.

We therefore developed a combined genomics- and model-based system using the ModelSEED2 reconstruction pipeline which captures MAG uncertainties in a probabilistic metabolic model. The uncertainties can be further mitigated with available multi-omics and experimental data. We apply this probabilistic framework to study the aforementioned ANME+SRB and wetland microbial communities, and discuss biological insights from our studies. Our computational methods are disseminated on GitHub and in the DOE KBase webplatform, which allows both programmers and experimentalists to use our tools for advancing their research.