

Learning microbial community metabolisms from terrabasepairs of DNA sequencing data

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**MICROBIAL COMMUNITIES DRIVE
BIOGEOCHEMICAL CYCLES**



1g mud

~ 1e9 microbes

3e15 DNA bp
(...ACTGGTACTGAA...)

\$1000 = 80e9 DNA bp

100 samples =
8e12 DNA bp for an experiment

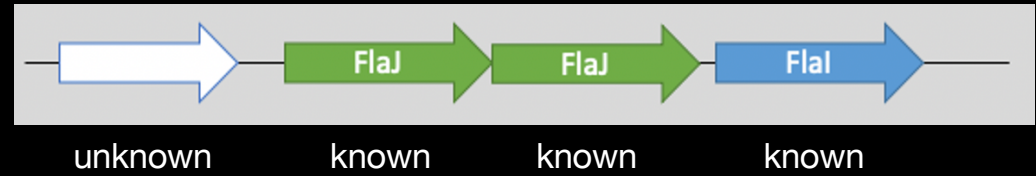
learn patterns from ~ 10e4 experiments

THIS IS STARTING TO LOOK LIKE DATA SCIENCE
(TO A BIOLOGIST)

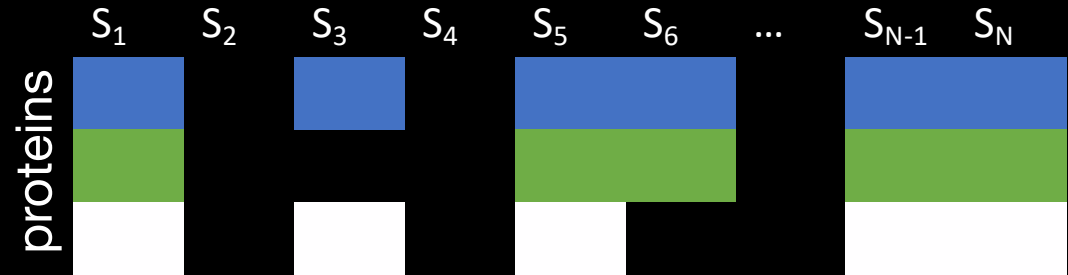
WORKFLOW

1. Sequence genomes directly from the environment
2. Infer proteins from DNA sequence
3. Infer protein function from homology search to known proteins
4. Infer protein function from association methods
5. Build metabolisms for individual microbes
6. Science!

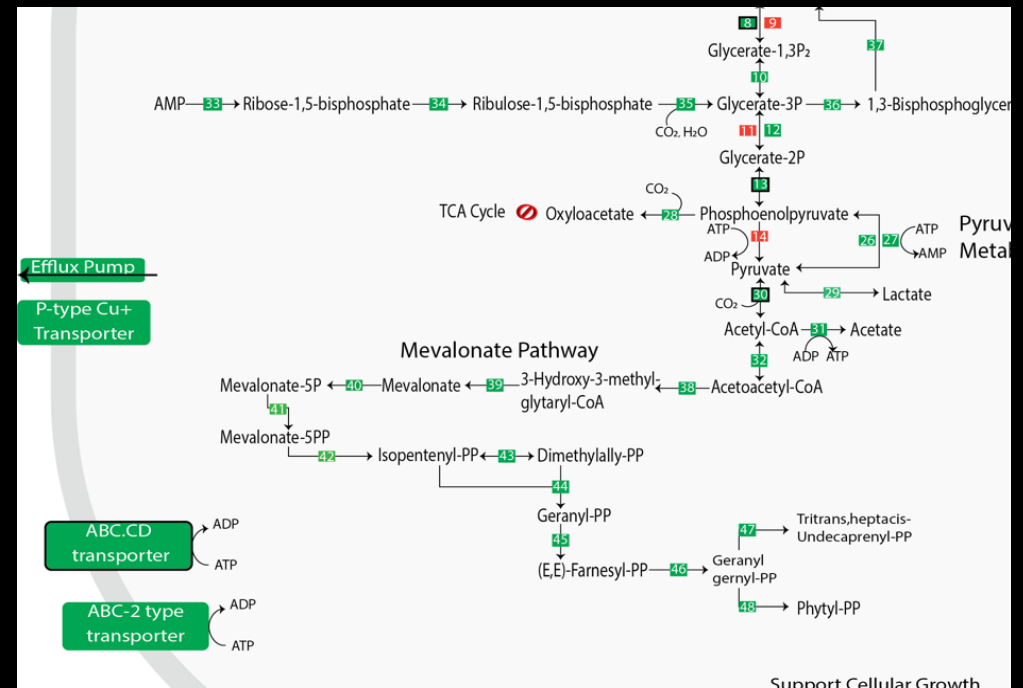
protein-coding genes in genomes



samples or genomes



biochemical pathways



Uncovering the Diversity and Activity of Methylophilic Methanogens in Freshwater Wetland Soils

Adrienne B. Narrowe,^a Mikayla A. Borton,^a David W. Hoyt,^b Garrett J. Smith,^c Rebecca A. Daly,^a Jordan C. Angle,^c Elizabeth K. Eder,^b Allison R. Wong,^b Richard A. Wolfe,^c Alexandra Pappas,^c Gil Bohrer,^d Christopher S. Miller,^e Kelly C. Wrighton^a

GBE Complex Evolutionary History of Translation Elongation Factor 2 and Diphthamide Biosynthesis in Archaea and Parabasalids

Adrienne B. Narrowe^{1,†}, Anja Spang^{2,3,†}, Courtney W. Stairs³, Eva F. Caceres³, Brett J. Baker⁴, Christopher S. Miller^{1,*,†}, and Thijs J.G. Ettema^{3,†}



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Methanogenesis in oxygenated soils is a substantial fraction of wetland methane emissions

Jordan C. Angle¹, Timothy H. Morin^{2,3}, Lindsey M. Solden¹, Adrienne B. Narrowe⁴, Garrett J. Smith¹, Mikayla A. Borton^{1,3}, Camilo Rey-Sanchez^{2,3}, Rebecca A. Daly¹, Golnazalsdat Mirfenderesgi², David W. Hoyt⁵, William J. Riley⁵, Christopher S. Miller⁴, Gil Bohrer^{2,3} & Kelly C. Wrighton^{1,3}