

Stanford



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Bio

BIO

I am a bioinformatician and microbiologist interested in studying the human microbiome and fine-scale microbial population genetics. See my personal website for more info- <https://mrilm.github.io/>

STANFORD ADVISORS

- Justin Sonnenburg, Postdoctoral Faculty Sponsor

LINKS

- Personal website: <https://mrilm.github.io/>

Publications

PUBLICATIONS

- **Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries.** *mSystems*
Olm, M. R., Crits-Christoph, A. n., Diamond, S. n., Lavy, A. n., Matheus Carnevali, P. B., Banfield, J. F.
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- **Necrotizing enterocolitis is preceded by increased gut bacterial replication, Klebsiella, and fimbriae-encoding bacteria** *SCIENCE ADVANCES*
Olm, M. R., Bhattacharya, N., Crits-Christoph, A., Firek, B. A., Baker, R., Song, Y. S., Morowitz, M. J., Banfield, J. F.
2019; 5 (12): eaax5727
- **Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms** *MICROBIOME*
Olm, M. R., West, P. T., Brooks, B., Firek, B. A., Baker, R., Morowitz, M. J., Banfield, J. F.
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- **dRep: a tool for fast and accurate genomic comparisons that enables improved genome recovery from metagenomes through de-replication** *ISME JOURNAL*
Olm, M. R., Brown, C. T., Brooks, B., Banfield, J. F.
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- **Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates** *GENOME RESEARCH*
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- **The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis** *MBIO*
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2020

- **Clades of huge phages from across Earth's ecosystems.** *Nature*

Al-Shayeb, B., Sachdeva, R., Chen, L., Ward, F., Munk, P., Devoto, A., Castelle, C. J., Olm, M. R., Bouma-Gregson, K., Amano, Y., He, C., Meheust, R., Brooks, et al
2020

- **Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut.** *PloS one*

Sher, Y., Olm, M. R., Raveh-Sadka, T., Brown, C. T., Sher, R., Firek, B., Baker, R., Morowitz, M. J., Banfield, J. F.

2020; 15 (3): e0229537

- **Impacts of microbial assemblage and environmental conditions on the distribution of anatoxin-a producing cyanobacteria within a river network** *ISME JOURNAL*

Bouma-Gregson, K., Olm, M. R., Probst, A. J., Anantharaman, K., Power, M. E., Banfield, J. F.

2019; 13 (6): 1618–34

- **Megaphages infect Prevotella and variants are widespread in gut microbiomes** *NATURE MICROBIOLOGY*

Devoto, A. E., Santini, J. M., Olm, M. R., Anantharaman, K., Munk, P., Tung, J., Archie, E. A., Turnbaugh, P., Seed, K. D., Blekhman, R., Aarestrup, F. M., Thomas, B. C., Banfield, et al
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- **Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome.** *mSystems*

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