

Matthew R. Olm, PhD

Department of Microbiology and Immunology

Stanford University

<https://mrolm.github.io> | mattolm@gmail.com | (480) 213 – 6684

EDUCATION:

- 2014 – 2019 **The University of California, Berkeley:** Berkeley, CA
Ph.D. in Microbiology (May 2019)
Thesis: Strain-resolved metagenomic analysis of the premature infant microbiome and other natural microbial communities
Advisor: Jillian F. Banfield
- 2010 – 2014 **The University of Pittsburgh:** Pittsburgh, PA
B.Sc. in Microbiology; Minor in Computer Science
Department of Biological Sciences

RESEARCH EXPERIENCE:

- 2020–present **Stanford University:** Stanford, CA
Postdoctoral fellow, Department of Microbiology and Immunology
Advisor: Justin Sonnenburg
- 2019–2020 **The University of California, Berkeley:** Berkeley, CA
Interim postdoctoral scholar, Earth and Planetary Science Department
Advisor: Jillian F. Banfield
- 2014–2019 **The University of California, Berkeley:** Berkeley, CA
Graduate student, Department of Plant and Microbial Biology
Advisor: Jillian F. Banfield
- 2011–2014 **The University of Pittsburgh:** Pittsburgh, PA
Undergraduate researcher, Department of Biological Sciences
Advisor: Graham F. Hatful

FELLOWSHIPS AND AWARDS:

- 2021 - 2024 F32 Postdoctoral fellowship from NIH NIDDK: “Understanding mechanisms by which microbial strains and metabolites in fermented foods decrease systemic inflammation “
- 2020 - 2021 T32 NIH Postdoctoral Fellowship from the Stanford Microbiology and Immunology training grant: “Molecular Basis of Host Parasite Interaction”
- 2019 Keystone National Institute of Allergy and Infectious Diseases Travel Scholarship

2014 – 2019 National Science Foundation Graduate Research Fellowship

2012 Howard Hughes Medical Institute Undergraduate Research Fellowship

PUBLICATIONS:

1. Pope, W.H., Anders, K.R., Baird, M., Bowman, C.A., Boyle, M.M., Broussard, G.W., Chow, T., Clase, K.L., Cooper, S., Cornely, K.A., DeJong, R.J., Delesalle, V.A., Deng, L., Dunbar, D., Edgington, N.P., Ferreira, C.M., Weston Hafer, K., Hartzog, G.A., Hatherill, J.R., Hughes, L.E., Ipapo, K., Krukoni, G.P., Meier, C.G., Monti, D.L., **Olm, M.R.**, Page, S.T., Peebles, C.L., Rinehart, C.A., Rubin, M.R., Russell, D.A., Sanders, E.R., Schoer, M., Shaffer, C.D., Wherley, J., Vazquez, E., Yuan, H., Zhang, D., Cresawn, S.G., Jacobs-Sera, D., Hendrix, R.W., Hatfull, G.F. “Cluster M mycobacteriophages Bongo, PegLeg, and Rey with unusually large repertoires of tRNA isotypes.” *Journal of virology*. 88, 2461–2480. 2014
2. Dedrick, R.M., Mavrich, T.N., Ng, W.L., Cervantes Reyes, J.C., **Olm, M.R.**, Rush, R.E., Jacobs-Sera, D., Russell, D.A., Hatfull, G.F. “Function, expression, specificity, diversity and incompatibility of actinobacteriophage parABS systems.” *Molecular Microbiology*. 101, 625–644. 2016
3. Brown, C.T., **Olm, M.R.**, Thomas, B.C., Banfield, J.F., “Measurement of bacterial replication rates in microbial communities.” *Nature Biotechnology*. 34, 1256–1263. 2016
4. **Olm, M.R.**, Butterfield, C.N., Copeland, A., Boles, T.C., Thomas, B.C., Banfield, J.F. “The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis.” *mBio* 8. 2017
5. **Olm, M.R.**, Brown, C.T., Brooks, B., Firek, B., Baker, R., Burstein, D., Soenjoyo, K., Thomas, B.C., Morowitz, M., Banfield, J.F. “Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates.” *Genome Research* 27, 601–612. 2017
6. **Olm, M.R.**, Brown, C.T., Brooks, B., Banfield, J.F. “dRep: a tool for fast and accurate genomic comparisons that enables improved genome recovery from metagenomes through de-replication.” *The ISME Journal*. 11, 2864–2868. 2017
7. Brooks, B., **Olm, M.R.**, Firek, B.A., Baker, R., Thomas, B.C., Morowitz, M.J., Banfield, J.F. “Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome.” *Nature Communications*. 8, 1814. 2017
8. Rahman, S.F., **Olm, M.R.**, Morowitz, M.J., Banfield, J.F. “Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome.” *mSystems* 3. 2018
9. Brown, C.T., Xiong, W., **Olm, M.R.**, Thomas, B.C., Baker, R., Firek, B., Morowitz, M.J., Hettich, R.L., Banfield, J.F. “Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles.” *mBio* 9. 2018

10. Brooks, B., **Olm, M.R.**, Firek, B.A., Baker, R., Geller-McGrath, D., Reimer, S.R., Soenjoyo, K.R., Yip, J.S., Dahan, D., Thomas, B.C., Morowitz, M.J., Banfield, J.F. “The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms.” *Microbiome* 6, 112. 2018
11. Rahman, S.F., **Olm, M.R.**, Morowitz, M.J., Banfield, J.F., **2019**. “Functional potential of bacterial strains in the premature infant gut microbiome is associated with gestational age.” *bioRxiv* [pre-print] 2019
12. Matheus Carnevali, P.B., Schulz, F., Castelle, C.J., Kantor, R.S., Shih, P.M., Sharon, I., Santini, J.M., **Olm, M.R.**, Amano, Y., Thomas, B.C., Anantharaman, K., Burstein, D., Becraft, E.D., Stepanauskas, R., Woyke, T., Banfield, J.F. “Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria.” *Nature Communications*. 10, 463. 2019
13. **Olm, M.R.***, West, P.T*, Brooks, B., Firek, B.A., Baker, R., Morowitz, M.J., Banfield, J.F. “Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms.” *Microbiome* 7, 26. 2019
14. Bouma-Gregson, K., **Olm, M.R.**, Probst, A.J., Anantharaman, K., Power, M.E., Banfield, J.F. “Impacts of microbial assemblage and environmental conditions on the distribution of anatoxin-a producing cyanobacteria within a river network.” *The ISME Journal* 13, 1618. 2019
15. Devoto, A.E., Santini, J.M., **Olm, M.R.**, Anantharaman, K., Munk, P., Tung, J., Archie, E.A., Turnbaugh, P.J., Seed, K.D., Blekhman, R., Aarestrup, F.M., Thomas, B.C., Banfield, J.F. “Megaphages infect *Prevotella* and variants are widespread in gut microbiomes.” *Nature Microbiology* 2019
16. **Olm, M.R.**, Bhattacharya, N., Crits-Christoph, A., Firek, B.A., Baker, R., Song, Y.S., Morowitz, M.J., Banfield, J.F.. “Necrotizing enterocolitis is preceded by increased gut bacterial replication, *Klebsiella*, and fimbriae-encoding bacteria.” *Science advances* 5, eaax5727. 2019
17. Sher, Y., **Olm, M.R.**, Raveh-Sadka, T., Brown, C.T., Sher, R., Firek, B., Baker, R., Morowitz, M.J., Banfield, J.F. “Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut.” *Plos one* 15, e0229537. 2020
18. Al-Shayeb, B., Sachdeva, R., Chen, L.-X., Ward, F., Munk, P., Devoto, A., Castelle, C.J., **Olm, M.R.**, Bouma-Gregson, K., Amano, Y., He, C., Méheust, R., Brooks, B., Thomas, A., Lavy, A., Matheus-Carnevali, P., Sun, C., Goltsman, D.S.A., Borton, M.A., Sharrar, A., Jaffe, A.L., Nelson, T.C., Kantor, R., Keren, R., Lane, K.R., Farag, I.F., Lei, S., Finstad, K., Amundson, R., Anantharaman, K., Zhou, J., Probst, A.J., Power, M.E., Tringe, S.G., Li, W.-J., Wrighton, K., Harrison, S., Morowitz, M., Relman, D.A., Doudna, J.A., Lehours, A.-C., Warren, L., Cate, J.H.D., Santini, J.M., Banfield, J.F. “Clades of huge phages from across Earth’s ecosystems.” *Nature*. 2020

19. **Olm, M.R.**, Crits-Christoph, A., Diamond, S., Lavy, A., Carnevali, P.B.M., Banfield, J.F. “Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries.” *mSystems* 5. 2020
20. West, P.T., Peters, S.L., **Olm, M.R.**, Feiqiao, B.Y., Lou, Y.C., Firek, B.A., Baker, R., Johnson, A.D., Morowitz, M.J., Hettich, R.L. “Genetic and behavioral adaptation of *Candida parapsilosis* to the microbiome of hospitalized infants revealed by in situ genomics, transcriptomics and proteomics.” *bioRxiv* [pre-print] 2020
21. Crits-Christoph, A., **Olm, M.R.**, Diamond, S., Bouma-Gregson, K., Banfield, J.F. “Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow.” *The ISME Journal* 1–13. 2020
22. Crits-Christoph, A., Bhattacharya, N., **Olm, M.R.**, Song, Y.S., Banfield, J.F. “Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity.” *Genome Research*. 2020
23. Lou, Y.C., **Olm, M.R.**, Diamond, S., Crits-Christoph, A., Firek, B.A., Baker, R., Morowitz, M.J., Banfield, J.F. “Infant gut strain persistence is associated with maternal origin, phylogeny, and functional potential including surface adhesion and iron acquisition.” *bioRxiv* [pre-print] 2021
24. Carnevali, P.B.M., Lavy, A., Thomas, A.D., Crits-Christoph, A., Diamond, S., Méheust, R., Olm, M.R., Sharrar, A., Lei, S., Dong, W. “Meanders as a scaling motif for understanding of floodplain soil microbiome and biogeochemical potential at the watershed scale.” *Microbiome* 9, 1–23. 2021
25. Crits-Christoph, A., Kantor, R.S., **Olm, M.R.**, Whitney, O.N., Al-Shayeb, B., Lou, Y.C., Flamholz, A., Kennedy, L.C., Greenwald, H., Hinkle, A., Hetzel, J., Spitzer, S., Koble, J., Tan, A., Hyde, F., Schroth, G., Kuersten, S., Banfield, J.F., Nelson, K.L. “Genome Sequencing of Sewage Detects Regionally Prevalent SARS-CoV-2 Variants.” *mBio* 12, e02703-20. 2021
26. **Olm, M.R.**, Crits-Christoph, A., Bouma-Gregson, K., Firek, B.A., Morowitz, M.J., Banfield, J.F. “inStrain profiles population microdiversity from metagenomic data and sensitively detects shared microbial strains.” *Nature Biotechnology*. 2021
27. **Olm, M.R.**, Sonnenburg, J.L. “Ancient human faeces reveal gut microbes of the past.” *Nature*. 2021

ORAL PRESENTATIONS:

- | | |
|------|--|
| 2021 | Molecular and Bioinformatic Methods in Ecology and Evolution Seminar Series
May 2021; University of Duisburg-Essen, Germany
Title: “Tracking microbial strains and quantifying in situ evolution with genome-resolved metagenomics” |
| 2021 | Applied Bioinformatics & Public Health Microbiology 2021
May 2021; Wellcome Genome Campus, UK |

Title: “Tracing the spread and evolution of microbial populations in hospital rooms and sewage with metagenomics”

- 2020 **Innovative Genomic Institute “Shelter in Place” Seminar Series**
May 2020; Innovative Genomics Institute; Berkeley, CA
Title: “Beyond strain-level: Tracking identical microbial populations and intra-specific variation in the human microbiome”
- 2019 **Keystone Symposia: *Microbiome: Therapeutic Implications***
October 2019; Killarney, Co. Kerry, Ireland
Title: “Metagenomic Identification of Fecal Microbial Signatures Preceding Acute Intestinal Inflammation in Premature Infants”
- 2017 **Microbiology & Molecular Genetics Seminar Series**
October 2017; University of Pittsburgh; Pittsburgh, PA.
Title: “Using genome-resolved metagenomics to study the developing infant microbiome”
- 2016 **Lake Arrowhead Microbial Genomics Conference**
September 2016; Lake Arrowhead, CA.
Title: “Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different *in situ* growth rates”

SOFTWARE DEVELOPMENT:

inStrain: <https://github.com/MrOlm/instrain>
Population genomics analyses from metagenomic data

dRep: <https://github.com/MrOlm/drep>
Rapid comparison and dereplication of genomes

tRep: <https://github.com/MrOlm/tRep>
Estimate the taxonomy of microbial genomes

SCIENTIFIC OUTREACH:

- 2017 – Contributor to microBE.net
- 2015 – Presenter at California Academy of Sciences NightLife events
- 2011 – 2014 Mentor to high school students in the Phagehunting program

SELECT POSTER PRESENTATIONS:

- 2018 **Stanford Microbiome Symposium 2018**
 September 2018; Stanford, CA.
Metagenomic analysis reveals bacterial replication rates increase two days prior to necrotizing enterocolitis diagnosis
- 2018 **17th International Symposium on Microbial Ecology**
 August 2018; Leipzig, Germany.
De novo assembly of eukaryotic genomes from metagenomes reveals strain-level overlap between infant and hospital fungal microbiomes
- 2017 **Applied Bioinformatics & Public Health Microbiology**
 June 2017; Cambridge, UK.
Genome-resolved metagenomics of infant fecal samples yields thousands of high-quality microbial genomes and reveals patterns of sub-species diversity
- 2016 **Lake Arrowhead Microbial Genomics Conference**
 September 2016; Lake Arrowhead, CA.
Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates
- 2013 **American Society for Microbiology General Meeting**
 August 2013; Denver, CO.
Partitioning System of Bacteriophage RedRock Increases Plasmid Maintenance in Mycobacterium smegmatis.
- 2012 **Science 2012**
 August 2012; Pittsburgh, PA
Study of Putative Partitioning System in Mycobacteriophage RedRock

TEACHING EXPERIENCE:

- Spring 2016 **Graduate Student Instructor**
 ESPM 112: Microbial Ecology with Professors Rodrigo Almeida and Jillian Banfield, University of California, Berkeley.
- Spring 2016 **Graduate Student Instructor**
 ESPM 112L: Metagenomics Computer Lab with Professor Jillian Banfield, University of California, Berkeley.
- Fall 2015 **Graduate Student Instructor**
 Biology 1A: Introduction to Biology
 University of California, Berkeley
- Fall 2013 **Teaching Assistant**
 NROSCI 1250: Human Physiology with Dr. Alan Sved
 University of Pittsburgh

Fall 2012

Lab Instructor

CHEM 0113-0114: General Chemistry Lab 1 and 2
University of Pittsburgh