

Matthew R. Olm, PhD

Department of Microbiology and Immunology

Stanford University

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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”
- 2021 Conceptualized and co-wrote successfully funded Chan Zuckerberg Biohub Investigators Program research grant with Dr. Justin Sonnenburg

- 2019 Keystone National Institute of Allergy and Infectious Diseases Travel Scholarship
- 2016 Conceptualized and co-wrote successfully funded Sloan Foundation Research Grant with Dr. Jillian Banfield
- 2014 – 2019 National Science Foundation Graduate Research Fellowship awardee
- 2012 Howard Hughes Medical Institute Undergraduate Research Fellowship awardee

INVITED ORAL PRESENTATIONS:

- 2022 **Biotecmar Bioinformatics Tools and Applications Workshop**
April 2022; All-Atlantic Joint Pilot Action AA-BIOTECMAR online workshop
Title: “Genome-resolved population genomics and strain-level comparisons”
- 2022 **Virginia Tech's Life Science Seminar Series**
February 2022; Virginia Tech, Blacksburg, VA
Title: “Metagenomics of Modern Hunter-gatherers to Understand the Human Microbiome”
- 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: Population genomics analyses from metagenomic data

Source Code: <https://github.com/MrOlm/instrain>

Documentation: <https://instrain.readthedocs.io>

10,000+ total downloads

dRep: Rapid comparison and dereplication of genomes

Source Code: <https://github.com/MrOlm/drep>

Documentation: <https://drep.readthedocs.io>

20,000+ total downloads

PROFESSIONAL ACTIVITIES AND OUTREACH:

2021 - 2022 Founding member of Sonnenburg Lab DEI Committee

2015 – 2019 Presenter at California Academy of Sciences NightLife events

2016 - 2017 Author for science dissemination website microBE.net

2011 – 2014 Mentor to high school students in the Phagehunting program

Continuous Peer reviewer for *Nature* (5 articles), *Cell* (2 articles), *Genome Research* (2 articles), *BMC Biology*, *Microbiome*, *ISME Journal*, *Nature Protocols*, *Molecular Systems Biology*, *Nature Microbiology*, *mSystems*, *BMC Genomics*, *Frontiers in Bioinformatics*

TEACHING EXPERIENCE:

Spring 2022 **Guest Lecturer**
MI 215: Principles of Biological Technologies with Dr. Peter Sarnow
Stanford University

Fall 2021 **Guest Lecturer**
MI 221: Gut Microbiota in Health and Disease with Drs. Bhatt and Sonnenburg
Stanford University

Spring 2021 **Guest Lecturer**
MI 215: Principles of Biological Technologies with Dr. Peter Sarnow
Stanford University

- Spring 2016 **Course Co-founder and Graduate Student Instructor**
 ESPM 112L: Metagenomics Computer Lab with Professor Jillian Banfield, University of California, Berkeley.
- Spring 2016 **Graduate Student Instructor**
 ESPM 112: Microbial Ecology with Professors Rodrigo Almeida and 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

PUBLICATIONS:

1. **Olm M. R.***, Dahan, D.*, Carter M. M., Merrill B. D., Yu F. B., Jain S., Meng X., Tripathi S., Wastyk H., Neff N., Holmes S., Sonnenburg E. D., Jha A. R., Sonnenburg J. L. (2022). Robust variation in infant gut microbiome assembly across a spectrum of lifestyles. *Science* 376, 1220–1223. <https://doi.org/10.1126/science.abj2972>
2. Merrill, B. D.*, Carter, M. M.*, **Olm, M. R.***, Dahan, D., Tripathi, S., Spencer, S. P., Yu, B., Jain, S., Neff, N., Jha, A. R., Sonnenburg, E. D., & Sonnenburg, J. L. (2022). Ultra-deep Sequencing of Hadza Hunter-Gatherers Recovers Vanishing Microbes. *BioRxiv*, 2022.03.30.486478. <https://doi.org/10.1101/2022.03.30.486478>
3. Lou, Y. C., Hoff, J., **Olm, M. R.**, West-Roberts, J., Diamond, S., Firek, B. A., Morowitz, M. J., & Banfield, J. F. (2022). Using strain-resolved analysis to identify contamination in metagenomics data. *BioRxiv*, 2022.01.16.476537. <https://doi.org/10.1101/2022.01.16.476537>
4. Bouma-Gregson, K., Crits-Christoph, A., **Olm, M. R.**, Power, M. E., & Banfield, J. F. (2022). *Microcoleus* (Cyanobacteria) form watershed-wide populations without strong gradients in population structure. *Molecular Ecology*, 31(1), 86–103. <https://doi.org/10.1111/mec.16208>
5. Carter, M. M., **Olm, M. R.**, & Sonnenburg, E. D. (2022). Microbiome assembly in The Gambia. *Nature Microbiology News & Views*, 7(1), 18–19. <https://doi.org/10.1038/s41564-021-01036-1>

6. **Olm, M. R., & Sonnenburg, J. L.** (2021). Ancient human faeces reveal gut microbes of the past. *Nature News & Views*. <https://doi.org/10.1038/d41586-021-01266-7>
7. **Olm, M. R., Crits-Christoph, A., Bouma-Gregson, K., Firek, B. A., Morowitz, M. J., & Banfield, J. F.** (2021). inStrain profiles population microdiversity from metagenomic data and sensitively detects shared microbial strains. *Nature Biotechnology*, 39(6), 727–736. <https://doi.org/10.1038/s41587-020-00797-0>
8. Mirzayi, C., Renson, A., Furlanello, C., Sansone, S.-A., Zohra, F., Elsafoury, S., Geistlinger, L., Kasselmann, L.J., Eckenrode, K., van de Wijgert, J., Loughman, A., Marques, F.Z., MacIntyre, D.A., Arumugam, M., Azhar, R., Beghini, F., Bergstrom, K., Bhatt, A., Bisanz, J.E., Braun, J., Bravo, H.C., Buck, G.A., Bushman, F., Casero, D., Clarke, G., Collado, M.C., Cotter, P.D., Cryan, J.F., Demmer, R.T., Devkota, S., Elinav, E., Escobar, J.S., Fettweis, J., Finn, R.D., Fodor, A.A., Forslund, S., Franke, A., Furlanello, C., Gilbert, J., Grice, E., Haibe-Kains, B., Handley, S., Herd, P., Holmes, S., Jacobs, J.P., Karstens, L., Knight, R., Knights, D., Koren, O., Kwon, D.S., Langille, M., Lindsay, B., McGovern, D., McHardy, A.C., McWeeney, S., Mueller, N.T., Nezi, L., **Olm, M. R.**, Palm, N., Pasolli, E., Raes, J., Redinbo, M.R., Rühlemann, M., Balfour Sartor, R., Schloss, P.D., Schriml, L., Segal, E., Shardell, M., Sharpton, T., Smirnova, E., Sokol, H., Sonnenburg, J.L., Srinivasan, S., Thingholm, L.B., Turnbaugh, P.J., Upadhyay, V., Walls, R.L., Wilmes, P., Yamada, T., Zeller, G., Zhang, M., Zhao, N., Zhao, L., Bao, W., Culhane, A., Devanarayan, V., Dopazo, J., Fan, X., Fischer, M., Jones, W., Kusko, R., Mason, C.E., Mercer, T.R., Sansone, S.-A., Scherer, A., Shi, L., Thakkar, S., Tong, W., Wolfinger, R., Hunter, C., Segata, N., Huttenhower, C., Dowd, J.B., Jones, H.E., Waldron, L. (2021). Reporting guidelines for human microbiome research: the STORMS checklist. *Nature Medicine*, 27(11), 1885–1892. <https://doi.org/10.1038/s41591-021-01552-x>
9. Lou, Y. C., **Olm, M. R.**, Diamond, S., Crits-Christoph, A., Firek, B. A., Baker, R., Morowitz, M. J., & Banfield, J. F. (2021). Infant gut strain persistence is associated with maternal origin, phylogeny, and traits including surface adhesion and iron acquisition. *Cell Reports Medicine*, 2(9), 100393. <https://doi.org/10.1016/j.xcrm.2021.100393>
10. West, P. T., Peters, S. L., **Olm, M. R.**, Yu, F. B., Gause, H., Lou, Y. C., Firek, B. A., Baker, R., Johnson, A. D., Morowitz, M. J., Hettich, R. L., & Banfield, J. F. (2021). Genetic and behavioral adaptation of *Candida parapsilosis* to the microbiome of hospitalized infants revealed by in situ genomics, transcriptomics, and proteomics. *Microbiome*, 9(1), 142. <https://doi.org/10.1186/s40168-021-01085-y>
11. 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. (2021). Meanders as a scaling motif for understanding of floodplain soil microbiome and biogeochemical potential at the watershed scale. *Microbiome*, 9(1), 1–23. <https://doi.org/10.1186/s40168-020-00957-z>
12. 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. (2021). Genome Sequencing of

Sewage Detects Regionally Prevalent SARS-CoV-2 Variants. *MBio*, 12(1), e02703-20. <https://doi.org/10.1128/mBio.02703-20>

13. Crits-Christoph, A., Bhattacharya, N., **Olm, M. R.**, Song, Y. S., & Banfield, J. F. (2021). Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity. *Genome Research*, 31(2), 239–250. <https://doi.org/10.1101/gr.268169.120>
14. Crits-Christoph, A., **Olm, M. R.**, Diamond, S., Bouma-Gregson, K., & Banfield, J. F. (2020). Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. *The ISME Journal*, 1–13. <https://doi.org/10.1038/s41396-020-0655-x>
15. Sher, Y., **Olm, M. R.**, Raveh-Sadka, T., Brown, C. T., Sher, R., Firek, B., Baker, R., Morowitz, M. J., & Banfield, J. F. (2020). Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut. *Plos One*, 15(3), e0229537. <https://doi.org/10.1371/journal.pone.0229537>
16. **Olm, M. R.**, Crits-Christoph, A., Diamond, S., Lavy, A., Carnevali, P. B. M., & Banfield, J. F. (2020). Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. *MSystems*, 5(1). <https://doi.org/10.1128/mSystems.00731-19>
17. 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., ... Banfield, J. F. (2020). Clades of huge phages from across Earth's ecosystems. *Nature*, 578(7795), 425–431. <https://doi.org/10.1038/s41586-020-2007-4>
18. **Olm, M. R.**, Bhattacharya, N., Crits-Christoph, A., Firek, B. A., Baker, R., Song, Y. S., Morowitz, M. J., & Banfield, J. F. (2019). Necrotizing enterocolitis is preceded by increased gut bacterial replication, *Klebsiella*, and fimbriae-encoding bacteria. *Science Advances*, 5(12), eaax5727. <https://doi.org/10.1126/sciadv.aax5727>
19. 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. (2019). Megaphages infect *Prevotella* and variants are widespread in gut microbiomes. *Nature Microbiology*, 4(4), 693. <https://doi.org/10.1038/s41564-018-0338-9>
20. Bouma-Gregson, K., **Olm, M. R.**, Probst, A. J., Anantharaman, K., Power, M. E., & Banfield, J. F. (2019). Impacts of microbial assemblage and environmental conditions on the distribution of anatoxin-a producing cyanobacteria within a river network. *The ISME Journal*, 13(6), 1618. <https://doi.org/10.1038/s41396-019-0374-3>
21. **Olm, M. R.***, West, P. T.*, Brooks, B., Firek, B. A., Baker, R., Morowitz, M. J., & Banfield, J. F. (2019). Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms. *Microbiome*, 7(1), 26. <https://doi.org/10.1186/s40168-019-0638-1>

22. Carnevali, P. B. M., 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. (2019). Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. *Nature Communications*, 10(1), 463. <https://doi.org/10.1038/s41467-018-08246-y>
23. 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*, 530139. <https://doi.org/10.1101/530139>
24. 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. (2018). The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms. *Microbiome*, 6(1), 112. <https://doi.org/10.1186/s40168-018-0493-5>
25. Brown, C. T., Xiong, W., **Olm, M. R.**, Thomas, B. C., Baker, R., Firek, B., Morowitz, M. J., Hettich, R. L., & Banfield, J. F. (2018). Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. *MBio*, 9(2), e00441-18. <https://doi.org/10.1128/mBio.00441-18>
26. Rahman, S. F., **Olm, M. R.**, Morowitz, M. J., & Banfield, J. F. (2018). Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome. *MSystems*, 3(1), e00123-17. <https://doi.org/10.1128/mSystems.00123-17>
27. Brooks, B., **Olm, M. R.**, Firek, B. A., Baker, R., Thomas, B. C., Morowitz, M. J., & Banfield, J. F. (2017). Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome. *Nature Communications*, 8(1), 1814. <https://doi.org/10.1038/s41467-017-02018-w>
28. Brown, C. T., **Olm, M. R.**, Thomas, B. C., & Banfield, J. F. (2017). Measurement of bacterial replication rates in microbial communities. *Nature Biotechnology*, 34(12), 1256–1263. <https://doi.org/10.1038/nbt.3704>
29. **Olm, M. R.**, Brown, C. T., Brooks, B., & Banfield, J. F. (2017). dRep: a tool for fast and accurate genomic comparisons that enables improved genome recovery from metagenomes through de-replication. *The ISME Journal*, 11(12), 2864–2868. <https://doi.org/10.1038/ismej.2017.126>
30. **Olm, M. R.**, Brown, C. T., Brooks, B., Firek, B., Baker, R., Burstein, D., Soenjoyo, K., Thomas, B. C., Morowitz, M., & Banfield, J. F. (2017). Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates. *Genome Research*, 27(4), 601–612. <https://doi.org/10.1101/gr.213256.116>
31. **Olm, M. R.**, Butterfield, C. N., Copeland, A., Boles, T. C., Thomas, B. C., & Banfield, J. F. (2017). The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis. *MBio*, 8(1), e01969-16. <https://doi.org/10.1128/mBio.01969-16>

32. Dedrick, R. M., Mavrich, T. N., Ng, W. L., Reyes, J. C. C., **Olm, M. R.**, Rush, R. E., Jacobs-Sera, D., Russell, D. A., & Hatfull, G. F. (2016). Function, expression, specificity, diversity and incompatibility of actinobacteriophage parABS systems. *Molecular Microbiology*, 101(4), 625–644. <https://doi.org/10.1111/mmi.13414>
33. 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., Hafer, K.W., 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. (2014). Cluster M Mycobacteriophages Bongo, PegLeg, and Rey with Unusually Large Repertoires of tRNA Isotypes. *Journal of Virology*, 88(5), 2461–2480. <https://doi.org/10.1128/JVI.03363-13>

***These authors contributed equally to this work**