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Full software and publication list: https://astrobiomike.github.io/research/

Summary

I am a bioinformatician at NASA's Ames Research Center in Mountain View, CA, USA. My formal educational background is in biology and microbial ecology, and my professional experience has been spent applying bioinformatics to questions about microbial ecology and evolution in various microbial systems ranging from deep-sea basalts at the bottoms of our oceans all the way up to the International Space Station.

I have extensive first-hand experience in many common bioinformatics approaches/analyses (e.g., marker-gene analysis, genomics, metagenomics, metatranscriptomics, comparative genomics, phylogenomics, pangenomics). And I am an adept coder in the programming languages of bash, python, and R, enabling me to not only access and utilize available tools and data for processing and analysis, but to also adjust and/or build tools as needed for any given project.

Having gone through it myself, I am passionate about and very much enjoy helping other biologists through the initial steep learning curve of needing to learn to use bioinformatics – which most of us are left to do with little or no guidance or support from our educational institutions. Simply put, our society as a whole is currently generating data much faster than it is developing the skills to work with it, and our educational infrastructures have not yet been able to adjust as much as needed. In that vein, I spend a lot of my free time building and maintaining a website designed to help biologists learn to utilize bioinformatics (microbialomics.org), and I am heavily involved in organizing and teaching at large, yearly bioinformatics workshops, as well as one-off smaller ones regularly.

Select publications

- **Lee, M.D.** (2019). <u>GToTree: a user-friendly workflow for phylogenomics.</u> *Bioinformatics*. <u>https://doi.org/10.1093/bioinformatics/btz188</u>
- **Lee, M.D.** (2019). <u>Applications and considerations of GToTree: a user-friendly workflow for phylogenomics</u>. *Evolutionary Bioinformatics*. <u>https://doi.org/10.1177/1176934319862245</u>
- Lee, M.D. (2019). <u>Happy Belly Bioinformatics</u>: an open-source resource dedicated to helping biologists utilize bioinformatics. *The Journal of Open-Source Education*. https://doi.org/10.21105/jose.00053
- O'Rourke, A.O. and **Lee, M.D.**, Nierman, W.C., Everroad, R.C., and Dupont, C.L. (2020). <u>Genomic and phenotypic characterization of *Burkholderia* isolates from the potable water system of the International Space Station. *PLoS ONE*. https://doi.org/10.1371/journal.pone.0227152</u>
- **Lee, M.D.**, Ahlgren, N.A., Kling, J. D., Walworth, N.G., Rocap, G., Saito, M.A., Hutchins, D.A., and Webb, E.A. (2019). <u>Marine Synechococcus</u> isolates representing globally abundant genomic lineages demonstrate a unique evolutionary path of genome reduction without a decrease in GC content. *Environmental Microbiology*. https://doi.org/10.1111/1462-2920.14552
- **Lee, M.D.**, Walworth, N.G., McParland, E.L., Fu, F.-X., Mincer, T.J., Levine, N.M., Hutchins, D.A., and Webb, E.A. (2017). The *Trichodesmium* consortium: conserved heterotrophic co-occurrence and genomic signatures of potential interactions. *ISMEJ*. https://doi.org/10.1038/ismej.2017.49
- Lee, M.D., Webb, E.A., Walworth, N.G., Fu, F.-X., Held, N.A., Saito, M.A., and Hutchins, D.A. (2017). Transcriptional activities of the microbial consortium living with the marine nitrogen-fixing cyanobacterium *Trichodesmium* reveal potential roles in community-level nitrogen cycling. *Applied and Environmental Microbiology*. https://doi.org/10.1128/AEM.02026-17

- **Lee, M.D.**, Walworth, N.G., Sylvan, J.B., Edwards, K.J., and Orcutt, B.N. (2015). <u>Microbial communities on seafloor basalts at Dorado Outcrop reflect level of alteration and highlight global lithic clades. *Frontiers in Microbiology*. https://doi.org/10.3389/fmicb.2015.01470</u>
- **Lee, M.D.**, Kling, J.D., Araya, R., and Ceh, J. (2018). <u>Jellyfish life stages shape associated microbial communities</u>, while a core microbiome is maintained across all. *Frontiers in Microbiology*. https://doi.org/10.3389/fmicb.2018.01534
- Walworth, N.G. and Lee, M.D., Suffridge, C., Qu, P., Fu., F-X., Saito, M.A., Webb, E.A., Sañudo-Wilhemly, S.A., And Hutchings, D.A. (2017). Functional genomics and phylogenetic evidence suggest genus-wide cobalamin production by the globally distributed marine nitrogen fixer *Trichodesmium*. Frontiers in Microbiology. https://doi.org/10.3389/fmicb.2018.00189
- O'Rourke, A.O., Zoumplis, A., Wilburn, P., **Lee, M.D.**, Lee, Z., Vecina, M., and Mercader, K. (2020). <u>Following</u> the Astrobiology roadmap: origins, habitability, and future exploration. Book chapter in *Astrobiology: current, evolving, and emerging perspectives* by Caister Academic. <u>https://doi.org/10.21775/9781912530304</u>
- Ahlgren, N.A., Belisle, B.S., and **Lee, M.D.** (2019). <u>Genomic mosaicism underlies the adaptation of marine Synechococcus</u> ecotypes to distinct oceanic iron niches. *Environmental Microbiology*. https://doi.org/10.1111/1462-2920.14893
- Kling, J.D., Lee, M.D., Fu, F-X., Phan, M.D., Wang, X., Qu, P., and Hutchins, D.A. (2019). <u>Transient exposure to unusually high temperatures reshapes coastal phytoplankton communities</u>. *ISMEJ*. https://doi.org/10.1038/s41396-019-0525-6
- Walworth, N.G., Fu., F-X., Lee, M.D., Cai, X., Saito, M.A., Webb, E.A., and Hutchins, D.A. (2017). <u>Nutrient colimited Trichodesmium</u> as nitrogen source or sink in a future ocean. *Applied and Environmental Microbiology*. https://doi.org/10.1128/AEM.02137-17
- Walworth, N.G., Hutchins, D.A., Dolzhenko, E., **Lee, M.D.**, Fu., F-X., Smith, A.D., and Webb, E.A. (2017). <u>Biogeographic conservation of the cytosine epigenome in the globally important marine, nitrogen-fixing cyanobacterium *Trichodesmium*. *Environmental Microbiology*. https://doi.org/10.1111/1462-2920.13934</u>
- Momper, L.M., Jungbluth, S.P., **Lee, M.D.**, and Amend, J.P. (2017). <u>Energy and carbon metabolisms in a deep terrestrial subsurface fluid microbial community. *ISMEJ*. https://doi.org/10.1038/ismej.2017.94</u>
- Ramirez, G.A., Hoffman, C.L., **Lee, M.D.**, Lesniewski, R.A., Barco, R., Garber, A., Toner, B.M., Wheat, C.G., Edwards, K.J., Orcutt, B.N. (2016). <u>Assessing marine microbial induced corrosion monitored in Santa Catalina Island, California. Frontiers in Microbiology</u>. https://doi.org/10.3389/fmicb.2016.01679
- Walworth, N.G., **Lee, M.D.**, Fu, F.-X., Hutchins, D.A., and Webb, E.A. (2016). <u>Molecular and physiological evidence of genetic assimilation to high CO2 in the marine nitrogen fixer *Trichodesmium*. *PNAS*. https://doi.org/10.1073/pnas.1605202113</u>
- Walworth, N.G., Fu, F.-X., Webb, E.A., Saito, M.A., Moran, D., McIlvin, M.R., Lee, M.D., and Hutchins, D.A. (2016). Mechanisms of increased *Trichodesmium* fitness under iron and phosphorus co-limitation in the present and future ocean. *Nature Communications*. https://doi.org/10.1038/ncomms12081