

# Mora Jove Groussman, Ph.D.

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**Bioinformatics Scientist experienced in building workflows for large sequencing datasets**

## PROFESSIONAL EXPERIENCE

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### University of Washington, School of Oceanography

January 2023 – January 2024

*Postdoctoral Scholar*

*Seattle, WA*

- Designed and implemented MarFERReT, a reproducible pipeline for processing large volumes of reference sequence data and enhancing bioinformatics data use for environmental sequence annotation.
- Developed reproducible bioinformatics pipelines using R and python for cross-validation of genetic reference data, establishing a github repository with code and technical documentation.
- Built, maintained and executed bioinformatics workflows for processing, annotation and distribution of large environmental sequencing datasets from hundreds of heterogeneous samples.
- Created and maintained public data repositories for nearly 200 million environmental gene sequences, increasing accessibility and re-use of data sets.
- Implemented advanced data visualization techniques to elucidate complex multi-dimensional transcriptomic datasets, identifying novel microbial interactions and metabolic pathways.

### University of Washington, School of Oceanography

June 2016 – December 2022

*Graduate Research Assistant*

*Seattle, WA*

- Published 10 papers in peer-reviewed journals and presented research at 5 international conferences, demonstrating expertise in scientific writing and communication.
- Developed key bioinformatics data pipelines for a novel machine learning study of marine microbial eukaryote metabolism, showcasing skills in ML applications for genomics.
- Applied multivariate statistical methods to analyze high-dimensional transcriptomic datasets encompassing hundreds of organisms and millions of gene sequences.
- Leveraged cloud computing (AWS) and High-Performance Computing (SLURM) for large-scale dataset processing and analysis.
- Utilized containerization (Docker, Singularity) to ensure reproducibility and portability of computational workflows.
- Mentored team members in bioinformatics algorithms, statistical techniques, and best practices for NGS data analysis.

## EDUCATION

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### University of Washington

December 2022

*Ph.D. in Oceanography*

*Seattle, WA*

- Dissertation: "Resolving the molecular ecology of marine microbial eukaryotes with metatranscriptomes."

### University of Washington

March 2016

*B.S. in Molecular, Cellular, and Developmental Biology (magna cum laude)*

*Seattle, WA*

## SKILLS

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Bioinformatics and Data Science: Genomics, Transcriptomics, Machine Learning, Algorithm Development

Pipeline Design and Implementation: Docker, GitHub. Programming: Python, R, Unix/Linux, SQL

Data Visualization and Statistical Analysis. High-Performance and Cloud Computing: AWS, SLURM

Scientific Writing and Presentation: 10 peer-reviewed publications, 5 conference presentations

Project Management and Team Leadership: Mentoring, Interdisciplinary Collaboration

NGS Technologies: Illumina sequencing

## PUBLICATIONS

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1. Groussman, R. D., Coesel, S. N., Schatz, M., Durham, B. D., & Armbrust, E. V. (2024). The North Pacific Eukaryotic Gene Catalog of metatranscriptome assemblies and annotations. *Scientific Data*, in revision. <https://doi.org/10.5281/zenodo.10472589>
2. Groussman, R. D., Blaskowski, S., Coesel, S. N., & Armbrust, E. V. (2023). MarFERReT, an open-source, version-controlled reference library of marine microbial eukaryote functional genes. *Scientific Data*, 10(1), 926. <https://doi.org/10.1038/s41597-023-02842-4>
3. Graff van Creveld, S., Coesel, S. N., Blaskowski, S., Groussman, R. D., Schatz, M. J., & Armbrust, E. V. (2023). Divergent functions of two clades of flavodoxin in diatoms mitigate oxidative stress and iron limitation. *Elife*, 12, e84392. <https://doi.org/10.7554/elife.84392>
4. Lambert, B. S., Groussman, R.D., Schatz, M. J., Coesel, S. N., Durham, B. P., Alverson, A. J., ... & Armbrust, E. V. (2022). The dynamic trophic architecture of open-ocean protist communities revealed through machine-guided metatranscriptomics. *Proceedings of the National Academy of Sciences*, 119(7). <https://doi.org/10.1073/pnas.2100916119>
5. Boysen, A. K., Durham, B. P., Kumler, W., Key, R. S., Heal, K. R., Carlson, L., Groussman, R.D., ... & Ingalls, A. E. (2022). Glycine betaine uptake and metabolism in marine microbial communities. *Environmental Microbiology*. <https://doi.org/10.1111/1462-2920.16020>
6. Park, J., Durham, B. P., Key, R. S., Groussman, R.D., Pinedo-Gonzalez, P., Hawco, N. J., ... & Bundy, R. M. (2022). Siderophore production and utilization by microbes in the North Pacific Ocean. *bioRxiv*. <https://doi.org/10.1101/2022.02.26.482025>
7. Groussman, R.D., Coesel, S., Durham, B.P., and Armbrust, E.V. (2021). "Diel-regulated transcriptional cascades of microbial eukaryotes in the North Pacific Subtropical Gyre". *Frontiers in Microbiology*, 2542. <https://doi.org/10.3389/fmicb.2021.682651>
8. Boysen, A. K., Carlson, L. T., Durham, B. P., Groussman, R.D., Aylward, F. O., Ribalet, F., ... & Ingalls, A. E. (2021). Particulate Metabolites and Transcripts Reflect Diel Oscillations of Microbial Activity in the Surface Ocean. *Msystems*, 6(3). <https://doi.org/10.1128/msystems.00896-20>
9. Coesel, S. N., Durham, B. P., Groussman, R.D., Hu, S. K., Caron, D. A., Morales, R. L., ... & Armbrust, E. V. (2021). Diel transcriptional oscillations of light-sensitive regulatory elements in open-ocean eukaryotic plankton communities. *Proceedings of the National Academy of Sciences*, 118(6). <https://doi.org/10.1073/pnas.2011038118>
10. Durham, B. P., Boysen, A. K., Carlson, L. T., Groussman, R.D., Heal, K. R., Cain, K. R., ... & Armbrust, E. V. (2019). Sulfonate-based networks between eukaryotic phytoplankton and heterotrophic bacteria in the surface ocean. *Nature microbiology*, 4(10), 1706-1715. <https://doi.org/10.1038/s41564-019-0507-5>
11. Becker, K. W., Collins, J. R., Durham, B. P., Groussman, R.D., White, A. E., Fredricks, H. F., ... & Van Mooy, B. A. (2018). Daily changes in phytoplankton lipidomes reveal mechanisms of energy storage in the open ocean. *Nature communications*, 9(1), 1-9. <https://doi.org/10.1038/s41467-018-07346-z>
12. Groussman, R.D., Parker, M. S., & Armbrust, E. V. (2015). Diversity and evolutionary history of iron metabolism genes in diatoms. *PLoS One*, 10(6), e0129081. <https://doi.org/10.1371/journal.pone.0129081>
13. Hennon, G. M., Ashworth, J., Groussman, R.D., Berthiaume, C., Morales, R. L., Baliga, N. S., ... & Armbrust, E. V. (2015). Diatom acclimation to elevated CO<sub>2</sub> via cAMP signalling and coordinated gene expression. *Nature Climate Change*, 5(8), 761-765. <https://doi.org/10.1038/nclimate2683>