

Michael Bertagna

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Top Open Source Projects:

Draft Buddy
Tetrahymena Gene Network Explorer
NASA JPL: Coralign

Summary

Innovative software engineer with roots in scientific research, bringing a research-driven, iterate-and-test approach to engineering challenges. Skilled in algorithm design, machine learning, and working with large-scale datasets, with a proven ability to self-motivate, lead, and deliver elegant solutions to complex problems. Articulate communicator who excels at confidently presenting complex technical findings.

Education

M.S. in Computer Science, Focus in Machine Learning and AI Dec. 2025
Northwestern University, Evanston, IL **GPA: 4.00/4.00**

B.S. in Biochemistry and Molecular Biology, Minor in Computer Science Dec. 2022
Chapman University, Orange, CA **GPA: 3.90/4.00**
Summa Cum Laude, Program Honors, Provost List, Dean's Merit Scholarship

Experience

Software Engineer Intern — Tarana Wireless, Inc. Jun. 2025 – Dec. 2025
Milpitas, CA

- Built an internal agentic AI platform with a chatbot interface and real-time access to databases and documentation
- Implemented refinement loops, self-correcting agents, Retrieval Augmented Generation (**RAG**) and Model Context Protocol (**MCP**) server integrations with **LangGraph** and **FastAPI** to orchestrate and provide context to agents.
- Accelerated technical troubleshooting for internal teams by automating data investigation and root cause analysis.

Research Specialist — The University of Chicago Aug. 2023 – Sep. 2024
Chicago, IL

- Co-developed the *Tetrahymena Gene Network Explorer*, an interactive dashboard for large-scale genetic analysis.
- Designed statistical pipelines in **Python/R** to process RNA-seq and microarray datasets and applied unsupervised ML to cluster 20,000+ genes.
- Equipped researchers with interactive tools to generate hypotheses, accelerating discovery of gene function.

Software Engineer Intern — NASA Jet Propulsion Laboratory Jun. 2022 – Aug. 2022
Pasadena, CA

- Co-developed *Coralign*, an open-source suite of vision algorithms for coronagraph optics alignment and calibration.
- Designed a novel iterative alignment algorithm, translated existing **MATLAB** code to **Python**, and built testing pipelines with **GitHub Actions** and **Pytest**.
- Delivered an automated, reproducible calibration process to replace tedious manual methods, supporting NASA's and other organizations' high-contrast imaging missions.

Skills

Programming: Python, C++, JavaScript, SQL

Data/ML/AI: Pandas, Numpy, SciPy, Jupyter, Bokeh, PyTorch, Sklearn, LangGraph, MCP

DevOps/Other: Git, CI/CD (GitHub Actions), AWS, Docker, Slurm, Linux/Unix

Publications

Michael A. Bertagna, L. J. Bright, et al. "Inferring gene-pathway associations from consolidated transcriptome datasets: an interactive gene network explorer for *Tetrahymena thermophila*," *NAR Genomics and Bioinformatics*, 7(2), lqaf067 (June 2025)