

# 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

<b>M.S. in Computer Science</b> , Focus in Machine Learning and AI Northwestern University, Evanston, IL	Dec. 2025 <b>GPA: 4.00/4.00</b>
<b>B.S. in Biochemistry and Molecular Biology</b> , Minor in Computer Science Chapman University, Orange, CA <i>Summa Cum Laude, Program Honors, Provost List, Dean's Merit Scholarship</i>	Dec. 2022 <b>GPA: 3.90/4.00</b>

## Experience

<b>Software Engineer Intern — Tarana Wireless, Inc.</b> Milpitas, CA	Jun. 2025 – Dec. 2025
• 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 ( <b>RAG</b> ) and Model Context Protocol ( <b>MCP</b> ) server integrations with <b>LangGraph</b> and <b>FastAPI</b> to orchestrate and provide context to agents.	
• Accelerated technical troubleshooting for internal teams by automating data investigation and root cause analysis.	
<b>Research Specialist — The University of Chicago</b> Chicago, IL	Aug. 2023 – Sep. 2024
• Co-developed the <i>Tetrahymena Gene Network Explorer</i> , an interactive dashboard for large-scale genetic analysis.	
• Designed statistical pipelines in <b>Python/R</b> 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.	
<b>Software Engineer Intern — NASA Jet Propulsion Laboratory</b> Pasadena, CA	Jun. 2022 – Aug. 2022
• Co-developed <i>Coralign</i> , an open-source suite of vision algorithms for coronagraph optics alignment and calibration.	
• Designed a novel iterative alignment algorithm, translated existing <b>MATLAB</b> code to <b>Python</b> , and built testing pipelines with <b>GitHub Actions</b> and <b>Pytest</b> .	
• 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)