Jonathan Strutz Scientist & Software Engineer

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EXPERIENCE

Bioinformatics Software Engineer, AI & Computational Biology | LanzaTech | Skokie, IL | Feb 2024–Present

- Lead development of a suite of 10+ **bioinformatics** pipelines to process genomics datasets (*Product owner, PostgreSQL, Luigi*) with a heavy emphasis on testing, continuous deployment, and reproducibility (*pytest, GitHub Actions, Docker*).
- Leverage **Infrastructure-as-Code** tools (*Ansible*) to rearchitect 3 on-prem servers (*Linux, Ubuntu*) to reproducibly process compute-heavy bioinformatics workloads and create a standardized, network-shared genomics data repository.
- Develop a **CLI tool** (*Click*) that preprocesses genomics data from disparate third-party vendors into a consistent format.
- Manage and optimize **AWS** infrastructure, reducing costs for some accounts by 50% while meeting business requirements.
- Build 4 **RAG** pipelines (*Haystack, FastAPI*) to allow engineers to quickly query 1000+ internal documents.
- Restrict visibility of Large Language Models based on SSO authentication provider user groups (LLMs, MSAL, Svelte).

Scientist, AI & Computational Biology | LanzaTech | Skokie, IL | 2022–2024

- Recommended genetic modifications using **computational modeling** (*Cobrapy, ODE-based Mechanistic Modeling*) that improved product selectivity from 54% to 80% (*► <u>Nature Biotechnology</u>*).
- Built a web app (AWS, Flask, Celery) that constructs 1000s of genome-scale models daily and validates against test datasets.
- Utilized **cheminformatics** tools (*RDKit*) to predict 1000s of alternative metabolic routes to 100s of value-added chemicals.

EDUCATION

Ph.D. Chemical & Biological Engineering | Northwestern University | 2022

- Built an open-source database (MongoDB) and web app to identify molecules in metabolomics datasets (# Bioinformatics).
- Created "<u>Pickaxe</u>", a **cheminformatics** python library (*RDKit*) to predict biochemical reactions (= <u>BMC Bioinformatics</u>).
- Built a machine learning pipeline (RDKit, Mordred, Cobrapy, Scikit-learn) to improve accuracy of biomolecule identification.
- Developed **mathematical framework** and software (*Biopython, Pandas, Numpy, Scipy, Matplotlib, Seaborn, Jupyter*) to translate noisy enzyme-metal binding signals encoded into DNA into a binary time-series readout (# <u>IACS</u>).

B.S. Chemical & Biomolecular Engineering (Minors: Biomedical Engineering & German) | Ohio State University | 2015

• Research Assistant in Wood Lab (protein purification, cloning, molecular biology) (2014–2016)

SKILLS

Software Engineering & Scientific Background

- Scientific Computing: Python, C, Rust, Swift, bash, Jupyter, Streamlit, Click, Numpy, Scipy, Pandas, Matplotlib, Seaborn, HPC
- Web Development: Python, JavaScript, TypeScript, Requests, Flask, FastAPI, Node.js, Express.js, Vue, Svelte, Celery, RabbitMQ
- Data Engineering: SQL, PostgreSQL, MySQL, SQLAlchemy, MongoDB, Pymongo, RDS, Data Architecture, Query Optimization
- Testing, CI/CD, & Dev Tools: pytest, Ansible, GitHub Actions, git, lazygit, conda, uv, pip, gcc, cargo, AWS, boto3, Docker, WSL
- Domain Expertise: Bioinformatics, Cheminformatics, Molecular Biology, Statistical Modeling, DoE, Data Visualization
- Al & Machine Learning: Model development, RAG, Haystack, NLP, Prompt engineering, Scikit-learn

Communication

- Write clear, readable code, reports, and documentation (Sphinx, Scientific writing, Markdown, Regular expressions, My blog)
- Passion for ongoing collaboration with key stakeholders and developers (Agile, User Story Mapping, GitHub, Jira)
- Proponent of clear, kind, and empathetic correspondence & feedback across all modes of modern workplace communication

CERTIFICATIONS

AWS Solutions Architect – Associate | Amazon Web Services | 2025