

# Jonathan Strutz *Scientist & Software Engineer*

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purpose: “Accelerate discovery by empowering scientists with value-driven software” }

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## EXPERIENCE

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**Software Engineer, Systems** | McMaster-Carr | Elmhurst, IL | June 2025–Present

**Bioinformatics Software Engineer, AI & Computational Biology** | LanzaTech | Skokie, IL | 2024–2025

- 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% ( 📄 [Nature Biotechnology](#) ).
  - 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.
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## EDUCATION

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**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 “[Pickaxe](#)”, a **cheminformatics** python library (*RDKit*) to predict biochemical reactions ( 📄 [BMC Bioinformatics](#) ).
- 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 ( 📄 [JACS](#) ).

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

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## SKILLS

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### 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*
- **AI & 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](#)*)
  - Proponent of clear, kind, and **empathetic** correspondence & feedback across all modes of modern workplace communication
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## CERTIFICATIONS

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**AWS Solutions Architect – Associate** | Amazon Web Services | 2025