Josh Loecker

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PROFESSIONAL SUMMARY

Computational Biologist with expertise in software development, bioinformatics, metabolic modeling, and RNA-seq analysis. Skilled in building maintainable backend software, high-performance pipelines, deploying scalable HPC solutions, and leading cross-disciplinary teams. **Passionate about developing robust and maintainable software that is usable by individuals without computational expertise.**

TECHNICAL SKILLS

Software Design & Engineering: Python, R, Snakemake, SQL, Object Oriented Programming

Bioinformatics: Bulk & single-cell RNA-seq, metabolic modeling, multi-omics integration

Systems & Tools: Docker, Git, Linux administration, CI/CD, cloud & cluster computing

AI/ML: Large Language Models (LLMs), integration with computational modeling and biological data

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EXPERIENCE

Computational Biology PhD Candidate / Bioinformatics & Software Engineering, PhD in Progress

PI: Dr. Tomas Helikar; University of Nebraska-Lincoln August 2021–Est. May 2026

- **MechAInistic**: AI agents design and execute in-silico experiments on constraint-based metabolic models to identify potential therapeutic targets for drug discovery
  - **Integrates 30 custom-made tools** for LLM-based function calling
  - Retrieves information from PubMed Central for up-to-date biomedical information
  - Connects to any OpenAI-compatible backend
  - **Multi-LLM architecture** attempts to reduce hallucinations
  - Results are **rooted in the metabolic model's biological mechanisms**
  - *Code available upon request, manuscript in preparation*
- **COMO:** Constraint-based Optimization of Metabolic Objectives
  - Automated **reconstruction of constraint-based metabolic models**
  - Incorporates **multi-omics integration** of proteomics, bulk, and single-cell RNA-sequencing data
  - Reduced Docker **build time from 4 hours to 20 minutes**
  - Translated hundreds of lines of legacy R code to modern Python
  - Provides a Python-based API and Jupyter Notebook frontend
- **AutoRNAseq:** Automated alignment of bulk RNA-sequencing samples
  - Automatically **downloads any reference genome** from Ensembl
  - **Built-in quality control** analysis on a per-sample basis
  - Dual input support: NCBI GEO/SRA accession or local FastQ files
  - Dynamic deployment options allow for a local desktop or remote compute cluster execution
- **Single-cell Analysis**
  - In the process of reconstructing 4,000 constraint-based metabolic models based on donor-specific single-cell RNA-sequencing data containing 2 million cells
  - This project will identify the impact of age on metabolism
- **Other**
  - **Supervised a team of undergraduates** by assigning tasks, reviewing code, mentoring development, and deploying production systems
  - **Managed high-performance computing workflows** on a Linux-based supercomputing cluster.

Bioinformatics Technician

PI: Dr. Patrick Ewing; U.S. Department of Agriculture May 2020–May 2021

- **Built an advanced RNA-sequencing pipeline** using high-performance computing to reduce manual labor required in downstream data analysis
- **Built and deployed specialized soil sieves** for bacterial analysis of pre- and post-crop season using a variety of fertilizers, herbicides, and pesticides.

Lab Technician

PI: Dr. Surtaj Iram; South Dakota State University August 2018–May 2020

- **Created a graphical user interface** in Python to automate data analysis
- Performed **MTT cell-viability assays** to determine the drug efficacy of multidrug-resistant cell lines
- Performed **ELISA assay techniques** for accurate antibody detection

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EDUCATION

Doctoral Candidate of Biochemistry with Specialization in Bioinformatics

University of Nebraska-Lincoln, PhD in Progress, Expected August 2026

Bachelor of Science in Biochemistry, Minor in Computer Science

South Dakota State University, Cum laude, 2021

AWARDS & PRESENTATIONS

- Oral Presentation, Department of Biochemistry Department Retreat, Lincoln, NE	August 2025
- Oral Presentation, Society for Mathematical Biology, Edmonton, Canada	July 2025
- Poster Presentation, Systems Immunology, Cold Spring Harbor, NY	April 2025
- Oral Presentation, Molecular Mechanisms of Disease, Lincoln, NE	April 2023 & April 2024
- Poster Presentation, “Building an Immune Digital Twin”, Orsay, France	May 2023
- Molecular Mechanisms of Disease Award Recipient	January 2022–January 2024
- South Dakota State University Chemistry Club President	August 2019–May 2021
- East Family Undergraduate Summer Research Fellowship	Summer 2019 & Summer 2020
- BioSNTR Undergraduate Summer Research Fellowship	Summer 2018
- Herbert Hodgeson Scholarship in Chemistry	Spring 2018

PUBLICATIONS (*Authors contributed equally to this work)

- Bessell B*, **Loecker J***, Zhao Z, Aghamiri S, Mohanty S, Amin R, et al. COMO: A pipeline for multi-omics data integration in metabolic modeling and drug discovery. Brief Bioinform. 2023. 10.1093/bib/bbad387.
- **Loecker J,** Ewing P. Benefits of the Snakemake Workflow Management Software in Comparison to Traditional Programming. *Undergraduate Honors Independent Study*. 2021. https://openprairie.sdstate.edu/honors_isp/8.