Jonathan Amory Rodiger

(978) 809-9233 | jonathanrodiger@gmail.com | Boston, MA
linkedin.com/in/jonathan-rodiger-4769a715b

Senior Bioinformatics Engineer with 7+ years' experience driving efficiency through bioinformatics software development, data analysis, and workflow optimization. Expertise includes full-stack web development, cloud platforms, relational database management, and agentic tools using large language models.

Skills

Programming Languages: Python, R, JavaScript, HTML, CSS
Frameworks & Libraries: Nextflow, Django, Flask, Plotly, Selenium, Bootstrap, Pandas
LLMs & Frameworks: OpenAI, Gemini, Claude, Ollama, Perplexity, LangChain, Retrieval Augmented Generation
DevOps: GitHub Actions, AWS CodePipeline + CodeBuild, Docker, Git
Databases & Cloud: PostgreSQL, pgvector, MySQL, AWS, GCP, HPC, SLURM
Bioinformatics Tools: JBrowse, Cytoscape, SIRIUS, AlphaFold, ESMFold, BLAST, GATK

Industry Knowledge
- NGS bioinformatics pipeline design and optimization
- Full stack web development and cloud infrastructure management
- Relational database modeling, administration, and performance tuning
- Agentic tool development with LLMs for advanced data applications

Open Source Contributions
- Developed SNP CRISPR, a SNP-targeted CRISPR design pipeline
- Previous lead developer of the Brain Arts Organization website
- Contributed bug fixes and updates to documentation for the React Native framework

Work Experience

Senior Bioinformatics Engineer II   September 2024 - April 2025
LifeMine Therapeutics, Cambridge MA
- Designed and implemented a mass spectrometry database schema, utilizing vector embeddings to represent spectral data and leveraging pgvector for spectral similarity searches
- Developed agentic web tools using LangChain, integrating multiple LLMs for advanced data aggregation, AI-driven interactive Plotly figure generation, and natural language database querying
- Led migration of bioinformatics pipelines (DNA-Seq, RNA-Seq) to Seqera Platform, optimizing performance and significantly reducing operational costs through strategic resource management

Senior Bioinformatics Engineer I   August 2022 - September 2024
LifeMine Therapeutics, Cambridge MA
- Developed and integrated dynamic LC-MS/RNA-Seq correlation analyses into a bioinformatics web platform, enhancing data accessibility and enabling interactive visualization
- Optimized database architecture and query performance by implementing a new schema based on non-redundant protein sequences, reducing data volume by over 50%
- Designed and implemented advanced user interfaces for internal data curation workflows, resulting in a 3x increase in platform usage

Bioinformatics Engineer II   April 2021 - August 2022
LifeMine Therapeutics, Cambridge MA
- Built a web portal providing user-friendly access to internal databases and enabling execution of advanced bioinformatics tools (e.g., AlphaFold, comparative genomics heatmaps)
- Implemented JBrowse as a cost-effective, open-source genome browser for internal genomic data, eliminating costly licensing fees associated with the prior system

Bioinformatics Software Developer   August 2018 - April 2021
Harvard Medical School - DRSC/Perrimon Lab, Boston MA
- Developed and maintained various online bioinformatics tools for CRISPR sgRNA design, transcription factor prediction, laboratory information management systems (LIMS) among others
- Performed variant calling on WGRS data using the Broad's GATK best practices workflow
- Bulk RNA-Seq QC and data analysis using a shared high performance computing cluster
- Experience with pipeline design and optimized existing pipelines through parallelization
- Full stack web development and relational database management

Graduate Teaching Assistant   January 2018 – May 2018
Boston University College of Engineering, Boston MA
- Teaching Assistant for BF527 Applications in Bioinformatics
- Assisted students with programming/analysis assignments on topics including: Linux/Unix, Python, Dynamic Programming, BLAST, RNA-Seq Analysis, Machine Learning, and more
- Held office hours, and graded homework/labs of students

Software Developer   June 2017 – August 2017
Mentorleaf.com, Carlisle PA
- Helped develop a matching algorithm to pair users with mentors based on interest metadata
- Developed front and back-end software services using JavaScript, Node.js, MongoDB, HTML, and CSS
- Leveraged Github workflow for team coordination and software delivery to cloud based platform
- Schema creation and analysis using Mongoose and Robo 3T

Education

Dickinson College, Carlisle, PA   Graduated May 2017
Bachelor of Science, Computer Science, Concentration in Biology
Honors: Founders Scholar 2013-2017 (merit scholarship)

Publications

REPTOR and CREBRF encode key regulators of muscle energy metabolism
Nature Communications - Aug 15, 2023
https://www.nature.com/articles/s41467-023-40595-1

Next-generation large-scale binary protein interaction network for Drosophila melanogaster
Nature Communications - Apr 15, 2023
https://www.nature.com/articles/s41467-023-37876-0

Paralog Explorer: A resource for mining information about paralogs in common research organisms
Computational and Structural Biotechnology Journal - Nov 24, 2022
https://www.sciencedirect.com/science/article/pii/S2001037022005359

SNP-CRISPR: A Web Tool for SNP-Specific Genome Editing
G3 - Feb 1, 2020
https://academic.oup.com/g3journal/article/10/2/489/6026318

Pooled CRISPR Screens in Drosophila Cells
Current Protocols in Molecular Biology - Nov 6, 2019
https://currentprotocols.onlinelibrary.wiley.com/doi/10.1002/cpmb.111

Full list:
https://scholar.google.com/citations?user=tBd4t0gAAAAJ