

# Alexander Larsen

Bioinformatics • Deep Learning • Software Engineering

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## SKILLS

### Managerial & Communication Skills

- **Managerial experience** of a Bioinformatics team: employee reviews, project tracking
- Clinician consultations, patient customer service, public speaking
- SOP & publication writing, grant writing, creation of publication visuals

### Software Engineering & Development

- Principles: Code review, **git** versioning, project management tools (Trello, **Jira**).
- Pipeline development & module creation: **Python**, Perl, AWS, **SQL**, command-line/**BASH**.
- Web Development: HTML, CSS, Javascript.
- Workflow management: **Docker**, **Nextflow**.

### Bioinformatics & Biophysical Modeling

- **NGS** protocols: optimization, data analysis, library preparation (**Illumina** NextSeq)
- Tools & Software: Bowtie2, BWA, **BLAST command line**, GATK, Samtools, Annovar, Picard, usearch, CD-HIT, FastQC, ClinVar, Kraken2, CLARK, MetaPhlan2, Pathoscope2, **NCBI Utilities**, R programming
- Algorithms: Vienna, Nupack, MSA, Hidden Markov Models, Smith-Waterman/Needleman-Wunsch, UPGMA, Nearest Neighbor agglomerative, DeBruijn

### Machine Learning & Data Science

- Deep Learning: Neural Networks, MLP, ConvNN, LSTM, VAE, Transformers, DNA/RNA LLMs,
- Machine Learning: Kmeans++, **Linear Regression / Logistic regression, regularization**, Classification, Random forests, Boosting, Bagging, Ensembling, SVM, KNN, A\*
- Statistical methods: Regression, **PCoA/PCA**, alpha/beta diversity analysis, **DeSEQ2**.
- Python Libraries: **PyTorch**, **numpy**, **pandas**, **matplotlib**, seaborn, biopython, primer3-py, **sklearn**, scipy, sqlalchemy, multiprocessing

### Laboratory Techniques & Protocols

- DNA/RNA/Protein extraction, Western Blotting, FISH, SDS-Page Electrophoresis, Mass Spectrometry, Neuronal electrophysiology, PCR

### High-Performance Computing (HPC)

- Defining environments, nodes, **Linux**, operating systems, user groups, job scheduling (SLURM), and resource management

## EXPERIENCE

### Deep Learning Doktorant

Roche - Helmholtz Zentrum Munich

Projects

- Project: Generative Modeling for **RNA therapeutics**. Focus on predicting siRNA efficacy with engineered features as well as chemically modified sequences and foundation model embeddings of contextual sequences in various **deep learning models** - ResNet, AttentionPooling, LSTMs, VAEs and extracting features of interest with integrated gradient saliency maps for **model explainability**.
- Curated the largest known dataset of publicly available chemically modified siRNAs for mRNA Knockdown..
- Benchmarking Datasets and simple models - XGBoost, RF, Lasso/Ridge linear regression, **Patent PaddleOCR Data** extraction, Generative design of modified siRNA. Genetic algorithms, beamsearch.

July 2024 – Current

Basel - Munich, DE

### Bioinformatics Scientist I

Sherlock Biosciences Inc.

Projects

- Manager of Bioinformatics Division at Sherlock Biosciences worked closely with multiple experimental and theoretical teams to develop and deploy new models and platforms
- Analysis and writing to support grant applications for MIT/Harvard's BROAD, B&M Gates Foundation, Agricultural firms, and US Department of Defence contracts towards creating FDA-cleared diagnostics

Nov 2020 – Nov 2023

Boston, MA

- Developed and maintained entire company bioinformatics pipelines using Python, Perl, SQL, bash, docker, and Vienna optimizing RNA structure, CRISPR predictive performance, LAMP constraints, Automatic dataset retrieval and Quality Control filtration, Single displacement Amplification ROI identification across four different amplification/readout chemistries.
- Achieved 99%+ reduction in genomic feature space for all company amplification technologies across Sense SDA, Cap SDA, LAMP, and **CRISPR** spaces reducing clinical diagnostic failure post-deployment.
- Identified novel thermostable **CRISPR-Cas proteins** for publication, patent, and LAMP + Cas diagnostic.
- Created software for **high specificity, inclusivity/LOD**, and thermodynamically stable guide targets tool. New package modules typically relied on novel algorithmic creation requiring optimization, multiprocessing, database curation, and external tool API wrappers.

### **Clinical Bioinformatician I, II**

*Aperionics Inc.*

**June 2018 – Nov 2020**

*Sterling, VA*

#### *Projects*

- Designed automated COVID-19 report end-to-end software. Analysis, formatting, clinical sign-off,
- Developed metagenomic analysis library that automatically queries patient data for report statistics formatting. Accomplished using Python, bash, SQL, CSS/HTML, git, Django, Docker, AWS CLI.
- Presented on bioinformatics clinical value to investors, posters, and at other local events.

### **Associate Research Assistant**

*University of Wisconsin Madison*

**Apr 2013 – May 2016**

*Madison, WI*

- Characterizing circadian rhythm genes and their temporal effect on long-term memory formation in drosophila. Particular effort towards the quality control of data and samples. – Professor Jerry Yin / Robin Fropf
- Characterizing zebrafish embryonic development, crayfish nerve reading frequencies, and rat hippocampal electrical activity. – Professor Tony Stretton

## **EDUCATION / CERTIFICATIONS**

### **Computational Biology PhD**

*Helmholtz / TUM*

**July 2024 – Current**

*Munich, DE*

- Generative Modeling for RNA therapeutics. Traditional Models vs Deep-Learning Foundation models

### **Bioinformatics M.S.**

*University of Maryland, Adelphi*

**Mar 2019 – Nov 2021**

*Adelphi, MD*

- Alignment, Statistical Analysis, SQL Databases, and Protein Structure. Biotechnology and Biomanufacturing.

### **Bioinformatics**

*Audited – UW Madison / MIT Open Courseware*

**June 2017 – Apr 2018**

*De Pere, WI*

- Graduate studies following UW Madison outlines for a master's in bioinformatics.
- Bioinformatic algorithms I/II, general algorithms/data structures, artificial intelligence.

### **Neurobiology B.S.**

*University of Wisconsin Madison*

**Sept 2012 – May 2016**

*Madison, WI*

- Graduated from a selective honors biology program which facilitated group-directed research, scientific writing, and analysis. – UW Madison Biocore program.

### **edX Courseware Certificates**

*MIT / UC Berkley / University of Maryland*

**May 2018 – Current**

*Various, US*

- BIF001x: DNA Sequences
- BIF002x: Proteins: Alignment, Analysis and Structure
- BIF003x: Statistical Analysis in Bioinformatics
- Bioinformatics MicroMasters Certificate
- Foundations of Data Science: Computational Thinking with Python
- MITx: 6.431x - Probability and Uncertainty
- MITx: 18.6501x - Fundamental of Statistics

## PUBLICATIONS

### *Published / In Progress*

- Larsen, A., Butnaru, D., Rotrattanadumrong, R., Yonchev, D., Gagneur, J., & Marsico, A. (2026). FENNEC: Fine-Tuned Ensemble Neural Networks Accelerate Chemically Modified siRNA Design and Screening. Manuscript in preparation, Institute of Computational Biology, Helmholtz Zentrum München; Roche Innovation Center Basel; TUM School of Computation, Information and Technology, Technical University of Munich.
- Baugher, D., Larsen, A., Chen, Y., & others. (2021). Female Urinary Microbiome Analysis and Artificial Intelligence Enhances the Infectious Diagnostic Yield in Precision Medicine. *Microbiol Infect Dis*, 5(4), 1–8.
- Larsen, A., Icenhour, C., Crandall, K., Valencia, C. A., & Chen, Y. (2020). Increased Virulent Microorganism Associations in the Urinary Microbiome of Interstitial Cystitis Patients. George Washington University.
- Larsen, A. W., Chen, Y., Crandall, K. A., Icenhour, C. R., & Valencia, A. C. (2022). Characterization of the Interstitial Cystitis/Bladder Pain Syndrome Microbiome in Clinically Diagnosed Patients. *Clinical Immunology & Research*, 6(1), 1–9.
- Pena JM, Manning BJ, Li X, Fiore ES, Carlson L, Shytle K, Nguyen PP, Azmi I, Larsen A, Wilson MK, Singh S, DeMeo MC, Ramesh P, Boisvert H, Blake WJ. Real-Time, Multiplexed SHERLOCK for in Vitro Diagnostics. *J Mol Diagn*. 2023 Jul;25(7):428-437. doi: 10.1016/j.jmoldx.2023.03.009.
- Phillips, E; Silverman, A; Liu, M; Brown, C; Carlson, P; Coticchia, C; Shytle, K; Larsen, A; Goyal, N; Cai, V; Huang, J; Hickey, J; Ryan, E; Acheampong, J; Ramesh, P; Collins, J; Blake, W . Detection of viral RNAs at ambient temperature via reporter proteins produced through the target-splinted ligation of DNA probes. *Nat. Biomed. Eng* (2023). <https://doi.org/10.1038/s41551-023-01028-y>.