

# Alexander Larsen

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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, creation of publication visuals.

### **Software Engineering & Development**

- Principles: Code review, **git** versioning, project management tools (Trello, **Jira**).
- Pipeline development & module creation: **Python**, Perl, C++, 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.

### **Statistical & Data Analysis**

- Machine Learning: Kmeans++, **Linear Regression / Logistic regression** (L1/L2), Classification, Random forests, Boosting, Bagging, Ensembling, SVM, KNN, A\*.
- Statistical methods: Bayesian analysis, Regression, **PCoA/PCA**, alpha/beta diversity analysis, **DeSEQ2**.
- Python Libraries: **numpy**, **pandas**, **matplotlib**, seaborn, biopython, primer3-py, **sklearn**, scipy, sqlalchemy.

### **Laboratory Techniques & Protocols**

- DNA/RNA 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

### **Bioinformatics Scientist I**

*Sherlock Biosciences Inc.*

**Nov 2020 – Current**

*Boston, MA*

#### *Projects*

- Primary developer on company bioinformatics pipelines optimizing RNA structure, CRISPR predictive performance, LAMP constraints, SDA ROI identification across two different chemistries.
- Achieved 99%+ reduction in genomic feature space for all company amplification technologies across Sense SDA, Cap SDA, LAMR 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.

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

*Aperiomics 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****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***University of Maryland / UC Berkley***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

**PUBLICATIONS***Published*

- 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>.