Alexander Larsen
Bioinformatics Scientist

PHONE	(920) 246-8971
E-MAIL	Alarsen525@gmail.com
GITHUB	www.github.com/Zinthrow
LINKEDIN	linkedin.com/in/a-w-larsen

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, 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/Needlman-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. multiprocessing

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   **Nov 2020 – Current**
Sherlock Biosciences Inc.   *Boston, MA*
   Projects
- Manager of Bioinformatics Division at Sherlock Biosciences worked closely 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
- 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　　　　　　　　　　　　　　　　　　**June 2018 – Nov 2020**
Aperiomics Inc.　　　　　　　　　　　　　　　　　　　　　　　　　　　　　*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　　　　　　　　　　　　　　　　　　　　**Apr 2013 – May 2016**
University of Wisconsin Madison　　　　　　　　　　　　　　　　　　　　　*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.　　　　　　　　　　　　　　　　　　　　　　　　**Mar 2019 – Nov 2021**
University of Maryland, Adelphi　　　　　　　　　　　　　　　　　　　　　*Adelphi, MD*
- Alignment, Statistical Analysis, SQL Databases and Protein Structure. Biotechnology and Biomanufacturing.

Bioinformatics　　　　　　　　　　　　　　　　　　　　　　　　　**June 2017 – Apr 2018**
Audited – UW Madison / MIT Open Courseware　　　　　　　　　　　　　　　　*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.　　　　　　　　　　　　　　　　　　　　　　　　**Sept 2012 – May 2016**
University of Wisconsin Madison　　　　　　　　　　　　　　　　　　　　　*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　　　　　　　　　　　　　　　　　　　　　**May 2018 – Current**
University of Maryland / UC Berkley　　　　　　　　　　　　　　　　　　　　*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.