ETHAN OKSEN

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Professional Experience

Washington, DC	fermPlot	Oct 2023 – Present

Founder

- Founded and currently operate fermPlot, a company developing a bioprocess platform for data processing and visualization.
- Built the fermPlot web application, which enables users to upload, visualize, and analyze bioprocess data, with a focus on flexibility and user experience. **Live Demo**: app.fermplot.com. **Technology**: Python, Dash, Plotly, Pandas, NumPy, JavaScript, Docker, Gunicorn, AWS EC2, Nginx, PostgreSQL, Git, pytest, and Locust.
- Implemented a CSV parser to handle data uploads, with an option for manual or automatic data grouping and labeling.
- Built an interactive plotting feature allowing users to select datasets and plot data across up to four axes.
- Developed feature to convert common CSV formats to normalized tables in PostgreSQL.
- Orchestrated application server deployment using GitHub Actions, Terraform, Ansible, and Docker.

Emeryville, CA	Lawrence Berkeley National Laboratory – Advanced Biofuels and Bioproducts Process Development Unit (ABPDU)	Aug 2017 – Oct 2021

Senior Research Associate / Bioprocess Engineer   *Jan 2020 – Oct 2021*

- Worked on over 30 industry partner projects, ranging from early-stage start-ups to large multinational companies, to develop and/or demonstrate fermentation and downstream processes.
- Later in my role, I became the primary point of contact for experiments — interfacing directly with scientists and engineers from industry partners and delegating tasks to team members.
- Held significant project management responsibility — working directly with companies to understand their goals, facilitating technology transfer, and developing statements of work.
- Created standard operating procedures for data export, parsing, and visualization.

Research Associate / Associate Bioprocess Engineer   *Nov 2018 – Jan 2020*

- Developed and demonstrated fermentation processes for industry and Department of Energy (DOE) programs.
- Used models to estimate the fuel properties of potential target molecules for genetic engineering projects to identify promising biofuel candidates. Included on a patent application for production of cyclopropane molecules.

Intern / Student Research Asst.   *Aug 2017 – Sep 2018*

Education

Baltimore, MD	Johns Hopkins University	Aug 2020 – Aug 2022

- M.S., Biotechnology, Concentration in Bioinformatics, GPA: 3.94
- Relevant Coursework: Advanced Genomics and Genetics Analyses, Gene Expression Data Analysis and Visualization, Bioinformatics: Tools for Genome Analysis, Next Generation DNA Sequencing and Analysis, and Bioassay Development.

Berkeley, CA	University of California, Berkeley, Extension	Jan 2019 – Feb 2020

- Advanced Biosciences Certificate, GPA: 4.0
- Relevant Coursework: Biochemistry, Cell Biology, and Biostatistics.

Berkeley, CA	University of California, Berkeley	Aug 2009 – Jun 2013

- B.A., Philosophy, GPA: 3.60

Projects

- **SRA Alignment Pipeline** (2023). Nextflow pipeline for downloading SRA FASTQs, performing quality control, aligning reads to reference sequences, and calling variants. This project is available at: github.com/eoksen/sra_alignment_pipeline. Technologies: Nextflow, Python, Bash, R, Docker.

Journal Articles, Inventions, and Conference Presentations

- **Full list**: ethanoksen.com/publications

Skills

Software and Technologies

- Programming Languages and Scripting: Python, R, JavaScript, Bash
- Data Analysis and Processing: Python — Pandas, NumPy, SciPy; R — dplyr, tidyr, base R
- Dashboards, Visualization, and Notebooks: Dash/Plotly, R Shiny, Matplotlib/Seaborn, ggplot2, Jupyter Notebook
- Containerization and Version Control: Docker, Git, GitHub
- Database Management: PostgreSQL, MySQL, SQLite
- Cloud Services and Application/Server Orchestration: AWS (EC2, S3, ECR), Terraform, Ansible, Nginx, Gunicorn
- Operating Systems and Environment: Linux (Debian), macOS, Windows

Bioinformatics

- Workflow Management: Nextflow
- Guide RNA Design: Benchling, CHOPCHOP
- Cloning, Primer Design, and Codon Optimization: Benchling
- Bioinformatics Libraries for R and Python: Bioconductor, BioPython
- Genome Alignment and Assembly: bbmap, Bowtie2, BWA, HISAT2, SPAdes
- RNA-seq Analysis: Cufflinks, DESeq2, HISAT2, HTSeq, TopHat
- Pre-Processing and Quality Control: FastQC, fastp, MultiQC, Trimmomatic
- Data Handling and File Conversion: bcftools, bedtools, samtools
- Variant Calling and Genotyping Tools: FreeBayes, Delly
- Variant Annotation Tools: Annovar, SnpEff, SnpSift

Laboratory

- Laboratory Information Systems: LabKey, Benchling
- Molecular Biology: DNA/RNA extraction and purification; PCR, qPCR; Illumina NGS; cloning workflows; Protein expression and purification; Flow Cytometry and cell sorting
- Lab Automation: Hamilton/Eppendorf liquid handlers, Sartorius AMBR 250 and Biolector for high throughput screening
- Data Collection and Integration: LabView
- Analytical Instrumentation: GC-MS, LC-MS/RI/UV, UV-Vis spectrometers