Victor Chen

https://github.com/VictorGChen

(925) 899-5519 — victor.g.chen@gmail.com

www.linkedin.com/in/victor-chen-bioinformatics

Bioinformatics Developer with experience developing diagnostic and an expertise in building production diagnostic algorithms and data platforms. Skilled in Python backend development, Python visualization tools, and translating complex biological data into scalable software solutions.

Experience

Stanford University, Snyder Lab – Research Assistant
Oct 2025 – Present

Research Assistant contributing to beneficial exposome research, analyzing cytokine responses to environmental and lifestyle exposures.

- Developing Python-based trajectory analysis pipeline for cytokine data using PCA, principal curves, and pseudotime modeling to identify time- and dose-sensitive response patterns across treatment concentrations.
- Implementing unsupervised clustering and dimensionality reduction algorithms (PCA, UMAP) with scikit-learn to track continuous cytokine trajectories, replacing inappropriate discrete clustering methods.
- Engineering data preprocessing workflows using pandas for multi-dimensional cytokine datasets with 45+ biomarkers, enabling robust statistical analysis of dose-dependent immune responses.

Kelliop Inc. – Bioinformatics Developer
Jul 2021 – Present

Bioinformatics Developer contributing to in vitro diagnostic platforms for neonatal care, pharmacogenomics, and oncology using lab-on-chip technologies and advanced sequencing pipelines.

- Developed DNA analysis algorithms using bioinformatics protocols for 2 neonatal ICU and 1 endometrial cancer diagnostic applications; improved multiplexing accuracy by 15%. All three applications entering clinical trial with promising results.
- Represented company at four ADLM conferences; led product demos and technical discussions with 40+ clinicians and stakeholders.
- Delivered technical demonstrations of DNA sequencing workflows for Lab-On-Chip IVD devices, enhancing clinical adoption of diagnostic tools.

Education

University of California, Santa Cruz

B.S. in Biomolecular Engineering and Bioinformatics – Bioinformatics Concentration, Minor in Computer Science

Projects

Interactive Cytokine Trajectory Analysis Dashboard – Full-Stack Bioinformatics Platform

- Built production-quality platform combining Python backend (Flask, pandas, scikit-learn, statsmodels) with JavaScript for cytokine research.
- Performs bioinformatics analysis for dimensionality reduction (PCA, UMAP), statistical testing, and trajectory modeling endpoints.
- Implemented ComBat batch correction pipeline reducing technical variation by 70-90% across multi-study datasets, enabling valid cross-study comparisons.

Allergen Detection ML Pipeline

- Developed allergen detection pipeline using Random Forest Regression to model serum IgE levels from NHANES and ImmPort datasets.
- Implemented comprehensive data engineering workflows to integrate and clean multi-source clinical datasets; analyzed feature impact using SHAP.
- Built classifiers to identify allergenic genes/proteins using genomic data and Bayesian models.

Encrypted Data Structures for Secure Search

- Collaborated with team through Git/GitHub to implement oblivious RAM protocols (Path ORAM and rORAM) in C++ for secure storage systems.
- Benchmarked I/O performance across database sizes (2^{14}–2^{16} blocks); reduced range query overhead by 300×.

Certifications

AWS Cloud Certified Practitioner
Amazon Web Services
Oct 2025

Skills

Programming & Development: Python, JavaScript (ES6+, D3.js), C/C++, SQL, Java, Bash, Git/GitHub, Linux/Unix
Machine Learning & Statistics: PyTorch, Scikit-learn, Pandas, NumPy, Bayesian Statistics, Dimensionality Reduction (PCA, UMAP, t-SNE), Statistical Testing (Mann-Whitney, Kruskal-Wallis, FDR correction)
Bioinformatics: Genomics, Sequence Analysis, UCSC Genome Browser, BLAST, GTEx, Batch Effect Correction (ComBat), Trajectory Analysis, Pseudotime Modeling
Data Engineering: Data pipeline development, Multi-study integration, Data normalization, Performance optimization
Professional: Technical Documentation, Cross-functional Collaboration, English (Fluent), Mandarin Chinese (Fluent)