

Gino Prasad

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Cancer Genomics | Machine Learning | Bioinformatics | Computer Vision | Data Science

Education

PhD, Computer Science (Bioinformatics): UC San Diego

Summer 2023 - Spring 2027

Academic Advisor: [Vineet Bafna](#), Professor of Computer Science, Bioinformatics and Systems Biology

GPA 4.0/4.0

- **Focus:** Applied Machine Learning for Cancer Genomics
- **Relevant Courses:** Generative AI modeling, Deep Learning, Population Genomics, Bioinformatics Algorithms, Recommender Systems

Bachelor of Science, Bioinformatics and Computer Science: UC San Diego

Fall 2020 - Spring 2023

Major: Bioinformatics (B.S.), Minor: Computer Science

GPA 3.97/4.0

- **Relevant Courses:** Machine Learning, Molecular Sequence Analysis, Probability & Statistics, Linear Algebra, Data Structures, Algorithms

Experience

Cancer Genomics / Machine Learning Researcher

Jun 2022 - Current

UC San Diego Bafna Lab

- Developed **Computer Vision** Models for FISH (Fluorescence in Situ Hybridization) Spatial Transcriptomics Data.
- Predicts **tumor amplification status** (ecDNA/HSR) in Cancer Cell Lines and Patient Tissue Images.
- **Technical Skills:** Tensorflow, OpenCV, Numpy, Pandas, Python, Linux, Git.
- Web development for [AmpliconRepository](#), a Public Web Database of Oncogene Amplifications using NGS data.
- **Technical Skills:** Cloud Computing, Statistical Analysis, Database querying using MongoDB and Python's SQLite3.

Machine Learning Research Assistant

Jun 2022 - Jun 2023

UC San Diego School of Medicine

- Co-developed Bento, a seqFISH toolkit for **cell type** identification and **gene regulatory analysis**.
- Built a **Convolutional Neural Network** for Spatial Transcriptomics Image data, to perform **nuclear segmentation**.
- Used a **U-Net Architecture** to predict nuclei boundaries, bypassing the need for DAPI staining.
- **Technical Skills:** TensorFlow, Keras, NumPy, Pandas, PyTorch, PyLab, Python, Linux, Git.

Computational Bioinformatics Research Assistant

Oct 2021 - Jun 2022

UC San Diego Yeo Lab

- Developed computational applications for **long-read Oxford Nanopore Sequencing Data** analysis.
- Created an Error Correction Pipeline for **RNA-seq Analysis** using the [Nanorevisor Deep Learning](#) Library.
- **Technical Skills:** Python, Bash, STAR, Minimap2, Samtools, Linux, Pandas.

Software Engineering Intern

Jun 2021 - Aug 2021

Dotdash

- Designed front-end software for Dotdash, the largest digital publisher in the US, managing sites like Investopedia and Verywell Health.
- Developed cross-platform web applications in a collaborative environment using Agile/Scrum.
- **Technical Skills:** JavaScript, Vue, HTML, SASS, Maven, Database Querying, APIs.

Phage Genomics Research Initiative

Oct 2020 - Jun 2021

UC San Diego Pogliano Lab

- Created a [BLAST parser website](#) using Google App Engine and Python ([GitHub](#)), used by the UCSD professor and class.
- Queries the NCBI BLAST data to perform comparative genomic analysis of Bacteriophage genes with unknown functions.
- **Technical Skills:** Flask, Python, HTML, Google Cloud App Engine.

Journal Publications

Luebeck et al. (2024), AmpliconSuite: Analyzing focal amplifications in cancer genomes.

Cancer Genetics, <https://doi.org/10.1016/j.cancergen.2024.08.015>

Mah et al. (2024), Bento: A toolkit for subcellular analysis of spatial transcriptomics data.

Genome Biology, <https://doi.org/10.1186/s13059-024-03217-7>

Chapman et al. (2023), Circular extrachromosomal DNA promotes inter- and intratumoral heterogeneity in high-risk medulloblastoma.

Nature Genetics, <https://doi.org/10.1038/s41588-023-01551-3>

Prichard et al. (2023), Identifying the core genome of the nucleus-forming bacteriophage family and characterization of Erwinia phage RAY.

Cell Reports, <https://doi.org/10.1016/j.celrep.2023.112432>

Dehkordi et al. (2023), OM2BFB: Detecting and elucidating Breakage Fusion Bridge structures in cancer genomes using Optical Mapping data.
bioRxiv, <https://doi.org/10.1101/2023.12.12.571349>

Lv et al., Spatial-Temporal Diversity of Extrachromosomal DNA Shapes Urothelial Carcinoma Evolution and Tumor-Immune Microenvironment.
Submitted to *Cancer Discovery*

Rajkumar, Prasad et al., Accurate Prediction of ecDNA in Interphase Cancer Cells using Deep Neural Networks.
In Preparation (Co-First Author Publication)

Skills

Programming	Python (PyTorch, TensorFlow, Keras, Pandas, NumPy), R, MATLAB, C++, Cloud Computing, Bash, Linux, Git, Java, SQL.
Machine Learning	Experience With Transformer Architectures , Convolutional Neural Networks , and ResNet Autoencoders .
Web Development	Developed applications with MongoDB, Django, Flask, Vue, and Google Cloud App Engine (GCP).

Mentoring

2023 - 2024	Data Science Capstone Mentor , Mentored 3 Data Science undergrads in a Computer Vision capstone competition to semantically segment cell imaging data using deep learning.	<i>UC San Diego</i>
2023 - 2024	Early Research Scholars Program Mentor , Mentored 2 Computer Science undergrads in a project to extract mutational signatures from The Cancer Genome Atlas (TCGA) genome sequencing data.	<i>UC San Diego</i>

Achievements

Oct 2024	Cancer Grand Challenge eDynamic Symposium , Presented a Computer Vision Model for Cancer Imaging	<i>Cancer Grand Challenge (NCI)</i>
Oct 2024	Cancer Grand Challenge Future Leaders Speaker , Presented on AI applications in Cancer Research	<i>Cancer Grand Challenge (NCI)</i>
June 2023	Summa Cum Laude Honors , Awarded for Exceptional GPA.	<i>UC San Diego</i>
April 2023	Undergraduate Research Conference , Presented on Computer Vision methods for FISH Imaging.	<i>UC San Diego</i>

Personal Projects

Autotune Implementation Using Phase Vocoder

 github.com/GinoP123/AutotunePV.git

May 2023

- Created an autotuner from scratch using Phase Vocoder and Yin pitch prediction.
- Able to autotune any audio clip to a specific major or minor scale using Hann window functions.
- Examples of popular songs autotuned [here](#).

Custom Search Engine for Linux File System

 github.com/GinoP123/FileSearch

Jul 2022

- Created a keyword-matching search engine with caching fully from scratch using dynamic programming.
- Added learning capability by including popularity and relevance weights.
- I personally use this tool all the time, and find it a huge time-saver for navigating in Linux.