Olivia Martinez

Bioinformatics Scientist

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- *Computational biologist with 5+ years of experience developing machine learning algorithms for genomic data analysis and drug discovery applications*
- *Expert in processing multi-omics datasets (RNA-seq, ChIP-seq, proteomics) with proficiency in Python, R, and high-performance computing environments*
- *Published researcher with 8 peer-reviewed publications in computational genomics and 450+ total citations*
- *Proven track record of translating complex biological questions into scalable computational solutions, reducing analysis time by up to 75%*
- *Strong collaborator bridging wet lab researchers and computational teams across pharmaceutical and academic settings*

EDUCATION

University of California, San Francisco

August 2019

Ph.D. in Bioinformatics and Computational Biology

Dissertation: "Deep Learning Approaches for Predicting Drug-Target Interactions in Cancer Therapeutics"
GPA: 3.9/4.0
Relevant Coursework: Machine Learning for Biological Data, Statistical Genomics, Structural Bioinformatics, Systems Biology, Advanced Algorithms

Stanford University

May 2014

Bachelor of Science in Molecular Biology

Minor: Computer Science
GPA: 3.7/4.0
Relevant Coursework: Genetics, Biochemistry, Data Structures, Database Systems, Biostatistics

TECHNICAL SKILLS

Programming & Scripting:
• Python: BioPython for sequence analysis, pandas/NumPy for large-scale genomic data manipulation, scikit-learn for machine learning
• R: Bioconductor packages for differential expression analysis, ggplot2 for publication-quality visualizations, DESeq2/edgeR for RNA-seq
• Bash: Pipeline automation for NGS data processing workflows, cluster job management
• SQL: Complex queries for biological databases, data warehouse optimization

Bioinformatics Tools & Platforms:
• Next-generation sequencing: GATK for variant calling, STAR/HISAT2 for alignment, Salmon for quantification
• Workflow management: Nextflow, Snakemake, Galaxy for reproducible pipeline development
• Cloud computing: AWS for genomics workflows, Docker containerization, Kubernetes orchestration
• Databases: NCBI, Ensembl, UniProt, TCGA, GTEx, STRING

Biological Expertise:
• Multi-omics data integration (genomics, transcriptomics, proteomics, metabolomics)
• Cancer genomics: Somatic mutation analysis, tumor heterogeneity, biomarker discovery
• Pharmacogenomics: Drug-target interaction prediction, ADMET modeling
• Molecular biology: Gene regulation, protein structure-function relationships, pathway analysis

PROFESSIONAL EXPERIENCE

Genentech

September 2021 - Present

Senior Bioinformatics Scientist

• Developed machine learning pipeline for predicting immunotherapy response using multi-modal patient data, improving

prediction accuracy by 35% over existing methods
• Led analysis of 500+ patient tumor samples using single-cell RNA-seq, identifying novel T-cell exhaustion signatures that informed 3 clinical trial designs
• Built automated quality control system for genomic data processing, reducing manual review time from 40 hours to 2 hours per study
• Collaborated with 8 cross-functional teams to integrate computational findings into drug development decisions, contributing to 2 IND applications
• Mentored 3 junior bioinformaticians and established best practices for reproducible research workflows

Broad Institute of MIT and Harvard

June 2019 - August 2021

Bioinformatics Analyst

• Analyzed whole-genome sequencing data from 2,000+ rare disease patients using GATK pipeline, identifying causal variants in 45% of cases
• Developed R Shiny application for interactive variant interpretation, enabling clinical geneticists to review cases 60% faster
• Implemented parallelized variant calling workflow using Cromwell/WDL, reducing processing time from 72 hours to 8 hours per sample
• Contributed to Cancer Genome Atlas (TCGA) pan-cancer analysis, processing 10TB+ of multi-omics data across 33 cancer types
• Published 4 first-author papers on computational methods for rare variant interpretation

UCSF Computational Biology Lab

September 2014 - May 2019

Graduate Research Assistant

• Designed deep learning architecture for drug-target interaction prediction, achieving 0.92 AUC on independent test sets
• Integrated chemical structure data with protein sequence features using graph neural networks, improving binding affinity predictions by 28%
• Analyzed RNA-seq data from 300+ cancer cell lines treated with experimental compounds, identifying synergistic drug combinations
• Created automated pipeline for processing ChIP-seq data, standardizing analysis across 15+ collaborative projects
• Presented research findings at 6 international conferences, winning 2 best poster awards

PUBLICATIONS

Graph Neural Networks for Predicting Drug-Target Interactions in Oncology Applications

2023

Nature Biotechnology

Martinez, O., Chen, L., Rodriguez, M., et al. (2023). *Nature Biotechnology*, 41(8), 1123-1135.
[Contributed: Designed GNN architecture, performed computational validation]

Single-Cell Analysis Reveals Novel Immune Escape Mechanisms in Melanoma

2022

Cell

Thompson, K., **Martinez, O.**, Park, S., et al. (2022). *Cell*, 185(12), 2234-2248.
[Contributed: Developed clustering algorithms, performed pathway enrichment analysis]

Automated Quality Control Framework for Large-Scale Genomic Studies

2022

Bioinformatics

Martinez, O., Kumar, A., Williams, J. (2022). *Bioinformatics*, 38(15), 3821-3829.
[First author: Designed QC pipeline, implemented software package]

Machine Learning Approaches for Rare Variant Interpretation in Clinical Genomics

2021

American Journal of Human Genetics

Lee, H., **Martinez, O.**, Davis, R., et al. (2021). *American Journal of Human Genetics*, 108(7), 1287-1301.
[Contributed: Developed ML models, performed statistical analysis]

AWARDS AND HONORS

Outstanding Early Career Scientist Award

2023

International Society for Computational Biology

"For innovative contributions to drug discovery through computational genomics"

Best Paper Award
2022

RECOMB Conference on Computational Biology

"Graph Neural Networks for Drug-Target Interaction Prediction"

NSF Graduate Research Fellowship
2015-2018

National Science Foundation

$138,000 fellowship for doctoral research in computational biology

First Place, Precision Medicine Hackathon
2021

Stanford Medicine

Developed AI model for predicting treatment response using electronic health records

Young Investigator Travel Award
2020

American Society of Human Genetics

RESEARCH PROJECTS

Cancer Immunotherapy Response Prediction Platform
2022-Present

- Integrated multi-omics data (WES, RNA-seq, flow cytometry) from 800+ patients across 5 clinical trials
- Developed ensemble machine learning model combining gradient boosting and neural networks
- Achieved 78% accuracy in predicting checkpoint inhibitor response, 15% improvement over clinical markers alone

Rare Disease Variant Interpretation Pipeline
2020-2021

- Built comprehensive annotation pipeline integrating 20+ databases (ClinVar, gnomAD, OMIM, etc.)
- Implemented machine learning classifier for pathogenicity prediction using 150+ genomic features
- Deployed system processing 500+ cases monthly for clinical genetics teams