Obed A. García

+1-773-679-5724 • ogarci12@ucsc.edu • Mountain View, CA

SUMMARY OF EXPERIENCE

- Over 12 years' experience in computational genomics.
- Expertise in bioinformatics, biostatistics, and computational Biology, specializing in the manipulation of large datasets and computational tools for Precision Medicine advancements.
- Proficient in processing NGS datafiles, immunoassays, and other wet laboratory work

EDUCATION

Ph.D.	Biological Anthropology (Population Genomics and Immunology), University of Michigan	2020
M.A.	Anthropology (Evolutionary Biology), University of Michigan	2015
B.A.	English and Jewish Studies, minor in Religion, Oberlin College	2009

EXPERIENCE

Postdoctoral Scholar, Ecology and Evolutionary Biology   **2023-present**
University of California, Santa Cruz
- Developing targeted HLA sequencing methods
- Improving methodology alongside the Human PanGenome Consortium for HLA calling and imputation

Computational Genomics Consultant, Global Health   **2022-present**
University of Washington, Seattle
- Aided with statistical study design and grant write-up for an R01
- Local ancestry inference and population stratification work for an HIV mucosal inflammation study. Populations include admixed US/Canada cohort, West African
- Performed rare variant imputation an QC for Rare Variant Burden Tests
- Calling HLA alleles from NGS dataset for Type I Diabetes study

Postdoctoral Scholar, Biomedical Data Science   **2020-2023**
Stanford University, Palo Alto
Served as a Biomedical Informatics and Data Science Fellow at the National Library of Medicine, allowing me to expand on my computational skillset including the manipulation of large datasets using computational methods
- Member of the HLA Expert Panel, the Rheumatologic Autoimmune Disease Working Group (ClinGen Consortium).
  - Designing an innovative tool and curation framework to facilitate the annotation of HLA allele-disease relationships, contributing to advancements in Precision Medicine
  - Designing the interface and the scoring mechanism to weigh Allele-Disease Associations
  - Created a series of Python scripts to facilitate updating our own database following the release updates from the IMGT database
- Conducted comprehensive testing of open-source HLA software to test reliability and enable external calls into the Pharmacogenomics Clinical Annotation Tool (pharmCAT). Currently writing a Python script to ingest the HLA specific HML files (XML formatted) into pharmCAT. Documentation written to date: https://pharmcat.org/using/Calling-HLA/
- Associate Member of the Human PanGenome Reference Consortium
  - Testing of graph-related tools such as the graph-genotyper developed by the consortium
- Investigated HLA susceptibility alleles for Type I and Type II Diabetes in the All of Us Cohort.
  - Population Genetics of multi-ancestry cohort including local ancestry, HLA imputation, and various statistical methods
  - Used various drug and phenotypes available through ICD-9/ICD-10 codes in the accompanying EHR records

Researcher, Anthropological Genomics
University of Michigan   **2012-2020**
- Performed Whole Genome Sequencing (WGS) and Whole Exome Sequencing (WES) mapping using BWA and DragMAP, alignment, and variant calling of data (GATK and DeepVariant)
- Ran a large wide range of immunoassays including dengue-specific IgG, IgM, various pro-inflammatory Cytokines, and Multiplex ELISAS

- Cultivated international research collaborations in Guatemala, Peru, and Mexico to study dengue, natural selection, and adaptive phenotypes to high-altitude

Research Technician and Lab Manager, Endocrinology, Metabolism, and Molecular Medicine   2009-2012
Northwestern University
- Researched Polycystic Ovary Syndrome (PCOS), Type II Diabetes, and other metabolic disorders
- Comprehensive analysis on Array data, Sanger sequencing, and Taqman assays
- Demonstrated expertise in primer design and PCR techniques to facilitate accurate genetic analysis and experimentation.
- Applied statistical design principles to optimize experimental protocols and enhance data reliability
- Generated cDNA from various mouse tissue samples
- Streamlined sample and data management systems by implementing a highly efficient 2D barcoded system and database, resulting in improved inventory organization and accessibility
- Successfully managed a laboratory team of five individuals, overseeing day-to-day operations, coordinating tasks, and ensuring efficient workflow

OTHER EXPERIENCE

Postdoctoral Scholar, Biomedical Data Science   2020-present
Stanford University, Palo Alto

- Mentored students in the Institute for Computational and Mathematical Engineering program and the Biomedical Informatics Program to reconstruct the natural selection, archaic introgression, and migration using publicly available computational tools.
    - The methods included IBD analysis, local ancestry, HLA imputation, and other genetics statistics. Wrote various scripts to reformat VCF datafiles into input for the software being used. Association studies were carried out with linear regression models and permutation tests.

Instructor, Biological Anthropology   2012-2020
University of Michigan, Ann Arbor

- Taught established curriculum and created new curriculum such as the intersections population genetics and Latin American history
- Mentored various undergraduate students to carry out independent research projects and submit to national conference
- Demonstrated a strong track record in obtaining highly competitive extramural national research grants, both national and internationally, NSF: $31,200 and Wenner-Gren: $19,959

Faculty, Mathematics   2009-2012
Dorothy Stang Popular Education High School, Chicago

- Taught Algebra and Geometry in both Spanish and English to Adults

SKILLS

Programming: Unix, R, Python, Nextflow, Snakemake, Singularity, Docker
NGS: BWA, DRAGMAP, GATK, DeepVariant, HLA calling (HLA-LA, Optitype, etc.), Picard, Samtools
Population Genetics: PCA, Admixture, Local Ancestry, Imputation (including rare-variant and HLA), Regression
Wet Lab: DNA/RNA extractions, PCR (including Real-Time, RT), Western Blotting, ELISAS (single and multiplex), Cell and Tissue culture work, Mouse-related genetic research
Languages: Spanish (Native Fluency), Hebrew (Basic Conversational), Latin
Professional Memberships: ClinGen Consortium (Ancestry and Diversity Working Group, Rheumatologic Autoimmune Disease Working Group, and HLA Expert Panel), Human PanGenome Reference Consortium (Associate Member), American Association of Anthropological Genetics (Board Member)