Javier Blanco Portillo, MS

Computational Biologist
Biology PhD Student

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Summary

I am a Mexican computational biologist specializing in ancestry deconvolution analyses and applications of machine learning to genetic data. Under the supervision of Dr. Marcus Feldman, I am currently pursuing a Ph.D. in Biology from Stanford University, and have published research in human population genetics in *Nature*, one of the leading journals in the field. My recent projects focus on the human settlement of the Hawaiian Islands while leveraging local ancestry in genome-wide association studies, and in conducting analyses of human genetic, epigenetic, environmental and cultural variation to quantify the importance of gene-culture coevolution as a force for recent human evolution.

Education

Stanford University   **Palo Alto, CA**
    PhD in Biology (Ecology & Evolution, 2nd Year)   *Started September 2019*
    Passed Qualification Exam on June 2nd, 2021

National Laboratory of Genomics for Biodiversity (LANGEBIO)   **Guanajuato, Mexico**
    M. Sc. in Integrative Biology   *July 2019*
    Thesis: Genomic Reconstruction of Human Trans-Pacific Population Dynamics

National Autonomous University of Mexico (UNAM)   **Morelos, Mexico**
    Undergraduate Program in Genomic Sciences   *June 2016*
    Graduated with honors via the High Academic Level modality

Research Experience

National Laboratory of Genomics for Biodiversity (LANGEBIO)   *June 2015 - June 2019*
    Human Evolutionary Genetics, *Human Population Genomics Lab*
    Beginning during the last year of the Undergraduate Program in Genomic Sciences, my research in Dr. Andrés Moreno's laboratory was focused on the population genetics of admixed human populations in the Americas and the Pacific, particularly on the fine-scale genetic structure of Chilean and Polynesian populations.

Stanford University   *August 2015 - Present*
    Human Evolutionary Genetics, *Bustamante Lab, Center for Computational, Evolutionary and Human Genomics (CEHG)*
    The close collaboration between the Moreno and Bustamante laboratories gave me the opportunity to visit the Center for Computational, Evolutionary and Human Genomics (CEGH) at Stanford University. Jointly with Dr. Alexander Ioannidis, I am currently involved in the genomic reconstruction of human trans-Pacific population dynamics through the application of some of the most advanced admixture deconvolution techniques in the field.
    Human Evolutionary Genetics & Cultural Evolution, *Feldman Lab*
    As a member of Dr. Marcus Feldman's laboratory, I am currently working on the settlement of the Hawaiian Archipelago and the development of genomic tools for populations currently underrepresented in genomic databases, in close collaboration with the Bustamante Lab.

Work Experience

Research Assistant, Stanford University   *February 2018 - June 2019*
    Human Diversity Biobank Database for Stanford University,
    Center for Computational, Evolutionary and Human Genomics (CEHG)
    Building on the extensive collection at Stanford begun by Luca Cavalli-Sforza and his collaborators, I was in charge of creating a comprehensive human diversity biobank database that serves as a valuable resource for future research, as well as assisting in the development of methods for its analysis.

Publications

Blanco-Portillo, Javier*; Ioannidis, Alexander*; Moraga, M.; Verdugo, R; Miquel, J.; Sandoval, K.; Hagelberg, E.; Barnes, K.; Parks, T.; Ávila-Arcos, M.; Adams, A.; Eng, C.; Burchard, E.; Mentzer, A.; Bustamante, C.; Moreno-Estrada, A. Genomic evidence for Native American contact in Polynesia predating the settlement of Easter Island. **Nature (2020).**
Featured by The New York Times, The Guardian, BBC News, Der Spiegel, Scientific American, Smithsonian Magazine, El País, and others.

Blanco-Portillo, Javier*; Ioannidis, Alexander*; Quinto, C.; Sandoval, K.; Hagelberg, E.; Parks, T.; Adams, A.; Eng, C.; Burchard, E.; Mentzer, A.; Bustamante, C.; Moreno-Estrada, A. The peopling of Polynesia: paths and timings inferred from genomic networks **(accepted for publication in Nature).**

Ioannidis, Alexander*; Agrawal, Devang*; Burgess, James; Rodriguez-Rodriguez, Juan Esteban; **Blanco-Portillo, Javier;** Pourshafeie, Armin; Sing-Long, Carlos. Principal Component Analysis for Incomplete Genomic Sequences **(manuscript in preparation).**

Ioannidis, Alexander*; Aounallah, Khaled*; Agrawal, Devang; **Blanco-Portillo, Javier**; Rodriguez-Rodriguez, Juan Esteban; Moreno-Estrada Andres; Bustamante, Carlos. Multiple Array Ancestry Specific Multidimensional Scaling **(manuscript in preparation).**

*First authors

Conference Presentations

Society for Molecular Biology and Evolution Annual Meeting, Québec City, Canada, 2020 (Canceled)
Oral presentation, "Genomic evidence for Native American contact in Polynesia predating the settlement of Easter Island"

American Society of Human Genetics Annual Meeting, San Diego, USA, 2018
Poster presentation (jointly with Alexander Ioannidis), "Ancestry Specific Methods for Reconstructing Human Settlement across the Pacific"

American Society of Human Genetics Annual Meeting, Orlando, USA, 2017
Poster presentation (jointly with Alexander Ioannidis), "Genetic Origins of Easter Island and Remote Oceania"

Society for Molecular Biology and Evolution Annual Meeting, Austin, USA, 2017
Oral presentation, "Genomic Insights Into the Ancestry and Human Demography of Remote Oceania"

Society for Molecular Biology and Evolution Satellite Meeting, San Antonio, USA, 2016
Poster presentation, "Fine-Scale Genetic Structure of Chilean Populations"

2nd Mexico Population Genomics Meeting, Mexico City, México, 2016
Poster presentation, "Reconstructing admixture and migration dynamics of post-Columbian Mexico."

1st Mexico Population Genomics Meeting, Querétaro, México, 2015
Poster presentation, "Fine-Scale Genetic Structure of Chilean Populations"

Seminars on Paleogenomics at the Center for Genomic Sciences, Cuernavaca, México, 2014
Organization committee

Teaching Awards

Excellence in Teaching Award (2019-2020 Winter Quarter)
Awarded by Stanford's Biology Department, Evolution Course (BIO-85)

Bioinformatics Skills and Stanford Courses

- **Code:** Proficient in R and Python; complete familiarity working on a Linux/Unix environment
- **Population genetics**: PLINK, ADMIXTURE, RFMix, AdmixTools, ALDER, EIGENSOFT, Beagle, SHAPEIT, GERMLINE, hapIBD, Refined IBD, IBDNe, asIBDNe, Tracts, Treemix, GWAS, Demographic modeling

- **Machine Learning:** Dimensionality reduction (UMAP, tSNE), Decision trees, SVMs, Neural networks (TensorFlow), Variational autoencoders
- **Graphic Design**: Adept at Adobe Illustrator, Photoshop, and InDesign
- Modern Statistics for Modern Biology (2019-2020 Autumn Quarter, A)
- Data Mining and Analysis (2019-2020 Autumn Quarter, CR)
- Theoretical Population Genetics (2019-2020 Winter Quarter, A)
- Teaching and Learning in Biology (2019-2020 Winter Quarter, A)
- Introduction to Scientific Python (2019-2020 Spring Quarter, S)
- Modeling Cultural Evolution (2020-2021 Winter Quarter, A)
- The Responsible Conduct of Research (2020-2021 Winter Quarter, +)
- Programming Methodology (2020-2021 Summer Quarter, *In progress*)

Languages

- Fluent in English and Spanish

References

- **Dr. Alexander Ioannidis (ioannidis@stanford.edu)**
  Postdoctoral Scholar, Bustamante Lab, Stanford University
- **Dr. Marcus Feldman (mfeldman@stanford.edu)**
  Princial Investigator, Biology Department, Stanford University
- **Dr. Andrés Moreno Estrada (andres.moreno@cinvestav.mx)**
  Principal Investigator & Head of Genomics Services, LANGEBIO, Cinvestav, Mexico
- **Dr. Carlos Bustamante (cdbadmin@stanford.edu)**
  Principal Investigator, Biomedical Data Science Department, Stanford University