

# Alejandro Ochoa

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Department of Biostatistics and Bioinformatics  
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<https://ochoalab.github.io/>

## Education

- 2013 PhD in Molecular Biology, Princeton University  
Dissertation: *Protein domain prediction using context statistics, the false discovery rate, and comparative genomics, with application to Plasmodium falciparum*  
Advisers: Mona Singh (Computer Science) and Manuel Llinás (Molecular Biology)
- 2006 BS in Biology and Mathematics, Massachusetts Institute of Technology

## Awards & Honors

- 2020 Whitehead Scholar, Whitehead Charitable Foundation. For Duke junior faculty with exceptional potential for research and research training in the biomedical sciences.
- 2008 NSF Graduate Research Fellowship. Computational Biology.
- 2008 Ford Foundation Diversity Fellowship Predoc. Comp. (Declined, listed as Honorable Mention.)
- 2006 MIT Department of Biology Merck Prize. Awarded to a graduating senior for outstanding research and academic performance in biophysics or bioinformatics.
- 2001 Mexican Math Olympiad Gold Medal. Awarded to top 15 competitors nationally.

## Employment

- 2018-now *Assistant Professor*, Duke Center for Statistical Genetics and Genomics, Department of Biostatistics and Bioinformatics, Duke University
- 2013-2018 *Postdoctoral Research Associate* at John D Storey's group, Lewis-Sigler Institute for Integrative Genomics, and Center for Statistics and Machine Learning, Princeton University

## Publications

### JOURNAL ARTICLES

- 2023 Zhuoran Hou, **Alejandro Ochoa**. Genetic association models are robust to common population kinship estimation biases. *Genetics*. iyado30. PMID [36843304](#).
- 2021 Brandon M Lane, Megan Chryst-Stangl, Guanghong Wu, Mohamed Shalaby, Sherif El Desoky,

Claire Middleton, Kinsie Huggins, Amika Sood, **Alejandro Ochoa**, Andrew F Malone, Ricardo Vancini, Sara Miller, Gentzon Hall, So Young Kim, David Howell, Jameela A Kari, Rasheed Gbadegesin. CLVS1, a candidate gene for steroid sensitive nephrotic syndrome, regulates podocyte oxidative stress and endocytosis. *JCI Insight*. 7(2) e152102. PMID [34874915](#).

Brian I Shaw, **Alejandro Ochoa**, Cliburn Chan, Chloe Nobuhara, Rasheed Gbadegesin, Annette M Jackson, Eileen T Chambers. HLA Loci and Recurrence of Focal Segmental Glomerulosclerosis In Pediatric Kidney Transplantation. *Transplant Direct*. 7(10) e748. PMID [34476293](#).

Young-Sook Kim, Graham D Johnson, Jungkyun Seo, Alejandro Barrera, Thomas N. Cowart, William H Majoros, **Alejandro Ochoa**, Andrew S Allen, Timothy E Reddy. Correcting signal biases and detecting regulatory elements in STARR-seq data. *Genome Res*. 31(5) 877-889. PMID [33722938](#).

**Alejandro Ochoa**, John D Storey. Estimating  $F_{ST}$  and kinship for arbitrary population structures. *PLoS Genet*. 17(1) e1009241. PMID [33465078](#).

**Alejandro Ochoa**, Mona Singh. Domain prediction with probabilistic directional context. *Bioinf*. 33(16) 2471-8. PMID [28407137](#).

Simon A Cobbold, Joana M Santos, **Alejandro Ochoa**, David H Perlman, Manuel Llinás. Proteome-wide analysis reveals widespread lysine acetylation of major protein complexes in the malaria parasite. *Sci Rep*. 2016;6:19722. PMID [26813983](#).

**Alejandro Ochoa**, John D Storey, Manuel Llinás, Mona Singh. Beyond the  $E$ -value: stratified statistics for protein domain prediction. *PLoS Comput Biol*. 11 e1004509. PMID [26575353](#).

Moriah L Szpara, Derek Gatherer, **Alejandro Ochoa**, Benjamin Greenbaum, Aidan Dolan, Rory J Bowden, Lynn W Enquist, Matthieu Legendre, Andrew J Davison. Evolution and diversity in human herpes simplex virus genomes. *J Virol*. 88:1209-27. PMID [24227835](#).

**Alejandro Ochoa**, Manuel Llinás, Mona Singh. Using context to improve protein domain identification. *BMC Bioinformatics*. 12:90. PMID [21453511](#).

Gevorg Grigoryan, **Alejandro Ochoa**, Amy E Keating. Computing van der Waals energies in the context of the rotamer approximation. *Proteins*. 68(4) 863-78. PMID [17554777](#).

#### MANUSCRIPTS IN SUBMISSION

Rachel K Cason, Eileen T Chambers, Tiffany Tu, Megan Chryst-Stangl, Kinsie Huggins, **Alejandro Ochoa**, Brandon M Lane, Annette M Jackson, Rasheed Gbadegesin. Genetic risk factors for childhood nephrotic syndrome are associated with pattern of therapy response. Submitted.

Yiqi Yao, **Alejandro Ochoa**. Limitations of principal components in quantitative genetic association models for human studies. Preprint: <https://doi.org/10.1101/2022.03.25.485885>

**Alejandro Ochoa**, John D Storey. New kinship and  $F_{ST}$  estimates reveal higher levels of differentiation in the global human population. Preprint: <https://doi.org/10.1101/653279>

**Alejandro Ochoa**, John D Storey.  $F_{ST}$  and kinship for arbitrary population structures I: Generalized definitions. Preprint: <https://doi.org/10.1101/083915>

#### ACKNOWLEDGMENTS

Irineo Cabreros, John D Storey. A Likelihood-Free Estimator of Population Structure Bridging Admixture Models and Principal Components Analysis. *Genetics*. 212(4) 1009-29. PMID [31028112](#).

- 2016 Prem Gopalan, Wei Hao, David M Blei, John D Storey. Scaling probabilistic models of genetic variation to millions of humans. *Nat Genet.* 48(12) 1587-90. PMID [27819665](#).
- 2014 Anton V Persikov, Mona Singh. De Novo Prediction of DNA-Binding Specificities for Cys2His2 Zinc Finger Proteins. *Nucleic Acids Res.* 42(1) 97-108. PMID [24097433](#).

## Distributed software

- 2021-2023 simgenphen: Simulate Genotypes and Phenotypes. R.  
<https://github.com/OchoaLab/simgenphen>.
- 2021-2022 genbin: R wrappers for binaries in genetics. R.  
<https://github.com/OchoaLab/genbin>.
- 2021-2023 simfam: Simulate and Model Family Pedigrees With Structured Founders. R, C++.  
Available on [CRAN](#) and <https://github.com/OchoaLab/simfam>.
- 2020-2023 ligera: Light GENetic Robust Association. R, C++.  
<https://github.com/OchoaLab/ligera>.
- 2019 human-differentiation-manuscript: Human differentiation analysis. R, bash, markdown.  
<https://github.com/StoreyLab/human-differentiation-manuscript>.
- 2019-2023 genio: Genetics Input/Output Functions. R, C++.  
Available on [CRAN](#) and <https://github.com/OchoaLab/genio>.
- 2019-2023 simtrait: Simulate Complex Traits from Genotypes. R.  
Available on [CRAN](#) and <https://github.com/OchoaLab/simtrait>.
- 2019-2022 popkinsuppl: Supplement to "popkin" package. R.  
<https://github.com/OchoaLab/popkinsuppl>.
- 2017-2023 popkin: Estimate Kinship and FST under Arbitrary Population Structure. R, C++.  
Available on [CRAN](#) and <https://github.com/StoreyLab/popkin>.
- 2017-2021 bnpsd: Model and Simulate Admixed Populations. R.  
Available on [CRAN](#) and <https://github.com/StoreyLab/bnpsd>.
- 2014-2020 dPUC2: Domain Prediction Using Context, Version 2. Perl, C.  
<https://github.com/alexviia/dpuc2>.
- 2014-2020 DomStratStats: Domain Stratified Statistics (q-values and local FDRs). Perl.  
<https://github.com/alexviia/DomStratStats>.
- 2014-2019 RandProt: High-order Markov random models for protein sequences. Perl.  
<https://github.com/alexviia/RandProt>.

## Invited Talks

- 2023 *American Mathematical Society (AMS) 2023 Spring Southeastern Sectional Meeting*. Georgia Institute of Technology, Atlanta, GA. 2023-03-19.
- 2022 *BERD Core Seminar*. Department of Biostatistics and Bioinformatics, Duke University, Durham, NC. 2022-08-26.
- 2022 *Latex in the Mathematical Sciences Conference 2022 (LatMath2022)*. Institute for Pure and Applied Mathematics, University of California, Los Angeles, Los Angeles, CA. 2022-07-08.
- 2022 *Duke University Program in Genetics and Genomics (UPGG) retreat*. Suite 4, Durham, NC. 2022-06-11.

- 2021 *Orientation for MB and PhD students.* Department of Biostatistics and Bioinformatics, Duke University, Durham, NC. 2021-08-19.
- 2021 *Statistics seminar.* Department of Mathematics and Statistics, Washington State University, Pullman, WA. 2021-03-10.
- 2021 *Master of Biostatistics Virtual Visit Day.* Department of Biostatistics and Bioinformatics, Duke University, Durham, NC. 2021-02-19.
- 2020 *University Program in Genetics and Genomics (UPGG) seminar.* Room 147, Nanaline Duke building, Duke University, Durham, NC. 2020-02-18.
- 2019 *Duke Computational Biology and Bioinformatics (CBB) retreat.* Holiday Inn Resort, Wrightsville Beach, NC. 2019-09-28.
- 2019 *Computational Biology and Bioinformatics (CBB) seminar.* French Family Science Center, Duke University, Durham, NC. 2019-02-04.
- 2019 *4th Mexico Population Genomics Meeting.* Amoxcalli Complex, Faculty of Sciences, University City, National Autonomous University of Mexico, Mexico City, DF, Mexico. 2019-01-11.
- 2018 *Population Biology seminar,* Department of Biology, Duke University, Durham, NC. 2018-09-27.
- 2018 *Department of Biostatistics and Bioinformatics,* Duke University, Durham, NC. 2018-02-21.
- 2018 *Department of Biostatistics,* Johns Hopkins University, Baltimore, MD. 2018-01-22.
- 2017 *Department of Biology,* University of Richmond, Richmond, VA. 2017-11-10.
- 2017 *Princeton Research Day.* Princeton University, Princeton, NJ. 2017-05-11.
- 2017 *Department of Genetics,* University of North Carolina, Chapel Hill, NC. 2017-02-13.
- 2016 *New York Area Population Genomics Workshop 2016.* Princeton University, Princeton, NJ. 2016-01-21.
- 2015 *Probabilistic Modeling in Genomics conference.* Cold Spring Harbor Laboratory, Cold Spring Harbor, NY. 2015-10-15.
- 2013 *Telepresentation for Yun Song's group.* UC Berkeley, Berkeley, CA. 2013-04-17.
- 2013 *Biological sequence analysis and probabilistic models conference.* HHMI Janelia Farm, Ashburn, VA. 2013-03-25.
- 2013 *NCBI, NIH,* Bethesda, MD. 2013-02-25.
- 2012 *Recruiting conference.* Department of Computer Science, Princeton University, Princeton, NJ. 2012-03-01.
- 2004 *Rotary Club Paso del Norte,* Ciudad Juarez, CHIH, Mexico. 2004-08-26.

## Conference posters

- 2022 **Zhuoran Hou, Alejandro Ochoa.** Genetic association models are robust to common population kinship estimation biases. *American Society of Human Genetics (ASHG) Annual Meeting.* Convention Center, Downtown, Los Angeles, CA.
- 2022 **Alejandro Ochoa,** Yuncheng Duan, Revathy Venukuttan, Shannon Clarke, Timothy Reddy. Development of Genomic Resource Modules for a Diverse Workforce. *NIH Centers for Excellence in Genomics Science (CEGS) Annual Meeting.* The Mary Duke Biddle Trent Semans Center for Health Education, Duke University, Durham, NC.
- 2020 **Alejandro Ochoa,** John D Storey. New kinship and  $F_{ST}$  estimates applied to the global human population. *American Society of Human Genetics (ASHG) Annual Meeting.* Virtual.
- 2019 **Alejandro Ochoa,** John D Storey. Relatedness and Differentiation in Arbitrary Population Struc-

tures. *4th Mexico Population Genomics Meeting*. Amoxcalli Complex, Faculty of Sciences, University City, National Autonomous University of Mexico, Mexico City, DF, Mexico.

2018 **Alejandro Ochoa**, John D Storey. Relatedness and Differentiation in Arbitrary Population Structures. *Probabilistic Modeling in Genomics*. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

2018 **Alejandro Ochoa**, John D Storey. Relatedness and Differentiation in Arbitrary Population Structures. *Population, Evolutionary and Quantitative Genetics Conference*. Madison Concourse Hotel, Madison, WI.

2016 **Alejandro Ochoa**, John D Storey, Srikanth Gottipati, Shashank Rohatagi, Andrew Forbes, Deborah Profit, Raymond Sanchez, Margaretta Nyilas, William Carson. Mixed Effects Modeling of Placebo Response Across 8 Placebo-controlled Aripiprazole Trials Spanning 20 Years in Acutely Relapsed Schizophrenia Patients. *Neuroscience Education Institute Psychopharmacology Congress*. Broadmoor Convention Center, Colorado Springs, CO.

2016 Srikanth Gottipati, **Alejandro Ochoa**, Shashank Rohatagi, Andrew Forbes, Deborah Profit, Raymond Sanchez, Margaretta Nyilas, William Carson. Canonical Loadings of PANSS Subscales Show Differential Placebo and Aripiprazole Drug Responses in Schizophrenia Patients. *Neuroscience Education Institute Psychopharmacology Congress*. Broadmoor Convention Center, Colorado Springs, CO.

2015 **Alejandro Ochoa**, John D Storey.  $F_{ST}$  generalized for arbitrary population structures. *John W. Tukey 100th Birthday Celebration conference*. Center for Statistics and Machine Learning, Princeton University, Princeton, NJ.

2013 **Alejandro Ochoa**, John D Storey, Manuel Llinás, Mona Singh. Forget the  $E$ -value: family-based  $q$ -values for protein domain prediction, and empirical error detection. *Biological sequence analysis and probabilistic models conference*. HHMI Janelia Farm, Ashburn, VA.

2010 **Alejandro Ochoa**, Manuel Llinás, Mona Singh. Using context to predict protein domains across diverse organisms. *Recomb Systems Biology conference*. Columbia University, New York, NY.

## Teaching

### DUKE UNIVERSITY

2022 Human Genetics. (Co-Lecturer Spring 2022)  
 2021-2022 UPGEN 778A-F Mini course: Genetic population structure and relatedness (Fall 2021, 2022)  
 2019-2022 SIBS lecture on genetic association studies (Summer 2019, 2021, 2022)  
 2019 BIOS 900 Current Problems in Biostatistics. Special lecture on kinship and  $F_{ST}$   
 2019 BIOS 710 Statistical Genetics and Genetic Epidemiology. Special lecture on kinship and  $F_{ST}$

### PRINCETON UNIVERSITY

2017 Intro to Genomics and Comp Bio. Quant Comp Bio, Comp Sci. (Co-Lecturer Fall 2017)  
 2016-2017 Discussion Leader. Summer Undergraduate Research Program (Summer 2016, 2017)  
 2014-2017 Statistical Treatment of Data. Mol Bio, Quant Comp Bio. (Workshop Fall 2014, 2015, 2016, 2017)  
 2011 Intro to Genomics and Comp Mol Bio. Mol Bio, Comp Sci. (TA Fall 2011)  
 2008 Core Laboratory. Mol Bio. (TA Spring 2008)

## MASSACHUSETTS INSTITUTE OF TECHNOLOGY

2005	Calculus. OME Project Interphase (TA Summer 2005)
2003-2004	Multivar Calculus and Diff Eqs. OME Seminar XL (Tutor Fall 2003, Spring 2004)
2003-2004	Calculus. MITE2S Program (TA Summer 2003, 2004)

## Mentoring

### CURRENT TRAINEES - PRIMARY ADVISER

2020-now	Tiffany Tu. PhD. Graduate rotation, Dissertation adviser. Ochoa Laboratory. Computational Biology and Bioinformatics Program, Duke University.
2021-now	Emmanuel Mokel. Undergraduate. Research Independent Study. Ochoa Laboratory. Department of Statistical Science, Duke University.
2022-now	Ratchanon "RP" Pornmongkolsuk. PhD. Graduate rotation, Dissertation adviser. Ochoa Laboratory. University Program in Genetics and Genomics, Duke University.

### CURRENT TRAINEES - SECONDARY ADVISER

2019-now	Xue "Scarlett" Zou. PhD. Dissertation committee. Allen Laboratory. Computational Biology and Bioinformatics Program, Duke University.
2022-now	Zhuoran Hou. PhD. Graduate rotation. Ochoa Laboratory. Department of Biostatistics and Bioinformatics, Duke University.
2020-now	Brandon M. Lê. PhD. Dissertation committee. Ashley-Koch Laboratory. University Program in Genetics and Genomics, Duke University.
2021-now	Cymfenee Dean-Phifer. PhD. Graduate rotation, Dissertation committee. Goldberg Laboratory. Computational Biology and Bioinformatics Program, Duke University.
2022-now	Changxin Wan. PhD. Dissertation committee. Ji Laboratory. Computational Biology and Bioinformatics Program, Duke University.
2023-now	Bide "Peter" Chen. PhD. Dissertation committee. Goldberg Laboratory. University Program in Genetics and Genomics, Duke University.

### PAST TRAINEES - PRIMARY ADVISER

2019-2020	Yiqi Yao. Master's. BCTIP internship, Master's project adviser. Ochoa Laboratory. Department of Biostatistics and Bioinformatics, Duke University. Now Senior Business Analyst at BenHealth.
2019-2022	Amika Sood. Postdoctoral. Postdoctoral adviser. Ochoa Laboratory. Department of Biostatistics and Bioinformatics, Duke University. Now Staff Scientist at Complex Carbohydrate Research Center (CCRC), The University of Georgia.
2020-2021	Zhuoran Hou. Master's. BCTIP internship. Ochoa Laboratory. Department of Biostatistics and Bioinformatics, Duke University. Now PhD Student at Duke University, BB.
2020-2022	Jiajie Shen. Master's. Research, Master's project adviser. Ochoa Laboratory. Department of Biostatistics and Bioinformatics, Duke University.

## PAST TRAINEES - SECONDARY ADVISER

2009	Neo Christopher Chung. PhD. Graduate rotation. Llinás Laboratory. Quantitative Computational Biology Program, Princeton University. Now Adjunct Faculty at University of Warsaw.
2010	Jeremy Bigness. PhD. Graduate rotation. Singh Laboratory. Quantitative Computational Biology Program, Princeton University. Now PhD Student at Brown University.
2011	Sebastian Nasamu. Undergraduate. Summer project. Llinás Laboratory. Department of Molecular Biology, Princeton University. Now Post-doctoral Research Fellow at Johns Hopkins Bloomberg School of Public Health.
2019	Yuncheng Duan. PhD. Graduate rotation. Ochoa Laboratory. Department of Biology, Duke University. Now PhD Student at Duke University, Allen Lab.
2019-2020	Shengyu Li. Master's. Master's project committee. Allen Laboratory. Department of Biostatistics and Bioinformatics, Duke University. Now PhD Student at Duke University, CBB.
2020-2022	Iman Hamid. PhD. Dissertation committee. Goldberg Laboratory. University Program in Genetics and Genomics, Duke University. Now Scientist at Variant Bio.
2020-2021	Bobby Boone IV. Master's. Master's project committee. Landstrom Laboratory. Department of Biostatistics and Bioinformatics, Duke University. Now Biostatistician II at University of Utah Health.
2020-2023	Rachel Cason. Resident physician. Scholarship Oversight Committee, Master's project committee. Gbadegesin Laboratory. Department of Pediatrics, Duke University.
2021-2022	Valerie Gartner. PhD. Dissertation committee. Wray Laboratory. University Program in Genetics and Genomics, Duke University.
2021-2022	Hongyu Du. Master's. Master's project committee. Allen Laboratory. Department of Biostatistics and Bioinformatics, Duke University.
2021-2022	Krista Pipho. PhD. Dissertation committee. Goldberg Laboratory. University Program in Genetics and Genomics, Duke University.
2021-2022	Weiliang "Frank" Tian. Master's. Master's project committee. Soderling Laboratory. Department of Biostatistics and Bioinformatics, Duke University.

## Research experience

2013-2018	Postdoctoral Research, Storey Lab, Princeton. Developed new definitions and tools to study arbitrary population structures. Also applied GWAS and mixed effects modeling to longitudinal psychiatric drug clinical trials.
2007-2013	Graduate Research Thesis, Singh Lab and Llinás Lab, Princeton. Developed probabilistic models and statistical methods that improve protein domain prediction. Studied the <i>Plasmodium falciparum</i> proteome, focusing on the AP2 transcription factors. Used experimental techniques (cloning, protein purification and protein-binding microarrays) to test predicted AP2 domains for DNA binding.
2007	Graduate Rotation, Tavazoie Lab, Princeton. Cloned an RNA aptamer for a phage display assay.
2006-2007	Graduate Rotation, Singh Lab, Princeton. Analyzed protein interactions predicted from the presence of interacting domain pairs.
2006	Graduate Rotation, Troyanskaya Lab, Princeton. Built and analyzed a potential "gold standard" of Gene Ontology terms integrated from predictions of multiple sources, in <i>Saccharomyces cere-</i>

*visiae* and *Homo sapiens*.

2005-2006 Undergraduate Research Assistant, Keating Lab, MIT. Analyzed full-atom computational protein designs using modified van der Waals potentials.

## Extracurricular University Activities

2006-2010 Latino Graduate Student Association, Princeton University. Board member: Technology Specialist 2007-2010 (handled website, email list, photos, calendar).

2002-2006 Association of Puerto Rican students, MIT. Regular member.

## Outreach

2017 Panelist at HISPA Latinos in College Conference. Princeton University.

2010 Ivy-plus recruiting fair at University of Puerto Rico (4 campuses) for Princeton.

2008-2011 Science and Engineering Expo. HHMI and Princeton University.

2007 Helped local high school students with college personal statements. PUPP, Princeton University.

## Languages

English. Native proficiency.

Spanish. Native proficiency.

French. Fluent reading and writing, conversational speaking.