

Alejandro Ochoa

Duke Center for Statistical Genetics and Genomics
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

- 2022 Lathisms: showcase of contributions of Latinx and Hispanic mathematicians during Hispanic Heritage Month. <https://www.lathisms.org/calendars/calendar-2022>
- 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 Rachel Kate Cason, Eileen T Chambers, Tiffany Tu, Megan Chryst-Stangl, Kinsie Huggins, Brandon M Lane, **Alejandro Ochoa**, Annette M Jackson, Rasheed Gbadegesin. Genetic risk variants

- for childhood nephrotic syndrome and corticosteroid response. *Frontiers in Pediatrics*. 11:1248733. PMID [37868272](#).
- 2023 Yiqi Yao, **Alejandro Ochoa**. Limitations of principal components in quantitative genetic association models for human studies. *eLife*. 79238. PMID [37140344](#).
- 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](#).
- 2021 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](#).
- 2021 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](#).
- 2021 **Alejandro Ochoa**, John D Storey. Estimating F_{ST} and kinship for arbitrary population structures. *PLoS Genet.* 17(1) e1009241. PMID [33465078](#).
- 2017 **Alejandro Ochoa**, Mona Singh. Domain prediction with probabilistic directional context. *Bioinf.* 33(16) 2471-8. PMID [28407137](#).
- 2016 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](#).
- 2015 **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](#).
- 2013 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](#).
- 2011 **Alejandro Ochoa**, Manuel Llinás, Mona Singh. Using context to improve protein domain identification. *BMC Bioinformatics*. 12(1) 90. PMID [21453511](#).
- 2007 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

- 2025 Tiffany Tu, **Alejandro Ochoa**, Amika Sood, Ashley Drabik, Megan Chryst-Stangl, Brandon M Lane, Guanghong Wu, Frank Donovan, Ursula Harper, Settara Chandrasekharappa, Christopher Esezobor, Adaobi Solarin, David Hooper, Christine Sethna, Sandra Amaral, Mahmoud Kallash, Michelle Rheault, Priya Verghese, Vikas Dharnidharka, Eloise Salmon, Patricia Weng, Tarak Srivastava, Michael E. Seifert, Cozumel Prueette, David Selewski, Keisha Gibson, Tracy Hunley, Asiri Abeyagunawardena, Shenal Thalgahagoda, Arvind Bagga, Aditi Sinha, Nicholas Webb, Larry Greenbaum, Ali Gharavi, Krzysztof Kiryluk, Mathias Kretzler, Lisa Guay-Woodford, Simone Sanna-Cherchi, Agnieszka Bierzynska, Ania Koziell, Gavin Welsh, Moin Saleem, Charles

Rotimi, Eileen T Chambers, Cliburn Chan, CureGN Consortium, PNRC Glomerular disease group, CIBMTR/NMDP Consortium, Annette M Jackson, Adebawale Adeyemo, Rasheed Gbadegesin. Polygenic Risk Scores and HLA Class II Variants are Biomarkers of Corticosteroid Response in Childhood Nephrotic Syndrome. PMID [40970117](#). Preprint: <https://doi.org/10.1101/2025.08.01.25332825>

2025 Zhuoran Hou, **Alejandro Ochoa**. Kinship estimation bias carries over to heritability estimation bias using variance components. PMID [40463130](#). Preprint: <https://doi.org/10.1101/2025.05.13.653659>

2025 Tiffany Tu, **Alejandro Ochoa**. Genetic association meta-analysis is susceptible to confounding by between-study cryptic relatedness. PMID [40463146](#). Preprint: <https://doi.org/10.1101/2025.05.10.653279>

2019 **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>

2016 **Alejandro Ochoa**, John D Storey. F_{ST} and kinship for arbitrary population structures I: Generalized definitions. Preprint: <https://doi.org/10.1101/083915>

ACKNOWLEDGMENTS

2019 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

MAJOR PACKAGES

2023-2025 popgeninfer: Tests and simulations of genotyping platform bias. R.
<https://github.com/OchoaLab/popgeninfer>.

2021-2025 simfam: Simulate and Model Family Pedigrees With Structured Founders. R, C++. Available on CRAN and <https://github.com/OchoaLab/simfam>.

2020-2024 jackstraw: Jackstraw Statistical Inference for Unsupervised Learning. R.
<https://github.com/ncchung/jackstraw>.

2020-2025 gcatest: Genotype Conditional Association Test. R.
<https://github.com/StoreyLab/gcatest>.

2020-2025 lfa: Logistic Factor Analysis for Categorical Data. R.
<https://github.com/StoreyLab/lfa>.

2019-2025 genio: Genetics Input/Output Functions. R, C++. Available on CRAN and <https://github.com/OchoaLab/genio>.

2019-2025 simtrait: Simulate Complex Traits from Genotypes. R. Available on CRAN and <https://github.com/OchoaLab/simtrait>.

2017-2024 popkin: Estimate Kinship and FST under Arbitrary Population Structure. R, C++.

Available on CRAN and <https://github.com/StoreyLab/popkin>.

2017-2023

bnpssd: Model and Simulate Admixed Populations. R.

Available on CRAN and <https://github.com/StoreyLab/bnpssd>.

2014-2020

dPUC2: Domain Prediction Using Context, Version 2. Perl, C.

<https://github.com/alexviiia/dpuc2>.

2014-2020

DomStratStats: Domain Stratified Statistics (q-values and local FDRs). Perl.

<https://github.com/alexviiia/DomStratStats>.

2014-2019

RandProt: High-order Markov random models for protein sequences. Perl.

<https://github.com/alexviiia/RandProt>.

MINOR PACKAGES

2025

domrec: DOMinant / RECessive reencoder. C++.

<https://github.com/OchoaLab/domrec>.

2021-2023

simgenphen: Simulate Genotypes and Phenotypes. R.

<https://github.com/OchoaLab/simgenphen>.

2021-2025

genbin: R wrappers for binaries in genetics. R.

<https://github.com/OchoaLab/genbin>.

2020-2023

ligera: Liight GEnetic Robust Association. R, C++.

<https://github.com/OchoaLab/ligera>.

2019-2022

popkinsuppl: Supplement to "popkin" package. R.

<https://github.com/OchoaLab/popkinsuppl>.

2019-2024

kinshipsymbols: Math symbols for statistical genetics. LaTeX.

<https://github.com/OchoaLab/kinshipsymbols>.

PAPER REPOSITORIES

2020-2025

bias-herit-paper: Characterization of heritability estimation biases, from biased kinship matrices and other causes. R, bash, LaTeX.

<https://github.com/OchoaLab/bias-herit-paper>.

2022-2025

meta-gwas-cryptic-inflation: Testing the effect of between-study relatedness on GWAS meta-analysis. R, bash.

<https://github.com/OchoaLab/meta-gwas-cryptic-inflation>.

2021-2025

bias-assoc-paper: Kinship bias association project. R, bash, LaTeX, markdown.

<https://github.com/OchoaLab/bias-assoc-paper>.

2019-2023

pca-assoc-paper: PCA association project. R, bash, LaTeX, markdown.

<https://github.com/OchoaLab/pca-assoc-paper>.

2019-2025

data: Instructions for real data processing shared across projects. R, bash, Perl, markdown.

<https://github.com/OchoaLab/data>.

2019

human-differentiation-manuscript: Human differentiation analysis. R, bash, markdown.

<https://github.com/StoreyLab/human-differentiation-manuscript>.

Invited Talks

2025

- Computing and Data Sciences Quantitative Biology Seminar Series.* Boston University, Boston, MA. 2025-12-04.
- 2025 *Latinx in the Mathematical Sciences Conference 2025 (LatMath2025).* Institute for Pure and Applied Mathematics, University of California, Los Angeles, Los Angeles, CA. 2025-03-07.
- 2024 *Society of Mathematical Biology (SMB) Summer Seminar Series: Diversity in Math Bio.* Virtual. 2024-07-30.
- 2024 *HLA and KIR region genomics in immune-mediated diseases consortium (virtual).* National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health (NIH), Bethesda, MD. 2024-06-11.
- 2024 *The 12th RECOMB Satellite Workshop on Computational Methods in Genetics.* Stata Center, Massachusetts Institute of Technology, Cambridge, MA. 2024-04-28. Presented by Tiffany Tu.
- 2024 *Princeton QCB seminar.* Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ. 2024-04-22.
- 2023 *Duke Computational Biology and Bioinformatics (CBB) retreat.* Holston Presbytery Camp and Retreat Center, Banner Elk, NC. 2023-11-18.
- 2023 *NIH Centers for Excellence in Genomics Science (CEGS) Annual Meeting.* Kimmel Center, New York University, New York, NY. 2023-10-11.
- 2023 *HLA and KIR region genomics in immune-mediated diseases consortium (virtual).* National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health (NIH), Bethesda, MD. 2023-06-16.
- 2023 *HCHS/SOL (Hispanic Community Health Study / Study of Latinos) Genetics Special Interest Group (Virtual).* Department of Biostatistics, Harvard University, Cambridge, MA. 2023-06-21.
- 2023 *NIH Centers for Excellence in Genomics Science (CEGS) Virtual Outreach Meeting.* The Jackson Laboratory, Bar Harbor, ME. 2023-04-20.
- 2023 *American Mathematical Society (AMS) 2023 Spring Southeastern Sectional Meeting.* Georgia Institute of Technology, Atlanta, GA. 2023-03-19.
- 2022 *American Society of Nephrology Kidney Week.* Orlando, FL. 2022-11-03. Presented by Rachel Kate Cason.
- 2022 *BERD Core Seminar.* Department of Biostatistics and Bioinformatics, Duke University, Durham, NC. 2022-08-26.
- 2022 *Latinx 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.
- 2022 *HLA and KIR region genomics in immune-mediated diseases consortium (virtual).* National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health (NIH), Bethesda, MD. 2022-04-28.
- 2021 *Orientation for MB and PhD students.* Department of Biostatistics and Bioinformatics, Duke University, Durham, NC. 2021-08-19.
- 2021 *American Transplant Congress.* Virtual. 2021-06-05. Presented by Brian I Shaw.
- 2021 *HLA and KIR region genomics in immune-mediated diseases consortium (virtual).* National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health (NIH), Bethesda, MD. 2021-04-06.
- 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 *American Society of Human Genetics (ASHG) Annual Meeting*. Virtual. 2020-10-27. Presented by Amika Sood.
- 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 (ProbGen) 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 (ProbGen) conference*. HHMI Janelia Farm, Ashburn, VA. 2013-03-25.
- 2013 National Center for Biotechnology Information (NCBI), National Institutes of Health (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

- 2025 Ratchanon Pornmongkolsuk, **Alejandro Ochoa**. Benchmark of genotype imputation of low-coverage ancient African genomes using SLiM forward-in-time genetic simulations. *American Society of Human Genetics (ASHG) Annual Meeting*. Convention Center, Boston, MA. 2025-10-15. Presented by Ratchanon Pornmongkolsuk.
- 2025 Zhuoran Hou, **Alejandro Ochoa**. A Kinship-Based Framework for LD Estimation Under Population Structure and Multi-Ancestry PRS. *American Society of Human Genetics (ASHG) Annual Meeting*. Convention Center, Boston, MA. 2025-10-17. Presented by Zhuoran Hou.
- 2025 Tiffany Tu, **Alejandro Ochoa**. Tests for harmonizing external controls in multiethnic case-control association studies with platform-specific genotyping biases. *The 13th RECOMB Satellite Workshop on Computational Methods in Genetics, and 29th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*. Centennial hall, Yonsei University, Seoul, Korea.

- 2025-04-25. Presented by Tiffany Tu.
- 2024 Ratchanon Pornmongkolsuk, **Alejandro Ochoa**. Evaluation of imputation methods for ancient African DNA. *American Society of Human Genetics (ASHG) Annual Meeting*. Convention Center, Denver, CO. 2024-11-08. Presented by Ratchanon Pornmongkolsuk.
- 2024 Zhuoran Hou, **Alejandro Ochoa**. Kinship estimation bias carries over to heritability estimation bias using variance components. *American Society of Human Genetics (ASHG) Annual Meeting*. Convention Center, Denver, CO. 2024-11-06. Presented by Zhuoran Hou.
- 2024 Tiffany Tu, **Alejandro Ochoa**. Genetic association meta-analysis is susceptible to confounding by between-study cryptic relatedness. *American Society of Human Genetics (ASHG) Annual Meeting*. Convention Center, Denver, CO. 2024-11-06. Presented by Tiffany Tu.
- 2024 Tiffany Tu, **Alejandro Ochoa**, Amika Sood, Cliburn Chan, Eileen T Chambers, Annette M Jackson, Adebawale Adeyemo, Rasheed Gbadegesin. Genome-wide Association Studies of Pediatric Nephrotic Syndrome identify variants associated with corticosteroid response. *American Society of Nephrology (ASN) Kidney Week*. Convention Center, San Diego, CA. 2024-10-25. Presented by Tiffany Tu.
- 2024 Tiffany Tu, **Alejandro Ochoa**. The presence of cryptic relatedness creates inflation in meta-analyses of genome-wide association studies. *The 12th RECOMB Satellite Workshop on Computational Methods in Genetics, and 28th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*. Stata Center, Massachusetts Institute of Technology, Cambridge, MA. 2024-04-28. Presented by Tiffany Tu.
- 2023 Tiffany Tu, Rasheed Gbadegesin, Adebawale Adeyemo, **Alejandro Ochoa**. A test of genotyping platform bias for multiethnic case/control association studies merging external controls. *American Society of Human Genetics (ASHG) Annual Meeting*. Walter E. Washington Convention Center, DC. 2023-11-04. Presented by Tiffany Tu.
- 2023 Ratchanon Pornmongkolsuk, **Alejandro Ochoa**. Single-locus imputation of ancient African DNA using novel regression-based approach. *American Society of Human Genetics (ASHG) Annual Meeting*. Walter E. Washington Convention Center, DC. 2023-11-03. Presented by Ratchanon Pornmongkolsuk.
- 2023 Shannon Clarke, Makenzie Beaman, Yuncheng Duan, Apoorva Iyengar, Revathy Venkuttan, Eden Harris, Allison Ashley-Koch, Rasheed Gbadegesin, Opeyemi Olabisi, William H Majoros, Timothy E Reddy, **Alejandro Ochoa**. Duke Genomic Scholars Program: Providing Accessible Genomic Training for a Diverse Workforce. *NIH Centers for Excellence in Genomics Science (CEGS) Annual Meeting*. Kimmel Center, New York University, New York, NY. 2023-10-11. Presented by Shannon Clarke.
- 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. 2022-10-27. Presented by Zhuoran Hou.
- 2022 **Alejandro Ochoa**, Yuncheng Duan, Revathy Venkuttan, Shannon Clarke, Timothy E 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. 2022-10-19.
- 2021 **Alejandro Ochoa**, Amika Sood. Joint inference of admixture and population history from the genetic covariance structure. *Probabilistic Modeling in Genomics (ProbGen) conference*. Virtual. 2021-04-14.
- 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. 2020-10-27.
- 2019 Alejandro Ochoa, John D Storey. Relatedness and Differentiation in Arbitrary Population Structures. *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 Alejandro Ochoa, John D Storey. Relatedness and Differentiation in Arbitrary Population Structures. *Probabilistic Modeling in Genomics (ProbGen) conference*. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY. 2018-11-05.
- 2018 Alejandro Ochoa, John D Storey. Relatedness and Differentiation in Arbitrary Population Structures. *Population, Evolutionary and Quantitative Genetics Conference*. Madison Concourse Hotel, Madison, WI. 2018-05-15.
- 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. 2016-11-03.
- 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. 2016-11-03. Presented by Srikanth Gottipati.
- 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. 2015-09-18.
- 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 (ProbGen) conference*. HHMI Janelia Farm, Ashburn, VA. 2013-03-25.
- 2010 Alejandro Ochoa, Manuel Llinás, Mona Singh. Using context to predict protein domains across diverse organisms. *Research in Computational Molecular Biology (RECOMB) 3rd Joint Conference on Systems Biology, Regulatory Genomics, and DREAM Challenges*. Columbia University, New York, NY. 2010-11-09.

Teaching

DUKE UNIVERSITY

- 2022-2024 Human Genetics. (Co-Lecturer Spring 2022-2024)
- 2021-2024 UPGEN 778A-F Mini course: Genetic population structure and relatedness (Fall 2021-2024)
- 2019-2024 SIBS lecture on genetic association studies (Summer 2019, 2021-2024)
- 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 2014-2017)
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

2022-now	Ratchanon "RP" Pornmongkolsuk. PhD. Graduate rotation, Dissertation adviser. Ochoa Laboratory. University Program in Genetics and Genomics, Duke University.
2022-now	Zhuoran Hou. PhD. Graduate rotation, Dissertation adviser. Ochoa Laboratory. Department of Biostatistics and Bioinformatics, Duke University.
2023-now	Bide "Peter" Chen. PhD. Dissertation committee, Dissertation adviser. Goldberg-Ochoa Laboratory. University Program in Genetics and Genomics, Duke University.
2023-now	Gabriel Kennedy. PhD. Dissertation committee, Dissertation adviser. Goldberg-Ochoa Laboratory. University Program in Genetics and Genomics, Duke University.
2025-now	Isabella Xu. Master's. Master's project adviser. Ochoa Laboratory. Department of Biostatistics and Bioinformatics, Duke University.

CURRENT TRAINEES - SECONDARY ADVISER

2021-now	Cymfenee Dean-Phifer. PhD. Graduate rotation, Dissertation committee. Hauser Laboratory. Computational Biology and Bioinformatics Program, Duke University.
2023-now	Grace E. Rhodes. PhD. Graduate rotation, Dissertation committee. Allen Laboratory. Department of Biostatistics and Bioinformatics, Duke University.
2023-now	Anvita Kulshrestha. PhD. Dissertation committee. Ashley-Koch Laboratory. University Program in Genetics and Genomics, Duke University.
2024-now	Jennifer Drucker Varner. Fellow. Scholarship Oversight Committee. Gbadegesin Laboratory. Department of Pediatrics, Duke University.
2024-now	Constantine Stavrianidis. PhD. Dissertation committee. Allen Laboratory. Computational Biology and Bioinformatics Program, Duke University.
2025-now	Ruolan Li. PhD. Dissertation committee. Allen Laboratory. Department of Biostatistics and Bioinformatics, Duke University.
2025-now	Ryan Schulken. Master's. Master's project committee. Majoros Laboratory. Department of Biostatistics and Bioinformatics, 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.
2020-2025	Tiffany Tu. PhD. Graduate rotation, Dissertation adviser. Ochoa Laboratory. Computational Biology and Bioinformatics Program, Duke University.
2020-2022	Jiajie Shen. Master's. Research, Master's project adviser. Ochoa Laboratory. Department of Biostatistics and Bioinformatics, Duke University.
2021-2022	Emmanuel Mokel. Undergraduate. Research Independent Study. Ochoa Laboratory. Department of Statistical Science, Duke University.
2023-2023	Danielle Mensah. Undergraduate. Research Independent Study. Ochoa Laboratory. Department of Computer Science, 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.
2019-2024	Xue "Scarlett" Zou. PhD. Dissertation committee. Allen Laboratory. Computational Biology and Bioinformatics Program, Duke University.
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	Brandon M. Lê. PhD. Dissertation committee. Ashley-Koch Laboratory. University Program in Genetics and Genomics, Duke University.
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 Genet-

	ics and Genomics, Duke University.
2021-2022	Weiliang "Frank" Tian. Master's. Master's project committee. Soderling Laboratory. Department of Biostatistics and Bioinformatics, Duke University.
2022-2025	Changxin Wan. PhD. Dissertation committee. Ji Laboratory. Computational Biology and Bioinformatics Program, Duke University.
2023-2024	Jinting Justin Liu. Master's. Master's project committee. Majoros Laboratory. Department of Biostatistics and Bioinformatics, Duke University.
2024-2024	Katelyn Jaggi. PhD. Graduate rotation. Ochoa Laboratory. University Program in Genetics and Genomics, Duke University.
2024-2024	Erick Figueroa Ildefonso. PhD. Graduate rotation. Ochoa Laboratory. University Program in Genetics and Genomics, Duke University.
2024-2025	Elisa Ma. Master's. Master's project committee. Landstrom and Allen Laboratory. Department of Biostatistics and Bioinformatics, Duke University.
2025-2025	Madison Strain. PhD. Dissertation committee. Ashley-Koch Laboratory. University Program in Genetics and Genomics, Duke University.

Research experience

2018-now	Principal investigator, Duke. I lead a team of trainees (graduate students, postdocs, master students and undergraduates) pursuing original research in statistical genetics and computational biology. Our lab focuses on models and applications for structured populations, including multi-ethnic and admixed cohorts and modeling cryptic relatedness.
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 cerevisiae</i> and <i>Homo sapiens</i> .
2005-2006	Undergraduate Research Assistant, Keating Lab, MIT. Analyzed full-atom computational protein designs using modified van der Waals potentials.

Organizations

2023-now	American Mathematical Society (AMS). Member.
2020-now	American Society of Human Genetics (ASHG). Member.

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. Member.

Outreach, admissions, committees, and other service

2020-now	Duke Center for Combinatorial Gene Regulation: Outreach and Engagement. Funded by a NIH Centers for Excellence in Genomics Science (CEGS) grant. Includes the Duke Genomic Scholars Program: providing accessible genomic training for a diverse workforce. Duke University.
2019-now	B&B Diversity and Inclusion Committee. Duke University.
2019-2024	CBB PhD Admissions Committee. Duke University.
2024	Promise and pitfalls of polygenic risk scores, faculty and postdoc panel, Triangle Center for Evolutionary Medicine's (TriCEM) annual Evolutionary Medicine Summer Institute (EMSI).
2024	B&B retreat, moderated session on Research Working Group. Duke University.
2024	Using Race, Ethnicity & Ancestry as Population Descriptors in Genetics and Genomics Research (NASEM report symposium), faculty panel. Duke University.
2023	CBB retreat, faculty panel. Duke University.
2023	Genomic Scholars Program, faculty panel. Duke University.
2023	Session moderator, o21: Human genome evolving I. ASHG annual meeting.
2023	Abstract reviewer, topic Evolutionary and Population Genetics. ASHG annual meeting.
2022	Session moderator, S41: Populations evolving: Modeling genetic variation to understand evolutionary processes. ASHG annual meeting.
2021-2022	Faculty Committee Member, Duke Next Generation Leaders. Duke University.
2021	B&B Faculty Search Committee. Duke University.
2021	B&B Master of Biostatistics Virtual Visit Day. Duke University.
2019	B&B informational interviewing practicum. Duke University.
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.
2008	Graduate school recruiting, student group panel, I represented the Latino Graduate Student Association (LGSA). 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.