

Audrey E. Hendricks, PhD

August 12, 2024

GENERAL INFORMATION

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| <i>Mailing Address:</i> | Department of Biomedical Informatics Anschutz Health Sciences Building 1890 N. Revere Court, Mailstop F600 Aurora, CO 80045 | <i>Google Scholar:</i> h-index = 24 i10-index = 40 4249 citations (2771 since 2019) 56 peer reviewed journal articles 6 first author (5 corresponding author) 1 co-first author and corresponding author 7 senior author (4 corresponding author) 2 co-senior author (1 co-corresponding author) |
| <i>E-mail</i> | audrey.hendricks@cuanschutz.edu | |
| <i>Website</i> | http://audreyhendricks.com | |
| <i>Github</i> | https://github.com/hendriau | |

CURRENT INTERESTS

I am a tenured Associate Professor of Statistics in the Department of Biomedical Informatics at the University of Colorado Anschutz with additional appointments including in the Department of Biostatistics and Informatics and the Department of Mathematical and Statistical Sciences. I am passionate about increasing inclusion and representation in all areas of science, including who completes the research, what questions are asked, and for whom the research is useful. In this aim, I co-direct two training programs to increase representation in genetics: Pathways in Genomic Data Science ([PATH-GDS](#)) and Pathways in Genomic Research Experiences for Undergraduates ([PATH-GREU](#)). I lead the Hendricks research team where we connect biomedical research and statistical/machine learning methods. Sitting at the interface between the applied and the theoretical enables our team to develop and use methods across a range of areas including: improving the utility and equity of large, publicly available genetic resources, identifying the biological mechanisms of healthy diets, elucidating the genomic underpinnings of conditions and traits, and, most recently, evaluating how genetic risk varies over internal and external environments including social determinants of health. We follow best practices of reproducibility and robust science by creating open source, well documented software and releasing all data and code used for our studies. Our team is highly collaborative working with people from a variety of backgrounds and education levels. We are always learning, improving, and pushing ourselves and others to be our best. In doing so, we produce first-class research for the broader community and train the next generation of genomics and health data scientists.

KEY WORDS

Statistics, biostatistics, genetics, ‘omics, common controls, summary data, obesity, big data, nutrition

EDUCATION

Visiting Postdoctoral Fellow (Sept. 2012-Aug. 2013); **Broad Institute of MIT and Harvard & Massachusetts General Hospital**; Mentor: *Assistant Professor of Medicine for Harvard Medical School-Diabetes Unit, Jose Florez*

Statistical Genetics Postdoctoral Fellow (Sept. 2011-Aug. 2013); **Wellcome Trust Sanger Institute, Cambridge University**; Mentors: *Head of Human Genetics & Metabolic Disease Group Leader, Inês Barroso; Analytical Genomics of Complex Traits Group Leader, Eleftheria Zeggini*

Ph.D in Biostatistics (2012); **Boston University**, Graduate School of Arts and Sciences
Dissertation: “Exploration of Gene Region Simulation, Correction for Multiple Testing, and Summary Methods”; Thesis Advisor: Kathryn L. Lunetta, PhD

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B.A. in Economics (2002); **University of Colorado Boulder**, College of Arts and Sciences; Magna Cum Laude

B.A. in Music (2002); **University of Colorado Boulder**, College of Music

PROFESSIONAL POSITIONS

Primary Appointment

Associate Professor (without tenure) – Department of Biomedical Informatics, University of Colorado Anschutz Medical Campus (Dec. 2022 – Present)

Associate Professor (with tenure) – Department of Mathematical and Statistical Sciences, University of Colorado Denver (Sept. 2020 – Dec. 2022)

Assistant Professor – Department of Mathematical and Statistical Sciences, University of Colorado Denver (Aug. 2013 – Aug. 2020)

Other Roles

Co-Director, Pathways in Genomic Research Experiences for Undergraduates (Sept. 2023 – present)

Co-Director, Pathways in Genomic Data Science (June 2023 – present)

Faculty Researcher, Ludeman Family Center for Women's Health Research (Sept. 2024 – present)

Associate Professor – secondary appointment, Department of Mathematical and Statistical Sciences, University of Colorado Denver (Dec. 2022 – Present)

Faculty, Human Medical Genetics Program, CU Anschutz Medical Campus (Oct. 2013 – Present)

Associate Professor – secondary appointment, Department of Biostatistics and Informatics, Colorado School of Public Health (Sept. 2020 – Present)

Associate Professor – secondary appointment, Colorado Center for Personalized Medicine, University of Colorado Anschutz Medical Campus (Sep. 2020 – Present)

Assistant Professor – secondary appointment, Department of Biostatistics and Informatics, University of Colorado School of Public Health (Oct. 2013 – Aug. 2020)

Assistant Professor – secondary appointment, Colorado Center for Personalized Medicine, University of Colorado Anschutz Medical Campus (Sep. 2018 – Aug. 2020)

Scientific Advisory Board, Human Code, (April 2017-Feb. 2018)

Consultant, Statistical Genetics, Wellcome Trust Sanger Institute (Aug. 2013-Dec. 2017)

Head of Human Genetics & Metabolic Disease Group Leader, Inês Barroso

Statistical Genetics Consultant for NHLBI Framingham Heart Study (March 2010-Aug. 2011)

Associate Dir. and Scientific Dir. of SHARe Project, Framingham Heart Study, NHLBI, Christopher O'Donnell
Director, Framingham Heart Study, NHLBI, Daniel Levy

DIVERSITY, INCLUSION, AND EQUITY TRAINING AND SERVICE

Member of Justice, Equity, Diversity, and Inclusion (JEDI) committee for the Western North American Region (WNAR) of the Biometrics Society (2021 – present)

Member of the Planning Committee for Hispanic Serving Research Universities (HSRU) Conference for Hispanic Women in Physical Sciences and Engineering (2023)

HEAL Foundations in Equity CU certificate, 4 out of 4 sessions, DEI Basics, Implicit Bias, Microaggressions, Equity in Action (2023-2024)

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Multicultural Mentoring, 2 out of 3 sessions, Bridging Differences for Better Mentoring and Creating Mutually Empowering Relationships (Fall 2022)

Equity Certificate Program, 2 out of 4 Modules, From Bystander to Active Allyship and Leading through an Equity Lens (Spring 2021)

ENAR Fostering Diversity in Biostatistics Workshop (March, 2021)

AWARDS AND FELLOWSHIPS

Personal

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| 2024 | Distinguished Alumni, Boston University Biostatistics (1 given per year) |
| 2022 | University of Colorado Denver Excellence in Research Award (1 given per year) |
| 2022 | College of Liberal Arts and Sciences Excellence in Diversity, Equity, and Inclusion in Research Award (1 given per year), University of Colorado Denver |
| 2022 | College of Liberal Arts and Sciences Excellence in Research Award (3 given per year), University of Colorado Denver |
| 2021 | The Perseverance Award, CU Denver Pandemic Research and Creative Activities Awards |
| 2020 | College of Liberal Arts and Sciences Excellence in Teaching Award (3 given per year), University of Colorado Denver |
| 2019 | College of Liberal Arts and Sciences Excellence in Research Award (3 given per year), University of Colorado Denver |
| 2018 | NIH Big Data Innovation Lab in Single Cell Dynamics Attendee (30 early career investigators chosen to attend), Bend, Oregon |
| 2013, '14, '19 | Young Upwardly Mobile Professors Award, University of Colorado - Denver |
| 2012 | Stellar Abstract Award, Program in Quantitative Genomics (PQG) Conference, Harvard School of Public Health |
| 2011 | Outstanding Advisor Award, FSILG, MIT |
| 2008 | Statistics in Epidemiology Travel Award to the American Statistical Associations Joint Statistical Meeting |
| 2008 | Boston University Women Graduates' Club Scholarship |
| 2007 | Kappa Alpha Theta Betty B. & James B. Lambert Foundation Scholarship |
| 2007 | Induction into Mu Sigma Rho, National Honor Society for Statistics |
| 2005-2007 | NIGMS Training Grant in Biostatistics, Boston University |
| 2002 | Magna Cum Laude in Economics, University of Colorado: In recognition of overall academic study and completion of Honors Thesis |
| 1997-2002 | Dean's List, University of Colorado Boulder |
| 2000 | International Study Abroad Merit Scholarship, Boulder, Colorado |
| 1999 | Winnifred Dick Ingals Scholarship, Denver, Colorado |
| 1998 | Dean's Scholarship, University of Colorado Boulder |

As Mentor

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| Spring 2024 | Souha Tifour, Outstanding MS Statistics Graduate, Dept. Mathematical & Statistical Sciences (one award per degree program) |
| Fall 2023 | Riley Lamont, Outstanding MS Statistics Graduate, Dept. Mathematical & Statistical Sciences (one award per degree program) |
| Fall 2022 | Adelle Price, Outstanding MS Statistics Graduate, Dept. Mathematical & Statistical Sciences (one award per degree program) |
| Fall 2022 | (Kelsey) Nikole Scribner-Trout, Summa Cum Laude, Dept. Mathematical & Statistical Sciences |
| Spring 2022 | Adelle Price, 3-minute talk (3MT) winner, State of Colorado |
| Winter 2020 | Adelle Price, 3-minute talk (3MT) winner, CU Denver Anschutz Medical Campus |

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| Fall 2021 | Ian Arriaga-MacKenzie, AJHG Cotterman Award for substantial contribution to the field of Human Genetics; <i>This award, earned for being first author on the Summix manuscript, is especially notable given the award is most often given to PhDs and post-docs. Mr. Arriaga-MacKenzie earned this award as a 5-year BS/MS student.</i> |
| Fall 2021 | Ian Arriaga-MacKenzie, College of Liberal Arts and Sciences CU Denver Outstanding MS student (one awarded per college) |
| Fall 2021 | Souha Tifour, College of Liberal Arts and Sciences CU Denver Outstanding BS student |
| Spring 2021 | Nicholas Weaver, Colorado/Wyoming Chapter of the American Statistical Association Maurice Davies Award for outstanding contribution by a student to statistics |
| Spring 2021 | Nicholas Weaver, CU Denver Department of Mathematical and Statistical Sciences, Lynn Bateman Memorial Award for Teaching Excellence by a TA |
| Fall 2020 | Nicholas Weaver, CU Denver Department of Mathematical and Statistical Sciences, Outstanding Teaching Assistant Award |
| Fall 2020 | Jessica Murphy, Outstanding MS Student College of Liberal Arts and Sciences CU Denver |
| Spring 2020 | Sam Chen, 3 rd place People's Choice Award for Technology, Engineering, and Math at CU Denver's Research and Creative Activities Symposium (RaCAS) |
| Spring 2020 | Catherine Fitch, 2 nd place Social Sciences at CU Denver's RaCAS |
| Fall 2019 | Ian Arriaga MacKenzi, Gregory Matesi, and Alexandria Ronco. Undergraduate Research Opportunity Program, University of Colorado Denver, Award to travel to the International Genetic and Epidemiology meeting to present research |
| Spring 2019 | Jordan Hall, CU Denver Graduate School Dean's Distinguished Student Service Award |

PUBLICATIONS (in descending chronological order; students/mentees[#], *corresponding author)

1. Kemp, J.F., Hambidge, K.M., Westcott, J.L., Ali, S.A., Saleem, S., Garces, A., Figueroa, L., Somannavar, M.S., Goudar, S.S., Long, J.M., **Hendricks, A.E.**, Krebs, N.F., Women First Preconception Maternal Nutrition Trial. Zinc supplementation initiated prior to or during pregnancy modestly impacted maternal status and high prevalence of hypozincemia in pregnancy and lactation: the Women First Preconception Maternal Nutrition Trial. *J Nutr.* **2024** 10.1016/j.tjnut.2024.04.018.
2. Hill, E.B., Tang, M., Long, J.M., Kemp, J.F., Westcott, J.L., **Hendricks, A.E.**, Reisdorph, N.A., Campbell, W.W., Krebs, N.F., and mini, M.E.D.T.T. mini-MED: study protocol for a randomized, multi-intervention, semi-controlled feeding trial of a Mediterranean-amplified vs. habitual Western dietary pattern for the evaluation of food-specific compounds and cardiometabolic health. *Trials* **2024**. 25, 101. 10.1186/s13063-024-07939-8.
3. Farias TDJ, Brugiapaglia S, Croci S, Magistrini P, Curcio C, Zguro K, Fallerini C, Fava F, Pettini F, Kichula KM, Pollock NR, Font-Porterias N, Palmer WH, Marin WM, Baldassarri M, Bruttini M, Hollenbach JA, **Hendricks AE**, Meloni I, Novelli F; GEN-COVID Multicenter Study Group; Renieri A, Furini S, Norman PJ, Amoroso A. HLA-DPB1*13:01 associates with enhanced, and KIR2DS4*001 with diminished protection from developing severe COVID-19. *HLA.* **2023** Oct 18. doi: 10.1111/tan.15251. PMID: 37850268.
4. Hill EB, Reisdorph RM, Rasolofomanana-Rajery S[#], Michel C, Khajeh-Sharafabadi M[#], Doenges KA, Weaver N[#], Quinn K, Sutliff AK, Tang M, Borengasser SJ, Frank DN, O'Connor LE, Campbell WW, Krebs NF, **Hendricks AE**, Reisdorph NA. Salmon Food-Specific Compounds and Their Metabolites Increase in Human Plasma and Are Associated with Cardiometabolic Health Indicators Following a Mediterranean-Style Diet Intervention. *The Journal of Nutrition.* **2023**. [10.1016/j.tjnut.2023.10.024](https://doi.org/10.1016/j.tjnut.2023.10.024)
5. Shankar, K., Ali, S.A., Ruebel, M.L., Jessani, S., Borengasser, S.J., Gilley, S.P., Jambal, P., Yazza, D.N., Weaver, N.[#], Kemp, J.F., Westcott, J.L., **Hendricks, A.E.**, Saleem, S., Goldenberg, R.L., Hambidge, K.M., Krebs, N.F. Maternal nutritional status modifies heat-associated growth restriction in women with chronic malnutrition. *PNAS Nexus.* **2023**. 2. 10.1093/pnasnexus/pgac309.

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A collaborative applied paper. I was the statistical expert and helped to ensure appropriate analysis and interpretation.

6. Tang M^{*,†}, Weaver NE^{#,†}, Frank DN, Ir D, Robertson CE, Kemp JF, Westcott J, Shankar K, Garces AL, Figueroa L, Tshetu AK, Lokangaka AL, Goudar SS, Somannavar M, Aziz S, Saleem S, McClure EM, Hambidge M, **Hendricks AE[‡]**, Krebs NF[‡], and the Women First Study Group. Longitudinal Reduction in Diversity of Maternal Gut Microbiota During Pregnancy Is Observed in Multiple Low-Resource Settings: Results. *Frontiers in Microbiology*. **2022**. Aug 1;13:823757. doi: 10.3389/fmicb.2022.823757. (PMCID: PMC9376441). [†] joint first authors; [‡] joint senior authors

A collaborative applied paper. I am joint senior author indicating my leadership in design, analysis, and interpretation of the study. Dr. Weaver, joint first author, was a PhD student in my team and was the analytical lead performing many novel analyses.

7. Wojcik GL, Murphy J[#], Edelson JL, Gignoux CR, Ioannidis AG, Manning A, Rivas MA, Buyske S, **Hendricks AE^{*}**. Opportunities and challenges for the use of common controls in sequencing studies. *Nat Rev Genet* **2022**. <https://doi.org/10.1038/s41576-022-00487-4>. (PMID: 35581355)
A review paper in the top-ranking genetics journal. I lead all aspects of the manuscript from conception to collaboration to writing. Ms. Jessica Murphy is a PhD student in my team and lead the development of informative figures and tables for the manuscript.

8. Murphy JI^{#,*}, Weaver NE[#], and **Hendricks, A.E.** Accessible analysis of longitudinal data with linear mixed effects models. *Dis Model Mech*. **2022** 15. (PMCID: PMC9092652)

A software paper providing a Shiny App and directions to enable easy and appropriate analysis of longitudinal data on the internet. Ms. This was Ms. Jessica Murphy's MS project. I was Ms. Murphy's MS advisor and mentor for this project. Dr. Weaver, a PhD student at the time, was Ms. Murphy's co-mentor.

9. Null M^{#,*}, Dupuis J, Sheinidashtegol P, Laver RM, Gignoux CR, **Hendricks AE**. RAREsim: A simulation method for very rare genetic variants. *American Journal of Human Genetics*. **2022** Mar 15:S0002-9297(22)00060-X. doi: 10.1016/j.ajhg.2022.02.009. (PMCID: PMC9069075).

A method development manuscript lead by former PhD student Dr. Megan Null. This method was part of Dr. Null's dissertation. I was Dr. Null's PhD advisor and mentor for this project.

10. Null M[#], Yilmaz F, Astling D, Yu HC, Cole J, Hallgrímsson B, Santorico SA, Spritz RA, Shaikh TH^{*}, **Hendricks AE^{*}**. Genome-wide analysis of copy number variants and normal facial variation in a large cohort of Bantu Africans. *Human Genetics and Genomics Advances*. **2022** Adv 3, 100082. (PMCID: PMC8756499)

A collaborative applied paper. I am senior author indicating my leadership in conceiving the study and analysis plan and mentoring the application. Dr. Null was a PhD student in my team.

11. Tang M, Matz KL, Berman LM, Davis KN, Melanson EL, Frank D, **Hendricks AE**, Krebs NF. Effects of complementary feeding with different protein-rich foods on infant growth and gut health: study protocol. *Frontiers in Pediatrics*, **2022** Jan 13;9:793215. doi: 10.3389/fped.2021.793215. (PMCID: PMC8793676)

A collaborative protocol paper. I designed the statistical design and analysis plan as well as performed the power analyses. I am second to last author indicating my senior role.

12. Arriaga-MacKenzie IS^{#,^}, Matesi G[#], Chen S[#], Ronco A[#], Marker KM[#], Hall JR[#], Scherenberg R[#], Khajeh-Sharafabadi M[#], Wu Y[#], Gignoux CR, Null M[#], **Hendricks AE^{*}**. Summix: A method for detecting and adjusting for population structure in genetic summary data. *Am J Hum Genet* **2021** Jul 1;108(7):1270-1282. doi: 10.1016/j.ajhg.2021.05.016. (PMCID: PMC8322937) [^]*Ian Arriaga-MacKenzie received the AJHG Cotterman award for outstanding contribution by a trainee in Human Genetics*

A method development manuscript that I lead in my team. I conceived of the idea, performed initial simulations and analyses, and mentored all trainees in the final simulations, applications, and coding. This manuscript includes 7 students who started working with me as undergraduates, including the first author. This was the first genetics project for most trainees including the first author.

13. Young AE, Kemp JF, Uhelson C, Westcott JL, Ali SA, Saleem S, Garces A, Figueroa L, Somannavar MS, Goudar SS, Hambidge MK, **Hendricks AE**, Krebs NF. Improved first trimester maternal iodine status with preconception supplementation: The Women First Trial. *Matern Child Nutr*, **2021** e13204. (PMCID: PMC8476419)

A collaborative application paper. I am second to last author indicating my senior role. I designed, performed, and interpreted statistical analysis and wrote and revised the analysis portions of the manuscript.

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14. Yilmaz F, Null M[#], Astling D, Yu HC, Cole J, Santorico SA, Hallgrimsson B, Manyama M, Spritz RA, **Hendricks AE**, Shaikh TH. Genome-wide copy number variations in a large cohort of bantu African children. *BMC Med Genomics* **2021** 14, 129.
A collaborative application paper from an R03 on which I was an investigator. Second to last author indicates my senior role. I provided expertise to ensure the computational analyses were employed and interpreted correctly.
15. Sutliff AK, Saint-Cyr M, **Hendricks AE**, Chen SS[#], Doenges KA, Quinn K, Westcott J, Tang M, Borengasser SJ, Reisdorph RM, Campbell WW, Krebs NF, Reisdorph NA. Lipidomics-Based Comparison of Molecular Compositions of Green, Yellow, and Red Bell Peppers. *Metabolites* **2021**. 11. DOI: 10.3390/metabo11040241 (PMCID: PMC8070949)
A collaborative application paper. I performed the statistical analysis and ensured appropriate interpretation of results.
16. Tang M, Weaver NE[#], Berman LM, Brown LD, **Hendricks AE**, Krebs NF. Different Blood Metabolomics Profiles in Infants Consuming a Meat- or Dairy-Based Complementary Diet. *Nutrients* **2021** Jan 27;13(2):388. doi: 10.3390/nu13020388. (PMCID: PMC7912106)
A collaborative application paper. I am second to last author indicating my senior role. I mentored Mr. Weaver, my PhD student, in performing all statistical analyses ensuring appropriate analysis, interpretation, and writing.
17. Okpara C^{#,*}, **Hendricks AE**, Cobb L. Beyond Aggravating and Mitigating Factors: The Analysis of Colorado's Death Penalty Cases (1999-2010). *Justice Evaluation Journal*, **2021**. DOI: 10.1080/24751979.2021.1877090
While this is outside of my research focus, I was motivated by the importance of the project and passion of Ms. Okpara. I was her MS project advisor and primary mentor for this manuscript helping ensure appropriate analysis and interpretation, as well as clear writing. Author order differs from where I typically publish with second author indicating the second most substantial and a senior role.
18. Hall L[#] and **Hendricks AE***. High-throughput analysis suggests differences in journal false discovery rate by subject area and impact factor but not open access status. *BMC Bioinformatics*. **2020**.
An applied manuscript implementing a novel method to estimate the empirical false discovery rate in journals using scraped abstracts. Here, we apply this method in over 90 journals and over 30,000 abstracts. Dr. Hall was my MS student; this manuscript developed from her MS project.
19. Marenne G, **Hendricks AE**, Perdikari A, Bounds R, Payne F, Keogh JM, Lelliott CJ, Henning E, Pathan S, Ashford S, Bochukova EG, Mistry V, Daly A, Hayward C, Interval, UK10K Consortium, Wareham NJ, O'Rahilly S, Langenberg C, Wheeler E, Zeggini E, Farooqi IS, Barroso I. (2020). Exome Sequencing Identifies Genes and Gene Sets Contributing to Severe Childhood Obesity, Linking PHIP Variants to Repressed POMC Transcription. *Cell Metab* **31**(6): 1107-1119 e1112, **2020**. (PMCID: PMC7267775)
A collaborative application paper. I am second author indicating my large role in the analysis and interpretation. I led the single variant analysis, and gene set analysis as well as collaborated and provided expertise on all other statistical aspects of the study.
20. Reisdorph NA, **Hendricks AE**, Tang M, Doenges KA, Reisdorph RM, Tooker BC, Quinn K, Borengasser SJ, Nkrumah-Elie Y, Frank DN, Campbell WW, Krebs NF. Nutrimetabolomics reveals food-specific compounds in urine of adults consuming a DASH-style diet. *Sci Rep* 10(1): 1157, **2020**. (PMCID: PMC6981146)
A collaborative application paper. I am second author. I led and performed most of the statistical analyses for this research including developing and applying a novel food score to quantify consumption of foods using untargeted metabolomics. I provided statistical expertise on all other aspects of the study.
21. Gilley SP, Weaver NE[#], Sticca EL[#], Jambal P, Palacios A, Kerns ME, Anand P, Kemp JF, Westcott JE, Figueroa L, Garcés AL, Ali SA, Pasha O, Saleem S, Hambidge KM, **Hendricks AE**, Krebs NF, Borengasser SJ. Longitudinal Changes of One Carbon Metabolites and Amino Acid Concentrations during Pregnancy in the Women First Maternal Nutrition Trial. *Current Developments in Nutrition*, **2020**. (PMCID: PMC7064164) <https://doi.org/10.1093/cdn/nzz132>
A collaborative application paper. I was the senior statistical collaborator on this project as represented by being third to last author. I designed and over saw all of the statistical analyses on this project. I have two students on this paper who completed the statistical analyses: Nicholas Weaver, a Math/Stat PhD Student and Evan Sticca, a Human Medical Genetics and Genomics PhD student.

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22. Kordas G, Rudra P, **Hendricks A**, Saba L, Kechris K. Insight into genetic regulation of miRNA in mouse brain. *BMC Genomics*, **2019**.
A collaborative application paper. I am a middle author on this paper. I provided guidance and insight into appropriate statistical methods for multiple testing and gene region analysis.
23. Tang M, Frank DN, Tshefu A, Lokangaka A, Goudar SS, Dhaded SM, Somannavar MS, **Hendricks AE**, Ir D, Robertson CE, Kemp JF, Lander RL, Westcott JE, Hambidge KM, Krebs NF. Different Gut Microbial Profiles in Sub-Saharan African and South Asian Women of Childbearing Age Are Primarily Associated with Dietary Intakes. *Frontiers in Microbiology*, **10**(1848), **2019**.
A collaborative application paper. I was the statistical expert on the paper advising on analysis and interpretation.
24. Yang Y, van der Klaauw A, Cacciottolo T, Stadler L, Keogh J, Henning E, Banton M, **Hendricks A**, Bochukova E, Mistry V, Lawler K, Liao L, Xu J, O'Rahilly S, Tong Q, UK10K Consortium, Barroso I, O'Malley B, Farooqi I, and Xu Y. Steroid Receptor Coactivator-1 Modulates the Function of Pomc Neurons and Energy Homeostasis. *Nature Communications*, **2019**. (PMCID: PMC6461669)
A collaborative application paper with a lot of laboratory work as well as some human genetics statistical analysis. I am a middle author. I was the statistical analyst and expert for the human genetics portion of the paper.
25. van der Klaauw AA, Croizier S, Mendes de Oliveira E, Stadler LKJ, Park S, Banton MC, Tandon P, **Hendricks AE**, Keogh JM, Riley SE, Papadia S, Henning E, Bounds R, Bochukova EF, Mistry V, O'Rahilly S, Simerly RB, INTERVAL, UK10K Consortium, Minchin JEN, Barroso I, Jones, EY, Bouret SG, Farooqi IS. Human Semaphorin 3 variants link melanocortin circuit development and energy balance. *Cell*, **2019**. Feb 7;176(4):729-742.e18. (PMCID: PMC6370916)
A collaborative application paper with a lot of laboratory work as well as some human genetics statistical analysis. I am a middle author. I was the statistical analyst and expert for the human genetics portion of the paper.
26. Riveros-McKay F, Mistry V, Bounds R, **Hendricks AE**, Keogh JM, Thomas, H, Henning E, Corbin LJ, Understanding Society Scientific Group, O'Rahilly S, Zeggini E, Wheeler E, Barroso I, Farooqi IS. Genetic architecture of human thinness compared to severe obesity, *PLoS Genetics*, **2019**. 15(1): e1007603. (PMCID: PMC6345421)
A collaborative application paper. I was the senior statistical expert on this paper advising and running the more complex statistical analyses. I also helped to write and revise the paper.
27. **Hendricks AE**, Billups S, Pike HNC[#], Farooqi IS, Zeggini E, Santorico SA, Barroso I, Dupuis J. ProxECAT: Proxy External Controls Association Test. A new case-control gene region association test using allele frequencies from public controls. *PLoS Genetics*, **2018**. (PMCID: PMC6191077)
Development of a new statistical genetics method and software. I was the driver of all aspects from conception to developing, and evaluating the method in simulations and real data, and writing the paper. I completed over 90% of the work. To ensure wide applicability and a robust method, I sought expertise and data as needed from the other authors on the paper.
28. Tang M[#], Andersen V, **Hendricks AE**, Krebs NF. Different Growth Patterns Persist at 24 Months of Age in Formula-Fed Infants Randomized to Consume a Meat- or Dairy-Based Complementary Diet from 5 to 12 Months of Age. *The Journal of Pediatrics*, **2018**. (PMCID: PMC6389371)
A collaborative application paper in longitudinal analysis of a nutritional intervention. I was the statistical expert on this paper advising on experimental design, analysis, and interpretation.
29. The TELOMAAS group & Tomaszewski, M. BMI is negatively associated with telomere length; a collaborative cross-sectional meta-analysis of 87 observational studies. *American Journal of Clinical Nutrition*, **2018**. (PMID: 30535086)
A collaborative application paper. I am a middle author on a meta-analysis with many contributors. I was the lead statistical analyst, correspondent, and author for our study's contribution to the paper.
30. Tang M[#], **Hendricks AE**, Krebs NF. A meat-or dairy-based complementary diet leads to distinct growth patterns in formula-fed infants: a randomized controlled trial. *American Journal of Clinical Nutrition*, **2018**. (PMCID: PMC6128676)
A collaborative application paper. I was the statistical expert on the project providing advice on experimental design, analysis, and interpretation. I also helped to revise the paper.

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31. Turcot V., Lu Y., Highland H. M., Schurmann C., Justice A. E., Fine R. S., Bradfield J.P., Esko T., Giri A., Graff M., Guo X., **Hendricks A.E.**,... Loos, R. J. F. Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, 50(1), 26–41. <https://doi.org/10.1038/s41588-017-0011-x>, 2018. (PMCID: PMC5945951)
A collaborative application paper. I am a middle author on a meta-analysis with many contributors. I was the lead statistical analyst, correspondent, and author for our study's contribution to the paper.
32. Moir L, Bochukova EG, Dumbell R, Banks G, Bains RS, Nolan PM, Scudamore C, Simon M, Watson K, Keogh J, Henning E, **Hendricks AE**, O'Rahilly S, Barroso I, Sullivan AE, Bersten DC, Whitelaw M, Kirsch S, Bentley E, Farooqi IS, Cox RD. Disruption of the homeodomain transcription factor orthopedia homeobox (Otp) is associated with obesity and anxiety. *Molecular Metabolism*, 2017. (PMCID: PMC5681237)
A collaborative application paper. I was the statistical lead for the analysis on human data for this paper providing comprehensive planning, application of the analysis, and interpretation. I also helped to write and revise the paper.
33. Tang M[#], Frank DN, **Hendricks AE**, Ir D, Esamai F, Liechty D, Hambidge KM, and Krebs NF. Iron in Micronutrient Powder Promotes an Unfavorable Gut Microbiota in Kenyan Infants. *Nutrients*, 2017. (PMCID: PMC5537890)
A collaborative application paper. I was the senior statistician this paper designing and overseeing the statistical tests and interpretation. I also helped to write and revise the paper.
34. **Hendricks AE***, Bochukova EG*, Marenne G, Keogh JM, Bounds R, Wheeler E, et al. Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. *Scientific Reports*, 2017 June, 1–14. (PMCID: PMC5758507) <https://doi.org/10.1038/s41598-017-03054-8> * Co-first authors
A collaborative application paper. I was the statistical lead for this paper completing over 90% of the statistical analysis and interpretation. I also helped to write and revise the paper.
35. Tachmazidou I, Süveges D, Min JL, Ritchie GRS, Steinberg J, Walter, K., ...**Hendricks, AE**, et al. Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *AJHG* 865–884. 2017. April. (PMCID: PMC5473732) <https://doi.org/10.1016/j.ajhg.2017.04.014>
A collaborative application paper. I provided statistical help and guidance regarding analysis of known obesity genes and gene-set enrichment. I also helped to write and revise the paper.
36. Lin H, Mueller-Nurasyid M, Smith A, Arking DE, Barnard J, Bartz TM, Lunetta KL, Lohman K, Kleber M, Lubitz SA, Feelhoed B, Trompet S, Niemeiher MN, Kacprowski T, Chasman DI, Klarin D, Sinner MF, Waldenberger M, Meitinger T, Harris TB, Launer LJ, Soliman EZ, Chen LY, Smith JD, Van Wagoner DR, Rotter JJ, Psaty BM, Sie Z, **Hendricks AE**, et al. Gene-gene interaction analyses for atrial fibrillation. *Scientific Reports*, 2016 Nov 8;6:35371. (PMCID: PMC5099695)
A collaborative application paper. I am a middle author on a meta analysis with many contributors. I was the lead analyst at the beginning of the project and designed the original study, then I moved to other projects and contributed as a statistical advisor.
37. Jeronic A, Memari Y, Ritchie G, **Hendricks AE**, Kolb-Kokocinski A, Matchan A, Vitart V, Hayward C, Kolcic I, Glodzik D, Wright A, Rudan I, Campbell H, Durbin R, Polašek O, Zeggini E, Perica VB. Whole exome sequencing in an isolated population from the Dalmatian island of Vis. *EJHG*, 2016 Oct;24(10):1479-87. (PMCID: PMC4950961).
A collaborative application paper. I was the senior statistical lead for this paper providing comprehensive planning and expertise regarding the analysis, and interpretation. I also helped to write and revise the paper.
38. Santorico SA, **Hendricks AE**. Progress in Methods for Rare Variant Association. *BMC Genetics*, 2016 Feb 3;17 Suppl 2:6. (PMCID: PMC4895384)
A review article. I took the lead on reviewing and writing the current state of the field in rare variant genetic association studies.
39. The UK10K project: rare variants in health and disease. *Nature*, 2015 Oct 1;526(7571):82-90. (PMCID: PMC4773891)

Audrey E. Hendricks, PhD

A large consortium project on which I was the lead statistician and analyst for the obesity group, was a leader in developing the QC and statistical analysis pipeline for the whole exome-sequencing. I was on several of the UK10K project groups including obesity, statistics, writing, and cohorts.

40. Zhang X, Johnson AD, **Hendricks AE**, Hwang SJ, Tanriverdi K, Ganesh SK, Smith NL, Peyser PA, Freedman JE, O'Donnell CJ. Genetic Associations with Expression for Genes Implicated in GWAS Studies for Atherosclerotic Cardiovascular Disease and Blood Phenotypes. *Hum Mol Gen*, **2014** Feb 1;23(3):782-95. (PMCID: PMC3900869)
A collaborative paper. I was the statistics and informatics expert on the paper. I developed the computational and analysis pipeline.
41. **Hendricks AE**, Dupuis J, Logue MW, Myers RH, Lunetta KL. Correction for multiple testing in a gene region. *EJHG*, **2014** Mar 22(3):414-8. (PMCID: PMC3925272)
A methodological paper comparing methods for testing multiple genetic variants within the same region. I was the driver of this paper including identifying the need, performing all analyses, visualizations. I also wrote the manuscript. Other authors on the manuscript provided expertise and guidance on the most appropriate ways to compare the methods, genetics expertise, and how to write the manuscript.
42. Pearce LR, Atanassova N, Banton MC, Bottomley B, van der Klaauw AA, Revelli JP, **Hendricks A**, Keogh JM, Henning E, Doree D, Jeter-Jones S, Garg S, Bochukova EG, Bounds R, Ashford S, Gayton E, Hindmarsh PC, Shield JP, Crowne E, Barford D, Wareham NJ, UK10K Consortium, O'Rahilly S, Murphy MP, Powell DR, Barroso I, Farooqi IS. KSR2 Mutations Are Associated with Obesity, Insulin Resistance, and Impaired Cellular Fuel Oxidation. *Cell*, **2013** Nov 7; 155(4):765-77. (PMCID: PMC3898740)
A collaborative application paper. I was the statistical lead for the human data analysis for this paper completing analysis, and interpretation. I also helped to write and revise the paper.
43. **Hendricks AE***, Dupuis J, Gupta M, Logue MW, Lunetta KL: A comparison of gene region simulation methods. *PLoS One*, **2012**; 7:e40925. (PMCID: PMC3399793)
44. Hadzi TC, **Hendricks AE**, Latourelle JC, Lunetta KL, Cupples LA, Gillis T, Mysore JS, Gusella JF, MacDonald ME, Myers RH, Vonsattel JP: Assessment of Cortical and Striatal Involvement in 523 Huntington Disease Brains. *Neurology*, **2012** Oct 16;79(16):1708-1715. (PMCID: PMC3468776)
45. Lee JH, Lee JM, Ramos EM, Gillis T, Mysore JS, Kishikawa S, Hadzi T, **Hendricks AE**, Hayden MR, Morrison PJ, Nance M, Ross CA, Margolis RL, Squitieri F, Gellera C, Gomez-Tortosa E, Ayuso C, Suchowersky O, Trent RJ, McCusker E, Novelletto A, Frontali M, Jones R, Ashizawa T, Frank S, Saint-Hilaire MH, Hersch SM, Rosas HD, Lucente D, Harrison MB, Zanko A, Abramson RK, Marder K, Sequeiros J, Landwehrmeyer GB, Shoulson I, Myers RH, MacDonald ME, and Gusella JF: TAA repeat variation in the *GRIK2* gene does not influence age at onset in Huntington's disease. *Biochemical and Biophysical Research Communications*, **2012** Aug 3;424(3):404-8. (PMCID: PMC3752397)
46. Dumitriu A, Moser C, Hadzi T, Williamson S, Pacheco C, **Hendricks AE**, Latourelle JC, Wilk J, Destefano A, Myers RH: Post-mortem Interval Influences α -Synuclein Expression in Parkinson Disease Brain. *Parkinson's Disease*, **2012**. 614212, doi:10.1155/2012/614212. (PMCID: PMC3317023)
47. Chen H[^], **Hendricks AE^{^*}**, Cheng Y, Cupples LA, Dupuis J, Liu CT: Comparison of statistical approaches to rare variant analysis for quantitative traits. *In BMC Proceedings*, **2011**. 5 Suppl 9:S113. (PMCID: PMC3287837) [^]Co-first authors ^{*}Corresponding author
48. Latourelle JC, **Hendricks AE**, Pankratz N, Wilk JB, Halter C, Nichols WC, Gusella JF, Destefano AL, Myers RH, Foroud T: Genomewide linkage study of modifiers of *LRRK2*-related Parkinson's disease. *Movement Disorders*, **2011** Sep; 26(11):2039-44. (PMCID: PMC3346677)
49. **Hendricks AE***, Latourelle JC, Lunetta KL, Cupples LA, Wheeler V, MacDonald ME, Gusella JF, Myers RH: Estimating the probability of *de novo* HD cases from transmissions of expanded penetrant CAG alleles in the Huntington Disease gene from male carriers of high normal alleles (27-35 CAG). *AJMG*, **2009**. 149A(7): 1375-81. (PMCID: PMC2724761)

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50. **Hendricks AE**, Zhu Y, Dupuis J: Genome-wide association and linkage analysis of quantitative traits: comparison of likelihood ratio test and conditional score statistic. *BMC Proceedings* **2009**. 3 Suppl 7:S100. (PMCID: PMC2795871)
51. Dragileva E, **Hendricks A**, Teed A, Gillis T, Lopez ET, Friedberg EC, Kucherlapati R, Edelman W, Lunetta KL, MacDonald ME, Wheeler VC: Intergenerational and striatal CAG repeat instability in Huntington's disease knock-in mice involve different DNA repair genes. *Neurobiol Dis* **2009**, 33:37-47. (PMCID: PMC2811282)
52. Swami M, **Hendricks AE**, Gillis T, Massood T, Mysore J, Myers RH, Wheeler VC: Somatic expansion of the Huntington's disease CAG repeat in the brain is associated with an earlier age of disease onset. *Hum Mol Genet* **2009**, 18:3039-3047. (PMCID: PMC2714728)
53. Manning AK, Ngwa JS, **Hendricks AE**, Liu CT, Johnson AD, Dupuis J, Cupples LA: Incorporating biological knowledge in the search for gene x gene interaction in genome-wide association studies. *BMC Proceedings* **2009**. 3 Suppl 7:S81 (PMCID: PMC2795984)
54. DeStefano AL, Latourelle J, Lew MF, Suchowersky O, Klein C, Golbe LI, Mark MH, Growdon JH, Wooten GF, Watts R, Guttman M, Racette BA, Perlmutter JS, Marlor L, Shill HA, Singer C, Goldwurm S, Pezzoli G, Saint-Hilaire MH, **Hendricks AE**, Gower A, Williamson S, Nagle MW, Wilk JB, Massood T, Huskey KW, Baker KB, Itin I, Litvan I, Nicholson G, Corbett A, Nance M, Drasby E, Isaacson S, Burn DJ, Chinnery PF, Pramstaller PP, Al-Hinti J, Moller AT, Ostergaard K, Sherman SJ, Roxburgh R, Snow B, Slevin JT, Cambi F, Gusella JF, Myers RH: Replication of association between ELAVL4 and Parkinson disease: the GenePD study. *Hum Genet* **2008**, 124:95-99. (PMCID: PMC2716559)
55. Latourelle JC, Sun M, Lew MF, Suchowersky O, Klein C, Golbe LI, Mark MH, Growdon JH, Wooten GF, Watts R, Guttman M, Racette BA, Perlmutter JS, Ahmed A, Shill HA, Singer C, Goldwurm S, Pezzoli G, Zini M, Saint-Hilaire MH, **Hendricks AE**, Williamson S, Nagle MW, Wilk JB, Massood T, Huskey KW, Laramie JM, DeStefano AL, Baker KB, Itin I, Litvan I, Nicholson G, Corbett A, Nance M, Drasby E, Isaacson S, Burn DJ, Chinnery PF, Pramstaller PP, Al-Hinti J, Moller AT, Ostergaard K, Sherman SJ, Roxburgh R, Snow B, Slevin JT, Cambi F, Gusella JF, Myers RH: The Gly2019Ser mutation in LRRK2 is not fully penetrant in familial Parkinson's Disease: the GenePD study. *BMC Medicine* **2008**, 6. (PMCID: PMC2596771)
56. Tobin JE, Latourelle JC, Lew MF, Klein C, Suchowersky O, Shill HA, Golbe LI, Mark MH, Growdon JH, Wooten GF, Racette BA, Perlmutter JS, Watts R, Guttman M, Baker KB, Goldwurm S, Pezzoli G, Singer C, Saint-Hilaire MH, **Hendricks AE**, Williamson S, Nagle MW, Wilk JB, Massood T, Laramie JM, DeStefano AL, Litvan I, Nicholson G, Corbett A, Isaacson S, Burn DJ, Chinnery PF, Pramstaller PP, Sherman S, Al-Hinti J, Drasby E, Nance M, Moller A, Ostergaard K, Roxburgh R, Sherman SJ, Roxburgh R, Snow B, Slevin JT, Cambi F, Gusella JF, Myers RH: Haplotypes and gene expression implicate the MAPT region for Parkinson disease: the GenePD Study. *Neurology* **2008**, 71:28-34. (PMCID: PMC2654275)

CONSORTIUM PUBLICATIONS

The publications listed above and on which my Google Scholar metrics are based are those on which I made a substantial contribution to the particular publication. Below are consortiums for which I played a considerable role. Given this, there are papers (that I do not list above or include in my metrics) on which I am listed as an author through my membership in the consortium.

UK10K Project (<http://www.uk10k.org>): I was one of four post-doctoral fellows funded directly on the UK10K project. I was the lead statistician and analyst on the obesity arm of the project and also contributed to the cohorts group, the statistics group, and the writing group. Since the UK10K project was one of the first large scale high-throughput sequencing studies, a substantial portion of my time was spent on identifying the appropriate quality control and statistical analysis frameworks to use for the whole-exome and whole-genome sequencing data.

Genome Sequencing Program (GSP) (<http://gsp-hg.org>): I developed and applied methods to use GSP as common control data and working with the Analysis Centers and the Common Controls Working Group.

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Population Architecture utilizing Genomics and Epidemiology (PAGE): My team is developing and applying methods to improve polygenic score transferability between diverse populations and identifying latent structural environmental variables and determinants of health.

BOOK CHAPTERS

Morris & Zeggini. Assessing Rare Variation in Complex Traits. Chapter: (Hendricks, AE) *Use of Appropriate Controls in Rare-Variant Studies* (239-252). Springer. 2015.

SOFTWARE and Internet Apps (Developed in the Hendricks Team)

1. **ProxeCAT** (2018). **Primary Developer:** Hendricks, AE. <https://github.com/hendriau/ProxECA>
2. **Summix**. (2021). **Primary Developers:** Arriaga-MacKenzie, I, Matesi G, & Hendricks AE. <https://www.bioconductor.org/packages/release/bioc/html/Summix.html>
3. **Summix Shiny App**. (2021). **Primary Developer:** Arriaga-MacKenzie, I. <https://shiny.clas.ucdenver.edu/Summix/>
4. **RAREsim**. (2022). **Primary Developer:** Null, M. <https://www.bioconductor.org/packages/release/bioc/html/RAREsim.html> and <https://github.com/meganmichelle/RAREsim>
5. **EasyLME Shiny App** (2022). **Primary Developer:** Murphy, J. <https://shiny.clas.ucdenver.edu/EasyLME/>
6. **Summix2**. (2024). **Primary Developers:** Stoneman, H & Price A. <https://www.bioconductor.org/packages/release/bioc/html/Summix.html>
7. **RAREsim2**. (2024). **Primary Developers:** Null, M., Barnard, RM, Murphy J. <https://github.com/hendriau/raresim>
8. **CCAFE**. (2024). **Primary Developers:** Stoneman, H. <https://github.com/wolffha/CCAFE/>

FUNDING HISTORY (Funded)

EXTERNAL

Seed Grant (PI: Hendricks) 03/01/2024 – 08/31/2024 0.05
PI; Evaluating polygenic score prediction accuracy across sample characteristics in the All of Us Research Program
University of Arizona subaward from NIH; \$40,000

1R25HG012994 (MPI: Duran/Liu/Hendricks) 09/18/2023 - 07/31/2028 0.05 Y1-Y5
MPI; Pathways in Genomics Research Experiences for Undergraduates from Underrepresented Groups
NIH/NHGRI \$338,547Y1 direct

R25HG012919 (Contact MPI: Hendricks; MPIs: French/Lange) 06/01/2023 - 05/30/2028 0.05 Y1-Y5
MPI; Research experience pathways in genomic data science (PATH-GDS) for underrepresented groups
NIH/NHGRI \$247,996Y1 direct

1R35HG011293 (PI: Hendricks) 9/01/2020-6/30/2025 0.525 FTE Y1; 0.3 FTE Y2-Y5
PI; “Methods to enable robust and efficient use of genetic summary data”
NIH/NHGRI \$281,663 Y1 direct

1R01DK126710; (PI: Tang, AMC) 02/2021 – 01/2026 0.08 Y1-Y2; 0.2 Y3-Y5
Co-I; “Dietary influence on infant growth and the gut microbiota”
NIDDK \$480k/yr direct cost

R01 AI158410 (PI: Norman, AMC) 9/1/2021 – 8/31/2025 0.05 Y1-Y5

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Co-I; Natural Killer cells and the Immunogenetics of COVID-19
NIH/NIAID

R01CA246586; (PI: Fishbein, AMC) 9/1/2020 – 8/31/2025 0.13 Y1; 0.15 Y2-Y5
Co-I; “Inherited genetic variation and penetrance of Hereditary Paraganglioma-Pheochromocytoma Syndrome”
NCI \$250k/yr direct cost

U01 AI090905; (PI: Norman, AMC) 7/1/2020 – 6/30/2025 0.05 Y1-Y5
Co-I; "Insights Into Immune-Related Diseases Born from Population Genomics"
NIAID \$549k/yr direct cost

INTERNAL

Seed Grant (PI: Hendricks) 09/01/2024 – 08/31/2025 0.05
PI; Evaluating polygenic score prediction accuracy across the menopause transition in the All of Us Research Program
Ludeman Center Health Equity Award for Intersectional Research in Women’s Health; \$50,000

FUNDING HISTORY (Previous)

EXTERNAL

R01 DK113957 (Krebs, AMC) 7/01/2018-3/30/2023 0.15 FTE (Y1-Y3); 0.08 FTE (Y4-Y5)
Co-I; “Predicting health outcomes of Mediterranean diet via metabolomics of foods and biospecimens”
NIH/NIDDK \$499,999 Y1 direct

INV-038612 (PI: Krebs, AMC) 11/2021-4/2022 0.05 FTE
Co-I; “Analyses of biomarkers of EED in Women First data”
Bill & Melinda Gates Foundation
\$99,999 direct

National Pork Board (PI: Tang, AMC) 5/2019-4/2022
Co-I; “Meat consumption during infancy on growth, gut health, sleep and neurodevelopment: a randomized controlled trial”
\$286,000 direct

OPP1055867 (Krebs/Hambidge, AMC) 6/1/2018-5/30/2021 0.2 FTE (Y6-Y8)
“Preconception Maternal Nutrition” – supplement to fund phenotyping and analysis of biomarkers
Bill & Melinda Gates Foundation/ Global Development

Foundation for Meat and Poultry Research and Education (Tang, AMC) 3/1/2019-8/30/2020
Co-I; “Meat as a first solid food on risk of overweight and neurodevelopment in infants”
\$192,884 direct

The Jayne Koskinas Ted Giovanis Foundation for Health and Policy (Bacher) 9/1/2018-8/31/2019
Co-I; “Uncovering the Life Clock of Red Blood Cells Using Single-Cell Analysis”
\$15,000 direct

R03-DE025363 (Shaikh, AMC) 07/01/2015-6/30/2017 0.2 FTE (Y1-Y2)
Co-I; “Genomewide Copy Number Variation Analysis and Association with Facial Shape Variation”
NIH/NIDCR \$150,000/yr
Funding request included a graduate research assistant under my supervision

Collaborative Research Travel Grant (Hendricks) 09/01/2015 – 12/31/2016

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PI; “Incorporating genome-wide information to find disease associated genes”

Burroughs Wellcome Fund \$10,000

To build collaboration with human geneticists to foster the development of a new statistical method.

INTERNAL

College of Liberal Arts and Sciences Dissemination Grant (Hendricks)

2018

PI; To support travel to the Joint Statistical Meeting to present Proxy External Controls Association Test.

\$2,000

Office of Research Services (Hendricks)

5/2017 – 8/2017

PI; “Identifying genetic determinants of immunotherapy success and brain metastasis in melanoma patients”

Funding to support a summer graduate student to complete analysis under my supervision.

\$2973.00

Office of Research Services (Hendricks)

11/2016

PI; To support collaborative travel to the Wellcome Trust Sanger Institute

\$1977.73

EXTERNAL PRESENTATIONS

Invited

| | |
|----------------|--|
| November 2024 | <i>Opportunities and Challenges for the Use of Common Controls in Sequencing Studies</i> , Foundations of Biomedical Data Science, Virtual. |
| November 2024 | <i>My Journey and Lessons Learned (so far...)</i> , 2024 Distinguished Alumni Award, Department of Biostatistics, Boston University, Boston. |
| August 2024 | <i>Pathways in Genomic Data Science</i> , Building an Inclusive and Representative Genomics Community, American Society for Human Genetics Webinar. https://learning.ashg.org/products/building-an-inclusive-and-representative-genomics-community-through-research-training-and-career-exposure-across-the-life-course-of-education-pathways#tab-product_tab_contents_1 |
| June 2024 | <i>Opportunities and Challenges for the Use of Common Controls in Sequencing Studies</i> , SeqSPACE National Cancer Institute (NCI) 2024, Virtual |
| May 2024 | <i>Detecting latent systemic structure in deep phenotyping and genotyping data</i> , STATGEN 2024, Pittsburgh, PA |
| March 2024 | <i>Assessing and Identifying Substructure</i> , PAGE, semi-annual meeting, Aurora, CO |
| September 2023 | <i>Opportunities in ‘omics informatics: from genetic summary data substructure to metabolomics derived food biomarkers</i> , Grand Rounds Laboratory Medicine, University of Washington, Seattle, WA. https://www.youtube.com/watch?v=BW1_VGwxuOU |
| March 2023 | <i>External Common Controls</i> , Biobank Rare Variant Analysis Consortium (BRaVA) Methods Meeting, Virtual |
| October 2022 | <i>Statistical problems and solutions in genetics and nutrition</i> , Department of Mathematics and Computer Science, Colorado College |
| September 2022 | <i>Methods and frameworks to increase the utility and equity of genetic summary data</i> , Program in Quantitative Genomics (PQG), Harvard University |
| March 2022 | <i>Enabling Equitable Use of Large Genetic Databases in Clinical Genomics</i> , New Mexico BioInformatics, Science and Technology (NMBIST) Symposium, Clinical Genomics, |

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Virtual

- March 2022 *Statistics in the News: how statistical thinking can help us be better consumers of the numbers, data, and statistics all around us*, Front Range Applied Mathematics Student Conference (FRAMSC), Keynote, Denver, CO
- Feb 2022 *Methods to increase the utility and equity of large genetic databases*, Statistical Genetics Working Group, Johns Hopkins University
- Oct 2021 *Methods to increase the utility and equity of large genetic databases*, quantitative cell and molecular biology (qCMB) program, Colorado State University
- Feb 2021 *Methods to increase the utility and equity of large genetic databases*, Statistical Genetics Working Group, Department of Biostatistics, Boston University, Virtual
- April 2020 *Evaluating Common Control Methods*, NHGRI's Genome Sequencing Project Annual Meeting, Virtual
- November 2019 *Estimating and modeling substructure within 'omics data*, Broad Institute of MIT and Harvard, Cambridge, MA
- April 2019 *Methods to Improve the use of Common Controls in Sequencing Studies*, University of Florida Department of Biostatistics, Gainesville, FL
- March 2019 *ProxECAT: A Case-Control Gene Region Association Test using Allele Frequencies from Public Controls*, Eastern North American Region of the International Biometric Society (ENAR), Philadelphia, PA
- March 2019 *Using Common Controls*, NHGRI's Genome Sequencing Project Annual Meeting, Bethesda, MD
- February 2019 *Statistical complications and solutions for using common controls in genetic sequencing studies*, Stat Alliance, Colorado State University
- January 2019 *Using Common Controls*, NHGRI's Genome Sequencing Project Common Controls Working Group, Virtual
- March 2018 *Proxy External Controls Association Test (ProxECAT)*, NHLBI Trans-Omics for Precision Medicine (TOPMed) Analysis Committee, Virtual
- November 2016 *Methods for association testing with massively different sequencing depths of coverage*, Wellcome Trust Genome Sciences Campus, UK
- June 2016 *A new method for gene region association testing with massively different sequencing depths of coverage*, Human Genetics Retreat, Wellcome Trust Sanger Institute, UK
- June 2015 *Methods for Studying Rare Variants in Next Generation Sequencing Data*, The Mathematical Sciences in Obesity, NIDDK Short Course – University of Alabama Birmingham
- April 2013 *Identifying and correcting for biases in experiments with external controls: An example from next generation sequencing*, Statistical Genetics Working Group, Boston University
- January 2012 *Evaluation of Gene Region Summary Methods*, First Friday Talks, Institute for Behavioral Genetics at the University of Colorado

Refereed (peer reviewed)

- October 2024 *Evaluating polygenic score prediction accuracy across the menopause transition in the All of Us Research Program*, National Conference for Women's Health Research, Colorado Springs, CO (poster)
- September 2022 *Phenome-wide PGS Portability in the Colorado Center for Personalized Medicine*,

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International Genetics and Epidemiology Society (IGES) Meeting, Paris, France

- May 2022 *Summix: A method for detecting and adjusting for population structure in genetic summary data*, Research in Computational Molecular Biology (RECOMB)-Genetics, La Jolla, CA
- January 2020 *Successful and sustainable undergraduate research in statistics through vertical integration of experience and horizontal integration of disciplines*, Joint Mathematical Meeting, Denver, CO
- October 2019 *Exome sequencing identifies multiple genes and gene-sets associated with severe childhood obesity*, American Society of Human Genetics, Houston (poster)
- August 2019 *Successful and sustainable undergraduate research in statistics through vertical integration of experience and horizontal integration of disciplines*, Joint Statistical Meeting, Denver (speed talk)
- October 2018 *Identifying Hidden Ancestries in Publicly Available Summary Data*, International Genetic and Epidemiology Society, San Diego
- October 2018 *Identifying Hidden Ancestries in Publicly Available Summary Data*, American Society of Human Genetics, San Diego (poster)
- August 2018 *ProxECAT: Proxy External Controls Association Test: A new case-control gene region association test using allele frequencies from public controls*, Joint Statistical Meeting, Vancouver (speed talk)
- October 2016 *A new method for gene region association testing with massively different sequencing depths of coverage*, International Genetic and Epidemiology Society, Toronto
- October 2016 *A new method for gene region association testing with massively different sequencing depths of coverage*, American Society of Human Genetics, Vancouver
- October 2014 *Next steps for whole exome sequenced cases: imputing non-coding regions and incorporating whole genome sequenced controls*, American Society of Human Genetics, San Diego (poster)
- June 2012 *Finding Obesity Genes by Whole Exome Sequencing in a UK Cohort of Severely Obese Children*, American Diabetes Association, Philadelphia
- November 2012 *Finding Obesity Genes by Whole Exome Sequencing in a UK Cohort of Severely Obese Children*, Program in Quantitative Genomics, Boston, MA (poster) *Stellar Abstract Award
- October 2012 *Whole Exome Sequencing Cases: Finding and Testing with External Controls*, American Society of Human Genetics, San Francisco, CA (poster)
- October 2010 *The Signal vs. Noise Balance: Exploring Gene Summary Methods*, American Society of Human Genetics, Washington D.C. (poster)
- October 2010 *Retaining Power: Is it Possible to Simply and Effectively Adjust for Multiple Comparisons in a Candidate Gene Region?* International Genetic and Epidemiology Society, Boston, MA (poster)
- October 2009 *A Comparison of Single and Multi-SNP Methods to Summarize Genetic Variation at Candidate Loci*, American Society of Human Genetics, Honolulu, HI (poster)
- October 2009 *A Comparison of Methods for Simulating a Gene Region with a Specified LD Structure*, International Genetic and Epidemiology Society Meeting, Kahuku, HI (poster)
- October 2008 *Genome-wide association and linkage analysis of quantitative traits: comparison of likelihood ratio test and conditional score statistic*, Genetic Association Workshop, St. Louis, MO (poster)

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August 2008

Estimating Risk for Transmission of Expanded CAG Alleles in the Huntington's Disease Gene from Male Carriers of Intermediate Alleles, American Statistical Association Joint Statistical Meeting Denver, CO (poster)

INTERNAL PRESENTATIONS

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| November 2023 | <i>Methods to estimate and leverage substructure from genetic summary data</i> , Human Medical Genetics and Genomics Annual Retreat, Colorado Springs, CO |
| November 2022 | <i>Successful and sustainable undergrad research in statistics</i> , Department of Biostatistics and Informatics, Colorado School of Public Health |
| May 2022 | <i>Revealing and utilizing hidden structure in 'omics data</i> , Center for Health Artificial Intelligence, University of Colorado Anschutz Medical Campus |
| April 2019 | <i>Methods to Improve the use of Common Controls in Sequencing Studies</i> , Department of Integrative Biology, University of Colorado Denver |
| April 2018 | <i>ProxECAT: Proxy External Controls Association Test. A new case-control gene region association test using allele frequencies from public controls</i> , The Power of Informatics to Advance Health Mini-Symposium, University of Colorado — Anschutz Medical Campus |
| March 2018 | <i>Genetic Analysis in the Era of Big Data</i> , Colorado Center for Personalized Medicine, University of Colorado — Anschutz Medical Campus |
| October 2017 | <i>Gene region association testing using summary level external controls</i> , Human Medical Genetics and Genomics 2017 Retreat, University of Colorado — Anschutz Medical Campus |
| April 2015 | <i>The Necessity of Bioinformatics in Next Generation Sequencing</i> , The Power of Informatics to Advance Health, University of Colorado — Anschutz Medical Campus |
| October 2014 | <i>Analysis Using Exome Sequenced Cases and Population Controls</i> , Human Medical Genetics and Genomics 2014 Retreat, University of Colorado — Anschutz Medical Campus |
| April 2014 | <i>Exome Sequencing of over 700 Severe Obesity Cases: Study Design, Challenges, & Initial Results</i> , Department of Integrative Biology Spring Seminar Series, University of Colorado — Denver |
| November 2013 | <i>Whole Exome Sequencing Case-Control using 1,000 Severe Obesity Cases Identifies Putative New Loci and Replicates Previously Established Loci</i> , Butcher Symposium, Colorado (poster) |
| October 2013 | <i>Exome Sequencing of over 700 Severe Obesity Cases: Study Design, Challenges, & Initial Results</i> , Human Medical Genetics and Genomics Program Seminar Series, University of Colorado — Anschutz Medical Campus |
| October 2013 | <i>Case-Control Analysis with Whole Exome Sequenced Cases: Challenges and Initial Results</i> , Statistical Genetics and Genetic Epidemiology Journal Club, CU – Anschutz Medical Campus |
| June 2013 | <i>SCOOP Case-Control Analysis: Challenges and Initial Results</i> , UK10K Annual Meeting, Cambridge, UK |
| May 2013 | <i>Insights from Exome Sequencing 1000 Severe Childhood Obese Cases</i> , Wellcome Trust Sanger Institute Human Genetics Retreat & Scientific Advisory Board Meeting, Cambridge, UK |

Audrey E. Hendricks, PhD

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|--------------|---|
| July 2012 | <i>Exome Sequencing in Severe Obese Children</i> , UK10K Annual Meeting, Cambridge, UK |
| July 2012 | <i>Case-Control Analysis using External Controls</i> , UK10K Annual Meeting, Cambridge, UK |
| March 2012 | <i>UK10K Obesity: From exome sequencing to potential hits</i> , Human Genetics Team Talks, Wellcome Trust Sanger Institute, Cambridge, UK |
| June 2011 | <i>Exploration of Gene Region Simulation, Correction for Multiple Testing, and Summary Methods</i> , Dissertation Committee and Audience, Boston University |
| January 2010 | <i>Gene Region Summary Methods</i> , Statistical Genetics Working Group, Boston University |

PROFESSIONAL AFFILIATIONS

Member, American Society of Human Genetics (ASHG)
Member, American Society of Nutrition (ASN)
Member, American Statistical Association (ASA)
Member, Eastern North American Region International Biometric Society (ENAR)
Member, International Genetic and Epidemiology Society (IGES)
Member, Global Alliance for Genomics and Health (GA4GH)
Member, Western North American Region International Biometric Society (WNAR)

FORMAL MENTORING/ADVISING (*Awards listed above)

Primary Advisor of PhD Thesis Research

| | |
|----------------|---|
| 2021 – Present | Jessica Murphy*, Department of Biostatistics and Informatics |
| 2021 – Present | Hayley Wolff, Human Genetics and Genomics Program |
| 2019 – 2022 | Nicholas Weaver*, Department of Mathematical and Statistical Sciences Dissertation: <i>Statistical tools for longitudinal microbiome data: Simulation frameworks, method comparisons, and development of association tests for longitudinal microbiome data</i> Current Position: Lecturer at Messiah College, PA |
| 2016 – 2020 | Megan Null, Department of Mathematical and Statistical Sciences Dissertation: <i>Advancement of understudied Variants and Groups within Statistical Genetics</i> Current Position: Assistant Professor College of Idaho (tenure-track) |

PhD External Mentor

| | |
|----------------|---|
| 2024 – Present | Henrietta Kadi, Joint Statistical Meetings Diversity Mentor-Mentee Pair |
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Primary Advisor of Statistics Certificate/BS Honors Project/Master's Project Research

| | |
|-------------|---|
| 2023 – 2024 | Nicholas Rogers, MS Statistics, <i>A Mathematical Description of Large Language Models and Analysis of ChatGPT's Responses</i> |
| 2022 – 2024 | Souha Tifour, MS Statistics, <i>Working towards Inclusivity in Genetic Studies: Unveiling the Influence of Reference Sample Size on Ancestry Estimation of Population Structure</i> |
| 2022 – 2023 | Riley Lamont*, MS Statistics, <i>Detecting Hidden Ancestry within Admixed Populations</i> |
| 2021 – 2023 | Sage Sigler, MS Statistics, <i>Rare Variant Association Methods Accounting for Ancestry When Using Summary Data as Common Controls</i> |
| 2020 – 2022 | Adelle Price*, MS Statistics, <i>Detection of Fine-Scale Population Structure in Genetic Summary Data with Summix under review</i> |

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| 2021 – 2022 | (Kelsey) Nikole Scribner-Trout, BS Mathematics, Honors Project Title: <i>Estimating Prostate Cancer Risk Proportion in Genetic Summary Data Using Summix</i> – Summa Cum Laude |
| 2021 – 2022 | Makayla Cowles, MS Statistics, <i>Evaluation of extending Proxy External Controls Association Test (ProxECAT) to Poisson Regression</i> |
| 2019 – 2021 | Ian Arriaga-MacKenzie*, MS Statistics, Project Title: <i>Summix: A method for detecting and adjusting for population structure in genetic summary data published</i> |
| 2019 – 2020 | Jessica Murphy*, MS Statistics, Project Title: <i>Accessible Analysis of Longitudinal Data with Linear Mixed Effects Models published</i> |
| 2019 – 2020 | Lee Panter, MS Statistics, Project Title: <i>Comparing Models of Subject-Clustered Single-Cell Data</i> |
| 2019 – 2020 | Valentinas Sungaila, MS Statistics, Project Title: <i>Exploring Gao et al. as a method for finding the effective number of independent tests in metabolomic data</i> |
| 2018 – 2019 | Matthew Lanz, MS Applied Mathematics, Project Title: <i>Causal Mediation Analysis: A method study and application</i> |
| 2018 | Sam May, Undergraduate Statistics Certificate, Project Title: <i>The EM Algorithm and its Application to Finite Mixtures</i> |
| 2017 | Daniel Klie, MS Statistics, Project Title: <i>Evaluating the Impact of the Promoting Success in Early College Mathematics through Graduate Teacher Training Project</i> |
| 2017 | Leonard Strnad, MS Statistics, Project Title: <i>Overview and TensorFlow Implementation of Diet Networks: Thin Parameters for Fat Genomics</i> |
| 2017 | Cailin McCloskey, MS Statistics, Project Title: <i>Studying the Genetics of Melanoma: Data Preparation, Quality Control, and Analysis Design</i> |
| 2016 - 2017 | Megan Sorenson, MS Statistics, Project Title: <i>Genome-wide analysis of copy number variation and common facial variation in a large cohort of Bantu Africans published</i> |
| 2016 - 2017 | Lauren Hall, MS Statistics, Project Title: <i>Is the False Discovery Rate Higher for Open Access Journals? A Comparison of FDR Estimates in Oncology Journals. published</i> |
| 2016 - 2017 | Chinyere Okpara, MS Statistics, Project Title: <i>Analysis of the Colorado Death Penalty Cases: Beyond Aggravating and Mitigating Factors published</i> |
| 2014 - 2015 | Alec McQuilkin, MS Applied Mathematics Statistics Concentration, Project Title: <i>Incorporating Relatedness in Gene Based Case-Only Analysis of Mendelian Traits</i> |
| 2014 - 2015 | Kraig Thomas, MS Applied Mathematics Statistics Concentration, Project Title: <i>Modeling Regular Season Winning Percentage in the NFL</i> |
| 2014 | Chad Jeffers, Undergraduate Statistics Certificate, Project Title: <i>Modeling Regular Season Winning Percentage in the NFL</i> |
| 2014 | Zhiyuan Guan, MS Applied Mathematics Statistics Concentration, Project Title: <i>How to appropriately account for autocorrelation in financial models</i> |

Post-doctoral Mentor

Summer 2021 and 2022
Summer 2023

Dr. Megan Null
Dr. Nicholas Weaver

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Statistical Mentor

| | | |
|---|----------------------|---------------|
| 2021 – 2023 | Dr. Emily Hill | T32 Nutrition |
| 2013 – 2020 | Dr. Minghua Tang | |
| CMH-Pilot (Tang, AMC) | 2/1/2014 – 1/31/2015 | CCTSI |
| Statistical Mentor ; “High protein consumption from meat vs. dairy as complementary” | | |
| 1 K01 DK111665-01 (Tang, AMC) | 9/01/2016-8/30/2020 | NIH/NIDDK |
| Statistical Mentor ; “Protein Quality Early in Life: Mechanisms of Growth and Later Obesity Development” | | |

Faculty Mentor (*chair)

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|----------------|----------------------|---|
| 2024 – present | Dr. Harriet Dashnow* | Asst Prof, Dept of Biomedical Informatics, CU Anschutz |
| 2023 – present | Dr. Jonathan Short | Asst Research Prof, Dept of Biomedical Informatics, CU Anschutz |
| 2022 – present | Dr. Gregory Way* | Asst Prof, Dept of Biomedical Informatics, CU Anschutz (chair '24-) |
| 2022 – present | Dr. Joanne Cole* | Asst Prof, Dept of Biomedical Informatics, CU Anschutz |
| 2021 – present | Dr. Priyanka deSouza | Asst Prof, College of Architecture and Planning, CU Denver |

Graduate Research Assistants

| | |
|-------------------------|--|
| 2021-Present | Hayley Stoneman, PhD Human Medical Genetics and Genomics |
| 2019-Present | Jessica Murphy*, MS Statistics (2020), PhD Biostatistics |
| 2022-2023 | Riley Lamont*, MS Statistics (2023) |
| 2021-2023 | Sage Sigler, MS Statistics (2023) |
| 2020-2022 | Adelle Price*, MS Statistics (2022) |
| 2020 | Mesbah Najafi, MS Statistics |
| 2019-2022 | Nicholas Weaver, PhD Applied Mathematics, concentration in Statistics (2022) |
| 2017 | Cailin McCloskey, MS Statistics (2017) |
| 2016 – 2017, 2019, 2020 | Megan Null, PhD Applied Mathematics with concentration in Statistics (2020) |

BS/MS Research Assistants

| | |
|-------------|---|
| 2021 – 2024 | Souha Tifour ^{#,*} , BS Math, MS Statistics (2024) |
| 2019 – 2021 | Ian Arriaga MacKenzi ^{#,*} , BS Math, MS Statistics (2021) |
| 2019 – 2020 | Gregory Matesi [#] , BS Math, MS Statistics (2022) |
| 2019 | Pitshou Nzazi Duki, BS Math, MS Statistics (2020) |

Undergraduate and post-bac Research Assistants

| | |
|-------------|---|
| 2024 – | Victor (Hugo) Lemus Gomez, post-bachelor's from Metropolitan State University of Denver |
| 2021 – 2024 | Sakaiza Rasolofomanana, post-bachelor's from Smith College |
| 2022 – 2023 | David Spacek, BS Computer Science |
| 2021 – 2023 | Nicolette Vere, post-bac, pre-med CU Denver |
| 2023 | Meghan Hinton, BS Mathematics |
| 2022 – 2023 | Makena Avichouser, BS Mathematics |
| 2021 – 2023 | Kelsey (Nikole) Scribner Trout*, BS Mathematics (2022) |
| 2021 – 2022 | Derek Gunnels [#] , BS Computer Science (2022) |
| 2021 | Silvia Zavarella [#] , BS Biology |
| 2020 – 2021 | Mobin Khajeh-Sharafabadi [#] , BS Psychology, Minor: Math (2021) |
| 2020 | Sam Chen ^{#,*} , BS Math |
| 2019 – 2021 | Catherine Fitch*, BS Public Health, Minor: Data Science (2021) |

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|-------------|--|
| 2019 | Andrew Zerwick, HS teacher |
| 2018 - 2020 | Alexandria Ronco [#] , BS Math (2020) |
| 2018 - 2019 | James Vance, BS Math (2019) |
| 2018 - 2019 | Jinyan Lyu, BS Math (2019) |
| 2018 - 2019 | Ryan Scherenberg [#] , BS Business (2019) |
| 2018 - 2019 | Yinfei Wu, BS-Math BS Economics (2019) |
| 2018 | Tiffany Dinh [#] , BS Biology (2019) |
| 2018 | Kendra Koach [#] , BS Math (2018) |

Lab Rotation/Internship/Summer Research Experiences

| | |
|------------------|--|
| 2024 Fall | Matthew Joel, Pathways in Genomic Data Science (PATH-GDS) rotation |
| 2024 Spring | Iris Ruz, Pathways in Genomic Research Experiences for Undergraduates (PATH-GREU) rotation |
| 2023 Summer | Madeline Chang, Olivia Lindberg, Majja Balts, Julie Lee, Jackelyn Valencia, undergraduate students participating in the Colorado Summer Institute for Biostatistics (CO-SIBs) |
| 2023 Summer | Jamie Lavigne, undergraduate from College of Mines, CORE summer program |
| 2023 Summer | Kathryn Allhouse, Biology Teacher Cherry Creek online HS and Community College of Denver, Summer Research Experience in data analysis of the microbiome with the RMSREE teacher training program |
| 2022/2023 Winter | Suraju Sadeeq, University of Colorado Anschutz Medical Campus, Human Medical Genetics and Genomics Program, PhD Student, Lab Rotation |
| 2022 Summer | Eric Mattys, Biology Teacher Centaurus High School, Summer Research Experience in genomics data science with the RMSREE teacher training program |
| 2021-22 AY | Morgan Holien, Kaitlin Swanson, Ava Flood, Monarch High School, Internship in analysis of food metabolites and health. |
| 2021 Summer | Sakaiza Rasolofomanana, post-bachelors, Summer Research Experience in Statistics, Metabolomics, and Nutrition |
| 2021 Summer | Daniel Kpormegbey, Department of Statistics, University of Connecticut, PhD student, Summer Research Experience in Statistical Genetics |
| 2021 Summer | Oluwagbenga (David) Agboola, Applied Statistics and Research Methods, University of Northern Colorado, PhD candidate, Summer Research Experience in Statistical Genetics |
| 2021 Spring | Hayley Stoneman, University of Colorado Anschutz Medical Campus, Human Medical Genetics and Genomics Program, PhD Student, Lab Rotation |
| 2020 Fall | Betzaida Maldonado, University of Colorado Anschutz Medical Campus, Human Medical Genetics and Genomics Program, PhD Student, Lab Rotation |
| 2019/2020 Winter | Katie Marker, University of Colorado Anschutz Medical Campus, Human Medical Genetics and Genomics Program, PhD Student, Lab Rotation |
| 2018/2019 Winter | Evan Sticca, University of Colorado Anschutz Medical Campus, Human Medical Genetics and Genomics Program, PhD Student, Lab Rotation |
| 2018 Spring | Hamish Pike, University of Colorado Anschutz Medical Campus, Human Medical Genetics and Genomics Program, PhD Student, Lab Rotation |
| 2016 Winter | Ben Kitchen, Denver School of Science and Technology, High School Junior, Intern |

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PhD Graduate Co-Mentors

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|----------------|--|
| 2021– Present | Hayley Stoneman, PhD Human Medical Genetics and Genomics |
| 2021 – Present | Jessica Murphy, PhD Biostatistics |
| 2020 – Present | Katie Marker, PhD student in Human Medical Genetics and Genomics |
| 2019 – 2022 | Nicholas Weaver, PhD, student in Applied Mathematics, Statistics concentration |
| 2018 – 2020 | Jordan Hall*, PhD, PhD student in Applied Mathematics |
| 2018 – 2020 | Megan Sorenson, PhD student in Applied Mathematics, Statistics concentration |

#EURECA! *workstudy students or Fellows*

Teaching Assistant Mentor

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| Fall 2018 | Amit Sengupta, Applied Mathematics PhD Student |
| AY 2017-2018 | Livia Bechtold, Applied Mathematics PhD Student |
| AY 2016-2017 | Michael Pilosov, Applied Mathematics PhD Student |
| AY 2015-2016 | Aaron Nielson, Applied Mathematics PhD Student |

Committees: PhD Thesis (*Committee chair)

Current:

Evan Sticca (PhD in Human Medical Genetics and Genomics, expected 2024)
Katie Marker* (PhD in Human Medical Genetics and Genomics, expected 2024)
Katie Kichula (PhD in Human Medical Genetics and Genomics, expected 2025)
Evan Shapiro (PhD in Applied Mathematics, expected 2026)
Kayley Smiley (PhD in Applied Mathematics, expected 2026)

Previous:

Kendra Ferrier* (2023, PhD in Human Medical Genetics and Genomics)
Hamish Pike* (2023, PhD in Human Medical Genetics and Genomics)
Emileigh Willems* (2020, PhD in Applied Mathematics concentration in Statistics)
Subrata Paul (2019, PhD in Applied Mathematics concentration in Statistics)
Genevieve Andersen* (2019, PhD in Human Medical Genetics and Genomics)
Monchai Kooakachai (2019, PhD in Applied Mathematics concentration in Statistics)
Aaron Nielson (2018, PhD in Applied Mathematics)
Sesha Dassanayaka* (2016, PhD in Applied Mathematics concentration in Statistics)
Daniel Yorgov (2016, PhD in Applied Mathematics concentration in Statistics)

Committees: Honors Project, Statistics Certificate, Masters Project

Mobin Khajeh-Sharafabadi (2023, MS in Biostatistics, University of Texas Houston)
Greg Matesi (2022, MS in Statistics)
Alyssa Newman (2021, MS in Applied Mathematics)
Aixin Zhang (2020, MS in Statistics)
Nicholas Weaver (2019, MS in Statistics)
Michael Ingram (2019, MS in Statistics)
Arlin Tawzer (2019, MS in Statistics)
Gordon Kordas (2019, MS in Biostatistics)
Kate Booth (2019, MS in Applied Mathematics)
Selah Chanthan (2019, MS in Statistics)
Emileigh Willems (2018, MS in Statistics)
Xingmeng Zhao (2017, MS in Applied Mathematics)
Jason Fagerness (2017, MS in Applied Mathematics)
Lucas Ortiz (2016, MS in Applied Mathematics Concentration in Statistics)
Long Fu (2016, MS in Applied Mathematics)

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Mengjie Yao (2016, MS in Applied Mathematics)
Nathaniel Brown (2015, MS in Applied Mathematics)
Takao Miller (2015, MS in Applied Mathematics)
Hannah Dauber (2015, MS in Applied Mathematics)
Lauren Hall (2014, Undergraduate Honors Project)
Melissa Bilbao (2014, MS in Applied Mathematics)
DeVon Farago (2014, Graduate Statistics Certificate)
Andie Nye (2014, MS in Applied Mathematics)

Mentoring Prior to Fall 2013

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| Fall 2012-Summer 2013 | Co-mentor Cambridge University MPhil Student, Nathan Nakatsuka, with Inês Barroso at the Wellcome Trust Sanger Institute |
| Fall 2004-Summer 2009, Fall 2012-Summer 2013 | Advisor, Kappa Alpha Theta – Zeta Mu Chapter, MIT, Cambridge, MA |
| Summer 2009-March 2011 | Advisory Board Chairman, Kappa Alpha Theta – Zeta Mu Chapter, MIT, Cambridge, MA |
| Fall 2003-Spring 2004 | Advisor, Kappa Alpha Theta – Eta Iota Chapter, MIT, San Diego, CA |

TEACHING

Learning Assistants

| | |
|-------------|---|
| Fall 2019 | Lu Vy. “Introduction to Statistical and Machine Learning”, University of Colorado Denver (MATH 4027/5027) |
| Spring 2019 | Samone Hubbart. “Applied Statistics”, University of Colorado Denver, (MATH 4830/5830) |
| Spring 2018 | Mari Kuker and Shannon Robinson. “Introduction to Statistics”, University of Colorado Denver, (MATH 2830) |

Courses Taught (Sole instructor, 3 credit courses)

University of Colorado Denver Department of Mathematical and Statistical Sciences

| | | |
|---|----------------|-----------|
| Applied Statistics (2014, 2015, 2019) | MATH 4830/5830 | CU Denver |
| Applied Regression Analysis (2015) | MATH 4387/5387 | CU Denver |
| Experimental Design (2014, 2016, 2018) (Developed new course in 2014) | MATH 4294/5394 | CU Denver |
| Introduction to Mathematical Statistics (2014) | MATH 4820/5320 | CU Denver |
| Introduction to Statistical and Machine Learning (2019) (Developed new course in 2019) | MATH 4027/5027 | CU Denver |
| Introduction to Statistics (Spring & Fall x2 2017, 2018) | MATH 2830 | CU Denver |
| Statistical and Machine Learning (2015, 2016, 2018, 2020) (previously Advanced Statistical Methods for Research) | MATH 6388 | CU Denver |
| Topics in Applied Mathematics – Experimental Design (2016) (Developed new course in 2016) | MATH 5027 | CU Denver |

Boston University, School of Public Health

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| Introduction to Statistical Computing (3x) | BIOS 723 | Boston University SPH |
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Readings Courses (1 credit)

| | |
|-------------|--|
| Summer 2019 | Non-parametric Longitudinal Analysis, 1 enrolled graduate student |
| Spring 2019 | Mixed Linear Effects Models with application to immune deficient mice studies, 1 enrolled graduate student |
| Fall 2017 | Deep Learning: A new application to genetics, 11 enrolled graduate students |
| Fall 2016 | A new method to incorporate publicly available data, 7 enrolled graduate students |
| Summer 2015 | Cluster Analysis, 2 enrolled graduate students |
| Fall 2014 | Kernels, 2 enrolled graduate students |

Independent Studies (3 credits)

| | |
|-------------|---|
| Summer 2022 | Adelle Price, Masters, <i>Statistical Genetics and Genomics</i> |
| Summer 2020 | Jessica Murphy, Masters, <i>Statistical Genetics and Genomics</i> |
| Summer 2020 | Gregory Matesi and Mesbah Najafi, Masters, <i>Introduction to Machine and Statistical Learning</i> |
| Spring 2020 | River Bond, PhD, <i>Introduction to Machine and Statistical Learning</i> |
| Fall 2019 | Lee Panter, Masters, <i>Single Cell Analysis with Generalized Estimating Equations and Linear Mixed Effects Models</i> |
| Summer 2019 | Jessica Murphy, Masters, <i>Linear Mixed Effects Models with an Application to Mouse Studies</i> |
| Spring 2019 | Gregory Matesi, undergraduate, <i>Mixture Models with an Application to Identifying Hidden Ancestries</i> |
| Fall 2018 | Alexandria Ronco, undergraduate, <i>Hidden Ancestries</i> |
| Fall 2018 | Jinyan Lyu, undergraduate, <i>Bootstrapping and Extensions</i> |
| Summer 2018 | Samuel May, <i>Master's Project Course: The EM Algorithm and its Application to Finite Mixtures</i> |
| Spring 2018 | Sebastian Del barco, undergraduate, <i>Distributions! A new look U.S. Median House Prices after the 2008 Housing Crisis</i> |
| Fall 2017 | Leonard Strnad, MS, <i>Master's Project Course: Deep Learning, Genomic Data and TensorFlow</i> |
| Fall 2017 | Cailin McCloskey, MS, <i>Master's Project Course: Studying the Genetics of Melanoma: Data Preparation, Quality Control, and Analysis Design</i> |
| Fall 2017 | Sebastian Del barco, undergraduate, <i>Generalized Linear Models with an Application to Time to Brain Metastasis and Response to Immunotherapy in Melanoma Patients</i> |
| Spring 2017 | Chinyere Okpara, MS, <i>Master's Project Course: Analysis of the Colorado Death Penalty Cases: Beyond Aggravating and Mitigating Factors</i> |
| Summer 2017 | Daniel Klie, MS, <i>Master's Project Course: Promoting Success in Early College Mathematics through Graduate Teacher Training Project</i> |

Lectures

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|-------------------------|--|
| Summer 2016-19, 2021-22 | Instructor (week of morning instruction), “Fitting Models to Data”, Colorado Summer Institute for Biostatistics (Co-SIBs), Colorado School of Public Health |
| Spring 2015-2018 | Faculty Lecturer, “Sequence Based Studies”, University of Colorado, Anschutz Medical Campus, HMGP7600: Graduate Survey of Human Genetics |
| Fall 2016 | Faculty Lecturer, “Methods for studying rare variants in next generation sequencing data”, University of Colorado, Anschutz Medical Campus, BSBT 6111: Introduction to Biomedical Data Science |

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|-------------------------|--|
| Fall 2014-2015 | Instructor (a week of instruction), “Exome Sequencing: annotation, quality control, and analysis”, Wellcome Genome Campus, Advanced Course on Exome Sequencing |
| Spring 2012 & Fall 2013 | Lecturer, “Complex Diseases & Exome Sequencing: An introduction to study design and analysis”, Wellcome Genome Campus, Advanced Course on Exome Sequencing |
| Spring 2011 | Lecturer, “Sequence Data: The statistical analysis of rare variants”, Boston University School of Public Health, (Applied Statistical Genetics; Biostatistics 859) |
| Fall 2009 | Lecturer, “Methods of Evidence-Based Medicine and Decision Analysis”, Boston University Medical School |
| Spring & Summer 2009 | Lecturer, “Statistical Genetics”, Upward Bound—a program for high school students who are aiming to be first generation college students |

Teaching Assistant

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|--|--------------------------|---|
| Biostatistics in Epidemiology Genetics and Genomics | BIOS 852 Genetics 701 | Boston University SPH Boston University SGMS |
| Introduction to Biostatistics | E-102 | Harvard Extension School |
| Introduction to Statistics | E-50 | Harvard Extension School |

UNIVERSITY SERVICE AND LEADERSHIP

Leadership Training

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| 2024 | ThriveForward mid-career Leadership Program, CU School of Medicine |
|------|--|

Administrative Responsibilities

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|----------------|--|
| 2023 – present | co-Director for Pathways in Genomics Undergraduate Research Experiences (PATH-GREU) for underrepresented groups; a 2-year program for Metropolitan State University of Denver undergraduate students to receive research training at the University of Colorado Denver and Anschutz Medical Campus funded by NIH/NHGRI (2023-2028) |
| 2023 – present | co-Director and contact PI for Pathways in Genomic Data Science (PATH-GDS) for underrepresented groups; 2-year program for MS statistics and applied mathematics students funded by NIH/NHGRI (2023-2028) |
| 2016 – 2020 | Organizer for the Statistical Genetics Working Group bi-weekly meetings |
| 2018 – 2020 | Organizer for Mathematical and Statistical Sciences Departmental Open House |

University Committees

| | |
|---------------|---|
| 2022 – 2023 | Research and Creative Activities Symposium planning committee |
| 2022 | Search Committee for Vice Chancellor for Technology Strategy and Innovation |
| 2021 – 2022 | Strategic Planning Committee: Interdisciplinary Computing Task Force |
| 2022 | Excellence in Teaching Review Committee |
| 2020 and 2021 | Excellence in Research Review Committee |

College Committees

| | |
|------|---|
| 2021 | CLAS Excellence in Teaching Review Committee |
| 2020 | CLAS Excellence in Research Review Committee |
| 2018 | CLAS Strategic Planning Initiative Student Success Subcommittee |

Audrey E. Hendricks, PhD

Department of Biomedical Informatics Committees

| | |
|----------------|--|
| 2023 – present | SOM Biostatistics course committee |
| 2023 – present | Diversity, Equity, and Inclusion Education Committee |
| 2023 | Post-doctoral search committee for Dr. Janani Ravi |
| 2022 – 2023 | Search Committee for Open Rank Professor of Clinical Informatics |

Mathematical and Statistical Sciences Departmental Committees

| | |
|----------------------|---|
| 2019-2020 | Graduate Admissions Committee |
| 2018-2019 | Search Committee for Assistant Professor of Optimization |
| 2017-2019 | Executive Committee |
| 2013-2014, 2015-2018 | Undergraduate Committee |
| 2013-2017 | Statistics Committee to revise statistics curriculum and creation of MS Statistics degree |
| 2013-2016 | Search Committee for Assistant Professor of Statistics |
| 2014-2015 | Graduate Committee |
| 2014-2015 | Merit Committee |

Human Medical Genetics and Genomics Program Committees

| | |
|----------------|---|
| 2024 – present | Graduate Advisory Committee (GAC) |
| 2020 | Human Medical Genetics and Genomics Virtual Retreat Committee |
| 2018 – 2020 | Human Medical Genetics and Genomics Seminar Committee |

SERVICE TO THE PROFESSION

Associate Editor

Human Genetics and Genomics Advances (2020 - present)

Study Sections / Review Panels

Adhoc Reviewer NIH Molecular Cancer Diagnosis and Classification (MCDC) (Summer 2024)

NHGRI Special Emphasis panel R25 Genome Research Undergraduates & R25 ELM Training Modules Genomics Research (Fall 2023)

TOPMed fellowship applications reviewer, round 1 (Fall 2023)

Adhoc Reviewer NIH Analytics and Statistics for Population Research Panel B (ASPB) (Spring 2023)

NHGRI Special Emphasis RFA-HG-22-002 Educational Hub for Enhancing Diversity in Computational Genomics and Data Science (Fall 2022)

NSF review panel (Fall 2022)

NHGRI Special Emphasis PAR-21-07: Research Experience in Genomic Research for Data Science. (Fall 2021)

Member of a NIH Study Section for Fellowships (Fall 2014, 2015, 2020; Summer 2016 – 2018)

Committees and Leadership Positions

Program Chair, 2024 STATGEN Conference for the Section on Statistical Genetics and Genomics (SSGG) for the American Statistical Association (2023-2024)

International Genetic and Epidemiology Society (IGES) Best Paper Competition Committee (2023, 2024)

Program Chair, 2023 Western North American Region (WNAR) of the Biometrics Society meeting (2022-2023)

Member of American Statistical Association's (ASA) Section on Statistical Genetics and Genomics (SSGG)

Membership Engagement Committee (MEC) (Spring 2021 – 2022)

Co-Chair Genome Sequencing Program (GSP) Common Controls Working Group (2021)

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Chair of Virtual Organizational Committee for the 2021 meeting for the Western North American Region (WNAR) of the Biometrics Society (2021)

International Genetic and Epidemiology Society (IGES) Young Investigator Committee (Fall 2015 – Fall 2018)

Boston Chapter of the American Statistical Association, Vice President (2010)

Boston Chapter of the American Statistical Association, Planning Committee (2009-2011)

Chaired/Moderated/Organized Sessions

American Society for Human Genetics

- 2024 (organizer), Webinar, *Building an inclusive and representative genomics community through research training and career exposure across the life course of education pathways*.
https://learning.ashg.org/products/building-an-inclusive-and-representative-genomics-community-through-research-training-and-career-exposure-across-the-life-course-of-education-pathways#tab-product_tab_overview

Joint Statistical Meeting

- 2024 (chair and co-organizer), *Considerations and Best Practices for Use of Race, Ethnicity, and Ancestry in Data Science Research*
- 2019 (impromptu chair), *SPEED: Statistical Methods for GWAs, Genetics, Genomics, and Other Omics Studies, Part 1*

NIH virtual workshop on Population Descriptors for Legacy Genomic Data: Challenges and Future Directions

- 2024, *What technical solutions exist (or should be developed) to assign population descriptors using genetic data-driven labels?* (moderator)

STATGEN

- 2024, *Speed Talks* (chair)
- 2024, *Methods and frameworks to disentangle genetics and environment in health and disease* (organizer)

Western North American Region (WNAR) of the Biometrics Society

- 2023, *Speed Talks* (chair)
- 2023, *Considerations and best practices for using race, ethnicity, ancestry in different areas of statistics and data science research* (organizer and co-chair)

Research in Computational Molecular Biology (RECOMB) – Genetics

- 2022, *Afternoon Session*

Genome Sequencing Program and Trans-Omics for Precision Medicine (GSP-TOPMed) Analysis Workshop

- 2020, *Variant Functional Annotation Resources*

International Genetic and Epidemiology Society Meeting

- 2019, *Polygenic Trait Genetics II*
- 2015, *Cross-Consortia and Mega-Cohorts: Ongoing and future directions*

Mentorship

Joint Statistical Meeting (JSM) Diversity Mentoring Program (2024)

Joint Statistical Meeting (JSM) Virtual Networking Session (2021)

American Society of Human Genetics (ASHG) Mentor-Mentee Lunch (2014, 2016, 2017, 2018)

International Genetic and Epidemiology Society (IGES) Mentor-Mentee Lunch (2018, 2019, 2020, 2023)

Other

Audrey E. Hendricks, PhD

Review abstracts for annual conference American Society of Human Genetics (2021, 2023)

Organized judging for trainee poster competition for International Genetic and Epidemiology Society Young Investigator Committee (Fall 2016 & 2018)

SCIENCE COMMUNICATION AND OUTREACH

| | |
|------------------|--|
| 2024 | Panel, Training programs, graduate school and beyond) for WNAR Diversity Summit |
| 2024 | Panel, Women in Biostatistics, Colorado School of Public Health |
| 2024 | Career Day, Superior Elementary School |
| 2021, 2022, 2023 | Poster session judge, Research and Creative Activities Symposium (RaCAS) at CU Denver |
| 2021- 2024 | Math Olympiad Coach, Superior Elementary School |
| July 2022 | <i>Statistics in the News</i> , Rocky Mountain Summer Research Education Experience, University of Colorado Denver |
| 2018, 2019, 2020 | Poster session judge, Data for Policy at CU Denver |
| July 2020 | <i>Statistics in the News in the time of COVID-19</i> , College of Liberal Arts and Sciences COVID-19 Lecture Series, University of Colorado Denver (https://www.youtube.com/watch?v=z3I9ns08Mng) |
| August 2019 | Panel on Research in Data Science, Data Science Symposium, CU Denver |
| May 2016 | Math Teacher's Circle |
| April 2016 | Lecture at The Carillon, an assisted living community, entitled <i>Stats in the News</i> |
| April 2016 | Panel for Women in STEM, CU Denver |
| March 2016 | <i>Statistics in the News</i> , Mini-STEM, University of Colorado Denver |

PEER REVIEW - JOURNALS

American Journal of Clinical Nutrition, American Journal of Human Genetics, Bioinformatics, Biostatistics, BMC Bioinformatics, BMC Biology, Cell Metabolism, Circulation, Clinical Genetics, The European Journal of Human Genetics, eLIFE, GAW Proceedings, Genetic Epidemiology, Human Genetics, Journal of the American Heart Association, Nature Genetics, PLoS Genetics, and others