Curriculum Vitae: updated December 6, 2023

I. IDENTIFYING DATA

Name	Zihuai He, PhD
Current Position	Assistant Professor
	Quantitative Sciences Unit
	Department of Neurology & Neurological Sciences
	Department of Medicine (Biomedical Informatics Research)
	Department of Biomedical Data Science
Current Affiliation	Stanford University

II. EDUCATION HISTORY

Colleges and Universities Attended

2010	BS, Mathematics and Physics, Tsinghua University, China
2016	PhD, Biostatistics, University of Michigan, USA

Residency and Fellowship Training

September 2016 - August 2018	Postdoctoral Research Scientist, Department of Biostatistics, Columbia University (laboratory of Dr. Iuliana Ionita-Laza)

III. EMPLOYMENT

Academic Appointments

November 2018 - present	Assistant Professor of Neurology and of Medicine (Biomedical Informatics Research), Stanford University School of Medicine, Stanford, CA, USA.
December 2023 - present	Assistant Professor of Biomedical Data Science (by courtesy), Stanford University School of Medicine, Stanford, CA, USA.

IV. HONORS AND AWARDS

2013	Best Performance on the Qualifying Exam	University of Michigan
2013 - 2015	Rackham Conference Travel Grant	University of Michigan
2015	Rackham Pre-doctoral Fellowship Award	University of Michigan

V. BIBLIOGRAPHY

Peer-reviewed original research (60 total, 5 submitted; 25 led as first or senior)

1. **He, Z.**, Zhang, M., Zhan, X., and Lu, Q. (2014). Modeling and testing for joint association using a genetic random field model. ***Biometrics***, 70 (3), 471-479.
2. Li, M., **He, Z.****, Zhang, M., Zhan, X., Wei, C., Elston, R.C., and Lu, Q. (2014). A generalized genetic random field method for the genetic association analysis of sequencing data. ***Genetic Epidemiology***, 38 (3), 242-253. ****Co-first author.***
3. Wei C., Li, M., **He, Z.***, Vsevolozhskaya O., Schaid, D.J., and Lu, Q. (2014). A weighted U-statistic for genetic association analyses of sequencing data. ***Genetic Epidemiology***, 38 (8), 699-708. *Conception and design of the method. Critical revision of the manuscript for important intellectual content.
4. **He, Z.**, Payne, E.K., Mukherjee, B., Lee, S., Smith, J.A., Ware, E.B., Sánchez, B.N., Seeman, T.E., Kardia, S.L.R., and Diez Roux, A.V. (2015). Association between stress response genes and features of diurnal cortisol curves in the Multi-Ethnic Study of Atherosclerosis. ***PLOS ONE***, e0126637.
5. Li, M., **He, Z.****, Schaid D.J., Cleves M.A., Nick T.G., and Lu Q. (2015). A powerful non-parametric statistical framework for family-based association analyses. ***Genetics***, 200 (1), 69-78. ****Co-first author.***
6. **He, Z.**, Zhang, M., Lee, S., Smith, J.A., Guo, X., Palmas, W., Kardia, S.L.R., Diez Roux, A.V., and Mukherjee, B. (2015). Set-based tests for genetic association in longitudinal studies. ***Biometrics***, 71(3), 606-615.
7. Wen, Y., **He, Z.***, Li, M., and Lu, Q. (2016). Risk prediction modeling of sequencing data using a forward random field method. ***Scientific Reports***, 6. *Conception and design of the method. Critical revision of the manuscript for important intellectual content.
8. Li, M., Li, J., **He, Z.***, Lu, Q., Witte, J.S., Macleod, S.L., Hobbs, C.A., Cleves, M.A., and the National Birth Defect Prevention Study (2016). Testing allele transmission for a SNP-set with a family-based generalized genetic random field method. ***Genetic Epidemiology***, 40(4), 341-351. *Conception and design of the method. Critical revision of the manuscript for important intellectual content.
9. **He, Z.**, Lee, S., Zhang, M., Smith, J.A., Guo, X., Palmas, W., Kardia, S.L.R., Ionita-Laza, I., and Mukherjee, B. (2017). Rare-variant association tests in longitudinal studies, with an application to the Multi-Ethnic Study of Atherosclerosis (MESA). ***Genetic Epidemiology***, 41(8), 801-810.
10. **He, Z.**, Zhang, M., Lee, S., Smith, J.A., Kardia, S.L.R., Diez Roux, A.V. and Mukherjee, B. (2017). Set-based tests for gene-environment interaction in longitudinal studies. ***Journal of the American Statistical Association,*** 112(519), 966-978.
11. **He, Z.**, Xu, B., Lee, S., Ionita-Laza, I. (2017). Unified sequence-based association tests allowing for multiple functional annotations, and meta-analysis of noncoding variation in Metabochip data. ***The American Journal of Human Genetics***, 101(3), 340-352.
12. Zhao, W., Ware, E.B., **He, Z.***, Kardia, S.L.R., Faul, J.D., Smith, J.A. (2017). Social and psychosocial factors modify the effect of genetic variants on body mass index: a gene environment interaction analysis in a longitudinal setting. ***International Journal of Environmental Research and Public Health***, 14(10), 1153. *Statistical analysis.
13. Li, M., **He, Z.****, Tong, X., Witte, J.S. and Lu, Q. (2018). Detecting Rare Mutations with Heterogeneous Effects Using a Family-Based Genetic Random Field Method. ***Genetics***, genetics-301266. ****Co-first author.***

14. **He, Z.**, Liu, L., Wang, K., Ionita-Laza, I. (2018). A semi-supervised approach for predicting cell type specific functional consequences of non-coding variation using MPRAs. ***Nature Communications***, 9(1), 5199.
15. Backenroth, D., **He, Z.***, Kiryluk, K., Boeva, V., Pethukova, L., Khurana, E., Christiano, A., Buxbaum, J., Ionita-Laza, I. (2018). FUN-LDA: A latent Dirichlet allocation model for predicting tissue-specific functional effects of noncoding variation. ***The American Journal of Human Genetics***, 102(5), 920-942. *Statistical analysis.
16. **He, Z.**, Xu, B., Buxbaum, J., Ionita-Laza, I. (2019) A genome-wide scan statistic framework for whole-genome sequence data analysis. ***Nature Communications***, 10(1), 3018.
17. Li, Y., Liu, Z., Yao, L., **He, Z.** (2020), Non-local Self-attentive Autoencoder for Genetic Functionality Prediction. The 29th International Conference on Information and Knowledge Management, (***CIKM 2020***), Galway, Ireland, Oct. 19 -23. (Peer reviewed conference paper)
18. Zhang, M., Yu, Y., Wang, S., Salvatore, M., G. Fritsche, L., **He, Z.*** and Mukherjee, B. (2020). Interaction analysis under misspecification of main effects: Some common mistakes and simple solutions. ***Statistics in Medicine***. *Conception and design of the method. Critical revision of the manuscript for important intellectual content.
19. Dujari, S., Gummidipundi, S., **He, Z.*** and Gold, C.A. (2020). Administration of Dexamethasone for Bacterial Meningitis: An Unreliable Quality Measure. ***The Neurohospitalist***, p.1941874420969556. *Supervision of the statistical analysis.
20. Diaz, J.L., Siththanandan, V.B., Lu, V., Gonzalez-Nava, N., Pasquina, L., MacDonald, J.L., Woodworth, M.B., Ozkan, A., Nair, R., **He, Z.***, Sahni, V., Sarnow, P., Palmer, T.D., Macklis, J.D., Tharin, S. (2020). An evolutionarily acquired microRNA shapes development of mammalian cortical projections. ***Proceedings of the National Academy of Sciences***, 117(46), pp.29113-29122. *Statistical analysis.
21. Julienne, H., Laville, V., Mccaw, Z.R., **He, Z.***, Guillemot, V., Lasry, C., Ziyatdinov, A., Vaysse, A., Lechat, P., Menager, H., Le Goff, W., Kraft, P., Ionita-Laza, I., Vilhjalmsson, B.J., Aschard, H. (2020). Decomposing the genetic burden of chronic diseases into multitrait signatures to support drug development. ***European Journal of Human Genetics***, 28(1), pp. 689-690. *Statistical analysis.
22. Le Guen, Y., Belloy, M.E., Napolioni, V., Eger, S.J., Kennedy, G., Tao, R., **He, Z**.**, Greicius, M.** (2021) A novel age-informed approach for genetic association analysis in Alzheimer's disease. ***Alzheimer's research & therapy, 13(1)***, pp.1-14. ***** Co-senior author***.
23. **He, Z.**, Liu, L., Wang, C., Le Guen, Y., Lee, J., Gogarten, S., Lu, Fred., Montgomery, S., Tang, H., Silverman, E., Cho, M.H., Greicius, M.D., Ionita-Laza, I. (2021). Identification of putative causal loci in whole-genome sequencing data via knockoff statistics. ***Nature Communications***, 12(1), pp.1-18.
24. **He, Z.**, Le Guen, Y., Liu, L., Lee, J., Ma, S., Yang, A.C., Liu, X., Rutledge, J., Losada, P.M., Song, B., Belloy, M.E., Butler III, R.R., Longo, F.M., Tang, H., Mormino, E.C., Wyss-Coray, T., Greicius, M.D., Ionita-Laza, I. (2021). Genome-wide analysis of common and rare variants via multiple knockoffs at biobank scale, with an application to Alzheimer disease genetics. ***The American Journal of Human Genetics***, 108(12), pp.2336-2353.
25. Xu, D., Wang, C., Khan, A., Shang, N., **He, Z.***, Gordon, A., Kullo, I.J., Murphy, S., Ni, Y., Wei, W.Q. and Gharavi, A., (2021). Quantitative disease risk scores from EHR with applications to clinical risk stratification and genetic studies. ***npj Digital Medicine***, 4(1), pp.1-13. *Technical support for the method development. Critical revision of the manuscript for important intellectual content.

26. Liu, Z., Yao, L., Wang, X., Monaghan, J., Schaette, R., **He, Z.*** and McAlpine, D. (2021). Generalizable Sample-efficient Siamese Autoencoder for Tinnitus Diagnosis in Listeners with Subjective Tinnitus. ***IEEE Transactions on Neural Systems and Rehabilitation Engineering***. *Critical revision of the manuscript for important intellectual content.
27. Baumer, F.M., McNamara, N.A., Fine, A.L., Pestana-Knight, E., Shellhaas, R.A., **He, Z.***, Arndt, D.H., Gaillard, W.D., Kelley, S.A., Nagan, M. and Ostendorf, A.P. (2021). Treatment Practices and Outcomes in Continuous Spike and Wave During Slow Wave Sleep (CSWS): A Multicenter Collaboration. ***The Journal of Pediatrics***. *Supervision of the statistical analysis.
28. Belloy, M., Eger, S., Le Guen, Y., Napolioni, V., Deters, K.D., Yang, H., Porter, T., Sperling, R., Laws, S., Mormino, E., **He, Z.***, Han, S., Altmann, A., Greicius, M.D. (2021). Klotho-VS Heterozygosity Reduces Brain Amyloid Burden in pre-symptomatic APOE4 Carriers. ***Neurobiology of Aging***, 101, pp.123-129. *Supervision of the statistical analysis.
29. Chamberlain, L.J., Bruce J., Olvera de la Cruz, M., Huffman, L., Steinberg, J.R., Bruguera, R., Pineda-Ramirez, J., Peterson, J.W., Gardner, R.M., **He, Z.***, Ordaz, Y., Connelly, E., Loeb, S. (2021). A Text-Based Intervention to Promote Literacy: An RCT. ***Pediatrics***, 148 (4): e2020049648. *Supervision of the statistical analysis.
30. Julienne, H., Laville, V., McCaw, Z.R., **He, Z.***, Guillemot, V., Lasry, C., Ziyatdinov, A., Vaysse, A., Lechat, P., Ménager, H. and Le Goff, W. (2021). Multitrait GWAS to connect disease variants and biological mechanisms. ***PLOS Genetics***, 17 (8), e1009713. *Statistical Analysis.
31. Lansinger, O.M., Biedermann, S., **He, Z.*** and Colevas, A.D. (2021). Do steroids matter? A retrospective review of premedication for taxane chemotherapy and hypersensitivity reactions. ***Journal of Clinical Oncology***, 39(32). *Statistical Analysis.
32. Guen, Y.L., Eger, S.J., Belloy, M.E., Kennedy, G., **He, Z.***, Napolioni, V. and Greicius, M.D., (2021). Sex-heterogenous effect on Alzheimer's disease risk at the BIN1 locus. ***Alzheimer's & Dementia***, 17, p.e053616. *Supervision of the statistical analysis.
33. Belloy, M.E., Eger, S.J., Guen, Y.L., Kennedy, G., **He, Z.***, Napolioni, V. and Greicius, M.D., (2021). APOE* 4-stratified genome-wide association study of Alzheimer's disease in over 350,000 individuals. ***Alzheimer's & Dementia***, 17, p.e055905. *Supervision of the statistical analysis.
34. Ma, S., Dalgleish, J., Lee, J., Wang, C., Liu, L., Gill, R., Buxbaum, J.D., Chung, W.K., Aschard, H., Silverman, E.K., Cho, M.H., **He, Z.***, Ionita-Laza, I. (2021). Powerful gene-based testing by integrating long-range chromatin interactions and knockoff genotypes. ***Proceedings of the National Academy of Sciences***, 118(47). *Conception and design of the method. Critical revision of the manuscript for important intellectual content.
35. Belloy, M.E., Eger, S.J., Le Guen, Y., Damotte, V., Ahmad, S., Ikram, M.A., Ramirez, A., Tsolaki, A.C., Rossi, G., Jansen, I.E., de Rojas, I., Parveen, K., Sleegers, K., Ingelsson, M., Hiltunen, M., Amin, N., Andreassen, O., Sanchez-Juan, P., Kehoe, P., Amouyel, P., Sims, R., Frikke-Schmidt, R., van der Flier, W.M., Lambert, J.C., **He, Z.***, Han, S.S., Napolioni, V., Greicius, M.D. (2022). Challenges at the APOE locus: a robust quality control approach for accurate APOE genotyping. ***Alzheimer's research & therapy***, 14(1), pp.1-17. *Supervision of the statistical analysis.
36. Abell, N.S., DeGorter, M.K., Gloudemans, M., Greenwald, E., Smith, K.S., **He, Z.*** and Montgomery, S.B. (2022). Multiple Causal Variants Underlie Genetic Associations in Humans. ***Science***, 375 (6586), pp.1247-1254. *Supervision of the statistical analysis. Analysis and interpretation of data. Critical revision of the manuscript for important intellectual content.

37. Le Guen, Y., Belloy, M.E., Grenier-Boley, B., de Rojas, I., Castillo-Morales, A., Jansen, I., Nicolas, A., Bellenguez, C., Dalmasso, C., Kucukali, F., Eger, S.J., Rasmussen, K.L., Thomassen, J.Q., Deleuze, J.F., **He, Z.***, Napolioni, V., Amouyel, P., Jessen, F., Kehoe, P.G., Van Duin, C., Tsolaki, M., Sanchez-Juan, P., Sleegers, K., Ingelsson M., Rossi, G., Hiltunen, M., Sims, R., van der Flier, W.M., Ramirez, A., Andreassen, O.A., Frikke-Schmidt, R., Williams, J., Ruiz, A., Lambert J.C. and Greicius, M.D. (2022). Rare APOE missense variant 1 R251G is associated 2 with reduced risk of Alzheimer's disease in APOE- 3 ε4 carriers. ***JAMA Neurology***, 79(7):652-663. *Supervision of the statistical analysis.
38. Belloy, M.E., Le Guen, Y.E., Eger, S.J., Napolioni, V., Greicius, M.D. and **He, Z.** (2022). A fast and robust strategy to remove variant level artifacts in Alzheimer's Disease Sequencing Project data. ***Neurology Genetics***, 8(5).
39. Baumer, F., Mytinger, J., Neville, K., Briscoe Abath, C., Gutierrez, C., Numis, A., Harini, C., **He, Z.***, Hessain, S., Berg, A., Loddenkemper, T., Chu, C., Gaillard, W., Pasupuleti, A., Samanata, D., Singh, R., Singhal, N., Wusthoff, C., Wirrell, E., Yozawitz, E., Knupp, K., Shellhaass, R. and Grinspan, Z. (2022). Inequities in therapy for infantile spasms: a call to action. ***Annals of Neurology***, 92(1):32-44. *Supervision of the statistical analysis. Analysis and interpretation of data. Critical revision of the manuscript for important intellectual content.
40. Belloy, M.E., Eger, S.J., Le Guen, Y., Damotte, V., Ahmad, S., Ikram, M.A., Ramirez, A., Tsolaki, A.C., Rossi, G., Jansen, I.E., de Rojas, I., Parveen, K., Sleegers, K., Ingelsson, M., Hiltunen, M., Amin, N., Andreassen, O., Sanchez-Juan, P., Kehoe, P., Amouyel, P., Sims, R., Frikke-Schmidt, R., van der Flier, W.M., Lambert, J.C., **He, Z.***, Han, S.S., Napolioni, V., Greicius, M.D. (2022). Challenges at the APOE locus: a robust quality control approach for accurate APOE genotyping. ***Alzheimer's research & therapy***, 14(1), pp.1-17. *Supervision of the statistical analysis.
41. Kassani, P.H., Lu, F., Guen, Y.L. and **He, Z.** (2022). Deep neural networks with controlled variable selection for the identification of putative causal genetic variants. ***Nature Machine Intelligence***.
42. Otero-Garcia, M., Mahajani, S.U., Wakhloo, D., Tang, W., Xue, Y., Morabito, S., Pan, J., Oberhauser, J., Madira, A.E., Shakouri, T., Deng, Y., Allison, T., **He, Z.***, Lowry, W.E., Kawaguchi, R., Swarup, V., Cobos, I. (2022). Molecular signatures underlying neurofibrillary tangle susceptibility in Alzheimer's disease. ***Neuron***. *Supervision of the statistical analysis.
43. Yang, Y., Wang, C., Liu, L., Buxbaum, J., **He, Z.***, Ionita-Laza, I. (2022). Knockoff Trio: A knockoff framework for the identification of putative causal variants in genetic association studies with trio design. ***The American Journal of Human Genetics***, in press. *Conception and design of the method. Critical revision of the manuscript for important intellectual content.
44. Gyawali, P.K., Liu, X., Zou, J. and **He, Z.** (2022). Ensembling improves stability and power of feature selection for deep learning models. ***Machine Learning in Computational Biology***, pp. 33-45.
45. **He, Z.**, Liu, L., Belloy, M.E., Le Guen, Y., Sossin, A., Liu, X., Qi, X., Ma, S., Wyss-Coray, T., Tang, H., Sabatti, C., Candes, E., Greicius, M.D., and Ionita-Laza, I. (2022). GhostKnockoff inference empowers identification of putative causal variants in genome-wide association studies. ***Nature Communications***, 13(1), p.7209.
46. Lu, F., Sossin, A., Abell, N., Montgomery, S.B. and **He, Z.** (2022). Deep learning-assisted genome-wide characterization of massively parallel reporter assays. ***Nucleic Acids Research***, 50(20), pp.11442-11454.

47. Goad, B.S., Lee-Messer, C., **He, Z.**, Porter, B.E. and Baumer, F.M. (2022). Connectivity increases during spikes and spike-free periods in self-limited epilepsy with centrotemporal spikes. ***Clinical Neurophysiology***, 144, pp.123-134. *Supervision of the statistical analysis.
48. Ma, S., Wang, C., Khan, A., Liu, L., Dalgleish, J., Kiryluk, K., **He, Z.*** and Ionita-Laza, I. (2023). BIGKnock: fine-mapping gene-based associations via knockoff analysis of biobank-scale data. ***Genome Biology***, 24(1), p.24. *Conception and design of the method. Critical revision of the manuscript for important intellectual content.
49. Le Guen, Y., Raulin, A.C., Logue, M.W., Sherva, R., Belloy, M.E., Eger, S.J., Chen, A., Kennedy, G., Kuchenbecker, L., O'Leary, J.P., Zhang, R., Merritt, V.C., Panizzon, M.S., Hauger, R.L., Gaziano, J.M., Bu, G., Thornton, T.A., Farrer, L.A., Napolioni, V., **He, Z.***, Greicius, M.D. (2023). Association of African Ancestry–Specific APOE Missense Variant R145C With Risk of Alzheimer Disease. ***JAMA***, 329(7), pp.551-560. *Supervision of the statistical analysis. Analysis and interpretation of data.
50. Le Guen, Y., Luo, G., Ambati, A., Damotte, V., Jansen, I., Yu, E., …, **He, Z.**, …, and Mignot E.J. (2023) (Author list is too long. Only include the first five authors and the last author). Multi-ancestry HLA analysis in Alzheimer's and Parkinson's diseases uncovers a shared adaptive immune response mediated by HLA-DRB1*04. ***Proceedings of the National Academy of Sciences***, 120(36), p.e2302720120. *Supervision of the statistical analysis.
51. Moskatel, L., **He, Z.**, Graber-Naidich, A., Zhang N. (2023). Real world evidence of changes in CGRP monoclonal antibody and onabotulinumtoxinA prescription practices at the start of the COVID-19 pandemic: an observational, retrospective study. ***Headache***, 63(8):1180-1182. *Supervision of the statistical analysis. Analysis and interpretation of data.
52. Moskatel, L.S., Graber-Naidich, A., **He, Z.** and Zhang, N. (2023). The introduction of the CGRP monoclonal antibodies and their effect on the prescription patterns of chronic migraine preventive medications in a tertiary headache center: A retrospective, observational analysis. ***Headache***. *Supervision of the statistical analysis.
53. Graber-Naidich, A., Lee, J., Younes, K., Greicius, M.D., Le Guen, Y. and He, Z. (2023). Loop diuretics association with Alzheimer's disease risk. ***Frontiers in Aging***, 4.
54. Gyawali, P.K., Le Guen, Y., Liu, X., Tang, H., Zou, J., **He, Z.** (2023). Improving genetic risk prediction across diverse population by disentangling ancestry representations. ***Communications Biology***, 6(1), p.964.
55. Oh, H.SH., Rutledge, J., ... , **He, Z.**, ... , Wyss-Coray, T. (2023) (Author list is too long. Only include the first five authors and the last author). Organ-specific aging signatures in the plasma proteome track health and disease. ***Nature***, 624, 164-172. *Supervision of the statistical analysis.

Peer-reviewed publications (submitted)

56. Liu, X., Butler III, R.R., Gyawali, P.K., Longo, F.M., **He, Z.** (2023) ScAtt: an Attention based architecture to analyze Alzheimer's disease at cell type level from single-cell RNA-sequencing data. Submitted.
57. Graber-Naidich, A., Lee, J., Younes, K., Greicius, M.D., Le Guen, Y. and **He, Z.** (2023). Bumetanide Exposure Association with Alzheimer's Disease Risk. ***Frontiers in Aging***, revision invited.

58. Winer, J.R., Lok, R., Weed, L., **He, Z.**, Poston, K.L., Mormino, E.C. and Zeitzer, J.M. (2023). Association of 24-hour activity patterns with risk of Alzheimer's disease, Parkinson's disease, and cognitive decline. Submitted. *Supervision of the statistical analysis.
59. Qi, X., Belloy, M.E., Gu, J., Liu, X., Tang, H. and **He, Z.** (2023). Robust inference with GhostKnockoffs in genome-wide association studies. arXiv preprint arXiv:2310.04030.
60. Chu, B.B., Gu, J., Chen, Z., Morrison, T., Candes, E., **He, Z.** and Sabatti, C. (2023). Second-order group knockoffs with applications to GWAS. arXiv preprint arXiv:2310.15069. ****Co-senior author.***

Peer-reviewed publications (other – 1 total)

1. Tang, H. and **He, Z.**** (2021) Advances and challenges in quantitative delineation of the genetic architecture of complex traits, ***Quantitative Biology***, 9 (2), pp.168-184. (Review) ****Co-first author.***

Book Chapters (1 total)

1. Mukherjee, B., Chen, Y., Ko, Y., **He, Z.***, Lee, S., Zhang, M., and Park, S.K. (2016). Statistical strategies for modeling gene-environment interactions in longitudinal cohort studies. ***Statistical Approaches to Gene-Environment Interactions for Complex Phenotypes***, Cambridge, MA: MIT Press, 2016. *Drafting of the manuscript. Critical revision of the manuscript for important intellectual content.

VI. GRANT FUNDING

Current:

09/2019 – 05/2024	Funder: NIH (R01) Title: Statistical and computational methods for integrative analysis of Alzheimer's Disease genetics Role: **PI**
06/2020 – 03/2025	Funder: NIH (P30) Title: Alzheimer's Disease Research Center Role: Co-Investigator (Principal Investigator: V. Henderson)
12/2020 – 11/2025	Funder: NIH (R01) Title: PREcision Care in Cardiac ArrEst – ICECAP (PRECICECAP) Role: Co-Investigator (Principal Investigator: K. Hirsch)
02/2022 – 01/2027	Funder: NIH (R01) Title: Hippocampal-dependent memory decline in aging and early Alzheimer's disease Role: Co-Investigator (Principal Investigator: E. Mormino)
01/2023 – 01/2026	Funder: Wu Tsai Neurosciences Institute

	Title: From gut to brain: reprogramming peripheral macrophages at the intestinal barrier to prevent age-associated inflammation and cognitive decline Role: Co-Investigator (Principal Investigator: K. I. Andreasson)
02/2023 – 01/2026	Funder: NIH (R01) Title: Metabolic mechanisms of cognitive decline in aging and AD mediated by inflammatory PGE2 signaling Role: Co-Investigator (Principal Investigator: K. I. Andreasson)
08/2022 – 07/2024	Funder: NIH (R01) Title: Neurostimulation of the Nucleus Basalis of Meynert for the cognitive-motor syndrome in Parkinson's disease Role: Co-Investigator (Principal Investigator: H.M. Bronte-Stewart)
12/2022 – 11/2027	Funder: NIH (R01) Title: Utilizing a Conductive Polymer- Stem Cell System to Augment EndogenousStroke Repair Mechanisms and Improve Functional Recovery Role: Co-Investigator (Principal Investigator: P. George)

Completed: None

VII. CLINICAL TRIALS

None

VIII. PATENTS

None

IX. EDITORIAL SERVICE

Editorial Positions

2018 – present Guest Associate Editor, *PLOS genetics*

Reviewer (2018 - present)

American Journal of Human Genetics, *Nucleic Acids Research*, *PLOS genetics*, *Journal of the American Statistical Association*, *Statistics in Medicine*, *Genetic Epidemiology*, *PLOS Computational Biology*, *BMC Public Health, PLOS One, Bioinformatics*

X. SERVICE AS GRANT REVIEWER

2018 *Alzheimer's Association Research Fellowship Program*

2023 *NIH study section: ASPB*

XI. UNIVERSITY ADMINISTRATIVE SERVICE

Head of data science research infrastructure, Department of Neurology – partnership with the Quantitative Sciences Unit.

Data Management & Statistics Associate Core Leader, Stanford Alzheimer's Disease Research Center.

Research advisory committee member, Department Neurology.

Dissertation committee:

Nicole Ersaro, PhD Candidate Biomedical Informatics 2021

Nathan Samuel Abell, PhD Candidate Genetics 2021

Mike Gloudemans, PhD Candidate Biomedical Informatics 2021

Yoo Jin Jung, PhD Candidate Neurosciences (2021 qualifying exam)

XII. SERVICE TO PROFESSIONAL ORGANIZATIONS

None

XIII. TEACHING EXPERIENCE

BIODS220, Stanford University
AI in Healthcare
October 2021
Guest Lecturer
Enrollment = 20–30

EPI 244, Stanford University
Genetic Epidemiology
February 2021
Guest Lecturer
Enrollment = 20–30

XIV. INVITED PRESENTATIONS

National Meetings:

1. 2013 "Random field modeling of association and correlation", The Kidney Disease Research (KDR) meeting, Ann Arbor, MI.
2. 2013 "Modeling and testing for joint association using a genetic random field model and its extensions", Michigan State University, Department of Statistics and Probability, East Lansing, MI.

3. 2013 "Modeling and testing for joint association using a genetic random field model and its extensions", University of Michigan, Department of Statistics, Ann Arbor, MI.
4. 2015 "Set-based tests for gene-environment interaction", University of Michigan, Department of Statistics, Ann Arbor, MI.
5. 2017 "A semi-supervised approach for predicting organism level and cell/tissue specific functional consequences of noncoding variants", Novarits Pharmaceuticals, Division of Advanced Exploratory Analytics, East Hanover, NJ.
6. 2019 "Statistical and computational methods for integrative analysis of noncoding genetic variation", University of California - San Francisco, San Francisco, CA.
7. 2019 "Statistical and computational methods for integrative analysis of noncoding genetic variation", Fred Hutchinson Cancer Research Center, Seattle, WA.
8. 2020 "Identification of putative causal loci in whole genome sequencing data via knockoff statistics", University of California - Berkeley, Berkeley, CA.
9. 2021 "Identification of putative causal loci in whole genome sequencing data via knockoff statistics", American Statistics Association San Francisco Chapter (SFASA) Seminar Presentations, Virtual Conference.
10. 2022 "Identification of putative causal genetic variants via GhostKnockoff", for the GREGoR consortium, Stanford University, Stanford, CA
11. 2022 "Feature Selection Methods to Identify Putative Causal Genetic Variants of Alzheimer's Disease", Stanford Data Science Institute, Stanford, CA.
12. 2023 "Advancing conditional independent feature selection in large-scale genetic studies with model-X knockoffs", Harvard University, Boston, MA.
13. 2023 "In silico identification of putative causal genetic variants", University of California, Riverside, CA.

International Meetings:

14. 2014 "Set-based tests for gene-environment interaction in longitudinal studies", invited session for the 2014 WNAR/IMS conference, Honolulu, U.S..
15. 2019 "A semi-supervised approach for predicting cell type specific functional consequences of non-coding variation using MPRAs", ENAR 2019 spring meeting, Philadelphia, U.S..
16. 2020 "Identification of putative causal loci in whole genome sequencing data via knockoff statistics", 2020 Joint Statistical Meetings, Virtual Conference.
17. 2020 "Identification of putative causal loci in whole genome sequencing data via knockoff statistics", ICSA 2020 Applied Statistics Symposium, Virtual Conference.
18. 2021 "Identification of putative causal loci in whole genome sequencing data via knockoff statistics", Tsinghua University, Center for Statistical Science, Beijing, China.
19. 2021 "Identification of putative causal loci in whole genome sequencing data via knockoff statistics", 2021 Joint Statistical Meetings, Virtual Conference.
20. 2022 "Identification of putative causal genetic variants via GhostKnockoff", Hong Kong University, Hong Kong, China.

21. 2022 "Feature selection methods for the identification of putative causal variants in genome-wide association studies", Keynote speaker for the Institute of Engineering, Tribhuvan University, Kathmandu, Nepal.
22. 2023 "Identification of putative causal genetic variants via GhostKnockoff", invited session for the 2014 WNAR/IMS conference, Anchorage, U.S..
23. 2023 "Identification of putative causal genetic variants via GhostKnockoff", The 6th International Conference on Econometrics and Statistics (EcoSta2023), Tokyo, Japan.

XV. TRAINEES

Graduate students:

Fred Lu, 2019-2020

Aaron Sossin, 2020-present

Undergraduate students: None

Postdoctoral scholars:

Dr. Peymann Kassani (PhD, Yonsei University), 2020-2022

Dr. Xiaoxia Liu (PhD, Dalian University of Technology), 2021-present

Dr. Prashnna Kumar Gyawali (PhD, Rochester Institute of Technology), 2021-2022

Dr. Xinran Qi (PhD, Medical College of Wisconsin), 2021-present

Dr. Jiaqi Gu (PhD, Hong Kong University), 2023-present

Junior statisticians:

Justin Lee, 2019-present

Rebecca Gardner, 2019-2021

Amy Lin, 2021-present

Bo Gu, 2022-present

KL2 trainees:

Dr. Maya Kasowski (Assistant Professor, Stanford University), 2021

Dr. Kelly Mahaney (Assistant Professor, Stanford University), 2021