

Stanford



Zihuai He

Assistant Professor (Research) of Neurology and of Medicine (BMIR)
Neurology & Neurological Sciences

 Curriculum Vitae available Online

Bio

BIO

Dr. He received his PhD from the University of Michigan in 2016. Following a postdoctoral training in biostatistics at Columbia University, he joined Stanford University as an assistant professor of neurology and of medicine in 2018. His research is concentrated in the area of statistical genetics and integrative analysis of omics data, attempting to develop new statistical methodologies that aid with the identification and interpretation of complex biological pathways involved in human diseases, particularly neurological disorders. His methodology interest includes high-dimensional data analysis, correlated (longitudinal, familial) data analysis and machine learning algorithms.

ACADEMIC APPOINTMENTS

- Assistant Professor (Research), Neurology & Neurological Sciences
- Assistant Professor (Research), Medicine - Biomedical Informatics Research
- Member, Bio-X
- Member, Wu Tsai Neurosciences Institute

HONORS AND AWARDS

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

PROFESSIONAL EDUCATION

- Ph.D., University of Michigan , Biostatistics (2016)
- B.S., Tsinghua University , Mathematics and Physics (2010)

LINKS

- Quantitative Science Unit: <https://med.stanford.edu/qsu.html>

Publications

PUBLICATIONS

- **FUN-LDA: A Latent Dirichlet Allocation Model for Predicting Tissue-Specific Functional Effects of Noncoding Variation: Methods and Applications** *AMERICAN JOURNAL OF HUMAN GENETICS*
Backenroth, D., He, Z., Kiryluk, K., Boeva, V., Pethukova, L., Khurana, E., Christiano, A., Buxbaum, J. D., Ionita-Laza, I.
2018; 102 (5): 920–42

- **A semi-supervised approach for predicting cell-type specific functional consequences of non-coding variation using MPRAs.** *Nature communications*
He, Z., Liu, L., Wang, K., Ionita-Laza, I.
2018; 9 (1): 5199
- **Rare-variant association tests in longitudinal studies, with an application to the Multi-Ethnic Study of Atherosclerosis (MESA)** *GENETIC EPIDEMIOLOGY*
He, Z., Lee, S., Zhang, M., Smith, J. A., Guo, X., Palmas, W., Kardia, S. R., Ionita-Laza, I., Mukherjee, B.
2017; 41 (8): 801–10
- **Unified Sequence-Based Association Tests Allowing for Multiple Functional Annotations and Meta-analysis of Noncoding Variation in Metabochip Data** *AMERICAN JOURNAL OF HUMAN GENETICS*
He, Z., Xu, B., Lee, S., Ionita-Laza, I.
2017; 101 (3): 340–52
- **Set-Based Tests for the Gene-Environment Interaction in Longitudinal Studies** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
He, Z., Zhang, M., Lee, S., Smith, J. A., Kardia, S. R., Roux, V., Mukherjee, B.
2017; 112 (519): 966–78
- **Set-Based Tests for Genetic Association in Longitudinal Studies** *BIOMETRICS*
He, Z., Zhang, M., Lee, S., Smith, J. A., Guo, X., Palmas, W., Kardia, S. R., Roux, A., Mukherjee, B.
2015; 71 (3): 606–15
- **Modeling and Testing for Joint Association Using a Genetic Random Field Model** *BIOMETRICS*
He, Z., Zhang, M., Zhan, X., Lu, Q.
2014; 70 (3): 471–79
- **Detecting Rare Mutations with Heterogeneous Effects Using a Family-Based Genetic Random Field Method.** *Genetics*
Li, M., He, Z., Tong, X., Witte, J. S., Lu, Q.
2018; 210 (2): 463–76
- **Interaction between Social/Psychosocial Factors and Genetic Variants on Body Mass Index: A Gene-Environment Interaction Analysis in a Longitudinal Setting** *INTERNATIONAL JOURNAL OF ENVIRONMENTAL RESEARCH AND PUBLIC HEALTH*
Zhao, W., Ware, E. B., He, Z., Kardia, S. R., Faul, J. D., Smith, J. A.
2017; 14 (10)
- **Testing Allele Transmission of an SNP Set Using a Family-Based Generalized Genetic Random Field Method** *GENETIC EPIDEMIOLOGY*
Li, M., Li, J., He, Z., Lu, Q., Witte, J. S., Macleod, S. L., Hobbs, C. A., Cleves, M. A., Natl Birth Defects Prevention Stud
2016; 40 (4): 341–51
- **Risk Prediction Modeling of Sequencing Data Using a Forward Random Field Method** *SCIENTIFIC REPORTS*
Wen, Y., He, Z., Li, M., Lu, Q.
2016; 6: 21120
- **Association between Stress Response Genes and Features of Diurnal Cortisol Curves in the Multi-Ethnic Study of Atherosclerosis: A New Multi-Phenotype Approach for Gene-Based Association Tests** *PLOS ONE*
He, Z., Payne, E. K., Mukherjee, B., Lee, S., Smith, J. A., Ware, E. B., Sanchez, B. N., Seeman, T. E., Kardia, S. R., Roux, A.
2015; 10 (5): e0126637
- **A Powerful Nonparametric Statistical Framework for Family-Based Association Analyses** *GENETICS*
Li, M., He, Z., Schaid, D. J., Cleves, M. A., Nick, T. G., Lu, Q.
2015; 200 (1): 69–U140
- **A Weighted U-Statistic for Genetic Association Analyses of Sequencing Data** *GENETIC EPIDEMIOLOGY*
Wei, C., Li, M., He, Z., Vsevolozhskaya, O., Schaid, D. J., Lu, Q.
2014; 38 (8): 699–708
- **A Generalized Genetic Random Field Method for the Genetic Association Analysis of Sequencing Data** *GENETIC EPIDEMIOLOGY*
Li, M., He, Z., Zhang, M., Zhan, X., Wei, C., Elston, R. C., Lu, Q.
2014; 38 (3): 242–53