Xihao Li

Contact Information

135 Dauer Drive
3107-D McGavran-Greenberg Hall
Chapel Hill, NC 27599

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Research Interests

Statistical Genetics, Integrative Analysis of Sequencing and Multi-Omics Data, Functional Genomics and Annotations, Data Integration and Meta-Analysis, Multivariate Analysis, Machine Learning, Big Data Computing

Education

Harvard University, Cambridge, MA

Ph.D., Biostatistics — Jan 2021

- Dissertation: *Modern Statistical Methods for Genetics and Genomic Studies*
- Advisor: Xihong Lin, Ph.D.

M.S., Biostatistics — May 2016

Peking University, Beijing, China

B.S., Statistics (major) and Economics (double major) — Jul 2014

Stanford University, Stanford, CA

Summer Program, Statistics — Jun 2013 - Aug 2013

Professional Experience

Assistant Professor — Aug 2023 - Present
Department of Biostatistics — Chapel Hill, NC
University of North Carolina at Chapel Hill

Assistant Professor — Aug 2023 - Present
Department of Genetics — Chapel Hill, NC
University of North Carolina at Chapel Hill

Postdoctoral Research Fellow — Mar 2021 - Jul 2023
Department of Biostatistics — Boston, MA
Harvard T.H. Chan School of Public Health

Statistical Consultant — Aug 2017 - Mar 2021
Harvard Biostatistics Consulting Center — Boston, MA

Biostatistician Intern — May 2017 - Aug 2017
Vertex Pharmaceuticals — Boston, MA

Biostatistician Intern — Jun 2015 - Aug 2015
Pfizer China Research & Development Center — Shanghai, China

Maternal & Child Health Intern — Jun 2014 - Aug 2014
UNICEF China — Beijing, China

Honors and Awards

CHARGE Travel Award — Oct 2023
Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium

Program in Quantitative Genomics (PQG) Travel Award — Nov 2022
Harvard T.H. Chan School of Public Health

Distinguished Student Paper Award in the Section on Statistics in Genomics and Genetics (SSGG) American Statistical Association — Aug 2022

Reviewers' Choice Abstract Award Oct 2021
The American Society of Human Genetics

Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research
Semifinalist The American Society of Human Genetics Oct 2020

Certificates of Distinction and Excellence in Teaching Fall 2019
Graduate School of Arts and Sciences, Harvard University

Certificates of Distinction and Excellence in Teaching Spring 2019
Graduate School of Arts and Sciences, Harvard University

Certificates of Distinction and Excellence in Teaching Fall 2018
Graduate School of Arts and Sciences, Harvard University

Distinction in Teaching Award Fall 2017
Department of Biostatistics, Harvard University

Robert B. Reed Prize for Excellence in Biostatistical Science Jan 2017
Department of Biostatistics, Harvard University

Peking University Leadership Scholarship May 2014
National School of Development, Peking University

Manuscripts Submitted (Preprints)

1. **Li, X.**, Chen, H., Selvaraj, M.S., et al., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, Rice, K.M., Rotter, J.I., Peloso, G.M., Natarajan P., Li, Z., Liu, Z., & Lin, X. A statistical framework for powerful multi-trait rare variant analysis in large-scale whole-genome sequencing studies. *bioRxiv*, 2023.10.30.564764, 1-71. **Under Revision** [preprint]

2. Hawkes, G.*, Beaumont, R.N.*, Li, Z.*, Mandla, R.*, **Li, X.***, et al., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, Liu, C.T., North, K.E., Justice, A.E., Locke, J., Owens, N., Murray, A., Patel, K., Frayling, T.M., Wright, C.F., Wood, A.R., Lin, X., Manning, A.K., & Weedon, M. Whole genome association testing in 333,100 individuals across three biobanks identifies rare non-coding single variant and genomic aggregate associations with height. *bioRxiv*, 2023.11.19.566520, 1-30. **Accepted in Principal at Nature Communications** [preprint]

3. Zhang, X.*, Brody, J.A.*, Graff, M.*, Highland, H.M.*, Chami, N.*, et al. (including **Li, X.**), Cupples, L.A., Lange, L.A., Liu, C.T., Loos, R.J.F., North, K.E., & Justice, A.E. Whole genome sequencing analysis of body mass index identifies novel african ancestry-specific risk allele. *medRxiv*, 2023.08.21.23293271, 1-33. **Under Revision** [preprint]

4. IGVF Consortium (including **Li, X.**). The Impact of Genomic Variation on Function (IGVF) Consortium. *arXiv*, 2307.13708, 1-30. [preprint]

5. Quick, C., Guan, L., Li, Z., **Li, X.**, Dey, R., Liu, Y., Scott, L., & Lin, X. A versatile toolkit for molecular QTL mapping and meta-analysis at scale. *bioRxiv*, 2020.12.18.423490, 1-26. [preprint]

Publications

1. Jiang, M.Z.*, Gaynor, S.M.*, **Li, X.**, et al., Reiner, A.P., Bowler, R.P., Lin, X., Auer, P.L., Raffield, L.M., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium & TOPMed Inflammation Working Group. Whole Genome Sequencing Based Analysis of Inflammation Biomarkers in the Trans-Omics for Precision Medicine (TOPMed) Consortium. *Human Molecular Genetics*. [pub]

2. Sun, Q., Yang, Y., Rosen, J.D., Chen, J., **Li, X.**, Guan, W., Jiang, M.Z., Wen, J., Pace, R.G., Blackman, S.M., Bamshad, M.J., Gibson, R.L., Cutting, G.R., O'Neal, W.K., Knowles, M.R., Kooperberg, C., Reiner, A.P., Raffield, L.M., Carson, A.P., Rich, S.S., Rotter, J.I., Loos, R.J.F., Kenny, E., Jaeger, B.C., Min, Y.I., Fuchsberger, C., & Li, Y. (2024). MagicalRsq-X: A cross-cohort transferable genotype imputation quality metric. *The American Journal of Human Genetics*. [pub]

3. **Li, X.**, Quick, C., Zhou, H., Gaynor, S.M., Liu, Y., Chen, H., Selvaraj, M.S., Sun, R., Dey, R., Arnett, D.K., Bielak, L.F., Bis, J.C., Blangero, J., Boerwinkle, E., Bowden, D.W., Brody, J.A., Cade, B.E., Correa, A., Cupples, L.A., Curran, J.E., de Vries, P.S., Duggirala, R., Freedman, B.I., Göring, H.H.H., Guo, X., Haessler, J., Kalyani, R.R., Kooperberg, C., Kral, B.G., Lange, L.A., Manichaikul, A., Martin, L.W., McGarvey, S.T., Mitchell, B.D., Montasser, M.E., Morrison, A.C., Naseri, T., O'Connell, J.R., Palmer, N.D., Peyser, P.A., Psaty, B.M., Raffield, R.M., Redline, S., Reiner, A.P., Reupena, M.S., Rice, K.M., Rich, S.S., Sitlani, C.M., Smith, J.A., Taylor, K.D., Vasan, R.S., Willer, C.J., Wilson, J.G., Yanek, L.R., Zhao, W., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Lipids Working Group, Rotter, J.I., Natarajan, P., Peloso, G.M., Li, Z., & Lin, X. (2023). Powerful, scalable and resource-efficient meta-analysis of rare variant associations in large whole genome sequencing studies. *Nature Genetics*, *55*(1), 154-164. [pub][software]

4. **Li, X.***, Yung, G.*, Zhou, H., Sun, R., Li, Z., Hou, K., Zhang, M.J., Liu, Y., Arapoglou, T., Wang, C., Ionita-Laza, I., & Lin, X. (2022). A multi-dimensional integrative scoring framework for predicting functional variants in the human genome. *The American Journal of Human Genetics*, *109*(3), 446-456. [pub]

5. Li, Z.*, **Li, X.***, Zhou, H., Gaynor, S.M., Selvaraj, M.S., Arapoglou, T., Quick, C., Liu, Y., Chen, H., Sun, R., Dey, R., Arnett, D.K., Auer, P.L., Bielak, L.F., Bis, J.C., Blackwell, T.W., Blangero, J., Boerwinkle, E., Bowden, D.W., Brody, J.A., Cade, B.E., Conomos, M.P., Correa, A., Cupples, L.A., Curran, J.E., de Vries, P.S., Duggirala, R., Franceschini, N., Freedman, B.I., Göring, H.H.H., Guo, X., Kalyani, R.R., Kooperberg, C., Kral, B.G., Lange, L.A., Lin, B.M., Manichaikul, A., Martin, L.W., Mathias, R.A, Meigs, J.B., Mitchell, B.D., Montasser, M.E., Morrison, A.C., Naseri, T., O'Connell, J.R., Palmer, N.D., Peyser, P.A., Psaty, B.M., Raffield, R.M., Redline, S., Reiner, A.P., Reupena, M.S., Rice, K.M., Rich, S.S., Smith, J.A., Taylor, K.D., Taub, M.A., Vasan, R.S., Weeks, D.E., Wilson, J.G., Yanek, L.R., Zhao, W., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Lipids Working Group, Rotter, J.I., Willer, C.J., Natarajan, P., Peloso, G.M., & Lin, X. (2022). A framework for detecting noncoding rare variant associations of large-scale whole-genome sequencing studies. *Nature Methods*. [pub][software]

6. **Li, X.***, Li, Z.*, Zhou, H., Gaynor, S.M., Liu, Y., Chen, H., Sun, R., Dey, R., Arnett, D.K., Aslibekyan, S., Ballantyne, C.M., Bielak, L.F., Blangero, J., Boerwinkle, E., Bowden, D.W., Broome, J.G., Conomos, M.P., Correa, A., Cupples, L.A., Curran, J.E., Freedman, B.I., Guo, X., Hindy, G., Irvin, M.R., Kardia, S.L.R., Kathiresan, S., Khan, A.T., Kooperberg, C.L., Laurie, C.C., Liu, X.S., Mahaney, M.C., Manichaikul, A.W., Martin, L.W., Mathias, R.A., McGarvey, S.T., Mitchell, B.D., Montasser, M.E., Moore, J.E., Morrison, A.C., O'Connell, J.R., Palmer, N.D., Pampana, A., Peralta, J.M., Peyser, P.A., Psaty, B.M., Redline, S., Rice, K.M., Rich, S.S., Smith, J.A., Tiwari, H.K., Tsai, M.Y., Vasan, R.S., Wang, F.F., Weeks, D.E., Weng, Z., Wilson, J.G., Yanek, L.R., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Lipids Working Group, Neale, B.M., Sunyaev, S.R., Abeçasis, G.R., Rotter, J.I., Willer,

C.J., Peloso, G.M., Natarajan, P., & Lin, X. (2020). Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. *Nature Genetics*, *52*(9), 969-983. [pub][software]

7. **Li, X.**, & Song, Y. (2020). Target population statistical inference with data integration across multiple sources - an approach to mitigate information shortage in rare disease clinical trials. *Statistics in Biopharmaceutical Research*, *12*(3), 322-333. [pub]

8. Hasbani, N.R., Westerman, K.E., Kwak, S.H., Chen, H., **Li, X.**, et al., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Atherosclerosis Working Group, TOPMed Diabetes Working Group, Wu, J.C., Malhotra, R., Peyser, P.A., Morrison, A.C., Vasan, R.S., Lin, X., Rotter, J.I., Meigs, J.B., Manning, A.K., & de Vries, P.S. (2023). Type 2 Diabetes Modifies the Association of CAD Genomic Risk Variants With Subclinical Atherosclerosis. *Circulation: Genomic and Precision Medicine*, *16*(6), e004176. [pub]

9. Wang, Y., Selvaraj, M.S., **Li, X.**, et al., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, Rotter, J.I., Lin, X., Natarajan, P., & Peloso, G.M. (2023). Rare variants in long non-coding RNAs are associated with blood lipid levels in the TOPMed whole-genome sequencing study. *The American Journal of Human Genetics*, *110*(10), 1704-1717. [pub]

10. Feofanova, E.V., Brown, M.R., Alkis, T., Manuel, A.M., **Li, X.**, Tahir U.A., Li, Z., Mendez K.M., Kelly, R.S., Qi, Q., Chen, H., Larson, M.G., Lemaitre, R.N., Morrison, A.C., Greiser, C., Wong, K.E., Gersztern, R.E., Zhao, Z., Lasky-Su, J., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, & Yu, B. (2023). Whole-genome sequencing analysis of human metabolome in multi-ethnic populations. *Nature Communications*, *14*, 3111. [pub]

11. Zhou, H., Arapoglou T., **Li, X.**, Li, Z., Zheng, X, Moore, J.E., Asok, A., Kumar, S., Blue, E.E., Buyske S., Cox, N., Felsenfeld A., Gerstein, M., Kenny, E., Li, B., Matise, T., Philippakis A., Rehm H., Sofia, H.J., Neale, B., Snyder G., Weng, Z., Sunyaev, S., & Lin, X. (2023). FAVOR: functional annotation of variants online resource and annotator for variation across the human genome. *Nucleic Acids Research*, *51*(D1), D1300-D1311. [pub]

12. Selvaraj, M.S., **Li, X.**, Li, Z., Pampana, A., Zhang, D.Y., Park, J., Aslibekyan, S., Bis, J.C., Brody, J.A., Cade, B.E., Chuang, L.M., Chung, R.H., Curran, J.E., de las Fuentes, L., de Vries, P.S., Duggirala, R., Freedman, B.I., Graff, M., Guo, X., Heard-Costa, N., Hidalgo, B., Hwu, C.M., Irvin, M.R., Kelly, T.N., Kral, B.G., Lange, L., Li, X., Martin, L., Lubitz, S.A., Manichaikul, A.W., Preuss, M., Montasser, M.E., Morrison, A.C., Naseri, T., O'Connell, J.R., Palmer, N.D., Peyser, P.A., Reupena, M.S., Smith, J.A., Sun, X., Taylor, K.D., Tracy, R.P., Tsai, M.Y., Wang, Z., Wang, Y., Wei, B., Wilkins, J.T., Yanek, L.R., Zhao, W., Arnett, D.K., Blangero, J., Boerwinkle, E., Bowden, D.W., Chen, Y.D.I., Correa, A., Cupples, L.A., Dutcher, S.K., Ellinor, P.T., Fornage, M., Gabriel, S., Germer, S., Gibbs, R., He, J., Kaplan, R.C., Kardia, S.L.R., Kim, R., Kooperberg, C., Loos, R.J.F., Martinez, K., Mathias, R.A., McGarvey, S.T., Mitchell, B.D., Nickerson, D., North, K.E., Psaty, B.M., Redline, S., Reiner, A.P., Vasan, R.S., Rich, S.S., Willer, C., Rotter, J.I., Rader, D.J., Lin, X., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, Peloso, G.M., & Natarajan, P. (2022). Whole genome sequence analysis of blood lipid levels in >66,000 individuals. *Nature Communications*, *13*, 5995. [pub]

13. Byun, J., Han, Y., Li, Y., Xia, J., Long, E., Choi, J., Xiao, X., Zhu, M., Zhou, W., Sun, R., Bossé, Y., Song, Z., Schwartz, A., Lusk, C., Rafnar, T., Stefansson, K., Zhang, T., Zhao, W., Pettit, R.W., Liu, Y., **Li, X.**, Zhou, H., Walsh, K.M., Gorlova, O., Zhu, D., Rosenberg, S.M., Pinney, S., Bailey-Wilson, J.E., Mandal, D., de Andrade, M., Gaba, C., Willey, J.C., You, M., Anderson, M., Wiencke, J.K., Albanes, D., Lam, S., Tardon, A., Chen, C., Goodman, G., Bojeson, S., Brenner, H., Landi, M.T., Chanock, S.J., Johansson, M., Muley, T., Risch, A., Wichmann, H.E., Bickeböller, H., Christiani, D.C., Rennert, G., Arnold, S., Field, J.K., Shete, S., Le Marchand, L., Melander, O., Brunnstrom, H., Liu, G., Andrew, A.S., Kiemeney, L.A., Shen, H., Zienolddiny, S., Grankvist, K., Johansson, M., Caporaso, N., Cox, A., Hong, Y.C., Yuan, J.M., Lazarus, P., Schabath, M.B., Aldrich, M.C., Patel, A., Lan, Q., Rothman, N., Taylor, F., Kachuri, L., Witte, J.S., Sakoda, L.C., Spitz, M., Brennan, P., Lin, X., McKay, J., Hung, R.J., & Amos, C.I. (2022). Cross-ancestry genome-wide meta-analysis of 61,047 cases and 947,237 controls identifies new susceptibility loci contributing to lung cancer. *Nature Genetics*, *54*(8), 1167-1177. [pub]

14. Gaynor, S.M., Westerman, K.E., Ackovic, L.L., **Li, X.**, Li, Z., Manning, A.K., Philippakis, A., & Lin, X. (2022). STAAR Workflow: A cloud-based workflow for scalable and reproducible rare variant analysis. *Bioinformatics*, *38*(11), 3116-3117. [pub]

15. West, E.R., Lapan, S.W., Lee, C., Kajderowicz, K.M., **Li, X.**, & Cepko, C.L. (2022). Spatiotemporal patterns of neuronal subtype genesis suggest hierarchical development of retinal diversity. *Cell Reports*, *38*(1), 110191. [pub]

16. Kim, D.H., **Li, X.**, Bian, S., Wei, L.J., & Sun, R. (2021). Utility of restricted mean survival time for analyzing time to nursing home placement among patients with dementia. *JAMA Network Open*, *4*(1), e2034745. [pub]

17. Sun, R., Xu, M., **Li, X.**, Gaynor, S.M., Zhou, H., Li, Z., Bossé, Y., Lam, S., Tsao, M.S., Tardon, A., Chen, C., Doherty, J., Goodman, G., Bojesen, S.E., Landi, M.T., Johansson M., Field, J.K., Bicheböller, H., Wichmann, H.E., Risch, A., Rennert, G., Arnold, S., Wu, X., Melander, O., Brunnström, H., Marchand, L.L., Liu, G., Andrew, A., Duell, E., Kiemeney, L.A., Shen, H., Haugen, A., Johansson, M., Grankvist, K., Caporaso, N., Woll, P., Teare, M.D., Scelo, G., Hong, Y.C., Yuan, J.M., Lazarus, P., Schabath, M.B., Aldrich, M.C., Albanes, D., Mak, R., Barbie, D., Brennan, P., Hung, R.J., Amos, C.I., Christiani, D.C., & Lin, X. (2021). Integration of multiomic annotation data to prioritize and characterize inflammation and immune-related risk variants in squamous cell lung cancer. *Genetic Epidemiology*, *45*(1), 99-114. [pub]

18. Wang, X., Ricciuti, B., Nguyen, T., **Li, X.**, Rabin, M.S., Awad, M.M., Lin, X., Johnson, B.E., & Christiani, D.C. (2021). Association between smoking history and tumor mutation burden in advanced non-small cell lung cancer. *Cancer Research*, *4*(1), e2034745. [pub]

19. Chao, C., Qian, Y., **Li, X.**, Sang, C., Wang, B., & Zhang, X.Y. (2021). Surgical Survival Benefits With Different Metastatic Patterns for Stage IV Extrathoracic Metastatic Non-Small Cell Lung Cancer: A SEER-Based Study. *Technology in Cancer Research & Treatment*, *20*, 15330338211033064. [pub]

20. Li, Z., **Li, X.**, Liu, Y., Shen, J., Chen, H., Zhou, H., Morrison, A.C., Boerwinkle, E., & Lin, X. (2019). Dynamic scan procedure for detecting rare-variant association regions in whole-genome sequencing studies. *The American Journal of Human Genetics*, *104*(5), 802-814. [pub]

21. Zhu, Z., Wang, X., **Li, X.**, Lin, Y., Shen, S., Liu, C.L., Hobbs, B.D., Hasegawa, K., Liang, L., International COPD Genetics Consortium, Boezen, H.M., Camargo, C.A., Cho, M.H., & Christiani, D.C. (2019). Genetic overlap of chronic obstructive pulmonary disease and cardiovascular diseases: A large-scale genome-wide cross-trait analysis. *Respiratory Research*, *20*(1), 64. [pub]

22. Zhu, Z., Lin, Y., **Li, X.**, Driver, J.A., & Liang, L. (2019). Shared genetic architecture between metabolic traits and Alzheimer's disease: a large-scale genome-wide cross-trait analysis. *Human Genetics*, *138*(3), 271-285. [pub]

23. Lin, C.K., Chen, T., **Li, X.**, de Marcellis-Warin, N., Zigler, C., & Christiani, D.C. (2019). Are per capita carbon emissions predictable across countries? *Journal of Environmental Management*, *237*, 569-575. [pub]

24. Lee, P.H., Lee, C., **Li, X.**, Wee, B., Dwivedi, T., & Daly, M. (2018). Principles and methods of in-silico prioritization of non-coding regulatory variants. *Human Genetics*, *137*(1), 15-30. [pub]

Talks and Presentations

Invited Talks and Lectures

- "Scalable statistical methods for integrative analysis of biobank-scale whole-genome sequencing studies", STATGEN 2024, Pittsburgh, PA May 2024
- "Scalable statistical methods for integrative analysis of biobank-scale whole-genome sequencing studies", MCBIOS 2024, Atlanta, GA Mar 2024
- "Whole Genome Sequencing Analyses of 45,176 Individuals Reveal Rare Coding and Noncoding Variants Associated with Kidney Function", TOPMed Annual Meeting 2024, Bethesda, MD Feb 2024
- "Rare Variant Analysis", Next Generation Statistical Methods for Genome Wide Association Studies: A Hands-On Course, NCI/DCEG, Rockville, MD Nov 2023
- "Statistical methods for integrative analysis of large-scale whole-genome sequencing studies", Department of Biostatistics, University of North Carolina at Chapel Hill, Chapel Hill, NC Feb 2023
- "Statistical methods for integrative analysis of large-scale whole-genome sequencing studies", Department of Epidemiology and Biostatistics, University of Maryland, College Park, MD Feb 2023
- "Statistical methods for integrative analysis of large-scale whole-genome sequencing studies", Division of Biostatistics and Data Science, Medical College of Georgia, Augusta University, Augusta, GA Feb 2023
- "Statistical methods for integrative analysis of large-scale whole-genome sequencing studies", Department of Computer Science and Statistics, University of Rhode Island, Kingston, RI Feb 2023
- "Statistical methods for integrative analysis of large-scale whole-genome sequencing studies", Department of Biostatistics and Data Science and Human Genetic Center, University of Texas Health Science Center at Houston, Houston, TX Jan 2023
- "Statistical methods for integrative analysis of large-scale whole-genome sequencing studies", Department of Biostatistics, University of Washington, Virtual Dec 2022

- "Scalable rare variant meta-analysis of sequencing studies using summary statistics and functional annotations", International Conference on Econometrics and Statistics (EcoSta) 2022, Virtual Jun 2022

- "Dynamic incorporation of multiple in-silico functional annotations empowers rare variant association analysis in large-scale whole genome sequencing studies", TOPMed F2F Spring Meeting 2019, Tysons, VA Apr 2019

Contributed Conference Presentations

- "MultiSTAAR: A statistical framework for powerful rare variant multi-trait analysis in biobank-scale sequencing studies", CHARGE Webinar Series, Virtual Jan 2024

- "MultiSTAAR: A statistical framework for powerful rare variant multi-trait analysis in biobank-scale sequencing studies", **Platform (Oral) Presentation, 8% Acceptance Rate**, American Society of Human Genetics (ASHG) 2023, Washington, D.C. Nov 2023

- "MultiSTAAR: A statistical framework for powerful rare variant multi-trait analysis in biobank-scale sequencing studies", **Travel Award**, CHARGE Investigator Meeting 2023, San Antonio, TX Oct 2023

- "MultiSTAAR: A statistical framework for powerful rare variant multi-trait analysis", Joint Statistical Meetings (JSM) 2023, Toronto, ON Aug 2023

- "Whole genome sequencing analyses of 87,652 individuals reveal rare variants in promoter of *HMGA1* associated with height", American Society of Human Genetics (ASHG) 2022, Los Angeles, CA Oct 2022

- "Whole genome sequencing analyses of 87,652 individuals reveal rare variants in promoter of *HMGA1* associated with height", CHARGE Investigator Meeting 2022, Seattle, WA Oct 2022

- "Powerful, scalable and resource-efficient rare variant meta-analysis of whole-genome sequencing studies using summary statistics and functional annotations", **Distinguished Student Paper Award in the Section on Statistics in Genomics and Genetics**, Joint Statistical Meetings (JSM) 2022, Washington, D.C. Aug 2022

- "A multi-dimensional integrative scoring framework for predicting functional variants in the human genome", Journal Club of the Biostatistics and Genomics Core at the Program of Sleep Medicine Epidemiology, Brigham and Women's Hospital/Harvard Medical School Mar 2022

- "A resource-efficient tool for phenome-wide rare variant association analysis in large-scale whole-genome sequencing studies, with application to TOPMed metabolomics data", **Reviewers' Choice Abstract Award**, American Society of Human Genetics (ASHG) 2021, Virtual Oct 2021

- "Powerful and resource-efficient rare variant meta-analysis for large-scale whole genome sequencing studies using summary statistics and functional annotations, with application to TOPMed lipid data", Program in Quantitative Genomics (PQG) Seminar Series, Virtual Dec 2020

- "Powerful and resource-efficient rare variant meta-analysis for large-scale whole

genome sequencing studies using summary statistics and functional annotations, with application to TOPMed lipid data", **Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research Semifinalist**, American Society of Human Genetics (ASHG) 2020, Virtual Oct 2020

- "Scalable Integrative Statistical Inference for Whole Genome Sequencing Association Studies", Genetic Epidemiology Journal Club/Working Group, Department of Human Genetics, Emory University Oct 2020

- "Dynamic incorporation of multiple in-silico functional annotations empowers rare variant association analysis of large-scale whole genome sequencing studies", American Society of Human Genetics (ASHG) 2019, Houston, TX Oct 2019

- "Omnibus weighting incorporating multiple functional annotations for whole genome sequencing rare variant association studies", Joint Statistical Meetings (JSM) 2019, Denver, CO Jul 2019

- "Dynamic incorporation of multiple in-silico functional annotations empowers rare variant association analysis in large-scale whole genome sequencing studies", Statistical Genetics Meeting, Broad Institute/HSPH Apr 2019

- "Omnibus weighting incorporating multiple functional annotations for whole genome sequencing rare variant association studies", Eastern North America Region (ENAR) 2019, Philadelphia, PA Mar 2019

- "A statistical framework on clinical trials for information integration across data sources with applications to rare disease clinical development", Joint Statistical Meetings (JSM) 2018, Vancouver, BC Aug 2018

- "Multivariate mixed models for predicting functional regions in the human genome", Joint Statistical Meetings (JSM) 2018, Vancouver, BC Jul 2018

- "Functional analysis and prediction of the effect sizes of disease-associated common and rare variants", Statistical Genetics Meeting, Broad Institute/HSPH Mar 2018

- "Multivariate mixed models for predicting functional regions in the human genome", Program in Quantitative Genomics (PQG) 2017, Boston, MA Nov 2017

Mentoring

Ph.D. Student Advisees

Wenbo Wang (Joint with Joseph Ibrahim) 2023 -

- Received Summer Institute of Statistical Genetics Scholarship, 2024

Yohhan Kumarasinghe (Graduate Research Assistant) 2023 -

- Received Summer Institute of Statistical Genetics Scholarship, 2024

Ph.D. Dissertation Committee

Yilun Li (Chair: Danyu Lin) 2023 - 2024
Euphy Wu (Chairs: Michael Love & Naim Rashid) 2023 -
Ji-Eun Park (Chairs: Michael Love & Di Wu) 2023 -
Yue Yang (Chair: Hongtu Zhu) 2023 -
Jie Chen (Chair: Hongtu Zhu) 2023 -
Junjian Wang (Chair: Jicai Jiang at NCSU) 2023 -

Master's Student Advisees

Kristy Ma 2023 -
Albert Yuan (Joint with Nora Franceschini) 2023 -

External Postdoctoral Advisee
Jacob Willams (Joint with Haoyu Zhang at NCI) 2023 -

Grants

Trans-Omics for Precision Medicine Fellowship Jan 2023 - Mar 2024
Li (PI) $78,000
- Powerful and resource-efficient multi-trait analysis for large-scale multi-ethnic whole-genome sequencing studies

UM1 TR004406 Apr 2023 - Feb 2030
Buse (PI), Role: Co-Investigator/Biostatistician
- North Carolina Translational and Clinical Science Institute (NC TraCS) - Biostatistics, Epidemiology, and Research Design (BERD)

Teaching Activities

Instructor at Harvard University
Harvard Biostatistics Summer Preparatory Course (∼12 students) Summer 2020

Teaching Fellow at Harvard University
Probability Theory and Applications I (∼25 students) Fall 2019
Analysis of Failure Time Data (∼12 students) Spring 2019
Probability Theory and Applications I (∼25 students) Fall 2018
Probability Theory and Applications I (∼25 students) Fall 2017

Teaching Assistant at Harvard University
Applied Longitudinal Analysis (∼60 students) Spring 2016
Basics of Statistical Inference (∼30 students) Fall 2015

Service

Member and Incoming Co-Chair
Seminar Committee, Aug 2023 -
Department of Biostatistics, UNC-Chapel Hill

Member
BIOS Web & Communications Committee, Aug 2023 -
Department of Biostatistics, UNC-Chapel Hill

Core Faculty
Curriculum in Biostatistics and Computational Biology, Feb 2024 -
Biological and Biomedical Sciences Program, UNC-Chapel Hill

Convenor (Co-Lead)
TOPMed Bone Mineralization Working Group, Feb 2024 -
National Heart, Lung, and Blood Institute

Organizing Committee Co-Vice-Chair
Boston Pharmaceutical Symposium 2024, Cambridge, MA Mar 2024 -
Boston Chapter of the American Statistical Association

Organizing Committee Member
TOPMed Annual Meeting 2024, Bethesda, MD Oct 2023 - Feb 2024
National Heart, Lung, and Blood Institute

Organizing Committee Co-Vice-Chair
Boston Pharmaceutical Symposium 2023, Cambridge, MA Mar 2023 - Oct 2023
Boston Chapter of the American Statistical Association

Organizing Committee Member

Boston Pharmaceutical Symposium 2022, Cambridge, MA — Mar 2022 - Oct 2022
Boston Chapter of the American Statistical Association

Conference Session Chair
New England Statistics Symposium (NESS) 2023, Boston, MA — Jun 2023
New England Statistical Society

Conference Session Chair
Joint Statistical Meetings (JSM) 2022, Washington, D.C. — Aug 2022
American Statistical Association

Conference Session Chair
Joint Statistical Meetings (JSM) 2018, Vancouver, BC — Aug 2018
American Statistical Association

Guest Editor
Mathematics

Journal Peer Reviewer
American Journal of Human Genetics
Bioinformatics
BMC Bioinformatics
Cell Genomics
Frontiers in Genetics
Genetic Epidemiology
Human Genetics and Genomics Advances
Human Molecular Genetics
JAMA Network Open
Journal of Clinical Pharmacy and Therapeutics
Journal of Computational Biology
Journal of Genetics and Genomics
Journal of Nonparametric Statistics
Journal of Translational Medicine
Molecular Genetics and Genomics
PLOS Computational Biology
PLOS Genetics
PLOS ONE
R Journal
Statistical Methods in Medical Research
The American Statistician

Professional Memberships

American Statistical Association
American Society of Human Genetics
Eastern North American Region, International Biometric Society
International Chinese Statistical Association (Permanent Member)
International Genetic Epidemiology Society

Skills

R (R package), Python, Workflow Language, Docker, SAS, Bash, LaTeX

Date of Preparation

April 20, 2024