

Jane Liang

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Education

- 2022 | **Harvard University**
Ph.D. in Biostatistics
Dissertation: *Innovative approaches for risk assessment in panel gene testing*
Advisor: Giovanni Parmigiani
Committee members: Danielle Braun & Peter Kraft
- 2015 | **University of California, Berkeley**
B.A. in Statistics, with Honors
Honors thesis: *Comparing dependence measures using simulation studies*
Supervisor: Haiyan Huang

Experience

- July 2022 – Present | **Stanford University School of Medicine, Quantitative Sciences Unit**
Palo Alto, CA
Senior Biostatistician
Collaborative data science for advancing clinical research in areas including hepatology, COVID-19, clinical trials, organ transplants, and diversity in medicine.
- Aug. 2017 – May 2022 | **Harvard T.H. Chan School of Public Health, Department of Biostatistics**
Dana-Farber Cancer Institute, Department of Data Science
Boston, MA
Graduate Student Researcher
Statistical methodology and software development for clinical risk assessment in panel gene testing.
- Oct. 2016 – July 2017 | **University of Tennessee Health Science Center**
Department of Preventive Medicine, Division of Biostatistics
Memphis, TN
Scientific Research Programmer
Writing, testing, and documenting software applications based on research requirements; maintaining Division's high performance computing systems.

Publications

- [1] **Jane W. Liang**, Kurt D. Christensen, Robert C. Green, and Peter Kraft. A framework evaluating the utility of multi-gene, multi-disease population-based panel testing that accounts for uncertainty in penetrance estimates. 2022. Submitted to *npj Genomic Medicine*. bioRxiv: [10.1101/2022.08.10.503415](https://doi.org/10.1101/2022.08.10.503415).
- [2] **Jane W. Liang**, Gregory E. Idos, Christine Hong, Stephen B. Gruber, Giovanni Parmigiani, and Danielle Braun. Statistical methods for Mendelian models with multiple genes and cancers. *Genetic Epidemiology*, 2022. doi: [10.1002/gepi.22460](https://doi.org/10.1002/gepi.22460).

- [3] **Jane W. Liang** and Saunak Sen. Sparse matrix linear models for structured high-throughput data. *The Annals of Applied Statistics*, 16(1):169–192, 2022. doi: [10.1214/21-aos1444](https://doi.org/10.1214/21-aos1444).
- [4] Anne Marie McCarthy, Yi Liu, Sarah Ehsan, Zoe Guan, **Jane W. Liang**, Theodore Huang, Kevin Hughes, Alan Semine, Despina Kontos, Emily Conant, et al. Validation of breast cancer risk models by race/ethnicity, family history and molecular subtypes. *Cancers*, 14(1):45, 2022. doi: [10.3390/cancers14010045](https://doi.org/10.3390/cancers14010045).
- [5] Gavin Lee*, **Jane W. Liang***, Qing Zhang, Theodore Huang, Christine Choirat, Giovanni Parmigiani, and Danielle Braun. Multi-syndrome, multi-gene risk modeling for individuals with a family history of cancer with the novel R package PanelPRO. *eLife*, 10:e68699, 2021. doi: [10.7554/eLife.68699](https://doi.org/10.7554/eLife.68699).
- [6] Yunqi Yang, Christine Hong, **Jane W. Liang**, Stephen Gruber, Giovanni Parmigiani, Gregory Idos*, and Danielle Braun*. A likelihood-based approach to assessing frequency of pathogenicity among variants of unknown significance (VUS) in susceptibility genes. *Statistics in Medicine*, 40(3):593–606, 2020. doi: [10.1002/sim.8791](https://doi.org/10.1002/sim.8791).
- [7] **Jane W. Liang**, Robert J. Nichols, and Saunak Sen. Matrix linear models for high-throughput chemical genetic screens. *Genetics*, 212(4):1063–1073, 2019. doi: [10.1534/genetics.119.302299](https://doi.org/10.1534/genetics.119.302299).
- [8] Alexandra H. Bartlett, **Jane W. Liang**, Jose Vladimir Sandoval-Sierra, Jay H. Fowke, Eleanor M. Simonsick, Karen C. Johnson, and Khyobeni Mozhui. Longitudinal study of leukocyte DNA methylation and biomarkers for cancer risk in older adults. *Biomarker Research*, 7(1):1–13, 2019. doi: [10.1186/s40364-019-0161-3](https://doi.org/10.1186/s40364-019-0161-3).
- [9] Hemant Gujar, **Jane W. Liang**, Nicholas C. Wong, and Khyobeni Mozhui. Profiling DNA methylation differences between inbred mouse strains on the Illumina Human Infinium MethylationEPIC microarray. *PLOS ONE*, 13(3):e0193496, 2018. doi: [10.1371/journal.pone.0193496](https://doi.org/10.1371/journal.pone.0193496).

* indicates equal contributions

Presentations

- [1] “PanelPRO: A general framework for multi-gene, multi-cancer Mendelian risk prediction models” (invited speaker). University of Tennessee Health Science Center (UTHSC) Biostatistics Seminar Series. Virtual, October 18, 2021.
- [2] “Aggregating across genes and cancers in Mendelian risk prediction modeling” (contributed speed talk). Joint Statistical Meetings (JSM) [🔗](#). Virtual, August 12, 2021.
- [3] “Aggregating across genes and cancers in Mendelian risk prediction modeling” (oral presentation) [🔗](#). Dana-Farber/Harvard Cancer Center Celebration of Early Career Investigators in Cancer Research (DF/HCC CECI) [🔗](#). Virtual, January 21, 2021.
- [4] “A general framework for multi-gene, multi-cancer Mendelian risk prediction models” (contributed paper). Eastern North American Region (ENAR) International Biometric Society Spring Meeting [🔗](#). Virtual, March 23, 2020.
- [5] “Sparse matrix linear models for structured high-throughput data” (contributed poster and lightning talk). Integrative Biostatistics Research for Imaging, Genomics & High-throughput Technologies in Precision Medicine (iBRIGHT), MD Anderson Cancer Center [🔗](#). Houston, TX, November 11, 2019.
- [6] “Matrix linear models for high-throughput data” (contributed lightning talk) [🔗](#). JuliaCon, University of California, Berkeley [🔗](#). Berkeley, CA, June 23, 2017.

Honors

- 2021 – 2022 | **Pedagogy Fellowship** [↗](#)
Harvard T.H. Chan School of Public Health, Office of Education
- Spring 2021 | **Certificate of Distinction in Teaching**
Harvard University, Derek Bok Center for Teaching and Learning
- 2020 – 2021 | **Certificate of Distinction in Teaching (×4)**
2019 – 2020 | Harvard T.H. Chan School of Public Health, Department of Biostatistics
- Jan. 2021 | **Best Oral Presentation**
Dana-Farber/Harvard Cancer Center Celebration of Early Career Investigators in Cancer Research (DF/HCC CECI) [↗](#)
- Dec. 2015 | **Phi Beta Kappa**
University of California, Berkeley
- Dec. 2015 | **Distinction in General Scholarship**
University of California, Berkeley

Competitive Travel and Conference Support

- Nov. 2019 | **Integrative Biostatistics Research for Imaging, Genomics & High-throughput Technologies in Precision Medicine (iBRIGHT)** [↗](#)
MD Anderson Cancer Center
- June 2017 | **JuliaCon** [↗](#)
University of California, Berkeley
- May 2017 | **50th Annual Barrett Memorial Lectures: Mathematical Foundations of Data Science** [↗](#)
University of Tennessee, Knoxville
- Feb. 2017 | **Workshop on the Interface of Statistics and Optimization (WISO)** [↗](#)
Statistical and Applied Mathematical Sciences Institute (SAMSI)
- Oct. 2016 | **Short Course on Systems Genetics**
The Jackson Laboratory

Teaching

- Aug. 2021 – May 2022 | **Harvard T.H. Chan School of Public Health, Office of Education**
Boston, MA
Pedagogy Fellow [↗](#)
Developing new course BST 219 (Core Principles of Data Science) and materials on practical/cluster computing; implementing solutions to other educational projects for the school and Department of Biostatistics.

Harvard T.H. Chan School of Public Health, Department of Biostatistics

Boston, MA

Teaching Fellow

Leading lab sections, designing course materials, holding office hours, monitoring online discussion boards, grading assignments, and supporting master's, doctoral, and clinical students from diverse fields.

Spring 2021	BIOSTAT 231/BST 231: Statistical Inference I (remote)
Fall 2020	BST 260: Introduction to Data Science ↗ (remote)
Spring 2020	BST 263: Statistical Learning (in-person and remote)
Fall 2019	BST 260: Introduction to Data Science ↗ (in-person)
Spring 2019	BST 210: Applied Regression Analysis (in-person)

McGoldrick Professional Development Program in Public Health [↗](#)**Harvard T.H. Chan School of Public Health, University of KwaZulu-Natal – Pietermaritzburg & the ARISE network**

Boston, MA

Teaching Assistant

Training researchers from low-and middle-income countries in quantitative methods and building a collaborative network in sub-Saharan Africa.

Feb. 2021	Health Data Science (remote)
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Harvard T.H. Chan School of Public Health, Department of Biostatistics

Boston, MA

Curriculum Fellow

Designing course materials, including exams, homework, and lab assignments.

Fall 2020	BST 260: Introduction to Data Science ↗
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Software

R: [PanelPRO](#)**Julia:** [MatrixLMnet](#), [MatrixLM](#), [GeneticScreens](#)

Service

Referee: *Cancer Epidemiology, Biomarkers & Prevention*; *PLOS ONE*

Skills

High proficiency: R, Julia, Python, LaTeX, distributed version control (Git, Mercurial), high performance cluster computing, Linux environments**Some proficiency:** C++, STATA, MATLAB