

Jane Liang

📍 Boston, MA, United States
✉ jwliang@g.harvard.edu
🏠 janewliang.github.io

Education

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

Experience

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| Aug. 2017 –
Present | Harvard T.H. Chan School of Public Health, Department of Biostatistics
Dana-Farber Cancer Institute, Department of Data Science
Boston, MA
Graduate Student Researcher
BayesMendel Lab ↗ , led by Giovanni Parmigiani & Danielle Braun
Also supervised by: Peter Kraft & Robert Green
Statistical methodology and software development for clinical risk assessment in panel gene testing. |
| Aug. 2021 –
Present | Harvard T.H. Chan School of Public Health, Office of Education
Boston, MA
Pedagogy Fellow ↗
Developing courses/course materials, training TAs, and implementing solutions to other educational projects for the school and Department of Biostatistics. |
| Oct. 2016 –
July 2017 | University of Tennessee Health Science Center
Department of Preventive Medicine, Division of Biostatistics
Memphis, TN
Scientific Research Programmer
Supervisor: Saunak Sen
Writing, testing, and documenting software applications based on research requirements; maintaining Division's high performance computing systems. |
| Jan. –
Sept. 2016 | Kaiser Permanente
Pleasanton, CA
Programming Analysis Associate
Data management, dashboard reporting, and bash scripting to monitor server environment activity. |

Publications



- [1] **Jane W. Liang**, Gregory E. Idos, Christine Hong, Stephen B. Gruber, Giovanni Parmigiani, and Danielle Braun. PanelPRO: a general framework for multi-gene, multi-cancer Mendelian risk prediction models. 2021. Submitted to *The Annals of Applied Statistics*. arXiv preprint: [arXiv:2108.12504](https://arxiv.org/abs/2108.12504) [stat.ME].
- [2] 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. 2021. To appear in *eLife*. doi: [10.7554/eLife.68699](https://doi.org/10.7554/eLife.68699).
- [3] **Jane W. Liang** and Saunak Sen. Sparse matrix linear models for structured high-throughput data. 2021. To appear in *The Annals of Applied Statistics*. arXiv preprint: [arXiv:1712.05767](https://arxiv.org/abs/1712.05767) [stat.CO].
- [4] 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).
- [5] **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).
- [6] 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).
- [7] 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] “Aggregating across genes and cancers in Mendelian risk prediction modeling” (contributed speed talk). Joint Statistical Meetings (JSM) [🔗](#). Virtual, August 12, 2021.
- [2] “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.
- [3] “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.
- [4] “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.
- [5] “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
Jan. 2021	Best Oral Presentation Dana-Farber/Harvard Cancer Center Celebration of Early Career Investigators in Cancer Research (DF/HCC CECI) 
2020 – 2021 2019 – 2020	Certificate of Distinction in Teaching Harvard T.H. Chan School of Public Health, Department of Biostatistics
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

	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)
	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 

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