Jane Liang

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Education

2022 (expected)	**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

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: Śaunak 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 Idos, Christine Hong, Stephen Gruber, Giovanni Parmigiani, and Danielle Braun. PanelPRO: a general framework for multi-gene, multi-cancer Mendelian risk prediction models. 2021. In preparation.

[2] Gavin Lee*, **Jane W. Liang***, Qing Zhang, Theodore Huang, Christine Choirat, Giovanni Parmigiani, and Danielle Braun. PanelPRO: A R package for multi-syndrome, multi-gene risk modeling for individuals with a family history of cancer. *arXiv preprint: arXiv:2010.13011 [stat.AP]*, 2020. Submitted to *eLife*.

[3] **Jane W. Liang** and Śaunak Sen. Sparse matrix linear models for structured high-throughput data. *arXiv preprint: arXiv:1712.05767 [stat.CO]*, 2020. To appear in *Annals of Applied Statistics*.

[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.

[5] **Jane W. Liang**, Robert J. Nichols, and Śaunak Sen. Matrix linear models for high-throughput chemical genetic screens. *Genetics*, 212(4):1063–1073, 2019. doi: 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.

[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.

* 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, Java, web scraping