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	**Department of Biostatistics, Harvard T.H. Chan School of Public Health** **Department of Data Sciences, Dana-Farber Cancer Institute** Boston, MA **Graduate Student Researcher** BayesMendel Lab ⬀, led by Giovanni Parmigiani & Danielle Braun Also supervised by: Peter Kraft & Robert C. Green Statistical methodology and software development for clinical risk assessment in panel gene testing.
Oct. 2016 – July 2017	**Division of Biostatistics, Department of Preventive Medicine** **University of Tennessee Health Science Center** 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):10, 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

Jan. 2021	**Best Oral Presentation** Dana-Farber/Harvard Cancer Center Celebration of Early Career Investigators in Cancer Research (DF/HCC CECI) ⬀

2020 – 2021	**Certificate of Distinction in Teaching**
2019 – 2020	Department of Biostatistics, Harvard T.H. Chan School of Public Health
2015	**Phi Beta Kappa**
	University of California, Berkeley
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

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

	Department of Biostatistics, Harvard T.H. Chan School of Public Health Boston, MA **Curriculum Fellow** Designing course materials, including exams, homework, and lab assignments.
Fall 2020	BST 260: Introduction to Data Science ↗

Service

Referee:	Cancer Epidemiology, Biomarkers & Prevention; PLOS One

Software

R:	PanelPRO
Julia:	MatrixLMnet, MatrixLM, GeneticScreens

Skills

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