

Jane Liang

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Education

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|---------------------------------------|---|
| Aug. 2017 –
May 2022
(expected) | Doctor of Philosophy in Biostatistics
Harvard T.H. Chan School of Public Health
<i>Boston, MA</i>
Dissertation : <i>Innovative approaches for risk assessment in panel gene testing</i>
Advisor: Giovanni Parmigiani, PhD
Committee members: Danielle Braun, PhD; Peter Kraft, PhD
Cancer training grant fellow (2020 – Present) ↗
Genomics training grant fellow (2017 – 2020) ↗ |
| Aug. 2012 –
Dec. 2015 | Bachelor of Arts in Statistics, with Honors
University of California, Berkeley
<i>Berkeley, CA</i>
Phi Beta Kappa, Distinction in General Scholarship
Honors thesis: <i>Comparing dependence measures using simulation studies</i>
Supervisor: Haiyan Huang, PhD |





Experience

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| Jan. –
March 2020 | Data Cleaning and Analysis Consultant
Department of Biostatistics, Epidemiology, and Informatics
University of Pennsylvania
<i>Philadelphia, PA</i>
Supervisor: Anne Marie McCarthy, PhD
Formatting and cleaning mammography screening and family history databases. |
| Oct. 2016 –
July 2017 | Scientific Research Programmer
Division of Biostatistics, Department of Preventive Medicine
University of Tennessee Health Science Center
<i>Memphis, TN</i>
Supervisor: Saunak Sen, PhD
Writing, testing, and documenting software applications based on research requirements; maintaining division's high performance computing systems. |
| Jan. – Sept. 2016 | Programming Analysis Associate
Kaiser Permanente
<i>Pleasanton, CA</i>
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. 2020. In preparation.
- [2] Gavin Lee*, Qing Zhang, **Jane W. Liang**, 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 \[stat.AP\]](https://arxiv.org/abs/2010.13011)*, 2020. In preparation.
- [3] **Jane W. Liang** and Saunak Sen. Sparse matrix linear models for structured high-throughput data. *arXiv preprint: [arXiv:1712.05767 \[stat.CO\]](https://arxiv.org/abs/1712.05767)*, 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. 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):10, 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).

Presentations

Jan. 21, 2021	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)  Boston, MA
March 23, 2020	A general framework for multi-gene, multi-cancer Mendelian risk prediction models (contributed paper) ENAR International Biometric Society Spring Meeting  Nashville, TN
Nov. 11, 2019	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

June 23, 2017 | **Matrix linear models for high-throughput data (lightning talk)** [↗](#)
 JuliaCon [↗](#)
 University of California, Berkeley
 Berkeley, CA

Teaching

	Teaching Fellow Department of Biostatistics Harvard T.H. Chan School of Public Health <i>Boston, MA</i> Leading lab sections, designing course materials, holding office hours, grading assignments, and supporting master's, doctoral, and clinical students from diverse fields.
Spring 2021	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)
	Teaching Assistant McGoldrick Professional Development Program in Public Health ↗ Harvard T.H. Chan School of Public Health, University of KwaZulu-Natal – Pietermaritzburg, and the ARISE network <i>Boston, MA</i> Training researchers from low-and middle-income countries in quantitative methods and building a collaborative network in sub-Saharan Africa.
Feb. 1-12, 2021	Health Data Science (remote)
	Curriculum Fellow Department of Biostatistics Harvard T.H. Chan School of Public Health <i>Boston, MA</i> Designing course materials, including exams, homework, and lab assignments.
Fall 2020	BST 260: Introduction to Data Science ↗




Honors

Jan. 21, 2021 | **Best Oral Presentation**
 Dana-Farber/Harvard Cancer Center Celebration of Early Career Investigators in Cancer Research (DF/HCC CECI) [↗](#)

Competitive Travel and Conference Support

Nov. 11-13, 2019 | **Integrative Biostatistics Research for Imaging, Genomics, & High-throughput Technologies in Precision Medicine (iBRIGHT)** [↗](#)
 MD Anderson Cancer Center

June 20-24, 2017 | **JuliaCon** [↗](#)
 University of California, Berkeley

May 1-3, 2017	50th Annual Barrett Memorial Lectures: Mathematical Foundations of Data Science  University of Tennessee, Knoxville
Feb. 8-10, 2017	Workshop on the Interface of Statistics and Optimization (WISO)  Statistical and Applied Mathematical Sciences Institute (SAMSI)
Oct. 16-22, 2016	Short Course on Systems Genetics  The Jackson Laboratory

Software

Software packages with primary or significant contribution.

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