

Jane Liang

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

Education

- | | |
|--------------------------|---|
| Aug. 2017 –
Present | Doctor of Philosophy in Biostatistics
Harvard T.H. Chan School of Public Health
Boston, MA
Dissertation (working title): <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
Berkeley, CA
Honors thesis: <i>Comparing dependence measures using simulation studies</i>
Supervisor: Haiyan Huang, PhD |

Work Experience

- | | |
|--------------------------|---|
| Oct. 2016 –
July 2017 | Scientific Research Programmer
Division of Biostatistics, Department of Preventive Medicine,
University of Tennessee Health Science Center
Memphis, TN
Supervisor: Saunak Sen, PhD |
| Jan. – Sept. 2016 | Programming Analysis Associate
Kaiser Permanente
Pleasanton, CA |





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] 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. 2020. *Submitted*.
- [3] **Jane W. Liang** and Saunak Sen. Sparse matrix linear models for structured high-throughput data. *arXiv preprint arXiv:1712.05767v3 [stat.CO]*: arxiv.org/abs/1712.05767, 2020. *Submitted*.
- [4] **Jane W. Liang**, Robert J. Nichols, and Saunak Sen. Matrix linear models for high-throughput chemical genetic screens. *Genetics*, 212(4):1063–1073, 2019. PMID: [31243057](#); PMCID: [PMC6707451](#).

- [5] 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. PMID: [31149338](#); PMCID: [PMC6537435](#).
- [6] 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. PMID: [29529061](#); PMCID: [PMC5846735](#).

* indicates equal contributions

Oral and Poster Presentations

March 23, 2020	A general framework for multi-gene, multi-cancer Mendelian risk prediction models (contributed paper) ENAR International Biometric Society Spring Meeting  JW Marriott Nashville Nashville, TN
Nov. 11, 2019	Sparse matrix linear models for structured high-throughput data (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 Experience


	Teaching Assistant Harvard T.H. Chan School of Public Health Boston, MA
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)
	Curriculum Fellow Harvard T.H. Chan School of Public Health Boston, MA
Fall 2020	BST 260: Introduction to Data Science

Honors and Awards

Dec. 2015	Phi Beta Kappa University of California, Berkeley Berkeley, CA
-----------	---

Dec. 2015 | **Distinction in General Scholarship**
University of California, Berkeley
Berkeley, CA

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
Houston, TX

June 20-24, 2017 | **JuliaCon** 
University of California, Berkeley
Berkeley, CA

May 1-3, 2017 | **50th Annual Barrett Memorial Lectures: Mathematical Foundations of Data Science** 
University of Tennessee, Knoxville
Knoxville, TN

Feb. 8-10, 2017 | **Workshop on the Interface of Statistics and Optimization (WISO)** 
Statistical and Applied Mathematical Sciences Institute (SAMSI)
Durham, NC

Oct. 16-22, 2016 | **Short Course on Systems Genetics** 
The Jackson Laboratory
Bar Harbor, ME

Skills

High proficiency: R, Julia, Python, C++, LaTeX, distributed version control (Git, Mercurial), Linux environments

Some proficiency: Java, MATLAB, web scraping