

Jane Liang

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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

Jan. – March. 2020	Consultant : cleaning mammography screening and family history databases Department of Biostatistics, Epidemiology, and Informatics University of Pennsylvania Philadelphia, PA Supervisor: Anne Marie McCarthy, PhD
Oct. 2016 – July 2017	Scientific Research Programmer Division of Biostatistics, Department of Preventive Medicine University of Tennessee Health Science Center Memphis, TN Supervisor: Śaunak 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](https://pubmed.ncbi.nlm.nih.gov/31243057/); PMCID: [PMC6707451](https://pubmed.ncbi.nlm.nih.gov/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](https://pubmed.ncbi.nlm.nih.gov/31149338/); PMCID: [PMC6537435](https://pubmed.ncbi.nlm.nih.gov/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](https://pubmed.ncbi.nlm.nih.gov/29529061/); PMCID: [PMC5846735](https://pubmed.ncbi.nlm.nih.gov/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

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| Dec. 2015 | Phi Beta Kappa
University of California, Berkeley
<i>Berkeley, CA</i> |
| Dec. 2015 | Distinction in General Scholarship
University of California, Berkeley
<i>Berkeley, CA</i> |

Competitive Travel and Conference Support

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| Nov. 11-13, 2019 | Integrative Biostatistics Research for Imaging, Genomics, & High-throughput Technologies in Precision Medicine (iBRIGHT) 
MD Anderson Cancer Center
<i>Houston, TX</i> |
| June 20-24, 2017 | JuliaCon 
University of California, Berkeley
<i>Berkeley, CA</i> |
| May 1-3, 2017 | 50th Annual Barrett Memorial Lectures: Mathematical Foundations of Data Science 
University of Tennessee, Knoxville
<i>Knoxville, TN</i> |
| Feb. 8-10, 2017 | Workshop on the Interface of Statistics and Optimization (WISO) 
Statistical and Applied Mathematical Sciences Institute (SAMSI)
<i>Durham, NC</i> |
| Oct. 16-22, 2016 | Short Course on Systems Genetics 
The Jackson Laboratory
<i>Bar Harbor, ME</i> |

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