

# Jane Liang

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## Education

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| 2022<br>(expected) | <b>Harvard University</b><br><b>Ph.D. in Biostatistics</b><br>Dissertation: <i>Innovative approaches for risk assessment in panel gene testing</i><br>Advisor: Giovanni Parmigiani<br>Committee members: Danielle Braun & Peter Kraft |
| 2015               | <b>University of California, Berkeley</b><br><b>B.A. in Statistics, with Honors</b><br>Honors thesis: <i>Comparing dependence measures using simulation studies</i><br>Supervisor: Haiyan Huang                                       |

## Experience

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| Aug. 2017 –<br>Present   | <b>Harvard T.H. Chan School of Public Health, Department of Biostatistics</b><br><b>Dana-Farber Cancer Institute, Department of Data Science</b><br>Boston, MA<br><b>Graduate Student Researcher</b><br>BayesMendel Lab <a href="#">🔗</a> , led by Giovanni Parmigiani & Danielle Braun<br>Also supervised by: Peter Kraft & Robert Green<br>Statistical methodology and software development for clinical risk assessment in panel gene testing. |
| Oct. 2016 –<br>July 2017 | <b>University of Tennessee Health Science Center</b><br><b>Department of Preventive Medicine, Division of Biostatistics</b><br>Memphis, TN<br><b>Scientific Research Programmer</b><br>Supervisor: Saunak Sen<br>Writing, testing, and documenting software applications based on research requirements; maintaining Division's high performance computing systems.   |
| Jan. –<br>Sept. 2016     | <b>Kaiser Permanente</b><br>Pleasanton, CA<br><b>Programming Analysis Associate</b><br>Data management, dashboard reporting, and bash scripting to monitor server environment activity.   |

## Publications

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- [1] **Jane W. Liang**, Gregory E. Idos, Christine Hong, Stephen B. Gruber, Giovanni Parmigiani, and Danielle Braun. PanelPRO: a general framework for multi-gene, multi-cancer Mendelian risk prediction models. 2022. Submitted to *Genetic Epidemiology*. arXiv preprint: [arXiv:2108.12504](https://arxiv.org/abs/2108.12504) [\[stat.ME\]](#).

- [2] Anne Marie McCarthy, Yi Liu, Sarah Ehsan, Zoe Guan, **Jane W. Liang**, Theodore Huang, Kevin Hughes, Alan Semine, Despina Kontos, Emily Conant, et al. Validation of breast cancer risk models by race/ethnicity, family history and molecular subtypes. *Cancers*, 14(1):45, 2022.
- [3] Gavin Lee\*, **Jane W. Liang**\*, Qing Zhang, Theodore Huang, Christine Choirat, Giovanni Parmigiani, and Danielle Braun. Multi-syndrome, multi-gene risk modeling for individuals with a family history of cancer with the novel R package PanelPRO. *eLife*, 10:e68699, 2021. doi: [10.7554/eLife.68699](https://doi.org/10.7554/eLife.68699).
- [4] **Jane W. Liang** and Saunak Sen. Sparse matrix linear models for structured high-throughput data. 2021. To appear in *The Annals of Applied Statistics*. arXiv preprint: [arXiv:1712.05767 \[stat.CO\]](https://arxiv.org/abs/1712.05767).
- [5] 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](https://doi.org/10.1002/sim.8791).
- [6] **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).
- [7] 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](https://doi.org/10.1186/s40364-019-0161-3).
- [8] 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).

\* indicates equal contributions

## Presentations

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- [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

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2021 – 2022	<b>Pedagogy Fellowship</b>  Harvard T.H. Chan School of Public Health, Office of Education
Spring 2021	<b>Certificate of Distinction in Teaching</b> Harvard University, Derek Bok Center for Teaching and Learning
Jan. 2021	<b>Best Oral Presentation</b> Dana-Farber/Harvard Cancer Center Celebration of Early Career Investigators in Cancer Research (DF/HCC CECI) 
2020 – 2021 2019 – 2020	<b>Certificate of Distinction in Teaching</b> Harvard T.H. Chan School of Public Health, Department of Biostatistics
Dec. 2015	<b>Phi Beta Kappa</b> University of California, Berkeley
Dec. 2015	<b>Distinction in General Scholarship</b> University of California, Berkeley

## Competitive Travel and Conference Support

Nov. 2019	<b>Integrative Biostatistics Research for Imaging, Genomics &amp; High-throughput Technologies in Precision Medicine (iBRIGHT)</b>  MD Anderson Cancer Center
June 2017	<b>JuliaCon</b>  University of California, Berkeley
May 2017	<b>50th Annual Barrett Memorial Lectures: Mathematical Foundations of Data Science</b>  University of Tennessee, Knoxville
Feb. 2017	<b>Workshop on the Interface of Statistics and Optimization (WISO)</b>  Statistical and Applied Mathematical Sciences Institute (SAMSI)
Oct. 2016	<b>Short Course on Systems Genetics</b> The Jackson Laboratory

## Teaching

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Aug. 2021 – Present	<b>Harvard T.H. Chan School of Public Health, Office of Education</b> Boston, MA <b>Pedagogy Fellow</b>  Developing new course BST 219 (Introduction to R for Data Science) and materials on practical/cluster computing; implementing solutions to other educational projects for the school and Department of Biostatistics.
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	<b>Harvard T.H. Chan School of Public Health, Department of Biostatistics</b> Boston, MA <b>Teaching Fellow</b> 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 <a href="#">↗</a> (remote)
Spring 2020	BST 263: Statistical Learning (in-person and remote)
Fall 2019	BST 260: Introduction to Data Science <a href="#">↗</a> (in-person)
Spring 2019	BST 210: Applied Regression Analysis (in-person)
	<b>McGoldrick Professional Development Program in Public Health <a href="#">↗</a></b> <b>Harvard T.H. Chan School of Public Health, University of KwaZulu-Natal – Pietermaritzburg &amp; the ARISE network</b> Boston, MA <b>Teaching Assistant</b> 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)
	<b>Harvard T.H. Chan School of Public Health, Department of Biostatistics</b> Boston, MA <b>Curriculum Fellow</b> Designing course materials, including exams, homework, and lab assignments.
Fall 2020	BST 260: Introduction to Data Science <a href="#">↗</a>

## Software

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**R:** [PanelPRO](#)  
**Julia:** [MatrixLMnet](#), [MatrixLM](#), [GeneticScreens](#)

## Service

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**Referee:** *Cancer Epidemiology, Biomarkers & Prevention; PLOS ONE*

## Skills

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