Jingyi Jessica Li

8125 Math Sciences Bldg.
Department of Statistics
University of California, Los Angeles, CA 90095-1554 USA
Homepage: http://jsb.ucla.edu/
Phone: 1(310) 206-2029
E-mail: jli@stat.ucla.edu

RESEARCH INTERESTS

My research is at the interface between statistics and biology. My primary research interest lies in developing new statistical methods for understanding biological questions, especially those related to large-scale genomic and transcriptomic data. The specific topics I have examined include

Bioinformatics / Statistical Genomics:

- Statistical methods for analyzing next-generation bulk and single-cell RNA sequencing data
- Simulators to generate realistic synthetic data for single-cell and spatial omics
- Using statistics to quantitate the Central Dogma, a fundamental principle in molecular biology
- Comparative genomics: developing novel statistical methods to investigate conserved or divergent biological phenomena in different tissue and cell types across multiple species
- Identification of gene-gene co-expression and protein-DNA and protein-RNA interactions using diverse genomic data

Statistics:

- Synthetic control data generation
- P-value-free control of false discovery rates
- Labeling ambiguity issue in multi-class classification
- Measures of association
- Neyman-Pearson classification that controls the prioritized type of error in binary classification
- High-dimensional linear model inference and variable selection
- Community detection in a bipartite network with node covariates

POSITIONS

2025–	**Professor and Program Head**, Biostatistics Program, Fred Hutchinson Cancer Center **Donald and Janet K. Guthrie Endowed Chair in Statistics** **Professor (Joint)**, Herbold Computational Biology Program **Affiliated Professor**, Department of Biostatistics, University of Washington **Co-Leader**, Biostatistics & Computational Biology Program, Fred Hutch/University of Washington/Seattle Children's Cancer Consortium
2022–	**Professor**, University of California, Los Angeles (on leave 2025–2026)
2019–2022	**Associate Professor (tenured)**, University of California, Los Angeles
2013–2019	**Assistant Professor**, University of California, Los Angeles Department of Statistics and Data Science (primary appointment) Department of Biostatistics (secondary appointment) Department of Human Genetics (secondary appointment) Department of Computational Medicine (secondary appointment) Interdepartmental Ph.D. Program in Bioinformatics Institute for Quantitative and Computational Biosciences (QCBio) Gene Regulation Program Area, Jonsson Comprehensive Cancer Center Director, Center of Statistical Research for Computational Biology (CSRCB)

SHORT-TERM

2022–2023	Radcliffe Fellow, Radcliffe Institute of Advanced Study, Harvard University Visiting Professor, Department of Statistics, Harvard University

EDUCATION

2013	Ph.D. in Biostatistics, with Designated Emphasis in Computational Biology Thesis: Statistical Methods for Analyzing High-throughput Biological Data Advisers: Peter J. Bickel and Haiyan Huang University of California, Berkeley, CA
2007	B.S. in Biological Sciences (summa cum laude), with minor in English Tsinghua University, China

HONORS AND AWARDS

2025	Mortimer Spiegelman Award, American Public Health Association (APHA)
2025	Guggenheim Fellowship, John Simon Guggenheim Memorial Foundation
2024	Highly Ranked Scholar – Lifetime, in the Specialty of RNA-Seq, ScholarGPS
2023	Overton Prize, International Society for Computational Biology (ISCB)
2023	Emerging Leader Award, Committee of Presidents of Statistical Societies (COPSS)
2023	EU-US Frontiers of Engineering Symposium Speaker (one of eight US speakers), US National Academy of Engineering
2022	Highly Ranked Scholar – Prior Five Years, in the Specialty of RNA-Seq, ScholarGPS
2022	Radcliffe Fellowship, Radcliffe Institute for Advanced Study at Harvard University
2020	MIT Technology Review 35 Innovators Under 35 China
2020	UCLA David Geffen School of Medicine W.M. Keck Foundation Junior Faculty Award
2019	CAREER Award, National Science Foundation
2018	Physical Sciences Entrepreneurship and Innovation Fund Fellowship, UCLA
2018	Junior Researcher Paper Award, International Chinese Statistical Association (ICSA) China Conference
2018	Math Scholar Award, Johnson & Johnson Women in STEM^{2}D (Science, Technology, Engineering, Math, Manufacturing and Design) Program (one winner per category, selected among 525 applications from 35 countries)
2018	Sloan Research Fellowship, Alfred P. Sloan Foundation
2017	Research Starter Award in Informatics, PhRMA Foundation
2016	Affordable Course Materials Initiative Award, UCLA
2016	Faculty Research Grant / Trans-disciplinary Seed Grant, UCLA
2016	Chancellor's Award for Teaching a *Fiat Lux* Freshman Seminar, UCLA
2015	Hellman Fellow, Hellman Foundation
2015	Faculty Career Development Award, UCLA
2013	ISCB Travel Fellowship for RECOMB 2013 (17th Annual International Conference on Research in Computational Molecular Biology)
2013	Chinese Government Award for Outstanding Self-financed Students Aboard, China Scholarship Council
2012	International Dissertation Field Work Grant, Institute of International Studies, UC Berkeley
2011	Stipend Awards in Recognition of Scholastic Achievements, Division of Biostatistics, UC Berkeley

2011	Best Presentation Award - CSHA Fellowship, Cold Spring Harbor Asia Conferences: Bioinformatics of Human and Animal Genomics, Suzhou, China
2010	Outstanding Graduate Student Instructor Award, UC Berkeley
2007	Distinguished Graduate of Class 2007, Tsinghua University
2007	Outstanding Undergraduate Thesis, Tsinghua University
2006	“12.9” Fellowship (awarded to ~30 students selected from all majors), Tsinghua University
2006	Role-Model College Student of Beijing
2004–2006	Merit-based Fellowships (awarded to the top 1% of students in each department), Tsinghua University

GRANTS

CURRENT PI GRANTS

U24 HG011735 (JAX TDCC PI: Adams; Subaward PI) **03/03/2025 – 02/28/2026**
NHGRI Genome Technology Program Opportunity Fund Total $200,000
“Statistical methods for enhancing the rigor of metacell partitioning in single-cell multi-omics data”

Single-Cell Biology Data Insights Grant (PI: Li) **07/01/2022 – 06/30/2025**
Chan-Zuckerberg Initiative $200,000
“Enhancing rigor and reliability of single-cell data science”

R35 GM140888 (PI: Li) **06/01/2021 – 05/31/2026**
NIH / NIGMS MIRA for established investigators $1,500,000
“Statistical methods for elucidating regulatory mechanisms and functional impacts of transcriptome variation at population and single-cell scales”

DMS 2113754 (MPI: Li/Tong) **07/01/2021 – 06/31/2025**
NSF Total $240,000 (Li: $120,000)
“Collaborative Research: Development of classification theory and methods for objective asymmetry, sample size limitation, labeling ambiguity, and feature importance”

DBI 1846216 (PI: Li) **07/01/2019 – 06/30/2025**
NSF Total $611,614
($12,000 REU supp; $20,000 ERC collaboration supp)
“CAREER: Advancing the bioinformatic infrastructure and methodology for single-cell RNA sequencing”

CURRENT CO-PI / CO-I GRANTS

R01 MH132689 (PI: Bhaduri) **08/15/2024 – 05/31/2029**
NIH / NIMH $21,860
“Elucidating regulation of cell fate specification in human cortical development to understand etiology of neurodevelopment disorders”

R01 HG012925 (PI: Wollman) **05/06/2024 – 02/29/2028**
NIH / NHGRI $211,473
“Whole organ transcriptome reconstruction by dimensionality reduced fluorescent in situ hybridization”

Internationalization of the High-Tech-Initiative (co-PI: Stefan Canzar) **08/21/2024 – 12/31/2025**
Bavaria California Technology Center (BaCaTeC) €15,000

"Statistical association of spatial transcriptomics and tissue structure for marker gene discovery"

Chan Zuckerberg Initiative (PI: Di Carlo) **08/21/2023 – 8/20/2026**
Chan-Zuckerberg Initiative $75,000
"Decoding intercellular communication using lab on a particle technology"

P01 CA244118 (PI: Ribas) **09/11/2020 – 06/30/2025**
NIH / NCI $92,789
"Combination therapies to defeat melanoma resistance"

COMPLETED

UCLA DGSOM W. M. Keck Foundation Junior Faculty Award (PI: Li)
01/01/2020 – 12/31/2023
W. M. Keck Foundation $500,000
"Discovering fundamental mechanisms of translational control to advance mRNA therapeutics and other biomedical technologies"

Sloan Research Fellowship (PI: Li) **09/15/2018 – 09/14/2023**
Alfred P. Sloan Foundation $65,000

Johnson & Johnson Women in STEM^{2}D Scholar Award (PI: Li) **01/21/2018 – 01/21/2024**
Johnson & Johnson $150,000
"Statistical modeling to quantitate the central dogma"

R01 GM120507 (PI: Li) **09/01/2016 – 05/31/2022**
NIH / NIGMS $1,250,000
"Robust identification and accurate quantification of RNA transcripts on a system wide scale"

Physical Sciences Entrepreneurship and Innovation Fund (PSEIF) Fellowship (PI: Li)
09/07/2018 – 09/06/2019
UCLA $100,000
"A flexible simulator for single-cell RNA sequencing experimental design"

DMS 1613338 (Co-PI; PI: Tong) **08/15/2016 – 08/14/2019**
NSF Total $120,000 (Li: $40,215)
"Development of a general classification framework under the Neyman-Pearson Paradigm, with biomedical and social applications"

PhRMA Foundation Research Starter Grant in Informatics (PI: Li)
01/15/2017 – 01/14/2018
PhRMA Foundation $100,000
"Computational methods for comparing large-scale epigenomic data and sequences"

Faculty Research Grant / Trans-disciplinary Seed Grant (PI: Li) **07/01/2016 – 06/30/2017**
UCLA $6,600

Chancellor's Award for Teaching a *Fiat Lux* Freshman Seminar (PI: Li)
07/01/2016 – 06/30/2017
UCLA $1,500

DMS 1557727 (MPI: Li/Abrams/Kang/Long/Shah) **09/15/2015 – 08/31/2016**
NSF Total $100,000 (Li: $33,762)

"QuBBD: Collaborative Research: Advancing mHealth using big data analytics: statistical and dynamical systems modeling of real-time adaptive m-Intervention for pain"

Hellman Fellows Award (PI: Li) **07/01/2015 – 06/30/2016**
Hellman Foundation $17,837
"A new statistical measure to capture complex gene interactions from massive genomic data"

Faculty Career Development Award (PI: Li) **07/01/2015 – 06/30/2016**
UCLA $10,000

PUBLICATIONS

Google Scholar: https://scholar.google.com/citations?hl=en&user=6FHAoRoAAAAJ

Selected Publications:
[Meth]: Statistical Methodologies; **[Bioinfo]:** Bioinformatics Tools; **[Data]:** Data Analysis

Note: * Co-first Authors; $^+$ Corresponding Authors; __ Trainees

RESEARCH PAPERS

JOURNAL ARTICLES (PUBLISHED / ACCEPTED)

1. **[Bioinfo]** Liu, P., and **Li, J.J.$^+$** (2025). mcRigor: a statistical method to enhance the rigor of metacell partitioning in single-cell data analysis. ***Nature Communications*** accepted. bioRxiv preprint.
    - Accepted by the 29th International Conference on Research in Computational Molecular Biology (RECOMB) 2025

2. **[Bioinfo, Meth]** Zhou, H.J., Ge, X., and **Li, J.J.$^+$** (2025). ClipperQTL: ultrafast and powerful eGene identification method. ***Genome Biology*** accepted. bioRxiv preprint.

3. Huang, E., Fu, T., Zhang, L., Yan, G., Yamamoto, R., Terrazas, S., Nguyen, T.L., Gonzalez-Figueroa, C., Khanbabaei, A., Bahn, J.H., Varada, R., Amoah, K., Hervoso, J., Paulsen, M.T., Magnuson, B., Ljungman, M., **Li, J.J.**, and Xiao, X. (2025). Unveiling the hidden role of RNA stability as a link between genetic variation and disease. ***Nature Genetics*** accepted.

4. Higgins, C., **Li, J.J.$^+$**, and Carey, M. (2025). Spatial transcriptomics iterative hierarchical clustering (stIHC): a novel method for identifying spatial gene co-expression modules. ***Quantitative Biology*** accepted.

5. Zhang, H., Li, X., Song, D., Yukselen, O., Nanda, S., Kucukural, A., **Li, J.J.**, Garber, M., and Walhout, A.J.M. (2025). Worm Perturb-Seq: massively parallel whole-animal RNAi and RNA-seq. ***Nature Communications*** 16:4785.

6. Song, B., Liu, D., Dai, W., McMyn, N., Wang, Q., Yang, D., Krejci, A., Vasilyev, A., Song, D., Williams, B., Cheng, X., Chao, L., Diao, Y., Buerckstuemmer, T., Siliciano, J.M., **Li, J.J.**, Siliciano, R., Huangfu, D., and Li, W. (2025). Decoding Heterogenous Single-cell Perturbation Responses. ***Nature Cell Biology*** 27:493–504.

7. Sankaran, K., Kodikara, S., **Li, J.J.**, and Le Cao, K.A. (2025). Semisynthetic simulation for microbiome data analysis. ***Briefings in Bioinformatics*** 26(1):bbaf051.

8. Sun, T., Yuan, J., Zhu, Y., Li, J., Yang, S., Zhou, J., Ge, X., Qu, S., Li, W.$^{+}$, **Li, J.J.$^{+}$**, and Li, Y.$^{+}$ (2024). Systematic evaluation of methylation-based cell type deconvolution methods for plasma cell-free DNA. ***Genome Biology*** 25:318.

9. Fernandez, E.G., Mai, W.X., Song, K., Bayley, N.A., Kim, J., Zhu, H., Pioso, M., Young, P., Andrasz, C., Cadet, D., Liau, L.M., Li, G., Yong, W.H., Rodriguez, F., Dixon, S.J., Souers, A.J., **Li, J.J.**, Graeber, T.G., Cloughesy, T.F. & Nathanson, D.A. (2024). Integrated molecular and functional characterization of the intrinsic apoptotic machinery identifies therapeutic vulnerabilities in malignant glioma. ***Nature Communications*** 15:10089.

10. **[Meth] Li, J.J.$^{+}$**, Zhou, H.J., Tong, X., and Bickel, P.J. (2024). Dissecting Gene Expression Heterogeneity: Generalized Pearson Correlation Squares and the K-Lines Clustering Algorithm. ***Journal of American Statistical Association*** 119(548):2450–2463.

11. Chen, Y., McDermott, M., Woyshner, K., Wang, L.D.$^{+}$, and **Li, J.J.$^{+}$** (2024). APIR: a flexible and powerful FDR-control framework for aggregating peptides identified by different database search algorithms from mass spectrometry data. ***Genomics, Proteomics, and Bioinformatics*** 22(2):qzae042.

12. **[Data]** Patowary, A., Zhang, P., Jops, C., Vuong, C.K., Ge, X., Hou, K., Kim, M., Gong, N., Margolis, M., Vo, D., Wang, X., Liu, C., Pasaniuc, B., **Li, J.J.**, Gandal, M.J., and De La Torre-Ubieta, L. (2024). Developmental isoform diversity in the human neocortex informs neuropsychiatric risk mechanisms. ***Science*** 384(6698):eadh7688.

13. **[Bioinfo]** Wang, W.*, Cen, Y.*, Lu, Z.*, Xu, Y., Sun, T., Xiao, Y., Liu, W., **Li, J.J.$^{+}$**, and Wang, C.$^{+}$ (2024). scCDC: a computational method for gene-specific contamination detection and correction in single-cell and single-nucleus RNA-seq data. ***Genome Biology*** 25:136.

14. **[Data]** Cui, Y., Ye, W., Li, J.S., **Li, J.J.**, Vilain, E., Sallam, T., and Li, W. (2024). A genome-wide spectrum of tandem repeat expansions in 338,963 humans. ***Cell*** 187(9):2336–2341.

15. **[Bioinfo]** Xia, L.*, Lee, C.*, and **Li, J.J.$^{+}$** (2024). Statistical method scDEED for detecting dubious 2D single-cell embeddings and optimizing t-SNE and UMAP hyperparameters. ***Nature Communications*** 15:1753.
    - Reported in *Nature Methods* Technology Feature Article “Seeing data as t-SNE and UMAP do” by Vivien Marx
    - Featured in *Nature Communications* Editors’ Highlights

16. **[Meth]** Wang, L., Wang, Y.X.R., **Li, J.J.**, and Tong, X. (2024). Hierarchical Neyman-Pearson classification for prioritizing severe disease categories in COVID-19 patient data. ***Journal of American Statistical Association*** 119:39–51.

17. **[Bioinfo]** Song, D., Wang, Q., Yan, G., Liu, T., and **Li, J.J.$^{+}$** (2024). scDesign3 generates realistic in silico data for multimodal single-cell and spatial omics. ***Nature Biotechnology*** 42:247–252.

18. Zhang, C., Zhang, S.$^{+}$, and **Li, J.J.$^{+}$** (2023). A Python package itca for information-theoretic classification accuracy: a criterion that guides data-driven combination of ambiguous outcome labels in multiclass classification. ***Journal of Computational Biology*** 30(11):1246–1249 (RECOMB 2023; software article).

19. **[Bioinfo]** Yan, G., Song, D., and **Li, J.J.$^{+}$** (2023). scReadSim: a single-cell RNA-seq and ATAC-seq read simulator. ***Nature Communications*** 14:7482.

20. Xi, N.M. and **Li, J.J.**$^+$ (2023). Benchmarking the autoencoder design for imputing single-cell RNA sequencing data. ***Computational and Structural Biotechnology Journal*** 21:4079-4095.

21. Yang, L., Chen, X., Lee, C., Shi, J., Lawrence, E.B., Zhang, L., Li, Y., Gao, N., Jung, S.Y., Creighton, C.J., **Li, J.J.**, Cui, Y., Arimura, S., Lei, Y., Li, W., Shen, L. (2023). Functional characterization of age-dependent p16 epimutation reveals biological drivers and therapeutic targets for colorectal cancer. ***Journal of Experimental & Clinical Cancer Research*** 42:113.

22. Wu, Y., Jin, M., Fernandez, M., Hart, K.L., Liao, A., Ge, X., Fernandes, S.M., McDonald, T., Chen, Z., Röth, D., Ghoda, L.Y., Marcucci, G., Kalkum, M., Pillai, R.K., Danilov, A.V., **Li, J.J.**, Chen, J., Brown, J.R., Rosen, S.T., Siddiqi, T., Wang, L. (2023). METTL3-mediated m6A modification controls splicing factor abundance and contributes to aggressive CLL. ***Blood Cancer Discovery*** 4(3):228–245.

23. Zong, W., Rahman, T., Zhu, L., Zeng, X., Zhang, Y., Zou, J., Liu, S., Ren, Z., **Li, J.J.**, Sibille, E., Lee, A.V., Oesterreich, S., Ma, T., Tseng, G.C. (2023). Transcriptomic congruence analysis for evaluating model organisms. ***Proc Natl Acad Sci. USA*** 120(6):e2202584120.

24. **[Meth]** Zhang, C., Chen, Y.E., Zhang, S.$^+$, and **Li, J.J.**$^+$ (2022). Information-theoretic classification accuracy: a data-driven approach to combining ambiguous outcome labels in multi-class classification. ***Journal of Machine Learning Research*** 23(341):1−65.
    - Accepted by the 27th International Conference on Research in Computational Molecular Biology (RECOMB) 2023

25. **[Bioinfo, Meth]** Zhou, H.J., Li, L., Li, Y., Li, W., and **Li, J.J.**$^+$ (2022). PCA outperforms popular hidden variable inference methods for QTL mapping. ***Genome Biology*** 23:210.

26. Say, I., Chen, Y.E., Sun, M.Z., **Li, J.J.**, and Lu, D.C. (2022). Machine learning predicts improvement of functional outcomes in traumatic brain injury patients after inpatient rehabilitation. ***Frontiers in Rehabilitation Sciences*** 3:1005168.

27. Cui, E.H.*, Song, D.*$^+$, Wong, W.K., and **Li, J.J.**$^+$ (2022). Single-cell generalized trend model (scGTM): a flexible and interpretable model of gene expression trend along cell pseudotime. ***Bioinformatics*** 38(16):3927–3934.

28. Song, D.*, Xi, N.M.*, **Li, J.J.**$^+$, and Wang, L.$^+$ (2022). scSampler: fast diversity-preserving subsampling of large-scale single-cell transcriptomic data. ***Bioinformatics*** 38(11):3126–3127.

29. Eisen, T.J., **Li, J.J.**, and Bartel, B.P. (2022). The interplay between translational efficiency, poly(A) tails, microRNAs, and neuronal activation. ***RNA*** 28:808–831.

30. **[Bioinfo, Meth]** Li, Y.*, Ge, X.*, Peng, F., Li, W.$^+$, and **Li, J.J.**$^+$ (2022). Exaggerated false positives by popular differential expression methods when analyzing human population samples. ***Genome Biology*** 23:79.

31. Sun, T., Song, D., Li, W.V., and **Li, J.J.**$^+$ (2022). Simulating single-cell gene expression count data with preserved gene correlations by scDesign2. ***Journal of Computational Biology*** 29(1):23–26 (RECOMB 2021; software article).

32. **[Meth, Bioinfo]** Ge, X.*, Chen, Y.E.*, Song, D., McDermott, M., Woyshner, K., Manousopoulou, A., Wang, N., Li, W., Wang, L.D., and **Li, J.J.**$^+$ (2021). Clipper: p-value-free FDR control on high-throughput data from two conditions. ***Genome Biology*** 22:288.

33. Shi, J., Xu, J., **Chen, Y.E.**, Li, J.S., Cui, Y., Shen, L, **Li, J.J.**, and Li, W. (2021). The concurrence of DNA methylation and demethylation is associated with transcription regulation. ***Nature Communications*** 12:5285.

34. Xi, N.M. and **Li, J.J.**$^+$ (2021). Protocol for executing and benchmarking eight computational doublet-detection methods in single-cell RNA sequencing data analysis. ***STAR Protocols*** 2(3):100699.

35. **[Bioinfo]** Jiang, R., Li, W.V., and **Li, J.J.**$^+$ (2021). An accurate and robust imputation method mbImpute for microbiome data. ***Genome Biology*** 22:192.

36. Wang, N., Lefaudeux, D., Mazumder, A., **Li, J.J.**, Hoffmann, A. (2021). Identifying the combinatorial control of signal-dependent transcription factors. ***PLOS Computational Biology*** 17(6):e1009095.

37. **[Meth] Li, J.J.**, Chen, Y., Tong, X. (2021). A flexible model-free prediction-based framework for feature ranking. ***Journal of Machine Learning Research*** 22(124):1–54.

38. Song, D., Li, K., Hemminger, Z., Wollman, R., and **Li, J.J.**$^+$ (2021). scPNMF: sparse gene encoding of single cells to facilitate gene selection for targeted gene profiling. ***Bioinformatics*** 37(Supplement_1):i358–i366.
    - Accepted by the Conference on Intelligent Systems for Molecular Biology (ISMB) and the European Conference on Computational Biology (ECCB) 2021

39. **[Bioinfo]** Sun, T., Song, D., Li, W.V.$^+$, and **Li, J.J.**$^+$ (2021). scDesign2: a transparent simulator that generates high-fidelity single-cell gene expression count data with gene correlations captured. ***Genome Biology*** 22:163.
    - Accepted by the 25th International Conference on Research in Computational Molecular Biology (RECOMB) 2021

40. Sun, Y.E., Zhou, H.J., and **Li, J.J.**$^+$ (2021). Bipartite tight spectral clustering (BiTSC) algorithm for identifying conserved gene co-clusters in two species. ***Bioinformatics*** 37(9):1225–1233.

41. Sun, M.Z., Babayan, D., Chen, J.-S., Wang, M.M., Naik, P.K., Reitz, K., **Li, J.J.**, Pouratian, N., Kim, W. (2021). Postoperative admission of adult craniotomy patients to the neuroscience ward reduces length of stay and cost. ***Neurosurgery*** 89(1):85–93.

42. **[Bioinfo]** Song, D. and **Li, J.J.**$^+$ (2021). PseudotimeDE: inference of differential gene expression along cell pseudotime with well-calibrated p-values from single-cell RNA sequencing data. ***Genome Biology*** 22:124.

43. **[Bioinfo]** Xi, N.M. and **Li, J.J.**$^+$ (2021). Benchmarking computational doublet-detection methods for single-cell RNA sequencing data. ***Cell Systems*** 12(2):176–194.

44. Guo, Y., Xue, Z., Yuan, R., **Li, J.J.**, Pastor, W.A., and Liu, W. (2021). RAD: a web application to identify region associated differentially expressed genes. ***Bioinformatics*** 37(17):2741–2743.

45. Xu, J., Shi, J., Cui, X., Cui, Y., **Li, J.J.**, Goel, A., Chen, X., Issa, J.-P., Su, J., and Li, W. (2021). Cellular heterogeneity–adjusted clonal methylation (CHALM) provides better prediction of gene expression. ***Nature Communications*** 12:400.

46. **[Bioinfo, Data]** Lyu, J.*, **Li, J.J.**$^{*+}$, Su, J., Peng, F., Chen, Y.E., Ge, X., and Li, W.$^+$ (2020). DORGE: Discovery of Oncogenes and tumor suppressoR genes using Genetic and Epigenetic features. ***Science Advances*** 6(46):eaba6784.

47. Yu, C., Zhang, M., Song, J., Zheng, X., Xu, G., Bao, Y., Lan, J., Luo, D., Hu, J., **Li, J.J.**, and Shi, H. (2020). Integrin-Src-YAP1 signaling mediates the melanoma acquired resistance to MAPK and PI3K/mTOR dual targeted therapy. ***Molecular Biomedicine*** 1:12.

48. **[Meth]** Liu, H., Xu, X., and **Li, J.J.**$^{+}$ (2020). A bootstrap lasso + partial ridge method to construct confidence intervals for parameters in high-dimensional sparse linear models. ***Statistica Sinica*** 30:1333–1355.

49. **[Bioinfo]** Li, W.V.*, Li, S.*, Tong, X., Deng, L., Shi, H.$^{+}$, and **Li, J.J.**$^{+}$ (2019). AIDE: a statistical method for annotation-based isoform discovery and abundance estimation from RNA-seq data. ***Genome Research*** 29:2056–2072.
    - Cover story of the December 2019 Issue

50. **[Data]** **Li, J.J.**$^{+}$, Chew, G.L., and Biggin, M.D.$^{+}$ (2019). Quantitative principles of *cis*-translational control by general mRNA sequence features in eukaryotes. ***Genome Biology*** 20:162.

51. **[Bioinfo]** Li, W.V. and **Li, J.J.**$^{+}$ (2019). A statistical simulator scDesign for rational scRNA-seq experimental design. ***Bioinformatics*** 35(14):i41–i50.
    - Accepted by the Conference on Intelligent Systems for Molecular Biology (ISMB) and the European Conference on Computational Biology (ECCB) 2019

52. Ge, X.*, Zhang, H.*, Xie, L., Li, W.V., Kwon, S.B., and **Li, J.J.**$^{+}$ (2019). EpiAlign: an alignment-based bioinformatic tool for comparing chromatin state sequences. ***Nucleic Acids Research*** 47(13):e77.

53. **[Meth]** Razaee, Z., Amini, A., and **Li, J.J.** (2019). Matched bipartite block model with covariates. ***Journal of Machine Learning Research*** 20(34):1–44.

54. Duong, D.$^{+}$, Ahmad, W.U., Eskin, E., Chang, K.-W., and **Li, J.J.**$^{+}$ (2019). Word and sentence embedding tools to measure semantic similarity of Gene Ontology terms by their definitions. ***Journal of Computational Biology*** 26(1):38–52.

55. **[Data]** Burke, J., Longhurst, A., Merkurjev, D., Sales-Lee, J., Rao, B., Moresco, J., Yates, J., **Li, J.J.**, and Madhani, H.D. (2018). Spliceosome profiling visualizes the operations of a dynamic RNP in vivo at nucleotide resolution. ***Cell*** 173(4):1014–1030.e17.

56. **[Bioinfo, Meth]** Li, W.V.*, Zhao, A., Zhang, S.$^{+}$, and **Li, J.J.**$^{*+}$ (2018). MSIQ: joint modeling of multiple RNA-seq samples for accurate isoform quantification. ***The Annals of Applied Statistics*** 12(1):510–539.

57. **[Bioinfo]** Li, W.V. and **Li, J.J.**$^{+}$ (2018). An accurate and robust imputation method scImpute for single-cell RNA-seq data. ***Nature Communications*** 9:997.

58. **[Meth]** Tong, X.$^{+}$, Feng, Y., and **Li, J.J.**$^{+}$ (2018). Neyman-Pearson classification algorithms and NP receiver operating characteristics. ***Science Advances*** 4(2):eaao1659.

59. Zhang, Y., Harris, C.J., Liu, Q., Liu, W., Ausin, I., Long, Y., Xiao, L., Feng, L., Chen, X., Xie, Y., Chen, X., Zhan, L., Feng, S., **Li, J.J.**, Wang, H., Zhai, J., and Jacobsen. S.E. (2018). Large-scale comparative epigenomics reveals hierarchical regulation of non-CG methylation in *Arabidopsis*. ***Proc Natl Acad Sci. USA*** 115(5):E1069–E1074.

60. Jonassaint, C.R., Kang, C., Abrams, D.M., **Li, J.J.**, Mao, J., Jia, Y., Long, Q., Sanger M., Jonassaint, J.C., De Castro, L., and Shah, N. (2018). Understanding patterns and correlates of daily

pain using the sickle cell disease mobile application to record symptoms via technology (SMART). ***British Journal of Hematology*** 183(2):306–308.

61. **[Data] Li, J.J.+**, Chew, G.L., and Biggin, M.D.+ (2017). Quantitating translational control: mRNA abundance-dependent and independent contributions and the mRNA sequences that specify them. ***Nucleic Acids Research*** 45(20):11821–11836.
    - Highlight talks at the International Conference on Research in Computational Molecular Biology (RECOMB) 2018 and the Conference on Intelligent Systems for Molecular Biology (ISMB) 2018

62. Clifton, S.M., Kang, C.+, **Li, J.J.+**, Long, Q., Shah, N., and Abrams, D.M.+ (2017). Hybrid statistical and mechanistic mathematical model guides mobile health intervention for chronic pain. ***Journal of Computational Biology*** 24(7):675–688.

63. Li, W.V., Chen, Y., and **Li, J.J.+** (2017). TROM: A testing-based method for finding transcriptomic similarity of biological samples. ***Statistics in Biosciences*** 9(1):105–136.

64. Gao, R. and **Li, J.J.+** (2017). Correspondence of *D. melanogaster* and *C. elegans* developmental stages revealed by alternative splicing characteristics of conserved exons. ***BMC Genomics*** 18(1):234.

65. Yang, Y.*, Yang, Y.C.T.*, Yuan J., Lu, Z.J.+, and **Li, J.J.+** (2017). Large-scale mapping of mammalian transcriptomes identifies conserved genes associated with different cell states. ***Nucleic Acids Research*** 45(4):1657–1672.

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67. Li, W.V., Razaee, Z.S., and **Li, J.J.+** (2016). Epigenome overlap measure (EPOM) for comparing tissue/cell types based on chromatin states. ***BMC Genomics*** 17(Supp 1):10.

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69. **[Data] Li, J.J.** and Biggin, M.D. (2015). Statistics requantitates the central dogma. ***Science*** 347(6226):1066–1067.

70. **[Data]** Gerstein, M.B.*, Rozowsky, J.*, Yan, K.K.*, Wang, D.*, Cheng, C.*, Brown, J.B.*, Davis, C.A.*, Hillier, L*, Sisu, C.*, **Li, J.J.***, Pei, B.*, Harmanci, A.O.*, Duff, M.O.*, Djebali, S.*, and 82 other authors from the modENCODE consortium (2014). Comparative analysis of the transcriptome across distant species. ***Nature*** 512(7515):445–448.

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72. **[Data] Li, J.J.**, Huang, H., Bickel, P.B., and Brenner, S.E. (2014). Comparison of *D. melanogaster* and *C. elegans* developmental stages, tissues, and cells by modENCODE RNA-seq data. ***Genome Research*** 24(7):1086–1101.
    - Top 10 papers selected at the 2014 RECOMB/ISCB Conference on Regulatory & Systems Genomics

73. **Li, J.J.**, Bickel, P.B., and Biggin, M.D. (2014). System wide analyses have underestimated protein abundances and transcriptional importance in mammals. ***PeerJ*** 2:e270.
    - "PeerJ Picks 2015" Collection
    - "Top Bioinformatics Papers – June 2015" Collection

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76. Gao, Q., Ho, C., Jia, Y., **Li, J.J.**, and Huang, H. (2012). Biclustering of linear patterns in gene expression data (CLiP). ***Journal of Computational Biology*** 19(6):619–631.

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78. **[Bioinfo] Li, J.J.**, Jiang, C.-R., Brown, B.J., Huang, H., and Bickel, P.J. (2011). Sparse linear modeling of RNA-seq data for isoform discovery and abundance estimation. ***Proc Natl Acad Sci. USA*** 108(50):19867–19872.

79. **[Data]** MacArthur, S.*, Li, X.Y.*, **Li, J.***, Brown, J.B., Chu, H.C., Zeng, L., Grondona, B.P., Hechmer, A., Simirenko, L., Keranen, S.V., Knowles, D.W., Stapleton, M., Bickel, P., Biggin, M.D., and Eisen, M.B. (2009). Developmental roles of 21 Drosophila transcription factors are determined by quantitative differences in binding to an overlapping set of thousands of genomic regions. ***Genome Biology*** 10:R80.
    - Highly accessed article on BioMed Central
    - Faculty of 1000 recommendation

CONFERENCE PROCEEDINGS (PUBLISHED / ACCEPTED)

80. Liu, P. and **Li, J.J.**$^{+}$ (2025). mcRigor: A statistical method to enhance the rigor of metacell partitioning in single-cell RNA-seq and ATAC-seq data analysis. ***Lecture Notes in Computer Science*** 15647:381–385. (RECOMB 2025 Proceeding; Sankararaman, S., ed.; Springer, Cham)

81. Song, D., Chen, S., Lee, C., Li, K., Ge, X., and **Li, J.J.**$^{+}$ (2025). Synthetic control removes spurious discoveries from double dipping in single-cell and spatial transcriptomics data analyses. ***Lecture Notes in Computer Science*** 15647:400–404. (RECOMB 2025 Proceeding; Sankararaman, S., ed.; Springer, Cham)

SUBMITTED

82. Li, Z., Patel, Z.M., Song, D., Yan, G., **Li, J.J.**, and Pinello, L. (2024). Systematic benchmarking of computational methods to identify spatially variable genes. ***Genome Biology*** under revision. bioRxiv preprint.

83. **[Bioinfo, Meth]** Wang, Q., Zhai, Z., Lian, Q., Song, D., and **Li, J.J.**$^{+}$ (2023). Categorization and analysis of 14 computational methods for estimating cell potency from single-cell RNA-seq data. ***Nature Communications*** under revision. arXiv preprint.

84. **[Bioinfo, Meth]** Song, D.*, Li, K.*, Ge, X., and **Li, J.J.$^{+}$** (2023). ClusterDE: a post-clustering differential expression (DE) method robust to false-positive inflation caused by double dipping. ***Cell*** under review. bioRxiv preprint.
    - Accepted by the 29th International Conference on Research in Computational Molecular Biology (RECOMB) 2025

85. **[Meth]** Wang, C., Zhang, Z., and **Li, J.J.$^{+}$** (2024). SyNPar: Synthetic null data parallelism for high-power false discovery rate control in high-dimensional variable selection. arXiv preprint.

86. Kanduri, C., Mamica, M., Olstad, E.W., Zucknick, M., **Li, J.J.**, and Sandve, G.K. (2024). Beware of counter-intuitive levels of false discoveries in omics: a tale of multiple testing on datasets with strong intracorrelations. ***Genome Biology*** under revision.

MANUSCRIPTS

87. Li, W.V., Tong, X., and **Li, J.J.$^{+}$** (2020). Bridging cost-sensitive and Neyman-Pearson paradigms in asymmetric binary classification. arXiv preprint.

REVIEWS & PERSPECTIVES

88. **[Meth]** Wang, C., Ge, X., Song, D., and **Li, J.J.$^{+}$** (2025). Comment on "Data fission: splitting a single data point": data fission for unsupervised learning: a discussion on post-clustering inference and the challenges of debiasing. ***Journal of American Statistical Association*** 120(549):174–175.

89. Fang, L., ..., **Li, J.J.$^{+}$**, Palmer, A.$^{+}$, Frantz, L.$^{+}$, Zhou, H.$^{+}$, Zhang, Z.$^{+}$, and Liu, G.E.$^{+}$ (2025). The farm animal genotype-tissue expression (FarmGTEx) project. ***Nature Genetics*** 57:786–796.

90. **[Bioinfo, Meth]** Yan, G., Hua, S.H., and **Li, J.J.$^{+}$** (2025). Categorization of 34 computational methods to detect spatially variable genes from spatially resolved transcriptomics data. ***Nature Communications*** 16:1141.

91. **Li, J.J.$^{+}$** (2024). Leadership at the Intersection of Statistics & Genomics: A COPSS-NISS Leadership Webinar with Drs. Rafael Irizarry and Mingyao Li. ***Statistics in Biosciences*** 16:547–555.

92. **[Bioinfo, Meth] Li, J.J.$^{+}$** (2023). How the Monty Hall problem is similar to the false discovery rate in high-throughput data analysis. ***Nature Biotechnology*** 41:754–755.

93. **[Bioinfo, Meth]** Jiang, R., Sun, T., Song, D., and **Li, J.J.$^{+}$** (2022). Statistics or biology: the zero-inflation controversy about scRNA-seq data. ***Genome Biology*** 23:31.

94. **[Meth]** Wang, Y.X.R., Li, L., **Li, J.J.**, and Huang, H. (2021). Network modeling in biology: statistical methods for gene and brain networks. ***Statistical Science*** 36(1):89–108.

95. **[Meth] Li, J.J.$^{+}$** and Tong, X. (2020). Statistical hypothesis testing versus machine-learning binary classification: distinctions and guidelines. ***Patterns*** 1(7):110115.

96. **Li, J.J.$^{+}$** (2020). A new bioinformatics tool to recover missing gene expression in single-cell RNA sequencing data. ***Journal of Molecular Cell Biology*** 13(1):1–2.

97. **Li, J.J.$^{+}$** (2019). Review of "Statistical modeling and machine learning for molecular biology" by Moses, A.M. ***The American Statistician*** 73(1):103-104.

98. **[Meth]** Li, W.V. and **Li, J.J.$^{+}$** (2018). Modeling and analysis of RNA-seq data: a review from a statistical perspective. ***Quantitative Biology*** 6(3):195-209.

99. Tong, X. and **Li, J.J.** (2017). Discussion of "Random-projection ensemble classification" by Cannings, T.I. and Samworth, R.J. ***Journal of the Royal Statistical Society: Series B*** 79(4):1025-1026.

BOOK CHAPTERS

100. **Li, J.J.** and Tong, X. (2016). Genomic Applications of the Neyman-Pearson Classification Paradigm. ***Big Data Analytics in Genomics*.** Springer (New York). DOI: 10.1007/978-3-319-41279-5; eBook ISBN: 978-3-319-41279-5; Hardcopy ISBN: 978-3-319-41278-8.

101. **Li, J.J.**, Huang, H., Qian, M., and Zhang, X. (2015). Chapter 24: Transcriptome analysis using next-generation sequencing data. ***Advanced Medical Statistics* (2nd Edition).** World Scientific Publishing Co. ISBN-10: 9814583294; ISBN-13: 978-9814583299.

THESIS

102. **Li, J.J.** (2013). Statistical Methods for Analyzing High-throughput Biological Data. Ph.D. Thesis, University of California, Berkeley.

TEACHING

UNDERGRADUATE COURSES

UCLA (as Instructor)

STAT 19:	Freshman Fiat Lux Seminar “Introduction to Modern Genomics Technologies” Spring 2016; “Junction at Statistics and Biology” Fall 2020, Winter 2021
STAT 20:	Lower-division Course “Introduction to Statistical Programming with R” Winter 2016
STAT 100B:	Upper-division Course “Introduction to Mathematical Statistics” Winter 2014, Winter 2016, Spring 2017, Winter 2022

UC Berkeley (as Graduate Student Instructor)

STAT 131A:	Upper-division Course “Statistical Inferences for Social and Life Scientists” Instructor: Haiyan Huang, Department of Statistics, Spring 2009

GRADUATE COURSES

UCLA (as Instructor)

STAT 200C:	PhD-level course “Large Sample Theory, Including Resampling” Spring 2016, Winter 2017 (renamed as STAT 203), Spring 2019, Fall 2020-2021, Fall 2023, Spring 2025
STAT 201B:	PhD-level course “Statistical Modeling and Learning” Winter 2020
STAT 205:	PhD-level course “Hierarchical Linear Models” Winter 2017, Fall 2017-2019, Winter 2021, Spring 2024, Winter 2025
STAT 207:	PhD-level course “Statistical Learning with Sparsity” Spring 2018
STAT M254 / BIOINFO M223:	PhD-level Course “Statistical Methods in Computational Biology”

Spring 2014-2019, Fall 2019, Winter 2021-2022, Spring 2024, Winter 2025

STAT 290: Seminar Course “Current Literature in Statistics”
Fall 2014, Winter 2014, Spring 2015

STAT 402: MAS-level course “Applied Regression”
Fall 2016

BIOINFO 201: Seminar Course “Advanced Methods in Computational Biology”
Spring 2019, 2019-2023

MC&IP M252: PhD-level Course “Molecular Mechanisms of Human Diseases I”
(Instructor for two statistics lectures)
Fall 2020, 2021

Workshop “Statistical Rigor in Genomics Data Analysis,” May 27, 2022

California State University, Northridge (as Instructor)

Workshop “Bridges-to-PhD Statistics Workshop,” Jan 22, 2021

Tsinghua University, China (as Instructor)

Summer Course “Biostatistical Methods with Applications in Biology,” School of Life Sciences, Summer 2014, Summer 2016

Chinese Academy of Sciences (as Instructor)

Summer Course “Biological Big Data and Data Mining,” Academy of Mathematics and Systems Science, Summer 2016

UC Berkeley (as Graduate Student Instructor)

STAT 200B: Master-level Course “Introduction to Probability and Statistics at an Advanced Level”
Instructor: Cari Caufman, Department of Statistics, Spring 2010

STAT 210A: PhD-level Course “Theoretical Statistics”
Instructor: Haiyan Huang, Department of Statistics, Fall 2010

STAT 215A: PhD-level Course “Statistical Models: Theory and Application”
Instructor: Bin Yu, Department of Statistics, Fall 2012

STUDENT ADVISING

MENTOR’ AWARDS

2021	Bruins in Genomics Summer Research Program Outstanding Mentorship Award

MENTEES’ AWARDS

2025	Guan’ao Yan received the Most Outstanding Statistician Award from UCLA Statistics
2024	Pan Liu received the Student Paper Award from the Section on Statistics in Genomics and Genetics, American Statistical Association
2024	Christy Lee received the UCLA Department of Statistics Stone Fellowship
2024	Guan’ao Yan received the UCLA Dissertation Year Fellowship
2024	Tianyi Sun received the Most Outstanding Statistician Award from UCLA Statistics
2024	Christy Lee and Pan Liu received the Warren Alpert Computational Biology and AI Network Fellowship
2023	Guan’ao Yan received the JXTX + CSHL 2023 Genome Informatics Scholarship
2023	Dongyuan Song received the UCLA Dissertation Year Fellowship

2023	Guan’ao Yan received UCLA Department of Statistics' inaugural Don Ylvisaker Award for the Best Practice of Statistics
2023	Kexin Li received the Most Outstanding Statistician Award from UCLA Statistics
2023	Christy Lee received the ISCB Travel Fellowship to attend ISMB/ECCB 2023
2023	Qingyang Wang received the National Science Foundation Graduate Research Fellowship
2023	Dongyuan Song received the JXTX + CSHL 2023 Biology of Genomes Scholarship
2022	Guan’ao Yan won the Interdisciplinary Opportunity Award at the UCI Center for Multiscale Cell Fate
2022	Guan’ao Yan received the Most Promising Statistician Award from UCLA Statistics
2022	Kexin Li received the UCLA Dissertation Year Fellowship
2022	Christy Lee received the NSF NRT MENTOR Fellowship
2022	Zhengtong Liu was selected for the UCLA Applied and Computational Mathematics REU Program Summer 2022
2021	Chris Dong received the NSF NRT MENTOR Fellowship
2021	Heather Zhou received the NHLBI UCLA Integrated Data Science Training in Cardiovascular Medicine (iDISCOVER) Fellowship
2020	Manasvi Malepati received the Bruins in Genomics Summer Research Symposium Presentation Award
2019	Heather Zhou received the NSF NRT MENTOR Fellowship
2019	Wei Li received the Most Outstanding Statistician Award from UCLA Statistics
2019	Yiling Chen received the Most Promising Statistician Award from UCLA Statistics
2018	Wei Li received the Pearl Cohen Poster Award on UCLA Bioscience Innovation Day
2018	Yiling Chen received the Biomedical Big Data Training Grant as the only international student recipient
2018	Ruochen Jiang received the Most Outstanding Masters Student Award from UCLA Statistics
2018	Wei Li received the UCLA Dissertation Year Fellowship
2016	Zahra Razaee received the UCLA Dissertation Year Fellowship
2015	Wei Li received the Most Promising Computational Statistician Award from UCLA Statistics

POSTDOCS

1. Changhu Wang	2024–	
2. Pan Liu	2024–	
3. Saidi Wang	2022–2023	Assistant Professor at Henan University, China
4. Xinzhou Ge	2021–2023	Assistant Professor of Statistics at Oregon State University

PHD STUDENTS

1. Ziqi Rong	2025–	UCLA Bioinformatics
2. Chenxin Jiang	2025–	UCLA Statistics
3. Mannix Burns	2023–	UCLA Molecular Biology (co-mentored with Dr. Steven E. Jacobsen)
4. Yihui Cen	2023–	UCLA Biomathematics
5. Weijian Wang	2023–	UCLA Bioinformatics (co-mentored with Dr. Grace Xinshu Xiao)
6. Chengfeng Jiang	2022–	UCLA Statistics
7. Zhiqian Zhai	2021–	UCLA Statistics

8. Qingyang Wang	2021–	UCLA Statistics
9. Chris Dong	2020–	UCLA Statistics
10. Christy Lee	2020–2025	UCLA Statistics
11. Guan'ao Yan	2020–2025	UCLA Statistics; Next Assistant Professor at Michigan State University
12. Dongyuan Song	2019–2024	UCLA Bioinformatics; Next Assistant Professor of Genetics and Genome Sciences at UConn
13. Wenbin Guo	2018–2021	UCLA Bioinformatics
14. Heather J. Zhou	2018–2023	UCLA Statistics; Currently Postdoc at City of Hope
15. Kexin Li	2018–2023	UCLA Statistics; Currently Data Scientist at Microsoft
16. Tianyi Sun	2017–2023	UCLA Statistics; Currently Biostatistician at FDA
17. Nan Xi	2016–2021	UCLA Statistics; Next Assistant Professor of Statistics at Loyola University of Chicago
18. Ruochen Jiang	2016–2021	UCLA Statistics; Currently Bioinformatics Scientist at Veracyte, Inc.
19. Xinzhou Ge	2016–2021	UCLA Statistics; Currently Assistant Professor of Statistics at Oregon State University
20. Yiling Chen	2016–2021	UCLA Statistics; Currently Scientist at Genentech
21. Jiaping Zhu	2015–2021	UCLA Statistics
22. Yidan Sun	2015–2021	UCLA Statistics; Next Visiting Assistant Professor of Statistics at UC Santa Barbara
23. Wei (Vivian) Li	2014–2019	UCLA Statistics; Next Assistant Professor of Biostatistics at Rutgers University; Currently Assistant Professor of Statistics at UC Riverside
24. Zahra Razaee	2014–2017	UCLA Statistics; Next Postdoctoral Scientist at Cedars-Sinai Medical Center

MS STUDENTS

1. Chenxin Jiang	2023–2025	UCLA Statistics
2. Wenbin Guo	2024–2024	UCLA Statistics
3. Stephanie Lu	2023–2025	UCLA Applied Statistics
4. Tianyang Liu	2020–2022	UCLA Applied Statistics
5. Xiaoru Zheng	2019–2020	UCLA Statistics
6. Yingqi Li	2019–2020	UCLA Statistics
7. Tianyi Xia	2018–2019	UCLA Statistics
8. Yu-Cheng Yang	2016–2017	UCLA Statistics; Currently Assistant Professor at Fudan University, China
9. Surui Sun	2015–2017	UCLA Statistics
10. Arturo Ramirez	2013–2015	UCLA Statistics

PHD ROTATION STUDENTS

1. Elaine Huang	Winter 2021	UCLA Bioinformatics
2. Leroy Bondhus	Fall 2018	UCLA Human Genetics
3. Soo Bin Kwon	Spring 2017	UCLA Bioinformatics
4. Lingyu Zhan	Winter 2017	UCLA Gene Regulation
5. Xinyuan Chen	Fall 2016	UCLA Human Genetics
6. Mudra Choudhury	Fall 2016	UCLA Bioinformatics
7. Douglas Arneson	Winter 2015	UCLA Bioinformatics

VISITING GRADUATE STUDENTS

1.	Jingzhi Sun	Summer 2024	Visiting MS student in Statistics from UC Davis
2.	Catherine Higgins	Summer 2024	Visiiting PhD student in Statistics from University of College Dublin

UNDERGRADUATE STUDENTS

1.	Joseph Lukas	2024–	Computational & Systems Biology major at UCLA
2.	Santiago Chang	2024–	Computational & Systems Biology major at UCLA
3.	Hengyuan Wang	2024–	Computational & Systems Biology major at UCLA
4.	Ria Ghosh	2024–	Computational & Systems Biology major at UCLA
5.	Yu Jin (Erin) Kwon	2023–2024	Computational & Systems Biology major at UCLA
6.	Lehan Zou	2022	Statistics major at UCLA
7.	Shiyu Ma	2022	Applied Math and Statistics major at UCLA
8.	Weijian Wang	2022	Visiting student from Zhejiang University, China
9.	Yihui Cen	2022	Visiting student from Zhejiang University, China
10.	Shuo Hua	2022	Visiting student from Tsinghua University, China
11.	Qiuran Lyu	2022	Visiting student from Renmin University, China
12.	Lucia Ramirez	2021	Bruins in Genomics Summer Program
13.	Zhengtong Liu	2020–2022	Applied Math and CS major at UCLA
14.	Melody Zhang	2020–2021	Biology major at UCLA
15.	Huy Nguyen	2020–2022	Statistics major at UCLA
16.	Jingfei Fang	2020	Math of Computational major at UCLA
17.	Manasvi Malepati	2020	Bruins in Genomics Summer Program
18.	Wenchu Pan	2019	Visiting student from Peking University, China
19.	Xindi Lin	2019	CSST student from Zhejiang University, China
20.	Dehong Xu	2018	CSST student from Beijing University of Posts and Telecommunications
21.	Mayra Varillas	2017	Bruins in Genomics Summer Program
22.	Tiffany Tu	2017	Bruins in Genomics Summer Program
23.	Kexin Li	2017	Visiting student from Tsinghua University, China
24.	Yue Cui	2016–2017	Statistics major at UCLA
25.	Longsheng Qian	2016–2017	Math/Econ major at UCLA
26.	Qianhao Yu	2016–2017	Applied Math & Statistics major at UCLA
27.	Jingwei Song	2016–2017	Statistics major at UCLA
28.	Yumeng Ma	2016	Visiting student from Tsinghua University, China
29.	Tianyi Sun	2016	Visiting student from Tsinghua University, China
30.	Yushi Tang	2016	CSST student from Peking University, China
31.	Yuqi Tian	2016	Summer student from Xiamen University, China
32.	Yiling Chen	2015–2016	Math/Applied Science major at UCLA
33.	Yimeng Jia	2015–2016	Statistics major at UCLA
34.	Jason Mao	2015–2016	Statistics major at UCLA
35.	Ruiqi Gao	2015–2016	Visiting student from Peking University, China
36.	Xin Xu	2014–2015	CSST student from Nankai University, China
37.	Yuting Ye	2014–2015	Visiting student from Tsinghua University, China
38.	Chang Ding	Spring, Fall 2014	Mathematics/Economics major at UCLA

THESIS COMMITTEES

PhD in Statistics:

1.	Navin Varadaraj Souda	2024–
2.	Yingqi Gao	2024–
3.	Siwei (Steven) Ye	2021–

4.	Stephen Vincent Smith	2021–
5.	Jireh Huang	2021–
6.	Yaxuan Zhu	2020–
7.	Yizhou Zhao	2020–
8.	Samuel O. Onyambu	2020–
9.	Gabriel Ruiz	2020–
10.	Yifei Xu	2019–2022
11.	Kun Zhou	2017–2020
12.	Zhixin Zhou	2017–2018
13.	Levon Demirdjian	2016–2018
14.	Seunghyun Min	2016–2019
15.	Joshua Gordon	2015–2017
16.	Qian Xiao	2014–2017
17.	Jianwen Xie	2015–2016
18.	Nikhyl Bryon Aragam	2013–2015

PhD in other majors:

1.	Yuning Chen	2025–	Molecular Biology
2.	Raag Agrawal	2023–	Human Genetics
3.	Chanyue (Charlotte) Hu	2023–	Bioinformatics
4.	Helena Kanya Winata	2023–	Bioinformatics
5.	Jingyuan Fu	2023–	Computer Science
6.	Aina M.I. Zurita	2023–	Human Genetics
7.	Arielle Hogan	2023–	Neuroscience
8.	Apeksha Sudha Singh	2023–	Biomathematics
9.	Jonathan Perrie	2022–	Bioinformatics
10.	Jack Freeland	2022–	Molecular Biology
11.	Runjia Li	2021–	Bioinformatics
12.	Shuya Wang	2021–	Molecular Biology
13.	Russell Littman	2020–2022	Bioinformatics
14.	Zhixin (Cyrillus) Tan	2020–	Bioinformatics
15.	Matias A. Rojas Leon	2020–2022	Civil Engineering
16.	Shuochuan Meng	2019–	Civil Engineering
17.	Leah Briscoe	2019–	Bioinformatics
18.	Thai Ha Vu	2019–	Bioinformatics
19.	Alec Matthew Chiu	2019–	Bioinformatics
20.	Mina Shahi	2019–	Bioengineering
21.	Dat Bach Duong	2018–2020	Computer Science
22.	Soo Bin Kwon	2018–2021	Bioinformatics
23.	Xingquan Guan	2018–2021	Civil Engineering
24.	Feiyang Ma	2018–2020	Molecular Biology
25.	Kikuye Koyano	2018–2021	Bioinformatics
26.	Xinhui Zhang	2017–	Biology
27.	Qin An	2017–2020	Human Genetics
28.	Zong Miao	2016–2020	Bioinformatics
29.	Hung-Hao Lo	2016–2019	Molecular Biology
30.	Jui-Ting Ju	2016–2019	Computer Science
31.	Sepideh Mazrouee	2016–2017	Computer Science
32.	Shanxi Jiang	2015–2018	Molecular, Cellular, and Integrative Physiology
33.	Yun-Hua Hsiao	2014–2018	Bioengineering

MS in Statistics:

1.	Yunan Yan	2024
2.	Bill Li	2022

3.	Sixuan Li	2021
4.	Ashley Kathleen Chiu	2021
5.	Juan Piao	2021
6.	Ritvik Yogesh Kharkar	2020
7.	Zijun Zhang	2019
8.	Yu Zhang	2019
9.	Shuai Zhu	2019
10.	Hua Kang	2018
11.	Maxim Ananyev	2018
12.	Soo Woo Choi	2017
13.	Yiwei Xu	2017
14.	Chufeng Hu	2017
15.	Qian Xiao	2015
16.	Muzhou Liang	2015
17.	Yuan Tian	2014

MAS in Statistics:

1.	Lynette Ho Ching To	2022
2.	Max Harris Belasco	2021
3.	Jason Osajima	2019
4.	Yueyan (Lilian) Gao	2019
5.	Hui Zhang	2018

MS in other majors:

1.	Rachana Jayaraman	2022	Bioinformatics
2.	Madeleine Claire Murphy	2022	Bioinformatics
3.	Yuelin (Kathleen) He	2021	Bioinformatics

FACULTY MENTORING & HOSTING

FACULTY MENTEE

2024–	Fabian Rosner	Assistant Professor of Civil and Environmental Engineering, UCLA

VISITING FACULTY

2024	Shan Yu	Assistant Professor of Statistics, University of Virginia

INVITED TALKS & PRESENTATIONS

KEYNOTE PRESENTATIONS

1. Spatial Biology Congress Asia, Guangzhou, China, June 26, 2025
2. Annual Meeting of Single Cell And Spatial Omics Community in Korea (SCSOK), June 23-24, 2025
3. Special Invited Talk, International Indian Statistical Association Conference, University of Nebraska-Lincoln, NE, June 14, 2025
4. Women in Data Science Symposium, Santa Clara University, Santa Clara, CA (Online), May 23, 2025
5. MCBIOS 2025 (The 21st Annual Meeting of the MidSouth Computational Biology and Bioinformatics Society), University of Utah, Salt Lake City, UT, Mar 28, 2025
6. "Modern Benchmarking: Advancing Computational Methods In Molecular Biology" Meeting, Ascona, Switzerland, Mar 23-27, 2025

7. Australian Bioinformatics and Computational Biology Society (ABACBS) Annual Conference, Sydney, Australia, Nov 4-6, 2024
8. International Conference on Intelligent Biology and Medicine (ICIBM), Houston, TX, Oct 10-12, 2024
9. Symposium “Bioinformatic Omics and Machine Learning,” University of Nebraska-Lincoln, Aug 19-21, 2024
10. The 15th RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges (RSGDREAM), Los Angeles, CA, Nov 28-29, 2023
11. The joint GIW 2023 and ISCB-Asia VI Conference, Singapore, Nov 18-21, 2023
12. ISCB Overton Prize Keynote, The 31st Conference on Intelligent Systems for Molecular Biology (ISMB) and The 22nd European Conference on Computational Biology (ECCB), Lyon, France, Jul 25, 2023
13. The 21st Asia Pacific Bioinformatics Conference, Changsha, Hunan, China, Apr 15, 2023
14. The 8th National Conference on Bioinformatics and Systems Biology of China and the 1st (Macao) International Bioinformatics Symposium, Macao, Oct 23, 2018

SEMINAR PRESENTATIONS AT UNIVERSITIES AND RESEARCH INSTITUTES

1. National Institute for Theory and Mathematics in Biology (NITMB) Seminar, Chicago, IL, Nov 7, 2025
2. Models, Inference & Algorithms Seminar, Broad Institute, Cambridge, MA, Nov 5, 2025
3. Department of of Mathematical Sciences, New Jersey Institute of Technology, Newark, NJ, Sep 26, 2025
4. QCBio Faculty Research Forum, University of California, Los Angeles, Jun 11, 2025
5. SenNet Omics and Image-Mapping Group Seminar (Online), Jun 10, 2025
6. Department of Statistics, University of California, Riverside, CA, May 13, 2025
7. Department of Statistics, University of Wisconsin, Madison, WI, Apr 23, 2025
8. Department of Biostatistics, St. Jude Children's Research Hospital, Memphis, TN, Apr 10, 2025
9. Department of Data Science, Dana-Farber Cancer Institute, Boston, MA, Apr 8, 2025
10. Department of Genetics and Genome Sciences, UConn Health, Farmington, CT, Mar 13, 2025
11. Department of Statistics, University of Connecticut, Storrs, CT, Mar 12, 2025
12. Biomedical Data Science Seminar, University of Virginia, Charlottesville, VA (Online), Jan 31, 2025
13. Division of Biostatistics and Health Data Science Seminar, University of Minnesota, Minneapolis, MN, Jan 22, 2025
14. Versiti Blood Research Institute, Milwaukee, WI, Jan 21, 2025
15. Faculty of Informatics and Data Science, University of Regensburg, Germany, Dec 5, 2024
16. Department of Information Systems, Business Statistics and Operations Management, Hong Kong University of Science and Technology, Hong Kong, Nov 1, 2024
17. Department of Computational Medicine, University of Michigan, Ann Arbor, MI, Oct 9, 2024
18. Department of Statistics, Oregon State University, Corvallis, OR, Oct 7, 2024
19. Department of Mathematical Sciences, University of Nevada, Las Vegas, NV, Oct 5, 2024
20. Program of Genetics, Bioinformatics, and Computational Biology, Virginia Tech, Blacksburg, VA (Online), Sep 25, 2024
21. Department of Biostatistics, University of North Carolina, Chapel Hill, NC, Sep 19, 2024
22. Center for Bioinformatics and Quantitative Biology, University of Illinois, Chicago, IL, Sep 9, 2024
23. Genomic Medicine Institute, Seoul National University College of Medicine, Seoul, Korea (Online), Aug 14, 2024
24. Department of Biostatistics, University of Washington, Seattle, WA, May 23, 2024
25. Biomedical Mathematics Colloquium, Institute for Basic Science, Korea (Online), May 10, 2024
26. Biostatistics Program, Fred Hutch Cancer Center, Seattle, WA, Apr 25, 2024
27. Section of Genetic Medicine, Department of Medicine, The University of Chicago, IL, Mar 27, 2024
28. Computational Biology and Bioinformatics Program, Duke University, Durham, NC, Mar 25, 2024
29. Department of Biostatistics, NYU School of Global Public Health, New York, NY, Mar 14, 2024

30. Institute for Research in Immunology and Cancer (IRIC), University of Montreal, QC, Canada, Mar 11, 2024
31. Department of Statistics, University of California, Davis, CA, Mar 7, 2024
32. Joint Webinar of Applied Public Health Statistics Section (APHS) of the American Public Health Association (APHA) and the Department of Biostatistics, Epidemiology and Environment Health Sciences (BEES) in the Jiann-Ping Hsu College of Public Health at Georgia Southern University (Online), Feb 26, 2024
33. Department of Statistics, University of California, Irvine, CA, Feb 22, 2024
34. Department of Computational Medicine, University of California, Los Angeles, CA, Feb 15, 2024
35. Biostatistics Seminar, McGill University, Montreal, QC, Canada (Online), Jan 17, 2024
36. Computational Biology Department, Carnegie Mellon University, Pittsburgh, PA, Nov 10, 2023
37. Department of Computational Biomedicine, Cedars-Sinai Medical Center, Los Angeles, CA, Nov 8, 2023
38. Department of Biostatistics, Vanderbilt University, Nashville (Online), TN, Oct 25, 2023
39. Department of Biomedical Engineering, Johns Hopkins University, Baltimore, MD, Oct 23, 2023
40. Center for Integrative Genomics, Georgia Institute of Technology, Atlanta, GA, Oct 20, 2023
41. Department of Biostatistics and Bioinformatics, Emory University, Atlanta, GA, Oct 19, 2023
42. Department of Statistics, Purdue University, West Lafayette, IN, Oct 13, 2023
43. Michelson Center for Convergent Biosciences, University of Southern California, Los Angeles, CA, Sep 22, 2023
44. Center of Computational Biology and Bioinformatics, Penn State University, State College, PA, Aug 23, 2023
45. French National Centre for Scientific Research (Centre National de la Recherche Scientifique (CNRS)), Grenoble, France, Jul 27, 2023
46. Special Seminar, University of Virginia, Charlottesville, VA, Jun 22, 2023
47. Microsoft Research New England, Cambridge, MA, Jun 7, 2023
48. Department of Statistics, Colorado State University, Fort Collins, CO, May 1, 2023
49. The Jackson Laboratory for Genomic Medicine, Farmington, CT, Mar 14, 2023
50. Department of Molecular and Systems Biology, Geisel School of Medicine, Dartmouth College, Hanover, NH, Feb 27, 2023
51. The Center for Computational & Genomic Medicine (CCGM), The Children's Hospital of Philadelphia (CHOP), Philadelphia, PA, Feb 8, 2023
52. Bioinformatics Interdepartmental Ph.D. Program, University of California, Los Angeles, CA, Feb 6, 2023
53. Center for Multiscale Cell Fate (CMCF) MathBio Seminar, University of California, Irvine, CA, Jan 19, 2023
54. Department of Biostatistics, MD Anderson Cancer Center, Houston, TX (Online), Dec 14, 2022
55. Technology Assessment in Health Care Seminar, Harvard University, Cambridge, MA (Online), Dec 1, 2022
56. Department of Statistics, Michigan State University, East Lansing, MI, Nov 22, 2022
57. Genome Sciences Seminar Series, Center for Public Health Genomics, University of Virginia, Charlottesville, VA, Nov 9, 2022
58. Data Matters Seminar Series, Data Science Initiative and Center for Computational Molecular Biology, Brown University, Providence, RI, Oct 27, 2022
59. Department of Biostatistics, Columbia University, New York, NY, Oct 20, 2022
60. The Herbert and Florence Irving Institute for Cancer Dynamics (IICD), Columbia University, New York, NY, Oct 19, 2022
61. Department of Statistics, University of Missouri, Columbia, MO, Oct 17, 2022
62. Department of Biostatistics, Yale University, New Haven, CT, Oct 11, 2022
63. Center for Biomedical Informatics and Genomics, Tulane University, New Orleans, LA (Online), Oct 5, 2022

64. Department of Statistics, Oregon State University, Corvallis, OR (Online), Oct 3, 2022
65. Department of Systems Biology, City of Hope, Duarte, CA, Sep 29 (Online), 2022
66. Department of Biostatistics, University of Nebraska Medical Center, Omaha, NE (Online), Apr 1, 2022
67. Department of Biomedical Data Science, Stanford University, Stanford, CA (Online), Feb 22, 2022
68. Department of Data Science and Operations, University of Southern California, Los Angeles, CA, Dec 3, 2021
69. Department of Statistics, George Washington University, Washington, D.C. (Online), Nov 19, 2021
70. Bioinformatics Seminar, School of Mathematics and Statistics, University of Sydney, Australia (Online), Aug 16, 2021
71. Department of Biostatistics, University of Michigan, Ann Arbor, MI (Online), Apr 1, 2021
72. Department of Statistics, Chinese University of Hong Kong, Hong Kong (Online), Mar 29, 2021
73. Department of Biostatistics, University of Pennsylvania, Philadelphia, PA (Online), Mar 23, 2021
74. Neyman Seminar, Department of Statistics, University of California, Berkeley, CA (Online), Feb 3, 2021
75. Department of Statistics, University of Illinois at Urbana-Champaign, IL (Online), Aug 27, 2020
76. Interdisciplinary Center for Quantitative Modeling in Biology, University of California, Riverside, CA, Feb 12, 2020
77. Biomed-X Research Seminar, Zhejiang University-University of Edinburgh Institute, Haining, China, Dec 23, 2019
78. Department of Statistics, University of California, Santa Barbara, CA, Oct 9, 2019
79. Computational and Systems Biology Seminar, Lyda Hill Department of Bioinformatics, The University of Texas Southwestern Medical Center, Dallas, TX, Sep 23, 2019
80. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Aug 30, 2019
81. The Comprehensive Cancer Center, Cancer Immunotherapeutics Program & Department of Immuno-Oncology, City of Hope, Duarte, CA, Mar 15, 2019
82. Department of Statistics and Actuarial Science, Simon Fraser University, Vancouver, BC, Feb 22, 2019
83. Department of Statistics, The University of British Columbia, Vancouver, BC, Feb 21, 2019
84. Department of Mathematics, California State University, Northridge, Feb 20, 2019
85. State Key Laboratory of Biotherapy, Sichuan University, Chengdu, China, Jan 23, 2019
86. School of Life Sciences, Tsinghua University, Beijing, China, Jan 18, 2019
87. Center for Statistical Science, Tsinghua University, Beijing, China, Jan 17, 2019
88. The First Affiliated Hospital, Sun Yat-Sen University, Guangzhou, China, Jan 14, 2019
89. Department of Biostatistics, University of Pittsburgh, Nov 1, 2018
90. Department of Biomathematics, University of California, Los Angeles, Oct 4, 2018
91. Omics Seminar, Cedars-Sinai Medical Center, Los Angeles, CA, Sep 25, 2018
92. Department of Statistics, University of Georgia, Athens, GA, Aug 23, 2018
93. Bioinformatics Interdepartmental Ph.D. Program, University of California, Los Angeles, CA, Apr 9, 2018
94. Physical Sciences Faculty Lunch Seminar, College of Letters and Sciences, University of California, Los Angeles, CA, Mar 19, 2018
95. Department of Biostatistics, Ohio State University, Columbus, OH, Feb 23, 2018
96. Department of Statistics, University of California, Los Angeles, CA, Jan 17, 2018
97. Medical and Population Genomics Seminar, University of California, Los Angeles, CA, Dec 6, 2017
98. Medical and Population Genomics Seminar, University of California, Los Angeles, CA, May 24, 2017
99. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jul 4, 2017
100. Center for Statistical Science, Tsinghua University, Beijing, China, Jul 3, 2017
101. School of Life Sciences, Tsinghua University, Beijing, China, Jul 3, 2017
102. Institute of Machine Learning and Systems Biology, Tongji University, Shanghai, China, Dec 21, 2016

103. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jun 24, 2016
104. Faculty Research Lunch Series, Quantitative and Computational Biosciences, University of California, Los Angeles, CA, May 6, 2016
105. Department of Data Sciences and Operations, Marshall School of Business, University of Southern California, Los Angeles, CA, Dec 4, 2015
106. Genomics Seminar, Johns Hopkins University, Baltimore, MD, Nov 17, 2015
107. Jonsson Comprehensive Cancer Center Gene Regulation Intramural Meeting, University of California, Los Angeles, CA, May 5, 2015
108. Department of Statistics, University of California, Riverside, CA, Feb 24, 2015
109. Department of Ecology and Evolutionary Biology, University of California, Los Angeles, CA, Feb 18, 2015
110. Department of Statistics, Pennsylvania State University, State College, PA, Jan 22, 2015
111. Center for Systems Genomics, Pennsylvania State University, State College, PA, Jan 21, 2015
112. Department of Biostatistics, University of California, Los Angeles, CA, November 19, 2014
113. MOE Key Laboratory of Bioinformatics and Bioinformatics Division, TNLIST / Department of Automation, Tsinghua University, Beijing, China, Jun 20, 2014
114. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jun 19, 2014
115. Department of Statistics, Columbia University, NY, May 1, 2014
116. Department of Molecular and Computational Biology, University of Southern California, CA, Mar 6, 2014
117. Department of Statistics, University of California, Los Angeles, CA, Jan 14, 2014
118. School of Life Sciences, Tsinghua University, Beijing, China, Dec 13, 2013
119. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Apr 11, 2013
120. Department of Statistics, University of Chicago, IL, Feb 25, 2013
121. Departments of Human Genetics and Statistics, University of California, Los Angeles, CA, Feb 1, 2013
122. Department of Statistics, University of California, Davis, CA, Jan 16, 2013

CONFERENCE AND SYMPOSIUM PRESENTATIONS

1. Forbeck Forum on AI in Cancer Research and Drug Discovery, Aspen, CO, Oct 19-22, 2025
2. Novel Statistical Approaches for Studying Multi-omics Data, Banff International Research Station (BIRS) Workshop, Banff, AB, Jul 17, 2025
3. 8th UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 14, 2025
4. Invited Talk, NHGRI Open Science Day, Washington University in St. Louis, MO, Jun 9, 2025
5. CGM Online Seminar (https://cgmonline.co/), May 30, 2025
6. The 3rd FunGen-AD xQTL Symposium (Online), May 5, 2025
7. Paper Talk at the 29th International Conference on Research in Computational Molecular Biology (RECOMB), Seoul, South Korea, Apr 28, 2025
8. Third International Conference on Single-cell and Spatial Omics (TICSSO-3) (Online), Mar 31, 2025
9. Invited Talk, Joint March Meeting and April Meeting: Global Physics Summit, Anaheim, CA, Mar 20, 2025
10. Invited Talk, Healthcare, Bioinformatics, and Computational Biology (HBC) Congress, Rayazi Research Group and Regional Student Group (RSG) of ISCB, Iran (Online), Feb 13, 2025
11. Invited Talk, Statistics Empowering Data Science (SEEDS) Conference, University of Southern California, Los Angeles, CA, Jan 9, 2025
12. Computational Biology of the Genome, Cold Spring Harbor Asia, Suzhou, China, Oct 21-25, 2024
13. Joint Statistical Meetings, Portland, OR, Aug 7, 2024
14. Horizontal Gene Transfer and Mobile Elements in Microbial Ecology and Evolution Program, Kavli Institute for Theoretical Physics, Santa Barbara, Aug 2, 2024

15. 7th UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 18, 2024
16. ICSA China Conference, Wuhan, China, Jun 30, 2024
17. WNAR/IMS/Graybill Meeting, Fort Collins, CO, Jun 11, 2024
18. STATGEN Conference, Pittsburgh, PA, May 2, 2024
19. Second International Conference on Single-cell and Spatial Omics (TICSSO-2) (Online), Mar 30, 2024
20. ENAR 2024 Spring Meeting, Baltimore, MD, Mar 13, 2024
21. Frontiers in Single Cell Genomics, Cold Spring Harbor Asia, Suzhou, China, Dec 4-8, 2023
22. Workshop on Spatial and Time-Resolved Single-Cell Transcriptomics Analysis, Michigan State University, East Lansing, MI, Nov 12-13, 2023
23. Computational Era of Life Sciences, EU-US Frontiers of Engineering Symposium, Murray Hill, NJ, Oct 15-18, 2023
24. The Conceptual Power of Single Cell Biology, Cell Symposia, San Diego, CA, Aug 28-30, 2023
25. Invited Talk, Joint Statistical Meetings, Toronto, ON, Aug 9, 2023
26. 6th UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 17, 2023
27. Single-Cell Plus - Data Science Challenges in Single-Cell Research, Banff International Research Station (BIRS) Workshop, Banff, AB, Jul 5, 2023
28. ICSA Applied Statistics Symposium, Ann Arbor, MI, Jun 14, 2023
29. Spatial Biology US, Jun 8, 2023
30. The 36th New England Statistics Symposium, Boston, MA, Jun 5, 2023
31. Highlight Talk at the 27th International Conference on Research in Computational Molecular Biology (RECOMB), Istanbul, Turkey, Apr 17, 2023
32. Chan-Zuckerberg Initiative Single-Cell Data Insights Cycle 1 Symposium, Mar 10, 2023
33. Mapping the Brain Webinar, UCLA Institute for Quantitative and Computational Biosciences (Online), Mar 1, 2023.
34. Spatial Biology & Spatial Omics, Informa Connect, Boston, MA, Mar 1, 2023
35. Educational Series, NIH Bridge to Artificial Intelligence (Bridge2AI) Program (Online), Feb 9, 2023
36. Two Invited Talks, The Plant and Animal Genome (PAG) Conference, San Diego, CA, Jan 13-18, 2023
37. Invited Talk, Biennial Conference of Chinese Biological Investigators Society (CBIS), Las Vegas, NV, Dec 19-22, 2022
38. NIDA's SCORCH (Single Cell Opioid Responses in the Context of HIV) Program Analysis Working Group Meeting (Online), Dec 1, 2022
39. Invited Talk, Emerging Methods in Translational Science: Contemporary Challenges in Prediction Modeling, Wake Forest School of Medicine (Online), Nov 18, 2022
40. Invited Talk, Chan-Zuckerberg Initiative Single-Cell Biology Annual Meeting, San Jose, CA, Nov 14-18, 2022
41. Invited Talk, Mathematics and Statistics of Genomic Epidemiology, Banff International Research Station (BIRS)-Casa Matemática Oaxaca (CMO) Workshop (Online), Nov 8, 2022
42. Invited Talk, 5th Annual Symposium on Multiscale Cell Fate, NSF-Simons Center for Multiscale Cell Fate Research, UC Irvine, CA, Oct 24, 2022
43. Invited Talk, Joint Statistical Meetings, Washington, D.C., Aug 11, 2022
44. 5th UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 29, 2022
45. Invited Talk, "Computational Challenges in Very Large-Scale 'Omics'" Workshop, Simons Institute for the Theory of Computing, Berkeley, CA, Jul 18-21, 2022
46. Chan-Zuckerberg Initiative Single-Cell Data Insights Kickoff Meeting, Jul 14, 2022
47. ICSA 2022 China Conference (Online), Jul 1, 2022
48. CGM Online Seminar (https://cgmonline.co/), Jun 29, 2022
49. ICSA Applied Statistics Symposium, Gainesville, FL, Jun 21, 2022

50. Invited Talk, Deep Learning for Genetics, Genomics and Metagenomics: Latest developments and New Directions, Banff International Research Station (BIRS) Workshop, Kelowna, BC, Jun 7, 2022
51. Invited Talk, "Statistics in the Big Data Era" Workshop, Simons Institute for the Theory of Computing, Berkeley, CA, Jun 2, 2022
52. Host and Speaker, Young Bioinformatics PI Seminar Series (Online), May 27, 2022
53. Invited Talk, USC Computational Biology Symposium, May 22, 2022
54. Discussant, International Seminar on Selective Inference (Online), Nov 11, 2021
55. Invited Talk, The 6th Annual MidAtlantic Bioinformatics Conference (Online), Nov 8, 2021
56. ICSA Applied Statistics Symposium (Online), Sep 12, 2021
57. Invited Talk, Joint Statistical Meetings (Online), Aug 12, 2021
58. Invited Talk, The 8th Young Scholar Forum of Interdisciplinary Research of Mathematics, Computer Science, and Life Science, Chinese Academy of Sciences (Online), May 15, 2021
59. ICSA Applied Statistics Symposium (Online), Dec 15, 2020
60. International Seminar on Selective Inference (Online), Dec 3, 2020
61. Invited Talk, Mathematics and Statistics of Genomic Epidemiology, Banff International Research Station (BIRS)- Casa Matemática Oaxaca (CMO) Workshop (Online), Nov 11, 2020
62. Human Cell Atlas Asia Meeting (Online), Oct 22, 2020
63. Invited Talk, Joint Statistical Meetings (Online), Aug 6, 2020
64. ENAR 2020 Spring Meeting (Online), Mar 25, 2020
65. The 11th ICSA International Conference, Zhejiang University, Hangzhou, China, Dec 20, 2019
66. Joint Statistical Meetings, Denver, CO, Jul 31, 2019
67. 4th UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 18, 2019
68. The 27th Conference on Intelligent Systems for Molecular Biology (ISMB) and the 18th European Conference on Computational Biology (ECCB), Basel, Switzerland, Jul 23, 2019
69. Invited Talk, Single-cell Data in Space and Time: Mathematical and Computational Challenges, Imperial College London, London, UK, Jun 17, 2019
70. The Data Science Expo, Los Angeles, CA, May 18, 2019
71. ENAR 2019 Spring Meeting, Mar 25, 2019
72. Invited Talk, Frontiers in Single-cell Technology, Application and Data Analysis, Banff International Research Station (BIRS) Workshop, Banff, AB, Feb 27, 2019
73. The 8th Annual Southern California Systems Biology Conference, University of California at Irvine, CA, Feb 9, 2019
74. ICSA Conference on Data Science, Xishuangbanna, China, Jan 12, 2019
75. DahShu Virtual Journal Club, Nov 16, 2018
76. The Past, Present and Future of RNA-seq Technology and Its Application to Drug Discovery, EMBL-EBI Industry Programme Workshop, Cambridge, MA, Nov 8, 2018
77. Joint Statistical Meetings, Vancouver, BC, Aug 1, 2018
78. 3rd UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 17, 2018
79. Regulatory and Systems Genomics (RegSys) Community of Special Interest (COSI) at the 26th Conference on Intelligent Systems for Molecular Biology (ISMB), Chicago, IL, Jul 10, 2018
80. The 5th International Biostatistics Symposium, Guangzhou, China, Jul 7, 2018
81. ICSA China Conference with the Focus on Data Science, Qingdao, China, Jul 4, 2018
82. ICSA Applied Statistics Symposium, New Brunswick, NJ, Jun 16, 2018
83. The 46th Annual Meeting of the Statistical Society of Canada, McGill University, Montreal, QB, Canada, Jun 5, 2018
84. UCLA College Physical Sciences "Welcome to Research" Symposium (How to thrive in the sciences at UCLA and beyond: research at the cutting edge), Los Angeles, CA, May 21, 2018
85. DahShu Virtual Journal Club (Online), Apr 30, 2018
86. Johnson & Johnson WiSTEM2D Symposium, New Brunswick, NJ, Apr 26, 2018
87. Highlight Talk at the 22nd International Conference on Research in Computational Molecular Biology (RECOMB), Paris, France, Apr 24, 2018
88. Joint Statistical Meetings, Baltimore, MD, Aug 3, 2017

89. The 1st North American Social Networks (NASN) Conference, Washington, D.C., Jul 28, 2017
90. 2nd UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 24, 2017
91. ICSA Applied Statistics Symposium, Chicago, IL, Jun 26, 2017
92. HDDA VII (The 7th International Workshop on Perspectives on High-dimensional Data Analysis), CIMAT, Guanajuato, Mexico, Jun 18, 2017
93. UCLA QCB 2nd Annual Symposium "Exploring the Frontiers of Biomedical Big Data," UCLA, Los Angeles, CA, Apr 28, 2017
94. Workshop "Harnessing Big Data for Precision Medicine: Infrastructure and Applications," Pacific Symposium on Biocomputing (PSB), The Big Island of Hawaii, HI, Jan 3, 2017
95. The 10th ICSA International Conference: Global Growth of Modern Statistics in the 21st Century, Shanghai Jiaotong University, Shanghai, China, Dec 20, 2016
96. International Indian Statistical Association Conference, Oregon State University, Corvallis, OR, Aug 20, 2016
97. Joint Statistical Meetings, Chicago, IL, Aug 2, 2016
98. 1st UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 22, 2016
99. The 3rd Taihu International Statistics Forum, Shanghai, China, Jul 10, 2016
100. The ICSA Conference on Data Science, Dali, China, Jul 3, 2016
101. Biological Big Data and Data Mining Workshop, Chinese Academy of Sciences, Beijing, China, Jun 25, 2016
102. ICSA Applied Statistics Symposium, Atlanta, GA, Jun 13, 2016
103. UCLA QCB 1st Annual Symposium "Exploring the Frontiers of Biomedical Big Data," UCLA, Los Angeles, CA, Jun 1, 2016
104. The 14th Asia Pacific Bioinformatics Conference, San Francisco, CA, Jan 13, 2016
105. Joint Statistical Meetings, Seattle, WA, Aug 9, 2015
106. Cold Spring Harbor Laboratory Systems Biology Meeting: Global Regulation of Gene Expression, Rio Mar, Puerto Rico, Jan 29, 2015 (Poster Presentation)
107. The 7th RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, San Diego, CA, Nov 14, 2014
108. Joint Statistical Meetings, Boston, MA, Aug 6, 2014
109. EITA-New Media and Bio 2014, MIT, Cambridge, MA, Jul 31, 2014
110. The 9th ICSA International Conference: Challenges of Statistical Methods for Interdisciplinary Research and Big Data, Hong Kong Baptist University, Hong Kong, Dec 23, 2013
111. The 6th RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, Toronto, Canada, Nov 12, 2013
112. The 17th RECOMB (Annual International Conference on Research in Computational Molecular Biology), Beijing, China, Apr 8, 2013
113. UC Systemwide Bioengineering Symposium, Berkeley, CA, Jun 23, 2012
114. Joint mod/mouse/ENCODE AWG/PI meeting, MIT, Cambridge, MA, May 22, 2012
115. Bay Area RNA Club, UCSF, San Francisco, CA, Jan 25, 2012
116. Cold Spring Harbor Asia Conference: Bioinformatics of Human and Animal Genomics, Suzhou, China, Nov 17, 2011
117. Joint mod/ENCODE Consortia Meeting, Washington DC, May 23, 2011

PUBLIC TALKS

1. Exploring Your Universe at UCLA, Nov 5, 2023
2. "Arriving at the Junction of Statistics and Biology," Harvard Radcliffe Institute, Mar 8, 2023
3. Exploring Your Universe at UCLA, Nov 7, 2021
4. The Science Show with Robyn Williams at ABC Australia, May 23, 2020
5. Exploring Your Universe at UCLA, Nov 1, 2020

EDITORIAL BOARD & REVIEWING ACTIVITIES

EDITORIAL BOARD

2025–	Area Editor, *Annals of Applied Statistics*
2024–	Advisory Board, *Cell Systems*
2024–2025	Associate Editor, *Annals of Applied Statistics*
2023–	Editorial Board, *Genome Biology*
2022–	Associate Editor, *Journal of American Statistical Association (Applications & Case Studies)*
2021–	Editorial Board, *Physiological Genomics*
2020–	Guest Editor, *PLOS Computational Biology*
2020–	Management Committee, *Journal of Computational and Graphical Statistics*
2015–	Associate Editor, *PeerJ*
2014–	Review Editor, *Frontiers in Genetics*

REVIEWER FOR SCIENTIFIC JOURNALS

1. *Annals of Applied Statistics*
2. *Bioinformatics*
3. *Biometrics*
4. *Biostatistics*
5. *BMC Bioinformatics*
6. *BMC Genomics*
7. *BMC Medical Genomics*
8. *BMC Research Notes*
9. *Cell*
10. *Cell Systems*
11. *Communications Biology*
12. *Computational Biology and Chemistry*
13. *Computational Statistics and Data Analysis*
14. *Computers in Biology and Medicine*
15. *eLife*
16. *Frontiers in Genetics*
17. *F1000Research*
18. *Gene Reports*
19. *Genes*
20. *Genetics*
21. *Genome Biology*
22. *Genome Research*
23. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
24. *Journal of American Statistical Association*
25. *Journal of Machine Learning Research*
26. *Nature Biotechnology*
27. *Nature Communications*
28. *Nature Machine Intelligence*
29. *Nature Methods*
30. *Nucleic Acids Research*
31. *NAR Genomics and Bioinformatics*
32. *PeerJ*
33. *PLOS Computational Biology*
34. *Proceedings of the National Academy of Sciences of the United States of America*
35. *Science*
36. *Science Bulletin*
37. *Science Translational Medicine*
38. *Statistica Sinica*

39. *Statistical Applications in Genetics and Molecular Biology*
40. *Statistics and Its Interface*
41. *Statistics in Medicine*

CONSULTANT FOR FUNDING AGENCIES

2023–	External Scientific Consultants, NIGRI Molecular Phenotypes of Null Alleles in Cells (MorPhiC)
2022–	Program Consultant, NIH Human BioMolecular Atlas Program (HuBMAP)

REVIEWER FOR CONFERENCES

1. ISMB/ECCB 2025: the 32nd Conference on Intelligent Systems for Molecular Biology
2. ISMB 2024: the 31st Conference on Intelligent Systems for Molecular Biology
3. RECOMB 2024: the 87th International Conference on Research in Computational Molecular Biology
4. ISMB/ECCB 2023: the 30th Conference on Intelligent Systems for Molecular Biology
5. RECOMB 2023: the 27th International Conference on Research in Computational Molecular Biology
6. RSGDREAM 2022: the 14th annual RECOMB/ISCB Conference on Regulatory and Systems Genomics with DREAM Challenges
7. ISMB 2022: the 29th Conference on Intelligent Systems for Molecular Biology
8. RECOMB 2022: the 26th International Conference on Research in Computational Molecular Biology
9. ISMB/ECCB 2021: the 29th Conference on Intelligent Systems for Molecular Biology
10. ISMB 2020: the 28th Conference on Intelligent Systems for Molecular Biology
11. ISMB/ECCB 2019: the 27th Conference on Intelligent Systems for Molecular Biology
12. APBC 2019: the 17th Asia Pacific Bioinformatics Conference
13. ICIBM 2018: International Conference on Intelligent Biology and Medicine
14. APBC 2016: the 14th Asia Pacific Bioinformatics Conference

REVIEWER FOR GRANT APPLICATIONS

2023–2024	Reviewer, Harvard Radcliffe Fellowship Program
2022–2026	Standing Member, NIH GCAT Study Section
2022	Reviewer, NIH IMST (Interdisciplinary Molecular Sciences and Training) Study Section
2022	Reviewer, NSF DMS (Division of Mathematical Sciences) Review Panel
2021	Reviewer, NIH IMST (Interdisciplinary Molecular Sciences and Training) Study Section
2021	Reviewer, NSF DBI (Division of Biological Infrastructure) Review Panel
2021	Reviewer, NIH GCAT (Genomics, Computational Biology and Technology) Study Section
2021	Reviewer, NIH Common Fund Program Special Emphasis Panel
2021	Ad Hoc Reviewer, NSF DBI (Division of Biological Infrastructure) Review Panel
2021	Reviewer, UCLA Society of Hellman Fellows Selection Committee
2021	Reviewer, NIGMS ESI MIRA Study Section
2020	Reviewer, Davidson Fellows Scholarship Program
2020	Reviewer, NIGMS ESI MIRA Study Section
2020	Reviewer, NIH GCAT (Genomics, Computational Biology and Technology) Study Section
2019	Reviewer, NSF DBI (Division of Biological Infrastructure) Review Panel
2018	External Reviewer, NSERC (Natural Sciences and Engineering Research Council of Canada), Discovery Grants
2018	Reviewer, NIH GCAT (Genomics, Computational Biology and Technology) Study Section
2018	Reviewer, PhRMA Foundation Informatics Advisory Committee
2017	Reviewer, NSF DMS (Division of Mathematical Sciences) Review Panel
2016 – 2020	Reviewer, Hong Kong General Research Fund (GRF)
2016	Reviewer, NIH/NIEHS Review Panel
2016	Reviewer, Israel Science Foundation
2016	Reviewer, NSF IIS (Division of Information and Intelligent Systems) Review Panel

2015	Specialist Reviewer, DOD CDMRP (Department of Defense Congressionally Directed Medical Research Programs) Review Panel

REVIEWER FOR TENURE AND PROMOTION

2025	University of California, Berkeley
2025	Duke-NUS Medical School
2025	Indiana University
2025	Yale University (2)
2024	University of Chicago
2024	University of Virginia
2024	University of Texas, Dallas
2024	University of California, Riverside
2024	Georgia Institute of Technology
2024	University of California, Irvine
2024	University of Southern California
2024	Mayo Clinic
2024	Johns Hopkins University
2024	Hong Kong University
2024	Peking University
2024	Harvard Medical School
2024	University of Maryland
2024	Duke University
2024	Chinese University of Hong Kong
2023	Rutgers University
2023	The Pennsylvania State University
2023	The University of Sydney
2022	University of California, Davis
2022	George Washington University
2022	Johns Hopkins Bloomberg School of Public Health
2022	National University of Singapore
2021	Tsinghua University, China

REVIEWER FOR DISSERTATIONS

2024	The University of Malaya, Malaysia
2024	The University of Melbourne, Australia

PROFESSIONAL SERVICES

2026–2027	Program Chair, American Statistical Association (ASA) Section on Statistical Learning and Data Science (SLDS)
2025	Mentor, Biomedical Data Science Innovation Lab (BDSIL) “Quantitative Approaches in Spatial Multi-Omics for Guiding Personalized Medicine”
2025	Co-organizer, Cold Spring Harbor Asia Course “Computational Genomics”
2025	Proceedings Program Committee, RECOMB 2025 Conference
2024–2025	Program Committee Chair, STATGEN 2025 Conference
2024	Student Paper Award Review Committee, American Statistical Association (ASA) Section on Statistics in Genomics and Genetics (SSGG)
2024	Proceedings Program Committee, RECOMB 2024 Conference
2023	Machine Learning in Computational and Systems Biology (MLCSB) COSI Program Committee, ISMB/ECCB 2023 Conference

2023	Proceedings Program Committee, RECOMB 2023 Conference
2022	Program Committee, RSGDREAM 2022 Conference
2022	Proceedings Program Committee, ISMB 2022 Conference
2022	Proceedings Program Committee, RECOMB 2022 Conference
2021	Proceedings Program Committee, ISMB/ECCB 2021 Conference
2020–	Management Committee, Journal of Computational and Graphical Statistics
2020–	WNAR Award Planning Committee
2020	Proceedings Program Committee, ISMB 2020 Conference
2019–	WNAR Member Engagement Committee
2019	Proceedings Program Committee, ISMB/ECCB 2019 Conference
2018	Local Organizing Committee Chair, International Conference on Intelligent Biology and Medicine

PROFESSIONAL ACTIVITIES

1. Session Chair, Joint Statistical Meetings, Portland, Corvallis, OR, Aug 4–8, 2024
2. Moderator, COPSS-NISS Leadership Webinar on the Intersection of Statistics and Genomics, Mar 29, 2024
3. Leader, Oxford Global's Spatial Omics Discussion Group, Apr 4, 2023
4. Panelist, ASA Section on Statistical Genomics and Genetics NIH Grant Panel, Jan 31, 2023
5. Discussant, “How to Build a Career in Math” Workshop, The MSRI Celebration of Women in Mathematics, May 12, 2022
6. Panelist, ConnectEd Junior Scholar Panel, Apr 13, 2022
7. Moderator, NISS Virtual Academic Career Fair: Finding a Position During the Pandemic, Dec 9, 2020
8. Session Chair, International Indian Statistical Association Conference, Oregon State University, Corvallis, OR, Aug 18–21, 2016
9. Session Chair and Organizer, Joint Statistical Meetings, Chicago, IL, Jul 30–Aug 4, 2016
10. Session Chair, 14th Asia Pacific Bioinformatics Conference, San Francisco, CA, Jan 11–13, 2016
11. Session Chair, Joint Statistical Meetings, Seattle, WA, Aug 8–13, 2015
12. Participant, SAMSI (Statistical and Applied Mathematical Sciences Institute) Innovations Lab (35 participants selected from > 350 applications), Research Triangle Park, NC, Jul 20–24, 2015
13. Session Chair and Organizer, Joint Statistical Meetings, Boston, MA, Aug 2–8, 2014
14. Participant, Women in Statistics Conference, Research Triangle Park, NC, May 15–17, 2014
15. Participant, SAMSI Social Network Data: Collection and Analysis Workshop, Research Triangle Park, NC, Oct 21–23, 2013
16. Participant, IPAM (Institute of Pure and Applied Mathematics) “Mathematical and Computational Approaches in High-Throughput Genomics” Program, Los Angeles, CA, Fall 2011
17. Volunteer, ICSA (International Chinese Statistical Association) Applied Statistics Symposium, San Francisco, CA, Jun 21–24, 2009

UNIVERSITY SERVICES

2025	Search Committee, UCLA Department of Statistics and Data Science
2024	Ad Hoc Committee, UCLA Department of Biostatistics
2024	Ad Hoc Committee, UCLA Department of Statistics and Data Science
2024	Ph.D. Fellowship Committee, UCLA Department of Statistics and Data Science
2024–2027	Review Committee, UCLA Chancellor’s Award for Postdoctoral Research
2024	Faculty Review Committee, UCLA Eugene V. Cota-Robles and/or Graduate Opportunity Program (GOP)
2021,2024	Selection Committee, UCLA Queen’s Road Foundation Fellowship Program
2021–2022	Search Committee, UCLA Department of Statistics

2021–2022	Search Committee, UCLA Department of Biostatistics
2021–2022	Evaluation Committee of PhD Written Qualifying Exam, UCLA Department of Statistics
2021–2022	Committee on Data, Information Technology, and Privacy, UCLA
2021	Selection Committee, UCLA Society of Hellman Fellows
2020–	Executive Steering Committee, UCLA Bioinformatics Graduate Program
2020–	Diversity Committee, UCLA Physical Sciences Division
2020–2021	Program Faculty, UCLA Bruins in Genomics Summer Program
2020	Ad Hoc Committee, UCLA Department of Statistics
2019–	Advisory Committee, UCLA Computational and Systems Biology Program
2019–2020	Search Committee, UCLA Department of Statistics
2019–2020	Search Committee, UCLA Department of Biostatistics
2019–2020	Search Committee, UCLA Department of Computational Medicine
2019	Organization Committee, UCLA Computational Genomics Summer Institute
2019	Ad Hoc Committee, UCLA Department of Statistics
2018–	Seminar Committee, UCLA Bioinformatics Graduate Program
2018–2019	Search Committee, UCLA Department of Ecology and Evolutionary Biology
2018	Evaluating Computational Biology, Genomics and Medicine Landscape Committee, UCLA
2018	Ad Hoc Committee, UCLA Department of Statistics
2018	Admission Committee, UCLA Department of Statistics
2017–	Admission Committee, UCLA Bioinformatics Graduate Program
2017–	Advising Committee, UCLA Bioinformatics Graduate Program
2015–	Curriculum Committee, UCLA Bioinformatics Graduate Program
2014–2015	Organizer, UCLA Statistics Seminar Series
2014–2015	Search Committee, UCLA Department of Statistics

UNIVERSITY ACTIVITIES

1. Program Faculty, UCLA Computational Genomics Summer Institute, Jul 15–Aug 2, 2024
2. Speaker, UCLA Exploring Your Universe, Nov 5, 2023
3. Program Faculty, UCLA Computational Genomics Summer Institute, Jul 17–Aug 4, 2023
4. Program Faculty, UCLA Computational Genomics Summer Institute, Jul 11–29, 2022
5. Speaker, UCLA Exploring Your Universe, Nov 7, 2021
6. Participant, UCLA Advancing Faculty Research Mentoring Workshop, Apr 16 & 23, 2021
7. Speaker, UCLA Exploring Your Universe, Nov 1, 2020
8. Program Faculty, UCLA Computational Genomics Summer Institute, Jul 15–Aug 7, 2019
9. Program Faculty, UCLA Computational Genomics Summer Institute, Jul 11–Aug 3, 2018
10. Program Faculty, UCLA Computational Genomics Summer Institute, Jul 6–20, 2017
11. Program Faculty, UCLA Computational Genomics Summer Institute, Jul 18–Aug 12, 2016
12. Participant, UCLA CEILS (Center for Education Innovation & Learning in the Sciences) Faculty Workshop on Best Practices in Teaching, Sep 17, 2015
13. Participant, UCLA Success in Science Workshop, Oxnard, CA, Feb 5–7, 2015

PROFESSIONAL AFFILIATIONS

2022–	Institute of Mathematical Statistics
2019–	ASA (American Statistical Association)
2019–	WNAR (Western North American Region of the International Biometrics Society)
2018–2019	IBS (International Biometric Society)
2013–	ISCB (International Society for Computational Biology)
2009–	ICSA (International Chinese Statistical Association)