Jingyi Jessica Li

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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:

- 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
- Labeling ambiguity issue in multi-class classification
- P-value-free control of false discovery rates
- Synthetic control data generation

POSITIONS

2022–	Professor, University of California, Los Angeles
2019–2022	Associate Professor (tenured), University of California, Los Angeles
2013–2019	Assistant Professor, University of California, Los Angeles

Department of Statistics (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

2023	Overton Prize, International Society for Computational Biology (ISCB)
2023	Emerging Leader Award, Committee of Presidents of Statistical Societies (COPSS)
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, 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

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”

Single-Cell Biology Data Insights Grant (PI: Li) **07/01/2022 – 12/31/2023**
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 $1,848,665
“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 – 06/31/2024**
NSF $240,000 (Li: $120,000)
“Collaborative Research: Development of classification theory and methods for objective asymmetry, sample size limitation, labeling ambiguity, and feature importance”

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”

DBI 1846216 (PI: Li) **07/01/2019 – 06/30/2024**
NSF $611,614 ($12,000 REU supp)
“CAREER: Advancing the bioinformatic infrastructure and methodology for single-cell RNA sequencing”

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”

COMPLETED

R01 GM120507 (PI: Li) **09/01/2016 – 05/31/2022**
NIH / NIGMS $1,667,725
“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 $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 $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

* co-first authors $^+$ corresponding authors __ trainees

RESEARCH PAPERS

PUBLISHED / ACCEPTED

1. Wang, L., Wang, Y.X.R., **Li, J.J.**, and Tong, X. (2022). Hierarchical Neyman-Pearson classification for prioritizing severe disease categories in COVID-19 patient data. ***Journal of American Statistical Association*** accepted. arXiv preprint.

2. Xia, L., Lee, C., and **Li, J.J.**$^+$ (2023). scDEED: a statistical method for detecting dubious 2D single-cell embeddings. ***Nature Communications*** accepted. bioRxiv preprint.

3. Yan, G., Song, D., and **Li, J.J.**$^+$ (2023). scReadSim: a single-cell RNA-seq and ATAC-seq read simulator. ***Nature Communications*** accepted. bioRxiv preprint.

4. 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.

5. Song, D., Wang, Q., Yan, G., Liu, T., and **Li, J.J.**$^+$ (2023). scDesign3 generates realistic in silico data for multimodal single-cell and spatial omics. ***Nature Biotechnology***.

6. 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.

7. 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.

8. 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.

9. 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

10. 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.

11. 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.

12. 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.

13. 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.

14. 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.

15. Li, Y.*, Ge, X.*, Peng, F., Li, W.$^{+}$, and **Li, J.J.$^{+}$** (2022). A large-sample crisis? Exaggerated false positives by popular differential expression methods. ***Genome Biology*** 23:79.

16. 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).

17. 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.

18. 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.

19. 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.

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

21. 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.

22. **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.

23. 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

24. 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

25. 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.

26. 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.

27. 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.

28. 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.

29. 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.

30. 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.

31. 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.

32. 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.

33. 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.

34. 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

35. **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.

36. 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

37. 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.

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

39. 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.

40. 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.

41. 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.

42. 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.

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

44. 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.

45. 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.

46. **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

47. 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.

48. 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.

49. 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.

50. 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.

51. Ye, Y. and **Li, J.J.$^{+}$** (2016). NMFP: a non-negative matrix factorization based preselection method to increase accuracy of identifying mRNA isoforms from RNA-seq data. ***BMC Genomics*** 17(Supp 1):11.

52. 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.

53. Liu, Z., Dai, S., Bones, J., Ray, S., Cha, S., Karger, B. L., **Li, J.J.**, Wilson, L., Hinckle, G., and Rossomando, A. (2015). A quantitative proteomic analysis of cellular responses to high glucose media in Chinese hamster ovary cells. ***Biotechnology Progress*** 31(4):1026–1038.

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

55. 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.

56. Boyle, A., Araya, C., Brdlik, C., Cayting, P., Cheng, C., Cheng, Y., Gardner, K., Hillier, L., Janette, J., Jiang, L., Kasper, D., Kawli, T., Kheradpour, P., Kundaje, A., **Li, J.J.**, and 25 other authors from the modENCODE and ENCODE consortia (2014). Comparative analysis of regulatory information and circuits across distant species. ***Nature*** 512(7515):453–456.

57. **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

58. **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

59. Fisher, W.W., **Li, J.J.**, Hammonds, A.S., Brown, J.B., Pfeiffer, B., Weiszmann, R., MacArthur, S., Thomas, S., Stamatoyannopoulos, J.A., Eisen, M.B., Bickel, P.B., Biggin, M.D., and Celniker, S.E. (2012). DNA regions bound at low occupancy by transcription factors do not drive patterned reporter gene expression in Drosophila. ***Proc Natl Acad Sci. USA*** 109(52):21330–21335.

60. The ENCODE Project Consortium (2012). An integrated encyclopedia of DNA elements in the human genome. ***Nature*** 489(7414):57–74.

61. 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.

62. Li, J., **Li, J.**, and Chen, B. (2012). Oct4 was a novel target of Wnt signaling pathway. ***Molecular and Cellular Biochemistry*** 362:233–240.

63. **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.

64. 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

SUBMITTED

65. <u>Song, D.</u>*, <u>Li, K.</u>*, <u>Ge, X.</u>, and **Li, J.J.**$^+$ (2023). ClusterDE: a post-clustering differential expression (DE) method robust to false-positive inflation caused by double dipping. ***Nature Biotechnology*** under review.

66. <u>Wang, W.</u>*, <u>Cen, Y.</u>*, Lu, Z.*, Xu, Y., <u>Sun, T.</u>, Xiao, Y., Liu, W., **Li, J.J.**$^+$, and Wang, C.$^+$ (2023). scCDC: a computational method for gene-specific contamination detection and correction in single-cell and single-nucleus RNA-seq data. ***Genome Biology*** under revision. bioRxiv preprint.

67. <u>Chen, Y.</u>, McDermott, M., Woyshner, K., Wang, L.D., and **Li, J.J.**$^+$ (2021). 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*** under revision. bioRxiv preprint.

68. **Li, J.J.**$^+$, Tong, X., and Bickel, P.J. (2019). Generalized Pearson correlation squares for a mixture of bivariate linear dependences. ***Journal of American Statistical Association*** under revision. arXiv preprint.

MANUSCRIPTS

69. 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

70. **Li, J.J.**$^+$ (2023). How the Monty Hall problem is similar to the false discovery rate in high-throughput data analysis. ***Nature Biotechnology***.

71. 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.

72. 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.

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

74. **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.

75. **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.

76. 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.

77. 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

78. **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.

79. **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

80. **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

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

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

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

ADVISING

MENTOR' AWARDS

2021	Bruins in Genomics Summer Research Program Outstanding Mentorship Award

MENTEES’ AWARDS

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 received the National Science Foundation Graduate Research Fellowship
2023	Dongyuan Song won 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. Saidi Wang	2022–2023	
2. Xinzhou Ge	2021–2023	Will be Assistant Professor of Statistics at Oregon State University

PHD STUDENTS

1. Chengfeng Jiang	2022–	UCLA Statistics
2. Zhiqian Zhai	2021–	UCLA Statistics
3. Qingyang Wang	2021–	UCLA Statistics
4. Chris Dong	2020–	UCLA Statistics
5. Guan’ao Yan	2020–	UCLA Statistics
6. Dongyuan Song	2019–	UCLA Bioinformatics
7. Wenbin Guo	2018–2021	UCLA Bioinformatics

8. Heather J. Zhou	2018–	UCLA Statistics
9. Kexin Li	2018–	UCLA Statistics
10. Tianyi Sun	2017–	UCLA Statistics
11. Nan Xi	2016–2021	UCLA Statistics; Currently Assistant Professor of Statistics at Loyola University of Chicago
12. Ruochen Jiang	2016–2021	UCLA Statistics; Currently Bioinformatics Scientist at Veracyte, Inc.
13. Xinzhou Ge	2016–2021	UCLA Statistics; Currently Postdoctoral Researcher at UCLA
14. Yiling Chen	2016–2021	UCLA Statistics; Currently Scientist at Genentech
15. Jiaping Zhu	2015–2021	UCLA Statistics
16. Yidan Sun	2015–2021	UCLA Statistics; Currently Visiting Assistant Professor of Statistics at UC Santa Barbara
17. Wei (Vivian) Li	2014–2019	UCLA Statistics; Currently Assistant Professor of Statistics at UC Riverside
18. Zahra Razaee	2014–2017	UCLA Statistics; Currently Postdoctoral Scientist at Cedars-Sinai Medical Center

MS STUDENTS

1. Christy Lee	2021–	UCLA Statistics
2. Tianyang Liu	2020–2022	UCLA Applied Statistics
3. Xiaoru Zheng	2019–2020	UCLA Statistics
4. Yingqi Li	2019–2020	UCLA Statistics
5. Tianyi Xia	2018–2019	UCLA Statistics
6. Yu-Cheng Yang	2016–2017	UCLA Statistics; Currently Assistant Professor at Fudan University, China
7. Surui Sun	2015–2017	UCLA Statistics
8. 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

UNDERGRADUATE STUDENTS

1. Lehan Zou	2022	Statistics major at UCLA
2. Shiyu Ma	2022	Applied Math and Statistics major at UCLA
3. Weijian Wang	2022	Visiting student from Zhejiang University, China
4. Yihui Cen	2022	Visiting student from Zhejiang University, China
5. Shuo Hua	2022	Visiting student from Tsinghua University, China
6. Qiuran Lyu	2022	Visiting student from Renmin University, China
7. Lucia Ramirez	2021	Bruins in Genomics Summer Program
8. Zhengtong Liu	2020–2022	Applied Math and CS major at UCLA
9. Melody Zhang	2020–2021	Biology major at UCLA
10. Huy Nguyen	2020–2022	Statistics major at UCLA
11. Jingfei Fang	2020	Math of Computational major at UCLA
12. Manasvi Malepati	2020	Bruins in Genomics Summer Program

13. Wenchu Pan	2019	Visiting student from Peking University, China
14. Xindi Lin	2019	CSST student from Zhejiang University, China
15. Dehong Xu	2018	CSST student from Beijing University of Posts and Telecommunications
16. Mayra Varillas	2017	Bruins in Genomics Summer Program
17. Tiffany Tu	2017	Bruins in Genomics Summer Program
18. Kexin Li	2017	Visiting student from Tsinghua University, China
19. Yue Cui	2016–2017	Statistics major at UCLA
20. Longsheng Qian	2016–2017	Math/Econ major at UCLA
21. Qianhao Yu	2016–2017	Applied Math & Statistics major at UCLA
22. Jingwei Song	2016–2017	Statistics major at UCLA
23. Yumeng Ma	2016	Visiting student from Tsinghua University, China
24. Tianyi Sun	2016	Visiting student from Tsinghua University, China
25. Yushi Tang	2016	CSST student from Peking University, China
26. Yuqi Tian	2016	Summer student from Xiamen University, China
27. Yiling Chen	2015–2016	Math/Applied Science major at UCLA
28. Yimeng Jia	2015–2016	Statistics major at UCLA
29. Jason Mao	2015–2016	Statistics major at UCLA
30. Ruiqi Gao	2015–2016	Visiting student from Peking University, China
31. Xin Xu	2014–2015	CSST student from Nankai University, China
32. Yuting Ye	2014–2015	Visiting student from Tsinghua University, China
33. Chang Ding	Spring, Fall 2014	Mathematics/Economics major at UCLA

THESIS COMMITTEES

PhD in Statistics:

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

PhD in other majors:

1. Helena Kanya Winata	2023–	Bioinformatics
2. Jingyuan Fu	2023–	Computer Science
3. Aina M.I. Zurita	2023–	Human Genetics
4. Arielle Hogan	2023–	Neuroscience
5. Apeksha Sudha Singh	2023–	Biomathematics
6. Jonathan Perrie	2022–	Bioinformatics
7. Jack Freeland	2022–	Molecular Biology
8. Runjia Li	2021–	Bioinformatics
9. Shuya Wang	2021–	Molecular Biology
10. Russell Littman	2020–2022	Bioinformatics

11.	Zhixin (Cyrillus) Tan	2020–	Bioinformatics
12.	Matias A. Rojas Leon	2020–2022	Civil Engineering
13.	Shuochuan Meng	2019–	Civil Engineering
14.	Leah Briscoe	2019–	Bioinformatics
15.	Thai Ha Vu	2019–	Bioinformatics
16.	Alec Matthew Chiu	2019–	Bioinformatics
17.	Mina Shahi	2019–	Bioengineering
18.	Dat Bach Duong	2018–2020	Computer Science
19.	Soo Bin Kwon	2018–2021	Bioinformatics
20.	Xingquan Guan	2018–2021	Civil Engineering
21.	Feiyang Ma	2018–2020	Molecular Biology
22.	Kikuye Koyano	2018–2021	Bioinformatics
23.	Xinhui Zhang	2017–	Biology
24.	Qin An	2017–2020	Human Genetics
25.	Zong Miao	2016–2020	Bioinformatics
26.	Hung-Hao Lo	2016–2019	Molecular Biology
27.	Jui-Ting Ju	2016–2019	Computer Science
28.	Sepideh Mazrouee	2016–2017	Computer Science
29.	Shanxi Jiang	2015–2018	Molecular, Cellular, and Integrative Physiology
30.	Yun-Hua Hsiao	2014–2018	Bioengineering

MS in Statistics:

1.	Bill Li	2022
2.	Sixuan Li	2021
3.	Ashley Kathleen Chiu	2021
4.	Juan Piao	2021
5.	Ritvik Yogesh Kharkar	2020
6.	Zijun Zhang	2019
7.	Yu Zhang	2019
8.	Shuai Zhu	2019
9.	Hua Kang	2018
10.	Maxim Ananyev	2018
11.	Soo Woo Choi	2017
12.	Yiwei Xu	2017
13.	Chufeng Hu	2017
14.	Qian Xiao	2015
15.	Muzhou Liang	2015
16.	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

INVITED TALKS & PRESENTATIONS

KEYNOTE PRESENTATIONS

1. The 15th RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges (RSGDREAM), Los Angeles, CA, Nov 28-29, 2023 (scheduled)
2. The joint GIW 2023 and ISCB-Asia VI Conference, Singapore, Nov 18-21, 2023 (scheduled)
3. 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
4. The 21st Asia Pacific Bioinformatics Conference, Changsha, Hunan, China, Apr 15, 2023
5. The 8th National Conference on Bioinformatics and Systems Biology of China and the 1st (Macao) International Bioinformatics Symposium, Macao, Oct 23, 2018

CONFERENCE AND SYMPOSIUM PRESENTATIONS

6. Frontiers in Single Cell Genomics, Cold Spring Harbor Asia, Suzhou, China, Dec 4-8, 2023 (scheduled)
7. Computational Era of Life Sciences , EU-US Frontiers of Engineering Symposium, Murray Hill, NJ, Oct 15-18, 2023 (scheduled)
8. The Conceptual Power of Single Cell Biology, Cell Symposia, San Diego, CA, Aug 28-30, 2023 (scheduled)
9. Invited Talk, Joint Statistical Meetings, Toronto, ON, Aug 9, 2023
10. Single-Cell Plus - Data Science Challenges in Single-Cell Research, Banff International Research Station (BIRS) Workshop, Banff, AB, Jul 5, 2023
11. ICSA Applied Statistics Symposium, Ann Arbor, MI, Jun 14, 2023
12. Spatial Biology US, Jun 8, 2023
13. The 36th New England Statistics Symposium, Jun 5, 2023
14. Chan-Zuckerberg Initiative Single-Cell Data Insights Cycle 1 Symposium, Mar 10, 2023
15. Mapping the Brain Webinar, UCLA Institute for Quantitative and Computational Biosciences, Mar 1, 2023.
16. Spatial Biology & Spatial Omics, Informa Connect, Mar 1, 2023
17. Educational Series, NIH Bridge to Artificial Intelligence (Bridge2AI) Program, Feb 9, 2023
18. Two Invited Talks, The Plant and Animal Genome (PAG) Conference, San Diego, CA, Jan 13-18, 2023
19. Invited Talk, Biennial Conference of Chinese Biological Investigators Society (CBIS), Las Vegas, NV, Dec 19-22, 2022
20. NIDA’s SCORCH (Single Cell Opioid Responses in the Context of HIV) Program Analysis Working Group Meeting, Dec 1, 2022
21. Invited Talk, Emerging Methods in Translational Science: Contemporary Challenges in Prediction Modeling, Wake Forest School of Medicine, Nov 18, 2022
22. Invited Talk, Chan-Zuckerberg Initiative Single-Cell Biology Annual Meeting, San Jose, CA, Nov 14-18, 2022
23. Invited Talk, Mathematics and Statistics of Genomic Epidemiology, Banff International Research Station (BIRS)-Casa Matemática Oaxaca (CMO) Workshop, Nov 8, 2022
24. Invited Talk, 5th Annual Symposium on Multiscale Cell Fate, NSF-Simons Center for Multiscale Cell Fate Research, UC Irvine, CA, Oct 24, 2022
25. Invited Talk, Joint Statistical Meetings, Washington, D.C., Aug 11, 2022
26. 5th UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 29, 2022
27. Invited Talk, “Computational Challenges in Very Large-Scale 'Omics'” Workshop, Simons Institute for the Theory of Computing, Berkeley, CA, Jul 18-21, 2022
28. Chan-Zuckerberg Initiative Single-Cell Data Insights Kickoff Meeting, Jul 14, 2022
29. ICSA 2022 China Conference, Jul 1, 2022
30. CGM Online Seminar (https://cgmonline.co/), Jun 29, 2022
31. ICSA Applied Statistics Symposium, Gainesville, FL, Jun 21, 2022

32. 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
33. Invited Talk, "Statistics in the Big Data Era" Workshop, Simons Institute for the Theory of Computing, Berkeley, CA, Jun 2, 2022
34. Host and Speaker, Young Bioinformatics PI Seminar Series, May 27, 2022
35. Invited Talk, USC Computational Biology Symposium, May 22, 2022
36. Discussant, International Seminar on Selective Inference, Nov 11, 2021
37. Invited Talk, The 6th Annual MidAtlantic Bioinformatics Conference, Nov 8, 2021
38. ICSA Applied Statistics Symposium, Sep 12, 2021
39. Invited Talk, Joint Statistical Meetings, Aug 12, 2021
40. Invited Talk, The 8th Young Scholar Forum of Interdisciplinary Research of Mathematics, Computer Science, and Life Science, Chinese Academy of Sciences, May 15, 2021
41. ICSA Applied Statistics Symposium, Dec 15, 2020
42. International Seminar on Selective Inference, Dec 3, 2020
43. Invited Talk, Mathematics and Statistics of Genomic Epidemiology, Banff International Research Station (BIRS)- Casa Matemática Oaxaca (CMO) Workshop, Nov 11, 2020
44. Human Cell Atlas Asia Meeting, Oct 22, 2020
45. Invited Talk, Joint Statistical Meetings, Aug 6, 2020
46. ENAR 2020 Spring Meeting, Mar 25, 2020
47. The 11th ICSA International Conference, Zhejiang University, Hangzhou, China, Dec 20, 2019
48. Joint Statistical Meetings, Denver, CO, Jul 31, 2019
49. 4th UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 18, 2019
50. The 27th Conference on Intelligent Systems for Molecular Biology (ISMB) and the 18th European Conference on Computational Biology (ECCB), Basel, Switzerland, Jul 23, 2019
51. Invited Talk, Single-cell Data in Space and Time: Mathematical and Computational Challenges, Imperial College London, London, UK, Jun 17, 2019
52. The Data Science Expo, Los Angeles, CA, May 18, 2019
53. ENAR 2019 Spring Meeting, Mar 25, 2019
54. Invited Talk, Frontiers in Single-cell Technology, Application and Data Analysis, Banff International Research Station (BIRS) Workshop, Banff, AB, Feb 27, 2019
55. The 8th Annual Southern California Systems Biology Conference, University of California at Irvine, CA, Feb 9, 2019
56. ICSA Conference on Data Science, Xishuangbanna, China, Jan 12, 2019
57. DahShu Virtual Journal Club, Nov 16, 2018
58. 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
59. Joint Statistical Meetings, Vancouver, BC, Aug 1, 2018
60. 3rd UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 17, 2018
61. 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
62. The 5th International Biostatistics Symposium, Guangzhou, China, Jul 7, 2018
63. ICSA China Conference with the Focus on Data Science, Qingdao, China, Jul 4, 2018
64. ICSA Applied Statistics Symposium, New Brunswick, NJ, Jun 16, 2018
65. The 46th Annual Meeting of the Statistical Society of Canada, McGill University, Montreal, QB, Canada, Jun 5, 2018
66. 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
67. DahShu Virtual Journal Club, Apr 30, 2018
68. Johnson & Johnson WiSTEM2D Symposium, New Brunswick, NJ, Apr 26, 2018
69. Highlight Talk at the 22nd International Conference on Research in Computational Molecular Biology (RECOMB), Paris, France, Apr 24, 2018
70. Joint Statistical Meetings, Baltimore, MD, Aug 3, 2017

71. The 1st North American Social Networks (NASN) Conference, Washington, D.C., Jul 28, 2017
72. 2nd UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 24, 2017
73. ICSA Applied Statistics Symposium, Chicago, IL, Jun 26, 2017
74. HDDA VII (The 7th International Workshop on Perspectives on High-dimensional Data Analysis), CIMAT, Guanajuato, Mexico, Jun 18, 2017
75. UCLA QCB 2nd Annual Symposium "Exploring the Frontiers of Biomedical Big Data," UCLA, Los Angeles, CA, Apr 28, 2017
76. Workshop "Harnessing Big Data for Precision Medicine: Infrastructure and Applications," Pacific Symposium on Biocomputing (PSB), The Big Island of Hawaii, HI, Jan 3, 2017
77. The 10th ICSA International Conference: Global Growth of Modern Statistics in the 21st Century, Shanghai Jiaotong University, Shanghai, China, Dec 20, 2016
78. International Indian Statistical Association Conference, Oregon State University, Corvallis, OR, Aug 20, 2016
79. Joint Statistical Meetings, Chicago, IL, Aug 2, 2016
80. 1st UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 22, 2016
81. The 3rd Taihu International Statistics Forum, Shanghai, China, Jul 10, 2016
82. The ICSA Conference on Data Science, Dali, China, Jul 3, 2016
83. Biological Big Data and Data Mining Workshop, Chinese Academy of Sciences, Beijing, China, Jun 25, 2016
84. ICSA Applied Statistics Symposium, Atlanta, GA, Jun 13, 2016
85. UCLA QCB 1st Annual Symposium "Exploring the Frontiers of Biomedical Big Data," UCLA, Los Angeles, CA, Jun 1, 2016
86. The 14th Asia Pacific Bioinformatics Conference, San Francisco, CA, Jan 13, 2016
87. Joint Statistical Meetings, Seattle, WA, Aug 9, 2015
88. Cold Spring Harbor Laboratory Systems Biology Meeting: Global Regulation of Gene Expression, Rio Mar, Puerto Rico, Jan 29, 2015 (Poster Presentation)
89. The 7th RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, San Diego, CA, Nov 14, 2014
90. Joint Statistical Meetings, Boston, MA, Aug 6, 2014
91. EITA-New Media and Bio 2014, MIT, Cambridge, MA, Jul 31, 2014
92. The 9th ICSA International Conference: Challenges of Statistical Methods for Interdisciplinary Research and Big Data, Hong Kong Baptist University, Hong Kong, Dec 23, 2013
93. The 6th RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, Toronto, Canada, Nov 12, 2013
94. The 17th RECOMB (Annual International Conference on Research in Computational Molecular Biology), Beijing, China, Apr 8, 2013
95. UC Systemwide Bioengineering Symposium, Berkeley, CA, Jun 23, 2012
96. Joint mod/mouse/ENCODE AWG/PI meeting, MIT, Cambridge, MA, May 22, 2012
97. Bay Area RNA Club, UCSF, San Francisco, CA, Jan 25, 2012
98. Cold Spring Harbor Asia Conference: Bioinformatics of Human and Animal Genomics, Suzhou, China, Nov 17, 2011
99. Joint mod/ENCODE Consortia Meeting, Washington DC, May 23, 2011

SEMINAR PRESENTATIONS AT UNIVERSITIES AND RESEARCH INSTITUTES

1. Department of Statistics, University of California, Riverside, CA, Apr 2, 2024 (scheduled)
2. Computational Biology and Bioinformatics Program, Duke University, Durham, NC, Mar 25, 2024 (scheduled)
3. Computational Biology Department, Carnegie Mellon University, Pittsburgh, PA, Nov 10, 2023 (scheduled)
4. Department of Computational Biomedicine, Cedars-Sinai Medical Center, Los Angeles, CA, Nov 8, 2023 (scheduled)

5. Department of Biostatistics, Vanderbilt University, Nashville, TN, Oct 25, 2023 (scheduled)
6. Department of Biomedical Engineering, Johns Hopkins University, Baltimore, MD, Oct 23, 2023 (scheduled)
7. Department of Biostatistics and Bioinformatics, Emory University, Atlanta, GA, Oct 19, 2023 (scheduled)
8. Department of Statistics, Purdue University, West Lafayette, IN, Oct 13, 2023 (scheduled)
9. Michelson Center for Convergent Biosciences, University of Southern California, Los Angeles, CA, Sep 22, 2023
10. Center of Computational Biology and Bioinformatics, Penn State University, State College, PA, Aug 23, 2023
11. French National Centre for Scientific Research (Centre National de la Recherche Scientifique (CNRS)), Grenoble, France, Jul 27, 2023
12. Special Seminar, University of Virginia, Charlottesville, VA, Jun 22, 2023
13. Microsoft Research New England, Cambridge, MA, Jun 7, 2023
14. Department of Statistics, Colorado State University, Fort Collins, CO, May 1, 2023
15. The Jackson Laboratory for Genomic Medicine, Farmington, CT, Mar 14, 2023
16. Department of Molecular and Systems Biology, Geisel School of Medicine, Dartmouth College, Hanover, NH, Feb 27, 2023
17. The Center for Computational & Genomic Medicine (CCGM), The Children's Hospital of Philadelphia (CHOP), Philadelphia, PA, Feb 8, 2023
18. Bioinformatics Interdepartmental Ph.D. Program, University of California, Los Angeles, CA, Feb 6, 2023
19. Center for Multiscale Cell Fate (CMCF) MathBio Seminar, University of California, Irvine, CA, Jan 19, 2023
20. Department of Biostatistics, MD Anderson Cancer Center, Houston, TX, Dec 14, 2022
21. Technology Assessment in Health Care Seminar, Harvard University, Cambridge, MA, Dec 1, 2022
22. Department of Statistics, Michigan State University, East Lansing, MI, Nov 22, 2022
23. Genome Sciences Seminar Series, Center for Public Health Genomics, University of Virginia, Charlottesville, VA, Nov 9, 2022
24. Data Matters Seminar Series, Data Science Initiative and Center for Computational Molecular Biology, Brown University, Providence, RI, Oct 27, 2022
25. Department of Biostatistics, Columbia University, New York, NY, Oct 20, 2022
26. The Herbert and Florence Irving Institute for Cancer Dynamics (IICD), Columbia University, New York, NY, Oct 19, 2022
27. Department of Statistics, University of Missouri, Columbia, MO, Oct 17, 2022
28. Department of Biostatistics, Yale University, New Haven, CT, Oct 11, 2022
29. Center for Biomedical Informatics and Genomics, Tulane University, New Orleans, LA, Oct 5, 2022
30. Department of Statistics, Oregon State University, Corvallis, OR, Oct 3, 2022
31. Department of Systems Biology, City of Hope, Duarte, CA, Sep 29, 2022
32. Department of Biostatistics, University of Nebraska Medical Center, Omaha, NE, Apr 1, 2022
33. Department of Biomedical Data Science, Stanford University, Stanford, CA., Feb 22, 2022
34. Department of Data Science and Operations, University of Southern California, Los Angeles, CA, Dec 3, 2021
35. Department of Statistics, George Washington University, Washington, D.C., Nov 19, 2021
36. Bioinformatics Seminar, School of Mathematics and Statistics, University of Sydney, Aug 16, 2021
37. Department of Biostatistics, University of Michigan, Ann Arbor, MI, Apr 1, 2021
38. Department of Statistics, Chinese University of Hong Kong, Hong Kong, Mar 29, 2021
39. Department of Biostatistics, University of Pennsylvania, Philadelphia, PA, Mar 23, 2021
40. Neyman Seminar, Department of Statistics, University of California, Berkeley, CA, Feb 3, 2021
41. Department of Statistics, University of Illinois at Urbana-Champaign, IL, Aug 27, 2020
42. Interdisciplinary Center for Quantitative Modeling in Biology, University of California, Riverside, CA, Feb 12, 2020

43. Biomed-X Research Seminar, Zhejiang University-University of Edinburgh Institute, Haining, China, Dec 23, 2019
44. Department of Statistics, University of California, Santa Barbara, CA, Oct 9, 2019
45. Computational and Systems Biology Seminar, Lyda Hill Department of Bioinformatics, The University of Texas Southwestern Medical Center, Dallas, TX, Sep 23, 2019
46. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Aug 30, 2019
47. The Comprehensive Cancer Center, Cancer Immunotherapeutics Program & Department of Immuno-Oncology, City of Hope, Duarte, CA, Mar 15, 2019
48. Department of Statistics and Actuarial Science, Simon Fraser University, Vancouver, BC, Feb 22, 2019
49. Department of Statistics, The University of British Columbia, Vancouver, BC, Feb 21, 2019
50. Department of Mathematics, California State University, Northridge, Feb 20, 2019
51. State Key Laboratory of Biotherapy, Sichuan University, Chengdu, China, Jan 23, 2019
52. School of Life Sciences, Tsinghua University, Beijing, China, Jan 18, 2019
53. Center for Statistical Science, Tsinghua University, Beijing, China, Jan 17, 2019
54. The First Affiliated Hospital, Sun Yat-Sen University, Guangzhou, China, Jan 14, 2019
55. Department of Biostatistics, University of Pittsburgh, Nov 1, 2018
56. Department of Biomathematics, University of California, Los Angeles, Oct 4, 2018
57. Omics Seminar, Cedars-Sinai Medical Center, Los Angeles, CA, Sep 25, 2018
58. Department of Statistics, University of Georgia, Athens, GA, Aug 23, 2018
59. Bioinformatics Interdepartmental Ph.D. Program, University of California, Los Angeles, CA, Apr 9, 2018
60. Physical Sciences Faculty Lunch Seminar, College of Letters and Sciences, University of California, Los Angeles, CA, Mar 19, 2018
61. Department of Biostatistics, Ohio State University, Columbus, OH, Feb 23, 2018
62. Department of Statistics, University of California, Los Angeles, CA, Jan 17, 2018
63. Medical and Population Genomics Seminar, University of California, Los Angeles, CA, Dec 6, 2017
64. Medical and Population Genomics Seminar, University of California, Los Angeles, CA, May 24, 2017
65. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jul 4, 2017
66. Center for Statistical Science, Tsinghua University, Beijing, China, Jul 3, 2017
67. School of Life Sciences, Tsinghua University, Beijing, China, Jul 3, 2017
68. Institute of Machine Learning and Systems Biology, Tongji University, Shanghai, China, Dec 21, 2016
69. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jun 24, 2016
70. Faculty Research Lunch Series, Quantitative and Computational Biosciences, University of California, Los Angeles, CA, May 6, 2016
71. Department of Data Sciences and Operations, Marshall School of Business, University of Southern California, Los Angeles, CA, Dec 4, 2015
72. Genomics Seminar, Johns Hopkins University, Baltimore, MD, Nov 17, 2015
73. Jonsson Comprehensive Cancer Center Gene Regulation Intramural Meeting, University of California, Los Angeles, CA, May 5, 2015
74. Department of Statistics, University of California, Riverside, CA, Feb 24, 2015
75. Department of Ecology and Evolutionary Biology, University of California, Los Angeles, CA, Feb 18, 2015
76. Department of Statistics, Pennsylvania State University, State College, PA, Jan 22, 2015
77. Center for Systems Genomics, Pennsylvania State University, State College, PA, Jan 21, 2015
78. Department of Biostatistics, University of California, Los Angeles, CA, November 19, 2014
79. MOE Key Laboratory of Bioinformatics and Bioinformatics Division, TNLIST / Department of Automation, Tsinghua University, Beijing, China, Jun 20, 2014

80. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jun 19, 2014
81. Department of Statistics, Columbia University, NY, May 1, 2014
82. Department of Molecular and Computational Biology, University of Southern California, CA, Mar 6, 2014
83. Department of Statistics, University of California, Los Angeles, CA, Jan 14, 2014
84. School of Life Sciences, Tsinghua University, Beijing, China, Dec 13, 2013
85. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Apr 11, 2013
86. Department of Statistics, University of Chicago, IL, Feb 25, 2013
87. Departments of Human Genetics and Statistics, University of California, Los Angeles, CA, Feb 1, 2013
88. Department of Statistics, University of California, Davis, CA, Jan 16, 2013

PUBLIC TALKS

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

EDITORIAL BOARD & REVIEWING ACTIVITIES

EDITORIAL BOARD

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

2022–	Program Consultant, The NIH Human BioMolecular Atlas Program (HuBMAP)

REVIEWER FOR CONFERENCES

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

REVIEWER FOR GRANT APPLICATIONS

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

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

PROFESSIONAL SERVICE

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, Queen's Road Foundation Fellowship Program
2021	Selection Committee, UCLA Society of Hellman Fellows
2020	Ad Hoc Committee, UCLA Department of Statistics
2020–	WNAR Award Planning Committee
2020–	Executive Steering Committee, UCLA Bioinformatics Graduate Program
2020–	Diversity Committee, UCLA Physical Sciences Division
2020–	Management Committee, Journal of Computational and Graphical Statistics
2019–	WNAR Member Engagement Committee
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	Ad Hoc Committee, UCLA Department of Statistics
2019–	Advisory Committee, UCLA Computational and Systems Biology Program
2018–2019	Search Committee, UCLA Department of Ecology and Evolutionary Biology
2018	Local Organizing Committee Chair, International Conference on Intelligent Biology and Medicine
2018–	Seminar Committee, UCLA Bioinformatics Graduate Program
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 of UCLA Statistics Seminar Series
2014–2015	Search Committee, UCLA Department of Statistics

UNIVERSITY ACTIVITIES

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

OTHER PROFESSIONAL ACTIVITIES

1. Machine Learning in Computational and Systems Biology (MLCSB) COSI Program Committee of the ISMB/ECCB 2023 Conference
2. Proceedings Program Committee of the RECOMB 2023 Conference
3. Leader of Oxford Global's Spatial Omics Discussion Group, Apr 4, 2023
4. Panelist of ASA Section on Statistical Genomics and Genetics NIH Grant Panel, Jan 31, 2023
5. Program Committee of the RSGDREAM 2022 Conference
6. Discussant of “How to Build a Career in Math” Workshop, The MSRI Celebration of Women in Mathematics, 2022.
7. Proceedings Program Committee of the ISMB/ECCB 2021 Conference
8. Proceedings Program Committee of the RECOMB 2022 Conference
9. Panelist of ConnectEd Junior Scholar Panel, 2022
10. Proceedings Program Committee of the ISMB/ECCB 2021 Conference
11. Moderator of NISS Virtual Academic Career Fair: Finding a Position During the Pandemic, 2020
12. Proceedings Program Committee of the ISMB 2020 Conference
13. Proceedings Program Committee of the ISMB/ECCB 2019 Conference
14. Session Chair at the International Indian Statistical Association Conference, Oregon State University, Corvallis, OR, Aug 18-21, 2016
15. Session Chair and Organizer at the Joint Statistical Meetings, Chicago, IL, Jul 30-Aug 4, 2016
16. Session Chair at the 14th Asia Pacific Bioinformatics Conference, San Francisco, CA, Jan 11-13, 2016
17. Session Chair at the Joint Statistical Meetings, Seattle, WA, Aug 8-13, 2015
18. Participant in the SAMSI (Statistical and Applied Mathematical Sciences Institute) Innovations Lab (35 participants selected from > 350 applications), Research Triangle Park, NC, Jul 20-24, 2015
19. Session Chair and Organizer at the Joint Statistical Meetings, Boston, MA, Aug 2-8, 2014
20. Participant in the Women in Statistics Conference, Research Triangle Park, NC, May 15-17, 2014
21. Participant in the SAMSI Social Network Data: Collection and Analysis Workshop, Research Triangle Park, NC, Oct 21-23, 2013
22. Participant in the IPAM (Institute of Pure and Applied Mathematics) “Mathematical and Computational Approaches in High-Throughput Genomics” Program, Los Angeles, CA, Fall 2011

23. Volunteer in ICSA (International Chinese Statistical Association) Applied Statistics Symposium, San Francisco, CA, Jun 21-24, 2009

PROFESSIONAL AFFILIATIONS

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)