

# 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
- 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
- Novel statistical methods for imputing missing data or extracting hidden information from various types of genomics data
- 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
- P-value free control of false discovery rates
- Labeling ambiguity issue in multi-class classification

## EMPLOYMENT

2019 - 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 (QCB)  
 Gene Regulation Program Area, Jonsson Comprehensive Cancer Center  
 Director, Center of Statistical Research for Computational Biology (CSRCB)

## 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

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<sup>2</sup>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 top 1% student in each department),  
 Tsinghua University

## GRANTS

### CURRENT

**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 for REU supplement)

“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<sup>2</sup>D Scholar Award (PI: Li)**

**01/21/2018 – 01/21/2022**

Johnson & Johnson \$150,000

“Statistical modeling to quantitate the central dogma”

**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”

**COMPLETED**

**Physical Sciences Entrepreneurship and Innovation Fund (PSEIF) Fellowship**

**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”

<b>Hellman Fellows Award (PI: Li)</b>		<b>07/01/2015 – 06/30/2016</b>
Hellman Foundation	\$17,837	
“A new statistical measure to capture complex gene interactions from massive genomic data”		
<b>Faculty Career Development Award (PI: Li)</b>		<b>07/01/2015 – 06/30/2016</b>
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. Ge, X., Chen, Y.E., Song, D., McDermott, M., Woyshner, K., Manousopoulou, A., Wang, N., Li, W., Wang, L.D., and **Li, J.J.**<sup>+</sup> (2021). Clipper: p-value-free FDR control on high-throughput data from two conditions. *Genome Biology* 22:288.
2. 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.
3. Xi, N.M. and **Li, J.J.**<sup>+</sup> (2021). Protocol for executing and benchmarking eight computational doublet-detection methods in single-cell RNA sequencing data analysis. *STAR Protocols* 2(3):100699.
4. Jiang, R., Li, W.V., and **Li, J.J.**<sup>+</sup> (2021). An accurate and robust imputation method mblImpute for microbiome data. *Genome Biology* 22:192.
5. 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.
6. **Li, J.J.**, Chen, Y., Tong, X.<sup>+</sup> (2021). A flexible model-free prediction-based framework for feature ranking. *Journal of Machine Learning Research* 22(124):1-54.
7. Song, D., Li, K., Hemminger, Z., Wollman, R., and **Li, J.J.**<sup>+</sup> (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
8. Sun, T.Y., Song, D.Y., Li, W.V.<sup>+</sup>, and **Li, J.J.**<sup>+</sup> (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
9. Sun, Y.E., Zhou, H.J., and **Li, J.J.**<sup>+</sup> (2021). Bipartite tight spectral clustering (BiTSC) algorithm for identifying conserved gene co-clusters in two species. *Bioinformatics* 37(9):1225-1233.

10. 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** nyab089.
11. Song, D. and **Li, J.J.**<sup>+</sup> (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.
12. Xi, N.M. and **Li, J.J.**<sup>+</sup> (2021). Benchmarking computational doublet-detection methods for single-cell RNA sequencing data. **Cell Systems** 12:1-19.
13. 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** btab075.
14. 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.
15. 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.
16. Lyu, J.\*<sup>\*</sup>, **Li, J.J.**<sup>\*\*</sup>, Su, J., Peng, F., Chen, Y.E., Ge, X., and Li, W.<sup>+</sup> (2020). DORGE: Discovery of Oncogenes and tumor suppressor genes using Genetic and Epigenetic features. **Science Advances** 6(46):eaba6784.
17. 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.
18. **Li, J.J.**<sup>+</sup> and Tong, X. (2020). Statistical hypothesis testing versus machine-learning binary classification: distinctions and guidelines. **Patterns** 1(7):110115.
19. Liu, H., Xu, X., and **Li, J.J.**<sup>+</sup> (2020). A bootstrap lasso + partial ridge method to construct confidence intervals for parameters in high-dimensional sparse linear models. **Statistica Sinica** 30:1333-1355.
20. Li, W.V.<sup>\*</sup>, Li, S.\*<sup>\*</sup>, Tong, X., Deng, L., Shi, H.<sup>+</sup>, and **Li, J.J.**<sup>+</sup> (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
21. **Li, J.J.**<sup>+</sup>, Chew, G.L., and Biggin, M.D.<sup>+</sup> (2019). Quantitative principles of cis-translational control by general mRNA sequence features in eukaryotes. **Genome Biology** 20:162.
22. Li, W.V. and **Li, J.J.**<sup>+</sup> (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
23. Ge, X.\*<sup>\*</sup>, Zhang, H.\*<sup>\*</sup>, Xie, L., Li, W.V., Kwon, S.B., and **Li, J.J.**<sup>+</sup> (2019). EpiAlign: an alignment-based bioinformatic tool for comparing chromatin state sequences. **Nucleic Acids Research** 47(13):e77.
24. Razaee, Z., Amini, A., and **Li, J.J.** (2019). Matched bipartite block model with covariates. **Journal of Machine Learning Research** 20(34):1-44.

25. Duong, D.<sup>+</sup>, Ahmad, W.U., Eskin, E., Chang, K.-W., and **Li, J.J.**<sup>+</sup> (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.
26. 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.
27. Li, W.V.<sup>\*</sup>, Zhao, A., Zhang, S.<sup>+</sup>, and **Li, J.J.**<sup>\*\*</sup> (2018). MSIQ: joint modeling of multiple RNA-seq samples for accurate isoform quantification. ***The Annals of Applied Statistics*** 12(1):510-539.
28. Li, W.V. and **Li, J.J.**<sup>+</sup> (2018). An accurate and robust imputation method scImpute for single cell RNA-seq data. ***Nature Communications*** 9:997.
29. Tong, X.<sup>+</sup>, Feng, Y., and **Li, J.J.**<sup>+</sup> (2018). Neyman-Pearson classification algorithms and NP receiver operating characteristics. ***Science Advances*** 4(2):eaao1659.
30. 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.
31. **Li, J.J.**<sup>+</sup>, Chew, G.L., and Biggin, M.D.<sup>+</sup> (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
32. 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. (2017). 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.
33. Clifton, S.M., Kang, C.<sup>+</sup>, **Li, J.J.**<sup>+</sup>, Long, Q., Shah, N., and Abrams, D.M.<sup>+</sup> (2017). Hybrid statistical and mechanistic mathematical model guides mobile health intervention for chronic pain. ***Journal of Computational Biology*** 24(7):675-688.
34. Li, W.V., Chen, Y., and **Li, J.J.**<sup>+</sup> (2017). TROM: A testing-based method for finding transcriptomic similarity of biological samples. ***Statistics in Biosciences*** 9(1):105-136.
35. Gao, R. and **Li, J.J.**<sup>+</sup> (2017). Correspondence of *D. melanogaster* and *C. elegans* developmental stages revealed by alternative splicing characteristics of conserved exons. ***BMC Genomics*** 18(1):234.
36. Yang, Y.<sup>\*</sup>, Yang, Y.C.T.<sup>\*</sup>, Yuan J., Lu, Z.J.<sup>+</sup>, and **Li, J.J.**<sup>+</sup> (2017). Large-scale mapping of mammalian transcriptomes identifies conserved genes associated with different cell states. ***Nucleic Acids Research*** 45(4):1657-1672.
37. Ye, Y. and **Li, J.J.**<sup>+</sup> (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.
38. Li, W.V., Razaee, Z.S., and **Li, J.J.**<sup>+</sup> (2016). Epigenome overlap measure (EPOM) for comparing tissue/cell types based on chromatin states. ***BMC Genomics*** 17(Supp 1):10.

39. 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.
40. **Li, J.J.** and Biggin, M.D. (2015). Statistics requantitates the central dogma. ***Science*** 347(6226):1066-1067.
41. 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.
42. 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.
43. **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
44. **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
45. 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.
46. The ENCODE Project Consortium (2012). An integrated encyclopedia of DNA elements in the human genome. ***Nature*** 489(7414):57-74.
47. 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.
48. Li, J., **Li, J.**, and Chen, B. (2012). Oct4 was a novel target of Wnt signaling pathway. ***Molecular and Cellular Biochemistry*** 362:233-240.
49. **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.
50. 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

51. **Li, J.J.<sup>+</sup>**, Tong, X., and Bickel, P.J. (2019). Generalized Pearson correlation squares for a mixture of bivariate linear dependences. *Annals of Applied Statistics* under review. [arXiv preprint](#).
52. **Jiang, R., Sun, T., Song, D., and Li, J.J.<sup>+</sup>** (2020). Statistics or biology: the zero-inflation controversy about scRNA-seq data. *Genome Biology* under review. [bioRxiv preprint](#).
53. **Zhang, C., Chen, Y.E., Zhang, S., and Li, J.J.<sup>+</sup>** (2021). Information-theoretic classification accuracy: a data-driven approach to combining ambiguous outcome labels in multi-class classification. *Journal of Machine Learning Research* under review. [arXiv preprint](#)

## MANUSCRIPTS

54. Li, W.V., Tong, X., and Li, J.J. (2020). Bridging cost-sensitive and Neyman-Pearson paradigms in asymmetric binary classification. [arXiv preprint](#).
55. Chen, Y., McDermott, M., Woyshner, K., Wang, L.D., and **Li, J.J.<sup>+</sup>** (2021). APIR: a flexible and powerful FDR-control framework for aggregating peptides identified by different database search algorithms from mass spectrometry data. [bioRxiv preprint](#).

**REVIEWS**

56. **Li, J.J.<sup>+</sup>** (2020). A new bioinformatics tool to recover missing gene expression in single-cell RNA sequencing data. *Journal of Molecular Cell Biology* mjaa053.
57. **Li, J.J.<sup>+</sup>** (2019). Review of "Statistical modeling and machine learning for molecular biology" by Moses, A.M. *The American Statistician* 73(1):103-104.
58. **Li, W.V.** and **Li, J.J.<sup>+</sup>** (2018). Modeling and analysis of RNA-seq data: a review from a statistical perspective. *Quantitative Biology* 6(3):195-209.
59. 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**

60. **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; Hardcover ISBN: 978-3-319-41278-8.
61. **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**

62. **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, 2019-2020
- MC&IP M252:** PhD-level Course “Molecular Mechanisms of Human Diseases I” (Instructor for two statistics lectures) Fall 2020, 2021

**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 Cauffman, 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

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

### PHD STUDENTS

1. Chris Dong (2020 - ) UCLA Statistics
2. Guan'ao Yan (2020 - ) UCLA Statistics
3. Dongyuan Song (2019 - ) UCLA Bioinformatics
4. Wenbin Guo (2018 - 2021) UCLA Bioinformatics
5. Heather J. Zhou (2018 - ) UCLA Statistics
6. Kexin Li (2018 - ) UCLA Statistics
7. Tianyi Sun (2017 - ) UCLA Statistics
8. Nan Xi (2016 - 2021) UCLA Statistics; Currently Assistant Professor of Statistics at Loyola University of Chicago
9. Ruochen Jiang (2016 - ) UCLA Statistics; Currently Bioinformatics Scientist at Veracyte, Inc.
10. Xinzhou Ge (2016 - 2021) UCLA Statistics; Currently Postdoctoral Researcher at UCLA
11. Yiling Chen (2016 - 2021) UCLA Statistics; Currently Postdoctoral Researcher at UC Irvine
12. Jiaping Zhu (2015 - ) UCLA Statistics
13. Yidan Sun (2015 - 2021): UCLA Statistics; Currently Visiting Assistant Professor of Statistics at UC Santa Barbara
14. Wei (Vivian) Li (2014 - 2019): UCLA Statistics; Currently Assistant Professor of Biostatistics at Rutgers University
15. Zahra Razaee (2014 - 2017): UCLA Statistics; Currently Postdoctoral Scientist at Cedars-Sinai Medical Center

**MS STUDENTS**

- |                                  |   |
|----------------------------------|---|
| 1. Xiaoru Zheng (2019 - 2020):   | UCLA Statistics   |
| 2. Yingqi Li (2019 - 2020):      | UCLA Statistics   |
| 3. Tianyi Xia (2018 - 2019):     | UCLA Statistics   |
| 4. Yu-Cheng Yang (2016 - 2017):  | UCLA Statistics; Currently Assistant Professor at Fudan University, China |
| 5. Surui Sun (2015 - 2017):      | UCLA Statistics   |
| 6. 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. Lucia Ramirez (2021)             | Summer student in the Bruins in Genomics Program                              |
| 2. Zhengtong Liu (2020 - 2021)      | Applied Math and CS major at UCLA   |
| 3. Melody Zhang (2020 - 2021)       | Biology major at UCLA   |
| 4. Huy Nguyen (2020 - 2021)         | Statistics major at UCLA  |
| 5. Jingfei Fang (2020)              | Math of Computational major at UCLA   |
| 6. Manasvi Malepati (2020)          | Summer student in the Bruins in Genomics Program                              |
| 7. Wenchu Pan (2019)                | Visiting student from Peking University, China                                |
| 8. Xindi Lin (2019)                 | Visiting CSST student from Zhejiang University, China                         |
| 9. Dehong Xu (2018)                 | Visiting CSST student from Beijing University of Posts and Telecommunications |
| 10. Mayra Varillas (2017)           | Summer student in the Bruins in Genomics Program                              |
| 11. Tiffany Tu (2017)               | Summer student in the Bruins in Genomics Program                              |
| 12. Kexin Li (2017)                 | Visiting student from Tsinghua University, China                              |
| 13. Yue Cui (2016 - 2017):          | Statistics major at UCLA  |
| 14. Longsheng Qian (2016 - 2017):   | Math/Econ major at UCLA   |
| 15. Qianhao Yu (2016 - 2017):       | Applied Math & Statistics major at UCLA                                       |
| 16. Jingwei Song (2016 - 2017):     | Statistics major at UCLA  |
| 17. Yumeng Ma (2016):               | Visiting student from Tsinghua University, China                              |
| 18. Tianyi Sun (2016):              | Visiting student from Tsinghua University, China                              |
| 19. Yushi Tang (2016):              | Visiting CSST student from Peking University, China                           |
| 20. Yuqi Tian (2016):               | Summer student from Xiamen University, China                                  |
| 21. Yiling Chen (2015 - 2016):      | Math/Applied Science major at UCLA  |
| 22. Yimeng Jia (2015 - 2016):       | Statistics major at UCLA  |
| 23. Jason Mao (2015 - 2016):        | Statistics major at UCLA  |
| 24. Ruiqi Gao (2015 - 2016):        | Visiting student from Peking University, China                                |
| 25. Xin Xu (2014 - 2015):           | Visiting CSST student from Nankai University, China                           |
| 26. Yuting Ye (2014 - 2015):        | Visiting student from Tsinghua University, China                              |
| 27. Chang Ding (Spring, Fall 2014): | Mathematics/Economics major at UCLA   |

**THESIS COMMITTEES**

PhD in Statistics:

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

## PhD in other majors:

1. Yun-hua Hsiao (Bioengineering, 2014 - 2018)
2. Shanxi Jiang (Molecular, Cellular, and Integrative Physiology, 2015 - 2018)
3. Sepideh Mazrouee (Computer Science, 2016 - 2017)
4. Jui-Ting Ju (Computer Science, 2016 - 2019)
5. Hung-Hao Lo (Molecular Biology, 2016 - 2019)
6. Zong Miao (Bioinformatics, 2016 - 2020)
7. Qin An (Human Genetics, 2017 - 2020)
8. Xinhui Zhang (Biology, 2017 - )
9. Kikuye Koyano (Bioinformatics, 2018 - 2021)
10. Feiyang Ma (Molecular Biology, 2018 - 2020)
11. Xingquan Guan (Civil Engineering, 2018 - 2021)
12. Soo Bin Kwon (Bioinformatics, 2018 - )
13. Dat Bach Duong (Computer Science, 2018 - 2020)
14. Mina Shahi (Bioengineering, 2019 - )
15. Alec Matthew Chiu (Bioinformatics, 2019 - )
16. Thai Ha Vu (Bioinformatics, 2019 - )
17. Leah Briscoe (Bioinformatics, 2019 - )
18. Shuochuan Meng (Civil Engineering, 2019 - )
19. Matias Andres Rojas Leon (Civil Engineering, 2020 - )
20. Zhixin (Cyrillus) Tan (Bioinformatics, 2020 - )
21. Russell Littman (Bioinformatics, 2020 - )
22. Shuya Wang (Molecular Biology, 2021 - )
23. Runjia Li (Bioinformatics, 2021 - )

## MS in Statistics:

1. Yuan Tian (2014)
2. Muzhou Liang (2015)
3. Qian Xiao (2015)
4. Chufeng Hu (2017)
5. Yiwei Xu (2017)
6. Soo Woo Choi (2017)
7. Maxim Ananyev (2018)
8. Hua Kang (2018)
9. Shuai Zhu (2019)
10. Yu Zhang (2019)
11. Zijun Zhang (2019)
12. Ritvik Yogesh Kharkar (2020)

13. Juan Piao (2021)
14. Ashley Kathleen Chiu (2021)
15. Sixuan Li (2021)

## MAS in Statistics:

1. Hui Zhang (2018)
2. Yueyan (Lilian) Gao (2019)
3. Jason Osajima (2019)
4. Max Harris Belasco (2021)

## MS in other majors:

1. Yuelin (Kathleen) He (Bioinformatics, 2021)

## INVITED TALKS & PRESENTATIONS

### CONFERENCE AND SYMPOSIUM PRESENTATIONS

1. Discussant, International Seminar on Selective Inference, Nov 11, 2021
2. Invited Talk, The 6<sup>th</sup> Annual MidAtlantic Bioinformatics Conference, Nov 8, 2021
3. ICSA Applied Statistics Symposium, Sep 12, 2021
4. Invited Talk, Joint Statistical Meetings, Aug 12, 2021
5. Invited Talk, The 8<sup>th</sup> Young Scholar Forum of Interdisciplinary Research of Mathematics, Computer Science, and Life Science, Chinese Academy of Sciences, May 15, 2021
6. ICSA Applied Statistics Symposium, Dec 15, 2020
7. International Seminar on Selective Inference, Dec 3, 2020
8. Human Cell Atlas Asia Meeting, Oct 22, 2020
9. Invited Talk, Joint Statistical Meetings, Aug 6, 2020
10. ENAR 2020 Spring Meeting, Mar 25, 2020
11. The 11<sup>th</sup> ICSA International Conference, Zhejiang University, Hangzhou, China, Dec 20, 2019
12. Joint Statistical Meetings, Denver, CO, Jul 31, 2019
13. The 27<sup>th</sup> Conference on Intelligent Systems for Molecular Biology (ISMB) and the 18<sup>th</sup> European Conference on Computational Biology (ECCB), Basel, Switzerland, Jul 23, 2019
14. Single-cell Data in Space and Time: Mathematical and Computational Challenges, Imperial College London, London, UK, Jun 17, 2019
15. The Data Science Expo, Los Angeles, CA, May 18, 2019
16. ENAR 2019 Spring Meeting, Mar 25, 2019
17. Frontiers in Single-cell Technology, Application and Data Analysis, Banff International Research Station (BIRS) Workshop, Banff, AB, Feb 27, 2019
18. The 8<sup>th</sup> Annual Southern California Systems Biology Conference, University of California at Irvine, CA, Feb 9, 2019
19. ICSA Conference on Data Science, Xishuangbanna, China, Jan 12, 2019
20. DahShu Virtual Journal Club, Nov 16, 2018
21. 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
22. Keynote Talk, The 8<sup>th</sup> National Conference on Bioinformatics and Systems Biology of China and the 1<sup>st</sup> (Macao) International Bioinformatics Symposium, Macao, Oct 23, 2018
23. Joint Statistical Meetings, Vancouver, BC, Aug 1, 2018
24. Regulatory and Systems Genomics (RegSys) Community of Special Interest (COSI) at the 26<sup>th</sup> Conference on Intelligent Systems for Molecular Biology (ISMB), Jul 10, 2018
25. The 5<sup>th</sup> International Biostatistics Symposium, Guangzhou, China, Jul 7, 2018
26. ICSA China Conference with the Focus on Data Science, Qingdao, China, Jul 4, 2018
27. ICSA Applied Statistics Symposium, New Brunswick, NJ, Jun 16, 2018
28. The 46<sup>th</sup> Annual Meeting of the Statistical Society of Canada, McGill University, Montreal, QB, Canada, Jun 5, 2018
29. 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

30. DahShu Virtual Journal Club, Apr 30, 2018
31. Johnson & Johnson WiSTEM2D Symposium, New Brunswick, NJ, Apr 26, 2018
32. Highlight Talk at the 22<sup>nd</sup> International Conference on Research in Computational Molecular Biology (RECOMB), Paris, France, Apr 24, 2018
33. Joint Statistical Meetings, Baltimore, MD, Aug 3, 2017
34. The 1<sup>st</sup> North American Social Networks (NASN) Conference, Washington, D.C., Jul 28, 2017
35. ICSA Applied Statistics Symposium, Chicago, IL, Jun 26, 2017
36. HDDA VII (The 7<sup>th</sup> International Workshop on Perspectives on High-dimensional Data Analysis), CIMAT, Guanajuato, Mexico, Jun 18, 2017
37. UCLA QCB 2<sup>nd</sup> Annual Symposium "Exploring the Frontiers of Biomedical Big Data," UCLA, Los Angeles, CA, Apr 28, 2017
38. Workshop "Harnessing Big Data for Precision Medicine: Infrastructure and Applications," Pacific Symposium on Biocomputing (PSB), The Big Island of Hawaii, HI, Jan 3, 2017
39. The 10<sup>th</sup> ICSA International Conference: Global Growth of Modern Statistics in the 21<sup>st</sup> Century, Shanghai Jiaotong University, Shanghai, China, Dec 20, 2016
40. International Indian Statistical Association Conference, Oregon State University, Corvallis, OR, Aug 20, 2016
41. Joint Statistical Meetings, Chicago, IL, Aug 2, 2016
42. The 3<sup>rd</sup> Taihu International Statistics Forum, Shanghai, China, Jul 10, 2016
43. The ICSA Conference on Data Science, Dali, China, Jul 3, 2016
44. Biological Big Data and Data Mining Workshop, Chinese Academy of Sciences, Beijing, China, Jun 25, 2016
45. ICSA Applied Statistics Symposium, Atlanta, GA, Jun 13, 2016
46. UCLA QCB 1<sup>st</sup> Annual Symposium "Exploring the Frontiers of Biomedical Big Data," UCLA, Los Angeles, CA, Jun 1, 2016
47. The 14<sup>th</sup> Asia Pacific Bioinformatics Conference, San Francisco, CA, Jan 13, 2016
48. Joint Statistical Meetings, Seattle, WA, Aug 9, 2015
49. Cold Spring Harbor Laboratory Systems Biology Meeting: Global Regulation of Gene Expression, Rio Mar, Puerto Rico, Jan 29, 2015 (Poster Presentation)
50. The 7<sup>th</sup> RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, San Diego, CA, Nov 14, 2014
51. Joint Statistical Meetings, Boston, MA, Aug 6, 2014
52. EITA-New Media and Bio 2014, MIT, Cambridge, MA, Jul 31, 2014
53. The 9<sup>th</sup> ICSA International Conference: Challenges of Statistical Methods for Interdisciplinary Research and Big Data, Hong Kong Baptist University, Hong Kong, Dec 23, 2013
54. The 6<sup>th</sup> RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, Toronto, Canada, Nov 12, 2013
55. The 17<sup>th</sup> RECOMB (Annual International Conference on Research in Computational Molecular Biology), Beijing, China, Apr 8, 2013
56. UC Systemwide Bioengineering Symposium, Berkeley, CA, Jun 23, 2012
57. Joint mod/mouse/ENCODE AWG/PI meeting, MIT, Cambridge, MA, May 22, 2012
58. Bay Area RNA Club, UCSF, San Francisco, CA, Jan 25, 2012
59. Cold Spring Harbor Asia Conference: Bioinformatics of Human and Animal Genomics, Suzhou, China, Nov 17, 2011
60. Joint mod/ENCODE Consortia Meeting, Washington DC, May 23, 2011

#### **SEMINAR PRESENTATIONS AT UNIVERSITIES AND RESEARCH INSTITUTES**

1. Department of Data Science and Operations, University of Southern California, Dec 3, 2021
2. Department of Statistics, George Washington University, Nov 19, 2021
3. Bioinformatics Seminar, School of Mathematics and Statistics, University of Sydney, Aug 16, 2021
4. Department of Biostatistics, University of Michigan, Apr 1, 2021
5. Department of Statistics, Chinese University of Hong Kong, Mar 29, 2021
6. Department of Biostatistics, University of Pennsylvania, Mar 23, 2021
7. Neyman Seminar, Department of Statistics, University of California, Berkeley, Feb 3, 2021
8. Department of Statistics, University of Illinois at Urbana-Champaign, IL, Aug 27, 2020

9. Interdisciplinary Center for Quantitative Modeling in Biology, University of California, Riverside, CA, Feb 12, 2020
10. Biomed-X Research Seminar, Zhejiang University-University of Edinburgh Institute, Haining, China, Dec 23, 2019
11. Department of Statistics, University of California, Santa Barbara, CA, Oct 9, 2019
12. Computational and Systems Biology Seminar, Lyda Hill Department of Bioinformatics, The University of Texas Southwestern Medical Center, Dallas, TX, Sep 23, 2019
13. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Aug 30, 2019
14. The Comprehensive Cancer Center, Cancer Immunotherapeutics Program & Department of Immuno-Oncology, City of Hope, Duarte, CA, Mar 15, 2019
15. Department of Statistics and Actuarial Science, Simon Fraser University, Vancouver, BC, Feb 22, 2019
16. Department of Statistics, The University of British Columbia, Vancouver, BC, Feb 21, 2019
17. Department of Mathematics, California State University, Northridge, Feb 20, 2019
18. State Key Laboratory of Biotherapy, Sichuan University, Chengdu, China, Jan 23, 2019
19. School of Life Sciences, Tsinghua University, Beijing, China, Jan 18, 2019
20. Center for Statistical Science, Tsinghua University, Beijing, China, Jan 17, 2019
21. The First Affiliated Hospital, Sun Yat-Sen University, Guangzhou, China, Jan 14, 2019
22. Department of Biostatistics, University of Pittsburgh, Nov 1, 2018
23. Department of Biomathematics, University of California, Los Angeles, Oct 4, 2018
24. Omics Seminar, Cedars-Sinai Medical Center, Los Angeles, CA, Sep 25, 2018
25. Department of Statistics, University of Georgia, Athens, GA, Aug 23, 2018
26. 3<sup>rd</sup> UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 17, 2018
27. Bioinformatics Interdepartmental Ph.D. Program, University of California, Los Angeles, CA, Apr 9, 2018
28. Physical Sciences Faculty Lunch Seminar, College of Letters and Sciences, University of California, Los Angeles, CA, Mar 19, 2018
29. Department of Biostatistics, Ohio State University, Columbus, OH, Feb 23, 2018
30. Department of Statistics, University of California, Los Angeles, CA, Jan 17, 2018
31. Medical and Population Genomics Seminar, University of California, Los Angeles, CA, Dec 6, 2017
32. 2<sup>nd</sup> UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 24, 2017
33. Medical and Population Genomics Seminar, University of California, Los Angeles, CA, May 24, 2017
34. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jul 4, 2017
35. Center for Statistical Science, Tsinghua University, Beijing, China, Jul 3, 2017
36. School of Life Sciences, Tsinghua University, Beijing, China, Jul 3, 2017
37. Institute of Machine Learning and Systems Biology, Tongji University, Shanghai, China, Dec 21, 2016
38. 1<sup>st</sup> UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 22, 2016
39. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jun 24, 2016
40. Faculty Research Lunch Series, Quantitative and Computational Biosciences, University of California, Los Angeles, CA, May 6, 2016
41. Department of Data Sciences and Operations, Marshall School of Business, University of Southern California, Los Angeles, CA, Dec 4, 2015
42. Genomics Seminar, Johns Hopkins University, Baltimore, MD, Nov 17, 2015
43. Jonsson Comprehensive Cancer Center Gene Regulation Intramural Meeting, University of California, Los Angeles, CA, May 5, 2015
44. Department of Statistics, University of California, Riverside, CA, Feb 24, 2015

45. Department of Ecology and Evolutionary Biology, University of California, Los Angeles, CA, Feb 18, 2015
46. Department of Statistics, Pennsylvania State University, State College, PA, Jan 22, 2015
47. Center for Systems Genomics, Pennsylvania State University, State College, PA, Jan 21, 2015
48. Department of Biostatistics, University of California, Los Angeles, CA, November 19, 2014
49. MOE Key Laboratory of Bioinformatics and Bioinformatics Division, TNLIST / Department of Automation, Tsinghua University, Beijing, China, Jun 20, 2014
50. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jun 19, 2014
51. Department of Statistics, Columbia University, NY, May 1, 2014
52. Department of Molecular and Computational Biology, University of Southern California, CA, Mar 6, 2014
53. Department of Statistics, University of California, Los Angeles, CA, Jan 14, 2014
54. School of Life Sciences, Tsinghua University, Beijing, China, Dec 13, 2013
55. Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Apr 11, 2013
56. Department of Statistics, University of Chicago, IL, Feb 25, 2013
57. Departments of Human Genetics and Statistics, University of California, Los Angeles, CA, Feb 1, 2013
58. Department of Statistics, University of California, Davis, CA, Jan 16, 2013

### **PUBLIC TALKS**

1. The Science Show with Robyn Williams at ABC Australia, May 23, 2020
2. Exploring Your Universe at UCLA, Nov 1, 2020

## **EDITORIAL BOARD & REVIEWING ACTIVITIES**

### **EDITORIAL BOARD**

1. *PeerJ* – Associate Editor (2015 - )
2. *Frontiers in Genetics* – Review Editor (2014 - )
3. *Journal of Computational and Graphical Statistics* – Management Committee (2020 - )
4. *PLOS Computational Biology* – Guest Editor (2020 - )
5. *Physiological Genomics* – Editorial Board (2021 - )
6. *Journal of American Statistical Association (Applications & Case Studies)* – Associate Editor (2022 - )

### **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 Systems*
10. *Communications Biology*
11. *Computational Biology and Chemistry*
12. *Computational Statistics and Data Analysis*
13. *Computers in Biology and Medicine*
14. *eLife*
15. *Frontiers in Genetics*
16. *F1000Research*

17. *Gene Reports*
18. *Genes*
19. *Genetics*
20. *Genome Biology*
21. *Genome Research*
22. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
23. *Journal of American Statistical Association*
24. *Journal of Machine Learning Research*
25. *Nature Biotechnology*
26. *Nature Communications*
27. *Nature Machine Intelligence*
28. *Nature Methods*
29. *Nucleic Acids Research*
30. *NAR Genomics and Bioinformatics*
31. *PeerJ*
32. *PLOS Computational Biology*
33. *Proceedings of the National Academy of Sciences of the United States of America*
34. *Science*
35. *Science Bulletin*
36. *Science Translational Medicine*
37. *Statistica Sinica*
38. *Statistical Applications in Genetics and Molecular Biology*
39. *Statistics and Its Interface*
40. *Statistics in Medicine*

#### **REVIEWER FOR CONFERENCES**

1. RECOMB 2022: the 26<sup>th</sup> International Conference on Research in Computational Molecular Biology
2. ISMB/ECCB 2021: the 29<sup>th</sup> Conference on Intelligent Systems for Molecular Biology
3. ISMB 2020: the 28<sup>th</sup> Conference on Intelligent Systems for Molecular Biology
4. ISMB/ECCB 2019: the 27<sup>th</sup> Conference on Intelligent Systems for Molecular Biology
5. APBC 2019: the 17<sup>th</sup> Asia Pacific Bioinformatics Conference
6. ICIBM 2018: International Conference on Intelligent Biology and Medicine
7. APBC 2016: the 14<sup>th</sup> Asia Pacific Bioinformatics Conference

#### **REVIEWER FOR GRANT APPLICATIONS**

1. Reviewer, NIH IMST (Interdisciplinary Molecular Sciences and Training) Study Section, 2021
2. Reviewer, NSF DBI Review Panel, 2021
3. Reviewer, NIH GCAT (Genomics, Computational Biology and Technology) Study Section, 2021
4. Reviewer, NIH Common Fund Program Special Emphasis Panel, 2021
5. Ad Hoc Reviewer, NSF (National Science Foundation) DBI, 2021
6. Reviewer, UCLA Society of Hellman Fellows Selection Committee, 2021
7. Reviewer, NIGMS ESI MIRA Study Section, 2021
8. Reviewer, Davidson Fellows Scholarship Program, 2020
9. Reviewer, NIGMS ESI MIRA Study Section, 2020
10. Reviewer, NIH GCAT (Genomics, Computational Biology and Technology) Study Section, 2020
11. Reviewer, NSF DBI Review Panel, 2019
12. External Reviewer, NSERC (Natural Sciences and Engineering Research Council of Canada), Discovery Grants, 2018
13. Reviewer, NIH GCAT Study Section, 2018
14. Reviewer, PhRMA Foundation Informatics Advisory Committee, 2018
15. Reviewer, NSF DMS Review Panel, 2017
16. Reviewer, Hong Kong General Research Fund (GRF), 2016, 2017, 2018, 2019, 2020
17. Reviewer, NIH/NIEHS Review Panel, 2016
18. Reviewer, Israel Science Foundation, 2016
19. Reviewer, NSF IIS Review Panel, 2016

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

## REVIEWER FOR TENURE AND PROMOTION

1. Tsinghua University, China, 2021

## PROFESSIONAL SERVICE

2021–2022 Search Committee, UCLA Department of Statistics  
 2021–2022 Search Committee, UCLA Department of Biostatistics  
 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  
 2014 Session Organizer, Joint Statistical Meetings

## UNIVERSITY ACTIVITIES

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

## OTHER PROFESSIONAL ACTIVITIES

1. Proceedings Program Committee of the RECOMB 2022 conference
2. Proceedings Program Committee of the ISMB/ECCB 2021 conference
3. Moderator of NISS Virtual Academic Career Fair: Finding a Position During the Pandemic, 2020
4. Proceedings Program Committee of the ISMB 2020 conference
5. Proceedings Program Committee of the ISMB/ECCB 2019 conference
6. Session Chair at the International Indian Statistical Association Conference, Oregon State University, Corvallis, OR, Aug 18-21, 2016
7. Session Chair and Organizer at the Joint Statistical Meetings, Chicago, IL, Jul 30-Aug 4, 2016
8. Session Chair at the 14th Asia Pacific Bioinformatics Conference, San Francisco, CA, Jan 11-13, 2016
9. Session Chair at the Joint Statistical Meetings, Seattle, WA, Aug 8-13, 2015
10. 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
11. Session Chair and Organizer at the Joint Statistical Meetings, Boston, MA, Aug 2-8, 2014
12. Participant in the Women in Statistics Conference, Research Triangle Park, NC, May 15-17, 2014
13. Participant in the SAMSI Social Network Data: Collection and Analysis Workshop, Research Triangle Park, NC, Oct 21-23, 2013
14. Participant in the IPAM (Institute of Pure and Applied Mathematics) "Mathematical and Computational Approaches in High-Throughput Genomics" Program, Los Angeles, CA, Fall 2011
15. Volunteer in ICOSA (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– ICOSA (International Chinese Statistical Association)