

# Jingyi Jessica Li

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Department of Statistics

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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:

- Computational method development for imputation and differential expression analysis of single-cell RNA sequencing data
- Statistical modeling of next-generation RNA sequencing data to identify and quantify full-length mRNA transcripts
- Using statistics to quantitate the Central Dogma
- Comparison of transcriptomes and/or epigenomes of various tissues and cells to reveal tissue/cell-associated genes and/or functional elements

Statistics:

- Neyman-Pearson (NP) classification: an umbrella algorithm; NP receiver operating characteristics (NP-ROC); feature ranking
- Measure of dependence: a generalized  $R^2$
- Hierarchical modeling to extract consistent information from multiple replicate samples
- Confidence intervals of coefficients in a high-dimensional linear model

## 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 (CSR CB)

## 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	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 <i>Fiat Lux</i> 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

#### UCLA DGSOM W. M. Keck Foundation Junior Faculty Award

**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

**07/01/2019 – 06/30/2024**

NSF \$599,611  
"CAREER: Advancing the bioinformatic infrastructure and methodology for single-cell RNA sequencing"

**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"**Sloan Research Fellowship****09/15/2018 – 09/14/2023**

Alfred P. Sloan Foundation \$65,000

**Johnson & Johnson Women in STEM<sup>2</sup>D Scholar Award****01/21/2018 – 01/21/2022**Johnson & Johnson \$150,000  
"Statistical modeling to quantitate the central dogma"**R01 GM120507 (PI: Li)****09/01/2016 – 05/31/2021**NIH / NIGMS \$1,667,725  
"Robust identification and accurate quantification of RNA transcripts on a system wide scale"**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"**COMPLETED****PhRMA Foundation Research Starter Grant in Informatics****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

1. Xi, N.M. and **Li, J.J.**<sup>+</sup> (2020). Benchmarking computational doublet-detection methods for single-cell RNA sequencing data. **Cell Systems** (in press).
2. Lyu, J.\* , **Li, J.J.**<sup>\*\*</sup>, Su, J., Peng, F., Chen, Y., Ge, X., and Li, W.<sup>+</sup> (2020). DORGE: Discovery of Oncogenes and tumor suppressor genes using Genetic and Epigenetic features. **Science Advances** (in press).
3. Xu, J., Shi, J., Cui, X., Cui, Y., **Li, J.J.**, Goel, A., Chen, X., Su, J., Issa, J.-P., and Li, W. (2020). Cellular heterogeneity-adjusted clonal methylation (CHALM) provides better prediction of gene expression. **Nature Communications** (in press).
4. **Li, J.J.**<sup>+</sup> and Tong, X. (2020). Statistical hypothesis testing versus machine-learning binary classification: distinctions and guidelines. **Patterns** 1(7):110115.
5. Wang, Y.X.R., Li, L., **Li, J.J.**, and Huang, H. (2020). Network modeling in biology: statistical methods for gene and brain networks. **Statistical Science** (in press).
6. Sun, Y.E., Zhou, H.J., and **Li, J.J.**<sup>+</sup> (2020). Bipartite tight spectral clustering (BiTSC) algorithm for identifying conserved gene co-clusters in two species. **Bioinformatics** btaa741.
7. 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.
8. Li, W.V.<sup>\*</sup>, Li, S.\* , 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
9. **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.
10. 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
11. 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.
12. Razaee, Z., Amini, A., and **Li, J.J.** (2019). Matched bipartite block model with covariates. **Journal of Machine Learning Research** 20(34):1-44.
13. 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. PubMed PMID: 30383443; PubMed Central PMCID: PMC6350067.
14. 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. PubMed PMID: 29727661; PubMed Central PMCID: PMC5940017.

15. 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. PubMed PMID: 29731954; PubMed Central PMCID: PMC5935499.
16. 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. PubMed PMID: 29520097; PubMed Central PMCID: PMC5843666.
17. 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. PubMed PMID: 29423442; PubMed Central PMCID: PMC5804623.
18. 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. PubMed PMID: 29339507; PubMed Central PMCID: PMC5798360.
19. **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. PubMed PMID: 29040683; PubMed Central PMCID: PMC5714229.
  - 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
20. 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. PubMed PMID: 29076140.
21. 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. PubMed PMID: 28581814; PubMed Central PMCID: PMC5510708.
22. 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. PubMed PMID: 28781712; PubMed Central PMCID: PMC5542419.
23. 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. PubMed PMID: 28302059; PubMed Central PMCID: PMC5353869.
24. 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. PubMed PMID: 27980097; PubMed Central PMCID: PMC5389511.
25. 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. PubMed PMID: 26818007; PubMed Central PMCID: PMC4895266.

26. 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. PubMed PMID: 26817822; PubMed Central PMCID: PMC4895267.
27. 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. PubMed PMID: 25857574.
28. Li, J.J. and Biggin, M.D. (2015). Statistics requantitates the central dogma. ***Science*** 347(6226):1066-1067. PubMed PMID: 25745146.
29. 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. PubMed PMID: 25164755; PubMed Central PMCID: PMC4155737.
30. 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. PubMed PMID: 25164757; PubMed Central PMCID: PMC4336544.
31. 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. PubMed PMID: 24985912; PubMed Central PMCID: PMC4079965.
  - Top 10 papers selected at the 2014 RECOMB/ISCB Conference on Regulatory & Systems Genomics
32. 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. PubMed PMID: 24688849; PubMed Central PMCID: PMC3940484.
  - "PeerJ Picks 2015" Collection
  - "Top Bioinformatics Papers - June 2015" Collection
33. Fisher, W.W., Li, J.J., Hammonds, A.S., Brown, J.B., Pfeiffer, B., Weiszmam, 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. PubMed PMID: 23236164; PubMed Central PMCID: PMC3535648.
34. The ENCODE Project Consortium (2012). An integrated encyclopedia of DNA elements in the human genome. ***Nature*** 489(7414):57-74. PubMed PMID: 22955616; PubMed Central PMCID: PMC3439153.
35. 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. PubMed PMID: 22697238; PubMed Central PMCID: PMC3375643.
36. Li, J., Li, J., and Chen, B. (2012). Oct4 was a novel target of Wnt signaling pathway. ***Molecular and Cellular Biochemistry*** 362:233-240. PubMed PMID: 22120493.

37. **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. PubMed PMID: 22135461; PubMed Central PMCID: PMC3250192.
38. 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. PubMed PMID: 19627575; PubMed Central PMCID: PMC2728534.
- Highly accessed article on BioMed Central
  - Faculty of 1000 recommendation

#### SUBMITTED

39. **Li, J.J.\***, Tong, X., and Bickel, P.J. (2019). Generalized Pearson correlation squares for a mixture of bivariate linear dependences. [arXiv preprint](#).
40. **Chen, Y.**, Tong, X., and **Li, J.J.\*** (2019). A general model selection criterion under the Neyman-Pearson binary classification paradigm. [arXiv preprint](#).
41. **Jiang, R.**, **Li, W.V.**, and **Li, J.J.\*** (2020). An accurate and robust imputation method mblImpute for microbiome data. [bioRxiv preprint](#).

#### MANUSCRIPTS

42. Li, W.V., Tong, X., and Li, J.J. (2020). Bridging cost-sensitive and Neyman-Pearson paradigms in asymmetric binary classification.
43. Sun, T.Y., Song, D.Y., Li, W.V., and Li, J.J. (2020). scDesign2: a statistical simulator that recapitulates gene correlations for benchmarking scRNA-seq data analysis.
44. Ge, X., Chen, Y., Li, W., Wang, L.D., and Li, J.J. (2020). Clipper: p-value-free FDR control on high-throughput data from two conditions.

#### REVIEWS

45. **Li, J.J.\*** (2020). A new bioinformatics tool to recover missing gene expression in single-cell RNA sequencing data. *Journal of Molecular Cell Biology* mjaa053.
46. **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.
47. **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.
48. 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

49. **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.

50. 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**

51. 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
- 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

#### **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
- STAT 201B:** PhD-level course “Statistical Modeling and Learning” Winter 2020
- STAT 205:** PhD-level course “Hierarchical Linear Models” Winter 2017, Fall 2017, Fall 2018, Fall 2019
- 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
- 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

#### **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****MENTEES’ AWARDS**

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	Ruo Chen 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**

- Dongyuan Song (Fall 2019)                      UCLA Bioinformatics
- Wenbin Guo (2018 - )                          UCLA Bioinformatics
- Heather J. Zhou (2018 - )                      UCLA Statistics
- Kexin Li (2018 - )                              UCLA Statistics
- Tianyi Sun (2017 - )                            UCLA Statistics
- Nan Xi (2017 - )                                UCLA Statistics
- Ruo Chen Jiang (2016 - )                      UCLA Statistics
- Xinzhou Ge (2016 - )                         UCLA Statistics
- Yiling Chen (2016 - )                         UCLA Statistics
- Yidan Sun (2015 - )                            UCLA Statistics
- Jiaping Zhu (2015 - )                         UCLA Statistics
- Wei (Vivian) Li (2014 - 2019):              UCLA Statistics; Currently Assistant Professor of Biostatistics at Rutgers University
- Zahra Razaee (2014 - 2017):                UCLA Statistics; Currently Postdoctoral Scientist at Cedars-Sinai Medical Center

**MS STUDENTS**

- Xiaoru Zheng (2019 - 2020): UCLA Statistics
- Yingqi Li (2019 - 2020): UCLA Statistics
- Tianyi Xia (2018 - 2019): UCLA Statistics
- Yu-Cheng Yang (2016 - 2017): UCLA Statistics; Currently Postdoctoral Researcher at Yale University
- Surui Sun (2015 - 2017): UCLA Statistics
- Arturo Ramirez (2013 - 2015): UCLA Statistics

### PHD ROTATION STUDENTS

- Leroy Bondhus (Fall 2018) UCLA Human Genetics
- Soo Bin Kwon (Spring 2017) UCLA Bioinformatics
- Lingyu Zhan (Winter 2017) UCLA Gene Regulation
- Xinyuan Chen (Fall 2016) UCLA Human Genetics
- Mudra Choudhury (Fall 2016) UCLA Bioinformatics
- Douglas Arneson (Winter 2015): UCLA Bioinformatics

### UNDERGRADUATE STUDENTS

- Jingfei Fang (2020) Math of Computations major at UCLA
- Manasvi Malepati (2020) Summer student in the Bruins in Genomics Program
- Wenchu Pan (2019) Visiting student from Peking University, China
- Xindi Lin (2019) Visiting CSST student from Zhejiang University, China
- Dehong Xu (2018) Visiting CSST student from Beijing University of Posts and Telecommunications
- Mayra Varillas (2017) Summer student in the Bruins in Genomics Program
- Tiffany Tu (2017) Summer student in the Bruins in Genomics Program
- Kexin Li (2017) Visiting student from Tsinghua University, China
- Yue Cui (2016 - 2017): Statistics major at UCLA
- Longsheng Qian (2016 - 2017): Math/Econ major at UCLA
- Qianhao Yu (2016 - 2017): Applied Math & Statistics major at UCLA
- Jingwei Song (2016 - 2017): Statistics major at UCLA
- Yumeng Ma (2016): Visiting student from Tsinghua University, China
- Tianyi Sun (2016): Visiting student from Tsinghua University, China
- Yushi Tang (2016): Visiting CSST student from Peking University, China
- Yuqi Tian (2016): Summer student from Xiamen University, China
- Yiling Chen (2015 - 2016): Math/Applied Science major at UCLA
- Yimeng Jia (2015 - 2016): Statistics major at UCLA
- Jason Mao (2015 - 2016): Statistics major at UCLA
- Ruiqi Gao (2015 - 2016): Visiting student from Peking University, China
- Xin Xu (2014 - 2015): Visiting CSST student from Nankai University, China
- Yuting Ye (2014 - 2015): Visiting student from Tsinghua University, China
- Chang Ding (Spring, Fall 2014): Mathematics/Economics major at UCLA

### THESIS COMMITTEES

#### PhD in Statistics:

- Nikhyl Bryon Aragam (2013 - 2015)
- Jianwen Xie (2015 - 2016)
- Qian Xiao (2014 - 2017)
- Joshua Gordon (2015 - 2017)
- Seunghyun Min (2016 - 2019)

- Levon Demirdjian (2016 - 2018)
- Zhixin Zhou (2017 - 2018)
- Kun Zhou (2017 - 2020)
- Yifei Xu (2019 - )
- Gabriel Ruiz (2020 - )
- Samuel Onyanacha Onyambu (2020 - )
- Yizhou Zhao (2020 - )

## PhD in other majors:

- Yun-hua Hsiao (Bioengineering, 2014 - 2018)
- Shanxi Jiang (Molecular, Cellular, and Integrative Physiology, 2015 - 2018)
- Sepideh Mazrouee (Computer Science, 2016 - 2017)
- Jui-Ting Ju (Computer Science, 2016 - 2019)
- Hung-Hao Lo (Molecular Biology, 2016 - 2019)
- Zong Miao (Bioinformatics, 2016 - 2020)
- Qin An (Human Genetics, 2017 - 2020)
- Xinhui Zhang (Biology, 2017 - )
- Kikuye Koyano (Bioinformatics, 2018 - )
- Feiyang Ma (Molecular Biology, 2018 - 2020)
- Xingquan Guan (Civil Engineering, 2018 - )
- Soo Bin Kwon (Bioinformatics, 2018 - )
- Dat Bach Duong (Computer Science, 2018 - 2020)
- Mina Shahi (Bioengineering, 2019 - )
- Alec Matthew Chiu (Bioinformatics, 2019 - )
- Thai Ha Vu (Bioinformatics, 2019 - )
- Leah Briscoe (Bioinformatics, 2019 - )
- Shuochuan Meng (Civil Engineering, 2019 - )
- Matias Andres Rojas Leon (Civil Engineering, 2020 - )

## MS in Statistics:

- Yuan Tian (2014)
- Muzhou Liang (2015)
- Qian Xiao (2015)
- Chufeng Hu (2017)
- Yiwei Xu (2017)
- Soo Woo Choi (2017)
- Maxim Ananyev (2018)
- Hua Kang (2018)
- Shuai Zhu (2019)
- Yu Zhang (2019)
- Zijun Zhang (2019)
- Ritvik Yogesh Kharkar (2020)

## MAS in Statistics:

- Hui Zhang (2018)
- Yueyan (Lilian) Gao (2019)
- Jason Osajima (2019)

**INVITED TALKS & PRESENTATIONS****CONFERENCE AND SYMPOSIUM PRESENTATIONS**

- Human Cell Atlas Asia Meeting, Oct 22, 2020
- Joint Statistical Meetings, Aug 6, 2020
- ENAR 2020 Spring Meeting, Mar 25, 2020

- The 11<sup>th</sup> ICSA International Conference, Zhejiang University, Hangzhou, China, Dec 20, 2019
- Joint Statistical Meetings, Denver, CO, Jul 31, 2019
- 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
- Single-cell Data in Space and Time: Mathematical and Computational Challenges, Imperial College London, London, UK, Jun 17, 2019
- The Data Science Expo, Los Angeles, CA, May 18, 2019
- ENAR 2019 Spring Meeting, Mar 25, 2019
- Frontiers in Single-cell Technology, Application and Data Analysis, Banff International Research Station (BIRS) Workshop, Banff, AB, Feb 27, 2019
- The 8<sup>th</sup> Annual Southern California Systems Biology Conference, University of California at Irvine, CA, Feb 9, 2019
- ICSA Conference on Data Science, Xishuangbanna, China, Jan 12, 2019
- DahShu Virtual Journal Club, Nov 16, 2018
- 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
- 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
- Joint Statistical Meetings, Vancouver, BC, Aug 1, 2018
- 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
- The 5<sup>th</sup> International Biostatistics Symposium, Guangzhou, China, Jul 7, 2018
- ICSA China Conference with the Focus on Data Science, Qingdao, China, Jul 4, 2018
- ICSA Applied Statistics Symposium, New Brunswick, NJ, Jun 16, 2018
- The 46<sup>th</sup> Annual Meeting of the Statistical Society of Canada, McGill University, Montreal, QB, Canada, Jun 5, 2018
- 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
- DahShu Virtual Journal Club, Apr 30, 2018
- Johnson & Johnson WiSTEM2D Symposium, New Brunswick, NJ, Apr 26, 2018
- Highlight Talk at the 22<sup>nd</sup> International Conference on Research in Computational Molecular Biology (RECOMB), Paris, France, Apr 24, 2018
- Joint Statistical Meetings, Baltimore, MD, Aug 3, 2017
- The 1<sup>st</sup> North American Social Networks (NASN) Conference, Washington, D.C., Jul 28, 2017
- ICSA Applied Statistics Symposium, Chicago, IL, Jun 26, 2017
- HDDA VII (The 7<sup>th</sup> International Workshop on Perspectives on High-dimensional Data Analysis), CIMAT, Guanajuato, Mexico, Jun 18, 2017
- UCLA QCB 2<sup>nd</sup> Annual Symposium “Exploring the Frontiers of Biomedical Big Data,” UCLA, Los Angeles, CA, Apr 28, 2017
- Workshop “Harnessing Big Data for Precision Medicine: Infrastructure and Applications,” Pacific Symposium on Biocomputing (PSB), The Big Island of Hawaii, HI, Jan 3, 2017
- 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
- International Indian Statistical Association Conference, Oregon State University, Corvallis, OR, Aug 20, 2016
- Joint Statistical Meetings, Chicago, IL, Aug 2, 2016
- The 3<sup>rd</sup> Taihu International Statistics Forum, Shanghai, China, Jul 10, 2016
- The ICSA Conference on Data Science, Dali, China, Jul 3, 2016
- Biological Big Data and Data Mining Workshop, Chinese Academy of Sciences, Beijing, China, Jun 25, 2016
- ICSA Applied Statistics Symposium, Atlanta, GA, Jun 13, 2016
- UCLA QCB 1<sup>st</sup> Annual Symposium “Exploring the Frontiers of Biomedical Big Data,” UCLA, Los Angeles, CA, Jun 1, 2016

- The 14<sup>th</sup> Asia Pacific Bioinformatics Conference, San Francisco, CA, Jan 13, 2016
- Joint Statistical Meetings, Seattle, WA, Aug 9, 2015
- Cold Spring Harbor Laboratory Systems Biology Meeting: Global Regulation of Gene Expression, Rio Mar, Puerto Rico, Jan 29, 2015 (Poster Presentation)
- The 7<sup>th</sup> RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, San Diego, CA, Nov 14, 2014
- Joint Statistical Meetings, Boston, MA, Aug 6, 2014
- EITA-New Media and Bio 2014, MIT, Cambridge, MA, Jul 31, 2014
- 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
- The 6<sup>th</sup> RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, Toronto, Canada, Nov 12, 2013
- The 17<sup>th</sup> RECOMB (Annual International Conference on Research in Computational Molecular Biology), Beijing, China, Apr 8, 2013
- UC Systemwide Bioengineering Symposium, Berkeley, CA, Jun 23, 2012
- Joint mod/mouse/ENCODE AWG/PI meeting, MIT, Cambridge, MA, May 22, 2012
- Bay Area RNA Club, UCSF, San Francisco, CA, Jan 25, 2012
- Cold Spring Harbor Asia Conference: Bioinformatics of Human and Animal Genomics, Suzhou, China, Nov 17, 2011
- Joint mod/ENCODE Consortia Meeting, Washington DC, May 23, 2011

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

- Department of Statistics, University of Illinois at Urbana-Champaign, IL, Aug 27, 2020
- Interdisciplinary Center for Quantitative Modeling in Biology, University of California, Riverside, CA, Feb 12, 2020
- Biomed-X Research Seminar, Zhejiang University-University of Edinburgh Institute, Haining, China, Dec 23, 2019
- Department of Statistics, University of California, Santa Barbara, CA, Oct 9, 2019
- Computational and Systems Biology Seminar, Lyda Hill Department of Bioinformatics, The University of Texas Southwestern Medical Center, Dallas, TX, Sep 23, 2019
- Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Aug 30, 2019
- The Comprehensive Cancer Center, Cancer Immunotherapeutics Program & Department of Immuno-Oncology, City of Hope, Duarte, CA, Mar 15, 2019
- Department of Statistics and Actuarial Science, Simon Fraser University, Vancouver, BC, Feb 22, 2019
- Department of Statistics, The University of British Columbia, Vancouver, BC, Feb 21, 2019
- Department of Mathematics, California State University, Northridge, Feb 20, 2019
- State Key Laboratory of Biotherapy, Sichuan University, Chengdu, China, Jan 23, 2019
- School of Life Sciences, Tsinghua University, Beijing, China, Jan 18, 2019
- Center for Statistical Science, Tsinghua University, Beijing, China, Jan 17, 2019
- The First Affiliated Hospital, Sun Yat-Sen University, Guangzhou, China, Jan 14, 2019
- Department of Biostatistics, University of Pittsburgh, Nov 1, 2018
- Department of Biomathematics, University of California, Los Angeles, Oct 4, 2018
- Omics Seminar, Cedars-Sinai Medical Center, Los Angeles, CA, Sep 25, 2018
- Department of Statistics, University of Georgia, Athens, GA, Aug 23, 2018
- 3<sup>rd</sup> UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 17, 2018
- Bioinformatics Interdepartmental Ph.D. Program, University of California, Los Angeles, CA, Apr 9, 2018
- Physical Sciences Faculty Lunch Seminar, College of Letters and Sciences, University of California, Los Angeles, CA, Mar 19, 2018
- Department of Biostatistics, Ohio State University, Columbus, OH, Feb 23, 2018

- Department of Statistics, University of California, Los Angeles, CA, Jan 17, 2018
- Medical and Population Genomics Seminar, University of California, Los Angeles, CA, Dec 6, 2017
- 2<sup>nd</sup> UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 24, 2017
- Medical and Population Genomics Seminar, University of California, Los Angeles, CA, May 24, 2017
- Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jul 4, 2017
- Center for Statistical Science, Tsinghua University, Beijing, China, Jul 3, 2017
- School of Life Sciences, Tsinghua University, Beijing, China, Jul 3, 2017
- Institute of Machine Learning and Systems Biology, Tongji University, Shanghai, China, Dec 21, 2016
- 1<sup>st</sup> UCLA Computational Genomics Summer Institute, University of California, Los Angeles, CA, Jul 22, 2016
- Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jun 24, 2016
- Faculty Research Lunch Series, Quantitative and Computational Biosciences, University of California, Los Angeles, CA, May 6, 2016
- Department of Data Sciences and Operations, Marshall School of Business, University of Southern California, Los Angeles, CA, Dec 4, 2015
- Genomics Seminar, Johns Hopkins University, Baltimore, MD, Nov 17, 2015
- Jonsson Comprehensive Cancer Center Gene Regulation Intramural Meeting, University of California, Los Angeles, CA, May 5, 2015
- Department of Statistics, University of California, Riverside, CA, Feb 24, 2015
- Department of Ecology and Evolutionary Biology, University of California, Los Angeles, CA, Feb 18, 2015
- Department of Statistics, Pennsylvania State University, State College, PA, Jan 22, 2015
- Center for Systems Genomics, Pennsylvania State University, State College, PA, Jan 21, 2015
- Department of Biostatistics, University of California, Los Angeles, CA, November 19, 2014
- MOE Key Laboratory of Bioinformatics and Bioinformatics Division, TNLIST / Department of Automation, Tsinghua University, Beijing, China, Jun 20, 2014
- Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Jun 19, 2014
- Department of Statistics, Columbia University, NY, May 1, 2014
- Department of Molecular and Computational Biology, University of Southern California, CA, Mar 6, 2014
- Department of Statistics, University of California, Los Angeles, CA, Jan 14, 2014
- School of Life Sciences, Tsinghua University, Beijing, China, Dec 13, 2013
- Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, Apr 11, 2013
- Department of Statistics, University of Chicago, IL, Feb 25, 2013
- Departments of Human Genetics and Statistics, University of California, Los Angeles, CA, Feb 1, 2013
- Department of Statistics, University of California, Davis, CA, Jan 16, 2013

## **PUBLIC TALKS**

- The Science Show with Robyn Williams at ABC Australia, May 23, 2020

## **EDITORIAL BOARD & REVIEWING ACTIVITIES**

### **EDITORIAL BOARD**

- *PeerJ* – Associate Editor (2015 - )
- *Frontiers in Bioinformatics and Computational Biology* – Review Editor (2014 - )
- *Journal of Computational and Graphical Statistics* – Management Committee (2020 - )
- *PLOS Computational Biology* – Guest Editor (2020 - )

#### **REVIEWER FOR SCIENTIFIC JOURNALS**

- *Annals of Applied Statistics*
- *Bioinformatics*
- *Biometrics*
- *Biostatistics*
- *BMC Bioinformatics*
- *BMC Genomics*
- *BMC Medical Genomics*
- *BMC Research Notes*
- *Communications Biology*
- *Computational Biology and Chemistry*
- *Computational Statistics and Data Analysis*
- *Computers in Biology and Medicine*
- *eLife*
- *Frontiers in Genetics*
- *F1000Research*
- *Gene Reports*
- *Genes*
- *Genetics*
- *Genome Biology*
- *Genome Research*
- *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
- *Journal of American Statistical Association*
- *Journal of Machine Learning Research*
- *Nature Biotechnology*
- *Nature Communications*
- *Nature Methods*
- *Nucleic Acids Research*
- *PeerJ*
- *PLOS Computational Biology*
- *Proceedings of the National Academy of Sciences of the United States of America*
- *Science*
- *Science Bulletin*
- *Science Translational Medicine*
- *Statistica Sinica*
- *Statistical Applications in Genetics and Molecular Biology*
- *Statistics and Its Interface*
- *Statistics in Medicine*

#### **REVIEWER FOR CONFERENCES**

- ISMB 2020: the 28<sup>th</sup> Conference on Intelligent Systems for Molecular Biology
- ISMB/ECCB 2019: the 27<sup>th</sup> Conference on Intelligent Systems for Molecular Biology
- APBC 2019: the 17<sup>th</sup> Asia Pacific Bioinformatics Conference
- ICIBM 2018: International Conference on Intelligent Biology and Medicine
- APBC 2016: the 14<sup>th</sup> Asia Pacific Bioinformatics Conference

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

- Reviewer, NIGMS ESI MIRA Study Section, 2020
- Reviewer, NIH GCAT (Genomics, Computational Biology and Technology) Study Section, 2020
- Reviewer, NSF (National Science Foundation) BIO Review Panel, 2019
- 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, 2018
- Reviewer, NSF (National Science Foundation) DMS Review Panel, 2017
- Reviewer, Hong Kong General Research Fund (GRF), 2016, 2017, 2018, 2019
- Reviewer, NIH/NIEHS Review Panel, 2016
- Reviewer, Israel Science Foundation, 2016
- Reviewer, NSF (National Science Foundation) IIS Review Panel, 2016
- Specialist Reviewer, DOD CDMRP (Department of Defense Congressionally Directed Medical Research Programs) Review Panel, 2015

## PROFESSIONAL SERVICE

- 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

- Participant in the CEILS (Center for Education Innovation & Learning in the Sciences) Faculty Workshop on Best Practices in Teaching, UCLA, Sep 17, 2015
- Participant in the Success in Science Workshop, Oxnard, CA, Feb 5-7, 2015

## OTHER PROFESSIONAL ACTIVITIES

- Program Faculty at the UCLA Bruins in Genomics Summer Program, 2020
- Proceedings Program Committee of the ISMB 2020 conference



- Organization Committee of the UCLA IPAM Computational Genomics Summer Institute, Jul 15-Aug 7, 2019
- Proceedings Program Committee of the ISMB/ECCB 2019 conference
- Program Faculty at the UCLA IPAM Computational Genomics Summer Institute, Jul 11-Aug 3, 2018
- Program Faculty at the UCLA Bruins in Genomics Summer Program, 2020
- Program Faculty at the UCLA IPAM Computational Genomics Summer Institute, Jul 6-20, 2017
- Session Chair at the International Indian Statistical Association Conference, Oregon State University, Corvallis, OR, Aug 18-21, 2016
- Session Chair and Organizer at the Joint Statistical Meetings, Chicago, IL, Jul 30-Aug 4, 2016
- Program Faculty at the UCLA IPAM Computational Genomics Summer Institute, Jul 18-Aug 12, 2016
- Session Chair at the 14th Asia Pacific Bioinformatics Conference, San Francisco, CA, Jan 11-13, 2016
- Session Chair at the Joint Statistical Meetings, Seattle, WA, Aug 8-13, 2015
- 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
- Session Chair and Organizer at the Joint Statistical Meetings, Boston, MA, Aug 2-8, 2014
- Participant in the Women in Statistics Conference, Research Triangle Park, NC, May 15-17, 2014
- Participant in the SAMSI Social Network Data: Collection and Analysis Workshop, Research Triangle Park, NC, Oct 21-23, 2013
- Participant in the IPAM (Institute of Pure and Applied Mathematics) “Mathematical and Computational Approaches in High-Throughput Genomics” Program, Los Angeles, CA, Fall 2011
- 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)