Jingyi Jessica Li

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Department of Statistics
University of California, Los Angeles, CA 90095-1554 USA
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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:

- 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
- Neyman-Pearson (NP) classification: an umbrella algorithm; NP receiver operating characteristics (NP-ROC); feature ranking

EMPLOYMENT

2013 - Assistant Professor, University of California, Los Angeles
    Department of Statistics (primary appointment)
    Department of Human Genetics (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

2018	Junior Researcher Paper Award, International Chinese Statistical Association (ICSA) China Conference
2018	Math Scholar Award, Johnson & Johnson Women in STEM^{2}D (Science, Technology, Engineering, Math, Manufacturing and Design) Program (one winner per category, selected among 525 applications from 35 countries)
2018	Sloan Research Fellowship, Sloan Foundation
2017	Research Starter Award in Informatics, PhRMA Foundation
2016	Affordable Course Materials Initiative Award, UCLA
2016	Faculty Research Grant / Trans-disciplinary Seed Grant, UCLA
2016	Chancellor's Award for Teaching a *Fiat Lux* Freshman Seminar
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

Sloan Research Fellowship **09/15/2018 – 09/14/2020**
Sloan Foundation $65,000

Johnson & Johnson Women in STEM^{2}D Scholar Award **01/21/2018 – 01/21/2021**
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"

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

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"

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

RESEARCH PAPERS

PUBLISHED

1. Li, W.V. and **Li, J.J.**$^+$ (2018). Modeling and analysis of RNA-seq data: a review from a statistical perspective. *Quantitative Biology* (in press).

2. 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.

3. Li, W.V., Zhao, A., Zhang, S.$^+$, and **Li, J.J.**$^+$ (2018). MSIQ: joint modeling of multiple RNA-seq samples for accurate isoform quantification. *Annals of Applied Statistics* 12(1):510-539. PubMed PMID: 29731954; PubMed Central PMCID: PMC5935499.

4. Li, W.V. and **Li, J.J.**$^+$ (2018). An accurate and robust imputation method scImpute for single cell RNA-seq data. *Nature Communications* 9:997. PubMed PMID: 29520097; PubMed Central PMCID: PMC5843666.

5. Tong, X.$^+$, Feng, Y., and **Li, J.J.$^+$** (2018). Neyman-Pearson classification algorithms and NP receiver operating characteristics. *Science Advances* 4(2):eaao1659. PubMed PMID: 29423442; PubMed Central PMCID: PMC5804623.

6. 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.

7. **Li, J.J.$^+$**, Chew, G.L., and Biggin, M.D.$^+$ (2017). Quantitating translational control: mRNA abundance-dependent and independent contributions and the mRNA sequences that specify them. *Nucleic Acids Research* 45(20):11821-11836. 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

8. 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*. PubMed PMID: 29076140.

9. Clifton, S.M., Kang, C.$^+$, **Li, J.J.$^+$**, Long, Q., Shah, N., and Abrams, D.M.$^+$ (2017). Hybrid statistical and mechanistic mathematical model guides mobile health intervention for chronic pain. *Journal of Computational Biology* 24(7):675-688. PubMed PMID: 28581814; PubMed Central PMCID: PMC5510708.

10. 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.

11. Li, W.V., Chen, Y. and **Li, J.J.$^+$** (2017). TROM: A testing-based method for finding transcriptomic similarity of biological samples. *Statistics in Biosciences* 9(1):105-136. PubMed PMID: 28781712; PubMed Central PMCID: PMC5542419.

12. Gao, R. and **Li, J.J.$^+$** (2017). Correspondence of *D. melanogaster* and *C. elegans* developmental stages revealed by alternative splicing characteristics of conserved exons. *BMC Genomics* 18(1):234. PubMed PMID: 28302059; PubMed Central PMCID: PMC5353869.

13. Yang, Y., Yang, Y.C.T., Yuan J., Lu, Z.J.$^+$, and **Li, J.J.$^+$** (2017). Large-scale mapping of mammalian transcriptomes identifies conserved genes associated with different cell states. *Nucleic Acids Research* 45(4):1657-1672. PubMed PMID: 27980097; PubMed Central PMCID: PMC5389511.

14. Ye, Y. and **Li, J.J.$^+$** (2016). NMFP: a non-negative matrix factorization based preselection method to increase accuracy of identifying mRNA isoforms from RNA-seq data. *BMC Genomics* 17(Supp 1):11. PubMed PMID: 26818007; PubMed Central PMCID: PMC4895266.

15. 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.

16. 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):1026-38. PubMed PMID: 25857574.

17. **Li, J.J.** and Biggin, M.D. (2015). Statistics requantitates the central dogma. *Science* 347(6226):1066-1067. PubMed PMID: 25745146.

18. 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.

19. 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.

20. **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

21. **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

22. 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. PubMed PMID: 23236164; PubMed Central PMCID: PMC3535648.

23. 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.

24. 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.

25. 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.

26. **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.

27. 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

28. Liu, H., Xu, X., and **Li, J.J.**$^+$ (2018). Constructing confidence intervals for high-dimensional linear model coefficients via Bootstrap Lasso+Partial Ridge. arXiv preprint arXiv:1706.02150. Under revision at *Statistica Sinica*.

29. Razaee, Z., Amini, A., and **Li, J.J.** (2018). Matched bipartite block model with covariates. arXiv preprint arXiv:1703.04943. Under revision at *Journal of Machine Learning Research*.

30. Li, W.V., Tong, X., and **Li, J.J.**$^+$ (2018). AIDE: a statistical method for annotation-based isoform discovery and abundance estimation from RNA-seq data. Under review at *Proc Natl Acad Sci. USA*.

MANUSCRIPTS

31. **Li, J.J.**$^+$, Tong, X., and Bickel, P.J. (2018). Generalized R^2 measures for a mixture of bivariate linear dependences.

32. Chen, Y., Tong, X., and **Li, J.J.**$^+$ (2018). A general model selection criterion under the Neyman-Pearson binary classification paradigm.

33. **Li, J.J.**$^+$, Chew, G.L., and Biggin, M.D.$^+$ (2018). Principles of *cis*-translational control by general mRNA features in six model eukaryotes.

34. Sun, Y. and **Li, J.J.**$^+$ (2018). A tight spectral clustering algorithm for bipartite networks with node covariates.

35. **Li, J.J.**$^+$ (2018). Review of "Statistical modeling and machine learning for molecular biology" by Moses, A.M. Invited review article for *The American Statistician*.

BOOK CHAPTERS

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

37. **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

38. **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)

STAT 205: PhD-level course "Hierarchical Linear Models"
Winter 2017, Fall 2017

STAT 207: PhD-level course "Statistical Learning with Sparsity"
Spring 2018

STAT M254 / BIOINFO M271 / BIOMATH M271:
PhD-level Course "Statistical Methods in Computational Biology"
Spring 2014, Spring 2015, Spring 2016, Spring 2017, Spring 2018

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

STAT 402: MAS-level course "Applied Regression"
Fall 2016

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

GRADUATE STUDENTS

Tianyi Sun (2017 -)	PhD student in Statistics at UCLA
Nan Xi (2017 -)	PhD student in Statistics at UCLA
Soo Bin Kwon (Spring 2017)	Ph D rotation student in Bioinformatics at UCLA
Lingyu Zhan (Winter 2017)	PhD rotation student in Gene Regulation at UCLA
Xinzhou Ge (2016 -)	MS student in Statistics at UCLA
Yiling Chen (2016 -)	PhD student in Statistics at UCLA
Xinyuan Chen (Fall 2016)	PhD rotation student in Human Genetics at UCLA
Mudra Choudhury (Fall 2016)	PhD rotation student in Bioinformatics at UCLA
Surui Sun (2015 -):	MS student in Statistics at UCLA
Yidan Sun (2015 -):	PhD student in Statistics at UCLA
Jiaping Zhu (2015 -)	PhD student in Statistics at UCLA
Douglas Arneson (Winter 2015):	PhD rotation student in Bioinformatics at UCLA
Wei Li (2014 -):	PhD student in Statistics at UCLA
Zahra Razaee (2014 - 2017):	PhD student in Statistics at UCLA
Arturo Ramirez (2013 - 2015):	MS student in Statistics at UCLA

UNDERGRADUATE STUDENTS

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:

- As the committee chair
  - Zahra Razaee (2016 -)
  - Wei Li (2016 -)
  - Yidan Sun (2017 -)
  - Jiaping Zhu (2017 -)
  - Yiling Chen (2017 -)
  - Nan Xi (2018 -)
- As a committee member
  - Nikhyl Bryon Aragam (2013 - 2015)
  - Jianwen Xie (2015 - 2016)
  - Qian Xiao (2014 -)
  - Joshua Gordon (2015 -)
  - Seunghyun Min (2016 -)
  - Levon Demirdjian (2016 -)
  - Zhixin Zhou (2017 -)

  - Kun Zhou (2017 -)

PhD in other majors:

  - Yun-hua Hsiao (Bioengineering, 2014 -)
  - Shanxi Jiang (Molecular, Cellular, and Integrative Physiology, 2015 -)
  - Sepideh Mazrouee (Computer Science, 2016 - 2017)
  - Jui-Ting Ju (Computer Science, 2016 -)
  - Hung-Hao Lo (Molecular Biology, 2016 -)
  - Zong Miao (Bioinformatics, 2016 -)
  - Qin An (Human Genetics, 2017 -)
  - Xinhui Zhang (Biology, 2017 -)
  - Kikuye Koyano (Bioinformatics, 2018 -)

MS in Statistics:

- As the committee chair
  - Surui Sun (2017)
  - Yu-Cheng Yang (2017)
- As a committee member
  - 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)

MAS in Statistics:

- As the committee member
  - Hui Zhang (2018)

INVITED TALKS & PRESENTATIONS

CONFERENCE AND SYMPOSIUM PRESENTATIONS

- Regulatory and Systems Genomics (RegSys) Community of Special Interest (COSI) at the 26th Conference on Intelligent Systems for Molecular Biology (ISMB), Jul 10, 2018
- The 5th 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, 2017
- The 46th Annual Meeting of the Statistical Society of Canada, McGill University, Montreal, QB, Canada, June 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 22nd International Conference on Research in Computational Molecular Biology (RECOMB), Paris, France, Apr 24, 2018
- Joint Statistical Meetings, Baltimore, MD, Aug 3, 2017
- The 1st North American Social Networks (NASN) Conference, Washington, D.C., Jul 28, 2017
- ICSA Applied Statistics Symposium, Chicago, IL, Jun 26, 2017
- HDDA VII (The 7th International Workshop on Perspectives on High-dimensional Data Analysis), CIMAT, Guanajuato, Mexico, Jun 18, 2017
- UCLA QCB 2nd 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 10th ICSA International Conference: Global Growth of Modern Statistics in the 21st 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 3rd Taihu International Statistics Forum, Shanghai, China, Jul 10, 2016
- The ICSA Conference on Data Science, Dali, China, July 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 1st Annual Symposium “Exploring the Frontiers of Biomedical Big Data,” UCLA, Los Angeles, CA, Jun 1, 2016
- The 14th 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 7th 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, July 31, 2014
- The 9th ICSA International Conference: Challenges of Statistical Methods for Interdisciplinary Research and Big Data, Hong Kong Baptist University, Hong Kong, Dec 23, 2013
- The 6th RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, Toronto, Canada, Nov 12, 2013
- The 17th RECOMB (Annual International Conference on Research in Computational Molecular Biology), Beijing, China, Apr 8, 2013
- UC Systemwide Bioengineering Symposium, Berkeley, CA, June 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 INSTITUTUTES

- Department of Biomathematics, University of California, Los Angeles, Oct 4, 2018
- Department of Statistics, University of Georgia, Athens, GA, Aug 23, 2018
- Omics Seminar, Cedars-Sinai Medical Center, Los Angeles, CA, Jul 24, 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
- 2nd 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, July 4, 2017

- Center for Statistical Science, Tsinghua University, Beijing, China, July 3, 2017
- School of Life Sciences, Tsinghua University, Beijing, China, July 3, 2017
- Institute of Machine Learning and Systems Biology, Tongji University, Shanghai, China, Dec 21, 2016
- 1st 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, June 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, June 20, 2014
- Institute of Applied Mathematics, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, June 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

EDITORIAL BOARD & REVIEWING ACTIVITIES

EDITORIAL BOARD

- *PeerJ* - Associate Editor (2015 -)
- *Frontiers in Bioinformatics and Computational Biology* - Review Editor (2014 -)

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*
- *Frontiers in Genetics*
- *F1000Research*
- *Gene Reports*
- *Genetics*
- *Genome Research*
- *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
- *Journal of American Statistical Association*
- *Journal of Machine Learning Research*
- *Nature Communications*
- *Nucleic Acids Research*
- *PeerJ*
- *PLOS Computational Biology*
- *Science*
- *Science Bulletin*
- *Statistica Sinica*
- *Statistical Applications in Genetics and Molecular Biology*
- *Statistics and Its Interface*

REVIEWER FOR CONFERENCES

- APBC 2016: the 14th Asia Pacific Bioinformatics Conference
- ICIBM 2018: International Conference on Intelligent Biology and Medicine

REVIEWER FOR GRANT APPLICATIONS

- Reviewer, NSF (National Science Foundation) DMS Review Panel, 2017
- Reviewer, Hong Kong general research fund (GRF), 2016
- 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

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 -	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 ACTIVIES

- 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

- 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

2013 -	ISCB (International Society for Computational Biology)
2009 -	ICSA (International Chinese Statistical Association)