

Li, Wei Vivian

University of California, Riverside
900 University Ave.
Riverside, CA 92521

Telephone: (951)827-3774
Email: weil@ucr.edu
Homepage: vivianli.org

EDUCATION

| | |
|--|-------------------|
| University of California, Los Angeles (UCLA) | 09/2014 - 06/2019 |
| Department of Statistics | |
| Ph.D. in Statistics | |
| Dissertation: Statistical methods for bulk and single-cell RNA sequencing data | |
| Advisor: Dr. Jingyi Jessica Li | |
| Huazhong University of Science & Technology (HUST) | 09/2010 - 06/2014 |
| School of Mathematics and Statistics | |
| B.S. in Statistics | |

EMPLOYMENT

| | |
|---|-------------------|
| Associate Professor | 07/2025 - |
| Assistant Professor | 07/2022 - 06/2025 |
| Department of Statistics | |
| University of California, Riverside | |
| Assistant Professor | 08/2019 - 06/2022 |
| Department of Biostatistics and Epidemiology, School of Public Health | |
| Department of Statistics and Biostatistics (courtesy appointment) | |
| Rutgers, The State University of New Jersey | |
| Teaching Assistant Consultant | 10/2018 - 06/2019 |
| Department of Statistics | |
| University of California, Los Angeles | |
| Graduate Student Researcher | 09/2016 - 06/2018 |
| Department of Statistics | |
| University of California, Los Angeles | |

HONORS AND AWARDS

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|---|------|
| Best Paper Award, RECOMB 2022 | 2022 |
| Busch Biomedical Grant Award, Rutgers | 2020 |
| The Caliburn Allocation Award of Research Computing, Rutgers | 2020 |
| The Most Outstanding Statistician Award, UCLA | 2019 |
| Physical Sciences Entrepreneurship & Innovation Award (co-inventor), UCLA | 2018 |
| Dissertation Year Fellowship, UCLA | 2018 |
| Pearl Cohen Poster Award, UCLA Biomedical & Life Science Innovation Day | 2018 |

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| Diversity Scholarship, UseR 2016 Conference | 2016 |
| Doctoral Student Travel Grant, UCLA | 2016 |
| The Most Promising Computational Statistician Award, UCLA | 2015 |
| Distinguished Graduate of Class 2014, HUST | 2014 |
| National Fellowship, Ministry of Education, China | 2013 |
| Student Award of Excellence (awarded to 20 students per year), HUST | 2013 |
| National Fellowship, Ministry of Education, China | 2012 |
| National Fellowship, Ministry of Education, China | 2011 |
| Outstanding Student Award (awarded to 3 students in each department), HUST | 2011 |

RESEARCH FUNDING

Ongoing:

California Education Learning Lab Grant (Salloum & Flores) 07/01/2023 - 06/30/2027
 Greater LA Data Science Pathways (GLADS-PATH)
 Role: Co-PI

NSF 2244480 (Chen & Fu) 04/01/2023 - 03/31/2026
 REU Site: Experience the full data science pipeline through research and practice
 Role: Senior Personnel

NIH/NCI R01 CA272578 (Cao) 07/15/2022 - 06/30/2027
 Hepatitis B virus integrations in KMT2B drive hepatocellular carcinoma
 Role: Co-I

NIH/NIDDK R01 DK126446 (Verzi) 09/23/2021 - 05/31/2026
 Mechanisms driving metabolic shifts in the intestinal epithelium
 Role: Co-I

NIH/NIGMS R35 GM142702 (Li) 09/01/2021 - 06/30/2026
 Novel statistical methods for multiscale analysis of single-cell transcriptomes
 Role: PI

Completed:

NIH/NIMH R21 MH126420 (Pang & Li) 07/01/2021 - 06/30/2024
 Multimodal profiling of neurons in 3D human cortical organoids using patch-seq
 Role: PI

NSF/IIS 2128307 (Zhang) 10/01/2021 - 09/30/2022
 EAGER: Integration and analysis of high-dimensional dataset
 Role: Co-PI

Rutgers Busch Biomedical Grant (Li) 10/01/2020 - 06/30/2022
A novel approach for joint modeling of multi-patient single-cell gene expression data
Role: PI

NJ ACTS Mini-Methods Grant (Li) 06/04/2020 - 02/28/2022
Statistical methods for single-cell differential gene network analysis
Role: PI

Rutgers School of Public Health Pilot Grant (Li) 11/01/2019 - 06/01/2021
Understanding gene co-expression patterns in single cells
Role: PI

PUBLICATIONS

— Corresponding authors [†] Current or past members of Li group

Google Scholar: <https://scholar.google.com/citations?user=HzjANkQAAAAJ>

Refereed Article:

1. Yang T[†], **Li WV**. (2025). Generalized probabilistic canonical correlation analysis for multi-modal data integration with full or partial observations. *BMC Bioinformatics*, in press.
2. Wang X, **Li WV**, **Li H**. (2025). spCLUE: a contrastive learning approach to unified spatial transcriptomics analysis across single-slice and multi-slice data. *Genome Biology*, 26(1), 1-23.
3. Antonio JM, Liu Y, Suntornsaratoon P, Jones A, Ambat J, Bala A, Kanattu JJ, Flores J, Bandyopadhyay S, Upadhyay R, Bhupana JN, Su X, **Li WV**, Gao N, Ferraris RP. (2025). Lactocaseibacillus rhamnosus GG-driven remodeling of arginine metabolism mitigates gut barrier dysfunction. *American Journal of Physiology-Gastrointestinal and Liver Physiology*, 329(1), G162-85.
4. Fu S[†], **Li WV**. (2025). Predicting and comparing transcription start sites in single cell populations. *PLOS Computational Biology*, 21(4), e1012878.
5. Wan D, Cheng A[†], Wang Y, Zhong G, **Li WV**, **Fan H**. (2024). Analyzing RNA-seq data from Chlamydia with super broad transcriptomic activation: Challenges, Solutions, and Implications for Other Systems. *BMC Genomics*, 25, 801.
6. **Yu S**, **Li WV**. (2024). spVC for the detection and interpretation of spatial gene expression variation. *Genome Biology*, 25(1), 103.
7. Singh M, Sahinalp C, Zeng J, **Li WV**, Kingsford C, Zhang Q, Przytycka T, Welch J, Ma J, Berger B. (2024). How has the AI boom impacted algorithmic biology?. *Cell Systems*, 15(6), 483-7.
8. Suntornsaratoon P, Antonio JM, Flores J, Upadhyay R, Veltri J, Bandyopadhyay S, Dadala R, Kim M, Liu Y, Balasubramanian I, Turner JR, Su X, **Li WV**, Gao N, Ferraris RP (2024). Lactobacillus rhamnosus GG stimulates dietary tryptophan-dependent production of barrier-protecting methylnicotinamide. *Cellular and Molecular Gastroenterology and Hepatology*, 18(2), 101346.

9. Suntornsaratoon P, Ferraris RP, Ambat J, Antonio JM, Flores J, Jones A, Su X, Gao N, **Li WV**. (2024). Metabolomic and transcriptomic correlative analyses in germ-free mice link *Lactobacillus rhamnosus* GG-associated metabolites to host intestinal fatty acid metabolism and β -oxidation. *Laboratory Investigation*, 104(4), 100330.
10. Li T, Qian K⁺, Wang X, **Li WV**, Li H. (2024). scBiG for representation learning of single-cell gene expression data based on bipartite graph embedding. *NAR Genomics and Bioinformatics*, 6(1), lqae004.
11. Wurihan W, Wang Y, Yeung S, Zou Y, Lai Z, Fondell JD, **Li WV**, Zhong G, Fan H. (2024). Expression activation of over 70% of *Chlamydia trachomatis* genes during the first hour of infection. *Infection and Immunity*, online ahead of print.
12. Lu B, Wang Y, Wurihan W, Cheng A⁺, Yeung S, Fondell JD, Lai Z, Wan D, Wu X, **Li WV**, Fan H. (2024). Requirement of GrgA for *Chlamydia* infectious progeny production, optimal growth, and efficient plasmid maintenance. *Mbio*, 15(1), e02036-23.
13. Ren H, Chen X, Wang J, Chen Y, Hafiz A, Xiao Q, Fu S⁺, Madireddy A, **Li WV**, Shi X, Cao J. (2023). Temporal and structural patterns of hepatitis B virus integrations in hepatocellular carcinoma. *Journal of Medical Virology*, 95(10), e29187.
14. Balasubramanian I, Bandyopadhyay S, Flores J, Bianchi-Smak Jared, Lin X, Liu H, Sun S, Golovchenko N, Liu Y, Wang D, Patel R, Joseph I, Suntornsaratoon P, Vargas J, Green P, Bhagat G, Lagana S, Ying W, Zhang Y, Wang Z⁺, **Li WV**, Singh S, Zhou Z, Kollias G, Farr L, Moonah S, Yu S, Wei Z, Bonder E, Zhang L, Kiela P, Edelblum K, Ferraris R, Liu T, Gao N. (2023). Infection and inflammation stimulate CD74+ Paneth cell subset to regulate disease progression. *The EMBO Journal*, e113975.
15. He X, Qian K⁺, Wang Z, Zeng S, Li H, and **Li WV**. (2023). scAce: an adaptive embedding and clustering method for single-cell gene expression data. *Bioinformatics*, btad546.
16. Liu J⁺, Kreimer A, and **Li WV**. (2023). Differential variability analysis of single-cell gene expression data. *Briefings in Bioinformatics*, bbad294.
17. Cheng A⁺, Hu, G, and **Li WV**. (2022). Benchmarking cell-type clustering methods for spatially resolved transcriptomics data. *Briefings in Bioinformatics*, bbac475.
18. Berger B, Tian D, **Li WV**, El-Kebir M, Tomescu AI, Singh R, Beerenwinkel N, Li Y, Boucher C, and Bar-Joseph Z. (2022). What are the keys to succeeding as a computational biologist in today's research climate? *Cell Systems*, 13(10), 781-785.
19. Qian K⁺, Fu S⁺, Li H, and **Li WV**. (2022). The scINSIGHT package for integrating single-cell RNA-seq data from different biological conditions. *Journal of Computational Biology*, Online Ahead of Print.
20. Qian K⁺, Fu S⁺, Li H, and **Li WV**. (2022). scINSIGHT for interpreting single-cell gene expression from biologically heterogeneous data. *Genome Biology*, 23, 82.
21. **Li WV**. (2022). Phitest for analyzing the homogeneity of single-cell populations. *Bioinformatics*, btac130.
22. Sun, T, Song, D, **Li WV**, and Li, JJ. (2022). Simulating single-cell gene expression count data with preserved gene correlations by scDesign2. *Journal of Computational Biology*, 29(1), 23-26.

23. **Li WV** and Li Y[†]. (2021). scLink: inferring sparse gene co-expression networks from single-cell expression data. *Genomics, Proteomics & Bioinformatics*, 19(3), 475-492.
24. Colon A, Hirday R, Patel A, Poddar A, Tuberty-Vaughan E, Fu T, Ai X, **Li WV**, and Cai L. (2021). A computational pipeline for functional gene discovery. *Scientific Reports*, 11, 23522.
25. Sheng J[†] and **Li WV**. (2021) Selecting gene features for unsupervised analysis of single-cell gene expression data. *Briefings in Bioinformatics*, bbab295.
26. **Li WV**, Zheng D, Wang R, and Tian B. (2021). MAAPER: model-based analysis of alternative polyadenylation using 3'end-linked reads. *Genome Biology*, 22, 222.
27. Zhang XS, Yin YS, Wang J, Battaglia T, Krautkramer K, **Li WV**, Li J, Brown M, Zhang M, Badri MH, Armstrong AJ, Strauch CM, Wang Z, Nemet I, Altomare N, Devlin JC, He L, Morton JT, Chalk JA, Needles K, Liao V, Mount J, Li H, Ruggles KV, Bonneau RA, Dominguez-Bello MG, Bäckhed F, Hazen SL, Blaser MJ. (2021). Maternal cecal microbiota transfer rescues early-life antibiotic-induced enhancement of type 1 diabetes in mice. *Cell Host & Microbe*, 29(8), 1249-1265.
28. Jiang R, **Li WV**, and Li JJ. (2021). mbImpute: an accurate and robust imputation method for microbiome data. *Genome Biology*, 22(1), 192.
29. Sun T, Song D, **Li WV**, and Li JJ. (2021). scDesign2: an interpretable simulator that generates high-fidelity single-cell gene expression count data with gene correlations captured. *Genome Biology*, 22(1), 1-37.
30. Zheng Y, Chen Z, Han L, Han Y, Zou X, Zhou B, Hu R, Hao J, Bai S, Xiao H, **Li WV**, Bueker A, Ma Y, Xie G, Yang J, Chen S, Li H, Cao J, and Shen L. (2020). Immune suppressive landscape in the human esophageal squamous cell carcinoma microenvironment. *Nature Communications*, 11(1), 1-17.
31. Wang J, Deng F, Zeng F, Shanahan AJ, **Li WV**, and Zhang L. (2020). Predicting long-term multicategory cause of death in patients with prostate cancer: random forest versus multinomial model. *American Journal of Cancer Research*, 10(5), 1344.
32. Xu J, Cheng Y, Yuan X, **Li WV**, and Zhang L. (2020). Trends and prediction in daily incidence of novel coronavirus infection in China, Hubei Province and Wuhan City: an application of Farr's law. *American Journal of Translational Research*, 12(4), 1355.
33. **Li WV**, Li S, Tong X, Deng L, Shi H, and Li JJ. (2019) AIDE: annotation-assisted isoform discovery with high precision. *Genome Research*, 29, 2056-2072.
34. **Li WV** and Li JJ. (2019). A statistical simulator scDesign for rational scRNA-seq experimental design. *Bioinformatics (ISMB/ECCB 2019)*, 35(14), i41-i50.
35. Ge X, Zhang H, Xie L, **Li WV**, Kwon SB, and Li JJ. (2019). EpiAlign: an alignment-based bioinformatic tool for comparing chromatin state sequences. *Nucleic Acids Research*, gkz287.
36. **Li WV** and Li JJ. (2018). An accurate and robust imputation method scImpute for single-cell RNA-seq data. *Nature Communications*, 9, 997.
37. **Li WV** and Li JJ. (2018). Modeling and analysis of RNA-seq data: a review from a statistical perspective. *Quantitative Biology*, 6(3), 195-209.

38. Li WV, Zhao A, Zhang S, and Li JJ. (2018). MSIQ: joint modeling of multiple RNA-seq samples for accurate isoform quantification. *Annals of Applied Statistics*, 12(1), 510-539.
39. Li WV, Chen Y, and Li JJ. (2017). TROM: a testing-based method for finding transcriptomic similarity of biological samples. *Statistics in Biosciences*, 9(1), 105-136.
40. Li WV, Razaee ZS, and Li JJ. (2016). Epigenome overlap measure (EPOM) for comparing tissue/cell types based on chromatin states. *BMC Genomics*, 17(1), S10.

PhD Dissertation:

41. Li WV. (2019). Statistical methods for bulk and single-cell RNA sequencing data. PhD dissertation, UCLA.

INVITED TALKS AND CONFERENCE PRESENTATIONS

Conference and Symposium Presentations:

- | | |
|---|---------|
| 1. Invited Talk, Biostatistics Symposium of Southern California | 02/2025 |
| 2. Invited Talk, Computational Modeling & Machine Learning in Biology & Medicine Workshop (UCR) | 12/2024 |
| 3. Invited Talk, ICSA 2024 China Conference | 06/2024 |
| 4. Invited Talk, 2024 ICSA Applied Statistics Symposium | 06/2024 |
| 5. Invited Talk, UCR RNA Center Retreat | 05/2024 |
| 6. Invited Talk, Front Line Genomics Single Cell and Spatial Online Webinar | 02/2024 |
| 7. Invited Talk, JSM 2023 | 08/2023 |
| 8. Invited Talk, WNAR 2023 | 06/2023 |
| 9. Invited Talk, The 2023 WiDS Riverside Conference | 04/2023 |
| 10. Invited Talk, JSM 2022 | 08/2022 |
| 11. Proceeding Talk, RECOMB 2022 | 05/2022 |
| 12. Invited Talk, Seventh International Conference on Statistics for Twenty-first Century. | 12/2021 |
| 13. Keynote Talk, IEEE International Conference on Bioinformatics and Biomedicine. Workshop on Computational Methods and Their Applications on Single Cell Multiomic Data | 12/2021 |
| 14. Talk, Machine Learning in Computational Biology 2021. | 11/2021 |
| 15. Invited Talk, Advanced Genetic Sequencing Virtual Conference. | 09/2021 |
| 16. Invited Poster, 1st Annual NJ ACTS Science Symposium. | 09/2021 |
| 17. Invited Talk, ICSA 2021 Applied Statistics Symposium. | 09/2021 |
| 18. Talk, RECOMB 2021. | 09/2021 |
| 19. Invited Talk, Joint Statistical Meetings. | 08/2021 |

20. Talk, 29th Conference on Intelligent Systems for Molecular Biology. 07/2021
21. Invited Talk, Fifth International Conference on Recent Trends in Statistical Theory and Applications. 06/2021
22. Invited Talk, Sixth International Conference on Statistics for Twenty-first Century. 12/2020
23. Poster, RECOMB/ISCB 2020 Conference on Regulatory and Systems Genomics. 11/2020
24. Talk, Human Cell Atlas Asia Meeting 2020. 10/2020
25. Talk, 2020 Joint Statistical Meetings. 08/2020
26. Invited Talk, RCAF Forum: Challenges and Opportunities in Computational Biology. 08/2020
27. Poster, 28th Conference on Intelligent Systems for Molecular Biology (ISMB 2020). 07/2020
28. Invited Talk, RCAF Webinar Series. 05/2020
29. Invited Talk, ENAR 2020 Spring Meeting. 03/2020
30. Invited Talk, Inaugural Lange Symposium Software Workshop. 02/2020
31. Invited Talk, 2019 Joint Statistical Meetings. 07/2019
32. Invited Talk, ENAR 2019 Spring Meeting. 03/2019
33. Talk, 8th Annual Southern California Systems Biology Conference. 02/2019
34. Invited Talk, 2018 IEEE 8th International Conference on Computational Advances in Bio and Medical Sciences. 10/2018
35. Talk and Poster, Inaugural Symposium on Multiscale Cell Fate. 10/2018
36. Talk, UCLA 4th Annual QCBio Retreat. 09/2018
37. Talk, 2018 Joint Statistical Meetings. 08/2018
38. Talk, 26th Conference on Intelligent Systems for Molecular Biology (ISMB 2018). 06/2018
39. Poster, UCLA Biomedical & Life Science Innovation Day. 06/2018
40. Invited Talk, DahShu Webinar. 04/2018
41. Invited Talk, 3rd Annual NGS Data Analysis & Informatics Conference. 02/2018
42. Poster, UCLA 3rd Annual QCBio Retreat. 09/2017
43. Talk, Asia Pacific Bioinformatics Conference 2016. 01/2016
44. Talk, USC/UCLA Bioinformatics Joint Meeting. 11/2015
45. Poster, UCLA 1st Annual QCBio Retreat. 09/2015

Seminar Presentations:

46. Department of Computational Medicine & Bioinformatics, University of Michigan. 10/2024

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| 47. Center of Mathematical Sciences, China University of Geosciences. | 07/2024 |
| 48. Interdisciplinary Center for Quantitative Modeling in Biology, University of California, Riverside. | 05/2023 |
| 49. Department of Statistics, The University of Virginia. | 04/2023 |
| 50. Department of Mathematics and Statistics, San Diego State University. | 04/2023 |
| 51. Data Science Seminar Series, University of California, Riverside. | 10/2022 |
| 52. Young Bioinformatics PI Seminar Series. | 05/2022 |
| 53. NCMDB/GGB/MCBL Seminar Series, University of California, Riverside. | 04/2022 |
| 54. NJ ACTS Biostatistics and Epidemiology Workshop, Rutgers University. | 05/2021 |
| 55. Department of Mathematics, Texas State University. | 04/2021 |
| 56. Bioinformatics-Human Genetics Seminar, UCLA. | 04/2021 |
| 57. Institute for Quantitative Biomedicine, Rutgers University. | 01/2021 |
| 58. Epigenetics User Group Meeting, Rutgers Department of Genetics | 02/2020 |
| 59. Systems Biology/Bioinformatics Meeting, Rutgers Cancer Institute of New Jersey | 10/2019 |
| 60. Department of Biostatistics and Epidemiology, Rutgers University. | 02/2019 |
| 61. Department of Statistics, University of Wisconsin-Madison. | 02/2019 |
| 62. Department of Public Health, University of California, Merced. | 01/2019 |
| 63. Department of Statistics, Pennsylvania State University. | 01/2019 |
| 64. Department of Statistics, University of Illinois at Urbana-Champaign. | 12/2018 |
| 65. Jonsson Comprehensive Cancer Center Gene Regulation Intramural Meeting, UCLA. | 03/2018 |

TEACHING EXPERIENCE

Instructor (UCR):

| | |
|---|-------------|
| STAT 140: Nonparametric techniques | Spring 2025 |
| STAT 208: Statistical Data Mining Methods | Winter 2025 |
| STAT 218: Survival Analysis | Fall 2024 |
| STAT 140: Nonparametric techniques | Spring 2024 |
| STAT 208: Statistical Data Mining Methods | Winter 2024 |
| STAT 218: Survival Analysis | Fall 2023 |
| STAT 140: Nonparametric techniques | Spring 2023 |
| STAT 208: Statistical Data Mining Methods | Winter 2023 |
| STAT 218: Survival Analysis | Fall 2022 |

Instructor (Rutgers):

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| BIST 0725: Generalized Linear Models | Spring 2022 |
| BIST 0613: Biostatistics Theory I | Fall 2021 |

BIST 0720: Advanced Biostatistical Computing
 BIST 0725: Generalized Linear Models

Spring 2021
 Spring 2020

Student Instructor (UCLA):

STATS 495A: Teaching College Statistics

Fall 2018

Teaching Assistant (UCLA):

| | |
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| STATS 207: Statistical Learning with Sparsity | Spring 2018 |
| STATS 203: Large Sample Theory, Including Resampling | Winter 2017 |
| STATS 205: Hierarchical Linear Models | Winter 2017 |
| STATS 101A: Introduction to Data Analysis and Regression | Summer 2016 |
| STATS M254: Statistical Methods in Computational Biology | Spring 2016 |
| STATS 200C: Large Sample Theory | Spring 2016 |
| STATS 13: Introduction to Statistical Methods for the Health and Life Sciences | Winter 2016 |
| STATS 10: Introduction to Statistical Reasoning | Fall 2015 |
| STATS 100B: Introduction to Mathematical Statistics | Summer 2015 |

Guest Lecturer:

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| Data Science Club | 06/2022 |
| Montgomery High School | |
| <i>Data Science Methods in Transcriptomic Studies II</i> | |
| Data Science Club | 03/2022 |
| Montgomery High School | |
| <i>Data Science Methods in Transcriptomic Studies I</i> | |
| RESH 0701: Doctoral Colloquium | 11/2021 |
| Rutgers School of Public Health | |
| <i>An Introduction to My Career Path as a Statistician</i> | |
| RESH 0701: Doctoral Colloquium | 11/2020 |
| Rutgers School of Public Health | |
| <i>Career As a Statistician in the Bioinformatics Field</i> | |
| DSO 530: Applied Modern Statistical Learning Methods | 04/2020 |
| Marshall School of Business, University of South California | |
| <i>Introduction to Cloud Computing</i> | |
| DSO 530: Applied Modern Statistical Learning Methods | 03/2019 |
| Marshall School of Business, University of South California | |
| <i>Cloud Computing with the Amazon Web Services</i> | |
| BIOINFO 201: Bioinformatics Interdisciplinary Research Seminar | 10/2018 |
| Bioinformatics Interdepartmental Ph.D. Program, UCLA | |
| <i>Statistical Methods for Isoform Quantification of Multiple Samples</i> | |
| STATS M254: Statistical Methods in Computational Biology | 06/2018 |
| Department of Statistics, UCLA | |
| <i>Statistical Methods for Isoform Quantification of Multiple Samples</i> | |

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|---|---------|
| STATS M254: Statistical Methods in Computational Biology Department of Statistics, UCLA <i>Imputation Methods for Single-cell RNA-seq Data</i> | 05/2018 |
| DSO 530: Applied Modern Statistical Learning Methods Marshall School of Business, University of South California <i>Cloud Computing with the Amazon Web Services</i> | 02/2018 |
| DSO 530: Applied Modern Statistical Learning Methods Marshall School of Business, University of South California <i>Introduction to the Amazon Web Services (AWS)</i> | 03/2017 |

ADVISING

Postdoc Scholar:

- Rui Ma (07/2024 - , Co-advised by Dr. Wenxiu Ma)

PhD Students (Thesis Advisor):

- | | |
|--------------------------------------|---|
| • Liming Zhao (07/2024 -) | PhD in Applied Statistics (UCR) |
| • Brian Tran (06/2023 - 06/2025) | PhD in Applied Statistics (UCR) |
| • Tianjian (Kiano) Yang (12/2022 -) | PhD in Applied Statistics (UCR) |
| • Yudi Mu (12/2022 -) | PhD in Applied Statistics (UCR, Co-advised by Dr. Ma) |
| • Shiwei Fu (08/2021 -) | PhD in Applied Statistics (UCR) |

PhD Students (Thesis Committee):

- | | |
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| • Nahee Kim (11/2024 -) | PhD in Applied Statistics (UCR) |
| • Jericho Lawson (01/2024 -) | PhD in Applied Statistics (UCR) |
| • Zehao Li (06/2023 -) | PhD in Genetics, Genomics & Bioinformatic (UCR) |
| • Cheng Zhong (06/2023 - 07/2023) | PhD in Computer Science (NJIT) |
| • Sabrina Stulting (05/2023 -) | PhD in CMDDB (UCR) |
| • Rui Ma (09/2022 - 06/2024) | PhD in Applied Statistics (UCR) |
| • Gregory Marshall (05/2022 -) | PhD in Microbiology and Molecular Genetics (Rutgers) |
| • Alireza Nohadani (12/2019 - 05/2020) | PhD in Computer Science (Rutgers) |
| • Tianyi Sun (10/2019 - 12/2023) | PhD in Statistics (UCLA) |
| • Aysegul Guvenek (10/2019 - 05/2020) | PhD in Biomedical Science (Rutgers) |

PhD Students (Qualifying Exam Committee):

- Shiyuan Chen (2024) PhD in GGB (UCR)
- Shiwei Fu (2024) PhD in Applied Statistics (UCR)
- Zehao Li (2024) PhD in GGB (UCR)
- Nahee Kim (2024) PhD in Applied Statistics (UCR)
- Shuang Jiang (2024) PhD in Applied Statistics (UCR)
- Jericho Lawson (2024) PhD in Applied Statistics (UCR)
- Minh Vu (2023) PhD in Mathematics (UCR)
- Jingong Huang (2023) PhD in Computer Science (UCR)
- Namhwa Lee (2023) PhD in Applied Statistics (UCR)
- Rui Ma (2022) PhD in Applied Statistics (UCR)
- Gregory Marshall (2022) PhD in Microbiology and Molecular Genetics (Rutgers)
- Wenxuan Xiong (2021) PhD in Biostatistics (Rutgers)
- Peng Zhang (2021) PhD in Biostatistics (Rutgers)

Graduate Students (Research Advisor):

- Lloyd Gilfillian (08/2022 - 09/2022) PhD in GGB (UCR)
- Song Chen (02/2022 - 06/2022) MS in Biostatistics (Rutgers)
- Maotian Li (02/2022 - 06/2022) MS in Biostatistics (Rutgers)
- Zhihan Wang (09/2021 - 05/2022) MS student in Statistics (Rutgers)
- Jiayi Liu (09/2021 - 08/2023) PhD in Molecular Biosciences (Rutgers)
- Jie Sheng (11/2020 - 07/2021) MS in Data Science (UW-Madison)
- Dayuan Wang (08/2020 - 12/2020) MS in Biostatistics (Rutgers)
- Shiwei Fu (06/2020 - 06/2021) MS in Statistics (UIUC)
- Yanzeng Li (12/2019 - 09/2020) MS in Biostatistics (Rutgers)
- Alireza Naghizadeh (06/2020 - 08/2020) PhD in Computer Science (Rutgers)

Graduate Students (Academic Advisor):

- Maotian Li (08/2021 - 06/2022) MS in Biostatistics (Rutgers)
- Rachel Lee (05/2021 - 05/2022) MS in Biostatistics (Rutgers)
- Kevin Zheng (01/2021 - 05/2022) MS in Biostatistics (Rutgers)
- Phoebe Chu (08/2020 - 12/2022) MS in Biostatistics (Rutgers)
- Changhan Lin (08/2020 - 05/2022) MS in Biostatistics (Rutgers)
- Adriel Staana (08/2020 - 12/2021) MS in Biostatistics (Rutgers)
- Daniel Yen (08/2020 - 05/2022) MS in Biostatistics (Rutgers)
- Zifan Guo (01/2020 - 05/2022) MS in Biostatistics (Rutgers)

Undergraduate Students (Research Advisor):

- John Seilbert (06/2025 -) BS in Mathematics (Bloomsburg University)
- Harley Nguyen (06/2024 -) BS in Human Computer Interaction (UC Irvine)
- Kya Olive (06/2024 - 08/2024) BS in Information Systems in Technology (CSUSB)
- Sweta Balaji (06/2024 - 08/2024) BS in Quantitative Sciences (Emory)
- Jordan Nguyen (06/2024 - 08/2024) BS in Mathematics (UCLA)
- Anika Singh (06/2023 - 08/2023) BS in Mathematics (Pasadena City College)
- Andrew Cheng (09/2020 - 11/2022) BS in Computer Science (Rutgers)

PROFESSIONAL SERVICE

Reviewer for Grant Applications:

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| NIH BDMA (Biodata Management and Analysis) Study Section | 02/2024 |
| NIH BDMA (Biodata Management and Analysis) Study Section | 10/2023 |
| NIH MGG (Molecular Genetics and Genomics) Special Emphasis Panel | 03/2023 |
| NIH BDMA (Biodata Management and Analysis) Study Section | 10/2022 |
| NIH BICAN (BRAIN Initiative Cell Atlas Network) Special Emphasis Panel | 03/2022 |
| NIH BDMA (Biodata Management and Analysis) Study Section | 10/2021 |
| Rutgers Busch Biomedical Grants Program | 07/2021 |

Reviewer for Conferences:

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| ACM Conference on Bioinformatics, Computational Biology, and Health Informatics | 2024 |
| International Conference on Research in Computational Molecular Biology (RECOMB) | 2024 |
| The 22nd European Conference on Computational Biology (ISMB/ECCB) | 2023 |
| International Conference on Research in Computational Molecular Biology (RECOMB) | 2022 |
| Pacific Symposium on Biocomputing | 2022 |

Reviewer for Scientific Journals:

Advanced Science
Annals of Applied Statistics
Applied Sciences
Big Data Minging and Analytics
Bioinformatics
BioMed Research International
Biometrics
Biostatistics
BMC Bioinformatics
BMC Genomics
Briefings in Bioinformatics
Cell Reports Methods
Cell Systems
Cells
Clinical and Translational Medicine
Communications Medicine
Exploratory Research and Hypothesis in Medicine
Frontiers in Genetics
Frontiers of Computer Science
GigaScience Gene Report
Genes
Genome Biology
Genome Research
Genomics, Proteomics & Bioinformatics
IEEE Access
IEEE/ACM Transactions on Computational Biology and Bioinformatics
Journal of Chemical Information and Modeling
Journal of Computational Biology
Journal of Molecular Cell Biology
Journal of the American Statistical Association
Laboratory Investigation
Molecular Ecology Resources

NAR Cancer
NAR Genomics and Bioinformatics
Nature Computational Science
Nature Biotechnology
Nature Communications
Nature Methods
Nucleic Acids Research
PeerJ
PLOS Computational Biology
PLOS Genetics
PLOS One
PNAS Nexus
Proteomics
Quantitative Biology
Science China Life Sciences
Statistics in Biosciences
Statistics in Medicine

Institutional Service:

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| Graduate Advisor for Admissions and Recruitment, UCR Graduate Program in Genetics, Genomics & Bioinformatics | 2024 - |
| Undergraduate Program Committee, UCR Department of Statistics | 2024 - |
| Session Chair, UCR RNA Center Retreat | 2024 |
| Colloquium Committee Co-chair, UCR Department of Statistics | 2023 - 2024 |
| Faculty Search Committee, UCR Department of Statistics | 2023 - 2024 |
| Faculty Judge, UCR Early Career Scientist Symposium | 2023 |
| MPH Course Committee, UCR Department of Statistics | 2023 - 2024 |
| Graduate Program Committee, UCR Department of Statistics | 2022 - 2023 |
| Graduate Admission Committee, UCR Department of Statistics | 2022 - 2023 |
| UCR Liaison of National Institute of Statistical Sciences | 2022 - |
| Faculty Facilitator, Rutgers Interprofessional Education Training | 2022 |
| Member, PhD Admission Committee, Rutgers Department of Biostatistics and Epidemiology | 2020 - 2022 |
| Bylaws and Elections Committee, Rutgers School of Public Health | 2020 - 2022 |
| Bioinformatics Research Committee, Rutgers University | 2020 |

Other Professional Service:

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| Session Organizer, WNAR 2025 | 2024 - 2025 |
| WNAR Student Paper Competition Committee, WNAR 2025 | 2025 |
| Organizing Committee, NISS Writing Workshop for Junior Researchers | 2025 |
| Program Committee, 29th International Conference on Research in Computational Molecular Biology (RECOMB) | 2024 - 2025 |
| Scientific Committee, NISS Graduate Student Network Research Conference | 2024 |
| Selection Committee, ASA Biopharmaceutical Section Nonclinical Biostatistics Conference Scholarship | 2024 |
| Program Committee and Session Organizer, ICSA 2024 China Conference | 2023 - 2024 |
| Program Committee, 28th International Conference on Research in Computational Molecular Biology (RECOMB) | 2023 - 2024 |

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| Co-organizer, NISS Webinar on Academic Perspectives on ChatGPT | 2023 |
| Invited Session Organizer, The 6th International Conference on Econometrics and Statistics (EcoSta) | 2023 |
| Moderator, NISS Virtual Career Fair | 2023 |
| Invited Panelist, UCLA Academic Career Panel | 2022 |
| Academic Subcommittee, National Institute of Statistical Sciences | 2022 - |
| Affiliates Committee, National Institute of Statistical Sciences | 2022 - |
| Invited Session Organizer, Joint Statistical Meetings | 2022 |
| Program Committee & Session Chair, 26th International Conference on Research in Computational Molecular Biology (RECOMB) | 2021 - 2022 |
| Selection Committee, ASA Biopharmaceutical Section Nonclinical Biostatistics Conference Scholarship | 2021 |

PROFESSIONAL AFFILIATIONS

Member:

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|---|-------------|
| Western North American Region International Biometric Society | 2023 - |
| Rutgers Cancer Institute of New Jersey | 2019 - 2022 |
| Eastern North American Region International Biometric Society | 2019 - 2022 |
| American Statistical Association | 2019 - |
| International Chinese Statistical Association | 2019 - |
| International Society for Computational Biology | 2019 - |

Student Member:

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| International Society for Computational Biology | 2017 - 2019 |
| International Chinese Statistical Association | 2015 - 2019 |
| American Statistical Association | 2014 - 2019 |

Last updated: July 11, 2025