Wenxiu Ma

Associate Professor
Department of Statistics
University of California Riverside
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EDUCATION

Ph.D. in Computer Science   2012
Stanford University   Advisor: Dr. Wing H. Wong

B.S. in Computer Science   2004
Peking University

EMPLOYMENT

Associate Professor   2021–Present
Department of Statistics, University of California Riverside
     Cooperative Faculty, Genetics, Genomics and Bioinformatics Program   2015–
     Cooperative Faculty, Department of Computer Science and Engineering   2015–
     Member, Data Science Center   2016–
     Member, Institute of Integrative Genome Biology   2016–
     Member, Center for Plant Cell Biology   2016–
     Member, Center for Infectious Disease and Vector Research   2016–

Assistant Professor   2015–2021
Department of Statistics, University of California Riverside

Postdoctoral Fellow   2012–2015
Department of Genome Sciences, University of Washington   Advisor: Dr. William S. Noble

Postdoctoral Fellow   2012
Department of Developmental Biology, Stanford University   Advisor: Dr. Matthew P. Scott

HONORS & AWARDS

NSF CAREER Award, Advances in Biological Informatics program   2018–2023

Regents' Faculty Fellowship, University of California Riverside   2017–2018

PUBLICATIONS

Publication list also available @ Google Scholar and PubMed
<u>underline</u>: lab members and advisees; ∗: equal contribution

Journal Articles, peer-reviewed

J22. <u>Y Hu</u>, **W Ma**#. "EnHiC: Learning fine-resolution Hi-C contact maps using a generative adversarial framework." *Bioinformatics (ISMB/ECCB 2021)*, Accepted. [GitHub]

J21. <u>J Zhou</u>, P Li, W Zeng, **W Ma**, Z Lu, R Jiang, Q Zhang, T Jiang. "IRIS: A method for predicting *in vivo*

RNA secondary structures using PARIS data." *Quantitative Biology*. 8(4):369–381, 2020.

J20. T Ye, **W Ma**#. "ASHIC: Hierarchical Bayesian modeling of diploid chromatin contacts and structures." *Nucleic Acids Research*. 48(21):e123, 2020. [GitHub]

J19. AA Virji, J Thekkiniath, **W Ma**, L Lawres, J Knight, A Swei, KL Roch, CB Mamoun. "Insights into the evolution and drug susceptibility of Babesia duncani from the sequence of its mitochondrial and apicoplast genomes." *International Journal for Parasitology*. 49(2019):105-113, 2019.

J18. T Barr, S Sureshchandra, P Ruegger, J Zhang, **W Ma**, J Borneman, K Grant, I Messaoudi. "Concurrent gut transcriptome and microbiota profiling following chronic ethanol consumption in nonhuman primates." *Gut Microbes*. 9(4):338-356, 2018.

J17. **W Ma**, F Ay, C Lee, G Gulsoy, X Deng, S Cook, J Hesson, C Cavanaugh, CB Ware, A Krumm, J Shendure, CA Blau, CM Disteche, WS Noble, Z Duan. "Using DNase Hi-C techniques to map global and local three-dimensional genome architecture at high resolution." *Methods*. 142(2018):59-73, 2018.

J16. Y Qiu, EK Pasoreck, AK Reddy, A Nagatani, **W Ma**, J Chory, M Chen. "Mechanism of early light signaling by the carboxy-terminal output module of *Arabidopsis* phytochrome B." *Nature Communications*. 8(1):1905, 2017.

J15. **W Ma**, L Yang, R Rohs, WS Noble. "DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding." *Bioinformatics*, 33(19):3003-3010, 2017. [Bitbucket]

J14. V Ramani, DA Cusanovich, RJ Hause, **W Ma**, R Qiu, X Deng, CA Blau, CM Disteche, WS Noble, J Shendure, Z Duan. "Mapping 3D genome architecture through *in situ* DNase Hi-C." *Nature Protocols*. 11(11):2104-2121, 2016.

J13. JB Berletch*, **W Ma***, F Yang, J Shendure, WS Noble, CM Disteche, X Deng. "Identification of genes escaping X inactivation by allelic expression analysis in a novel hybrid mouse model." *Data in Brief*, 5:761-769, 2015.

J12. X Deng*, **W Ma***, V Ramani, A Hill, F Yang, F Ay, JB Berletch, CA Blau, J Shendure, Z Duan, WS Noble, CM Disteche. "Bipartite structure of the inactive mouse X chromosome." *Genome Biology*. 16:152, 2015.

J11. JB Berletch*, **W Ma***, F Yang, J Shendure, WS Noble, CM Disteche, X Deng. "Escape from X inactivation varies in mouse tissues." *PLOS Genetics*. 11(3):e1005079, 2015.

J10. F Yang, X Deng, **W Ma**, JB Berletch, N Rabaia, G Wei, JM Moore, GN Filippova, J Xu, Y Liu, WS Noble, J Shendure, CM Disteche. "The lncRNA Firre anchors the inactive X chromosome to the nucleolus by binding CTCF and maintains H3K27me3 methylation." *Genome Biology*. 16:52, 2015.

J9. **W Ma**, F Ay, C Lee, G Gulsoy, X Deng, S Cook, J Hesson, C Cavanaugh, C Ware, T Krumm, J Shendure, CA Blau, CM Disteche, WS Noble, Z Duan. "Fine-scale chromatin interaction maps reveal the cis-regulatory landscape of human lincRNA genes." *Nature Methods*. 12(1):71-78, 2015.

J8. **W Ma**, WS Noble and TL Bailey. "Motif-based analysis of large nucleotide datasets using MEME-ChIP." *Nature Protocols*. 9(6):1428-1450, 2014.

J7. J Cao, J Ni, **W Ma**, V Shiu, LA Milla, S Park, ML Spletter, S Tang, J Zhang, X Wei, SK Kim, MP Scott. "Insight into insulin secretion from transcriptome and genetic analysis of insulin-producing cells of drosophila." *Genetics*. 197:175-192, 2014.

J6. X Deng, JB Berletch, **W Ma**, DK Nguyen, JB Hiatt, WS Noble, J Shendure, CM Disteche. "Mammalian X upregulation is associated with enhanced transcription initiation, RNA half-life, and MOF-mediated H4K16 acetylation." *Developmental Cell*. 25(1):55-68, 2013.

J5. KA Peterson, Y Nishi, **W Ma**, A Vedenko, L Shokri, X Zhang, M McFarlane, JM Baizabal, JP Junker, A van Oudenaarden, T Mikkelsen, BE Bernstein, TL Bailey, ML Bulyk, WH Wong, AP McMahon. "Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning." *Genes & Development*. 26(24):2802-2816, 2012.

J4. JS Park, **W Ma**, LL O'Brien, E Chung, JJ Guo, JG Cheng, MT Valerius, JA McMahon, WH Wong, AP McMahon. "Six2 and Wnt regulate self-renewal and commitment of nephron progenitors through shared gene regulatory networks." *Developmental Cell*. 23(3):637-651, 2012.

J3. EY Lee, H Ji, Z Ouyang, B Zhou, **W Ma**, SA Vokes, AP McMahon, WH Wong, MP Scott. "Hedgehog pathway-regulated gene networks in cerebellum development and tumorigenesis." *Proceedings of the National Academy of Sciences*. 107(21):9736-9741, 2010.

J2. H Ji, H Jiang, **W Ma**, DS Johnson, RM Myers, WH Wong. "An integrated software system for analyzing ChIP-chip and ChIP-seq data." *Nature Biotechnology*. 26(11):1293-1300, 2008.

J1. J Choi, LK Southworth, KY Sarin, AS Venteicher, **W Ma**, W Chang, P Cheung, S Jun, MK Artandi, N Shah, SK Kim, SE Artandi. "TERT promotes epithelial proliferation through transcriptional control of a Myc-and Wnt-related developmental program." *PLoS Genetics*. 4(1):e10, 2008.

Conference Proceedings, peer-reviewed

P1. M Salloum, D Jeske, **W Ma**, V Papalexakis, C Shelton, V Tsotras, S Zhou. "Developing an Interdisciplinary Data Science Program." *In Proceedings of the 52nd ACM Technical Symposium on Computer Science Education (SIGCSE '21)*, Pages 509-515, March 2021.·

Book Chapters

C3. **W Ma**, G Bonora, JB Berletch, X Deng, WS Noble, CM Disteche. "X-chromosome inactivation and escape from X inactivation in mouse." *Methods in Molecular Biology*. 1861:205-219, 2018.

C2. **W Ma**, WH Wong. "The analysis of ChIP-seq data." *Methods in Enzymology*. 497:51-73, 2011.

C1. H Ji, H Jiang, **W Ma**, WH Wong. "Using CisGenome to analyze ChIP-chip and ChIP-seq data." *Current Protocols in Bioinformatics*. 2:2, 2011.

Dissertation

D1. **W Ma**. "Computational Algorithms and Statistical Modeling of ChIP Sequencing Analysis." *Stanford University*. 2012.

Software

S4. DiffGR: Detecting differentially interacting genomic regions from Hi-C contact maps.
https://github.com/wmalab/DiffGR

S3. EnHiC: Learning fine-resolution Hi-C contact maps using a generative adversarial framework.
https://github.com/wmalab/EnHiC

S2. ASHIC: Hierarchical Bayesian modeling of diploid chromatin contacts and structures.
https://github.com/wmalab/ASHIC

S1. sequence-shape: DNA sequence+shape kernels for alignment-free modeling of transcription factor binding.
https://bitbucket.org/wenxiu/sequence-shape.git

FUNDING

Current Support

R35 GM133678 (Ma)   9/1/19 – 8/30/24
NIH/NIGMS
Computational modeling of spatial genome organization and gene regulation
The research goal of this project is to 1) develop computational approaches to enhance the resolution of existing Hi-C data, infer fine-scale 3D chromatin structures, and investigate the dynamics of 3D genome organization across different cell lines, tissue types, and developmental stages; 2) build scalable and interpretable machine learning models that leverage 1D epigenomic data to predict cell type-specific 3D chromatin interactions and gene expression.
Role: PI

DBI 1751317 (Ma)   4/1/18 – 3/31/23
NSF
CAREER: Computational and statistical methods for allele-specific chromatin structure analysis
The research objectives of this project are to establish a new computational and statistical framework for modeling the three-dimensional (3D) chromatin structures in an allele-specific manner and investigate the impact of chromatin organization on allelic gene regulation.
Role: PI

Gift fund (Tsotras, Jeske, Ma, Papalexakis, Shelton, Zhou)   7/1/18 – 6/30/23
Center for Advancing Women in Technology
Technology Pathway Initiative: Advancing diversity in computing through the undergraduate program in data science
This gift fund is to support a new data science degree to increase the numbers of women and underrepresented groups in high-tech fields.
Role: co-PI

R01 GM087388 (Chen)   9/17/20 – 7/31/24
NIH/NIGMS
Function of photobodies in plant photoreceptor signaling
The major goals of this project are to determine the function of the photobody in a temperature-dependent nuclear transcriptional switch and to determine the significance and mechanism of gene recruitment to photobodies.
Role: Co-Investigator

Previous Support

Seed Grant (Chen, Ma)   7/1/18 – 6/30/19
UCR Academic Senate
Spatial genome reorganization by plant light signaling
Role: Co-PI

Regents' Faculty Fellowship (Ma)   8/1/17 – 6/30/19
UCR Academic Senate
Computational algorithms and statistical modeling of allele-specific chromosome structures
Role: PI

R01 GM087388 (Chen)   9/1/16 – 6/30/20
NIH/NIGMS
Function of photobodies in plant light signaling
Role: Co-Investigator

Seed Grant (Messaoudi, Brown, Borneman, Ma)   7/1/16 – 6/30/17
UCR Academic Senate
Mechanisms of accelerated aging in geriatric HIV+ subjects
Role: Co-PI

R01 GM113943 (Disteche)   8/1/15 – 5/31/19
NIH/NIGMS
Molecular studies of sex chromosome aneuploidy
Role: Sub-contractor

PRESENTATIONS

"Learning fine-resolution chromosome conformation interaction maps."
4th International Conference on Econometrics and Statistics (EcoSat 2021), Virtual event   Jun 2021

"Statistical and computational methods for analyzing chromatin spatial organization data."
Women In Data Science (WiDS) Riverside, Virtual event   May 2021

"Statistical and computational methods for analyzing chromatin spatial organization data."
11th ICSA International Conference, Hangzhou, China   Dec 2019

"Statistical and computational methods for analyzing chromatin spatial organization data."
Special Session on Data Science, AMS Fall Western Sectional Meeting, Riverside, CA   Nov 2019

"Statistical and computational methods for analyzing chromatin spatial organization data."
Statistical Genomics Workshop, Plant & Animal Genome Conference XXVII, San Diego, CA   Jan 2019

"Statistical and computational methods for analyzing chromatin spatial organization data."
NSF Project / Bioinformatics Workshop, University of California Riverside   Apr 2018

"Statistical and computational methods for analyzing chromatin spatial organization data."
Computational and Statistical Interface to Big Data Conference, Thuwal, Saudi Arabia   Mar 2018

"Statistical and computational methods for analyzing chromatin spatial organization data."
Data Science Seminar, University of California Riverside   Jan 2018

"DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding."
Department of Economics, University of California Riverside   Feb 2017

"DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding."
10th ICSA International Conference, Shanghai, China   Dec 2016

"DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding."
Department of Mathematics and Statistics, San Diego State University   Nov 2016

"DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding."
ICSA Conference on Data Science, Dali, China   Jul 2016

"Statistical inference of allele-specific contacts from high-throughput chromatin conformation data."
25th ICSA Applied Statistics Symposium, Atlanta, GA   Jun 2016

"Zooming into the 3D Genome Architecture."

Bioinformatics and Systems Biology Seminar, University of California San Diego   Jun 2016

"Allele-specific gene expression and chromosome conformation analyses on mouse X chromosomes."
CMDB/GGB/MCBL Joint Seminar, University of California Riverside   Apr 2016

"Identification of bipartite structure of inactive mouse X chromosome using DNase Hi-C data."
6th Annual Southern California Systems Biology Conference, University of California Irvine   Jan 2016

"Zooming into the 3D genome architecture."
Department of Computer Science and Engineering, University of California Riverside   Nov 2015

"Zooming into the 3D genome architecture of gene regulation."
Department of Molecular and Computational Biology, University of Southern California   Jan 2015

"Zooming into the 3D genome architecture of gene regulation."
Department of Genome Sciences, University of Washington   Aug 2014

"Fine-scale chromatin interaction maps reveal cis-regulatory landscape of human lincRNA genes."
ENCODE Consortium Meeting, Stanford, CA   Jul 2014

"Computational algorithms and statistical models for analyzing ChIP-seq data."
Progenitor Cell Consortium Meeting, Stanford University, Stanford, CA   Jul 2011

TEACHING

Instruction

NASC093 Freshman Advising Seminar   Fall 2017

STAT155 Probability and Statistics for Science and Engineering   Winter 2016–2019

STAT167 Introduction to Data Science   Spring 2017–2021

STAT209 Software Tools for Big Data Analysis   Spring 2021

STAT255N Topics in Applied Statistics - Statistical and Computational Genomics   Fall 2015

STAT288 Literature Seminar   Spring 2019

Course Development

STAT209 Software Tools for Big Data Analysis   2019–2021
Proposed and developed a new graduate-level big data computing course.

STAT167 Introduction to Data Science   2016–2017
Proposed and developed a new undergraduate-level data science course.

STAT255N Topics in Applied Statistics - Statistical and Computational Genomics   2015
Developed a new graduate-level course on statistical and computational genomics.

Other Teaching

DataFest `R/tidyverse` Workshop   2019
Taught 2 sessions (5 hours each) to undergraduate students at Highlander Statistics Society and coached them for the ASA DataFest competition.

DataFest `R/tidyverse` Workshop   2018
Taught 4 sessions (3 hours each) to undergraduate students at Highlander Statistics Society and coached them for the ASA DataFest competition.

ADVISING

Postdoctoral Scholars

Tiantian Ye   2021–
Prior degree: Ph.D., Genetics, Genomics & Bioinformatics, University of California Riverside, 2020.

Biswanath Chowdhury   2020–
Prior degree: Ph.D., BioPhysics, Molecular Biology and Bioinformatics, University of Calcutta, India, 2020.

Li Ma   2020–
Prior degree: Ph.D., Computational Biology, Shanghai Institute of Biology Science, Chinese Academy of Science, China, 2019.

Eleonora Khabirova   2017–2018
Prior degree: Ph.D., Mathematical Genomics and Medicine, University of Cambridge, UK, 2016.
Current position: Postdoc, Wellcome Sanger Institute, UK.

Ph.D. Students

Jinli Zhang, Genetics, Genomics & Bioinformatics   2020–
Prior degree: M.S., Biology, specialized in Bioinformatics, Shanghai Jiao Tong University, China, 2014

Yangyang Hu, Computer Science   2016–
Prior degree: M.S., Computer Technology, China University of Geosciences, China, 2016.

Luke Klein, Applied Statistics   2015–
Prior degree: M.S., Statistics, University of California Riverside, 2015.

Huiling Liu, Applied Statistics   2016–2021
Dissertation: "Statistical Differential Analyses of Hi-C contact maps."
Prior degree: M.A., Statistics, Columbia University, 2016.

Tiantian Ye, Genetics, Genomics & Bioinformatics   2015–2020
Dissertation: "Hierarchical Bayesian Modeling of Diploid Chromatin Contacts and Structures."
Prior degree: B.S., Biotechnology, Zhejiang University, China, 2015.

Fangjie Xie, Applied Statistics (co-advised with Dr. Shizhong Xu)   2015–2019
Dissertation: "Significance tests for random effects and correction for bias of estimated QTL variances in GWAS."
Prior degree: M.S., Statistics, University of California Riverside, 2015.

Other Ph.D. Students (Rotation Projects)

Qiong Jia, Genetics, Genomics & Bioinformatics   Winter 2020
Shiyang He, Genetics, Genomics & Bioinformatics   Winter 2020
Lei Yu, Genetics, Genomics & Bioinformatics   Fall 2018
Xinru Qiu, Genetics, Genomics & Bioinformatics   Fall 2018
Theodore Kataras, Genetics, Genomics & Bioinformatics   Fall 2017
David Hillis, Genetics, Genomics & Bioinformatics   Spring 2017
Jose Lomeli, Genetics, Genomics & Bioinformatics   Fall 2016
Qihua Liang, Genetics, Genomics & Bioinformatics   Fall 2015

Visiting Students

Jianyu Zhou, Ph.D. student from Tsinghua University   2019
Cheng Wang, Ph.D student from King Abdullah University of Science and Technology   2018

Masters Students

Hung Chih (Jimmy) Ni, Computer Science   2020–2021
Prior degree: B.S., Computer Science, National Tsing-Hua University, Taiwan, 2017.

Tiantian Ye, Computer Science (concurrently with her PhD in GGB)   2018–2020
Prior degree: B.S., Biotechnology, Zhejiang University, China, 2015.

Douglas Kirsher, Bioengineering   2019–2020
Prior degree: B.E., Bioengineering, University of California Riverside, 2019.

Jingfei Zhang, Statistics   2016–2017
Prior degree: B.S., Biochemistry, University of Hong Kong, Hong Kong SAR, China.

Undergraduate Students

Sydney Pun, Computer Science	Fall 2020 –
Piyush Mundhra, Mathematics & Computer Science	2020–2021
Douglas Kirsher, Bioengineering	2019
Xiaodi Fan, Computer Science	2017

Dissertation / Qualifying Exam / Guidance Committee

Ph.D. Dissertation Committee

Le Zhang, Genetics, Genomics & Bioinformatics	2020–
Amy Boyd, Genetics, Genomics & Bioinformatics	2020–
Theodore Kataras, Genetics, Genomics & Bioinformatics	2020–
Jianhai Zhang, Genetics, Genomics & Bioinformatics	2018–
Yuzhu Duan, Genetics, Genomics & Bioinformatics	2018–
Samantha VanSchalkwyk, Applied Statistics	2020
Weihua Pan, Computer Science	2019
Edward Schuberg, Applied Statistics	2019
Sakar Sigdel, Applied Statistics	2018
Supawadee Wichitchan, Applied Statistics	2017
Jolly Shrivastava, Genetics, Genomics & Bioinformatics	2017

Ph.D. Qualifying Exam Committee

Ryan Traband, Botany & Plant Sciences	2021
Lei Yu, Genetics, Genomics & Bioinformatics	2020
Xinru Qiu, Genetics, Genomics & Bioinformatics	2020
Samantha VanSchalkwyk, Applied Statistics	2018
Hao Chen, Computer Science	2018
Yuzhu Duan, Genetics, Genomics & Bioinformatics	2018
Edward Schuberg, Applied Statistics	2017
Supawadee Wichitchan, Applied Statistics	2016
Lichao Li, Genetics, Genomics & Bioinformatics	2016
Stephen Bolaris, Genetics, Genomics & Bioinformatics	2015

Ph.D. Guidance Committee

Shiyang He, Genetics, Genomics & Bioinformatics	2020–
Qiong Jia, Genetics, Genomics & Bioinformatics	2020–2021
Theodore Kataras, Genetics, Genomics & Bioinformatics	2016–2019
Jianhai Zhang, Genetics, Genomics & Bioinformatics	2017–2018

Yuzhu Duan, Genetics, Genomics & Bioinformatics	2016–2018
David Hillis, Genetics, Genomics & Bioinformatics	2016–2018
Jose Lomeli, Genetics, Genomics & Bioinformatics	2016–2019

PROFESSIONAL ACTIVITIES

Grant Review Panel

National Science Foundation, Directorate for Biological Sciences   2019

Conference Program Committee

International Conference on Research in Computational Molecular Biology, Satellite Meeting on Massively Parallel Sequencing (RECOMB-SEQ)   2017–2021

ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)   2018

IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)   2017

International Workshop on Data Mining in Bioinformatics (BIOKDD)   2017

International Conference on Intelligent Systems for Molecular Biology (ISMB)   2016

Journal Referee

Analytical Biochemistry: Methods in the Biological Sciences
Bioinformatics
BMC Genomics
Cell Reports
Computational and Structural Biotechnology Journal
Computational Statistics and Data Analysis
Frontiers in Non-coding RNA
Genome Biology
Genomics Proteomics and Bioinformatics
IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)
Journal of Bioinformatics and Computational Biology
Journal of Computational Biology
Journal of the Royal Statistical Society, Series C
Nature Communications
Nucleic Acid Research
PLOS Computational Biology
PLOS One
Proceedings of the National Academy of Sciences (PNAS)
Scientific Reports
Statistical Applications in Genetics and Molecular Biology
Statistics in Biosciences

Conference Sub-referee

Research in Computational Biology (RECOMB)	2013–2015
Uncertainty in Artificial Intelligence (UAI)	2013–2015
International Conference on Machine Learning (ICML)	2014
International Conference on Intelligent Systems for Molecular Biology (ISMB)	2013 & 2015
Workshop on Algorithms in Bioinformatics (WABI)	2015

ASE/IEEE International Conference on BioMedical Computing (BioMedCom)	2013

Professional Society Membership

American Statistical Association (ASA)	2018–Present
International Chinese Statistical Association (ICSA)	2015–Present
International Society for Computational Biology (ISCB)	2014–Present

UNIVERSITY SERVICE

Campus Service

Executive committee, High Performance Computing Center (HPCC) advisory board	2017–
Program committee, New Data Science undergraduate program	2016–
Search committee, Bioinformatics programmer for IIGB metabolomics core	2017–2018
Search committee, System administrator for HPCC	2016–2017
Search committee, Data Science cluster hire	2016–2017
Search committee, Food, Bugs, Gut, Brain and Behavior (FBGBB) cluster hire	2016–2017

Department Service

Undergraduate program committee	2020–
Undergraduate mentoring committee	2017–
Facility upgrade, computer and equipment committee	2015–
Growth committee	2019
Lead faculty advisor for Statistics undergraduate students	2018–2019
LPSOE/LSOE search committee	2018–2019
Department colloquium committee	2017–2018

PUBLIC SERVICE

Judge, ASA/UCLA DataFest	2017–2021
Workshop speaker, ASA Orange County/Long Beach Chapter Gave a R data scrubbing/wrangling workshop to 100+ high school students.	2020
Faculty mentor, SISTERS program, CNAS, UCR Host annual outreach workshops to middle school girls at University Heights Middle School.	2018–2019