

Wenxiu Ma

Assistant 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

Assistant Professor	2015–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–
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](#)
underline: lab members and advisees; *: equal contribution

Journal Articles, peer-reviewed

- J22. Y Hu, **W Ma**. “EnHiC: Learning fine-resolution Hi-C contact maps using a generative adversarial framework.” *Bioinformatics (ISMB/ECCB 2021)*, Accepted. [[GitHub](#)]
- J21. J Zhou, 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

Dollar amounts indicate the total award amount (including indirect cost).

Current Support

R35 GM133678 (Ma) 9/1/19 – 8/30/24 \$1,883,220
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 \$688,224
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 \$400,000
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 – 07/31/24 \$2,340,177
NIH/NIGMS \$0 (subaward)

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 \$10,000
UCR Academic Senate

Spatial genome reorganization by plant light signaling

Role: Co-PI

Regents' Faculty Fellowship (Ma) 8/1/17 – 6/30/19 \$3,000
UCR Academic Senate

Computational algorithms and statistical modeling of allele-specific chromosome structures

Role: PI

R01 GM087388 (Chen) NIH/NIGMS Function of photobodies in plant light signaling Role: Co-Investigator	9/1/16 – 6/30/20	\$1,918,068 \$53,234 (subaward)
Seed Grant (Messouadi, Brown, Borneman, Ma) UCR Academic Senate Mechanisms of accelerated aging in geriatric HIV+ subjects Role: Co-PI	7/1/16 – 6/30/17	\$50,000
R01 GM113943 (Disteche) NIH/NIGMS Molecular studies of sex chromosome aneuploidy Role: Sub-contractor	8/1/15 – 5/31/19	\$1,717,582 \$108,061 (subcontract)

PRESENTATIONS

“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 Developing a new graduate-level big data computing course.	2019–2021
STAT167 Introduction to Data Science Proposed and developed a new undergraduate-level data science course.	2016–2017
STAT255N Topics in Applied Statistics - Statistical and Computational Genomics Developed a new graduate-level course on statistical and computational genomics.	2015

Other Teaching

DataFest R/tidyverse Workshop Taught 2 sessions (5 hours each) to undergraduate students at Highlander Statistics Society and coached them for the ASA DataFest competition.	2019
DataFest R/tidyverse Workshop Taught 4 sessions (3 hours each) to undergraduate students at Highlander Statistics Society and coached them for the ASA DataFest competition.	2018

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
- Huiling Liu, Applied Statistics 2017–
Prior degree: M.A., Statistics, Columbia University, 2016.
- 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.
- 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 Prior degree: B.S., Computer Science, National Tsing-Hua University, Taiwan, 2017.	2020–2021
Tiantian Ye, Computer Science (concurrently with her PhD in GGB) Prior degree: B.S., Biotechnology, Zhejiang University, China, 2015.	2018–2020
Douglas Kirsher, Bioengineering Prior degree: B.E., Bioengineering, University of California Riverside, 2019.	2019–2020
Jingfei Zhang, Statistics Prior degree: B.S., Biochemistry, University of Hong Kong, Hong Kong SAR, China.	2016–2017

Undergraduate Students

Sydney Pun, Computer Science	Fall 2020 –
Piyush Mundhra, Mathematics & Computer Science	Fall 2020 –
Douglas Kirsher, Bioengineering	Winter, Spring 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

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–
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
 Jose Lomeli, Genetics, Genomics & Bioinformatics

2016–2018
 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	2017–2020
Faculty mentor, SISTERS program, CNAS, UCR	2018–
Host annual outreach workshops to middle school girls at University Heights Middle School.	