

Wenxiu Ma

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Department of Statistics
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EDUCATION

Ph.D. in Computer Science 2012
Stanford University

B.S. in Computer Science 2004
Peking University

ACADEMIC APPOINTMENT

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, Institute of Integrative Genome Biology 2016 -
Member, Center for Plant Cell Biology 2016 -
Member, Center for Infectious Disease and Vector Research 2016 -

RESEARCH INTERESTS

Computational Biology and Bioinformatics

Genome Architecture, Transcriptional Regulation, Gene Expression Profiling, Epigenetics, High-throughput Sequencing Analysis, Motif Analysis, Systems Biology, Cancer Genomics.

Statistical Modeling and Machine Learning

Bayesian Inference, Empirical Bayes, Hierarchical Models, Kernel Methods.

RESEARCH EXPERIENCE

Postdoctoral Fellow 2012 - 2015
Department of Genome Sciences, University of Washington *Advisor: Prof. William S. Noble*

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

Graduate Research Assistant 2005 - 2012
Department of Statistics, Stanford University *Advisor: Prof. Wing H. Wong*

PUBLICATIONS

1. **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*. 2018 Jan 31. pii: S1046-2023(17)30240-2. doi: 10.1016/j.jymeth.2018.01.014. [Epub ahead of print].
2. 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.

3. **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.
4. V Ramani, DA Cusanovich, RJ Hause, **W Ma**, R Qiu, X Deng, CA Blau, CM Disteche, WS Noble, J Shendure, Z Duan. “Mapping three-dimensional genome architecture through *in situ* DNase Hi-C.” *Nature Protocols*. 11(11):2104-2121, 2016.
5. 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. [* co-first author]
6. 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. [* co-first author]
7. 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. [* co-first author]
8. 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 lincRNA Firre anchors the inactive X chromosome to the nucleolus by binding CTCF and maintains H3K27me3 methylation.” *Genome Biology*. 16:52, 2015.
9. **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.
10. **W Ma**, WS Noble and TL Bailey. “Motif-based analysis of large nucleotide datasets using MEME-ChIP.” *Nature Protocols*. 9(6):1428-1450, 2014.
11. 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.
12. 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.
13. 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.
14. 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.
15. **W Ma**, WH Wong. “The analysis of ChIP-seq data.” *Methods in Enzymology*. 497:51-73, 2011.
16. 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.
17. 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.
18. 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.
19. 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.

Dissertation

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

PRESENTATIONS

- Seminar*, Data Science Center, University of California Riverside
 “Statistical and computational methods for analyzing chromatin spatial organization data.” *Jan 2018*
- Seminar*, Econometrics Colloquia Seminar, Department of Economics, University of California Riverside
 “DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding.” *Feb 2017*
- Talk*, Invited Session, 10th ICSA International Conference, Shanghai, China
 “DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding.” *Dec 2016*
- Seminar*, Department of Mathematics and Statistics, San Diego State University
 “DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding.” *Nov 2016*
- Talk*, Invited Session, ICSA Conference on Data Science, Dali, China
 “DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding.” *Jul 2016*
- Talk*, Invited Session, 25th ICSA Applied Statistics Symposium, Atlanta, GA
 “Statistical inference of allele-specific contacts from high-throughput chromatin conformation data.” *Jun 2016*
- Seminar*, Bioinformatics and Systems Biology Seminar, University of California, San Diego
 “Zooming into the 3D Genome Architecture.” *Jun 2016*
- Seminar*, CMDDB/GGB/MCBL Joint Seminar, University of California, Riverside
 “Allele-specific gene expression and chromosome conformation analyses on mouse X chromosomes.” *Apr 2016*
- Talk*, 6th Annual Southern California Systems Biology Conference, University of California, Irvine
 “Identification of bipartite structure of inactive mouse X chromosome using DNase Hi-C data.” *Jan 2016*
- Colloquium*, Department of Computer Science and Engineering, University of California, Riverside
 “Zooming into the 3D genome architecture.” *Nov 2015*
- Seminar*, Department of Molecular and Computational Biology, University of Southern California
 “Zooming into the 3D genome architecture of gene regulation.” *Jan 2015*
- Seminar*, Department of Genome Sciences, University of Washington
 “Zooming into the 3D genome architecture of gene regulation.” *Aug 2014*
- Lightning Talk*, ENCODE Consortium Meeting, Stanford, CA
 “Fine-scale chromatin interaction maps reveal cis-regulatory landscape of human lincRNA genes.” *Jul 2014*
- Talk*, Progenitor Cell Consortium Meeting, Stanford University, Stanford, CA
 “Computational algorithms and statistical models for analyzing ChIP-seq data.” *Jul 2011*

TEACHING EXPERIENCE

- Instructor** *NASC093 Freshman Advising Seminar*
 College of Natural & Agricultural Sciences, University of California, Riverside *Fall 2017*
- Instructor** *STAT167 Introduction to Data Science*
 Department of Statistics, University of California, Riverside *Spring 2017, Spring 2018*
- Instructor** *STAT155 Probability and Statistics for Science and Engineering*
 Department of Statistics, University of California, Riverside *Winter 2016, Winter 2017, Winter 2018*
- Instructor** *STAT255N Topics in Applied Statistics - Statistical and Computational Genomics*
 Department of Statistics, University of California, Riverside *Fall 2015*
- Teaching Assistant** *CS161 Design and Analysis of Algorithms*
 Department of Computer Science, Stanford University *Summer 2009*
- Teaching Assistant** *CS228 Probabilistic Graphical Models*
 Department of Computer Science, Stanford University *Winter 2009*
- Teaching Assistant** *CS161 Design and Analysis of Algorithms*
 Department of Computer Science, Stanford University *Summer 2006*

PROFESSIONAL EXPERIENCE

Program Committee Member

9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB) 2018

22nd International Conference on Research in Computational Molecular Biology (RECOMB), Satellite Meeting on Massively Parallel Sequencing, 2018

7th IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS) 2017

16th International Workshop on Data Mining in Bioinformatics (BIOKDD) 2017

21st International Conference on Research in Computational Molecular Biology (RECOMB), Satellite Meeting on Massively Parallel Sequencing, 2017

24th International Conference on Intelligent Systems for Molecular Biology (ISMB) 2016.

Referee/Reviewer

Journals: Analytical Biochemistry: Methods in the Biological Sciences, BMC Genomics, Bioinformatics, Cell Reports, Frontiers in Non-coding RNA, Genome Biology, IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB), Journal of Bioinformatics and Computational Biology, Journal of the Royal Statistical Society, Series C, Nucleic Acid Research, PLOS One, Scientific Reports, Statistical Applications in Genetics and Molecular Biology, Statistics in Biosciences.

Conferences: 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.

Membership

International Society for Computational Biology (ISCB)

2014 - Present

International Chinese Statistical Association (ICSA)

2015 - Present

HONORS & AWARDS

Regents' Faculty Fellowship, University of California Riverside

2017 - 2018