

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 -

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*

Undergraduate Research Assistant 2003 - 2004
Department of Computer Science and Technology, Peking University *Advisor: Prof. Xiaoming Li*

TEACHING EXPERIENCE

Instructor *STAT155 Probability and Statistics for Science and Engineering*
Department of Statistics, University of California, Riverside *Winter 2016*

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

Department of Computer Science, Stanford University

*CS228 Probabilistic Graphical Models**Winter 2009***Teaching Assistant**

Department of Computer Science, Stanford University

*CS161 Design and Analysis of Algorithms**Summer 2006***PUBLICATIONS**

1. 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]
2. 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]
3. 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]
4. 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.
5. **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.
6. **W Ma**, WS Noble and TL Bailey. "Motif-based analysis of large nucleotide datasets using MEME-ChIP." *Nature Protocols*. 9(6):1428-1450, 2014.
7. 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.
8. 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.
9. 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.
10. 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.
11. **W Ma**, WH Wong. "The analysis of ChIP-seq data." *Methods in Enzymology*. 497:51-73, 2011.
12. 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.
13. 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.
14. 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.
15. 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

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*

PROFESSIONAL EXPERIENCE

Program Committee Member

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, 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