

## **Jianrong Wang, Ph.D.**

*Office Address:* 428 S. Shaw Ln., Rm 2507J Engineering Building, East Lansing, MI 48824.

*E-mail:* [wangj164@msu.edu](mailto:wangj164@msu.edu).

*Office Phone:* 517-432-0370

*Website:* <https://cmse.msu.edu/directory/faculty/jianrong-wang>

### **● EDUCATION**

2007-2012: Ph.D. Bioinformatics, Georgia Institute of Technology.

2003-2007: B.S. Control Science and Engineering, Tsinghua University.

### **● PROFESSIONAL EXPERIENCE**

2017.01-present: Assistant Professor, Michigan State University, Department of Computational Mathematics, Science and Engineering.

2016.03-2016.12: Postdoctoral Researcher, Stanford University, Department of Genetics.

*Project:* Integrative dissection of enhancer regulation and its application in GWAS studies.

*Advisor:* Professor Anshul Kundaje.

2012-2016: Postdoctoral Research Associate, MIT, EECS Department, Computer Science and Artificial Intelligence Laboratory (CSAIL), Broad Institute of MIT and Harvard.

*Project:* Probabilistic modeling of patterns of enhancer regulation in diverse cellular contexts.

*Advisor:* Professor Manolis Kellis.

2008-2012: Research Assistant, Georgia Institute of Technology, School of Biology.

*Dissertation:* Computational algorithm development for epigenomic analysis.

*Advisor:* Professor I. King Jordan.

### **● TEACHING EXPERIENCE**

2019: CMSE-201, “Introduction to Computational Modeling”, Flipped-class course on Python programming, computational modeling and data analysis.

2019: CMSE-801, “Introduction to Computational Modeling”, Graduate-level flipped-class course on Python programming and mathematical modeling.

2018: CMSE-491/CMSE-890, “Computational Medicine”, New course on bioinformatics, systems biology, computational genomics, multi-omics integration and genotype-phenotype mapping, including algorithm lectures, interactive journal clubs, and real-world projects.

2018: CMSE-201, “Introduction to Computational Modeling”, Flipped-class course on Python programming, computational modeling and data analysis.

2017: Computational Biology 3-week Workshop Series: Interactive workshop on bioinformatics and its applications for students with diverse backgrounds, including real-world data processing, programming, statistical analysis and visualizations.

2017: Modular course material development for “Computational biology: programming, statistics and RNA-seq analysis”.

2008: Teaching Assistant, School of Biology, Georgia Institute of Technology.

2007: Teaching Assistant, School of Physics, Georgia Institute of Technology.

### ● RESEARCH INTERESTS

1. Probabilistic modeling of long-range three-dimensional enhancer-gene networks in diverse cellular contexts and inference of hierarchical regulatory logic of combinatorial transcription factors on gene expression.
2. Network-based prediction and functional annotation of non-coding genetic variants associated with complex traits and phenotypes.
3. Machine learning algorithms to predict regulatory elements of gene expression (insulators, enhancers and boundary elements), large-scale chromatin domains, and histone modification signatures ('histone-code') based on genomics, epigenomics and transcriptomics data.
4. Statistical and computational methods for efficient design, analysis and interpretation of biological big-data generated from new high-throughput techniques.

### ● GRANTS

2018-2022 NIH-NIGMS, R01GM131398, Role: PI

Statistical modeling of long-range chromatin interactions on gene regulation and underlying molecular mechanisms.

2018-2019 NSF-BEACON Center, Sub-award, Role: PI

Evolutionary rewiring of regulatory networks by transposable elements.

2018-2023 NSF NRT-IMPACTS, Role: co-PI

Intersecting computational and data science to address grand challenges in plant biology.

### ● PUBLICATIONS

Jiao Chen, Jianrong Wang and Yanni Sun. A contig binning tool to reconstruct viral haplotypes. *Under revision*.

Bryce Warren, Brian Petroff, Paul Cooke, Manjunatha Ketumaranahalli, Hao Wang, Jianrong Wang, Soo Ahn, Gustavo Blanco, Gladys Sanchez and Margaret Petroff. Multiple lesions contribute to infertility in males lacking Autoimmune Regulator (AIRE) protein. *Under Revision*.

Jianrong Wang, Peyton Greenside, Anshul Kundaje and Manolis Kellis. De-novo inference of enhancer-gene networks in diverse cellular contexts reveals the long-range regulatory impact of disease-associated variants. *In preparation*.

Sean Lam-Vien Nguyen, Jacob William Greenberg, Hao Wang, Benjamin William Collaer, Jianrong Wang, Margaret Green Petroff. Visualizing murine placental extracellular vesicle data with tidyNano: a computational framework for analyzing and visualizing nanoparticle data in R. 2019 *PLOS ONE* (*accepted*).

Feng Shao, Jianrong Wang, Hongen Xu, Zuogang Peng. FishTEDB: a collective database of transposable elements identified in the complete genomes of fish. 2018 *Database Vol 2018 1-9*.

Lavanya Rishishwar, Lu Wang, Jianrong Wang, Soojin V Yi, Joseph Lachance and I. King Jordan. Evidence for positive selection on recent human transposable element insertions. 2018 *Gene* 675:69-79.

Eugenio Marco, Wouter Meuleman, Jialiang Huang, Kimberly Glass, Luca Pinello, Jianrong Wang, Manolis Kellis and Guo-Cheng Yuan. Multi-scale chromatin state annotation using a hierarchical hidden Markov model. 2017 *Nature Communications* 8:15011.

Evan A. Clayton, Lu Wang, Lavanya Rishishwar, Jianrong Wang, John F. McDonald and I. King Jordan. Patterns of transposable element expression and insertion in cancer. 2016 *Frontiers in Molecular Biosciences* 3:76.

Jianrong Wang, Cristina Vicente-Garcia, Davide Seruggia, Eduardo Molto, Ana Fernandez-Minan, Ana Neto, Elbert Lee, Jose Luis Gomez-Skarmeta, Lluís Montoliu, Victoria V. Lunyak and I. King Jordan. MIR retrotransposon sequences provide insulators to the human genome. 2015 *Proc Natl Acad Sci USA* 112(32):E4428-4437.

Roadmap Epigenomics Consortium *et al.* Integrative analysis of 111 reference human epigenomes. 2015 *Nature* 518:317-330.

Daudi Jjingo, Andrew B. Conley, Jianrong Wang, Leonardo Marino-Ramirez, Victoria V. Lunyak and I. King Jordan. Mammalian-wide interspersed repeat (MIR)-derived enhancers and the regulation of human gene expression. 2014 *Mobile DNA* 5:14.

Jianrong Wang, Victoria V. Lunyak and I. King Jordan. BroadPeak: a novel algorithm for identifying broad peaks in diffuse ChIP-seq datasets. 2013 *Bioinformatics* 29(4):492-493.

Daudi Jjingo, Jianrong Wang, Andrew B. Conley, Victoria V. Lunyak and I. King Jordan. Compound cis-regulatory elements with both boundary and enhancer sequences in the human genome. 2013 *Bioinformatics* 29(24):3109-3112.

Ke Xu, Jianrong Wang, Navin Elango and Soojin V. Yi. The evolution of lineage-specific clusters of single nucleotide substitutions in the human genome. 2013 *Molecular Phylogenetics and Evolution* 69(1):276-285.

Aswathy Sebastian, Lavanya Rishishwar, Jianrong Wang, Karen F. Bernard, Andrew B. Conley, Nael A. McCarty and I. King Jordan. Origin and evolution of the cystic fibrosis transmembrane regulator protein R domain. 2013 *Gene* 523(2):137-146.

Jianrong Wang, Victoria V. Lunyak and I. King Jordan. Chromatin signature discovery via histone modification profile alignments. 2012 *Nucleic Acids Research* 40(21):10642-10656.

Benjamin J. Blackwell, Mary F. Lopez, Jianrong Wang, Bryan Krastins, David Sarracino, James R.

Tollervey, Marek Dobke, I. King Jordan and Victoria V. Lunnyak. Protein interactions with piALU RNA indicates putative participation of retroRNA in the cell cycle, DNA repair and chromatin assembly. 2012 *Mobile Genetic Elements* 2(1):26-35.

Jianrong Wang, Victoria V. Lunnyak and I. King Jordan. Genome-wide prediction and analysis of human chromatin boundary elements. 2012 *Nucleic Acids Research* 40(2):511-529, (Cover Story).

Jianrong Wang\*, Glenn J. Geesman\*, Sirkka Liisa Hostikka, Michelle Atallah, Benjamin Blackwell et al. Inhibition of activated pericentromeric SINE/Alu repeat transcription in senescent human adult stem cells reinstates self-renewal. 2011 *Cell Cycle* 10(17):3016-3030.

Jianrong Wang, Ahsan Huda, Victoria V. Lunnyak and I. King Jordan. A Gibbs sampling strategy applied to the mapping of ambiguous short-sequence tags. 2010 *Bioinformatics* 26(20):2501-2508.

Jianrong Wang, Nathan J. Bowen, Leonardo Marino-Ramirez and I. King Jordan. A c-Myc regulatory subnetwork from human transposable element sequences. 2009 *Molecular Biosystems* 5(12):1831-1839.

#### ● **ACADEMIC SERVICE**

1. Member of NSF review panel for DMS/NIGMS program: 02/2019.
2. Ad hoc Reviewer for NSF TRIPODS+X program: 06/2018.
3. Grant reviewer for Fonds de recherch  du Quebec – Nature et technologies: 12/2018.
4. Member of Outreach Committee for NRT IMPACTS program for high-school and undergraduate student engagement and inter-disciplinary graduate student career development.
5. Chair of Awards Committee for CMSE Department, MSU.
6. Member of Committee for Frontiers in Computing and Data Science 2020 Annual Workshop.
7. Guest editor for a special issue of journal Methods: since 05/2019.
8. Referee for scientific journals: PNAS, Nucleic Acids Research, Scientific Reports, Epigenetics and Chromatin, PLOS ONE, BMC Genomics, Gene, Molecular Biosystems, ISMB/ECCB and MLSB/ECCB.

#### ● **BOOK CHAPTERS**

Leverage large-scale biological networks to decipher the genetic basis of human diseases using machine learning. Methods in Molecular Biology, 2019 (under revision).

#### ● **PRESENTATIONS**

2019.06 “Machine learning for epigenomics data integration and gene regulation”, 2019 ICIBM Conference, Ohio State University.

2019.06 “Statistical modeling of genomics and epigenomics big-data reveals human disease mechanisms”, 2019 ICSA Symposium, Raleigh.

2019.05 “Integrative statistical modeling to construct enhancer regulatory networks”, 2019 ASBMB Symposium.

2018.01 “Statistical integrative modeling of genomics and epigenomics big-data reveals tissue-specific gene regulation mechanisms”, Institute for Integrative Toxicology seminar series of Michigan State University, East Lansing.

2017 “Machine learning in functional genomics reveals mechanistic insights of human disease”, CSE seminar series of Michigan State University, East Lansing.

2017 “Computational algorithm development for cancer-associated regulatory pathway identification.” Cancer Research Network seminar series of Michigan State University, East Lansing.

2017 “Probabilistic modeling to re-construct 3D chromatin structure and new insights on gene regulation.” Computational Biology Journal Club, Michigan State University, East Lansing.

2016 “De-novo inferences of three-dimensional enhancer-gene networks in diverse cellular contexts and its application in human diseases.” Seminar talk at Tsinghua University, Beijing.

2016 “Regulatory genomics and epigenomics reveal mechanistic insights of human disease.” Seminar talk at Lehigh University, Bethlehem.

2016 “Regulatory genomics and epigenomics reveal mechanistic insights of human disease.” Seminar talk at University of Georgia, Athens.

2016 “Integrative analysis of long-range enhancer regulation based on multi-omic dataset to dissect human disease mechanisms.” Seminar talk at Zhejiang University, Hangzhou.

2015 “Learning three dimensional regulation of gene expression.” ENCODE AWG Conference Call.

2013 “Interpreting eQTLs by linking enhancers to target genes.” American Society of Human Genetics 63<sup>rd</sup> Annual Meeting (ASHG), Boston. (Selected talk)

2013 “Linking target genes to enhancers and its application on gene expression predictions.” Epigenomics Program and Center for Cell Circuits Joint Seminar Series, Broad Institute of MIT and Harvard.

2011 “Deciphering the histone code with the EpiAlignTree algorithm.” Statistical Analysis for Next Generation Sequencing Conference, The University of Alabama at Birmingham. (Selected talk)

2010 “Computational Epigenomics: genome-wide prediction of chromatin boundary elements in the human genome.” Scientific Retreat of School of Biology, Georgia Institute of Technology. (Selected talk)

#### ● HONORS AND AWARDS

2007: Outstanding Student Award for Graduation in Beijing Area;

2007: Outstanding Student Award for Graduation in Tsinghua University;

2006: Chinese National Scholarship;

2005: Academic Excellence Scholarship of Tsinghua University;

2004: Honeywell Scholarship.

#### ● POSTDOCTORAL SCIENTIST MENTORING

Binod Manandhar: Postdoctoral Scientist, started from 2019.09.

#### ● GRADUATE STUDENT MENTORING

Binbin Huang: Ph.D. student in CMSE, started from 2017.01.

Hao Wang: Ph.D. student in CMSE, started from 2017.08.

Jiaxin Yang: Ph.D. student in CMSE, starting from 2019.08.

Hongjie Ke: Master student in Statistics, 2018.04-2019.02.

#### ● UNDERGRADUATE STUDENT MENTORING

Kayla Makela: Undergraduate Research Assistant.

Nate Olsen: Undergraduate Research Assistant.

Kaela Burger: Undergraduate Research Assistant.

Linghao Song: Undergraduate Research Assistant.

Alex Deneau: Undergraduate Research Assistant.

Sai Ramesh: Undergraduate Research Assistant.

Max Brombach: Undergraduate Research Assistant.

Junyi Bao: Undergraduate Research Assistant.

Albert Xue: NSF REU trainee.

Chinaza Nanwulezi: NSF REU trainee.

Tongyu Yang: MSU EnSURE Research Intern.

#### ● OTHER MENTORING ACTIVITY

*Thesis committee member for:*

Nolan Bornowski, Ph.D student in Plant Biology

Reid Blanchett: Ph.D student in Genetics.

Jake Reske: Ph.D student in Genetics.

Menglun Wang: Ph.D student in Mathematics.

Huaxin Li: Ph.D student in Probability & Statistics.

Wenjie Qi: Ph.D student in BME.

David Filipovic, Ph.D. student in BME.

Kayla Anne Marie Johnson, Dual Ph.D student in BMB and CMSE.

#### ● STUDENT ACHIEVEMENTS

2019.05: NRT-IMPACTS fellowships to Ph.D. student Hao Wang.

2019.04: Master student Hongjie Ke successfully get admitted to the Ph.D. program of statistics in the University of Maryland.

2019.03: Ph.D. student Hao Wang get Honorable Mention for Fitch H. Beach Award (Top one of CMSE Dept.).

2019.02: Undergraduate research assistant Junyi Bao successfully get admitted to the master program of statistics in Cornell University.

2019.01: NRT-IMPACTS fellowships to Ph.D. students Binbin Huang and Hao Wang.

2018.12: Undergraduate research assistant Linghao Song successfully get admitted to the master program of bioinformatics in the University of Chicago.

2018.05: Ph.D. student Binbin Huang get BEACON fellowship.

2018.03: Ph.D. student Hao Wang get First Place for DewGood Award for Public Service (Top one of College of Engineering).

2018.03: Ph.D. student Hao Wang get Outstanding Poster Award in Interdisciplinary Areas.

- **SOFTWARE DEVELOPED**

BroadPeak: Broad-peak calling algorithm for diffuse histone modifications based on high-throughput ChIP-seq data;

ChAT: Unsupervised algorithm to infer complex combinatorial chromatin signatures, with different histone modifications and signal shapes, that are indicative of distinct functional regulatory elements;

Boundary-HMM: Statistical algorithm (based on hidden Markov model and maximal-segment model) to predict large-scale chromatin domains and associated boundary elements/insulators;

GibbsAM: Gibbs sampling algorithm to probabilistically map short ambiguous multi-mapping ChIP-seq sequence reads.