

## Daifeng Wang

Phone: (608) 262-8567

Office: Room 517, 1500 Highland Ave, Madison, WI 53705

Email: [daifeng.wang@wisc.edu](mailto:daifeng.wang@wisc.edu)

Website: <http://daifengwanglab.org>

### RESEARCH AREAS

Bioinformatics, Machine Learning, Computational Genomics, Computational Medicine

### PROFESSIONAL EXPERIENCE

*Assistant Professor*, Department of Biostatistics & Medical Informatics, and *Investigator*, Waisman Center, University of Wisconsin-Madison (07/2019 – )

*Assistant Professor*, Department of Biomedical Informatics, Stony Brook University (08/2016 – 06/2019)

*Associate Research Scientist*, Department of Molecular Biophysics and Biochemistry, Yale University (08/2015 – 07/2016)

### EDUCATION AND TRAINING

*Postdoctoral Associate*, Computational Biology & Bioinformatics Program and Department of Molecular Biophysics and Biochemistry, Yale University (01/2012 – 07/2015)

*Ph.D.* (2011), *Master of Science* (2006), Electrical and Computer Engineering, The University of Texas at Austin

*Bachelor of Science* (2004), Electronics and Information Engineering, Huazhong University of Science and Technology, Wuhan, China

### PEER-REVIEWED PAPERS (\*co-first-author, equal contribution; #corresponding author)

Published/accepted/in-press:

- Nam Nguyen, Ian K. Blaby, **Daifeng Wang**<sup>#</sup>, ManiNetCluster: A Manifold Learning Approach to Reveal the Functional Linkages Across Multiple Gene Networks, accepted as oral presentation by ICIBM 2019 and recommended to publish in *BMC Genomics*, <https://doi.org/10.1101/470195>
- Mohamed Salama, Mengling Liu, Christopher J. Clarke, Mel Pilar Espaillet, John Haley, Ting Jin, **Daifeng Wang**, Lina M. Obeid, Yusuf A. Hannun, PKC $\alpha$  is required for Akt-mTORC1 activation in Non-Small Cell Lung Carcinoma (NSCLC) with EGFR mutation, *Nature Oncogene*, accepted
- **Daifeng Wang**<sup>\*</sup>, Shuang Liu<sup>\*</sup>, ..., PsychENCODE Consortium, Nenad Sestan, Andrew E. Jaffe, Kevin White, Zhiping Weng, Daniel H. Geschwind, James Knowles, Mark Gerstein, Comprehensive functional genomic resource and integrative model for the human brain, *Science*, 362, 1266, 2018
- Michael J Gandal, Pan Zhang, ..., **Daifeng Wang**, ..., PsychENCODE Consortium, ..., Daniel H. Geschwind, Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder, *Science*, 362, 1265, 2018
- Mingfeng Li<sup>\*</sup>, Gabriel Santpere<sup>\*</sup>, ..., **Daifeng Wang**, ..., BrainSpan Consortium, PsychENCODE Consortium: Developmental Subgroup, ..., Nenad Sestan, Integrative Functional Genomic Analysis of Human Brain Development and Neuropsychiatric Risk, *Science*, 362, 1264, 2018
- Adam P Arkin, Robert W Cottingham, ..., **Daifeng Wang**, Fangfang Xia, Hyunseung Yoo, Shinjae Yoo, Dantong Yu, KBase: The United States Department of Energy Systems Biology Knowledgebase, *Nature Biotechnology*, 36(7):566-569, 2018

- Zongdong Li, Natasha M. Nesbitt, Lisa E. Malone, Dimitri V. Gnatenko, Song Wu, **Daifeng Wang**, Wei Zhu, Geoffrey D. Girnun, Wadie F. Bahou, Heme degradation enzyme biliverdin IXB reductase is required for stem cell glutamine metabolism, *Biochemical Journal*, 475(6):1211-1223, 2018
- Pedro Alves, Shuang Liu, **Daifeng Wang**<sup>#</sup> and Mark Gerstein<sup>#</sup>, Multiple-Swarm Ensembles: Improving the Predictive Power and Robustness of Predictive Models and Its Use in Computational Biology, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(3):926-933, 2018
- **Daifeng Wang**<sup>#</sup>, John D. Haley and Patricia Thompson<sup>#</sup>, Comparative gene co-expression network analysis of epithelial to mesenchymal transition reveals lung cancer progression stages, *BMC Cancer*, 17:830, 2017
- **Daifeng Wang**, Fei He, Sergei Maslov, Mark Gerstein, DREISS: Using state-space models to infer the dynamics of gene expression driven by external and internal regulatory networks, *PLoS Computational Biology*, 12(10): e1005146, 2016
- **Daifeng Wang**, Koon-Kiu Yan, Joel Rozowsky, Eric Pan, Mark Gerstein, Temporal dynamics of collaborative networks driven by large scientific consortia, *Trends in Genetics*, 32, 251-253, 2016
- Koon-Kiu Yan<sup>\*</sup>, **Daifeng Wang**<sup>\*</sup>, Anurag Sethi, Robert Kitchen, Paul Muir, Chao Cheng, Mark Gerstein, Cross-Disciplinary Network Comparison: Matchmaking between Hairballs, *Cell Systems*, 2(3):147-157, 2016
- Paul Muir, Shantao Li, Shaoke Lou, **Daifeng Wang**, Daniel Spakowicz, Leonidas Salichos, Jing Zhang, Farren Isaacs, George M. Weinstock, Joel Rozowsky, Mark Gerstein, The real cost of sequencing: scaling computation to keep pace with data generation, *Genome Biology*, 17:53, 2016
- Fei He, Shinjae Yoo, **Daifeng Wang**, Sunita Kumari, Mark Gerstein, Doreen Ware, Sergei Maslov, Large-scale atlas of microarray data reveals biological landscape of gene expression in Arabidopsis, *The Plant Journal*, 86(6), 472-480, 2016
- The PsychENCODE Consortium including **Daifeng Wang**, The PsychENCODE Project Consortium, *Nature Neuroscience*, 18, 1707-1712, 2015
- **Daifeng Wang**, Koon-Kiu Yan, Cristina Sisu, Chao Cheng, Joel Rozowsky, William Meyerson, Mark Gerstein, Loregic: A method to characterize the cooperative logic of regulatory factors, *PLoS Computational Biology* 11(4): e1004132, 2015
- Chao Cheng, Erik Andrews, Koon-Kiu Yan, Matthew Ung, **Daifeng Wang**, Mark Gerstein, An Approach for Determining and Measuring Network Hierarchy: Application to Comparing the Phosphorylome and the Regulome, *Genome Biology*, 16:63, 2015
- Shuang Liu, Anjali Datta, Derek Ho, Jordan Dwelle, **Daifeng Wang**, Thomas E. Milner, H. Grady Rylander III, Mia K. Markey, Effect of image registration on longitudinal analysis of retinal nerve fiber layer thickness of non-human primates using Optical Coherence Tomography (OCT), *BMC Eye and Vision*, 2:3, 2015
- Mark Gerstein<sup>\*</sup>, Joel Rozowsky<sup>\*</sup>, Koon-Kiu Yan<sup>\*</sup>, **Daifeng Wang**<sup>\*</sup>, Chao Cheng<sup>\*</sup>, ..., Steven Brenner, Brenton Graveley, Susan Celniker, Thomas Gingeras, and Robert Waterston, Comparative Analysis of the Transcriptome across Distant Species, *Nature* 512, 445–448, 2014
- Alan P. Boyle<sup>\*</sup>, Carlos L. Araya<sup>\*</sup>, ..., **Daifeng Wang**, ..., Robert H. Waterston, Mark Gerstein, Kevin P. White, Manolis Kellis, Michael Snyder, Comparative analysis of regulatory information and circuits across diverse species, *Nature* 512, 453–456, 2014
- Koon-Kiu Yan<sup>\*</sup>, **Daifeng Wang**<sup>\*</sup>, Joel Rozowsky, Henry Zheng, Mark Gerstein, OrthoClust: An orthology-based network framework for expression clustering across multiple species, *Genome Biology*, 15:R100, 2014

- Cristina Sisu, Baikang Pei, ..., Rachel Harte, **Daifeng Wang**, Michael Rutenberg Schoenberg, Wyatt Clark, Mark Diekhans, Joel Rozowsky, Tim Hubbard, Jennifer Harrow, Mark Gerstein, Comparative analysis of pseudogenes across three phyla, *Proceedings of the National Academy of Sciences* (PNAS), vol. 111, no. 37, pp. 13361–13366, 2014
- **Daifeng Wang**, Mia K. Markey, Claus O. Wilke and Ari Arapostathis, Eigen-genomic System Dynamic-pattern Analysis (ESDA): Modeling mRNA degradation and self-regulation, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, vol. 9, no. 2, pp. 430-437, 2012
- **Daifeng Wang**, Ari Arapostathis, Claus O. Wilke, and Mia K. Markey, Principal-Oscillation-Pattern Analysis of Gene Expression, *PLoS ONE* 7(1): e28805, 2012
- Sean X. Shi, Anand Ramalingam, **Daifeng Wang**, and David Z. Pan, Latch Modeling for Statistical Timing Analysis, Proceedings of the IEEE Conference on Design, Automation and Test in Europe 2008
- Wei Wu, **Daifeng Wang**, Ari Arapostathis and K. Davey, Optimal Power Generation Scheduling of a Shipboard Power System, Proceedings of the IEEE Electric Ship Technologies Symposium 2007
- **Daifeng Wang** and Brian L. Evans, Codebook Design for Noncoherent MIMO Communications Via Reflection Matrices, Proceedings of the IEEE Global Telecommunications Conference 2006

#### Revision/Submitted/Preprint:

- Ting Jin, Flaminia Talos, **Daifeng Wang**<sup>#</sup>, a deep learning model based on semi-restricted Boltzmann Machine reveals gene regulatory networks for predicting early cancer patient outcomes, submitted

#### **BOOK REVIEWS AND CHAPTERS**

- **Daifeng Wang**, Systems Biology: Constraint-Based Reconstruction and Analysis by Bernhard O. Palsson, The Quarterly Review of Biology, 92:3, 303-304, 2017
- **Daifeng Wang**, Epigenomics in Health and Disease by Mario Fraga and Agustin F. Fernandez, The Quarterly Review of Biology, 93:2, 163-164, 2018
- **Daifeng Wang**, Chao Cheng, Chapter 27: Genomics and Systems Biology, *Cooperative and Graph Signal Processing*, Editors: Petar M. Djuric and Cedric Richard, Elsevier, 2018, ISBN: 978-0-12-813677-5

#### **HONORS AND AWARDS**

- Best Poster Award, ACM Conference on Bioinformatics, Computational Biology & Health Informatics 2018
- Faculty of 1000 Best Poster Presentation Award, 10<sup>th</sup> Great Lakes Bioinformatics Conference, International Society for Computational Biology 2015
- NSF Extreme Science and Engineering Discovery Environment Startup Allocation Grant 10/2015
- Graduate Student Professional Development Award, The University of Texas at Austin 2009
- Nominated for Texas Exes Teaching Awards to Teaching Assistant 2008
- Graduate Student Travel Award, IEEE GLOBECOM 2006
- Advanced Class of Elite Range (ACER), Huazhong University of Science and Technology

#### **SELECTED RESEARCH EXPERIENCE**

*Assistant Professor*, Stony Brook University (08/2016 – 06/2019) and University of Wisconsin – Madison (07/2019 -)

- Interpretable machine learning models for understanding molecular mechanisms and functional genomics in human aging and brain disorders (PsychENCODE)

- Multi-scale modeling, prediction and analysis of gene regulatory networks and circuits with applications to brain disorders, cancer, neuroscience and bioenergy
- Translational bioinformatics and computational medicine

*Postdoctoral Associate and Associate Research Scientist, Yale University (01/2012 – 07/2016)*

- Bioinformatics and Functional genomics in the projects of Encyclopedia of DNA Elements (ENCODE/modENCODE/PsychENCODE), Extracellular RNA Communication (ERC), The Cancer Genome Atlas (TCGA), Pan-Cancer analysis of Whole Genomes (PCAWG) and 1000 Genomes
- Plant gene network analysis as leading developer in DOE Systems Biology Knowledgebase (KBase)
- Academic social networks driven by large scientific consortia (Big Science)

*Graduate Research Assistant, University of Texas at Austin (12/2007 – 12/2011)*

- Principal dynamic characteristics of high dimensional temporal gene expression data
- Functional annotations & pathway analysis of mouse brain neuro-genomic data, in collaboration with the Waggoner Center for Alcohol and Addiction Research, UT-Austin
- Clinical decision support systems about tissue expansion implant breast reconstruction, in collaboration with MD Anderson cancer center

## **SELECTED TEACHING AND MENTORING EXPERIENCE**

*Assistant Professor, Stony Brook University*

- BMI 511 Translational Bioinformatics (Fall 2017, 2018)
- CSE 523/524 Advanced Project in Computer Science I/II (Faculty advisor)
- CSE 393 Introduction to Biomedical Informatics (Spring 2018, guest lecturer)
- PhD students: Nam Nguyen (Computer Science, 07/2017 –), Ting Jin (Biomedical Informatics, 08/2017 –)
- Masters students: Sanjeevani Choudhery, Neha Mane, Rahul Bhansali
- Rotation: Manojit Mosur Swamynathan (Molecular and Cellular Biology, 01-04/2017)
- Undergraduate: So Yeon Min (MIT EECS, funded by Google Summer of Code 2017)
- Dissertation committee: Dr. Cheng Chang (Electrical & Computer Engineering, 03/2018)

*Graduate Teaching Assistant, University of Texas at Austin*

- EE331 Electric Circuits, Electronics and Machinery, EE411 Circuit Theory, EE445S Real-Time Digital Signal Processing Lab, EE382V-3 VLSI Communication/Digital Signal Processing Systems

## **SELECTED INVITED TALKS AND ORAL PRESENTATIONS**

- “The PsychENCODE Consortium: What Did We Learn and What is next?”, PsychENCODE symposium, 2019 World Congress of Psychiatric Genetics, Anaheim, CA, 10/2019
- “ManiNetCluster: A novel manifold learning approach to reveal the functional links between gene networks”, International Conference on Intelligent Biology and Medicine (ICIBM 2019), Columbus, OH, 06/2019
- “Interpretable deep learning modeling embedding gene regulatory network for understanding functional genomics in neuropsychiatric disorders”, Network Biology 2019 at Cold Spring Harbor Laboratory, NY, 03/2019
- “Larger-Scale Transcriptome and Epigenome Mappings, Modeling and Analyses in Developing and Diseased Human Brain”, American College of Neuropsychopharmacology Annual Meeting, Hollywood, FL, 12/2018
- “Comprehensive functional genomic resource and integrative model for the adult brain”, American Society of Human Genetics Annual Meeting, San Diego, CA, 10/2018

- “Comparative gene network analysis of epithelial to mesenchymal transition reveals lung cancer progression stages”, International Conference on Intelligent Biology & Medicine, Los Angeles, 06/2018
- “Comprehensive functional genomic resource and integrative model for the adult brain”, NIMH PsychENCODE Consortium In-Person Workshop, Yale University, New Haven, CT, 05/2018
- “Using state-space models to infer the dynamics of gene expression driven by external and internal regulatory networks”, Systems Genomics Workshop, International Plant & Animal Genome Conference XXV, San Diego, CA, 01/2017
- NIMH PsychENCODE Workshop, Society for Neuroscience conference, San Diego, CA, 11/2016
- “Temporal dynamics of collaborative networks driven by large scientific consortia”, Intelligent Systems for Molecular Biology (ISMB), Orlando, FL, 07/2016 (Highlights talk)
- “Systematic multi-scale modeling and analysis for gene regulation”, 1st SysMod SIG meeting, Intelligent Systems for Molecular Biology (ISMB), Orlando, FL, 07/2016
- “DREISS: dynamics of gene expression driven by external and internal regulatory networks based on state space model”, the eighth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, Philadelphia, PA, 11/2015
- “Using state-space models to infer the dynamics of gene expression driven by external and internal regulatory networks”, Yale Institute for Network Science and Kavli Institute for Neuroscience, Yale University, 11/2015
- “Loregic: A method to characterize the cooperative logic of regulatory factors”, 10<sup>th</sup> Great Lakes Bioinformatics Conference, International Society for Computational Biology, Purdue University, 05/2015
- NHGRI ENCODE consortium meeting, Boston, Massachusetts, 2012
- “Development of a Bayesian Network to Model Decisions about Tissue Expansion Implant Breast Reconstruction”, 3<sup>rd</sup> Annual International Conference in Computational Surgery, Houston, Texas, 2011

#### **SELECTED POSTER PRESENTATIONS AND ABSTRACTS**

- ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB) 2018
- Sanjeev Choudhery (Master’s research project), “Machine learning analysis reveals functional developmental and predictive gene modules associated with cortical thickness changes for Autism Spectrum Disorder (ASD)” on Society of Biological Psychiatry Annual Meeting, New York City, 2018
- Computational Aspects of Biological Information 2016 at Microsoft Research New England, Cambridge, MA
- The New York Area Meeting in Quantitative Biology, Computational and Statistical Genomics: Applications to Disease, Cold Spring Harbor Laboratory, New York, 2016
- Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor Laboratory, New York, 2016
- The eighth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, Philadelphia, Pennsylvania, November 15-18, 2015
- The Great Lakes Bioinformatics Conference, West Lafayette, Indiana, May 18-20, 2015
- Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, San Diego, California, 2014
- Biological Data Science, Cold Spring Harbor Laboratory, New York, 2014
- Annual International Conference on Research in Computational Molecular Biology, Pittsburgh, PA, 2014
- Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor Laboratory, New York, 2014
- CSHL Genome Informatics 2013, Cold Spring Harbor Laboratory, New York, 2013
- ACM Conference on Bioinformatics, Comp. Biology & Biomedical Informatics, Washington D.C., 2013

- Plant Biology 2013, American Society of Plant Biologists, Providence, Rhode Island, 2013
- The Biology of Genomes 2013, Cold Spring Harbor Laboratory, New York, 2013
- Department of Energy Joint Genome Institute User Meeting, Walnut Creek, California, 2013
- ENCODE consortium meeting, Boston, Massachusetts, 2012
- American Medical Informatics Association Annual Symposium, Washington D.C., 2011
- Biomedical Engineering Society (BMES) 2011 Annual Meeting, Hartford, CT, 2011
- The third Annual International Conference in Computational Surgery, Houston, Texas, 2011

## RESEARCH GRANTS

- *Discovery and Validation of Neuronal Enhancers Associated with the Development of Psychiatric Disorders*, NIMH 1U01MH116492, Co-I (Site Project Director), 07/2018 – 06/2023
- *Identification of gene regulatory networks for direct conversion of fibroblasts into bladder epithelia*, Interdisciplinary pilot grant of Cancer Center, College of Engineering and Applied Sciences at Stony Brook University, PI with co-PI Dr. Flaminia Talos, 07/2017 – 06/2019
- *Large-Scale Comparative Regulatory Network Analysis in Photosynthetic Organisms*, Stony Brook University – Brookhaven National Laboratory seed grant, PI with co-PI Dr. Ian Blaby, 07/2017 – 12/2018

## PEER-REVIEW EXPERIENCE

Proposals: NIH P01 (ad hoc 2018, special emphasis panelist 2019), NSF (virtual panelist 2019)

Journals and conferences: PLoS Genetics, PLoS Computational Biology, Schizophrenia Research, Nucleic Acids Research, Oxford Bioinformatics, AACR Cancer Research, AACR Molecular Cancer Research, Scientific Reports, PLoS One, Information Sciences, Evolutionary Bioinformatics, BMC Bioinformatics, Algorithms for Molecular Biology, Cancer Management and Research, Cancer Informatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Journal of Bioinformatics and Computational Biology, 2005 IEEE Signal Processing Systems Workshop, IEEE Transactions on Signal Processing, IEEE International Symposium on Circuits and Systems, RECOMB 2009