

Daifeng Wang

CONTACT INFORMATION

Work: (631) 638-1329

Email: daifeng.wang@stonybrook.edu

Website: <https://daifengwang.com>

RESEARCH AREAS

Biomedical data science, bioinformatics, computational biology and medicine, network science

PROFESSIONAL EXPERIENCE

August 2016 – Present, *Assistant Professor*, Department of Biomedical Informatics and *Faculty member* of Stony Brook Cancer Center, Stony Brook University

February 2017 – Present, *Assistant Professor*, Department of Electrical and Computer Engineering and *Adjunct Assistant Professor*, Department of Computer Science, Stony Brook University

August 2015 – July 2016, *Associate Research Scientist*, Department of Molecular Biophysics and Biochemistry, Yale University

EDUCATION AND TRAINING

Postdoctoral Associate, Computational Biology & Bioinformatics Program and Department of Molecular Biophysics and Biochemistry, Yale University, 2012-2015

Mentor: Dr. Mark B. Gerstein, Albert L. Williams Professor of Biomedical Informatics

Ph.D., Electrical and Computer Engineering, The University of Texas at Austin, 2011

Certificate, Statistical Foundations, Division of Statistics and Scientific Computation, The University of Texas at Austin, 2011

Master of Science, Electrical and Computer Engineering, The University of Texas at Austin, 2006

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

HONORS AND AWARDS

- Faculty of 1000 Best Poster Presentation Award, 10th Great Lakes Bioinformatics Conference, International Society for Computational Biology 2015
- The 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
- The Top Academic Outstanding Student, Huazhong University of Science and Technology

PEER-REVIEWED PUBLICATIONS (*co-first-author, equal contribution)

- **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*, **Daifeng Wang***, Anurag Sethi, Robert Kitchen, Paul Muir, Chao Cheng, Mark Gerstein, Matchmaking hairballs – insights from cross-disciplinary network comparison, **Cell Systems**, 2, 147-157, 2016 (featured front-matter)
- 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, Logic: A method to characterize the cooperative logic of regulatory factors, **PLoS Computational Biology** 11(4): e1004132, 2015 (featured article)
- 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*, Joel Rozowsky*, Koon-Kiu Yan*, **Daifeng Wang***, Chao Cheng*, ..., Steven Brenner, Brenton Graveley, Susan Celniker, Thomas Gingeras, and Robert Waterston, Comparative Analysis of the Transcriptome across Distant Species, **Nature** 512, 445–448, 2014 (News & Views, Nature)
- Alan P. Boyle*, Carlos L. Araya*, ..., **Daifeng Wang**, Peter Weisdepp, Yi-Chieh Wu, Dan Xie, Koon-Kiu Yan, Elise A. Feingold, Peter J. Good, Michael J. Pazin, Haiyan Huang, Peter J. Bickel, Steven E. Brenner, Valerie Reinke, 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 (News & Views, Nature)
- Koon-Kiu Yan*, **Daifeng Wang***, 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, Jing Leng, Adam Frankish, Yan Zhang, Suganthi Balasubramanian, 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**, Eric Pan, Gang Fang, Sunita Kumari, Fei He, Koon-Kiu Yan, Doreen Ware, Sergei Maslov, Mark Gerstein, Comparative network analysis of gene co-expression networks reveals the conserved and species-specific functions of cell-wall related genes between Arabidopsis and Poplar, Proceedings of 4th ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM BCB 2013)

- **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

MEDIA COVERAGE

- “Shared genetics in humans, worms and flies”, [Yale Daily News](#), 2014, personal Interview
- “Evolution used similar molecular toolkits to shape flies, worms, and humans”, [Yale News](#), 2014
- “Tiny, Vast Windows Into Human DNA”, [The New York Times](#), September 2, 2014
- “Scientists looking across human, fly and worm genomes find shared biology”, [National Institutes of Health \(NIH\)](#), 2014

SELECTED RESEARCH EXPERIENCE

August 2016 – Present: *Assistant Professor*, Stony Brook University

- Systems identification of novel biomarker and drug-target genes driving epithelial–mesenchymal transition (EMT) in cancer
- Integrated network analysis of genomics and metabolomics
- Principal spatiotemporal dynamic interactions and patterns in complex networks and systems

January 2012 – July 2016: *Postdoctoral Associate and Associate Research Scientist*, Yale University

- Bioinformatics, genome informatics and computational systems biology 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
- Bioinformatics software as leading developer in DOE Systems Biology Knowledgebase (KBase)
- Academic social networks driven by large scientific consortia (Big Science)

December 2007 – December 2011: *Graduate Research Assistant*, University of Texas at Austin.

- 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

SELECTED TEACHING EXPERIENCE

Graduate Teaching Assistant, University of Texas at Austin

- Undergraduate Courses: EE331 Electric Circuits, Electronics and Machinery, EE411 Circuit Theory, EE445S Real-Time Digital Signal Processing Lab

- Graduate Courses: EE382V-3 VLSI Communication/Digital Signal Processing Systems (this course was designed for working professionals of high-tech companies in Austin, TX).

SELECTED WORK EXPERIENCE

- June-August 2008: *Graduate Research Intern*, Qualcomm Research Center, San Diego, CA.
- June 2007-January 2008: *Software Engineer Co-op*, Cisco Systems, Austin, TX.
- May-August 2005: *Software Engineer Intern*, National Instruments, Austin, TX.

INVITED TALKS AND ORAL PRESENTATIONS

- “Using state-space models to infer the dynamics of gene expression driven by external and internal regulatory networks”, Systems Genomics Workshop of the International Plant and Animal Genome Conference XXV, San Diego, CA, January 2017
- NIMH PsychENCODE In-Person Workshop, 2016 Society for Neuroscience (SfN) conference, San Diego, CA, November 2016
- “Temporal dynamics of collaborative networks driven by large scientific consortia”, Intelligent Systems for Molecular Biology (ISMB), Orlando, FL, July 2016 (Highlights talk)
- “Systematic multi-scale modeling and analysis for gene regulation”, 1st SysMod SIG meeting on Computational modeling of biological systems, Intelligent Systems for Molecular Biology (ISMB), Orlando, FL, July 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, November 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, November 2015
- “Loregic: A method to characterize the cooperative logic of regulatory factors”, 10th Great Lakes Bioinformatics Conference, International Society for Computational Biology, Purdue University, May 2015
- NHGRI ENCODE consortium meeting, Boston, Massachusetts, 2012
- “Development of a Bayesian Network to Model Decisions about Tissue Expansion Implant Breast Reconstruction”, 3rd Annual International Conference in Computational Surgery, Houston, Texas, 2011

POSTER PRESENTATIONS AND ABSTRACTS

- Computational Aspects of Biological Information (CABI) 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
- CSHL Systems Biology: Global Regulation of Gene Expression 2016, 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

- The seventh Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges and Cytoscape Workshops, San Diego, California, 2014
- CSHL Biological Data Science, Cold Spring Harbor Laboratory, New York, 2014
- 18th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2014), Pittsburgh, Pennsylvania, 2014
- CSHL Systems Biology: Global Regulation of Gene Expression 2014, Cold Spring Harbor Laboratory, New York, 2014
- CSHL Genome Informatics 2013, Cold Spring Harbor Laboratory, New York, 2013
- 4th ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM BCB 2013), Washington DC, 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

PEER-REVIEW EXPERIENCE

PLoS Genetics, Scientific Reports, PLoS One, Information Sciences, Evolutionary Bioinformatics, Algorithms for Molecular Biology, 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, 13th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2009)