

Daifeng Wang

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SUMMARY

Interpretable machine learning approaches and bioinformatics tools for understanding functional genomics and gene regulation in complex biological systems such as human brain and brain diseases.

PROFESSIONAL EXPERIENCE

- **Assistant Professor**, Department of Biostatistics and Medical Informatics and Department of Computer Sciences (affiliate), University of Wisconsin – Madison, 07/2019 – present
- **Investigator**, Waisman Center, University of Wisconsin – Madison, 07/2019 – present
- **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 and Bioinformatics Program and Department of Molecular Biophysics and Biochemistry, Yale University, 01/2012 – 07/2015
- **Ph.D.**, Electrical and Computer Engineering, The University of Texas at Austin, 12/2011
- **Master of Science**, Electrical and Computer Engineering, The University of Texas at Austin, 06/2006
- **Bachelor of Science**, Electronics and Information Engineering, Huazhong University of Science and Technology, Wuhan, China, 06/2004

PUBLICATIONS

(*co-first-author, equal contribution; #co-corresponding author; last author as corresponding author)

- Chirag Gupta, Pramod Chandrashekar, Chenfeng He, Ting Jin, Saniya Khullar, Qiang Chang, **Daifeng Wang**, Bringing machine learning to research on intellectual and developmental disabilities: taking inspiration from neurological diseases, accepted, *Journal of Neurodevelopmental Disorders* (IDDRC 2022 special issue on computational neuroscience)
- Nam D Nguyen, Jiawei Huang, **Daifeng Wang**, a deep manifold-regularized learning model for improving phenotype prediction from multi-modal data, *Nature Computational Science*, 2, 38–46, 2022
- Cui-Xiang Lin, Hong-Dong Li, Chao Deng, Weisheng Liu, Shannon Erhardt, Fang-Xiang Wu, Xing-Ming Zhao, Jun Wang, **Daifeng Wang**, Bin Hu, Jianxin Wang, Genome-wide prediction and integrative functional characterization of Alzheimer's disease-associated genes, *Briefings in Bioinformatics*, 23(1):bbab522, 2022
- Ali Fathi, Sakthikumar Mathivanan, Linghai Kong, Andrew J Petersen, Cole R. K. Harder, Jasper Block, Julia Marie Miller, Anita Bhattacharyya, **Daifeng Wang**, Su-Chun Zhang, Chemically Induced Senescence in Human Stem Cell-Derived Neurons Promotes Phenotypic Presentation of

Neurodegeneration, *Aging Cell*, e13541, 2021

- Jiawei Huang, Jie Sheng, **Daifeng Wang**, Manifold learning analysis suggests strategies for aligning single-cell multi-modalities and revealing functional genomics for neuronal electrophysiology, accepted, *Communications Biology*, 4, 1308, 2021
- Ting Jin, Peter Rehani, Mufang Ying, Jiawei Huang, Shuang Liu, Panos Roussos, **Daifeng Wang**, scGRNom: a computational pipeline of integrative multi-omics analyses for predicting cell-type disease genes and regulatory networks, *Genome Medicine*, 13, 95, 2021
- Minjie Shen, Yu Guo, Qiping Dong, Yu Gao, Michael E. Stockton, Meng Li, Sudharsan Kannan, Tomer Korabelnikov, Keegan A. Schoeller, Carissa L. Sirois, Chen Zhou, Jonathan Le, **Daifeng Wang**, Qiang Chang, Qian-Quan Sun, Xinyu Zhao, FXR1 regulation of parvalbumin interneurons in the prefrontal cortex is critical for schizophrenia-like behaviors, *Molecular Psychiatry*, 2021
- Kunling Huang, Yuchang Wu, Junha Shin, Ye Zheng, Alireza Fotuhi Siahpirani, Yupei Lin, Zheng Ni, Jiawen Chen, Jing You, Sunduz Keles, **Daifeng Wang**, Sushmita Roy, Qiongshi Lu, Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder, *PLoS Genetics*, 17(2): e1009309, 2021
- Ting Jin*, Nam D Nguyen*, Flaminia Talos, **Daifeng Wang**, ECMarker: Interpretable machine learning model identifies gene expression biomarkers predicting clinical outcomes and reveals molecular mechanisms of human disease in early stages, *Bioinformatics*, 37 (8), 1115-1124, 2021
- Nam D Nguyen, Ting Jin, **Daifeng Wang**, Varmole: A biologically drop-connect deep neural network model for prioritizing disease risk variants and genes, btaa866, *Bioinformatics*, 37 (12), 1772-1775, 2021
- Yu Gao, Minjie Shen, Jose Carlos Gonzalez, Qiping Dong, Sudharsan Kannan, Johnson Hoang, Brian E. Eisinger, Qiang Chang, **Daifeng Wang**#, Linda Overstreet-Wadiche, Xinyu Zhao, RGS6 mediates effects of voluntary running on adult hippocampal neurogenesis, *Cell Reports*, 32(5):107997, 2020
- Koon-Kiu Yan*, **Daifeng Wang***, Kun Xiong, Mark Gerstein, Comparing technological development and biological evolution from a network perspective, *Cell Systems*, 10(3), P219-222, 2020
- Jing Zhang et al. including **Daifeng Wang**, An integrative ENCODE resource for cancer genomics, *Nature Communications*, 11, 3696, 2020
- Nam D Nguyen, **Daifeng Wang**, Multi-view learning for understanding functional multiomics, *PLoS Computational Biology*, 16(4): e1007677, 2020
- Nam Nguyen, Ian K. Blaby, **Daifeng Wang**, ManiNetCluster: A Manifold Learning Approach to Reveal the Functional Linkages Across Multiple Gene Networks, *BMC Genomics*, 20, 1003, 2019
- John A Haley, Christian F Ruiz, Emily D Montal, **Daifeng Wang**, John D Haley, Geoffrey D Girnun, Decoupling of Nrf2 Expression Promotes Mesenchymal State Maintenance in Non-Small Cell Lung Cancer, *Cancers*, 2019, 11(10), 1488
- Mohamed Salama, Mengling Liu, Christopher J. Clarke, Mel Pilar Espailat, John Haley, Ting Jin, **Daifeng Wang**, Lina M. Obeid, Yusuf A. Hannun, PKC α is required for Akt-mTORC1 activation in Non-Small Cell Lung Carcinoma (NSCLC) with EGFR mutation, *Nature Oncogene*, 2019
- **Daifeng Wang***, Shuang Liu*, ..., 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*, Gabriel Santpere*, ..., **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
- PsychENCODE consortium including **Daifeng Wang**, Revealing the brain's molecular architecture, **Science**, 2018 Dec 14;362(6420):1262-1263
- 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**[#] and Mark Gerstein[#], 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**[#], John D. Haley and Patricia Thompson[#], 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*, **Daifeng Wang***, 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*, 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
- Alan P. Boyle*, Carlos L. Araya*, ..., **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*, **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, ..., 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, Mia K. Markey, Principal-Oscillation-Pattern Analysis of Gene Expression, *PLoS ONE* 7(1): e28805, 2012
- Sean X. Shi, Anand Ramalingam, **Daifeng Wang**, 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**, Brian L. Evans, Codebook Design for Noncoherent MIMO Communications Via Reflection Matrices, Proceedings of the IEEE Global Telecommunications Conference 2006

BOOK REVIEWS AND CHAPTERS

- Justin Snider, **Daifeng Wang**, Daniel F. Bogenhagen, John D. Haley, Pulse SILAC Approaches to the Measurement of Cellular Dynamics, Advances in Experimental Medicine and Biology book series (volume 1140), pp 575-583
- **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

SOFTWARE AND COMPUTATIONAL INFRASTRUCTURE

- Data science core in Waisman Center for bioinformatics and biostatistical analyses with AWS cloud computing and high performance computing platforms, <https://www.dropbox.com/s/o8owobhul62xkqu/WaismanCenter-AWS.pdf?dl=0>
- ManiNetCluster, R package for revealing the functional links between gene networks using manifold learning, <https://github.com/daifengwanglab/ManiNetCluster>
- ECTMarker, Python package (Pytorch), an interpretable neural network model for identifying gene expression biomarkers predicting clinical phenotypes and outcomes and revealing underlying gene regulatory mechanisms, <https://github.com/daifengwanglab/ECTMarker>
- Varmole, Python package (Pytorch), a biologically drop-connect deep neural network model for prioritizing disease risk variants and genes, <https://github.com/daifengwanglab/Varmole>
- scGRNom, R pipeline for predicting gene regulatory networks via multi-omics data (e.g., cell-type gene regulatory networks), <https://github.com/daifengwanglab/scGRNom>
- deepManReg, Python package (Pytorch), a deep manifold-regularized learning model for improving phenotype prediction from multi-modal data, <https://github.com/daifengwanglab/deepManReg>
- scMNC, R pipeline, Manifold learning analysis for aligning single-cell multi-modalities and revealing functional genomics for cellular electrophysiology, <https://github.com/daifengwanglab/scMNC>
- scNET, R pipeline of single cell network biology for drug repurposing and phenotype prediction in Alzheimer's disease, <https://github.com/daifengwanglab/scNET>

RESEARCH EXPERIENCE

- **Assistant Professor**, University of Wisconsin – Madison, 07/2019 – present
 - Interpretable machine learning models and tools for understanding functional genomics and gene regulation in complex biological systems, especially at cellular resolution
 - Neurodevelopmental, neurodegenerative, and neuropsychiatric diseases
 - Data science core for the Waisman Center
- **Assistant Professor**, Stony Brook University, 08/2016 – 06/2019
 - Systems identification of gene regulatory networks in human diseases (cancers, brain disorders) by machine learning and network science approaches
 - Co-director of Biostatistics & Bioinformatics Shared Resource in Stony Brook Cancer Center
- **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), Extracellular RNA Communication (ERC), Pan-Cancer analysis of Whole Genomes (PCAWG) and 1000 Genomes
 - Gene network analysis as leading developer in DOE Systems Biology Knowledgebase
 - Academic social networks driven by large scientific consortia (Big Science)
- **Graduate Research Assistant**, University of Texas at Austin, 12/2006 – 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

TEACHING EXPERIENCE

- University of Wisconsin – Madison, July 2019 – present
 - BMI/CS 776 Advanced Bioinformatics (Spring 2021, Spring 2020, Spring 2022)
 - CS 540 Introduction to Artificial Intelligence (Fall 2020, co-teaching with Drs. Yin Li and Anthony Gitter)
 - STAT/BMI 877 Statistical Methods for Molecular Biology (Fall 2020, Spring 2022, guest lecturer)
- Stony Brook University, August 2016 – June 2019
 - BMI 511 Translational Bioinformatics (Fall 2017, Fall 2018)
 - CSE 523/524 Advanced Project in Computer Science I/II (Faculty advisor)
 - CSE 393 Introduction to Biomedical Informatics (Spring 2018, guest lecturer)

MENTORING EXPERIENCE

- Postdoctoral Associates
 - Pramod Chandrashekar (2020 – Present)
 - Chirag Gupta (2021 – Present)
 - Chenfeng He (2021 – Present)
 - Kalpana Hanthanan Arachdhilage (2021 – Present)
- Ph.D. students
 - Ting Jin, Biomedical Data Science (2017 – Present)
 - Saniya Khullar, Biomedical Data Science & CIBM Traineeship (2020 – Present)
 - Sayali Alatar, Computer Sciences (2021 – Present)
 - Noah Cohen Kalafut, Computer Sciences (2021 – Present)
- Master's students
 - Jie Sheng, Data Science in Statistics (2020 – Present)
 - Xiaoyu Liu, Data Science in Statistics (2021 – Present)
 - Chen Yang, Mathematics (2021 – Present)
- Undergraduate students
 - Jonathan Bryan, Neurobiology & Undergraduate Research Scholar (2020 – Present)
 - Marin Suzuki, Arjun Malik, Dhruv Gupta, Julia Paciorek, Boya Zhang, Isabella Escalante, Undergraduate Research Scholar (2021 – Present)
- Recent Alumni
 - Nam Nguyen, Ph.D., in Computer Science (2017 – 2021)
 - Jiawei Huang, M.S., Data Science in Statistics (2020 – 2021)
 - Yudi Mu, M.S., Data Science in Statistics (2020 – 2021)
 - Mufang Yin, M.S., Data Science in Statistics (2019 – 2020)

- Krittikak Chaiyakul, Biomedical Data Science (Ph.D. rotation, Spring 2021)
- Sahas Kumar Dandapantula, Difei Kang, Undergraduate Research Scholar, Computer Sciences (2020 – 2021)
- Peter Rehani, Undergraduate Researcher, Integrative biology (2019 – 2020)

HONORS AND AWARDS

- NSF Career Award 2022 – 2027
- Best Poster Award, ACM Conference on Bioinformatics, Computational Biology & Health Informatics 2018
- Faculty of 1000 Best Poster Presentation Award, 10th 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

PEER-REVIEW AND EDITOR EXPERIENCE

- **Grant reviewers:** NSF (2019), AHA Data Science (2019, 2020), UW Health Animal (2020), NIH (2018-2022)
- **Journal reviewers:**
 - Nature Medicine, Nature Communications, Communications Biology, Communications Medicine, iScience (Cell), Scientific Reports, PLoS One
 - Genome Biology, Genome Medicine, PLoS Genetics, Human Molecular Genetics, Trends in Molecular Medicine, Nucleic Acids Research
 - PLoS Computational Biology, Oxford Bioinformatics, Patterns (Cell), Machine learning, Genomics, Proteomics & Bioinformatics, Evolutionary Bioinformatics, BMC Bioinformatics, Algorithms for Molecular Biology, Information Sciences, IEEE/ACM Transactions on Computational Biology and Bioinformatics
 - Molecular Psychiatry, Alzheimer's & Dementia: The Journal of the Alzheimer's Association, Schizophrenia Research, Cancer Research, Clinical and Translational Medicine, Molecular Cancer Research, Cancers, Journal of Visualized Experiments, Cancer Management and Research, Cancer Informatics
- **Conference reviewers:** RECOMB, NeurIPS, ICLR, ICIBM, ICML
- **Journal editors:** JND special issue on computational neuroscience 2022 for NICHD IDDRCs

PROFESSIONAL MEMBERSHIPS

- International Society for Computational Biology
- Institute of Electrical and Electronics Engineers
- Society for Neuroscience
- Organization for Computational Neurosciences

- American Society of Human Genetics

INVITED TALKS AND ORAL PRESENTATIONS (select)

- Annual Wisconsin Epigenetics Symposium, 10/2021
- Bioinformatics and Computational Biology Seminar, Purdue University, 03/2021
- Genetics Colloquium, University of Wisconsin – Madison, Madison, WI, 02/2021
- NIH/NIA Psych-AD and Resilience-AD Joint Meeting, 12/2020 (Co-presenting with Dr. Roussos, MSSM & Dr. Finkbeiner, UCSF)
- Quantitative Biomedical Research Center Seminar Series, Department of Population and Data Sciences, University of Texas Southwestern Medical Center, 12/2020
- DOE Biological Systems Science Division Scientific Focus Area (SFA) workshop, LBNL/LLNL, 10/2020
- John D. Wiley Seminar, Waisman Center, University of Wisconsin – Madison, Madison, WI, 07/2020
- Annual RECOMB Conference on Regulatory and Systems Genomics, with DREAM Challenges, 2020
- Biomedical Data Science Visit Day, University of Wisconsin – Madison, Madison, WI, 02/2020
- BMI student training seminar, University of Wisconsin – Madison, Madison, WI, 12/2019
- Gene discovery session, Director’s meeting of Eunice Kennedy Shriver Intellectual & Developmental Disabilities Research Centers, NICHD, Seattle, WA, 11/2019
- Board of Visitors, Waisman Center, University of Wisconsin – Madison, Madison, WI, 10/2019
- PsychENCODE symposium, 2019 World Congress of Psychiatric Genetics, Anaheim, CA, 10/2019
- NIMH PsychENCODE Consortium In-Person Workshop, University of Chicago, Chicago, IL, 10/2019
- Computation and Informatics in Biology and Medicine (CIBM) Seminar, University of Wisconsin – Madison, Madison, WI, 10/2019
- Institute of Brain Science (IOBS), Fudan University, Shanghai, China, 09/2019
- College of Computer Science, Central South University, Changsha, Hunan, China, 09/2019
- International Conference on Intelligent Biology and Medicine (ICIBM 2019), Columbus, OH, 06/2019
- Network Biology 2019 at Cold Spring Harbor Laboratory, NY, 03/2019
- American College of Neuropsychopharmacology Annual Meeting, Hollywood, FL, 12/2018
- American Society of Human Genetics Annual Meeting, San Diego, CA, 10/2018
- International Conference on Intelligent Biology & Medicine, Los Angeles, 06/2018
- 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”, International Plant & Animal Genome Conference, San Diego, CA, 01/2017
- NIMH PsychENCODE Workshop, Society for Neuroscience conference, San Diego, CA, 11/2016
- Intelligent Systems for Molecular Biology (ISMB), Orlando, FL, 07/2016 (Highlights talk)
- 1st SysMod SIG meeting, Intelligent Systems for Molecular Biology (ISMB), Orlando, FL, 07/2016
- RECOMB Conference on Regulatory and Systems Genomics, with DREAM Challenges, Philadelphia, PA, 11/2015
- Yale Institute for Network Science and Kavli Institute for Neuroscience, Yale University, 11/2015
- 10th Great Lakes Bioinformatics Conference, International Society for Computational Biology, Indiana, 05/2015