

Yijie Wang

Computer Science Department
Indiana University at Bloomington
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Education

- 2010-2015 | **Texas A&M University, USA**
PhD in Electrical Engineering
Thesis: Module Identification for Biological Networks
Honor: Asia Pacific Bioinformatics Conference *Best paper award* (2013),
GlobalSIP travel award (2014), ACM-BCB travel award (2012)
Advisor: Xiaoning Qian
- 2006-2009 | **Dalian University of Technology, China**
MSc in Automation
Thesis: Correlation analysis and prediction of multivariate chaotic time series
Honor: Best Master thesis award (2009), Push Heavy Machinery Co. Ltd.
Fellowship (2008)
Advisor: Min Han
- 2002-2006 | **Dalian University of Technology, China**
BSc in Automation

Experience

- 2019-now | **Indiana University at Bloomington, Computer Science Department**
Tenure-track assistant professor. Research on computational biology and bioinformatics.
- 2015-2019 | **Computational Biology Branch, NCBI/NLM/NIH, MD, USA**
Research fellow. Research on various biological data driven topics, such as comparative analysis of single cell RNA-seq datasets, constructing context-specific gene regulatory networks, and design of RNA complexes, with a focus on algorithm development and mathematical optimization.
Advised by Teresa M Przytycka
- Summer 2012 | **Los Alamos National Laboratory, NM, USA**
Summer Intern. Research and development of a parallel algorithm for particle movement problems for GPUs under the supervision of Allen McPherson.

Honor/Awards

- 2022 | *NIH Maximizing Investigators Research Award (MIRA)*

2017	<i>Best Paper Award</i> , RECOMB 2017. <i>The Fellows Award for Research Excellence</i> , NIH 2017
2014	<i>Travel award</i> , GlobalSIP 2014
2013	<i>Best Paper Award</i> , Asia Pacific Bioinformatics Conference (APBC) 2013.
2012	<i>Travel award</i> , ACM-BCB 2012.
2009	<i>Best Master Thesis Award</i> , Dalian University of Technology, China.

Funding

2022-2027	R35: Maximizing Investigators' Research Award (MIRA)	\$1,975,000
2022-2023	IU Faculty Research Support Program—Seed Funding (FRSP-SF)	\$20,000

Publications

Peer-reviewed conference (*shared first authorship)

2022	X. Huang, A. Ang, and <u>Y. Wang</u> . A l_0 norm penalized 1st-order Graph Trend Filtering equivalent to k-means clustering with graph cut regularization. AISTATS 2023 . submitted Y. Wang, Y. Zhou, and Jianzhu Ma. Learning Sparse Group Models Through Boolean Relaxation. ICLR 2023 . Accepted (recommendation score: 8, 8, 8, 6)
2021	A. Ang*, J. Ma, N. Liu, K. Huang, and <u>Y. Wang</u> *. <i>Fast Projection onto the Capped Simplex with Applications to Sparse Regression in Bioinformatics</i> . NeurIPS 2021 , the top machine learning conference.
2019	<u>Y. Wang</u> , J. Fear, I. Berger, H. Lee, B. Oliver and T.M. Przytycka. <i>Reconstruction of Gene Regulatory Networks by Integrating Biological Model and a Recommendation System</i> . RECOMB 2020 , Annual International Conference on Research in Computational Molecular Biology. <u>Y. Wang</u> and T.M. Przytycka. <i>Accurate sub-population detection and mapping across single cell experiments with PopCom</i> . RECOMB 2019 , Annual International Conference on Research in Computational Molecular Biology, Accepted and invited by <i>Cell Systems</i> .
2018	<u>Y. Wang</u> , J. Honinka, P. Swiderski, and T. M. Przytycka. <i>AptaBlocks: Accelerating the Design of RNA-based Drug Delivery Systems</i> . RECOMB 2018 , Annual International Conference on Research in Computational Molecular Biology, Paris, France, April 21-24, 2018.

- 2017 Y. Wang*, D.Y. Cho*, H. Lee, B. Oliver, and T. Przytycka. *NetREX: Network Rewiring using EXpression - Towards Context Specific Regulatory Networks*
RECOMB 2017, Annual International Conference on Research in Computational Molecular Biology, Hong Kong, China, May 3-7, 2017.
RECOMB Best Paper Award
- Y. Wang and X. Qian. *Finding Low-Conductance sets with Dense interactions (FLCD) for better protein complex prediction.*
CNB-MAC 2017, The Fourth International Workshop on Computational Network Biology: Modeling, Analysis, and Control, Boston, MA, August 20, 2017.
- 2016 P. Dao, J. Hoinka, Y. Wang, M.Takahashi, J. Zhou, F. Costa, J. Rossi, J. Burnett, R. Backofen, and T. M. Przytycka. *AptaTRACE: Elucidating Sequence-Structure Binding Motifs by Uncovering Selection Trends in HT-SELEX Experiments.*
RECOMB 2016. Annual International Conference on Research in Computational Molecular Biology, Santa Monica, CA, April 18-21 2016.
- 2014 Y. Wang and X. Qian. *Biological network clustering by robust NMF.*
CNB-MAC 2014, The Third International Workshop on Computational Network Biology: Modeling, Analysis, and Control, Newport Beach, CA, September 20, 2014.
- Y. Wang and X. Qian. *Stochastic coordinate descent Frank-Wolfe algorithm for large-scale biological network alignment.*
GlobalSIP 2014. 2014 IEEE Global Conference on Signal and Information Processing, Atlanta, GA, December 03-05, 2014.
- Y. Wang and X. Qian. *Joint Clustering of Protein Interaction Networks by Block Modeling.*
ICASSP 2014. 2014 IEEE International Conference on Acoustics, Speech, and Signal Processing, Florence, Italy, May 4-9, 2014.
- Y. Wang and X. Qian. *Joint Clustering of Protein Interaction Networks through Markov Random Walk.*
APBC 2014. The 12th Asia Pacific Bioinformatics Conference, Shanghai, China, January 17-19, 2014.
- 2013 Y. Wang and X. Qian. *Identifying Overlapping Functional Modules in Biological Networks by Markov Random Walk.*
GlobalSIP 2013. 2013 IEEE Global Conference on Signal and Information Processing, Austin, TX, December 03-05, 2013.
- Y. Wang and X. Qian. *Blockmodel Module Identification in Protein Interaction Networks through Markov Random Walk.*
EUSIPCO 2013. The 21th European Signal Processing Conference, Marrakech, Morocco, September 9-13, 2013.
- Y. Wang and X. Qian. *A Novel Subgradient-based Optimization Algorithm for Blockmodel Functional Module Identification.*
APBC 2013. The 11th Asia Pacific Bioinformatics Conference, Vancouver, CA, January 17-19, 2013.
APBC Best Paper Award

- 2012 | Y. Wang and X. Qian. *Functional Module Identification by Block Modeling using Simulated Annealing with Path Relinking*.
ACM-BCB 2012. The 13rd ACM Conference on Bioinformatics, Computational Biology and Biomedicine, Orlando, FL, October 7-10, 2012.
- 2008 | M. Han, X. Wang and Y. Wang. *Applying ICA on Neural Network to Simplify BOF Endpoints Predicting Model*.
WCCI 2008. The 5th IEEE World Congress on Computational Intelligence, Hong Kong, China, June 1-6, 2008.
- 2007 | Y. Wang and M. Han. *Prediction of Multivariate Chaotic Time Series Based on Optimized Phase Space Reconstruction*.
CCC 2007, The 26th Chinese Control Conference, Zhangjiajie, China, July 26-31, 2007.
- *shared first authorship

Peer-reviewed journal (†shared last authorship)

- 2022 | Y. Wang†, J. Fear, I. Berger, H. Lee, B. Oliver and T.M. Przytycka†. Reconstruction of Gene Regulatory Networks by Integrating Biological Model and a Recommendation System. *Communications Biology*. Accepted.
E. Jafari and Y. Wang. AIscEA: Unsupervised Integration of Single-cell Gene Expression and Chromatin Accessibility via Their Biological Consistency. *Bioinformatics*, btac683, 2022.
Y. Shao, K. Zhao, Z. Cao, Z. Peng, X. Peng, P. Li, J. Ma†, Y. Wang†. MobilePrune: Neural Network Compression via ℓ_0 Sparse Group Lasso on the Mobile System. *Sensor (Basel)*, 22(11):4081, 2022.
- 2021 | X. Huang, K. Huang, T. Johnson, M. Radovich, J. Zhang, J. Ma and Y. Wang. ParsVNN: parsimony visible neural networks for uncovering cancer-specific and drug-sensitive genes and pathways. *NAR Genomics and Bioinformatics*, 3(4): lqab097, 2021.
- 2019 | Y. Wang, J. Honinka, and T. M. Przytycka. Subpopulation Detection and Their Comparative Analysis across Single-Cell Experiments with scPopCorn. *Cell Systems*, 8(6): 506-513, 2019
- 2018 | Y. Wang, J. Honinka, P. Swiderski, and T. M. Przytycka. AptaBlocks: Accelerating the Design of RNA-based Drug Delivery Systems. *Nucleic Acids Research*, 46(16): 8133-8142, 2018
Y. Wang*, D.Y. Cho*, H. Lee, J. Fear, B. Oliver, and T. Przytycka. Reprogramming of regulatory network using expression uncovers sex-specific gene regulation in *Drosophila*. *Nature Communications*, 9(1): 4061, 2018
- 2017 | Y. Wang and X. Qian. Finding Low-Conductance sets with Dense interactions (FLCD) for better protein complex prediction. *BMC System Biology*, 11(suppl 3): 22, 2017.

- S.Yoon, K. Huang, V. Reebye, D. Spalding, T. M. Przytycka, Y. Wang, P. Swiderski, L. Li, B. Armstrong, I. Reccia, D. Zacharoulis, K. Dimas, T. Kusano, J. Shively, N. Habib, and J. J. Rossi. Aptamer drug conjugates (ApDCs) of active metabolites of nucleoside analogues and cytotoxic agents inhibit pancreatic tumor cell growth. *Molecular Therapy—Nucleic Acids*, 6: 80-88, 2017.
- 2016 P. Dao, J. Hoinka, M. Takahashi, J. Zhou, M. Ho, Y. Wang, F. Costa, J. J. Rossi, R. Backofen, J. Burnett, T. M. Przytycka. AptaTRACE Elucidates RNA Sequence-Structure Motifs from Selection Trends in HT-SELEX Experiments. *Cell Systems*, 3(1): 62-70, 2016.
- Y. Wang and X. Qian. Stochastic block coordinate Frank-Wolfe algorithm for large-scale biological network alignment. *EURASIP Journal on Bioinformatics and Systems Biology*, 1: 1-9, 2016.
- 2014 S. Jia, L. Gao, J. Nastos, Y. Wang, X. Zhang, and H. Wang. Defining and identifying cograph communities in complex networks. *New Journal of Physics* 17: 013044, 2014.
- Y. Wang and X. Qian. Joint Clustering of Protein Interaction Networks through Markov Random Walk. *BMC System Biology*, 8(suppl 1): S9, 2014.
- Y. Wang and X. Qian. Functional Module Identification in Protein Interaction Networks by Interaction Patterns. *Bioinformatics*, 30(1): 81-93, 2014.
- 2013 Y. Wang and X. Qian. A Novel Subgradient-based Optimization Algorithm for Blockmodel Functional Module Identification. *BMC Bioinformatics*, 14(Suppl 2): S23, 2013.
- 2009 M. Han and Y. Wang. Analysis and Modeling of Multivariate Chaotic Time Series Based on Neural Network. *Expert Systems with Applications*, 36(2): 1280-1290, 2009.

Presentations

- 2018 **AptaBlocks: Accelerating the Design of RNA-based Drug Delivery Systems**
RECOMB 2018, Paris, France, April 2018.
- 2017 **NetREX: Network Rewiring using EXpression - Towards Context Specific Regulatory Networks**
Poster presentation. The Fellows Award for Research Excellence. NIH Research Festival, Bethesda, MD, September, 2017.
- Current advances of computational tools dedicated to the analysis of HT-SELEX data**
RNA Consortium 2017, Duarte, CA, May 2017.
- 2015 **Module Identification for Biological Networks**
University of California, San Francisco, CA, March 2015.
- Module Identification for Biological Networks**
National Center for Biotechnology Information, Bethesda, MD, January 2015.

- 2014 | **Biological network clustering by robust NMF**
The Third International Workshop on Computational Network Biology: Modeling, Analysis, and Control, Newport Beach, CA, September 2014.
- Stochastic coordinate descent Frank-Wolfe algorithm for large-scale biological network alignment**
2014 IEEE Global Conference on Signal and Information Processing, Atlanta, GA, December 2014.
- Joint Clustering of Protein Interaction Networks through Markov Random Walk**
The 12th Asia Pacific Bioinformatics Conference, Shanghai, China, January 2014.
- 2013 | **A Novel Subgradient-based Optimization Algorithm for Blockmodel Functional Module Identification**
Best Paper Award. The 11th Asia Pacific Bioinformatics Conference, Vancouver, CA, January 2013.
- 2012 | **Functional Module Identification by Block Modeling using Simulated Annealing with Path Relinking**
The 13rd ACM Conference on Bioinformatics, Computational Biology and Biomedicine, Orlando, FL, October 2012.