Yijie Wang

Computer Science Department
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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

2019.08-	**Indiana University at Bloomington, Computer Science Department** Tenure track assistant professor. Research on computational biology and bioinformatics.
2015.09 - 2019.07	**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

2017	***Best Paper Award***, RECOMB 2017. ***The Fellows Award for Research Excellence***, NIH 2017
2014	***Travel award***, GlobalSIP 2014

2013	***Best Paper Award***, Asia Pacific Bioinformatics Conference (APBC) 2013.
2012	***Travel award***, ACM-BCB 2012.
2009	***Best Master Thesis Award***, Dalian University of Technology, China.

Publications
Peer-reviewed conference

2019	Y. Wang and T.M. Przytycka. *Accurate sub-population detection and mapping across single cell experiments with PopCom*. **RECOMB 2019**, Annual International Conference on Research in Computational Molecular Biology, Accepted and invited by ***Cell Systems***.
2018	Y. Wang, J. Honinka, P. Swiderski, and T. M. Przytycka. *AptaBlocks: Accelerating the Design of RNA-based Drug Delivery Systems.* **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

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
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 Communication*s, 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, <u>Y. Wang</u>, 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.

<u>Y. Wang</u> 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, <u>Y. Wang</u>, X. Zhang, and H. Wang. Defining and identifying cograph communities in complex networks. *New Journal of Physics* 17: 013044, 2014.

<u>Y. Wang</u> and X. Qian. Joint Clustering of Protein Interaction Networks through Markov Random Walk. *BMC System Biology*, 8(suppl 1): S9, 2014.

<u>Y. Wang</u> and X. Qian. Functional Module Identification in Protein Interaction Networks by Interaction Patterns. *Bioinformatics*, 30(1): 81-93, 2014.

2013   <u>Y. Wang</u> 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 <u>Y. Wang</u>. Analysis and Modeling of Multivariate Chaotic Time Series Based on Neural Network. *Expert Systems with Applications*, 36(2): 1280-1290, 2009.

Presentations

2019   **scPopCorn:** Subpopulation Detection and Their Comparative Analysis across Single-Cell Experiments with scPopCorn, Washington D.C., USA, May 2019

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.

Teaching Experience

2019	**Adv. Topics in deep neural networks**, Indiana University at Bloomington. Lecture for teaching and mentoring students in advanced deep learning topics
2014	**Data Mining in Bioinformatics**, Texas A&M University. Guest lecture on module identification in biological networks.
2011	**Topics in Introductory Computer Science,** Texas A&M University. Teaching assistant, responsible for lecturing discussion sections.
2008	**The Principle of Automatic Control**, graduate courses (EE) at Dalian University of Technology. Responsible for organizing, setting up and teaching the Matlab programming practical.