Jiang Shu

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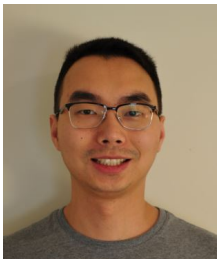

Education

2014–2018 **Ph.D. Computer Science**, *University of Nebraska - Lincoln*, Lincoln, Nebraska.

2011–2013 **M.S. Statistics**, *University of Nebraska - Lincoln*, Lincoln, Nebraska.

2003–2007 **B.S. Mathematics and Applied Mathematics**, *Huazhong Normal University*, Wuhan, China.

Employments

Jan. 2014 – present **Research Assistant**, Systems Biology and Biomedical Informatics Lab, University of Nebraska - Lincoln.

Developed a meta-LASSO regression model to reconstruct dynamic regulatory networks in cancers using multi-dimensional biological data;Performed network analysis on the complex biological system to identify the functional modules related cancer progression; Designed a computational method to identify the potential human absorbable exogenous microRNAs utilizing machine learning techniques; Built a computational pipeline for the motif detection among the short sequences using the large-scale sampling and graph algorithms.

May 2012 – Dec. 2013 **Research Assistant**, Computational Biology Lab, University of Nebraska - Lincoln.

Conducted meta-analyses of transcriptional regulation based on 500GB data from ENCODE Project; Reconstructed the regulatory networks of genes that code for ribosomal proteins; Created several data visualization templates in R; Designed and maintained a MySQL database for ENCODE data and performed customized data analysis.

Jun. 2007 – Sep. 2009 **Data Analyst**, Wuhan Katsu World Medical Electronics Technology Ltd., Wuhan, China.

Analyzed monthly sales data and maintained an internal databases using MySQL; Assisted the marketing team on identifying new clients and increasing sales..

Honors and Awards

May 2018 **Travel Award**, Conference on Predictive Inference and Its Applications, Iowa State University.

May 2018 **Young Investigator Travel Award**, 1st Midwest Statistical Machine Learning Colloquium, Iowa State University.

Sep. 2016 **Best Poster Award**, Nebraska Center for the Prevention of Obesity Diseases, University of Nebraska – Lincoln.

Jul. 2016 **Fellowship**, Open Science Grid Summer School, University of Wisconsin – Madison.

Sep. 2015 **Best Poster Award**, Nebraska Center for the Prevention of Obesity Diseases, University of Nebraska – Lincoln.

Jun. 2014 **Winning Abstract**, NetSciReg'14 – Network Models in Cellular Regulation, University of California – Berkeley.

Jun. 2014 **Best Poster Award**, Nebraska Gateway to Nutrigenomics, University of Nebraska – Lincoln.

2007, 2008 **Outstanding Staff Award**, Wuhan Katsu World Medical Electronics Technology Ltd .

2006 **Best Internship Group**, Huazhong Normal University.

Skills

Statistical Analysis: R, SAS

Programming Languages: Python, Bash Shell, SQL

Operating Systems: Unix/Linux, Windows, OS X

Slected Publications

[#] Co-first authors.

Gao T[#], **Shu J**[#], Cui J (2018). A systematic approach to RNA-associated motif discovery. *BMC Genomics*. doi:10.1186/s12864-018-4528-x.

Shu J, Vieira Resende e Silva B, Gao T, Xu Z, Cui J (2017). Dynamic and modularized microRNA regulation and its implication in human cancers. *Scientific Reports*. doi:10.1038/s41598-017-13470-5.

Shu J, Cui J (2017). MiRDR-OSG: MicroRNA dynamic regulation analysis utilizing open science grid. *IEEE Bioinformatics and Biomedicine (BIBM)*. doi: 10.1109/BIBM.2017.8217941.

Salas E, **Shu J**, Cserhati M, Weeks D, Ladunga I (2016). Pluralistic and stochastic gene regulation: examples, models and consistent theory. *Nucleic Acids Research*. doi:gkw042v1-gkw042.

Shu J, Chiang K, Zempleni J, Cui J (2015). Computational characterization of exogenous microRNAs that can be transferred into human circulation. *PLOS ONE*. doi:10.1371/journal.pone.0140587.

Chiang K, **Shu J**, Zempleni J, Cui J (2015). Dietary MicroRNA Database (DMD): An archive database and analytic tool for microRNAs in human foods. *PLOS ONE*. doi:10.1371/journal.pone.0128089.

Shu J, Chiang K, Zhao D, Cui J (2015). Human absorbable microRNA prediction based on an ensemble manifold ranking model. *IEEE Bioinformatics and Biomedicine (BIBM)*. doi: 10.1109/BIBM.2015.7359697.