CURRICULUM VITAE

Personal Information			
Name	Xionghui Zhou	Gender	Male
Position Title		Associate Professor	
Working Department		Department of Artificial Intelligence, College of Informatics.	
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Study Informaiton

My research aera includes cancer systems biology and data mining. For several years, I have paid my attention to identify prognostic signatures and construct prognosis models for cancer patients, using network biology as tool. Recently, I am working on cancer early detection by using cell-free DNA fragmentation.

Professional Memberships

Member of Bioinformatics Division, Chinese Association for Artificial Intelligence
Member of China Computer Federation

Other Roles

Education & Working Experience

Education
2005.9 - 2009.7 Jinan University in Guangdong Computer Science, Bachelor
2009.9 - 2014.7 School of Computer, Wuhan University Computer Science, PhD
Experience
2014.7-2017.12 College of Informatics, Huazhong Agricultural University Lecturer
2018.1-present College of Informatics, Huazhong Agricultural University Associate Professor
2019.4 – 2020.10 Cincinnati Children's Hospital Medical Center Research fellow

Publications

1. Ze-Jia Cui#, Min Gao#, Yuan Quan, Bo-Min Lv, Xin-Yu Tong, Teng-Fei Dai, Xiong-Hui Zhou*, and Hong-Yu Zhang*.(2021) Systems Pharmacology-Based Precision Therapy and Drug Combination Discovery for Breast Cancer. Cancers (Basel). 2021 Jul; 13(14): 3586.
2. Xiong-Hui Zhou, Xin-Yi Chu, Gang Xue, Jiang-Hui Xiong, Hong-Yu Zhang*.(2019) Identifying cancer prognostic modules by module network analysis. Bmc Bioinformatics 20 2019,20:85.
3. Ling-Hao Yu, Qin-Wei Huang, Xiong-Hui Zhou*. (2019) Identification of Cancer Hallmarks Based on the Gene Co-expression Networks of Seven Cancers. Frontiers in Genetics 2019,10:https://doi.org/10.3389/fgene.2019.00099.
4. Wei-Lin Hu, Xiong-Hui Zhou*. (2017) Identification of prognostic signature in cancer based on DNA methylation interaction network. Bmc Medical Genomics, 2017, 10(4):63.
5. Xiwen Xu#, Xiong-Hui Zhou#, Ruiru Wang, Wenlei Peng, Yue An, Lingling Chen*. (2016) Functional analysis of long intergenic non-coding RNAs in phosphate starved rice using competing endogenous RNA network, Scientific Reports 6, 2016, doi: 10.1038/srep20715
6. Xionghui Zhou, Juan Liu. (2014) A computational model to predict bone metastasis in breast cancer by integrating the dysregulated pathways. BMC Cancer 2014, 14:618.
7. Xionghui Zhou, Juan Liu, Wei Wang. (2014) Construction and investigation of breast-cancer-specific ceRNA network based on the mRNA and miRNA expression data. IET systems biology 8(3):pp.96-103.
8. Xionghui Zhou, Juan Liu, Xinhuo Ye, Wei Wang, Jianghui Xiong. (2013) Ensemble classifier based on context specific miRNA regulation modules: a new method for cancer outcome prediction. BMC Bioinformatics, 14(Suppl 12):S6.
9. Xionghui Zhou, Juan Liu, Jianghui Xiong. (2012) Predicting distant metastasis in breast cancer using ensemble classifier based on context specific miRNA regulation modules, 2012 IEEE International Conference on Bioinformatics and Biomedicine (BIBM). pp. 1-6. (Regular paper).

Additional Information