Xiaowen Chen

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Education Experience

2008-2011 Ph.D. in Biological Physics, Area of Specialization: Bioinformatics

Harbin Medical University, College of Bioinformatics Science and Technology

Harbin, China

2004-2006 M.S. in Mathematics, Area of Specialization: Basic Mathematics

Harbin Institute of Technology, School of Mathematics

Harbin, China

2000-2004 B.A. in Mathematics

Harbin normal university, School of Mathematics

Harbin, China

Grants

Sponsor: National Natural Science Foundation of China

Contract number: 31401134

Title: Identification and function study of interactions between small molecules and miRNAs based on the heterogeneous network

Contribution: Principal Investigator

Amount: CNY 200,000

Grant Period: Jan. 1, 2015 to Dec. 30, 2017

Research Experience

- Developing a high-throughput algorithm to identify links between small molecules and miRNAs in 23 different cancers through evaluating the extent of expression pattern similarity of differentially expressed genes between cancer-related miRNA regulations and small molecules perturbation based on the Kolmogorov-Smirnov test.
- Analyzing the topological property of the heterogeneous network containing two type of nodes.
- Dissecting the functional miRNA/small molecule modules in small molecule-miRNA networks and investigating biological mechanisms from miRNA/small molecule modules based on biological and chemical features including biological process, miRNA family, two-dimensional structure of drug and drug interaction information.
- Developing an algorithm to identify overrepresented adverse drug reaction (ADR)-pathway combinations through merging clinical phenotypic data, biological pathway data, and drug-target interactions.
- Using the text-mining tool PathNER to compile the known ADR-pathway associations mentioned in abstracts or titles in the PubMed.
- Understanding the pathogenesis of ADRs through network analysis on biology and pharmacology.
- Developing a random walk with restart-based algorithm to infer potential protein-ADR relations.
- Identifying the feed-forward loops in the regulatory network.
- Predicting human microRNA precursors using GA-SVM.

Qualifications

Programming Ability Matlab is well used to write applications to process data or implement algorithms. Familiar with MySQL database. R/Bioconductor, Excel, Access, Illustrator and other softwares can be skillfully used for data

processing, analyzing and drawing figures.

Software Application Ability Investigate, install, test, use and integrate software under Windows platforms. Experience of using Cytoscape, PathNER, ClueGo, etc.

Public Databases NCBI, Ensembl, Gene Ontology, KEGG, miRBase, Drugbank, SIDER, STRING, TTD, etc.

Publications

First author and co-first author

1. **Xiaowen Chen**, Hongbo Shi, Feng Yang, Lei Yang, Yingli Lv, Shuyuan Wang, Enyu Dai, Dianjun Sun, Wei Jiang (2016) Large-scale identification of adverse drug reaction- related proteins through a random walk model. *Sci. Rep*. 6, 36325; doi: 10.1038/srep 36325.

2. **Xiaowen Chen**, Yanqiu Wang, Pingping Wang, Baofeng Lian, Chunquan Li, Jing Wang, Xia Li, Wei Jiang (2015) Systematic analysis of the associations between adverse drug reactions and pathways. Biomed Res Int 2015: 670949.

3. Wei Jiang, **Xiaowen Chen**, Mingzhi Liao, Wei Li, Baofeng Lian, Lihong Wang, Fanlin Meng, Xinyi Liu, Xiujie Chen, Yan Jin, Xia Li (2012) Identification of links between small molecules and miRNAs in human cancers based on transcriptional responses. Sci Rep 2: 282.

4. Yanqiu Wang, **Xiaowen Chen**, Wei Jiang, Li Li, Wei Li, Lei Yang, Mingzhi Liao, Baofeng Lian, Yingli Lv, Shiyuan Wang, Shuyuan Wang Li X (2011) Predicting human microRNA precursors based on an optimized feature subset generated by GA-SVM. Genomics 98: 73-78.

Coauthor

1. Wang J, Meng F, Dai E, Yang F, Wang S, **Chen X**, Yang L, Wang Y, Jiang W (2016) Identification of associations between small molecule drugs and miRNAs based on functional similarity. Oncotarget.

2. Meng F, Wang J, Dai E, Yang F, **Chen X**, Wang S, Yu X, Liu D, Jiang W

(2016) Psmir: a database of potential associations between small molecules and miRNAs. Sci Rep 6: 19264.

3. Lv Y, Wang S, Meng F, Yang L, Wang Z, Wang J, **Chen X**, Jiang W, Li Y, Li X (2015) Identifying novel associations between small molecules and miRNAs based on integrated molecular networks. Bioinformatics 31: 3638-3644.

4. Meng F, Dai E, Yu X, Zhang Y, **Chen X**, Liu X, Wang S, Wang L, Jiang W (2014) Constructing and characterizing a bioactive small molecule and microRNA association network for Alzheimer's disease. J R Soc Interface 11: 20131057.

5. Jiang W, Zhang Y, Meng F, Lian B, **Chen X**, Yu X, Dai E, Wang S, Liu X, Li X, Wang L (2013) Identification of active transcription factor and miRNA regulatory pathways in Alzheimer's disease. Bioinformatics 29: 2596-2602.

6. Li X, Jiang W, Li W, Lian B, Wang S, Liao M, **Chen X**, Wang Y, Lv Y, Yang L (2012) Dissection of human MiRNA regulatory influence to subpathway. Brief Bioinform 13: 175-186.

7. Wang C, Jiang W, Li W, Lian B, **Chen X**, Hua L, Lin H, Li D, Li X, Liu Z (2011) Topological properties of the drug targets regulated by microRNA in human protein-protein interaction network. J Drug Target 19: 354-364.

8. Liao M, Jiang W, **Chen X**, Lian B, Li W, Lv Y, Wang Y, Wang S, Li X (2010) Systematic analysis of regulation and functions of co-expressed microRNAs in humans. Mol Biosyst 6: 1863-1872.

9. Chen X, Jiang W, Wang Q, Huang T, Wang P, Li Y, **Chen X**, Lv Y, Li X (2012) Systematically characterizing and prioritizing chemosensitivity related gene based on Gene Ontology and protein interaction network. BMC Med Genomics 5: 43.

Teaching experience

Associate professor:	Liner algebra and application, Harbin Medical University, 2013-2016
Associate professor:	Operations research, Harbin Medical University, 2013-2016
Instructor:	Operations research, Harbin Medical University, 2006-2013
Instructor:	Numerical analysis, Harbin Medical University, 2006-2010
Instructor:	Matlab, Harbin Medical University, 2006-2010