

## **Xiaowen Chen**

The Jackson Laboratory for Genomic Medicine

10 Discovery Drive, Farmington, CT 06032-2374, USA

## **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**

1. 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  
Grant Period: Jan. 1, 2015 to Dec. 30, 2017
2. Sponsor: The Science Foundation of Heilongjiang Province Education  
Department  
Contract number: 12531391  
Title: Identification of associations between side effects and sub-pathways  
based on chemical system biological method  
Grant Period: Jan. 1, 2013 to Dec. 30, 2015

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3. Sponsor: The Science Foundation of Heilongjiang Province Health

Department

Contract number: 2012-806

Title: Identification of associations between adverse drug effect and biological pathways

Grant Period: Jan. 1, 2013 to Dec. 30, 2015

4. Sponsor: China Postdoctoral Science Foundation

Contract number: 160765

Title: Identification of side effects-related targets

Grant Period: Jan. 1, 2015 to Dec. 30, 2018

5. Sponsor: China Postdoctoral start-up Funding

Contract number: LBH-Q19116

Title: Identification of important noncoding RNAs regulator using deep machine learning in AML

Grant Period: Jan. 1, 2020 to Dec. 30, 2023

### **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.

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- 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**

**Co-corresponding author**

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1. Jie Wu, Li Zhang, Qian Song, Lei Yu, Shuyuan Wang, Bo Zhang, Weida Wang, Peng Xia, **Xiaowen Chen**<sup>\*</sup>, Yun Xiao<sup>\*</sup>, Chaohan Xu<sup>\*</sup>. (2020) Systematical identification of cell-specificity of CTCF-gene binding based on epigenetic modifications. Briefings in Bioinformatics. DOI: 10.1093/bib/bbaa004.
2. Hui Liu, Shuyuan Wang, Wencan Wang, Weida Wang, Peng Xia, Lei Yu, Ye Lu, **Xiaowen Chen**<sup>\*</sup>, Chaohan Xu<sup>\*</sup> (2020) Context-specific Coordinately Regulatory Network Prioritize Breast Cancer Genetic Risk Factors. *Frontiers in Genetics* 11, 255
3. Shuyuan Wang, Wencan Wang, Qianqian Meng, Shunheng Zhou, Haizhou Liu, Xueyan Ma, Xu Zhou, Hui Liu, **Xiaowen Chen**<sup>\*</sup>, and Wei Jiang<sup>\*</sup> (2018) Inferring Novel Autophagy Regulators Based on Transcription Factors and Non-Coding RNAs Coordinated Regulatory Network. *Cells* 2018, 7(11), 194.

### **First author and co-first author**

1. Sheng Li<sup>#</sup>, **Xiaowen Chen**<sup>#</sup>, Jiahui Wang, Cem Meydan, Jacob L Glass, Alan H Shih, Ruud Delwel, Ross L Levine, Christopher E Mason, Ari M Melnick (2020) Somatic Mutations Drive Specific, but Reversible, Epigenetic Heterogeneity States in AML. *Cancer Discovery*, 10 (12), 1934-1949
2. Wojciech Rosikiewicz<sup>#</sup>, **Xiaowen Chen**<sup>#</sup>, Pilar M Dominguez<sup>#</sup>, Hussein Ghamlouch, Said Aoufouchi, Olivier A Bernard, Ari Melnick, Sheng Li (2020) TET2 deficiency reprograms the germinal center B cell epigenome and silences genes linked to lymphomagenesis. *Science advances* 6 (25), eaay5872
3. **Xiaowen Chen**, Haitham Ashoor, Ryan Musich, Jiahui Wang, Mingsheng Zhang, Chao Zhang, Mingyang Lu, Sheng Li (2020) epihet for intra-tumoral epigenetic heterogeneity analysis and visualization. *Sci. Rep.* (have been accepted and waiting publication)
4. **Xiaowen Chen**, Hongbo Shi, Feng Yang, Lei Yang, Yingli Lv, Shuyuan Wang, Enyu Dai, Dianjun Sun, Wei Jiang (2016) Large-scale identification of

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adverse drug reaction- related proteins through a random walk model. *Sci. Rep.* 6, 36325; doi: 10.1038/srep 36325.

5. **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.

6. 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.

7. 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. Haitham Ashoor, **Xiaowen Chen**, Wojciech Rosikiewicz, Jiahui Wang, Albert Cheng, Ping Wang, Yijun Ruan, Sheng Li (2020) Graph embedding and unsupervised learning predict genomic sub-compartments from HiC chromatin interaction data. *Nature Communications* 11 (1) 1-11.

2. Peishan Li, Ming Lu, Jiayuan Shi, Zheng Gong, Li Hua, Qing Li, Bora Lim, Xiang H-F Zhang, **Xiaowen Chen**, Sheng Li, Leonard D Shultz, Guangwen Ren (2020) Lung mesenchymal cells elicit lipid storage in neutrophils that fuel breast cancer lung metastasis. *Nature Immunology* 21 (11) 1444-1455.

3. HD Yang L, Wang S, Zhang Q, Pan Y, Lv Y, Chen X, Zuo Y (2018) Clinical significance of the immune microenvironment in ovarian cancer patients. *Mol Omics* 14 (5), 341-351.

4. S Wang, Q Zhang, D Xu, Y Pan, Y Lv, X Chen, Y Zuo, L Yang (2018) Characterize the difference between TMPRSS2-ERG and non-TMPRSS2-ERG fusion patients by clinical and biological characteristics in prostate cancer. *Gene* 679, 186-194.

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5. L Yang, S Wang, M Zhou, X Chen, W Jiang, Y Zuo, Y Lv (2017) Molecular classification of prostate adenocarcinoma by the integrated somatic mutation profiles and molecular network. *Scientific reports* 7 (1), 1-14.
6. L Yang, S Wang, M Zhou, X Chen, Y Zuo, Y Lv (2016) Characterization of BioPlex network by topological properties. *Journal of theoretical biology* 409, 148-154.
7. L Yang, S Wang, M Zhou, X Chen, Y Zuo, Y Lv. (2016) Characterize the relationship between essential and TATA-containing genes for *S. cerevisiae* by network topologies in the perturbation sensitivity network. *Genomics* 108 (3-4), 177-183.
8. 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*.
9. 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.
10. 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.
11. XM Zhang, L Guo, MH Chi, HM Sun, XW Chen (2015) Identification of active miRNA and transcription factor regulatory pathways in human obesity-related inflammation. *BMC bioinformatics* 16 (1), 76.
12. 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.
13. 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.

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14. 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.
15. 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.
16. 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.
17. 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.

### **Working experience**

- Postdoctoral Associate:* The Jackson Laboratory, 4/17/17 to now
- Associate professor:* Harbin medical university, 2013.09-now
- Instructor:* Harbin medical university, 2009.09-2012.09
- Teaching assistant:* Harbin medical university, 2006.09-2009.09