

Guangxu Jin, Ph.D.

6565 Fannin ST, B5-033, Houston, TX 77054

(281) 627-1455 (Cell) • GJin@tmhs.org

Professional Highlights

- In-depth knowledge in Mathematics and Network Biology
- Development of new pathway analysis methods for translational studies
- Modeling of the signaling mechanisms for drug repositioning, drug combination, and drug resistance
- Expertise in cDNA microarray, Proteomics, RPPA, and next generation sequencing data analyses
- Skills in Python, R, Perl, C/C++/C#, MATLAB, SQL/MySQL, ASP.net/PHP, Unix/Linux, Mac OS X

Research Experience

The Methodist Hospital Research Institute, Houston, TX

Postdoctoral Fellow with Dr. Stephen T.C. Wong, 10/2008 – present
Department of Systems Medicine and Bioengineering
A novel method of transcriptional response analysis to facilitate drug repositioning for cancer therapy

Exchange student with Dr. Stephen T.C. Wong, 12/2007 – 10/2008
Department of Systems Medicine and Bioengineering

Education

Ph.D., Chinese Academy of Sciences, Beijing, P.R. of China. Applied Mathematics 9/2005 – 7/2008

M.S., Shenyang Normal University, Shenyang, P.R. of China. Applied Mathematics 9/2002 – 7/2005

B.S., Shenyang Normal University, Shenyang, P.R. of China. Applied Mathematics 9/1998 – 7/2002

Grants and Research Supports

Current Support

NCI 1U54 CA149196-01 (PI Stephen Wong) 4/2009 – 3/2014
NCI Center for Systematic Modeling of Cancer Development
To identify protein markers for breast cancer stem

cells and niche and develop multi-scale computational model to predict treatment responses.

CPRIT RP101334 (Core PI: Stephen Wong) 3/2011 – 2/2016
Gulf Coast Consortia CPRIT High-throughput Screening Program
Data Analysis – Support from Bioinformatics Core (BIC)
To provide advanced bioinformatics design and services to assist in the experimental design and data interpretation obtained by selected high throughput drug screening projects and to create and manage databases of results and raw data generated by drug screening projects to enable off-line secondary data analysis and data mining applications.

Pending Support

NCI NLM R01 (PI Stephen Wong) 4/2013 – 03/2015
TRACT: A modeling tool for transcriptional response analysis of drug resistance
TRACT is proposed to identify the resistance signaling mechanisms for ER- and HER2- targeted therapies by applying transcriptional response data.
Status: Submission data 2/2/2012
Progress: Submitted

Patent

Network-based Signatures for Drug Repositioning
File Number: MKT201119

Professional activities

Memberships

American Association Cancer Research 1/2011 – present
Associate Member

American Chemical Society 2/2012 – present
Member

ICSB membership 4/2012 – present

Referee

BMC Systems Biology, BMC Research Notes, Journal of Theoretical Biology, Mathematical Biosciences, Computer Methods in Biomechanics

and Biomedical Engineering, IEEE/ACM Transactions on Computational Biology and Bioinformatics, ISB2011, ICIC2012, CCC2012.

Invited Presentations

- | | |
|--|--------|
| Repositioning of Drugs for Cancer and Reconstruction of Unknown Targeted Signaling Pathways
<i>Southern Biomedical Engineering Conference, Houston, TX</i> | 5/2012 |
| A Network Biology Strategy to Facilitate Faster-to-Market Drug Repositioning for Cancer Therapy.
<i>U54 CMCD Annual Symposium, Houston, TX</i> | 2/2012 |
| Network-based Models on Signaling Pathways.
<i>NCI-ICBP CMCD Annual Symposium, Houston, TX</i> | 2/2011 |
| Network-based Signatures for Drug Repositioning and Combination for the Breast Tumor Initiating Cells
<i>6th Annual Breast Cancer Research and Education Program, Montgomery, TX</i> | 9/2010 |

Peer-Reviewed Publications

Journals

Jin, G., Fu, C., Zhao, H., Cui, K., Chang, J. and Wong, S.T. (2012) A novel method of transcriptional response analysis to facilitate drug repositioning for cancer therapy. ***Cancer research***, **72**, 33-44.

Zhao, H., Cui, K.M., Nie, F., Wang, L.L., Brandl, M.B., **Jin, G.X.**, Li, F.H., Mao, Y., Xue, Z., Rodriguez, A. *et al.* (2012) The effect of mTOR inhibition alone or combined with MEK inhibitors on brain metastasis: an in vivo analysis in triple-negative breast cancer models. ***Breast Cancer Res Tr***, **131**, 425-436.

Jin, G., Zhao, H., Zhou, X. and Wong, S.T. (2011) An enhanced Petri-net model to predict synergistic effects of pairwise drug combinations from gene microarray data. ***Bioinformatics***, **27**, i310-316.

Jin, G.X., Cui, K.M., Zhou, X.B. and Wong, S.T.C. (2009) Unraveling the Signal-Transduction Networks in Cancer Metastasis. ***IEEE Signal Proc Mag***, **26**, 129-132.

Jin, G., Zhou, X., Cui, K., Zhang, X.S., Chen, L. and Wong, S.T. (2009) Cross-platform method for identifying candidate network biomarkers for prostate cancer. ***IET systems biology***, **3**, 505-512.

Wang, R.S., **Jin, G.X.**, Zhang, X.S. and Chen, L.N. (2009) Modeling post-transcriptional regulation activity of small non-coding RNAs in Escherichia coli. **BMC bioinformatics**, **10**.

Jin, G., Zhou, X., Wang, H., Zhao, H., Cui, K., Zhang, X.S., Chen, L., Hazen, S.L., Li, K. and Wong, S.T. (2008) The knowledge-integrated network biomarkers discovery for major adverse cardiac events. **Journal of proteome research**, **7**, 4013-4021.

Jin, G., Zhang, S., Zhang, X.S. and Chen, L. (2007) Hubs with network motifs organize modularity dynamically in the protein-protein interaction network of yeast. **PLoS one**, **2**, e1207.

Zhang, S.H., **Jin, G.X.**, Zhang, X.S. and Chen, L.N. (2007) Discovering functions and revealing mechanisms at molecular level from biological networks. **Proteomics**, **7**, 2856-2869.

Conferences

Jin, G., Gao, J., Wong S. (2012) A new computational model using multi-objective optimization to identify activated cancer signaling networks from heterogeneous genomic data. **ISMB**, 2012

Jin, G., Gao, J., Wong S. (2012) A computational model of pathway activation facilitates target discovery, **NCI ICBP 2nd Mathematical Modeling Meeting**, 2012, 5

Jin, G., Gao, J., Wong, S. (2012) Activated signaling mechanism of glioblastoma recurrence derived from genetics, epigenetics, and genomics abnormalities, **AACR Meeting Abstracts**, 2012, 4940

Jin, G., Zhao, H., Cong, Y., Fu, C., Chang, J., Lewis, M. and Wong, S. (2011) Abstract 4370: Network-based signatures for drug repositioning and combination for the breast tumor initiating cells. **Cancer Res**, **71**, 4370.

Jin, G., Gao, J., and Wong, S. (2011) Feeding genetics, epigenetics, and genomics abnormalities back to derive activated pathways for specific types of cancer. **TCGA Annual Meeting**, **1**: 30

Jin, G., Zhou, X., Lewis, M., Rosen, J. and Wong, S. (2010) Signal-Transduction Based Network Biomarkers for Tumor-Initiating Cells in a p53-Null Mouse Model of Breast Cancer. **Cancer Res**, **69**, 2138.

Zhao, H., Cui, K., Nie, F., **Jin, G.**, Li, F., Wu, L., Wang, L., Brandl, M., Yilidirim, N., Zhang, S. *et al.* (2010) Effects of Rapamycin on Breast Cancer

Cell Migration through the Cross-Talk of MAPK Pathway. **Cancer Res**, **69**, 5080.

Zhao, H., **Jin, G.**, Wong, H., Cui, K., Li, F., Zhang, S., Wong, S., Zhou, X., Chang, J. and Wong, S. (2009) Abstract #3573: Drug reposition for brain metastasis of breast cancer. **AACR Meeting Abstracts**, **2009**, 3573.

Cui, K., **Jin, G.**, Zhao, H., Li, F., Wang, L., Zhou, X. and Wong, S. (2009) Abstract #2452: Knowledge-based metastatic prostate cancer targets discovery. **AACR Meeting Abstracts**, **2009**, 2452.

Wang, R.S., **Jin, G.**, Zhang, X.S., Chen, L. (2008) Reconstruction of post-transcriptional regulatory signals in E. coli. **Bioinformatics and Biomedicine (BIBM'08)**: 339-342.

Jin, G., Zhou, X., Cui, K., and Wong, S. (2008) The network biomarker discovery in prostate cancer from both genomics and proteomics levels. **Lecture Notes in Operations Research**, 9: 144-151.

Jin, G., Zhang, S., Zhang, X.S., and Chen, L. (2007) New Insights into Network Motif Clusters from the Views of Cellular Localizations and Signal Pathways. **Lecture Notes in Operations Research**, 8: 100-109.

Book Chapters

Jin, G. (2012) Network topology motif. Encyclopedia of Systems Biology, 590, **Springer**, LLC. (In press)

Jin, G. (2012) Single-Input Module. Encyclopedia of Systems Biology, 464, **Springer**, LLC. (In press)

Jin, G. (2012) Feed Forward Loop. Encyclopedia of Systems Biology, 463, **Springer**, LLC. (In press)

Jin, G., Zhou, X., Cui, K., and Wong, S. (2010) The challenges in blood proteomic biomarker discovery. Computational Biology, 273-299. **Springer** New York.