

BIOGRAPHICAL SKETCH

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NAME Guangxu Jin, Ph.D.		POSITION TITLE Assistant Professor	
eRA COMMONS USER NAME (credential, e.g., agency login) GJIN2011			
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)			
INSTITUTION AND LOCATION	DEGREE (if applicable)	MM/YY	FIELD OF STUDY
Shenyang Normal University, Shenyang	B.S.	09/02	Applied Mathematics
Shenyang Normal University, Shenyang	M.S.	09/05	Applied Mathematics
Chinese Academy of Sciences, Beijing	Ph.D.	09/08	Bioinformatics

A. Personal Statement

Dr. Jin's research develops mathematical and computational biology models for translational studies. His research experiences have launched a long-term interest in the modeling of the effects of targeted therapy drugs at the molecular off-target level. He has extensive experience in signaling pathway analyses and developed the computational models for identification of the off-targets for drug repositioning and drug combination studies. A new type of signaling network elements, called cancer signaling bridges (CSBs), has been developed for cancer drug repositioning (Jin et al, *Cancer Research*, 2012, Zhao and Jin et al, *Cancer Research* 2013, Jin et al, *Drug Discovery Today*, 2014, *Stem Cells*, 2014). The new computational model based on the CSBs is helpful to address the activated signaling pathways associated with the targeted-therapy drugs. Another computational model, called Enhanced Petri Net, has been developed for drug combination study (Jin et al, *Bioinformatics*, 2011). The unique of this model is at its superiority in predicting the changed signaling pathways caused by targeted therapy. Moreover, he has more than 6 years experience in translational research. Recently, he has published a drug database with visualization of drug and signaling pathway information (Fu and Jin et al, *Bioinformatics*, 2013).

B. Positions and Professional Activities**Positions and Employment**

2007-2008 Research Fellow, The Methodist Hospital Research Institute& Weil Cornell Medical College, TX
 2008-2012 Postdoc Fellow, The Methodist Hospital Research Institute& Weil Cornell Medical College, TX
 2012-2014 Instructor and Research Associate, The Methodist Hospital Research Institute& Weil Cornell Medical College, TX
 2014- Assistant Professor, Wake Forest School of Medicine, NC

Other Experience and Professional Memberships

2011- Member, American Association Cancer Research
 2012- Member, American Chemical Society
 2012- Member, International Society for Computational Biology
 2011- Program Committee Member, IEEE International Conference on Systems Biology

C. Publications**Selected Journal Publications:**

1. **Jin G**, Wong ST. (2014) Toward better drug repositioning: Prioritizing and integrating existing methods into efficient pipelines. *Drug Discovery Today*. **19**(5); 637-644

2. Choi DS, Blanco E, Kim YS, Rodriguez AA, Zhao H, Huang TH, Chen CL, **Jin G**, Landis MD, Burey LA, Qian W, Granados SM, Dave B, Wong HH, Ferrari M, Wong ST, Chang JC. (2014) Chloroquine eliminates cancer stem cells through deregulation of Jak2 and DNMT1. *Stem cells*. doi: 10.1002/stem.1746.
3. **Jin G**, Wong ST. (2014) Enhanced Petri Net: Elucidating the Pathway-Level Mechanism of Targeted-Therapy Drugs. *Information Technology*. 56(2): 67-75.
4. Zhao H*, **Jin G***, Cui K, Ren D, Liu T, Chen P, Wong S, Li F, Fan Y, Rodriguez A, Chang J, Wong ST. (2013) Novel Modeling of Cancer Cell Signaling Pathways Enables Systematic Drug Repositioning for Distinct Breast Cancer Metastases. *Cancer Res*; **73**(20); 1-15. (*Co-first author)
5. Fu C*, **Jin G***, Gao J, Zhu R, Ballesteros-Villagrana E, Wong ST. (2013) DrugMap Central (DMC), an on-line query and visualization tool to facilitate drug repositioning studies. *Bioinformatics*, **29**(14):1834-6. (*Co-first author)
6. Li, F., Yin, Z., **Jin, G.**, Zhao, H., Wong, S. T. Chapter 17: bioimage informatics for systems pharmacology. *PLoS Comput Biol* **9**, e1003043, doi:10.1371/journal.pcbi.1003043 (2013).
7. Liu, T., Ren, D., Zhu, X., Yin, Z., **Jin, G.**, Zhao, Z., Robinson, D., Li, X., Wong, K., Cui, K. et al. (2013) Transcriptional signaling pathways inversely regulated in Alzheimer's disease and glioblastoma multiform. *Scientific reports*, **3**, 3467.
8. **Jin G**, Fu C, Zhao H, Cui K, Chang J, Wong ST (2012) A novel method of transcriptional response analysis to facilitate drug repositioning for cancer therapy. *Cancer Res*, **72**: 33-44.
9. **Jin G**, Zhao H, Zhou X, Wong ST (2011) An enhanced Petri-net model to predict synergistic effects of pairwise drug combinations from gene microarray data. *Bioinformatics* **27**(13): i310-i316.
10. **Jin G**, Cui K, Zhou X, Wong S (2009) Unraveling the Signal-Transduction Networks in Cancer Metastasis. *IEEE Signal Proc Mag* **26**: 129-132.
11. **Jin G**, Zhou X, Cui K, Zhang XS, Chen L, Wong ST (2009) Cross-platform method for identifying candidate network biomarkers for prostate cancer. *IET Syst Biol* **3**: 505-512.
12. **Jin G**, Zhou X, Wang H, Zhao H, Cui K, Zhang XS, Chen L, Hazen SL, Li K, Wong ST (2008) The knowledge-integrated network biomarkers discovery for major adverse cardiac events. *J Proteome Res* **7**: 4013-4021.
13. **Jin G**, Zhang S, Zhang XS, Chen L (2007) Hubs with network motifs organize modularity dynamically in the protein-protein interaction network of yeast. *PLoS One* **2**: e1207.
14. Wang RS, **Jin G**, Zhang XS, Chen L (2009) Modeling post-transcriptional regulation activity of small non-coding RNAs in Escherichia coli. *BMC Bioinformatics* **10 Suppl 4**: S6.
15. Zhang S, **Jin G**, Zhang XS, Chen L (2007) Discovering functions and revealing mechanisms at molecular level from biological networks. *Proteomics* **7**: 2856-2869.
16. 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.
17. Wang, L., Zhao, H., Cui, K., Yao, L., Ren, M., Hao, A., Smollen, P., Nie, F., **Jin, G.**, Liu, Q. et al. (2012) Identification of novel small-molecule inhibitors of glioblastoma cell growth and invasion by high-throughput screening. *Bioscience trends*, **6**, 192-200.
18. Wang, L., Liu, Q., Zhao, H., Cui, K., Yao, L., Nie, F., **Jin, G.**, Hao, A. and Wong, S.T. (2013) Differential effects of low- and high-dose GW2974, a dual epidermal growth factor receptor and HER2 kinase inhibitor, on glioblastoma multiforme invasion. *Journal of neuroscience research*, **91**, 128-137.
19. Fu, C., Deng, S., Jing, L., and **Jin, G.** (2012) Identification of Oncogenic Genes for Colon Adenocarcinoma from Genomics Data. *IEEE systems biology*, **6**:263-266
20. Zhao, H., Cui, K., Nie, F., Wang, L., Brandl, M. B., **Jin, G.**, Li, F., Mao, Y., Xue, Z., Rodriguez, A., et al. (2011). 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 Treat.* **131** (2), 425-436

Conferences (Abstracts and posters):

21. Jin, G., Wong S. (2014) "One Patient-One Pathway": Constructing personalized signaling pathways for better prediction of disease conditions and design of treatment strategies. AACR 5325.
22. Jin, G., Wong S. (2013) Systematic drug repositioning for cancer study. LINKS Symposium 2013, 15.

23. 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. ISMB2012, 31
24. Jin, G., Gao, J., Wong S. (2012) A computational model of pathway activation facilitates target discovery, NCI ICBP 2nd Mathematical Modeling Meeting, 5
25. Jin, G., Gao, J., Wong, S. (2012) Activated signaling mechanism of glioblastoma recurrence derived from genetics, epigenetics, and genomics abnormalities, AACR Meeting Abstracts, 4940
26. 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.
27. 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
28. 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.
29. 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.
30. Zhao, H., Jin, G., Wong, H., Cui, K., Li, F., Zhang, S., Wong, S., Zhou, X., Chang, J. and Wong, S. (2009) Drug reposition for brain metastasis of breast cancer. AACR Meeting Abstracts, 3573.
31. Cui, K., Jin, G., Zhao, H., Li, F., Wang, L., Zhou, X. and Wong, S. (2009) Knowledge-based metastatic prostate cancer targets discovery. AACR Meeting Abstracts, 2452.

Book Chapters:

32. Jin, G., Wong ST. (2014) Proteomics Based Theranostics. Cancer Theranostics, **Elsevier**.
33. Jin, G. (2013) Network motif of Gene regulatory network. Encyclopedia of Systems Biology, 459, **Springer**, LLC.
34. Jin, G. (2013) Dense overlapping regulons. Encyclopedia of Systems Biology, 465, **Springer**, LLC.
35. Jin, G. (2013) Regulation and autoregulation. Encyclopedia of Systems Biology, 462, **Springer**, LLC.
36. Jin, G. (2013) Network topology motif. Encyclopedia of Systems Biology, 590, **Springer**, LLC.
37. Jin, G. (2013) Single-Input Module. Encyclopedia of Systems Biology, 464, **Springer**, LLC.
38. Jin, G. (2013) Feed Forward Loop. Encyclopedia of Systems Biology, 463, **Springer**, LLC.
39. Jin, G., Zhou, X., Wong H., and Wong, S. (2010) The challenges in blood proteomic biomarker discovery. Computational Biology, 273-299. **Springer**, New York.

Patents:

40. Guangxu Jin, Hong Zhao, Stephen T.C. Wong. (2012) Drug Repositioning Methods For Targeting Breast Tumor Initiating Cells. *US Patent* 20,120,296,090

D. Research Support

Previous 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.

Role: Member, Using mathematical model to predict drug response at the molecular level.

Current Support

Program Director/Principal Investigator (Last, First, Middle):

Current Support

LINCS NIH U01 grant: 1 U01 HL111560-01 (PI Xiaobo Zhou)
**itNETZ: The Integrative and Translational Network-Based Cellular
Signature Analyzer**

7/2011 – 6/2016

Role: Member, Modeling of drug response signaling pathways for the LINCS data.