

## *Curriculum vitae*

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### Education

- 1997** **BS, Material Sciences**, Tsinghua University, Beijing, China  
**2000** **MS, Material Sciences**, Tsinghua University, Beijing, China  
**2006** **MS, Electrical Engineering**, University of Minnesota, Minneapolis, MN, USA  
**2006** **PhD, Biostatistics**, University of Minnesota, Minneapolis, MN, USA

### Faculty Academic Appointments

2006 - 2013	Assistant Professor	Population & Data Sciences	UT Southwestern Medical Center
2013 - 2019	Associate Professor (with Tenure)	Population & Data Sciences	UT Southwestern Medical Center
2017 - 2019	Associate Professor	Bioinformatics	UT Southwestern Medical Center
2019 - Present	Professor	Population & Data Sciences	UT Southwestern Medical Center
2019 - Present	Professor	Bioinformatics	UT Southwestern Medical Center
2020 – Present	Mary Dees McDermott Hicks Chair in Medical Science		UT Southwestern Medical Center

### Honors and Awards

- 2014 Co-lead the co-best performance team in Broad-DREAM Gene Essentiality Prediction Challenge (Broad Institute & DREAM organization)  
2013 Co-lead the best Performing Team in “NIEHS-NCATS-UNC-DREAM Toxicogenetics Challenge” (National Institute of Environmental Health Sciences, National Center for Advancing Translational Sciences, The University of North Carolina at Chapel Hill and the DREAM & DREAM organization)  
2012 Co-lead the best Performing Team in “NCI-DREAM Drug Sensitivity Prediction Challenge” (National Cancer Institute & DREAM organization)  
2006 Delta Omega National Society, Pi Chapter (Delta Omega National Society)  
2004-2006 Merck Doctoral Fellowship (Merck, Inc.)  
2004 New Student Scholarship, School of Public Health (University of Minnesota)  
1999 Guang-Hua Graduate Student Scholarship (Tsinghua University)  
1997 Graduated with honors (Tsinghua University)  
1993-1997 Honor Student (Tsinghua University)  
1994 Guang-Hua Undergraduate Student Scholarship (Tsinghua University)  
1993-1996 Outstanding Student Award (Tsinghua University)

## Patents

- A Blood-Based Screening Tool for Alzheimer's Disease (UTSD: 2679), O'Bryant S, Barber R, **Xiao G**, German D, This patent has been licensed to Cx Precision Medicine
- Developed a Prognostic and Predictive Gene Signature for Adjuvant Chemotherapy in Non-Small-Cell Lung Cancer Patients (patent #UTSD2627), Xie, Y; **Xiao, G**; Tang, H; Wistuba, I; Minna, J.

## Publications

### Original Research Articles

1. **Xiao G**, Pan W. Gene Function Prediction by a Combined Analysis of Gene Expression Data and Protein-Protein Interaction Data. *Journal of Bioinformatics and Computational Biology* 2005; 3:1371-1389.
2. Pan W, **Xiao G**, Huang X. Using Input Dependent Weights for Model Combination and Model Selection with Multiple Sources of Data. *Statistica Sinica* 2006; 16:523-540.
3. **Xiao G**, Martinez-Vaz B, Pan W, Khodursky A, Operon information improves gene expression estimation for cDNA microarrays. *BMC Genomics* 2006; 7:87.
4. Renthal W, Krishnan V, Covington H, Kumar A, Russo SJ, Maze I, Graham A, Tsankova N, Kippin TE, **Xiao G**, Neve RL, Haggarty SJ, McKinsey T, Bassel-Duby R, Olson EN, Nestler EJ. Histone Deacetylase 5 Epigenetically Controls Behavioral Adaptations to Chronic Emotional Stimuli. *Neuron* 2007 Nov 8;56(3):517-29.
5. Li N, Wu B, Wei P, Xie B, Xie Y, **Xiao G** and Pan W. Functional group based linkage analysis of gene expression trait loci. *BMC Proceedings* 2007 (1):S117.
6. **Xiao G**, Pan W. Consensus clustering of gene expression data and its application to gene function prediction. *Journal of Computational and Graphical Statistics*, 2007, 16(3):1-19.
7. Zachariou V, Liu R, Laplant Q, **Xiao G**, Renthal W, Chan GC, Storm DR, Aghajanian G, Nestler EJ. Distinct Roles of Adenylyl Cyclases 1 and 8 in Opiate Dependence: Behavioral, Electrophysiological, and Molecular Studies. *Biol Psychiatry*. 2008 Jan 25;
8. Ding LH, Xie Y, Park S, **Xiao G**, Story MD, Enhanced Identification and Biological Validation of Differential Gene Expression via Illumina Whole Genome Expression Arrays Through the Use of the Model Based Background Correction Methodology, *Nucleic Acids Research*, 2008, 1-10
9. Hatanpaa KJ, Bigio EH, Cairns NJ, Womack KB, Weintraub S, Morris JC, Foong C, **Xiao G**, Hladik C, Mantanona TY, White CL 3rd. TDP-43 immunohistochemistry reveals extensive neuritic pathology in FTLD-U: a Midwest-Southwest Consortium for FTLD study. *J Neuropathol Exp Neurol*, Apr 2008;67(4):271-279
10. Pulipparacharuvil S, Renthal W, Hale CF, Taniguchi M, **Xiao G**, Kumar A, Dewey CM, Nestler EJ, Cowan CW. Cocaine Regulates MEF2 to Control Synaptic and Behavioral Plasticity, *Neuron* 2008, V59 621-633
11. Sakata I, Nakano Y, Osborne-Lawrence S, Rovinsky SA, Lee CE, Perello M, Anderson JG, Coppapi R, **Xiao G**, Lowell BB, Elmquist JK, Zigman JM, Characterization of a Novel Ghrelin Cell Reporter Mouse, *Regulatory Peptides*, 2009 Jun 5;155(1-3):91-8. PMID: 19361544
12. Yezhuvath US, Lewis-Amezcua K, Varghese R, **Xiao G**, Lu H, On the assessment of cerebrovascular reactivity using hypercapnia BOLD MRI. *NMR in Biomedicine*, 2009 Apr 22, PMID: 19388006
13. Park S, Hatanpaa KJ, Xie Y, Mickey BE, Madden CJ, Raisanen JM, Ramnarain DB, **Xiao G**, Saha D, Boothman DA, Zhao D, Bachoo RM, Pieper RO, and Habib AA, The receptor interacting protein (RIP1) inhibits p53 induction through NF- $\kappa$ B activation and confers a worse prognosis in glioblastoma, *Cancer research*, 2009 Apr 1;69(7):2809-16. PMID: 19339267
14. Lu Z, Yezhuvath US, **Xiao G**, Improving fMRI sensitivity by normalization of basal physiologic state, *Human Brain Mapping*. 2009 Jul 7, PMID: 19585589

15. Wilkinson M\*, **Xiao G\***, Kumar A, Laplant Q, Renthal W, Sikder D, Kodadek T, and Nestler E, Imipramine Treatment and Resiliency Exhibit Similar Chromatin Regulation in the Mouse Nucleus Accumbens in Depression Models, *Journal of Neuroscience* 29(24) 7820-7832 PMID: 19535594 (As co-first author)
16. Renthal W\*, Kumar A\*, **Xiao G\***, Wilkinson M., Covington HE., Maze I., Sikder D., Robison AJ., LaPlant Q., Dietz DM., Russo, SJ., Vialou V., Chakravarty S., Kodadek, TJ., Stack A., Kabbaj M., Nestler EJ. (2009) Genome-wide analysis of chromatin regulation by cocaine reveals a role for sirtuins. *Neuron*, 62, 335-348.
17. **Xiao G\***, Reilly C. and Khodursky, AB. (2009), Improved Detection of Differentially Expressed Genes Through Incorporation of Gene Locations. *Biometrics*, 65:805–814. doi:10.1111/j.1541-0420.2008.01161.x,
18. Chong BF, Dantzer P, Germeroth T, Hafner M, Wilson AJ, **Xiao G**, Wong HK. Induced Sézary syndrome PBMCs poorly express immune response genes up-regulated in stimulated memory T cells. *J Dermatol Sci*. 2010 Jul 22
19. Xie Y, JK, Pan W, **Xiao G**, Khodursky A. A Bayesian Approach to Joint Modeling of Protein-DNA Binding, Gene Expression and Sequence Data. *Statistics in Medicine*. 2010 Feb 20;29(4):489-503.PMID:20049751.
20. Laplant Q, Vialou V, Covington HE 3rd, Dumitriu D, Feng J, Warren BL, Maze I, Dietz DM, Watts EL, Iñiguez SD, Koo JW, Mouzon E, Renthal W, Hollis F, Wang H, Noonan MA, Ren Y, Eisch AJ, Bolaños CA, Kabbaj M, **Xiao G**, Neve RL, Hurd YL, Oosting RS, Fan G, Morrison JH, Nestler EJ. Dnmt3a regulates emotional behavior and spine plasticity in the nucleus accumbens. *Nature Neuroscience*. 2010 Sep 13(9):1137-43.
21. O'Bryant SE, **Xiao G**, Barber R, Reich J, McDade R, Doody R, Fairchild T, Adams P, Diaz-Arrastia R, A Serum Protein-Based Algorithm for the Detection of Alzheimer's Disease, *Archives of Neurology*, 2010 Sep;67(9):1077-81.
22. Jeong Y, Xie Y, **Xiao G**, Behrens C, Girard L, Wistuba II, Minna JD, Mangelsdorf DJ. Nuclear Receptor Expression Defines a Set of Prognostic Biomarkers for Lung Cancer. *PLoS Med* 7(12): 2010 Dec 14;7(12)e1000378. PMID: 21179495; PMCID: PMC3001894.
23. **Xiao G\***, Wang, X, and Khodursky AB, Modelling Three-dimensional Chromosome Structure Using Gene Expression Data. *Journal of American Statistician Association*, 2011 106(493):61-72.
24. O'Bryant SE., **Xiao G.**, Barber R, Huebinger R, Wilhelmsen K, Edwards M, Graff-Radford N, Doody R, Diaz-Arrastia R, A Blood-Based Screening Tool for Alzheimer's Disease That Spans Serum and Plasma: Findings from TARC and ADNI, *PLoS ONE* 2011;6(12):e28092. PMID: 22163278; PMCID: PMC3233542.
25. O'Bryant SE, **Xiao G**, Barber R, Reisch J, Hall J, Cullum CM, Doody R, Fairchild T, Adams P, Wilhelmsen K, Diaz-Arrastia R. A blood-based algorithm for the detection of Alzheimer's disease. *Dement Geriatr Cogn Disord*. 2011;32(1):55-62. PMID: 21865746.
26. Wang S, Wang Y, Xie Y, **Xiao G**, A Novel Approach to DNA Copy Number Data Segmentation, *Journal of Bioinformatics and Computational Biology*. 2011 Feb;9(1):131-48. PubMed PMID: 21328710; PubMed Central PMCID: PMC3084615.
27. Aslan S, Huang H, Uh J, Mishra V, **Xiao G**, van Osch M, Lu H. White matter cerebral blood flow is inversely correlated with structural and functional connectivity in the human brain, *NeuroImage*, 2011 Jun 1;56(3):1145-53. PMID: 21385618; PMCID: PMC3085605.
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29. Xie Y, **Xiao G**, Coombes KR, Behrens C, Solis LM, Raso G, Girard L, Erickson HS, Roth J, Heymach JV, Moran C, Danenberg K, Minna JD, Wistuba II. Robust gene expression signature from formalin-fixed paraffin-embedded samples predicts prognosis of non-small-cell lung cancer patients. *Clin Cancer Res*. 2011 Sep 1;17(17):5705-14. PMID: 21742808; PMCID: PMC3166982.

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31. He C, Bassik MC, Moresi V, Sun K, Wei Y, Zou Z, Loh J, Fisher J, Sun Q, Korsmeyer S, Packer M, May H, Hill JA, Virgin HW, Gilpin C, **Xiao G**, Bassel-Duby, Scherer PE, Levine B, Exercise-induced Bcl-2-regulated autophagy is required for muscle glucose homeostasis, *Nature*, 2012 Jan 26; 481:511-515. PMID: 22258505
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33. Hoshiyama H, Tang J, Batten K, **Xiao G**, Rouillard JM, Shay JW, Xie Y, Wright WE. Development of Methods for Quantitative Comparison of Pooled shRNAs by Mass Sequencing. *J Biomol Screen*. 2012 Feb;17(2):258-65. PMID: 21956173.
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35. Xu F, Liu P, Pascual JM, **Xiao G**, Lu H. Effect of hypoxia and hyperoxia on cerebral blood flow, blood oxygenation, and oxidative metabolism. *Journal of cerebral blood flow and metabolism*. 2012; 32(10):1909-18. PMCID: 3463882.
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37. Allen JD, Xie Y, Chen M, Girard L, **Xiao G\***. Comparing Statistical Methods for Constructing Large Scale Gene Networks, *PLoS ONE*. 2012;7(1):e29348. PMID: 22272232; PMCID: PMC3260142.
38. Allen JD, Wang S, Chen M, Girard L, Minna J, Xie Y, **Xiao G\***. Probe mapping across multiple microarray platforms, *Briefings in Bioinformatics*, 2012 Sep;13(5):547-54. doi: 10.1093/bib/bbr076. PMID: 22199380
39. Wang X, Chen M, Khodursky AB and **Xiao G\***, Bayesian Joint Analysis of Gene Expression Data and Gene Functional Annotations, *Statistics in Biosciences*. 2012 Nov; 4(2): 300-318.
40. Zhang Y, Xie Y, Berglund ED, Coate KC, He TT, Katafuchi T, **Xiao G**, Potthoff MJ, Wei W, Wan Y, Yu RT, Evans RM, Kliewer SA, Mangelsdorf DJ. The starvation hormone, fibroblast growth factor-21, extends lifespan in mice. *eLife* 2012;1:e00065.
41. Wang R, Wei Y, An Z, Zou Z, **Xiao G**, Bhagat G, White M, Reichelt J, Levine B, Akt-Mediated Regulation of Autophagy and Tumorigenesis Through Beclin 1 Phosphorylation, *Science*. 2012 Nov; 338(6109):956-959.
42. Wang X, Zang M, **Xiao G\***, Epigenetic Change Detection and Pattern Recognition via Bayesian Hierarchical Hidden Markov Models, *Statistics in Medicine*, 2012 Oct 25. doi: 10.1002/sim.5658.
43. O'Bryant S, **Xiao G**, Edwards M, Devous M, Gupta VB, Martins R, Zhang F Barber B, Biomarkers of Alzheimer's Disease Among Mexican Americans, *J Alzheimers Dis*. 2013;34(4):841-9. doi: 10.3233/JAD-122074..
44. **Xiao G**, Wang X, Laplant Q, Nestler E, and Xie Y, Detection of Epigenetic Changes Using ANOVA with Spatially Varying Coefficients, *Statistical Applications in Genetics and Molecular Biology*, 2013 Mar 13;12(2):189-205. doi: 10.1515/sagmb-2012-0057.
45. Tang H, **Xiao G**, Behrens C, Schiller J, Allen J, Chow CW, Suraokar M, Corvalan A, Mao J, White MA, Wistuba II, Minna JD, Xie Y. A 12-gene set predicts survival benefits from adjuvant chemotherapy in non-small cell lung cancer patients. *Clin Cancer Res*. 2013 Mar 15;19(6):1577-86. PMID:23357979 | PMCID:PMC3619002

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47. Tung KC, Uh J, Mao D, Xu F, **Xiao G**, Lu H. Alterations in resting functional connectivity due to recent motor task. *Neuroimage*. 2013 Sep;78:316-24. PMID:23583747 | PMCID:PMC3672369
48. Zhong R, Kim MS, White MA, Xie Y, **Xiao G**\*. SbacHTS: spatial background noise correction for high-throughput RNAi screening. *Bioinformatics*. 2013 Sep 1;29(17):2218-20. doi: 10.1093/bioinformatics/btt358. Epub 2013 Jun 28. PMID:23814141 | PMCID:PMC3740628
49. Wu K, Xie D, Zou Y, Zhang T, Pong RC, **Xiao G**, Fazli L, Gleave M, He D, Boothman DA, Hsieh JT. The mechanism of DAB2IP in chemoresistance of prostate cancer cells. *Clin Cancer Res*. 2013 Sep 1;19(17):4740-9. PMID:23838317 | PMCID:PMC4806645
50. He C, Wei Y, Sun K, Li B, Dong X, Zou Z, Liu Y, Kinch LN, Khan S, Sinha S, Xavier RJ, Grishin NV, **Xiao G**, Eskelinen EL, Scherer PE, Whistler JL, Levine B. Beclin 2 functions in autophagy, degradation of G protein-coupled receptors, and metabolism. *Cell*. 2013 Aug 29;154(5):1085-99. PMID:23954414 | PMCID:PMC4231430
51. Wei Y, Zou Z, Becker N, Anderson M, Sumpter R, **Xiao G**, Kinch L, Koduru P, Christudass CS, Veltri RW, Grishin NV, Peyton M, Minna J, Bhagat G, Levine B. EGFR-mediated Beclin 1 phosphorylation in autophagy suppression, tumor progression, and tumor chemoresistance. *Cell*. 2013 Sep 12;154(6):1269-84. PMID:24034250 | PMCID:PMC3917713
52. Potts MB, Kim HS, Fisher KW, Hu Y, Carrasco YP, Bulut GB, Ou YH, Herrera-Herrera ML, Cubillos F, Mendiratta S, **Xiao G**, Hofree M, Ideker T, Xie Y, Huang LJ, Lewis RE, MacMillan JB, White MA. Using functional signature ontology (FUSION) to identify mechanisms of action for natural products. *Sci Signal*. 2013 Oct 15;6(297):ra90. PMID:24129700 | PMCID:PMC4075427
53. O'Bryant SE, **Xiao G**, Barber R, Cullum CM, Weiner M, Hall J, Edwards M, Grammas P, Wilhelmsen K, Doody R, Diaz-Arrastia R; Texas Alzheimer's Research and Care Consortium. Molecular neuropsychology: creation of test-specific blood biomarker algorithms. *Dement Geriatr Cogn Disord*. 2014;37(1-2):45-57. PMID:24107792 | PMCID:PMC4400831
54. **Xiao G**, Ma S, Minna J, Xie Y. Adaptive prediction model in prospective molecular signature-based clinical studies. *Clin Cancer Res*. 2014 Feb 1;20(3):531-9. doi: 10.1158/1078-0432.CCR-13-2127. Epub 2013 Dec 9. PMID:24323903 | PMCID:PMC3946561
55. Yang J, Wang X, Kim M, Xie Y, **Xiao G**\*. Detection of candidate tumor driver genes using a fully integrated Bayesian approach. *Stat Med*. 2014 May 10;33(10):1784-800. doi: 10.1002/sim.6066. Epub 2013 Dec 18. PMID:24347204 | PMCID:PMC3981913
56. Wang T, Xie Y, **Xiao G**\*. dCLIP: a computational approach for comparative CLIP-seq analyses. *Genome Biol*. 2014 Jan 7;15(1):R11. doi: 10.1186/gb-2014-15-1-r11. PMID:24398258 | PMCID:PMC4054096
57. Yun J, Wang T, **Xiao G**\*. Bayesian hidden Markov models to identify RNA-protein interaction sites in PAR-CLIP. *Biometrics*. 2014 Jun;70(2):430-40. PMID:24571656 | PMCID:PMC4061157
58. Wang T, Chen B, Kim M, Xie Y, **Xiao G**\*. A model-based approach to identify binding sites in CLIP-Seq data. *PLoS One*. 2014;9(4):e93248. PMID:24714572 | PMCID:PMC3979666

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64. Xue Z, Ye Q, Anson SR, Yang J, **Xiao G**, Kowbel D, Glass NL, Crosthwaite SK, Liu Y. Transcriptional interference by antisense RNA is required for circadian clock function. *Nature*. 2014 Oct 30;514(7524):650-3. Epub 2014 Aug 17. PMID:25132551 | PMCID:PMC4214883
65. Xu F, Liu P, Pascual JM, **Xiao G**, Huang H, Lu H. Acute effect of glucose on cerebral blood flow, blood oxygenation, and oxidative metabolism. *Hum Brain Mapp*. 2015 Feb;36(2):707-16. doi: 10.1002/hbm.22658. Epub 2014 Oct 16. PMID:25324201
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68. Zhong R, Dong X, Levine B, Xie Y, **Xiao G\***. iScreen: Image-Based High-Content RNAi Screening Analysis Tools. *J Biomol Screen*. 2015 Sep;20(8):998-1002. doi: 10.1177/1087057114564348. Epub 2014 Dec 29. PMID:25548139
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92. Li X, Wang X, **Xiao G\***. A comparative study of rank aggregation methods for partial and top ranked lists in genomic applications. *Briefings in Bioinformatics*, 2017 Aug 22. (Corresponding Author)

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122. Zhang M, Li Q, Yu D, Yao B, Guo W, Xie Y, **Xiao G\***. GeNeCK: a web server for gene network construction and visualization. *BMC Bioinformatics*. 2019 Jan 7;20(1):12. PMID: 30616521
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124. Wang S, Yang DM, Rong R, Zhan X, **Xiao G\***. Pathology Image Analysis Using Segmentation Deep Learning Algorithms. *Am J Pathol*. 2019 Sep;189(9):1686-1698.. PMID: 31199919.
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127. Zhang M, Wang T, **Xiao G**, Xie Y. Large-Scale Profiling of RBP-circRNA Interactions from Public CLIP-Seq Datasets. *Genes* (Basel). 2020 Jan 3;11(1). pii: E54. doi: 10.3390/genes11010054. PMID: 31947823
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130. Park S, Wang X, Lim J, Xiao G, Lu T, Wang T. Bayesian multiple instance regression for modeling immunogenic neoantigens. *Stat Methods Med Res*. 2020 Oct;29(10):3032-3047. PMID: 32401701
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132. Jiang S, Xiao G, Koh AY, Chen Y, Yao B, Li Q, Zhan X. HARMONIES: A Hybrid Approach for Microbiome Networks Inference via Exploiting Sparsity. *Frontiers in Genetics*. 2020 Jun 3;11:445. PMID: 32582274
133. Wang S, Rong R, Yang DM, Fujimoto J, Yan S, Cai L, Yang L, Luo D, Behrens C, Parra ER, Yao B, Xu L, Wang T, Zhan X, Wistuba II, Minna J, Xie Y, **Xiao G\***. Computational staining of pathology images to study the tumor microenvironment in lung cancer. *Cancer Res*. 2020 Jan 8. PMID: 31915129.

134. Zhang M, Sheffield T, Zhan X, Li Q, Yang DM, Wang Y, Wang S, Xie Y, Wang T, **Xiao G**\*. Spatial molecular profiling: platforms, applications and analysis tools. *Briefings in Bioinformatics*. 2020 Aug 6. PMID: 32770205

#### Chapters, Monographs and Editorials

1. Wang T, Yun J, Xie Y, **Xiao G**, Finding RNA–Protein Interaction Sites Using HMMs, *Methods Molecular Biology*, 2017;1552:177-184. PMID: 28224499
2. Yao, J., Ganti, D., Luo, X., **Xiao, G.**, Xie, Y., Yan, S. & Huang, J., Computer-assisted diagnosis of lung cancer using quantitative topology features, 2015, *Lecture Notes in Computer Science* (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics). Springer Verlag, Vol. 9352. p. 288-295 8 p.
3. Yu D, Kim M, **Xiao G**, Hwang TH. Review of biological network data and its applications. *Genomics Inform.* 2013 Dec;11(4):200-10. Review. PMID:24465231 | PMCID:PMC3897847

#### Proceedings of Meetings

1. **Xiao G.**, Barber R., Reisch J., Doody R., Fairchild T., Adams P. Royall R., Diaz-Arrastia R., O'Bryant S., Developing and validating of Diagnostic Algorithm for Alzheimer's Disease, Alzheimer's & Dementia Volume 7, Issue 4, Supplement, Alzheimer's Association International Conference 2011
2. Huang C, Zhang A, **Xiao G**. Deep Integrative Analysis for Survival Prediction. Pac Symp Biocomput. 2018;23:343-352. PMID: 29218895 Free
3. Zhu, X., Yao, J., **Xiao, G.**, Xie, Y., Rodriguez-Canales, J., Parra, E. R., Behrens, C., Wistuba, I. I. & Huang, J., Imaging-genetic data mapping for clinical outcome prediction via supervised conditional Gaussian graphical model, Jan 17 2017, Proceedings - 2016 IEEE International Conference on Bioinformatics and Biomedicine, BIBM 2016. Institute of Electrical and Electronics Engineers Inc., p. 455-459 5 p. 7822559
4. Zhu, X., Yao, J., Luo, X., **Xiao, G.**, Xie, Y., Gazdar, A. & Huang, J., Lung cancer survival prediction from pathological images and genetic data - An integration study, Jun 15 2016, 2016 IEEE International Symposium on Biomedical Imaging: From Nano to Macro, ISBI 2016 - Proceedings. IEEE Computer Society, Vol. 2016-June. p. 1173-1176 4 p. 7493475

#### GRANT SUPPORT

##### ACTIVE

RP190107 (Xiao) CPRIT Digital pathology analysis for lung cancer patient care Major Goal: (1) Develop algorithms for pathology image preprocessing and analysis in lung cancer. (2) Develop clinical outcome prediction models from pathology imaging features. (3) Integrate pathology imaging data with molecular profiling data for lung cancer outcome prediction. Role: PD/PI	03/01/19 – 02/28/22	2.4 calendar
5 P30 CA142543-06 (Arteaga) NIH Cancer Center Support Grant Major Goal: This is a Cancer Center Support Grant for the University of Texas Southwestern Medical Center.	08/03/10 – 07/31/20	1.20 calendar
1 U19 AI142784-01 (Levine)	03/15/19 – 02/29/24	1.2 calendar

NIAID

RP1: Autophagy modulators as novel broad-spectrum anti-infective agents

Major Goal: To develop host-directed broad-spectrum anti-infective agents against NIAID priority pathogens by targeting the autophagy pathway.

Role: Co-investigator

P50CA070907 (Minna) 09/01/2019 – 08/31/2020 0.53 calendar

Administrative Supplement \$67,082

University of Texas SPORE (Specialized Programs of Research Excellence) in Lung Cancer-CORE C

Major Goal: The core will provide bioinformatics, biostatistics and database support for all SPORE projects and other cores.

Role: Co-Investigator, Data Sciences Core C

Completed

1RO1CA17221-01A1 (Xiao) 09/26/13-08/31/18

NIH

Integrative Analysis to Identify Therapeutic Targets for Lung Cancer

Role: PI

Univ of Florida Subcontract (Xiao) 08/01/15-07/31/18

NIH

Equivalent Partial Correlation Methods for Integrative Genetic Network Analysis

Role: Subcontract-PI

5 R33 DA027592 (Xiao) 09/01/2011 – 08/31/2014

NIH/NIDA

Integrated Analysis for Molecular Mechanisms of Cocaine Addiction

Role: PI

DMS-0907562-03 (Xiao) 07/01/2009-06/30/2012

National Science Foundation

Bayesian Hierarchical Methods for Modeling Chromosomal Spatial Correlation

Role: PI

1 R01AG039389-01A1 (Xiao) 04/15/2012 – 03/31/2014

University of North Texas

A Blood Based Screener for Alzheimer's Disease

Role: Subcontract PI

UL1 RR024982-02 (Packer) July 01 2008 – June 30 2009

NIH/NCRR

Adaptive prediction for genomic or proteomic signatures based clinical trials

Role: Pilot award PI

RP120717-C1; RP121026-02 (Hsieh) 09/01/12-08/31/17

CPRIT

C1: Translational Core

Role: Co-Investigator

RP120732-C2 (Xie) 09/01/12-08/31/17

CPRIT

C2: Biostatistics, Bioinformatics and Database Core

Role: Co-Investigator

W81XWH-10-1-0176-02 (PI: Hsieh) 5/1/2010 – 4/30/2013

ARMY/DOD

Suppression of BRCA2 by Mutant Mitochondrial DNA in Prostate Cancer

Role: Co-Investigator

W81XWH-11-1-0491-01 (PI: Hsieh) 06/01/2011-05/31/2014

US DEPARTMENT OF DEFENSE

Role of microRNA in Agressive Prostate Cancer

Role: Co-Investigator

5 R01 MH084021-04 (Lu) 07/01/2011-06/30/2013

NIH

Normalized Functional MRI in Human Brain Disorders

Role: Co-Investigator

2 UL1 TR000451-06 (Toto) 07/24/2012-07/23/2013

NIH-NATIONAL INSTITUTES OF HEALTH

UT STAR – Bridge funding - BERD

Role: Co-Investigator

1 R21 NS078656-01A1 (Lu) 09/01/2012-08/31/2014

NIH

Vascular Physiology in Brain White Matter

Role: Co-I

5 P30 AG012300-19 (Rosenberg) 08/01/2011-06/30/2016

NIH-NATIONAL INSTITUTES OF HEALTH

Neurobiology of Alzheimer's Disease and Aging - Core C Data

Role: Co-I

1 U01 NS082148-01 (German) 09/30/2012-08/31/2017

NIH-NATIONAL INSTITUTES OF HEALTH

Diagnostic and prognostic biomarkers for Parkinson's disease – Project B

Role: Co-I

5 R01 CA159144-02 (Hsieh) 09/21/2011-07/31/2016

NIH-NATIONAL INSTITUTES OF HEALTH

Targeting Aggressive Prostate Cancer with Novel Theranostic Nanomedicine

Role: Co-I

### **Grant Review Activities**

2016	NCI study section ZCA1 SRB-5 (J1)	NCI
2019	NCI study section ZCA1 SRB-5 (J1)	NCI
2018	NCI (LRP) study section	NCI
2019	NCI (LRP) study section	NCI
2019	NCI ITCR U24 study section	NCI
2020	NCI study section ZCA1 SRB-5 (J1)	NCI

### **Editorial Activities**

2014-present Associate Editor, PLoS ONE

2017 – present Editorial Board, Genes

2018 – present Editorial Board, PLoS ONE

Ad Hoc Reviewer:

Cell, PNAS, Biometrics, Bioinformatics, BMC Genomics, Circulation, Nature Communication, Annals of Applied Statistics, Statistics in Medicine, PNAS, PLoS Computational Biology, Genetic Epidemiology, PLoS ONE, Journal of American Statistician Association

### **Invited Lectures**

- “Bayesian model for joint analysis of gene expression data and gene functional annotations,” Division of Biostatistics, University of Minnesota, MN, 2006.
- “Bayesian model for joint analysis of gene expression data and gene functional annotations,” Division of Biostatistics, St. Jude Children Research Hospital, TN, 2006.
- “Improved detection of differentially expressed genes through incorporation of gene locations,” Department of Biostatistics, University of Michigan, Ann Arbor, MI, 2006.
- “Improved detection of differentially expressed genes through incorporation of gene locations,” Division of Biostatistics, University of Kansas Medical Center, Kansas City, MO, 2006.
- “Improved detection of differentially expressed genes through incorporation of gene locations,” Department of Biostatistics, Emory University, Atlanta, GA, 2006.
- “Improved detection of differentially expressed genes through incorporation of gene locations,” Department of Statistics, Iowa State University, Ames, IA, 2006.
- “Improved detection of differentially expressed genes through incorporation of gene locations,” School of Medicine, University of Utah, Salt Lake City, UT, 2006.
- “Improved detection of differentially expressed genes through incorporation of gene locations,” Division of Biostatistics, Indiana University School of Medicine, Indianapolis, IN, 2006.
- “Improved detection of differentially expressed genes through incorporation of gene locations,” The University of Texas Southwestern Medical Center, Dallas, TX, 2006.
- “Improved detection of differentially expressed genes through incorporation of gene locations,” Division of Biostatistics, University of South Florida, Moffitt Cancer Center and Research Institute, Tampa, FL, 2006.

- “Improved detection of differentially expressed genes through incorporation of gene locations,” Division of Biostatistics, The Washington University, St. Louis, MO, 2006.
- “Improved detection of differentially expressed genes through incorporation of gene locations,” Department of statistics, Southern Methodist University, Dallas, TX, 2007.
- “Incorporating Biological Information into Microarray Data Analysis, Division of Medical informatics,” Department of Clinical Sciences, University of Texas Southwestern Medical Center, Dallas, TX, 2007
- “Modeling Three-dimensional Chromosome Structures Using Gene Expression Data,” Department of Clinical Sciences, UT Southwestern Medical Center, Dallas, TX, 2009.
- “Modeling spatial correlation in gene regulation,” Department of Computer Sciences, Southern Methodist University, Dallas, TX, 2008.
- “Modeling Three-dimensional Chromosome Structures Using Gene Expression Data,” Department of Statistics, Texas A&M University, College Station, TX, 2009
- “Detection of tumor driver genes using a fully integrated Bayesian approach.” School of Information Science and Technology, Tsinghua University, China. 2013.
- “Detection of tumor driver genes using a fully integrated Bayesian approach”, Statistical and Computational Theory and Methodology for Big Data Analysis, Calgary, Canada, 2014
- “Detection of tumor driver genes using a fully integrated Bayesian approach” International Conference on Ordered Data Analysis, Dallas, Tx, 2014
- “Machine Learning and Spatial Modeling in Pathological Imaging Analysis”, Department of Mathematics, University of Texas at Arlington, Tx, 2017
- “Machine Learning and Spatial Modelling in Lung Cancer Pathological Imaging Analysis”, Tianjin Medical University, General Hospital, Tianjin, China, 2018
- “AI-based Whole Slide Image Analysis in Head & Neck Cancer”, NCI, Washington DC, 2018
- “Machine Learning and Spatial Modelling in Lung Cancer Pathological Imaging Analysis”, Department of Mathematics, University of Texas at Dallas, Tx, 2018
- “Artificial Intelligence (AI) based Digital Pathology”, ACP MetroCon, Dallas, TX2018
- “Artificial Intelligence (AI) based Digital Pathology”, Tianjin Medical University, General Hospital, Tianjin, China, 2019
- “Machine Learning and Spatial Modelling in Lung Cancer Pathological Image Analysis”, Department of Biomedical Informatics, Ohio State University, 2019
- “Machine Learning and Spatial Modelling in Lung Cancer Pathological Image Analysis”, Division of Biostatistics, University of Minnesota, 2019
- “Deep learning and Spatial Modelling in Cancer Pathological Image Analysis”, UT MD Anderson Cancer Center, 2019

## **TEACHING**

### **Medical and graduate school didactic and small group teaching**

- Introduction to High-Throughput Data Analysis ( 2007)
- Introduction to Biostatistics: summer course (2011-2013)
- BSCI 5096.01 Special Topics: Analysis of High Content/High Complexity Data Sets (2013)
- Advanced Data Analysis and Statistical Learning (2016 ,2017, 2018)
- Artificial Intelligence in Biomedical Research (2018)

## **Graduate student trainees**

### Current

- Minzhe Zhang, (Ph.D. student, Integrative Biology program, UTSW, 2016 --- present)
- Shen Yin, (Ph.D. student, UTSW-SMU Joint Biostatistics Program, 2017 --- present)
- Xinyi Zhang, (Ph.D. student, Integrative Biology program, UTSW, 2018 --- present)
- Zhuoyu Wen, (Ph.D. student, Integrative Biology program, UTSW, 2019 --- present)

### Previous

- Tao Wang, Ph.D. (Integrative Biology program, UTSW, 2012 --- 2014)
- Lie Li (Ph.D. student in Statistics, SMU, 2014-2017)
- Xiao Zang (Cancer Biology program, UTSW, 2013 --- 2015)
- Rui Zhong (Cancer Biology program, UTSW, 2011 --- 2014)
- Ke Wang (Ph.D. in Statistics, SMU, graduated in summer 2011)
- Miao Zang (Ph.D. in Statistics, SMU, graduated in summer 2012)
- Tsungwei Ma (Ph.D., Integrative Biology program, UTSW, 2013 --- 2017)
- Bo Ci, (Ph.D., Integrative Biology program, UTSW, 2015 --- 2019)
- Gaoxiang Jia, (Ph.D. in UTSW-SMU Joint Biostatistics Program, 2015-2018)
- Shidan Wang, (Ph.D. student, Integrative Biology program, UTSW, 2015 --- 2019)

## **Postdoctoral trainees**

<u>Name</u>	<u>Graduate School</u>	<u>Duration</u>	<u>Current Position</u>
Dr. Hao Tang	UTSW	2011 - 2013	Assistant Professor
Dr. Beibei Chen	UTSW	2011 – 2013	Data Scientist
Dr. Jonghyun Yun	UTSW	2012 – 2014	Assistant Professor
Dr. Jichen Yang	UTSW	2012 – 2014	Data Scientist
Dr. Dongyeon Yu	UTSW	2013 – 2014	Assistant Professor
Dr. Jungisk Nok	UTSW	2014 – 2015	Assistant Professor
Dr. Sangin Lee	UTSW	2014 - 2016	Assistant Professor
Dr. Faliu Yi	UTSW	2015 – 2017	Data Scientist
Dr. Qiwei Li	UTSW	2016 – 2019	Assistant Professor