

# Curriculum Vitae of Guanghua (Andy) Xiao

UT Southwestern Medical Center

5323 Harry Hines Blvd.

Dallas, TX 75390-8551

Phone: (214) 648-4110

Fax: (214) 648-1663

Email: Guanghua.Xiao@utsouthwestern.edu

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## EDUCATION

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

## PROFESSIONAL EXPERIENCE

### Associate Professor (with Tenure)

- **2013 – Present**  
Clinical Sciences, UT Southwestern Medical Center

### Assistant Professor

- **2006 – 2012**  
Clinical Sciences, UT Southwestern Medical Center

## HONORS, AWARDS AND FELLOWSHIPS

- 2012            **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**, Division of Biostatistics, 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, 1995, 1996 **Outstanding Student Award** (Tsinghua University)

## PROFESSIONAL MEMBERSHIP

- International Biometric Society (2006-present)
- American Statistician Association (2006-present)

## PEER-REVIEWED PUBLICATIONS

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. Renthall 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**, Renthall 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 FTL-DU: a Midwest-Southwest Consortium for FTL-DU study. *J Neuropathol Exp Neurol*, Apr 2008;67(4):271-279.
10. Pulipparacharuvil S, Renthall 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, Coppari 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-Amezcu 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, Renthall 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. Renthall 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. (**As co-first author**).
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, (**\*Corresponding Author**).
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. (\*Corresponding author).
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. (As co-first Author).
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.
28. Huang H, Fan X, Weiner M, Martin-Cook K, **Xiao G**, Davis J, Devous M, Rosenberg R, Diaz-Arrastia R. Distinctive disruption patterns of white matter tracts in Alzheimer's disease with full diffusion tensor characterization. *Neurobiol Aging*. 2011 Aug 26. PMID: 21872362.
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.
30. Orvdahl A, Sumpter R, **Xiao G**, Ng A, Zou Z, Tang Y, Narimatsu M, Gilpin C, Sun Q, Roth M, Forst C, Wrana J, Zhang Y, Luby-Phelps K, Xavier R, Xie Y, Levine B. Image-Based Genome-Wide siRNA Screen Identifies Host Factors Involved in Selective Autophagy. *Nature*. 2011 Dec 1;480(7375):113-7. PMID: 22020285.
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.

32. Barber RC, Edwards MI, **Xiao G**, Huebinger RM, Diaz-Arrastia R, Wilhelmsen KC, Hall JR, O'Bryant SE. Serum granulocyte colony-stimulating factor and Alzheimer's disease. *Dement Geriatr Cogn Dis Extra*. 2012 Jan; 2(1):353-60.
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.
34. Han T, Kato M, Xie S, Wu L, Mirzaei H, Pei J, Chen M, Xie Y, Allen J, **Xiao G**, McKnight S. Cell-free Formation of RNA Granules: Bound RNAs Identify Features and Components of Cellular Assemblies. *Cell*, 11 May 2012 (Vol. 149, Issue 4, pp. 768-779).
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. PMID: 23463882.
36. Wu K, Gore C, Yang L, Fazli L, Gleave M, Pong RC, **Xiao G**, Zhang L, Yun EJ, Tseng SF, Kapur P, He D, Hsieh JT. Slug, a unique androgen-regulated transcription factor, coordinates androgen receptor to facilitate castration resistance in prostate cancer. *Molecular endocrinology* 2012 Sep;26(9):1496-507.
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; PMID: PMC3260142. (**\*Corresponding author**).
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 (**\*Corresponding author**).
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, Klier 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. (**\*Corresponding author**).
43. Huebinger R, **Xiao G**, Wilhelmsen KC, Diaz-Arrastia R, Zhang F, O'Bryant SE, Barber RC, Comparison of protein concentrations in serum versus plasma from Alzheimer's patients, *Advances in Alzheimer's Disease*, Vol.1, No.3, 51-58 (2012) doi:10.4236/aad.2012.13007.
44. Wu K, Liu J, Tseng SF, Gore C, Ning Z, Sharifi N, Fazli L, Gleave M, Kapur P, **Xiao G**, Sun X, Oz OK, Min W, Alexandrakis G, Yang CR, Hsieh CL, Wu HC, He D, Xie D, Hsieh JT. The role of DAB2IP in androgen receptor activation during prostate cancer progression. *Oncogene*. 2013 Apr 22. doi: 10.1038/onc.2013.143. [Epub ahead of print].
45. 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, *Journal of Alzheimer's disease*, 2013 Jan 1;34(4):841-9. doi: 10.3233/JAD-122074.
46. **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 13:1-17.

47. Chen M, Zang M, Wang X, **Xiao G**. A powerful Bayesian meta-analysis method to integrate multiple gene set enrichment studies. *Bioinformatics*. 2013 Apr 1;29(7):862-9.
48. Tung KC, Uh J, Mao D, Xu F, **Xiao G**, Lu H. Alterations in resting functional connectivity due to recent motor task. *Neuroimage*. 2013 Apr 11;78C:316-324.
49. Tang H, **Xiao G**, Behrens C, Schiller J, Allen J, Chow C, Suraokar M, Corvalan A, Mao J, White M, Wistuba I, Minna J, Xie Y. A 12-Gene Set Predicts Survival Benefits from Adjuvant Chemotherapy in Non-Small-Cell Lung Cancer Patients, *Clinical cancer Research*, 2013 Mar 15;19(6):1577-86.
50. Zhong R, Kim M, White M, Yang X, **Xiao G\***, Spatial Background Noise Correction for High-Throughput RNAi Screening, *Bioinformatics*, 2013 Jul 15. [Epub ahead of print] PMID:23814141, (**\*Corresponding author**).
51. Wu K, Xie D, Zou Y, Zhang T, Pong RC, **Xiao G**, Fazli L, Gleave ME, He D, Boothman DA, Hsieh JT. The mechanism of DAB2IP in chemo-resistance of prostate cancer cells. *Clin Cancer Res*. 2013 Jul 9. [Epub ahead of print] PMID: 23838317.
52. He C, Wei Y, Sun K, Li B, Dong X, Zou Z, Liu Y, Kinch LN, Khan S, Sinha S, Rammik J, 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.
53. 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.
54. 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. *Science Signaling*. 2013 Oct 15;6(297):ra90. PMID: 24129700.
55. O'Bryant SE, **Xiao G**, Barber R, Cullum CM, Weiner M, Hall J, Edwards M, Grammas P, Wilhelmsen K, Doody R, Diaz-Arrastia R. Molecular Neuropsychology: Creation of Test-Specific Blood Biomarker Algorithms. *Dement Geriatr Cogn Disord*. 2013 Jan 3;37(1-2):45-57. [Epub ahead of print] PMID: 24107792.
56. Yu D, Kim M, Xiao G, Hwang TH. Review of Biological Network Data and Its Applications. *Genomics Inform*. 2013 Dec;11(4):200-210. PMID: 24465231.
57. O'Bryant S, **Xiao G**, Barber B, Cullum CM, Weiner M, Hall J, Edwards M, Grammas P, Wilhelmsen K, Doody R, Diaz-Arrastia R, Molecular Neuropsychology: Creation of Test-Specific Blood Biomarker Algorithms, *Dementia and Geriatric Cognitive Disorders*, *Dement Geriatr Cogn Disord*. 2014;37(1-2):45-57. doi: 10.1159/000345605.
58. Moro L, Arbin A, Guerra F, Greco F, Marra E, Gandee L, **Xiao G**, Lotan Y, Gasparre G, and Hsieh JT, Mitochondrial DNA depletion sensitizes cancer cells to PARP inhibitors by translational and post-translational repression of BRCA2, *Oncogenesis*, Dec 16, 2013, 2, e82; doi:10.1038/oncsis.2013.45.
59. Yang J, Wang X, Kim M, Xie Y, **Xiao G\***, Detection of candidate tumor driver genes using a fully integrated Bayesian approach, *Statistics in Medicine*, 2013 Dec 18. doi: 10.1002/sim.6066.
60. **Xiao G**, Ma S, Minna J, Xie Y, Adaptive prediction model in prospective molecular-signature-based clinical studies, *Clinical Cancer Research*, 2014 Feb 1;20(3):531-9. doi: 10.1158/1078-0432.CCR-13-2127.
61. Wang T, Xie Y and **Xiao G\***, dCLIP: a computational approach for comparative CLIP-seq analyses, *Genome Biology*, 2014, 15:R11 doi:10.1186/gb-2014-15-1-r11.

62. 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 Apr 8;9(4):e93248. doi: 10.1371/journal.pone.0093248. eCollection 2014. PMID: 24714572.
63. Yun J, Wang T, **Xiao G**. Bayesian hidden Markov models to identify RNA-protein interaction sites in PAR-CLIP. Biometrics. 2014 Feb 24. doi: 10.1111/biom.12147. [Epub ahead of print]. PMID: 24571656.

## MANUSCRIPTS UNDER REVIEW/REVISION

## MANUSCRIPTS IN PREPARATION

## CONFERENCE CONTRIBUTIONS

## PRESENTATIONS

### Invited

1. “Bayesian model for joint analysis of gene expression data and gene functional annotations,” Division of Biostatistics, University of Minnesota, MN, 2006.
2. “Bayesian model for joint analysis of gene expression data and gene functional annotations,” Division of Biostatistics, St. Jude Children Research Hospital, TN, 2006.
3. “Improved detection of differentially expressed genes through incorporation of gene locations,” Department of Biostatistics, University of Michigan, Ann Arbor, MI, 2006.
4. “Improved detection of differentially expressed genes through incorporation of gene locations,” Division of Biostatistics, University of Kansas Medical Center, Kansas City, MO, 2006.
5. “Improved detection of differentially expressed genes through incorporation of gene locations,” Department of Biostatistics, Emory University, Atlanta, GA, 2006.
6. “Improved detection of differentially expressed genes through incorporation of gene locations,” Department of Statistics, Iowa State University, Ames, IA, 2006.
7. “Improved detection of differentially expressed genes through incorporation of gene locations,” School of Medicine, University of Utah, Salt Lake City, UT, 2006.
8. “Improved detection of differentially expressed genes through incorporation of gene locations,” Division of Biostatistics, Indiana University School of Medicine, Indianapolis, IN, 2006.
9. “Improved detection of differentially expressed genes through incorporation of gene locations,” The University of Texas Southwestern Medical Center, Dallas, TX, 2006.
10. “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.
11. “Improved detection of differentially expressed genes through incorporation of gene locations,” Division of Biostatistics, The Washington University, St. Louis, MO, 2006.
12. “Improved detection of differentially expressed genes through incorporation of gene locations,” Department of statistics, Southern Methodist University, Dallas, TX, 2007.
13. “Incorporating Biological Information into Microarray Data Analysis, Division of Medical informatics,” Department of Clinical Sciences, University of Texas Southwestern Medical Center, Dallas, TX, 2007
14. “Modeling Three-dimensional Chromosome Structures Using Gene Expression Data,” Department of Clinical Sciences, UT Southwestern Medical Center, Dallas, TX, 2009.
15. “Modeling spatial correlation in gene regulation,” Department of Computer Sciences, Southern Methodist University, Dallas, TX, 2008.
16. “Modeling Three-dimensional Chromosome Structures Using Gene Expression Data,” Department of Statistics, Texas A&M University, College Station, TX, 2009

17. “Modeling Three-dimensional Chromosome Structures Using Gene Expression Data,” Joint Statistical Meeting, Washington DC, 2009.
18. “Joint Modeling of Epigenetic Data, Transcription Factor Binding Data, and Expression Data,” Joint Statistical Meeting, Vancouver, British Columbia, Canada, 2010.
19. “Modeling Three-dimensional Chromosome Structures Using Gene Expression Data,” International Biometrics Society (ENAR), New Orleans, LA, 2010.

## **Contributed**

### **GRANT SUPPORT**

#### **Current Grant Support**

- Title of Project: Integrative Analysis to Identify Therapeutic Targets for Lung Cancer  
Funding Source: NIH RO1  
Role: Principal Investigator  
Duration: 10/01/2013 - 09/31/2018  
Total amount of award: \$1,649,625
- Title of Project: Secondary Data Analyses for Substance Abuse Research  
Funding Source: NIH R21/R33  
Role: Principal Investigator  
Duration: 9/1/2009 to 8/31/2013  
Total amount of award: \$1,136,918
- Title of Project: Blood-Based Screening Tool for Alzheimer’s Disease  
Funding Source: NIH R01  
Role: UTSW Sub-contract Principal Investigator  
Duration: 4/15/2012 to 3/31/2014  
Total amount of award: \$21,784
- Title of Project: UT STAR – Bridge Funding - BERD  
Funding Source: NIH Clinical and Translational Science Award (CTSA)  
Role: Co-Investigator  
Duration: 7/24/2012 to 7/23/2013  
Total amount of award: \$376,719
- Title of Project: Vascular Physiology in Brain White Matter  
Funding Source: NIH R21  
Role: Co-Investigator  
Duration: 9/1/2012 to 8/31/2014  
Total amount of award: \$301,697
- Title of Project: Suppression of BRCA2 by Mutant Mitochondrial DNA in Prostate Cancer  
Funding Source: Department of Defense  
Role: Co-Investigator  
Duration: 5/1/2010 to 4/30/2013

Total amount of award: \$449,957

- Title of Project: Role of microRNA in Aggressive Prostate Cancer  
Funding Source: Department of Defense  
Role: Co-Investigator  
Duration: 6/15/2011 to 6/14/2014  
Total amount of award and dates: \$450,000
- Title of Project: Targeting Aggressive Prostate Cancer with Novel Theranostic NanoMED  
Funding Source: NIH R01  
Role: Co-Investigator  
Duration: 9/21/2011 to 7/31/2016  
Total amount of award: \$1,136,291
- Title of Project: C1: Translational Core  
Funding Source: CPRIT  
Role: Co-Investigator  
Duration: 9/1/2012 to 8/31/2017  
Total amount of award: \$997,473
- Title of Project: Neurobiology of Alzheimer's Disease and Aging – Core C Data  
Funding Resource: NIH  
Role: Co-Investigator  
Duration: 8/1/2011 to 6/30/2016  
Total amount of award: \$666,533
- Title of Project: C2: Biostatistics, Bioinformatics and Database Core  
Funding Resource: CPRIT  
Role: Co-Investigator  
Duration: 9/1/2012 to 8/31/2017  
Total amount of award: \$712,445
- Title of Project: Diagnostic and Prognostic Biomarkers for Parkinson's Disease  
Funding Source: NIH  
Role: Co-Investigator  
Duration: 9/30/2012 to 8/31/2017  
Total amount of award: \$3,226,510
- Title of Project: Texas Alzheimer's Research and Care Consortium  
Funding Source: State of Texas  
Role: Co-Investigator  
Duration: 9/1/2007 to 8/31/2013  
Total amount of award: \$15,600,000

**Pending Grants**



### **Completed Grant Support**

- Title of Project: Bayesian Hierarchical Methods for Modeling Chromosomal Spatial Correlation  
Funding Source: National Science Foundation  
Role: Principal Investigator (% effort)  
Duration: 7/1/2009 to 6/30/2012  
Total amount of award: \$75,000
  
- Title of Project: CTSA Pilot award: Systematic Approaches for molecular profiling data in Alzheimer's Disease  
Funding Resource: NIH/NCRR  
Role: Pilot award, Principal Investigator (% effort)  
Duration: 6/1/2008 to 5/31/2010  
Total amount of award: \$20,000
  
- Title of Project: CTSA Pilot award: Adaptive prediction for genomic or proteomic signatures based clinical trials  
Funding Source: NIH/NCRR  
Role: Pilot award, Principal Investigator (% effort)  
Duration: 6/1/2010 to 5/31/2011  
Total amount of award: \$27,510
  
- Title of Project: Novel Biomarkers for Predicting Response to Treatment in Diabetic Nephropathy  
Funding Source: American Heart Association  
Role: Co-Investigator  
Duration: 1/1/2008 to 12/31/2010  
Total amount of award: \$521,739
  
- Title of Project: North and Central Texas Clinical and Translational Science Initiative – U54-D. Research Design and Statistics  
Funding Source: NIH  
Role: Co-Investigator  
Duration: 9/14/2007 to 7/23/2012  
Total amount of award: \$314,860
  
- Title of Project: Normalized Functional MRI in Human Brain Disorders  
Funding Source: NIH  
Role: Co-Investigator  
Duration: 9/8/2008 to 6/30/2012  
Total amount of award: \$846,157
  
- Title of Project: Quantitative Measurement of Spinal Cord Perfusion in Humans Using MRI  
Funding Source: NIH  
Role: Co-Investigator

Duration: 2/1/2009 to 1/31/2011  
Total amount of award: \$296,406

- Title of Project: Cognition and Cerebrovascular Function Across Lifespan  
Funding Source: NIH  
Role: Co-Investigator  
Duration: 9/15/2009 to 8/31/2011  
Total amount of award: \$253,926

## TEACHING

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

- Introduction to High-Throughput Data Analysis (taught one lecture, 2007)
- Introduction to Biostatistics: summer course (taught one lecture, 2011, 2012)
- BSCI 5096.01 Special Topics: Analysis of High Content/High Complexity Data Sets

### Graduate student trainees

- Advisor for Tao Wang (Integrative Biology program, UTSW, 2012 --- present)
- Co-advisor for Rui Zhong (Cancer Biology program, UTSW, 2011 --- 2014)
- Co-advisor for Ke Wang (Ph.D. in Statistics, SMU, graduated in summer 2011)  
Thesis: "Analyzing High-throughput Data via Hierarchical Bayesian Spatial Modeling"
- Co-advisor for Miao Zang (Ph.D. in Statistics, SMU, graduated in summer 2012)  
Thesis: "Bayesian meta-analysis in pathway enrichment analysis"

### Postdoctoral trainees

- Jichen Yang (UTSW)
- Jonghyun Jun (UTSW)
- Donghyeon Yu (UTSW)
- Faliu Yi (UTSW)

## STUDENT ADVISING AND COMMITTEE MEMBERSHIP

### ACADEMIC SERVICE

- **2007-present, Member** on Biomarker Subcommittee, Texas Alzheimer's Research and Care Consortium
- **2007-present, Member** on Genetic Subcommittee, Texas Alzheimer's Research and Care Consortium

### JOURNAL REFEREE

- Journal of American Statistician Association
- Biometrics
- Bioinformatics
- Genome Biology
- American Statistician
- Briefings in Bioinformatics

- Statistics in Medicine
- IEEE Transactions on Signal Processing
- BMC Genomics
- BMC Bioinformatics
- Journal of Bioinformatics and Computational Biology
- PloS ONE
- Bayesian Analysis
- Journal of Investigative Medicine
- Annals of Applied Statistics

#### **TECHNOLOGICAL AND OTHER SCIENTIFIC INNOVATIONS**

- **Patent pending:** A Serum Protein–Based Algorithm for the Detection of Alzheimer Disease. (O’Bryant S, Xiao G, Barber B, Diaz-Arrastia R, Reisch R, Doody R, Adams P, Fairchild T and Rule Based Medicine).
- Developed a Prognostic and Predictive Gene Signature for Adjuvant Chemotherapy in Non-Small-Cell Lung Cancer Patients (Tang, Hao; Xiao, Guanghua; Wistuba, Ignacio; Minna, John; Xie, Yang).
- Co-led UTSW-MC team to win the NCI-DREAM Drug Sensitivity Prediction Challenge. The news was highlighted on the NCI website.