Curriculum Vitae of Yang Xie

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EDUCATION

2006	**PhD, Biostatistics** (Advisor: Dr. Wei Pan), University of Minnesota, Minneapolis, MN, USA
2003	**MS, Biostatistics**, University of Minnesota, Minneapolis, MN, USA
2000	**MS, Epidemiology**, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China
1997	**MD, Medicine**, Peking University Health Science Center, Beijing, China

PROFESSIONAL EXPERIENCE

2013 – Present	**Associate Professor (with Tenure)**, Department of Clinical Sciences, UT Southwestern Medical Center
2011 – Present	**Founding Director**, Simmons Cancer Center Bioinformatics Shared Resources, UT Southwestern Medical Center
2010 – Present	**Founding Director**, Quantitative Biomedical Research Center, UT Southwestern Medical Center
2006 – 2013	**Assistant Professor,** Department of Clinical Sciences, UT Southwestern Medical Center

HONORS, AWARDS AND FELLOWSHIPS

- 2014 **Co-best performance team** (Team Leader) in Broad-DREAM Gene Essentiality Prediction Challenge sub challenge 1
- 2013 **Best Performing Team** (Team leader) in “The NIEHS-NCATS-UNC DREAM Toxicogenetics Challenge” (both sub-challenges), NIEHS, NCATS & DREAM organization
- 2012 **Best Performing Team** (Team leader) in “NCI-DREAM Drug Sensitivity Prediction Challenge,” National Cancer Institute & DREAM organization
- 2008 **Travel Award** for American Association for Cancer Research (AACR) Cancer Biostatistics Workshop —Developing Targeted Agents. Sonoma, CA.
- 2008 **Scholarship** for Internal Biometrics Society Young Researcher Workshop. Arlington, VA.
- 2008 **Bayesian Conference Travel Award**. Houston, TX., MD Anderson Cancer Center
- 2006 **Jacob E. Bearman Student Achievement Award**. Minneapolis, MN., University of Minnesota
- 2005-2006 **Doctoral Dissertation Fellowship**, University of Minnesota Graduate School.
- 1997 **Outstanding Student of Beijing City**, Peking University Health Science Center, Beijing, China.
- 1996-1997 **Guanghua Excellent Students Award (First Prize)**, Peking University Health Science Center, China.

- 1992-1995 **Scholarship for Excellent Student (First Prize)**, Peking University Health Science Center, China.

PROFESSIONAL ACTIVITIES

Membership

- Associate Editor, Biostatistics (2014-)
- Member**,** American Statistical Association (2004-present)
- Member, International Biometric Society (2006-present)
- Member**,** Society of Clinical Trials (2006-present)
- Member, International Society for Computational Biology (2012-present)

Committees

- Section chair, Clinical Trial Design Session, the International Biometrics Society (ENAR) Meeting (2010)
- Organizer, Invited session for Joint Statistical Meeting (2010)

Grant Review

- June, 2012 Susan G. Komen for Cure Research Programs Grants Review Panel, 2012
- Feb, 2014 NIH Biodata Management and Analysis Study Section [BDMA], Feb, 2014
- June, 2014 NIH Biodata Management and Analysis Study Section [BDMA], June, 2014
- July, 2014 NIH Biodata Management and Analysis Study Section [BDMA], July, 2014
- Nov, 2014 NCI Cancer Management and Prevention Special Emphasis Panel, ZCA1 RPRB-B (J1),
- June, 2015 NIH, Biodata Management and Analysis Study Section [BDMA], June, 2015
- Oct, 2015 NIH, Cancer Management and Prevention, Special Emphasis Panel, ZCA1 RPRB-B (J1)
- Nov, 2015 NIH, Center for Scientific Review, Special Emphasis Panel, ZRG1 BST-H 40 P

Journal Review:

- 2014 Associate Editor, Biostatistics
- Bioinformatics, Genome Biology, Journal of Bioinformatics and Computational Biology, Cancer Epidemiology, Biomarkers & Prevention, Journal of Clinical Oncology, Journal of Pharmacogenomics, BMC Bioinformatics, BMC genomics, PLoS One, Statistics in Medicine, Nature Methods.

PEER-REVIEWED PUBLICATIONS

Articles

1. Zuo Q, Zhang K, **Xie Y**. (1998) HIV/AIDS epidemic characteristics and risk factors in China. *Journal of Jinan University* (6):22-23.

2. **Xie Y**. (1999) Experiences of investigation and health education among the overseas workers. *Chinese Population Medicine*. (10):4-5.

3. **Xie Y**, Liao S. (2000) Quality assessment of infrastructure of STD service in Hainan province. *Chinese Journal of Prevention and Control of STD and AIDS*.

4. Ross JA, **Xie Y**, Davies SM, Shu XO, Pendergrass T, Robison LL. (2003) Prescription medication use during pregnancy and risk of infant leukemia (United States). *Cancer Causes and Control (14), 447-451*.

5. Ross JA, **Xie Y**, Kiffmeyer WR, Bushhouse S, Robison LL. (2003) Cancer in the Minnesota Hmong population. *Cancer* (12), 3076-3079.

6. **Xie Y**, Davies SM, Xiang Y, Robison LL, Ross JA. (2003) Trends in leukemia incidence and survival in the United States (1973-1998). *Cancer* (9), 2229-2235.

7. **Xie Y**, Jeong KS, PanW, Khodursky AB and Carlin BP. (2004) A case study on choosing normalization methods and test statistics for microarray data. *Comparative and Functional Genomics* (5), 432-444.

8. Spector LG, **Xie Y**, Robison LL, Heerema N, Hilden JH, Lange B, Felix C, Davies SM, Slavin J, Potter JD, Reaman GH, Blair CK, Ross JA . (2005) Maternal Diet and Infant Leukemia: The DNA Topoisomerase II Inhibitor Hypothesis. *Cancer Epidemiology, Biomarkers and Prevention* (14): 651-655.

9. MartinezVaz BM$^{\#}$, **Xie Y**$^{\#}$, Pan W, Khodursky AB. (2005) Genome-wide localization of mobile elements: experimental, statistical and biological considerations. *BMC Genomics* (6):81.

10. **Xie Y**, Pan W, and Khodursky AB. (2005) A note on using permutation based false discovery rate estimate to compare different analysis methods for microarray data. *Bioinformatics* (23):4280-4288. 2005.

11. **Xie Y**, Carlin BP. (2006) Measures of Bayesian learning and identifiability in hierarchical models. *Journal of Statistical Planning and Inference* (136): 3458-3477.

12. Jeong KS, **Xie Y**, Hiasa H and Khodursky AB. (2006) Analysis of Pleiotropic Transcriptional Profiles: a Case Study of DNA Gyrase Inhibition. *PLoS Genetics*, Sep 29;2(9):e152.

13. 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.

14. **Xie Y**, Pan W, Jeong KS, Khodursky AB. (2007) Incorporating prior information via shrinkage: a combined analysis of genome-wide location data and gene expression data. *Statistics in Medicine* (26): 2258-2275.

15. Blaira C, Roeslera M, **Xie Y**, Gamisc AS, Olshand AF, Heeremae NA, Robisonf LL, Rossa JA. (2008) Vitamin supplement use among children with Down syndrome and risk of Leukemia: A Children’s Oncology Group (COG) Study. *Pediatric Perinatal Epidemiol* 22: 288-295.

16. Pan W, Jeong KS, **Xie Y**, Khodursky AB. (2008) A Nonparametric Empirical Bayes Approach to Joint Modeling Multiple Sources of Genomic Data. *Statistical Sinica*18:709-729.

17. Shivapurkar N, Stastny V, **Xie Y**, Prinsen C, Thunnissen F, Minna J, Gazdar AF. (2008) Differential Methylation of a short CpG rich sequence within exon 1 of TCF21 gene: a promising cancer biomarker assay. *Cancer Epidemiology, Biomarkers and Prevention* (17):995-1000 (Appears on the cover-page of the journal).

18. Ding L*, **Xie Y***, Park S, Xiao G, Story M.(2008) 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* (36):e58. (***co-first author**.)

19. Shivapurkar N, Stastny V, Okumura N, Girard L, **Xie Y**, Prinsen C, Thunnissen F,Minna J, Gazdar AF. Cytoglobin, the newest member of the globin family, functions as a tumor suppressor gene. *Cancer Research*, 68, 7448-7456, September 15, 2008. doi: 10.1158/0008-5472.

20. Zhang W, Peyton M, **Xie Y,** Soh J, Minna JD, Gazdar AF, Frenkel EP Histone deacetylase inhibitor romidepsin enhances anti-tumor effect of erlotinib in non-small cell lung cancer (NSCLC) cell lines. *J Thorac Oncol.* 2009 Feb;4(2):161-6. PMID: 19179890

21. Xie CQ, Jeong Y, Fu M, Bookout AL, Garcia-Barrio MT, Sun T, Kim BH, Xie Y, Root S, Zhang J, Xu RH, Chen YE, Mangelsdorf DJ. Expression Profiling of Nuclear Receptors in Human and Mouse Embryonic Stem Cells. Mol Endocrinol. 2009 Feb 5. PMID: 19196830

22. Zhang W, Peyton M, **Xie Y**, Soh J, Minna JD, Gazdar AF, Frenkel EP Histone deacetylase inhibitor romidepsin enhances anti-tumor effect of erlotinib in non-small cell lung cancer (NSCLC) cell lines. *J Thorac Oncol*. 2009 Feb;4(2):161-6. PMID: 19179890

23. **Xie Y***, Wang X, Story M. Statistical Methods of Background Correction for Illumina BeadArray. *Bioinformatics*, 2009, Mar 15;25(6):751-7. doi: 10.1093/bioinformatics/btp040. PMID: 19193732

24. Park S, Hatanpaa K, **Xie Y**, Mickey B, Madden C, Raisanen J, Ramnarain D, Xiao G, Saha D, Boothman D, Zhao D, Bachoo R, Pieper R, Habib A. The receptor interacting protein (RIP1) inhibits p53 induction through NF-κB activation and confers a worse prognosis in glioblastoma, *Cancer Research*, 2009 Apr 1;69(7):2809-16. doi: 10.1158/0008-5472.CAN-08-4079.

25. Gandhi J, Zhang J, **Xie Y**, Soh J, Shigematsu H, Zhang W, Yamamoto H, Peyton M, Girard L, Lockwood W, Lam W, Varella-Garcia M, Minna J, Gazdar A. Molecular changes in lung cancers and sensitivity to tyrosine kinase inhibitors. *PloS ONE* 2009;4(2):e4576 PMID: 19238210

26. Galindo CL, McIver LJ, McCormick JF, Skinner MA, **Xie Y**, Gelhausen RA, Ng K, Kumar NM, Garner HR. Global microsatellite content distinguishes humans, primates, animals, and plants. *Mol Biol Evol.* 2009 Dec;26(12):2809-19. Epub 2009 Aug 28. PMID : 19717526 .

27. Yorio JT, **Xie Y**, Yan J, Gerber DE. Lung Cancer Diagnostic and Treatment Intervals in the United States: A Health Care Disparity? *Journal of Thoracic Oncology*: November 2009 - Volume 4 - Issue 11 - pp 1322-1330 doi: 10.1097/JTO.0b013e3181bbb130, PMID: 19752757

28. Allen JD, Chen M, **Xie Y*** (2009) Model-Based Background Correction (MBCB): R methods and GUI for Illumina Bead-array Data. *J Canc Sci Ther* 1: 025-027. doi:10.4172/1948-5956.1000004

29. Arnold SA, Rivera LB, Miller AF, Carbon JG, Dineen SP, Castrillon DH, **Xie Y**, Sage EH, Puolakkainen P, Bradshaw AD, and Brekken RA. Lack of host SPARC enhances vascular function and accelerates metastasis in an orthotopic murine model of pancreatic carcinoma. *Disease Models and Mechanisms* 2010 Jan-Feb;3(1-2): 57–72. PMID: 20007485

30. **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.

31. Cai D, Shames DS, Raso MG, **Xie Y**, Kim YH, Pollack JR, Girard L, Sullivan JP, Gao B, Peyton M, Nanjundan M, Byers L, Heymach J, Mills G, Gazdar AF, Wistuba I, Kodadek T, Minna JD. Steroid receptor coactivator-3 expression in lung cancer and its role in the regulation of cancer cell survival and proliferation. *Cancer Res.* 2010; 15;70(16):6477-85. PubMed PMID: 20663904; PubMedCentral PMCID: PMC2922434.

32. 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*. 2010 Dec 14;7(12):e1000378. PubMed PMID: 21179495; PMCID: PMC3001894.

33. Gerber DE, Rasc**o** DW, Le P, Yan J, Dowell JE, **Xie Y**. Predictors and Impact of Second-Line Chemotherapy for Advanced Non-small Cell Lung Cancer in the United States: Real-World Considerat*ions for Maint*enance Therapy. *J Thorac Oncol*. 2010 Dec 17. PubMed PMID: 21173713.

34. Wang S, Wang Y, **Xie Y,** Xiao G. A novel approach to DNA copy number data segmentation. *J Bioinform Comput Biol*. 2011 Feb;9(1):131-48. PubMed PMID: 21328710; PubMed Central PMCID: PMC3084615.

35. Gerber DE, Rasco DW, Le P, Yan J, Dowell JE, **Xie Y**. Predictors and impact of second-line chemotherapy for advanced non-small cell lung cancer in the United States: real-world considerations for maintenance therapy. *J Thorac Oncol*. 2011 Feb;6(2):365-71. PubMed PMID: 21173713; PubMed Central PMCID: PMC3025081.

36. Sunaga N, Shames DS, Girard L, Peyton M, Larsen JE, Imai H, Soh J, Sato M, Yanagitani N, Kaira K, **Xie Y**, Gazdar AF, Mori M, Minna JD. Knockdown of oncogenic KRAS in non-small cell lung cancers suppresses tumor growth and sensitizes tumor cells to targeted therapy. *Mol Cancer Ther.* 2011 Feb;10(2):336-46. PubMed PMID: 21306997; PubMed Central PMCID: PMC3061393.

37. Chen M., **Xie Y**. and Story M. An Exponential-Gamma Convolution Model for Background Correction of Illumina BeadArray Data. *Communications in Statistics*, 2011, 40(17), 3055-3069. PMID: 21769162 PMCID: PMC3137271.

38. **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. Epub 2011 Jul 8. PubMed PMID: 21742808; PubMed Central PMCID: PMC3166982.

39. Orvedahl A, Sumpter R Jr, Xiao G, Ng A, Zou Z, Tang Y, Narimatsu M, Gilpin C, Sun Q, Roth M, Forst CV, Wrana JL, Zhang YE, Luby-Phelps K, Xavier RJ, **Xie Y**, Levine B. Image-based genome-wide siRNA screen identifies selective autophagy factors. *Nature.* 2011 Dec 1;480(7375):113-7. PubMed PMID: 22020285; PubMed Central PMCID: PMC3229641.

40. Greer RM, Peyton M, Larsen JE, Girard L, **Xie Y**, Gazdar AF, Harran P, Wang L, Brekken RA, Wang X, Minna JD. SMAC mimetic (JP1201) sensitizes non-small cell lung cancers to multiple chemotherapy agents in an IAP-dependent but TNF-α-independent manner. *Cancer Res.* 2011 Dec 15;71(24):7640-8. Epub 2011 Nov 2. PubMed PMID: 22049529.

41. Gerber DE, Rasco DW, Skinner CS, Dowell JE, Yan J, Sayne JR, **Xie Y**. Consent timing and experience: modifiable factors that may influence interest in clinical research. *Journal of oncology practice*. 2012;8(2):91-6. PMCID: 3457835.

42. 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. Epub 2012 Jan 17. PubMed PMID: 22272232; PubMed Central PMCID: PMC3260142.

43. 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. PubMed PMID: 21956173.

44. Han TW, Kato M, Xie S, Wu LC, Mirzaei H, Pei J, Chen M, **Xie Y**, Allen J, Xiao G, McKnight SL. Cell-free formation of RNA granules: bound RNAs identify features and components of cellular assemblies. ***Cell***. 2012 May;149(4):768-79.

45. Tao W, Edwards JT, Tu F, **Xie Y**, Sharma SK. Incidence of unanticipated difficult airway in obstetric patients in a teaching institution. *Journal of anesthesia*. 2012 June; 26(3):339-345.

46. Allen JD, Wang S, Chen M, Girard L, Minna JD, **Xie Y**, Xiao G. Probe mapping across multiple microarray platforms. *Briefings in bioinformatics*. 2012 Sep;13(5):547-54. PMCID: 3431719.

47. Dowell JE, Dunphy FR, Taub RN, Gerber DE, Ngov L, Yan J, **Xie Y**, Kindler HL. A multicenter phase II study of cisplatin, pemetrexed, and bevacizumab in patients with advanced malignant mesothelioma. *Lung cancer*. 2012;77(3):567-71.

48. Ma S., Dai Y., Huang J., and **Xie, Y**., Identification of Breast Cancer Prognosis Markers via Integrative Analysis, *Computational Statistics and Data Analysis*, 2012 Volume 56, Issue 9, September 2012, Pages 2718–2728.

49. 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. PMCID: 3466591.

50. Sato M, Larsen JE, Lee W, Sun H, Shames DS, Dalvi MP, Ramirez RD, Tang H, DiMaio JM, Gao B, **Xie Y**, Wistuba II, Gazdar AF, Shay JW, Minna JD. Human lung epithelial cells progressed to malignancy through specific oncogenic manipulations. *Mol Cancer Res*. 2013 Jun;11(6):638-50. doi: 10.1158/1541-7786.MCR-12-0634-T. Epub 2013 Feb 28

51. 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. PMCID: 23502341.

52. 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.

53. Liu J, Huang J, **Xie Y**, Ma S. Sparse group penalized integrative analysis of multiple cancer prognosis datasets. *Genet Res* (Camb). 2013 Jun;95(2-3):68-77. doi: 10.1017/S0016672313000086. PMID: 23938111

54. Ding LH, Park S, Peyton M, Girard L, **Xie Y**, Minna JD, Story MD. Distinct transcriptome profiles identified in normal human bronchial epithelial cells after exposure to γ-rays and different elemental particles of high Z and energy. *BMC Genomics*. 2013 Jun 1;14:372. doi: 10.1186/1471-2164-14-372. PMID: 23724988

55. Chakraborty S, Li L, Tang H, **Xie Y**, Puliyappadamba VT, Raisanen J, Burma S, Boothman DA, Cochran B, Wu J, Habib AA. Cytoplasmic TRADD confers a worse prognosis in glioblastoma. *Neoplasia*. 2013 Aug;15(8):888-97. PMID: 23908590 Free PMC Article

56. Wu Q, Ishikawa T, Sirianni R, Tang H, McDonald JG, Yuhanna IS, Thompson B, Girard L, Mineo C, Brekken RA, Umetani M, Euhus DM, Xie Y, Shaul PW. 27-Hydroxycholesterol Promotes Cell-Autonomous, ER-Positive Breast Cancer Growth. *Cell Rep***.** 2013 Nov 14;5(3):637-45. doi: 10.1016/j.celrep.2013.10.006. Epub 2013 Nov 7. PMID: 24210818

57. Ahn DH, Mehta N, Yorio JT, **Xie Y**, Yan J, Gerber DE. Influence of Medical Comorbidities on the Presentation and Outcomes of Stage I-III Non-Small-Cell Lung Cancer. *Clin Lung Cancer*. 2013 Nov;14(6):644-50. doi: 10.1016/j.cllc.2013.06.009. Epub 2013 Jul 22. PMID: 23886797]

58. Wang T, **Xie Y**, Xiao G, dCLIP: a computational approach for comparative CLIP-seq analyses. ***Genome Biology***, 2014 Jan 7;15(1):R11.7 PMCID: PMC4054096

59. Chen B, Yun J, Kim MS, Mendell JT, **Xie Y***. PIPE-CLIP: a comprehensive online tool for CLIP-seq data analysis. Genome Biol. 2014 Jan 22;15(1):R18. doi: 10.1186/gb-2014-15-1-r18. PMID: 24451213 [PubMed - in process]

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, PMCID: PMC3946561

61. Zhao Q, Shi X, **Xie Y**, Huang J, Shia B, Ma S. Combining multidimensional genomic measurements for predicting cancer prognosis: observations from TCGA. ***Brief Bioinform.*** 2014 Mar 13. [Epub ahead of print] PMID: 24632304
62. Shi X, Liu J, Huang J, Zhou Y, **Xie Y**, Ma S. A penalized robust method for identifying gene-environment interactions. ***Genet Epidemiol***. 2014 Apr;38(3):220-30. doi: 10.1002/gepi.21795. Epub 2014 Feb 24. PMID: 24616063 [PubMed - indexed for MEDLINE]
63. 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
64. Gazdar A, Robinson L, Oliver D, Xing C, Travis WD, Soh J, Toyooka S, Watumull L, **Xie Y**, Kernstine K, Schiller JH. Hereditary lung cancer syndrome targets never smokers with germline EGFR gene T790M mutations. ***J Thorac Oncol***. 2014 Apr;9(4):456-63. PMID: 24736066
65. 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***, 2014 May 10;33(10):1784-800. PMCID: PMC3981913
66. Zhong R, Kim J, Kim HS, Kim M, Lum L, Levine B, Xiao G, White MA, **Xie Y***. Computational detection and suppression of sequence-specific off-target phenotypes from whole genome RNAi screens. ***Nucleic Acids Res***. 2014 Jul;42(13):8214-22. doi: 10.1093/nar/gku306. Epub 2014 Jun 27. PMID: 24972830
67. Gerber DE, Laccetti AL, Chen B, Yan J, Cai J, Gates S, **Xie Y**, Lee SJ. Predictors and intensity of online access to electronic medical records among patients with cancer. ***J Oncol Pract***. 2014 Sep;10(5):e307-12. doi: 10.1200/JOP.2013.001347. Epub 2014 Jul 8. PMID: 25006222
68. Kwon I, Xiang S, Kato M, Wu L, Theodoropoulos P, Wang T, Kim J, Yun J, **Xie Y**, McKnight SL. Poly-dipeptides encoded by the C9orf72 repeats bind nucleoli, impede RNA biogenesis, and kill cells. ***Science.*** 2014 Sep 5;345(6201):1139-45. doi: 10.1126/science.1254917. Epub 2014 Jul 31. PMID: 25081482
69. Augustyn A, Borromeo M, Wang T, Fujimoto J, Shao C, Dospoy PD, Lee V, Tan C, Sullivan JP, Larsen JE, Girard L, Behrens C, Wistuba II, **Xie Y**, Cobb MH, Gazdar AF, Johnson JE, Minna JD. ASCL1 is a lineage oncogene providing therapeutic targets for high-grade neuroendocrine lung cancers. ***Proc Natl Acad Sci U S A***. 2014 Oct 14;111(41):14788-93. doi: 10.1073/pnas.1410419111. Epub 2014 Sep 29. PMID: 25267614
70. Zhong R, Allen JD, Xiao G, **Xie Y***. Ensemble-based network aggregation improves the accuracy of gene network reconstruction. ***PLoS One***. 2014 Nov 12;9(11):e106319. doi: 10.1371/journal.pone.0106319. 2014. PMID: 25390635 **(*Corresponding Author)**
71. Bansal M, Yang J, Karan C, Menden MP, Costello JC, Tang H, Xiao G, Li Y, Allen J, Zhong R, Chen B, Kim M, Wang T, Heiser LM, Realubit R, Mattioli M, Alvarez MJ, Shen Y; NCI-DREAM Community, Gallahan D, Singer D, Saez-Rodriguez J, **Xie Y***, Stolovitzky G*, Califano A*; NCI-DREAM Community. A community computational challenge to predict the activity of pairs of compounds. ***Nat Biotechnol***. 2014 Dec;32(12):1213-22. doi: 10.1038/nbt.3052. Epub 2014 Nov 17. PMID: 25419740 [PubMed - in process]
72. Zhong R, Dong X, Levine B, **Xie Y**, Xiao G. iScreen: Image-Based High-Content RNAi Screening Analysis Tools. ***J Biomol Screen***. 2014 Dec 29. pii: 1087057114564348. [Epub ahead of print] PMID: 25548139
73. Yang J, Tang H, Li Y, Zhong R, Wang T, Wong S, Xiao G, and **Xie Y*****,** DIGRE: Drug Induced Genomic Residual Effect Model for Successful Prediction of Multidrug Effects. *CPT: Pharmacometrics & Systems Pharmacology*, 2014 (In Press)
74. Wang T, Zhan X, Bu CH, Lyon S, Pratt D, Hildebrand S, Choi JH, Zhang Z, Zeng M, Wang KW, Turer E, Chen Z, Zhang D, Yue T, Wang Y, Shi H, Wang J, Sun L, SoRelle J, McAlpine W, Hutchins N, Zhan X, Fina M, Gobert R, Quan J, Kreutzer M, Arnett S, Hawkins K, Leach A, Tate C, Daniel C, Reyna C, Prince

L, Davis S, Purrington J, Bearden R, Weatherly J, White D, Russell J, Sun Q, Tang M, Li X, Scott L, Moresco EM, McInerney GM, Karlsson Hedestam GB, **Xie Y**, Beutler B. Real-time resolution of point mutations that cause phenovariance in mice. ***Proc Natl Acad Sci U S A***. 2015 Jan 20. pii: 201423216. [Epub ahead of print] PMID: 25605905 [PubMed - as supplied by publisher]

75. Zang X, Chen M, Zhou Y, Xiao G, **Xie Y***, Wang X*, Meta-analysis Identification of CDKN3 Gene Expression as a Prognostic Biomarker in Lung Adenocarcinoma, ***Cancer Informatics***, 2015 (In Press)
76. Sei E, Wang T, Hunter OV, **Xie Y***, Conrad NK*. HITS-CLIP Analysis Uncovers a Link between the Kaposi's Sarcoma-Associated Herpesvirus ORF57 Protein and Host Pre-mRNA Metabolism. PLoS Pathog. 2015 Feb 24;11(2):e1004652.
77. Tang, H., Sebti, S., Titone, R., Zhou, Y., Isidoro, C., Ross, T., Hibshoosh, H., Xiao, G., Packer, M., **Xie, Y***., and Levine, B*. Decreased BECN1 mRNA Expression in Human Breast Cancer is Associated with Estrogen Receptor-Negative Subtypes and Poor Prognosis, ***EBioMedicine, 2015,*** (In Press)
78. Meyer JJ, Foster RD, Lev-Cohain N, Yokoo T, Dong Y, Schwarz RE, Rule W, Tian J, **Xie Y**, Hannan R, Nedzi L, Solberg T, Timmerman R. A Phase I Dose-Escalation Trial of Single-Fraction Stereotactic Radiation Therapy for Liver Metastases. ***Ann Surg Oncol.*** 2015 May 12. [Epub ahead of print] PMID: 25963478
79. Wang T, Xiao G, Chu Y, Zhang MQ, Corey DR, **Xie Y*.** Design and bioinformatics analysis of genome-wide CLIP experiments. ***Nucleic Acids Res.*** 2015 Jun 23;43(11):5263-74. PMID: 25958398
80. Fan D, Coughlin LA, Neubauer MM, Kim J, Kim MS, Zhan X, Simms-Waldrip TR, **Xie Y**, Hooper LV, Koh AY. Activation of HIF-1α and LL-37 by commensal bacteria inhibits Candida albicans colonization., ***Nat Med***. 2015 Jul;21(7):808-14. Epub 2015 Jun 8. PMID: 26053625
81. Ding LH, Park S, **Xie Y,** Girard L, Minna JD, Story MD. Elucidation of changes in molecular signalling leading to increased cellular transformation in oncogenically progressed human bronchial epithelial cells exposed to radiations of increasing LET. ***Mutagenesis.*** 2015 Sep;30(5):685-94. PMID: 26001755
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84. Shi X, Zhao Q, Huang J, **Xie Y,** Ma S. Deciphering the associations between gene expression and copy number alteration using a sparse double Laplacian shrinkage approach. ***Bioinformatics.*** 2015 Sep 3. pii: btv518. [Epub ahead of print] PMID: 26342102
85. Chu Y, Wang T, Dodd D, **Xie Y**; Janowski B, Corey D, Intramolecular Circularization Increases Efficiency of RNA Sequencing, ***Nucleic Acids Res***. 2015 (Accepted)

(***Corresponding Author, #Co-first Author**).

Reviews, Chapters, Monographs and Editorials

1. Minna JD, Girard L, **Xie, Y**. (2007) TumormRNA Expression Profiles Predicting Responses to Chemotherapy. ***Journal of Clinical Oncology***(28):4329 - 4336.
2. Ahn C, Kang S, and **Xie, Y**. (2007) Optimal biological dose for molecular-targeted therapies. ***Wiley Encyclopedia of Clinical Trials***. 1–8.

3. **Xie Y**, and Minna JD. Predicting the future for people with lung cancer. ***Nature Medicine.*** 2008 14, 812 - 813 (2008) doi:10.1038/nm0808-812
4. **Xie Y**, Ahn C. Statistical methods for integrating multiple types of genomic data. ***Statistical Methods in Molecular Biology***. (Edited by Bang H, Zhou XK, Van Epps HL and Mazumdar M).2010 Jan; 620:511-529. DOI: 10.1007/978-1-60761-580-4
5. **Xie Y,** Minna JD. Non-small-cell lung cancer mRNA expression signature predicting response to adjuvant chemotherapy. ***J Clinical Oncology.*** 2010 Oct 10;28(29):4404-7. PMID: 20823415.
6. **Xie, Y**. and Minna, J. D. (2012), 'A Lung Cancer Molecular Prognostic Test Ready for “Prime Time”', ***Lancet,*** 2012 Mar 3;379(9818):785-7**.**

PATENTS

A Prognostic and Predictive Gene Signature for Adjuvant Chemotherapy in Non-Small-Cell Lung Cancer Patients (patent #UTSD2627) - 2012
Prognosis signature/assay for kidney cancer

PRESENTATIONS

Invited

1. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. Division of Biostatistics, University of Kansas Medical Center, Kansas City, MO. 2006.
2. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. Division of Biostatistics, St. Jude Children Research Hospital, Memphis, TN. 2006.
3. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. Huntsman Cancer Institute, University of Utah, Salt Lake City, UT. 2006
4. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. Department of Health Studies, University of Chicago, Chicago, IL. 2006
5. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. School of Medicine, Johns Hopkins University, Baltimore, MD. 2006.
6. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. Division of Biostatistics, University of Minnesota, Minneapolis, MN. 2006
7. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. Department of Biostatistics, University of North Carolina, Chapel Hill, NC. 2006.
8. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. Division of Biostatistics, Washington University, St. Louis, MO. 2006.
9. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. Winship Cancer Institute, Emory University, Atlanta, GA. 2006.
10. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. Division of Biostatistics, Indiana University School of Medicine, Indianapolis, IN. 2006.

11. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. Division of Biostatistics, University of South Florida, Moffitt Cancer Center and Research Institute, Tampa, FL. 2006.

12. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. Division of Biostatistics, The University of Texas Southwestern Medical Center, Dallas, TX. 2006.

13. “A Bayesian approach to jointly modeling DNA protein binding data, gene expression data and DNA sequence data”. SMU-UTSW-MAG (microarray analysis interest group) , UTSW Dallas, TX. 2007.

14. “Gene Expression Signatures of Drug Sensitivity in Lung Cancer.” Hamon Center for Therapeutic Oncology, UTSW. 2007.

15. “Gene Expression Signatures of Drug Sensitivity in Lung Cancer.” Department of Computer Sciences, Southern Methodist University, Dallas, TX. 2007.

16. “Background correction for Illumina beadarray”. Department of Statistics, Southern Methodist University, Dallas, TX. 2008.

17. “Robust Gene Expression Signature from Formalin-Fixed Paraffin-Embedded Samples Predict Prognosis of Non-Small-Cell Lung Cancer Patients.” American Statistical Association Chapter Meeting, Dallas, TX. 2010.

18. “Robust Gene Signature from Formalin Fixed Paraffin Embedded (FFPE) Samples Refines Prognosis of Lung Cancer.” Department of Biomedical Engineering, University of Texas at Dallas, Dallas, TX. 2011.

19. “Robust Gene Signature from Formalin Fixed Paraffin Embedded (FFPE) Samples Refines Prognosis of Lung Cancer.” Department of Clinical Sciences, Distinguished Speaker Seminar, UTSW, Dallas, TX. 2011.

20. “Predicting synergistic effects of compound combinations using genomic data.” 5th RECOMB conference on regulatory and systems genomics, San Francisco, CA. 2012.

21. “A 12-gene set derived by network analysis and siRNA synthetic lethality data that predicts survival benefits from adjuvant chemotherapy in non-small cell lung cancer patients.” Lung cancer workshop---progress toward translation, Pittsburgh, PA. 2012.

22. “Identify and Validate Gene Expression Markers for Prognosis and Response to Adjuvant Chemotherapy in Lung Cancer Patients.” Department of Biostatistics and Computational Biology, Harvard University. 2013.

23. “Identify and Validate Gene Expression Markers for Prognosis and Response to Adjuvant Chemotherapy in Lung Cancer Patients.” University of Texas, MD Anderson Cancer Center, Houston, TX. 2013.

24. “Integrative Analysis and Systems Biology Approaches for Cancer Predictive Signatures.” Department of Mathematics, University of Texas, Arlington, TX. 2013.

25. “Bioinformatics in translational cancer research.” School of Information Science and Technology, Tsinghua University, China. 2013.

26. “Integrative Analysis and Systems Biology Approaches for Cancer Predictive Signatures.” Joint Statistical Meeting, Montreal, Quebec, Canada. 2013.

27. “Computational models to predict the sensitivity of cancer cell lines to compounds using genomic data.” Center for Computational Biology and Bioinformatics, Indiana University, Indianapolis, IN. 2013.

28. “Computational models to predict the sensitivity of cancer cell lines to compounds using genomic data.” Novartis Institutes for Biomedical Research, Emeryville, CA. 2013.

29. “Lung Cancer Explorer (LCE): an open web portal to explore gene expression and clinical associations in lung cancer.” World Conference on Lung Cancer, Sydney, Australia. 2013.

30. “Molecular Signatures for the Accurate Classification of NSCLC and Neuroendocrine Tumors.” World Conference on Lung Cancer, Sydney, Australia. 2013.

Contributed

1. “Model based background correction for Illumina microarray data”. Joint Statistics Meeting, Salt Lake City, Utah. 2007.

2. “Statistical methods to preprocess Illumina microarray data”. International Biometrics Society (ENAR), Arlington, VA. 2008.

3. “Adaptive prediction in genomic signatures based clinical trials.” Joint Statistical Meeting, Washington, DC. 2009.

4. “Adaptive prediction in genomic signatures based clinical trials.” International Biometrics Society (ENAR), New Orleans, LA. 2010.

GRANT SUPPORT

Current Grant Support

1. Title of Project: Integrative Analysis to Identify Regulation Targets of RNA-Binding Proteins
   Funding Source: NIH R01
   Role: PI
   Duration: 4/1/2016 to 3/31/2021
   Total amount of award: $1,295,584

2. Title of Project: C2: Biostatistics, Bioinformatics and Database Core
   Funding Source: CPRIT
   Role: PI
   Duration: 9/1/2012 to 8/31/2017
   Total amount of award: $712,445

3. Title of Project: SPORE in Lung Cancer – Core C
   Funding Source: NCI Specialized Programs of Research Excellence (P50)
   Role: Co-Director of Biostatistics and Bioinformatics Core
   Duration: 9/1/2015 to 8/31/2016
   Total amount of award: $1,650,776

4. Title of Project: DIS3L2 in Childhood Wilms Tumor: Mechanism to Medicines
   Funding Source: CPRIT
   Role: Co-Investigator
   Duration: 3/1/2016 to 2/28/2017
   Total amount of award: $285,000

5. Title of Project: Bioinformatics Core Facility at UT Southwestern Medical Center
   Funding Source: CPRIT
   Role: Co-Investigator

Duration: 06/01/2015 to 05/31/2016
Total amount of award: $1,268,871

6. Title of Project: Targeting Metastatic Pathways
   Funding Source: CPRIT
   Role: Co-Investigator
   Duration: 03/01/2016 – 02/28/2017
   Total amount of award: $285,000

7. Title of Project: Cancer Center Support Grant
   Funding Source: NIH P30
   Role: Co-Investigator
   Duration: 8/3/2010 to 7/31/2015
   Total amount of award: $4,720,203

Completed Grant Support

8. Title of Project: Project 1. Molecular Biomarker ID
   Funding Source: CPRIT
   Role: Co-Investigator
   Duration: 7/1/2011 to 6/30/2016
   Total amount of award: $1,873,655

9. Title of Project: UT STAR – Bridge Funding – Biomedical Informatics
   Funding Source: NIH Clinical and Translational Science Award (CTSA)
   Role: Co-Investigator
   Duration: 7/24/2012 to 7/23/2013
   Total amount of award: $989,356

10. Title of Project: Risk Estimates and Mechanisms of Lung Cancer Pathogenesis after Space Radiation
    Funding Source: NASA
    Role: Project lead and Biostatistics and Bioinformatics Core Director
    Duration: 1/1/2011 to 12/31/2015
    Total amount of award: $4,726,895

11. Title of Project: Predicting Adjuvant Chemotherapy Response in Lung Cancer
    Funding Source: NIH R01 (priority score 1%)
    Role: PI
    Duration: 9/1/2010 to 2/28/2016
    Total amount of award: $1,290,837

12. Title of Project: CTSA Pilot - Xie- Optimal designs for Phase I clinical trials with late-onset toxicities
    Funding Source: NIH

    Role: Pilot Award PI
    Duration: 6/1/2009 to 5/31/2010
    Total amount of award: $25,600

13. Title of Project: CTSA Pilot – Xie - Expression of Nuclear Receptors in Lung Cancer as Diagnostic and Therapeutic Targets
    Funding Source: NIH
    Role: Pilot Award PI
    Duration: 9/1/2009 to 4/30/2010
    Total amount of award: $45,000

14. Title of Project: SPORE in Lung Cancer – Core C
    Funding Source: NIH
    Role: Co-Investigator
    Duration: 8/31/2003 to 8/31/2008
    Total amount of award: $1,329,195

15. Title of Project: Radiation Leukemogenesis Project 3
    Funding Source: NASA
    Role: Co-Investigator
    Duration: 12/1/2004 to 7/31/2009
    Total amount of award: $291,348

16. Title of Project: HZE Particle Radiation & Lung Cancer Pathogenesis-Core D2
    Funding Source: NASA
    Role: Co-Investigator
    Duration: 4/1/2005 to 3/31/2010
    Total amount of award: $109,847

17. Title of Project: HZE Particle Radiation & Lung Cancer Pathogenesis-Supplement
    Funding Source: NASA
    Role: Co-Investigator
    Duration: 8/1/2010 to 12/31/2010
    Total amount of award: $320,513

18. Title of Project: NASA Specialized Center of Research on Radiation Carcinogenesis
    Funding Source: NASA
    Role: Co-Investigator
    Duration: 7/1/2009 to 6/30/2010
    Total amount of award: $130,370

19. Title of Project: Stereotactic Body Radiation Therapy for Underserved Populations of Men with Low and Intermediate Risk Prostate Cancer
    Funding Source: NIH
    Role: Co-Investigator
    Duration: 5/15/2008 to 5/14/2011
    Total amount of award: $617,202

20. Title of Project: Role for RIP1 in Gliomagenesis
Funding Source: NIH
Role: Co-Investigator
Duration: 9/29/2009 to 7/31/2013
Total amount of award: $996,825

21. Title of Project: Concerted Attack on Patient Specific Oncogenic Vulnerabilities in Lung Cancer
Funding Source: NIH RC2
Role: Co-Investigator
Duration: 9/29/2009 to 8/31/2011
Total amount of award: $2,456,853

TEACHING

- **2008** **Course**: Bioinformatics and DNA Microarray Data Analysis
- **2008-2012** **Course**: Biostatistics for clinical sciences II, 2008 – 2012
- **2013-2014** Co-designed and co-direct a new course: BSCI 5096.01 “Special Topics: Analysis of High Content/High Complexity Data Sets.”
- **2014-2015** Co-design and teach a new graduate core course on “Introduction to Biostatistics and Bioinformatics”
- **2015-2016** Design and teach a new graduate course “Advanced data analysis and statistical learning ”

STUDENT ADVISING AND COMMITTEE MEMBERSHIP

Students

Student Name	Degree Program	Duration	Role
Rui Zhong	PhD in Cancer Biology		Advisor
Tao Wang	PhD in Integrative Biology		Co-Advisor
Michelle Ma	PhD in Integrative Biology		Advisor
Xiao Zang	PhD in Integrative Biology		Advisor
Shidan Wang	PhD in Integrative Biology		Advisor
Bo Ci	PhD in Integrative Biology		Advisor

Postdoctoral trainees

Student Name	Graduate School	Duration	Current Position
Dr. Hao Tang	UTSW	2011 - 2013	Assistant Professor
Dr. Beibei Chen	UTSW	2012 – Present	Computational Biologist
Dr. Jonghyun Yun	UTSW	2012 - 2015	Assistant Professor
Dr. Sangin Lee	UTSW	2014 - 2016	Assistant Professor
Dr. Jungsik Noh	UTSW	2014 - 2015	

ACADEMIC SERVICE

- **2006 – 2014**, Cancer Center Protocol Review & Monitoring Committee, UT Southwestern Medical Center
- **2006 – 2014**, Cancer Center Data Monitoring & Safety Committee, UT Southwestern Medical Center
- **2010 – Present Member**, Cancer Center Lab Correlative Studies Committee, UT Southwestern Medical Center
- **2011 – Present Member**, Scientific Computing Committee, UT Southwestern Medical Center
- **2010 – Present Member**, PhD Students' Qualifying Exam Committees (Ganesh Kadamur Bhavani, Patrick Dospoy), UT Southwestern Medical Center
- **2009 Member**, faculty representatives committee in the division of Biostatistics at the Department of Clinical Sciences, UT Southwestern Medical Center
- **2015- Present** UT SOUTHWESTERN MEDICAL CENTER six-year plan research sub-committee
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Last updated: July 14, 2016