

March 2017

CURRICULUM VITAE

Zongli Xu

Education

1996 M.D. Public Health, Xinjiang Medical University, China
 1999 M.S. Biostatistics, Xinjiang Medical University, China
 2002 Ph.D. Biostatistics, Sun Yat-Sen University, Guangzhou, China

Professional Work Experience

2004 – 2010 Research Fellow, Epidemiology Branch, National Institute of Environmental Health Sciences, Research Triangle Park, NC
 2003 –2004 Postdoctoral Research Associate, Computational Biology, University of North Carolina at Chapel Hill, NC

Professional Appointments

2010 – Present Staff Scientist, Epidemiology branch, National Institute of Environmental Health Sciences, Research Triangle Park, NC

Certifications

SAS Certified Base Programmer for SAS 9
 SAS Certified Advanced Programmer for SAS 9

Editorial Service

Academic editor for journal *PLoS One*
 Academic editor for journal *BioMed Research International*
 Academic editor for journal *Advances in Medicine*

Peer-Reviewed Publications:

1. **Zongli Xu**, Sabine A. S. Langie, Patrick De Boever, Jack A. Taylor and Liang Niu. RELIC: a novel dye-bias correction method for Illumina Methylation BeadChip. *BMC Genomics* 2016
2. Lauren Wilson, Sophia Harlid, **Zongli Xu**, Dale sandler, and Jack Taylor, An epigenome-wide study of body mass index and DNA methylation in blood using participants from the Sister Study cohort. *International Journal of Obesity*, 2016
3. Harlid S, **Xu Z**, Taylor JA. Soy Formula and Epigenetic Modifications: Analysis of Vaginal Epithelial Cells from Infant Girls in the IFED Study. *Environ Health Perspect.* 2016 Aug 19
4. **Xu Z**, Taylor JA, Leung YK, Ho SM, Niu L. oxBS-MLE: an efficient method to estimate 5-methylcytosine and 5-hydroxymethylcytosine in paired bisulfite and oxidative bisulfite treated DNA. *Bioinformatics.* 2016 Aug 13.

5. Markunas CA, Wilcox AJ, **Xu Z**,..., Taylor JA. Maternal Age at Delivery Is Associated with an Epigenetic Signature in Both Newborns and Adults. PLoS One. 2016 Jul 6;11(7)
6. **[co-first author]** Niu L, **Xu Z**, Taylor JA. RCP: a novel probe design bias correction method for Illumina Methylation BeadChip. Bioinformatics. 2016 May
7. Joubert BR, **Xu Z**, London SJ. DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. Am J Hum Genet. 2016
8. Figueroa JD, **Xu Z**, ..., Rothman N. Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. Hum Mol Genet. 2016
9. Dong J..., **Xu Z**, Chen H. Genome-wide Meta-analysis on the Sense of Smell Among US Older Adults. Medicine (Baltimore). 2015
10. Wilson LE, Kim S, **Xu Z**, Harlid S, Sandler DP, Taylor JA. Non-Steroidal Anti-Inflammatory Drug Use and Genomic DNA Methylation in Blood. PLoS One. 2015
11. **Zongli Xu**, Liang Niu, Leping Li and Jack A. Taylor, ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip. Nucleic Acids Research, 2015
12. Hair BY, **Xu Z**, Kirk EL, Harlid S, Sandhu R, Robinson WR, Wu MC, Olshan AF, Conway K, Taylor JA, Troester MA. Body mass index associated with genome-wide methylation in breast tissue. Breast Cancer Res Treat. 2015 Jun;151(2):453-63.
13. Wilson LE, Kim S, **Xu Z**, Harlid S, Sandler DP, Taylor JA. Non-Steroidal Anti-Inflammatory Drug Use and Genomic DNA Methylation in Blood. PLoS One. 2015
14. Liu R, Umbach DM, Peddada SD, **Xu Z**, Tröster AI, Huang X, Chen H. Potential sex differences in nonmotor symptoms in early drug-naive Parkinson disease. Neurology. 2015 May 26;84(21):2107-15.
15. Harlid S, **Xu Z**, Panduri V, D'Aloisio AA, DeRoo LA, Sandler DP, Taylor JA. In utero exposure to diethylstilbestrol and blood DNA methylation in women ages 40-59 years from the sister study. PLoS One. 2015 Mar 9;10(3)
16. **[co-first author]** Christina A. Markunas, **Zongli Xu**, S. Sophia Harlid, Paul A. Wade, Rolv T. Lie, Jack A. Taylor, and Allen J. Wilcox. Identification of DNA methylation changes in newborns related to maternal smoking during pregnancy. Environ Health Perspect, Environ Health Perspect. 2014 Oct;122(10):1147-53
17. **[co-first author]** Harlid S, **Xu Z**, Panduri V, Sandler DP, Taylor JA. CpG Sites Associated with Cigarette Smoking: Analysis of Epigenome-Wide Data from the Sister Study. Environ Health Perspect. 2014 Jul;122(7):673-8
18. **Xu Z**, Taylor JA. Genome-wide age-related DNA methylation changes in blood and other tissues relate to histone modification, expression and cancer. Carcinogenesis. 2014 Feb;35(2):356-64

This study has been reported by several news presses:

- NIH record (http://nihrecord.od.nih.gov/newsletters/2014/02_28_2014/digest.htm); NIEHS new release (<http://www.nih.gov/news/health/feb2014/niehs-03.htm>);
 - Healthline news (<http://www.healthline.com/health-news/cancer-dna-mythelation-the-key-to-cancer-risk-020614>)
 - North Carolina health news: (<http://www.northcarolinahealthnews.org/2014/02/17/n-c-based-research-sheds-understanding-on-cancer-aging-link/>)
19. **[co-first author]** Bensen JT, **Xu Z**, McKeigue PM, Smith GJ, Fonham ET, Mohler JL, Taylor JA. Admixture mapping of prostate cancer in African Americans participating in the North Carolina-Louisiana Prostate Cancer Project (PCaP). Prostate. 2014 Jan;74(1):1-9
 20. Huang L, Bao Y, **Xu Z**, Lei X, Chen Y, Zhang Y, Zhang J. Neonatal bilirubin levels and childhood asthma in the US Collaborative Perinatal Project, 1959-1965. Am J Epidemiology. 2013 Dec 15;178(12):1691-7
 21. Deroo LA, Bolick SC, **Xu Z**, Umbach DM, Shore D, Weinberg CR, Sandler DP, Taylor JA. Global DNA methylation and one-carbon metabolism gene polymorphisms and the risk of breast cancer in the Sister Study. Carcinogenesis. 2014 Feb;35(2):333-8
This paper has been selected as Intramural papers of the month in Dec. 2013 (<http://www.niehs.nih.gov/news/newsletter/2013/12/dir/>).
 22. Godfrey AC, **Xu Z**, Weinberg CR, Getts RC, Wade PA, Deroo LA, Sandler DP, Taylor JA. Serum microRNA expression as an early marker for breast cancer risk in prospectively collected samples from the Sister Study cohort. Breast Cancer Res. 2013
 23. **Xu, Zongli**, Bolick, Sophia C.E, DeRoo, Lisa A, Weinberg, Clarice R, Sandler, Dale P, and Taylor, Jack A "Epigenome-wide Association Study of Breast Cancer Using Prospectively Collected Sister Study Samples", J Natl Cancer Inst. 2013 May 15;105(10):694-700
The findings have been reported by NIEHS newsletter Environmental Factor in 2013 (<http://www.niehs.nih.gov/news/newsletter/2013/5/science-taylor/>).
 24. **[co-first author]** Bensen JT, **Xu Z**, Smith GJ, Mohler JL, Fonham ET, Taylor JA. Genetic polymorphism and prostate cancer aggressiveness: A case-only study of 1,536 GWAS and candidate SNPs in African-Americans and European-Americans. Prostate. 2013 Jan;73(1)
 25. White AJ, Sandler DP, Bolick SC, **Xu Z**, Taylor JA, Deroo LA., "Recreational and household physical activity at different time points and DNA global methylation". Eur J Cancer. 2013 Mar 6
 26. Sucheston LE, Bensen JT, **Xu Z**, Singh PK, Preus L, Mohler JL, Su LJ, Fonham ET, Ruiz B, Smith GJ, Taylor JA. "Genetic ancestry, self-reported race and ethnicity in African Americans and European Americans in the PCaP cohort". PLoS One. 2012;7(3)
 27. Kim S, Parks CG, **Xu Z**, Carswell G, DeRoo LA, Sandler DP, Taylor JA , Association between genetic variants in DNA and histone methylation and telomere length. PLoS One. 2012;7(7):e40504. Epub 2012 Jul 11.

28. Shaughnessy DT, Gangarosa LM, Schliebe B, Umbach DM, **Xu Z**, MacIntosh B, Knize MG, Matthews PP, Swank AE, Sandler RS, DeMarini DM, Taylor JA. Inhibition of fried meat-induced colorectal DNA damage and altered systemic genotoxicity in humans by crucifera, chlorophyllin, and yogurt. PLoS One. 2011 Apr 25;6(4):e18707.
29. Meadows KL, Andrews DM, **Xu Z**, Carswell GK, Laughlin SK, Baird DD, Taylor JA. Genome-wide analysis of loss of heterozygosity and copy number amplification in uterine leiomyomas using the 100K single nucleotide polymorphism array. Exp Mol Pathol. 2011 Aug;91(1):434-9. Epub 2011 Apr 8.
30. **Xu Z**, Bensen JT, Smith GJ, Mohler JL, Taylor JA. GWAS SNP Replication among African American and European American men in the North Carolina-Louisiana prostate cancer project (PCaP). Prostate. 2011 Jun 1;71(8):881-91. doi: 10.1002/pros.21304. Epub 2010 Nov 17.
31. Rothman N, Garcia-Closas M, **Xu Z**, Silverman DT, Chanock SJ. A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nat Genet. 2010 Nov;42(11):978-84. Epub 2010 Oct 24
32. Fang F, Umbach DM, **Xu Z**, Ye W, Sandler DP, Taylor JA, Kamel F. No association between DNA repair gene XRCC1 and amyotrophic lateral sclerosis. Neurobiol Aging. 2010 Aug 16.
33. Yu-Jing Fang, Han-Bing Deng, G Neil Thomas, Chi Hung Tzang, Cai-Xia Li, **Zong-Li Xu**, Mengsu Yang, Brian Tomlinson "Linkage of Angiotensinogen Gene Polymorphisms with Hypertension in a Sibling Study of Hong Kong Chinese" Journal of Hypertension, 2010
34. **Zongli Xu**, Jack A. Taylor "Integrating GWAS and Candidate Gene Information into Functional SNP Selection for Genetic Association Studies" Nucleic Acids Research, 2009
This study has been reported by several news presses:
 - *Nature Medicine*: <http://www.nature.com/nm/journal/v16/n1/full/nm0110-7a.html>
 - *NIEHS news*: <https://www.niehs.nih.gov/news/newsletter/2009/september/science-intramural.cfm>
35. Christina Markunas, David M. Umbach, **Zongli Xu**, Jack, A. Taylor. "Assessing candidate gene nsSNPs for phenotypic differences in double-strand break repair using radiation-induced γ H2A.X foci" Journal of Cancer Epidemiology , 2008
36. **Zongli Xu**, Norman L. Kaplan, Jack A. Taylor, "TAGster: Efficient Selection of LD tag SNPs in Single or Multiple Populations", 2007, Bioinformatics. 2007 Dec 1;23(23):3254-5
37. **Zongli Xu**, Norman L. Kaplan, Jack A. Taylor, "LD tag SNP selection for candidate gene association studies using HapMap and gene resequencing data" Eur J Hum Genet. 2007 Oct;15(10):1063-70.
38. Li Qian, **Zongli Xu**, Belinda Wilson, Jau-Shyong Hong, and Patrick M. Flood, "Sinomenine, a natural dextrorotatory morphinan analog, is anti-inflammatory and neuroprotective through inhibition of microglial NADPH oxidase" Journal of Neuroinflammation, 2007 Sep 19;4:23

39. Li Qian, Kai Soo Tan, Sung-Jen Wei, Hung-Ming Wu, **Zongli Xu**, Belinda Wilson, Ru-Bin Lu, Jau-Shyong Hong, and Patrick M. Flood, "Microglia-Mediated Neurotoxicity Is Inhibited by Morphine through an Opioid Receptor-Independent Reduction of NADPH Oxidase Activity" Journal of Immunology. 2007, 179: 1198-1209
40. King AA, Shaughnessy DT, Mure K, Leszczynska J, Ward WO, Umbach DM, **Xu Z**, Ducharme D, Taylor JA, Demarini DM, Klein CB. "Antimutagenicity of cinnamaldehyde and vanillin in human cells: Global gene expression and possible role of DNA damage and repair" Mutation Research. 2007, 616(1-2):60-69
41. Jack A. Taylor, **Zong-Li Xu**, Norman L. Kaplan, Richard W. Morris, "How well do HapMap haplotypes identify common haplotypes of genes: A comparison with benchmark haplotypes of 334 genes resequenced in the Environmental Genome Project" Cancer Epidemiology Biomarkers & Prevention, 2006, 15(1):133-137
42. Zou F, **Xu Z**, Vision T, "Assessing the Significance of Quantitative Trait Loci in Replicable Mapping Populations", Genetics. 2006, 174(2):1063-1068
43. **Zongli Xu**, Fei Zou, Todd. J.Vision, "High resolution QTL mapping in genotypically selected samples from experimental crosses." Genetics. 2005, 170(1):401-408
44. Fang YJ, Thomas GN, **Xu ZL**, Fang JQ, Critchley JA, Tomlinson B. An affected pedigree member analysis of linkage between the dopamine D2 receptor gene TaqI polymorphism and obesity and hypertension. Int J Cardiol. 2005,102(1):111-116
45. WeiHua Jia, Bingjian Feng, **Zongli Xu**, Xiaoshi Zhang, Ping Huang, Lixi Huang, Xingjuan Yu, Qisheng Feng, Minghong Yao, Yinyao Shugart, Yixin Zeng, "Familial risk and clustering of nasopharyngeal carcinoma in Guangdong, China" Cancer. 2004, 101(2):363-369
46. Weihua Jia, **Zongli Xu**, Bingjian Feng, Lixi Huang, Xingjuan Yu, Qisheng Feng, Feng Zhang, Yixin Zeng, "Epidemiological Study of Nasopharyngeal Carcinoma Risk in Relatives of High-risk Families in Guangdong." Chinese Journal of Cancer. 2004, 23(7):767-770
47. **Zong-Li Xu**, Yu-Jing Fang, Ji-Qian Fang, "A model for Sibpair linkage analysis on multi-response traits and its application to gene mapping of essential hypertension." Journal of Biomathematics. 2003, 18(2):176-181
48. **Zong-Li Xu**, Fang Jiqian, "A method of Bayesian linkage analysis on complex binary traits in general Pedigrees" Journal of Biomathematics. 2003, 18(1):15-20
49. **Zong-Li Xu**, Ji-Qian Fang, "The statistical methods to synthesize linkage studies", Chinese Journal of preventive medicine, 2002, 36(3):196-198
50. Junshu Wu, Bin Yang, Zheng Wang, Guofu Huang, **Zongli Xu**, "The effects of Tear Naturals II and Celluvisc on tear film after LASIK", Chinese Journal of Practical Ophthalmology, 2002, 20(3): 186-190
51. Bin Yang, Zheng Wang, Junshu Wu, Guofu Huang, **Zongli Xu**, "The early changes of tear film after laser in situ keratomileusis", Chinese Journal of Ophthalmology, 2002,

38(2): 76-80

52. **Zong-Li Xu**, Ji-Qian Fang, “Meta analysis for Linkage studies.” Life Science Research, 2001, 5(4): 308-313
53. Hua Yao, **Zong-Li Xu**, Qing Xu, “A discussion on data analysis methods for lysozyme measurement in saliva”. Journal of Xingjiang Medical University.1999, 22(1): 68-72,

Software or Web Server (Peer-reviewed)

Freely available software and web tools I have developed for statistical analysis of genomic datasets.

- **ENmix**: An R software package for data preprocessing and quality control for Illumina HumanMethylation450 BeadChip. Web address: <http://www.bioconductor.org/packages/release/bioc/html/ENmix.html>
- **SNPinfo**: a web server for SNP selection and functional information. It can comprehensively utilize computational, experimental and epidemiological information together with genome wide association study (GWAS) results and linkage disequilibrium (LD) information to prioritize SNPs for further genetic mapping studies. Web address: <http://snpinfo.niehs.nih.gov/> .
- **TAGster**: a software package to select, evaluate and visualize LD tag SNPs for single or multiple populations. Website: <http://www.niehs.nih.gov/research/resources/software/epidemiology/tagster/> . Written in Perl and R.
- **mPopTag**: a software tool to select or evaluate linkage disequilibrium (LD) tag SNPs for multiple populations. Website: <http://www.niehs.nih.gov/research/resources/software/mpoptag>. Written in Perl.

Book Chapters

1. Xuyu Zhuo, Ji-Qian Fang, Chuanhua Yu, **Zongli Xu** and Ying Lu “Meta-Analysis” *Advanced Medical Statistics*, World Scientific, 2003
2. **Zong-Li Xu**, Li Li, Ji-Qian Fang, “Statistical Analysis Methods for Genetics Data”. *Medical Statistics and Computer experiment*. Second edition. ShangHai Science and technology publishing house, 2001. (This is a textbook for graduate student recommended by the office in charge of graduate affairs in Chinese Education Ministry).
3. Zhao-Hai Li, Yu-Ming Xie, **Zong-Li Xu**, “Statistics in genetics”. *Advanced Medical Statistics*, People`s Medical publishing house, 2001
4. George Y.H. Chi, Kun Jin, Gang Chen, Lu Cui, **Zong-Li Xu**, “Some Statistical Issues of Relevance to Confirmatory Trials”. *Advanced Medical Statistics*, People`s Medical publishing house, 2001
5. Xu-Yu Zhou, **Zong-Li Xu**, Chuan-Hua Yu, “Meta analysis method”. *Advanced Medical Statistics*, People`s Medical publishing house, 2001
6. Ming Tan, **Zong-Li Xu**, “Describing Data, Variability and Over-Dispersion in Medical Research”. *Advanced Medical Statistics*, People`s Medical publishing house, 2001

Presentations at Scientific Meetings

1. **Zongli Xu**, Jack A. Taylor “Epigenome-wide DNA methylation changes in blood from infants with facial clefts in the Norway Facial Clefts Study” The American Society of Human Genetics (ASHG), at San Diego, October, 2014
2. **Zongli Xu**, Jack A. Taylor “Age-related DNA methylation changes in blood and other tissues relate to histone modification, stem cell gene repression, and cancer” The Biology of Genome, Cold Spring Harbor, New York, May, 2013
3. **Zongli Xu**, Jack A. Taylor “DNA methylation in blood is associated with breast cancer: A study in prospective samples from the Sister Study” Joint Statistical meeting, at San Diego, Aug, 2012
4. **Zongli Xu**, Jack A. Taylor “SNPinfo: Integrating GWAS and Candidate Gene Information into Functional SNP Selection for Genetic Association Studies” Human Genetics and Genomics, University of New England, Maine, July 19-24, 2009
5. **Zongli Xu** “SNPinfo: Integrating GWAS and Candidate Gene Information into Functional SNP Selection for Genetic Association Studies” School of Public Health, University of North Carolina at Chapel Hill. Sept. 24, 2009
6. **Zongli Xu**, Jack A. Taylor “Integrating GWAS and Candidate Gene Information into Functional SNP Selection for Genetic Association Studies” The Biology of Genome, Cold Spring Harbor, New York, May 8-12, 2008
7. **Zongli Xu**, Normal L. Kaplan, Jack A. Taylor. “mPopTag: Efficient Selection of LD tag SNPs in Single or Multiple Populations” The Biology of Genome, Cold Spring Harbor, New York, May 8-12, 2007
8. **Zongli Xu**, Normal L. Kaplan, Jack A. Taylor. “LD Tag SNPs Selection for candidate gene association studies using HapMap and gene resequencing data” The American Society of Human Genetics 56th Annual Meeting, New Orleans, Louisiana. October 9-13, 2006
9. **Zongli Xu**, Normal L. Kaplan, Jack A. Taylor. “LD Tag SNPs Selection for candidate gene association studies” The 3rd Annual International HapMap Project Community Analysis Meeting. Cambridge, Massachusetts, May 8-10, 2006
10. **Zongli Xu**, Fei Zou, Todd. J. Vision, “High resolution QTL mapping in genotypically selected samples from experimental crosses.” ENAR. Mar 28-31, 2004 Pittsburgh, USA.
11. Maria, **Zongli Xu**, Todd. J. Vision “The Genetic Architecture of crop Domestication: a Meta-analysis.” ASPB 2003: Mechanisms of Genetic Variation, October 22-26, 2003, Snowbird, Utah, USA
12. **Zong-Li Xu** “Meta analysis for linkage studies”. International Symposium on Mapping and Identification of Genes underlying complex diseases and traits. May 24-26, 2001 Changsha, China.