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CURRICULUM VITAE AND BIBLIOGRAPHY

EMPLOYMENT & TRAINING

- 2010 – Present. Staff Scientist, Epidemiology branch, National Institute of Environmental Health Sciences, Research Triangle Park, NC
- Oct. 2004 – 2010. Research Fellow, Epidemiology branch, National Institute of Environmental Health Sciences, Research Triangle Park, NC
- Jan. 2003 – Sep. 2004. Postdoctoral Research Associate, Computational Biology, University of North Carolina at Chapel Hill, NC

EDUCATION

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

RESEARCH INTERESTS

- Genetic epidemiology
- Epigenetics
- Bioinformatics & statistical genetics

BIBLIOGRAPHY

Articles:

1. 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.
2. 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.

3. **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.
4. 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
5. 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.
6. 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
7. **Zongli Xu**, Jack A. Taylor "Integrating GWAS and Candidate Gene Information into Functional SNP Selection for Genetic Association Studies" Nucleic Acids Research, 2009
8. 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 γH2A.X foci" Journal of Cancer Epidemiology , 2008
9. **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
10. **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.
11. 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
12. 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
13. 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
14. 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
15. Zou F, **Xu Z**, Vision T, "Assessing the Significance of Quantitative Trait Loci in Replicable Mapping Populations", Genetics. 2006, 174(2):1063-1068

16. **Zongli Xu**, Fei Zou, Todd. J.Vision, "High resolution QTL mapping in genotypically selected samples from experimental crosses." Genetics. 2005, 170(1):401-408
17. 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
18. 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
19. 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
20. **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 Biomathmatics**.** 2003, 18(2):176-181
21. **Zong-Li Xu,** Fang Jiqian, "A method of Bayesian linkage analysis on complex binary traits in general Pedigrees" Journal of Biomathmatics. 2003, 18(1):15-20
22. **Zong-Li Xu**, Ji-Qian Fang, "The statistical methods to synthesize linkage studies", Chinese Journal of preventive medicine, 2002, 36(3):196-198
23. 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
24. 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
25. **Zong-Li Xu**, Ji-Qian Fang, "Meta analysis for Linkage studies." Life Science Research, 2001, 5(4): 308-313
26. 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 Tools (Peer-reviewed):

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

- 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/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.

- 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://www.niehs.nih.gov/snpinfo/.

Programs written for publications

- LRmain.c: A modified code to perform permutation tests for marker regression in correlated data. Written in C.
- repPermu: To perform permutation test in repeated measure data of recombinant inbred (RI) line. Written with SAS Micro.
- Simuline: A simulation tool for evaluation of statistical methods. It can be used to simulate marker genotype data from several experimental design (F2, Backcross to P1, Backcross to P2, Recombinant Inbreed (RI1)) as well as repeated measure data for these experimental designs. Written in C++.

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

Abstracts:

1. **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
2. **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
3. **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

4. **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
5. **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.
6. 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
7. **Zong-Li Xu**, Ji-Qian Fang. "Meta analysis for linkage studies". International Symposium on Mapping and Identification of Genes underlying complex diseases and traits. May 24-26, 2001 Changsha, China.
8. Yu-Jing Fang, G Nell Thomas, Brian Tomlinson, **Zong-Li Xu**, Ji-Qian Fang, Jullan AJH Critchley. "Linkage analysis of the uncoupling protein 1 gene in Hong Kong Chinese with hypertensive family history." International Symposium on Mapping and Identification of Genes underlying complex diseases and traits. May 24-26, 2001. Changsha, China.