

# Curriculum Vitae

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### EDUCATION:

2004–2005	Postdoctoral	Bioinformatics	Department of Psychiatry, UT Health Science Center at San Antonio, San Antonio, TX
2002–2004	Postdoctoral	Statistical Genetics	Department of Statistics, University of Florida, Gainesville, FL
1994–1997	Ph.D.	Statistical Genetics	Zhejiang University, Hangzhou, China
1991–1994	M.Sc.	Quantitative Genetics	Zhejiang University, Hangzhou, China
1983–1985	Associate	Agronomy	Zhejiang University, Hangzhou, China

### PROFESSIONAL EXPERIENCE:

2019–	Research Professor, Department of Biostatistics, University of Florida, Gainesville, FL
2018–	Adjunct Professor, Department of Mathematics and Statistics, University of Arkansas at Little Rock, Little Rock, AR
2018–	Associate Member, Winthrop P. Rockefeller Cancer Institute, University of Arkansas for Medical Sciences, Little Rock, AR
2018–2019	Professor of Biostatistics, Department of Pediatrics, University of Arkansas for Medical Sciences, Little Rock, AR
2016–2018	Associate Professor of Biostatistics, Department of Pediatrics, University of Arkansas for Medical Sciences, Little Rock, AR
2015–2016	Associate Professor, Department of Biostatistics and Bioinformatics, Tulane University, New Orleans, LA

2013–2015	Scientist, UAB Comprehensive Cancer Center, Cancer Control and Population Science Program
2009–2015	Associate Professor, Department of Biostatistics/Department of Medicine, University of Alabama at Birmingham, Birmingham, AL
2006–2009	Assistant Professor, Department of Psychiatry and Neurobehavioral Sciences, University of Virginia, Charlottesville, VA
2005–2006	Research Associate, Department of Psychiatry and Neurobehavioral Sciences, University of Virginia, Charlottesville, VA
1997–2002	Assistant Professor, Department of Agronomy, Zhejiang University, Hangzhou, China
1993–1996	Teaching Assistant, Department of Agronomy, Zhejiang University, Hangzhou, China
1988–1994	Research Assistant, Maize Research Institute, Zhejiang Agricultural Science Academy, Dongyang, China
1985–1988	Teacher, Shanglu High School, Dongyang, China

#### **RESEARCH INTERESTS:**

1. **Statistical Genetics:** Development of innovative statistical methodology for genetic and genomic studies of complex traits in humans, plants and animals (e.g., joint linkage and association mapping method, GMDR for detecting gene-gene and gene-environment interactions)
2. **Bioinformatics:** Development of novel computationally efficient bioinformatics tools scaled to large data sets for data mining that aim at hypothesis exploration and discovery (e.g., querying pathway and ontology databases and *in silico* mapping)
3. **Genetic Epidemiology:** Planning study design and performing data analysis of genetic epidemiological studies for complex human disorders using both linkage and association approaches (e.g., genome-wide association studies)
4. **Biostatistics:** Clinical trial design, longitudinal data analysis, survival analysis, latent variable analysis and mixture modeling
5. **Computational Biology:** Development and application of algorithms or models to process biological data for understanding living system and relationships among various biological systems
6. **Population Genetics:** Development and application of new statistical approaches to genetic population inference, DNA structure analysis, genetic diversity evaluation, and paternity inference through mathematical and population genetic bridges such as coalescence model and phylogeny construction
7. **Genetics and Epigenetics of Birth Defects, Drug Addictions, and other Psychiatric Disorders:** Application of the specialized state-of-the-art methods to identification of genetic and environmental risk factors underlying birth defects, drug addictions, and other

psychiatric disorders

8. Biological Mechanisms and Nature-Nurture Interactions underlying Child Health and Development: Applying high-throughput biotechnologies and bioinformatics tools to decipher the mechanisms by which maternal-child nutrition and physical activity optimize health and development
9. Plant Genetics and Breeding: Principles of plant genetics and breeding, theory of heterosis, selection theory, genetic analysis in plant breeding, genetic resource and germplasm preservation, molecular breeding, maize breeding

#### **HONORS AND AWARDS:**

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|------|---|
| 1993 | 1991–1993 excellent graduate student award (top ~5% of graduate students)   |
| 1994 | Early admission to Ph.D. program through competition (top ~5% of graduate students)   |
| 2007 | The 1 <sup>st</sup> prize of Zhejiang Province's Science and Technology Award in 2006 (Title: Genetic model and analysis methods for diallel designs and germplasm resource exploration; Authors: Jun Zhu, Jin Hu, Haiming Xu, <b>Xiang-Yang Lou</b> , Daofan Ji) |

#### **PROFESSIONAL MEMBERSHIPS:**

Member, American Society of Human Genetics  
Member, International Genetic Epidemiology Society  
Member, Association of Chinese Geneticists in America  
Member, International Chinese Statistical Association  
Member, Genetics Society of China  
Member, Biomathematics Society of China  
Member, Central Arkansas Chapter (CASA) of ASA

#### **OTHER PROFESSIONAL ACTIVITIES:**

Panelist, National Science Foundation (NSF) Review Panel  
NIH-BGES (Behavioral Genetics and Epidemiology Study Section)  
NIH Special Emphasis Panel/Scientific Review Group ZRG1 PSE-P 55  
Member, Natural Science Foundation of China (NSFC) Review Panel  
*Ad hoc* Grant Reviewer, National Science Foundation (NSF)  
*Ad hoc* Grant Reviewer, Experimental and Translational Medicine Research Committee, Scottish Government  
*Ad hoc* Grant Reviewer, Israel Science Foundation  
*Ad hoc* Grant Reviewer, The Wellcome Trust/DBT India Alliance

*Ad hoc* Grant Reviewer, UAB CCTS/COCD Translational Research Intramural (Pilot) Grant Program

Guest Associate Editor, *Statistics and Its Interface*

Guest Editor, *BioMed Research International*

Editor, *Biometrics & Biostatistics International Journal*

Editor, *Pediatrics & Neonatal Biology Open Access*

Review Editor, *Frontiers in Statistical Genetics and Methodology*

Editorial Board, *International Scholarly Research Network (ISRN) Applied Mathematics*

Editorial Board, *Dataset Papers in Science*

Editorial Board, *Journal of Medical Statistics and Informatics*

Editorial Board, *Austin Statistics*

Editorial Board, *Enliven: Biostatistics and Metrics*

Editorial Board, *International Journal of Clinical Biostatistics and Biometrics*

Editorial Board, *Ommega Journal of Pediatrics*

Program Committee Member, *IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2010)–Workshop on Data Mining for High Throughput Data from Genome-wide Association Studies; IEEE International Conference on Bioinformatics & Biomedicine (BIBM 2011)*.

Journal Reviewer for *American Journal of Human Genetics, PLoS Genetics, Bioinformatics, Genetic Epidemiology, Nucleic Acids Research, Journal of Theoretical Biology, Genetics, Theoretical and Applied Genetics, Statistical Applications in Genetics and Molecular Biology, Briefings in Bioinformatics, BMC Bioinformatics, BMC Genomics, BMC Genetics, PLoS One, Scientific Reports, Statistics and Probability Letters, Journal of Multivariate Analysis, Computational Statistics and Data Analysis, Journal of Biomedical Informatics, Theoretical Biology and Medical Modelling, Journal of Clinical Oncology, Molecular Psychiatry, Biological Psychiatry, Cancer Research, Journal of Alzheimer's Disease, Obesity, Human Genetics, Psychological Medicine, Drug and Alcohol Dependence, Behavioral and Brain Functions, Neural Regeneration Research, International Journal of Obesity, Journal of Obesity, American Journal of Translational Research, Molecular Genetics and Genomics, International Journal of Cancer, Genetica, Human Heredity, Frontiers in Statistical Genetics and Methodology, Current Genomics, Behavior Genetics, Genetics Research, Gene, International Journal of Molecular Sciences, Genetic Testing, Euphytica, Journal of Genetics, Journal of Insect Science, Scientific World Journal, International Scholarly Research Network (ISRN) Biomathematics, Austin Statistics, Australian Journal of Crop Science, Journal of Medical Statistics and Informatics, Rice, Meta Gene, Journal of Genetics and Genomics, Chinese Journal of Rice Science, Acta Agriculturae Zhejiangensis, Journal of Zhejiang Agricultural Sciences, Journal of Fujian Agriculture and Forestry, African Journal of Agricultural Research, African Journal of Plant Science, Journal of Metabolomics and Systems Biology*

## PUBLICATIONS:

1. **Lou XY**, Hou TT, Liu SY, Xu HM, Lin F, Tang XY, MacLeod SL, Cleves MA, Hobbs CA (2020). Innovative approach to identify multi-genomic and environmental interactions associated with birth defects in family-based hybrid designs. *Genetic Epidemiology* (accepted)
2. Ballard H, Fuell W, Elwy R, **Lou XY**, Albert GW (2020). Effects of growth hormone therapy in pediatric patients with growth hormone deficiency and Chiari I malformation: A retrospective study. *Child's Nervous System* 36 (4): 835–839. PMID: 31502034
3. Li T, Badger TM, Bellando BJ, Sorensen ST, **Lou XY**, Ou XW (2020). Brain cortical structure and executive function in children may be influenced by parental choices of infant diets. *American Journal of Neuroradiology* (in press). PMID: 32527846
4. Tang X, Andres A, West DS, **Lou XY**, Krukowski RA (2020). Eating behavior and weight gain during pregnancy. *Eating Behaviors* 36: 101364. PMID: 32032810
5. Xu T, Monir M, **Lou XY**, Xu HM, Zhu J (2020). Conditional and unconditional genome-wide association study reveal complicate genetic architecture of human body weight and impacts of smoking. *Scientific Reports* 10: 12136. PMID: 32699216; PMCID: PMC7376032
6. Lin F, Qi G, Xu T, **Lou XY**, Hong YB, Xu HM (2020). Joint association analysis method to dissect complex genetic architecture of multiple genetically related traits. *Crop Journal* (accepted).
7. Hou TT, Lin F, Bai S, Cleves MA, Xu HM, **Lou XY** (2019). Generalized multifactor dimensionality reduction approaches to identification of genetic interactions underlying ordinal traits. *Genetic Epidemiology* 43 (1): 24–36. PMID: 30387901 (the senior author)
8. Feng K, Rowell AC, Andres A, Bellando BJ, **Lou XY**, Glasier CM, Ramakrishnaiah RH, Badger T, Ou X (2019). Diffusion tensor MRI of white matter of healthy full-term newborns: Relationship to neurodevelopmental outcomes. *Radiology* 292 (1): 179–187. PMID: 31161971; PMCID: PMC6614910
9. Jenkins MM, Almli LM, Pangilinan F, Chong JX, Blue EE, Shapira SK, White J, McGoldrick D, Smith JD, Mullikin JC, Bean CJ, Nembhard WN, **Lou XY**, Shaw GM, Romitti PA, Keppler-Noreuil K, Yazdy MM, Kay DM, Carter TC, Olshan AF, Voltzke K, Nascone-Yoder N, Finnell RH, Lupo PJ, Feldkamp NL, NISC Comparative Sequencing Program, The University of Washington Center for Mendelian Genomics, Nickerson DA, Bamshad MJ, Brody LC, Reefhuis J, and The National Birth Defects Prevention Study (2019). Exome sequencing of family trios from the National Birth Defects Prevention Study: Tapping into a rich resource of genetic and environmental data. *Birth Defects Research* 111 (20): 1618–1632. PMID: 31328417 PMCID: PMC6889076
10. Sharma NS, Lal CV, Li JD, **Lou XY**, Viera L, Abdalla T, King R, Sethi J, Kanagarajah P, Restrepo-Jaramillo R, Sales-Conniff A, Wei S, Jackson PL, Blalock JE, Gaggar A, Xu X (2018). The neutrophil chemoattractant peptide proline-glycine-proline is associated with

- acute respiratory distress syndrome (ARDS). *American Journal of Physiology-Lung Cellular and Molecular Physiology* 315 (5): L653–L661. PMID: 30091378.
11. Du XM, Liu SY, Sun JL, Zhang GY, Jia YH, Pan ZE, Xiang HT, He SP, Xia QJ, Xiao SH, Shi WJ, Quan ZW, Liu JG, Ma J, Pang BY, Wang LR, Sun GF, Gong WF, Jenkins JN, **Lou XY**, Zhu J, Xu HM (2018). Dissection of complicate genetic architecture and breeding perspective of cottonseed traits by genome-wide association study. *BMC Genomics* 19 (1): 451. PMID: 29895260.
  12. Liu C, Chu C, Zhang J, Wu D, Xu D, Li P, Chen Y, Liu B, Pei L, Zhang L, Liu S, Qi T, **Lou XY**, Li L (2018). *IRX3* is a genetic modifier for birth weight, adolescent obesity, and transaminase metabolism. *Pediatric Obesity* 13 (3): 141–148. PMID: 28316138.
  13. Xu X, Abdalla T, Bratcher PE, Jackson PL, Sabbatini G, Wells JM, **Lou XY**, Quinn R, Blalock JE, Clancy JP, Gaggar A (2017). Doxycycline improves clinical outcomes during cystic fibrosis exacerbations. *European Respiratory Journal* 49 (4): 1601102. PMID: 28381428.
  14. **Lou XY** (2017). Hidden Markov model approaches for biological studies. *Biometrics & Biostatistics International Journal* 5 (4): 00139.
  15. Zhang YX, Zhou LY, Shen XH, Chen DB, Wu WX, Zhan XD, Liu QE, Zhu AK, **Lou XY**, Xu HM, Cheng SH, Cao LY (2017). Genetic dissection of yield traits in super hybrid rice Xieyou9308 using both unconditional and conditional genome-wide association mapping. *Scientific Reports* 7 (1): 824. PMID: 28400567.
  16. **Lou XY** (2017). Hidden Markov models and their applications to biomedical studies. *Journal of Zhengzhou University (Medical Sciences)* 52 (3): 237–246.
  17. Xu HM, Xu LF, Hou TT, Luo LF, Chen GB, Sun XW, **Lou XY** (2016). GMDR: Versatile software for detecting gene-gene and gene-environment interactions underlying complex traits. *Current Genomics* 17 (5): 396–402. PMID: 28479868; PMCID: PMC5320543. (the senior author)
  18. Zhou LY, Liu SY, Wu WX, Chen DB, Zhan XD, Zhu AK, Zhang YX, Cheng SH, Cao LY, **Lou XY**, Xu HM (2016). Dissection of genetic architecture of rice plant height and heading date by multiple-strategy-based association studies. *Scientific Reports* 6: 29718. PMCID: PMC4942822.
  19. Yan Q, Weeks DE, Tiwari HK, Yi N, Zhang K, Gao G, Lin WY **Lou XY**, Chen W, Liu N (2016). Rare-variant kernel machine test for longitudinal data from population and family samples. *Human Heredity* 80 (3):126–138. PMID: 27161037; PMCID: PMC4940283.
  20. **Lou XY** (2015). UGMDR: A unified conceptual framework for detection of multifactor interactions underlying complex traits. *Heredity* 114 (3): 255–261. PMID: 25335557; PMCID: PMC4815578.
  21. Qi T, Cao YJ, Cao LY, Gao YM, Zhu SJ, **Lou XY**, Xu HM (2015). Dissecting genetic architecture underlying seed traits in multiple environments. *Genetics* 199 (1): 61–71. PMID: 25335503; PMCID: PMC4286693.

22. Xu HM, Jiang BB, Cao YJ, Zhang YX, Zhan XD, Shen XH, Cheng SH, **Lou XY**, Cao LY (2015). Detection of epistatic and gene-environment interactions underlying three quality traits in rice using high-throughput genome-wide data. *BioMed Research International* Vol. 2015: 135782. PMID: 26345334; PMCID: PMC4539430. (the co-senior author)
23. Park T, Van Steen K, **Lou XY**, Xiong M (2015) Statistical analysis of high-dimensional genetic data in complex traits (Editorial). *BioMed Research International* Vol. 2015: 564273. PMID: 26346557; PMCID: PMC4539419.
24. Yan Q, Tiwari HK, Yi N, Gao G, Zhang K, Lin WY, **Lou XY**, Cui X, Liu N (2015). A sequence kernel association test for dichotomous traits in family samples under a generalized linear mixed model. *Human Heredity* 79 (2): 60–68. PMID: 25791389; PMCID: PMC4825859.
25. Xu HM, Kong XD, Chen F, Huang JX, **Lou XY**, Zhao JY (2015). Transcriptome analysis of *Brassica napus* pod using RNA-Seq and identification of lipid-related candidate genes. *BMC Genomics* 16: 858. PMID: 26499887; PMCID: PMC4619414. (the co-senior author)
26. Yan Q, Weeks DE, Celedón JC, Tiwari HK, Li B, Wang X, Lin WY, **Lou XY**, Gao G, Liu N, Chen W (2015). Associating multivariate quantitative phenotypes with genetic variants in family samples with a novel kernel machine regression method. *Genetics* 201 (4):1329–1339. PMID: 26482791; PMCID: PMC4676518.
27. Chen GB, Liu N, Klimentidis YC, Zhu X, Zhi D, Wang X, **Lou XY** (2014). A unified GMDR method for detecting gene-gene interactions in family and unrelated samples with application to nicotine dependence. *Human Genetics* 133 (2): 139–150. PMID: 24057800; PMCID: PMC3947150. (the senior author)
28. Lin WY, **Lou XY**, Gao GM, Liu NJ (2014). Rare variant association testing by adaptive combination of p-values. *PLoS One* 9 (1): e85728. PMID: 24454922; PMCID: PMC3893264.
29. Xu HM, Sun XW, Qi T, Lin WY, Liu N, **Lou XY** (2014). Multivariate dimensionality reduction approaches to identify gene-gene and gene-environment interactions underlying multiple complex traits. *PLoS One* 9 (9): e108103. PMID: 25259584; PMCID: PMC4178067. (the senior author)
30. Qi T, Jiang BB, Zhu ZH, Wei CS, Gao YM, Zhu SJ, Xu HM, **Lou XY** (2014). Mixed linear model approach for mapping quantitative trait loci underlying crop seed traits. *Heredity* 113 (3): 224–232. PMID: 24619175; PMCID: PMC4815641. (the co-senior author)
31. Yi N, Xu S, **Lou XY**, Mallick H (2014). Multiple comparisons in genetic association studies: a hierarchical modeling approach. *Statistical Applications in Genetics and Molecular Biology* 13 (1): 35–48. PMID: 24259248; PMCID: PMC5003626.
32. Yan Q, Tiwari HK, Yi N, Lin WY, Gao G, **Lou XY**, Cui X, Liu N (2014). Kernel-machine testing coupled with a rank-truncation method for genetic pathway analysis. *Genetic Epidemiology* 38 (5): 447–456. PMID: 24849109; PMCID: PMC4073214
33. Jiang BB, Yu SZ, Xiao BG, **Lou XY**, Xu HM (2014). Constructing linkage map based on a four-way cross population. *Journal of Zhejiang University (Agriculture & Life Science)* 40

- (4): 387–396. PMID: PMC4274998
34. **Lou XY** (2014). Gene-gene and gene-environment interactions underlying complex traits and their detection (Mini-review). *Biometrics & Biostatistics International Journal* 1 (2): 00007. PMID: PMC4288817.
  35. Lin WY, Yi N, **Lou XY**, Zhi D, Zhang K, Gao G, Tiwari HK, Liu N (2013). Haplotype kernel association test as a powerful method to identify chromosomal regions harboring uncommon causal variants. *Genetic Epidemiology* 37 (6): 560–570. PMID: 23740760; PMID: PMC4116485.
  36. Zhu ZH, Hayart Y, Xiao BG, Yang J, Cao LY, **Lou XY**, Xu HM (2012). Statistical method for mapping QTLs for complex traits based on two backcross populations. *Chinese Science Bulletin* 57 (21): 2645–2654. PMID: PMC3924781.
  37. Li M, **Lou XY**, Lu Q (2012). On epistasis: A methodological review for detecting gene-gene interactions underlying various types of phenotypic traits. *Recent Patents on Biotechnology* 6(3): 230–236. PMID: 23003010.
  38. Chen GB, Zhu J, **Lou XY** (2011). A faster pedigree-based generalized multifactor dimensionality reduction method for detecting gene-gene interactions. *Statistics and Its Interface* 4 (3): 295–304. PMID: 21927640; PMID: PMC3173778. (the senior author)
  39. Xu HM, Wei CS, Tang YT, Zhu ZH, Sima YF, **Lou XY** (2011). A new mapping method for quantitative trait loci of silkworm. *BMC Genetics* 12: 19. PMID: 21276233; PMID: PMC3042969. (the senior author)
  40. Wu JX, **Lou XY**, Gonda M (2011). Stochastic deletion-insertion algorithm to construct dense linkage maps. *Statistics and Its Interface* 4 (3): 381–388. PMID: 21927641; PMID: PMC3173768.
  41. Chen GB, Xu Y, Xu HM, Li MD, Zhu J, **Lou XY** (2011). Practical and theoretical considerations in study design for detecting gene-gene interactions using MDR and GMDR approaches. *PLoS One* 6 (2): e16981. PMID: 21386969; PMID: PMC3046176. (the senior author)
  42. Wu JX, Jenkins JN, McCarty JC, **Lou XY** (2011). Comparisons of four approximation algorithms for large-scale linkage map construction. *Theoretical & Applied Genetics* 123 (4): 649–655. PMID: 21611760; PMID: PMC3172867.
  43. Chen GB, Ingram KH, de los Campos G, Yi NJ, **Lou XY**, Pomp D, Allison DB (2011). A two-step modeling strategy for testing and estimating genetic susceptibility to the ill-effects of adiposity: Illustration in an outbred F2 mice population. *International Journal of Obesity* 35: S21–S21.
  44. **Lou XY**, Allison DB (2011) Statistics in Human Genetics and Molecular Biology by REILLY, C. *Biometrics* 67: 1672–1673 (Book Reviews).
  45. Chi XF, **Lou XY**, Shu QY (2010). Combining DNA pooling with selective recombinant genotyping for increased efficiency in fine mapping. *Theoretical & Applied Genetics* 120 (4): 775–783. PMID: 19898814; PMID: PMC2829194. (the senior author)



46. Li MD, Xu Q, **Lou XY**, Payne TJ, Niu T, Ma JZ (2010). Association and interaction analysis of variants in CHRNA5/CHRNA3/CHRNA4 gene cluster with nicotine dependence in African and European Americans. *American J Medical Genetics B Neuropsychiatric Genetics* 153B (3): 745–756. PMID: 19859904; PMCID: PMC2924635.
47. Dou BD, Hou BW, Xu HM, **Lou XY**, Chi XF, Yang JB, Wang F, Ni ZF, Sun QX (2009). Efficient mapping of a female sterile gene in wheat (*Triticum aestivum* L.). *Genetics Research* 91 (5): 337–343. PMID: 19922697.
48. Li MD, Mangold JE, Seneviratne C, Chen GB, Ma JZ, **Lou XY**, Payne TJ (2009). Association and interaction analyses of *GABBR1* and *GABBR2* with nicotine dependence in European- and African-American populations. *PLoS One* 4 (9): e7055. PMID: 19763258; PMCID: PMC2739294.
49. Chi XF, **Lou XY**, Yang MCK, Shu QY (2009). An optimal DNA pooling strategy for progressive fine mapping. *Genetica* 135 (3): 267–281. PMID: 18506582. (the senior author)
50. Shi CH, Shi Y, **Lou XY**, Xu HM, Zheng X, Wu JG (2009). Identification of endosperm and maternal plant QTLs for protein and lysine contents of rice across different environments. *Crop and Pasture Science (Australian Journal of Agricultural Research)* 60 (3): 295–301.
51. **Lou XY**, Chen GB, Yan L, Ma JZ, Mangold JE, Zhu J, Elston RC, Li MD (2008). A combinatorial approach to detecting gene-gene and gene-environment interactions in family studies. *American Journal of Human Genetics* 83 (4): 457–467. PMID: 18834969; PMCID: PMC2561932
52. Chen GB, Payne TJ, **Lou XY**, Ma JZ, Zhu J, Li MD (2008). Association of amyloid precursor protein-binding protein, family B, member 1 with nicotine dependence in African and European American smokers. *Human Genetics* 124 (4): 393–398. PMID: 18777128.
53. Li MD, **Lou XY**, Chen GB, Ma JZ, Elston RC (2008). Gene-gene interactions among *CHRNA4*, *CHRNA2*, *BDNF* and *NTRK2* in nicotine dependence. *Biological Psychiatry* 64 (11): 951–957. PMID: 18534558; PMCID: PMC2592606.
54. Chi XF, **Lou XY**, Shu QY (2008). Progressive fine mapping in experimental populations: An improved strategy toward positional cloning. *Journal of Theoretical Biology* 253 (4): 817–823. PMID: 18533192. (the senior author)
55. Li MD, Ma JZ, Payne TJ, **Lou XY**, Zhang D, Dupont RT, Elston RC (2008). Genome-wide linkage scan for nicotine dependence in European Americans and its converging results with African Americans in the Mid-South Tobacco Family sample. *Molecular Psychiatry* 13 (4): 407–416. PMID: 17579606.
56. Zheng X, Wu JG, **Lou XY**, Xu HM, Shi CH (2008). The QTL analysis on maternal and endosperm genome and their environmental interactions for characters of cooking quality in rice (*Oryza sativa* L.). *Theoretical & Applied Genetics* 116 (3): 335–342. PMID: 17989953.
57. Han LD, Xu HM, Zhu J, **Lou XY** (2008). Analysis of genetic effects of nuclear-cytoplasmic interaction on quantitative traits: Genetic models for seed traits of plants. *Theoretical & Applied Genetics* 116 (6): 769–776. PMID: 18283427.

58. Zheng X, Wu JG, **Lou XY**, Xu HM, Shi CH (2008). Mapping and analysis of QTLs on maternal and endosperm genomes for histidine and arginine in Rice (*Oryza sativa* L.) across environments. *Acta Agronomica Sinica* 34(3): 369–375.
59. **Lou XY**, Chen GB, Yan L, Ma JZ, Zhu J, Elston RC, Li MD (2007). A generalized combinatorial approach for detecting gene-by-gene and gene-by-environment interactions with application to nicotine dependence. *American Journal of Human Genetics* 80 (6): 1125–1137. PMID: 17503330; PMCID: PMC1867100.
60. **Lou XY**, Ma JZ, Sun D, Payne TJ, Li MD (2007). Fine mapping of a linkage region on chromosome 17p13 reveals that *GABARAP* and *DLG4* are associated with vulnerability to nicotine dependence in European-Americans. *Human Molecular Genetics* 16 (2): 142–153. PMID: 17164261.
61. Beuten J, Ma JZ, Payne TJ, **Lou XY**, Dupont RT, Crews KM, Elston RC, Li MD (2007). Association of specific haplotypes of neurotrophic tyrosine kinase receptor 2 gene (*NTRK2*) with vulnerability to nicotine dependence in African-Americans and European-Americans. *Biological Psychiatry* 61 (1): 48–55. PMID: 16713586.
62. Beuten J, Ma JZ, **Lou XY**, Payne TJ, Li MD (2007). Association analysis of the protein phosphatase regulatory subunit B1 (*PPP1R1B*) gene with nicotine dependence in European- and African-American smokers. *American J Medical Genetics B Neuropsychiatric Genetics* 144 (3): 285–290. PMID: 17171661.
63. Li MD, Sun D, **Lou XY**, Beuten J, Payne TJ, Ma JZ (2007). Linkage and association studies in African- and Caucasian-American populations demonstrate that *SHC3* is a novel susceptibility locus for nicotine dependence. *Molecular Psychiatry* 12 (5): 462–473. PMID: 17179996.
64. **Lou XY**, Ma JZ, Yang MCK, Zhu J, Liu PY, Deng HW, Elston RC, Li MD (2006). Improvement of mapping accuracy by unifying linkage and association analysis. *Genetics* 172 (1): 647–661. PMID: 16172505; PMCID: PMC1456190.
65. **Lou XY**, Yang MCK (2006). Estimating effects of a single gene and polygenes on quantitative traits from a diallel design. *Genetica* 128 (1–3): 471–484. PMID: 17028974. (the senior author)
66. **Lou XY**, Ma JZ, Payne TJ, Beuten J, Crew KM, Li MD (2006). Gene-based analysis suggests association of the nicotinic acetylcholine receptor  $\beta$ 1 subunit (*CHRNB1*) and M1 muscarinic acetylcholine receptor (*CHRM1*) genes with vulnerability to nicotine dependence. *Human Genetics* 120 (3): 381–389. PMID: 16874522.
67. Li MD, Payne TJ, Ma JZ, **Lou XY**, Zhang D, Dupont RT, Crews KM, Somes G, Williams NJ, Elston RC (2006). A genomewide search finds major susceptibility loci for nicotine dependence on chromosome 10 in African Americans. *American Journal of Human Genetics* 79 (4): 745–751. PMID: 16960812; PMCID: PMC1592559.
68. **Lou XY**, Zhu J, Zhang QD, Zang RC, Chen YB, Yu ZL, Zhao YJ (2005). Genetic control of the *opaque-2* gene and background polygenes over some kernel traits in maize (*Zea mays* L.). *Genetica* 124 (2): 291–300. PMID: 16134340.

69. Li MD, Beuten J, Ma JZ, Payne TJ, **Lou XY**, Garcia V, Duenes AS, Crews KM, Elston RC (2005). Ethnic- and gender-specific association of the nicotinic acetylcholine receptor  $\alpha 4$  subunit gene (*CHRNA4*) with nicotine dependence. *Human Molecular Genetics* 14 (9): 1211–1219. PMID: 15790597.
70. **Lou XY**, Casella G, Todhunter RJ, Yang MCK, Wu R (2005). A general statistical framework for unifying interval and linkage disequilibrium mapping: Toward high-resolution mapping of quantitative traits. *Journal of the American Statistical Association* 100 (469): 158–171.
71. **Lou XY**, Casella G, Littell RC, Yang MCK, Johnson JA, Wu RL (2003). A haplotype-based algorithm for multilocus linkage disequilibrium mapping of quantitative trait loci with epistasis. *Genetics* 163 (4): 1533–1548. PMID: 12702696; PMCID: PMC1462520.
72. **Lou XY**, Todhunter RJ, Lin M, Lu Q, Liu T, Bliss SP, Casella G, Acland GM, Lust G, Wu RL (2003). The extent and distribution of linkage disequilibrium in Canine. *Mammalian Genome* 14 (8): 555–564. PMID: 12925888.
73. Lin M, **Lou XY**, Chang M, Wu RL (2003). A general statistical framework for mapping quantitative trait loci in nonmodel systems: Issue for characterizing linkage phases. *Genetics* 165 (2): 901–913. PMID: 14573497; PMCID: PMC1462782.
74. Wu RL, Ma CX, **Lou XY**, Casella G. (2003). Molecular dissection of allometry, ontogeny and plasticity: A genomic view of developmental biology. *BioScience* 53 (11): 1041–1047.
75. Liu PY, Zhu J, **Lou XY**, Lu Y (2003). A method for marker-assisted selection based on QTLs with epistatic effects. *Genetica* 119 (1): 75–86. PMID: 12903749.
76. Chi XF, Wu DX, **Lou XY**, Xia YW, Shu QY (2003). Comparative studies on the starch gelatinization characteristics of five cereal crops (in Chinese). *Acta Agrochemical Sinica* 29 (2): 300–304.
77. **Lou XY**, Zhu J (2002). Analysis of genetic effects of major genes and polygenes on quantitative traits. I. Genetic model for diploid plants and animals. *Theoretical & Applied Genetics* 104 (2–3): 414–421. PMID: 12582714.
78. **Lou XY**, Zhu J (2002). Analysis of genetic effects of major genes and polygenes on quantitative traits. II. Genetic models for seed traits of crops. *Theoretical & Applied Genetics* 105 (6–7): 964–971. PMID: 12582922.
79. Wu RL, **Lou XY**, Ma CX, Wang XL, Larkins BA, Casella G. (2002). An improved genetic model generates high-resolution mapping of QTL for protein quality in maize endosperm. *Proceedings of the National Academy of Sciences of the United States of America* 99 (17): 11281–11286. PMID: 12177407; PMCID: PMC123248.
80. Cao LY, **Lou XY**, Si HM, He LB, Sun ZX (2002). Comparison between two methods of establishing DH population for mapping *lox-3* gene in rice (*Oryza sativa* L.) (in Chinese). *Hereditas* (BEIJING) 24 (2): 159–162. PMID: 16118132.
81. Yu ZL, Zhao JH, **Lou XY** (1999). Analyses of genetic effects on kernel traits in maize (*Zea mays* L.) (in Chinese). *Zhejiang Agricultural Science* 99 (4): 171–174.

82. **Lou XY**, Zhu J, Zhang QD, Zang RC, Chen YB (1998). A genetic study on the effects of *opaque-2* and polygenes on kernel quality traits in maize. In: Chen LS, Ruan SG, Zhu J (eds), *Advanced Topics in Biomathematics: Proceedings of International Conference on Mathematical Biology*, Singapore: World Scientific Pub Co pp 143–148.
83. **Lou XY**, Zhang QD, Yu ZL, Zhao JH (1998). Studies on genetic effects of some quantitative ear traits in maize (*Zea mays* L.) (in Chinese). *Zhejiang Agricultural Science* 98 (1): 21–24.

#### **MANUSCRIPTS IN SUBMISSION OR PREPARATION:**

1. **Lou XY**. Generalized Multifactor Dimensionality Reduction (GMDR) (Book chapter, Cambridge University Press, submitted and expected to appear in 2016).
2. Sinumporn S, Zhang YX, Zhang PP, Chen YY, Anis GB, Wu WX, Cao YR, **Lou XY**, Cheng SH, Cao LY. A nonsynonymous mutation of *ONAC43* causes early leaf senescence in rice. *Plant Molecular Biology*.
3. Cheng AQ, **Lou XY**, Xu HM, Lai CQ, Zhu J. Impacts of Physical Activities on Genetic Architecture of Epistasis and Ethnic-Specific Effects of Calibrated Factor VIII Level in the Multiethnic Study of Atherosclerosis (MESA). (to be submitted).
4. Wang LW, **Lou XY**, Xu HM, Lai CQ, Zhu J. Dissecting impacts of nutrition on epistasis and ethnicity-specific effects of calibrated factor VIII level in the multiethnic study of atherosclerosis (MESA) (to be submitted).
5. Zhang B, **Lou XY**, Zhu J. Impact of gender and cigarette on genetic architecture of BMI. (in preparation).
6. Lou XY, Ma JZ, Payne TJ, Chen GB, Niu T, Wang J, Li MD. Searching susceptibility loci for nicotine dependence through a pathway-based association analysis approach.

#### **GRANT SUPPORT:**

##### *Grant support as PI or Co-PI*

Principal Investigator (07/15/2015–08/31/2021), Division of Mathematical Sciences, NSF (No. DMS1462990/DMS1632985/DMS1701433/DMS2002865, \$1,545,157). “A telescopic algorithm for two-dimensional hidden Markov models with application to genetic studies”

Principal Investigator (01/27/2017–07/31/2020), UAMS Research Scholar Pilot Grant Awards in Child Health (271-G1-51898-01, \$50,000). “New statistical approach for studying interplays between maternal genes, child genes, environmental and lifestyle factors within a family-based hybrid design”

Principal Investigator (07/01/2008–03/31/2015), National Institute on Drug Abuse, NIH (No. R01DA025095, \$1,136,250). “Detection of multifactor interactions with application to nicotine dependence”

Co-PI (09/01/2011–08/31/2012), National Institute of General Medical Sciences, NIH (No. R01GM077490, \$1,250,000 from 09/01/2007 to 08/31/2012). “Genome-wide structured association testing and regional admixture mapping”

Principal Investigator (01/01/2001–12/31/2003), Natural Science Foundation of China (No. 30000097, RMB140,000). “Developing a mapping method for QTL with conditional genetic effect and the dynamic gene expressions of QTLs for some agronomic traits in rice (*Oryza sativa* L.)”

Principal Investigator (07/01/1999–12/31/2002), Zhejiang Education Commission Grant (No. 19990032, RMB20,000). “Mapping a storable gene (*lox-3*) in rice (*Oryza sativa* L.) and its utilization in breeding”

Principal Investigator (under revision), National Institute of General Medical Sciences, NIH (No. 1R01GM111482-01A1). “Innovative statistical frameworks for emerging challenges in family studies”

Co-Principal Investigator (under revision), National Institute of General Medical Sciences, NIH (No. 1R01GM114333-01). “Statistical methods for family-based whole genome sequence studies of complex human traits with application to Jackson Heart Study”

#### *Grant support as Co-I*

Co-Investigator (07/20/2018–05/31/2023), National Institute of Nursing Research (NINR), NIH (R01NR015988, \$424,498/\$641,638 first year direct/total). “Implementing a guidelines-based M-health intervention for high risk asthma patients”

Co-Investigator (08/10/2019–06/30/2024), Eunice Kennedy Shriver National Institute of Child Health and Human Development (NICHD), NIH (R01HD099099, \$399,102/\$605,004 first year direct/total). “Effects of maternal obesity and inflammation on offspring brain development”

Co-Investigator (04/01/2020–03/31/2022), National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK), NIH (R21DK122317, \$125,000/\$172,767 first year direct/total). “Phentermine/topiramate to end obesity and uric acid stones trial”

Biostatistician (09/01/2018–08/07/2023), United States Department of Agriculture-Agricultural Research Service (USDA-ARS). “Impact of early dietary factors on child development and health” (6026-51000-010-00-D)

Biostatistician (08/01/2013–07/31/2019), United States Department of Agriculture-Agricultural Research Service (USDA-ARS). “Impact of early dietary factors on child development and health” (6026-51000-010-00-D)/”Effects of diet and physical activity on maternal/child/adolescent health and development” (6026-51000-010-06-S)

Co-Investigator (09/01/2018-08/07/2023), National Center on Birth Defects and Developmental Disabilities (NCBDD), Centers for Disease Control and Prevention (CDC) (No. U01DD001229, \$995,000 first year total). “Component A: Arkansas proposal to participate in the birth defects study to evaluate pregnancy exposures (BD-STEPS II)”

Co-Investigator (04/01/2012–03/31/2018), Eunice Kennedy Shriver National Institute of Child Health and Human Development, NIH (No. R01HD039054, \$6,082,366). “Genomic/epigenomic factors and non-syndromic congenital heart defect risk”

Co-Investigator (09/01/2013–08/31/2018), National Center on Birth Defects and

- Developmental Disabilities (NCBDD), Centers for Disease Control and Prevention (CDC) (No. U01DD001039, \$641,630). “Birth Defects Study to Evaluate Pregnancy ExposureS (BD-STEPS)”
- Co-Investigator (12/01/2015–11/30/2018), DoD/PCRP/Idea Development Award (PC14030, \$330,750). “Effects of CD24-RCC2 signaling on prostate cancer metastasis”
- Co-Investigator (01/01/2017–12/31/2020), Natural Science Foundation of China (No. 31671570, RMB620,000 direct). “Study on new methods for association mapping and molecular design of complex traits by integrated analysis of multiple omics data”
- Co-Investigator (09/01/2012–08/31/2017), National Institute of Arthritis and Musculoskeletal and Skin Diseases, NIH (No. R01AR059781, \$3,687,250). “Epigenomewide DNA methylation study for osteoporosis risk”
- Co-Investigator (09/01/15–08/30/16), UAB Comprehensive Cancer Center NCTN-LAPS Program Translational Research Initiative Awards, “p53 and CD24 expression in localized prostate cancer to predict the risk of metastasis”
- Co-Investigator (01/01/2015–12/31/2016), Natural Science Foundation of China (No. 31470083, RMB300,000). “Development of new approach for association mapping of multiple traits and its application in breeding design”
- Co-Investigator (01/01/2013–12/31/2016), Natural Science Foundation of China (No.31271608, RMB700,000). “Developing new methods for analyzing genetic architecture and candidate genes for complex traits”
- Co-Investigator (07/01/2009–04/30/2014), National Institute on Drug Abuse, NIH (No. DA-12844, \$5,338,931). “Fine mapping susceptibility loci for nicotine dependence”
- Co-Investigator (03/01/2006–02/28/2009), National Institute on Drug Abuse, NIH (No. DA-12844, \$1,409,332). “Fine mapping susceptibility loci for nicotine dependence”
- Co-Investigator (09/01/2005–08/31/2006), National Institute on Drug Abuse, NIH (No. DA-12844, \$ 170,494). “Mapping of susceptibility loci for nicotine dependence”
- Co-Investigator (01/01/2006–12/31/2008), Natural Science Foundation of China (No. 30571198, RMB260,000). Project title “Genetic model for mapping embryo, endosperm and maternal plant QTLs underlying seed quality traits in cereal crops and its application to a rice breeding study”
- Co-Investigator (01/01/2005–12/31/2007), Natural Science Foundation of China (No. 30471067, RMB200,000). Project title “Identification of special genes in rice genome”
- Co-Investigator (01/2000–12/2002), Natural Science Foundation of China (No. 39970473). “Developing new methods for improving genetic population and predicting heterosis based on QTL effects”
- Co-Investigator (01/1999–12/2002), Key Project of Natural Science Foundation of China (39830250). “Studies on the mechanism of inheritance and environmental control for cereal quality traits in rice (*Oryza sativa* L.)”
- Co-Investigator (01/1998–12/2001), Important Project of Natural Science Foundation of

- China (39893354). “Developing genetic models and statistical methods for mapping QTLs”
- Co-Investigator (01/1999–12/2001), Natural Science Foundation of Zhejiang Province (398265). “Identification, location, and exploitation of important genes for cereal quality traits in *indica* rice”
- Co-Investigator (01/1997–12/1999), Natural Science Foundation of China (39670390). “Genetic mechanism of quantitative traits with developmental behavior in crop and their utilization”.
- Co-Investigator (01/1994–12/1996), Transcentury Training Program Foundation for the Talents of the National Education Commission of China. “Genetic studies on quantitative cereal quality traits in crop”
- Co-Investigator (01/1991–02/1994), Key Project of the Science and Technology Committee of Zhejiang Province in the 8<sup>th</sup> Five Year Plan. “Maize breeding”
- Co-Investigator (09/1988–12/1990), Key Project of the Science and Technology Committee of Zhejiang Province in the 7<sup>th</sup> Five Year Plan. “Maize breeding”

**PRESENTATIONS/PUBLISHED ABSTRACTS/POSTERS:**

- Unifying multilocus linkage and linkage disequilibrium mapping: A human model. Division of Biostatistics, School of Public Health, Yale University. May 18, 2004
- Unifying multilocus linkage and association mapping: A human model. Department of Epidemiology and Biostatistics, Case Western Reserve University School of Medicine. November 6, 2004
- GMDR: A novel strategy for detecting multifactor interactions. The 3<sup>rd</sup> International Conference of Quantitative Genetics, Hangzhou, Zhejiang, China. August 23, 2007 (<http://ibi.zju.edu.cn/icqg/programs.htm>).
- GMDR: A novel strategy for detecting multifactor interactions. Maize Research Institute, Zhejiang Agricultural Science Academy (Invited Speaker), Dongyang, Zhejiang, China. September 7, 2007.
- GMDR: A novel strategy for detecting multifactor interactions. Institute of Bioinformatics, Zhejiang University (Invited Speaker), Hangzhou, Zhejiang, China. September 29, 2007.
- Generalized MDR approaches to detecting multifactor interactions in population-based and family-based studies. Department of Biostatistics, University of Alabama at Birmingham, Birmingham, AL. October 20, 2008.
- Generalized MDR approaches to detecting multifactor interactions in population-based and family-based studies. Department of Psychiatry and Neurobehavioral Sciences, University of Virginia, Charlottesville, VA. December 5, 2008.
- Generalized combinatorial approaches to detecting multifactor interactions in population-based and family-based studies. The Joint Conference of the Society for Mathematical Biology and the Chinese Society for Mathematical Biology, Hangzhou,

Zhejiang, China. June 15, 2009 (<http://122.224.176.110:8080/program.htm>).

The meaning of interactions and the GMDR approach. China National Rice Research Institute (Invited Speaker), Hangzhou, Zhejiang, China. July 14, 2011.

The challenges and opportunities of statistical genetics in the post-genomic era. China National Rice Research Institute (Invited Speaker), Hangzhou, Zhejiang, China. August 25, 2012.

The challenges and opportunities of statistical genetics in the post-genomic era. Zhejiang A & F University (Invited Speaker), Hangzhou, Zhejiang, China. September 7, 2012.

GMDR: A conceptual framework for detection of multifactor interactions underlying complex traits. Michigan Technological University. Houghton, Michigan. February 26, 2014.

GMDR: A conceptual framework for detection of multifactor interactions underlying complex traits. Invited Session 201426 - Recent Advances in Statistical Genetics, organized by Taesung Park, Seoul National University. 2014 Joint Applied Statistics Symposium of International Chinese Statistical Association (ICSA) & Korean International Statistical Society (KISS). Portland Mariot Downtown Waterfront, Portland, OR, June 15–18, 2014

UGMDR: A unified conceptual framework for detection of multifactor interactions underlying complex traits. China National Rice Research Institute (Invited Speaker). Hangzhou, Zhejiang, China. December 26, 2014

UGMDR: A unified conceptual framework for detection of multifactor interactions underlying complex traits. Kansas State University. Manhattan, Kansas. February 23, 2015

UGMDR: A unified conceptual framework for detection of multifactor interactions underlying complex traits. George Washington University. Washington, DC. March 6, 2015

UGMDR: A unified conceptual framework for detection of multifactor interactions underlying complex traits. St. Jude Children’s Research Hospital. Memphis, TN. March 12, 2015

UGMDR: A unified conceptual framework for detection of multifactor interactions underlying complex traits. UC Riverside. Riverside, CA. April 28, 2015

Challenges in studying gene-gene and gene-environment interactions and the GMDR approach. Mississippi State University, Mississippi State, MS. August 19, 2015

The role of gene-gene and gene-environment interactions in biology and the GMDR approach. University of Arkansas for Medical Sciences. Little Rock City, AR. September 29, 2015

The role of gene-gene and gene-environment interactions in biology and the GMDR approach. Tulane University, New Orleans, LA, November 11, 2015

The versatile GMDR approach for identification of gene-gene and gene-environment interactions. 2016 International Chinese Statistical Association (ICSA)–China Statistics Conference, Qingdao, Shandong, China, June 24–25, 2016

New family-based association analytical framework for studying the interplays between maternal genes, child genes, and environmental factors: A generalized linear model/logistic approach. UAMS Pediatrics Biostatistics and Journal Club, Little Rock, AR. March 30, 2017



- GMDR: A machine learning method for identifying multifactor interactions. University of Florida, Gainesville, FL, February 11, 2019
- GMDR: A machine learning method for identifying multifactor interactions. University of Arkansas at Little Rock, Little Rock, AR, March 01, 2019
- GMDR: A machine learning method for identifying multifactor interactions. 16th Annual MidSouth Conference on Computational Biology and Bioinformatics (MCBIOS 2019), Birmingham, AL. March 28–30, 2019
- Health data ecosystem for improving outcome prediction. 2019 Zhejiang University Quantitative Genetics Symposium, Hangzhou, Zhejiang, China. May 24–26, 2019
- Li MD, **Lou XY**, Chen GB (2008). “Linkage Studies of Nicotine Dependence” at the Short Course on the Genetics and Epigenetics of Addiction (National Institute on Drug Abuse, Bethesda, MD, Mar 31–Apr 4, 2008)
- Lou XY**, Zhu J (2001). Analysis of genetic effects of major genes and polygenes on quantitative traits. The 2<sup>nd</sup> Meeting of Plant Genomics in China. Hangzhou, Zhejiang, China, August 2001.
- Lou XY**, Ma JZ, Yang MCK, Zhu J, Liu PY, Deng HW, Elston RC, Li MD (2005). Improvement of mapping accuracy by unifying linkage and association analyses. The 55<sup>th</sup> Annual Meeting of the American Society of Human Genetics, Salt Lake City, UT, October 25–29, 2005.
- Lou XY**, Ma JZ, Sun D, Payne TJ, Li MD (2006). Fine mapping of a linkage region on chromosome 17p13 reveals that GABARAP and DLG4 are associated with vulnerability to nicotine dependence in European-Americans”. The 56<sup>th</sup> Annual Meeting of the American Society of Human Genetics, New Orleans, LA, October 9–13, 2006.
- Li MD, Beuten J, Ma JZ, **Lou XY**, Payne TJ (2006). Association analysis of the protein phosphatase regulatory subunit B1 gene with nicotine dependence in European-Americans and African-Americans. 68<sup>th</sup> Annual Scientific Meeting of the College on Problems of Drug Dependence. Scottsdale, AZ.
- Li MD, Sun D, **Lou XY**, Beuten J, Payne TJ, Ma JZ (2006). Linkage and association studies in African- and Caucasian-American populations demonstrate that SHC3 is a novel susceptibility locus for nicotine dependence. Program No. 393.4. 2006 Neuroscience Meeting Planner. Atlanta, GA: Society for Neuroscience.
- Lou XY**, Chen GB, Yan L, Ma JZ, Zhu J, Elston RC, Li MD (2007). A generalized combinatorial approach for detecting gene by gene and gene by environment interactions. The 57<sup>th</sup> Annual Meeting of the American Society of Human Genetics, San Diego, CA, October 23–27, 2007.
- Chen GB, **Lou XY**, Yan L, Zhu J, Li MD (2007). GMDR: A package for detecting gene-by-gene and gene-by-environment interactions underlying complex traits. The 57<sup>th</sup> Annual Meeting of the American Society of Human Genetics, San Diego, CA, October 23–27, 2007.

- Li MD, **Lou XY**, Chen GB, Ma JZ, Elston RC (2007). Interactive Contributions of CHRNA4, CHRN2, BDNF and NTRK2 to Nicotine Dependence. The 57<sup>th</sup> Annual Meeting of the American Society of Human Genetics, San Diego, CA, October 23–27, 2007.
- Lou XY**, Chen GB, Yan L, Ma JZ, Zhu J, Elston RC, Li MD (2007). GMDR: A novel strategy for detecting multifactor interactions. The 3<sup>rd</sup> International Conference of Quantitative Genetics, Hangzhou, Zhejiang, China. August 19–24, 2007.
- Chi XF, **Lou XY**, Shu QY (2007). Optimizing DNA pooling strategy for progressive fine genetic mapping. The 3<sup>rd</sup> International Conference of Quantitative Genetics, Hangzhou, Zhejiang, China. August 19–24, 2007.
- Xu HM, Yang J, **Lou XY**, Shi CH, Zhu J (2007). Mixed model approach for mapping quantitative trait loci underlying crop seed traits. The 3<sup>rd</sup> International Conference of Quantitative Genetics, Hangzhou, Zhejiang, China. August 19–24, 2007.
- Lou XY**, Chen GB, Yan L, Mangold JE, Ma JZ, Zhu J, Elston RC, Li MD (2008). A generalized combinatorial approach for detecting gene by gene and gene by environment interactions. The 17<sup>th</sup> Annual Meeting of the International Genetic Epidemiology Society, St. Louis, Missouri, September 14–16, 2008.
- Chen GB, **Lou XY**, Xu HM, Xu Y, Zhu J, Li MD (2009). Power and design considerations for detecting gene-gene interactions: Analytical and simulation comparison of GMDR and MDR. The International Genetic Epidemiology Society 18<sup>th</sup> Annual Conference, Kahuku, Hawaii, October 18–20, 2009.
- Lou XY**, Ma JZ, Payne TJ, Chen GB, Niu T, Wang J, Li MD (2009). Searching susceptibility loci for nicotine dependence through a pathway-based association analysis. The 59<sup>th</sup> annual meeting of the American Society of Human Genetics (ASHG), Honolulu, Hawaii, October 20–24, 2009.
- Li MD, Mangold JE, Seneviratne C, Chen GB, Ma JZ, **Lou XY**, Payne TJ (2009). Association and interaction analyses of GABBR1 and GABBR2 with nicotine dependence in both European- and African-American populations. The 59<sup>th</sup> annual meeting of the American Society of Human Genetics (ASHG), Honolulu, Hawaii, October 20–24, 2009.
- Tucci M, **Lou XY**, Tiwari H, Guay-Woodford L (2010). Positional cloning of a novel glomerulocystic kidney disease gene. 2010 Pediatric Academic Societies' Annual Meeting, Vancouver, Canada, May 1–4, 2010.
- Chen GB & **Lou XY** (2010). A faster pedigree-based generalized multifactor dimensionality reduction method for detecting gene-gene interactions. UAB School of Public Health Research Day, Birmingham, AL, April 5, 2010.
- Li MD, Wang J, Niu T, Saadvandi J, Morris R, Ait-Daoud N, Campbell J, Haning W, Mawhinney J, Kahn R, Anderson A, Iturriaga E, **Lou XY**, Elkashef A, Johnson BA (2010). Transcriptome profiling and pathway analysis of genes differentially expressed in response to topiramate for treatment of methamphetamine dependence. The 72<sup>nd</sup> Annual Scientific Meeting of the College on Problems of Drug Dependence. Scottsdale, AZ, June 12–17, 2010.

- Chen GB, **Lou XY** (2010). MDR and Its Extensions for Identification of Interactions. The2010 SSG Retreat. Columbiana, AL. August 8–10, 2010.
- Chen GB, Zhu J, **Lou XY** (2010). A faster pedigree-based generalized multifactor dimensionality reduction method for detecting gene-gene interactions. The 60<sup>th</sup> annual meeting of the American Society of Human Genetics (ASHG), Washington, D.C., November 2–6, 2010.
- Tucci MC, **Lou XY**, Guay-Woodford LM (2010). Identification of a novel disease gene in dominantly transmitted glomerulocystic kidney disease. The 43rd Annual Meeting of American Society of Nephrology, Denver, CO, November 16–21, 2010. *Journal of American Society of Nephrology* 21: 2010 (SA-PO2451).
- Chen GB, Ingram KH, de los Campos G, Yi NJ, Lou XY, Pomp D, Allison DB (2011). A two-step modeling strategy for testing and estimating genetic susceptibility to the ill-effects of adiposity: Illustration in an outbred F2 Mice Population. *International Journal of Obesity* 35: S21.
- Chen GB & **Lou XY** (2011). A faster pedigree-based generalized multifactor dimensionality reduction method for detecting gene x gene interactions. UAB School of Public Health Research Day, Birmingham, AL, April 5, 2011.
- Lou XY**, Chen GB, Yan L, Liu N, Klimentidis YC, Zhu X, Zhi D, Wang X (2012). A PCA-based generalized multifactor reduction method for correcting population stratification. The 21<sup>st</sup> Annual IGES (the International Genetic Epidemiology Society) Conference, Stevenson, Washington, October 18–20, 2012.
- Lou XY**, Chen GB, Liu N, Klimentidis YC, Zhu X, Zhi D, Wang X (2012). A unified generalized multifactor reduction method for detecting gene-gene interactions in family and unrelated samples with application to nicotine dependence. The 62<sup>nd</sup> annual meeting of the American Society of Human Genetics (ASHG), San Francisco, California, November 6–10, 2012.
- Lou XY** (2013). GMDR: A conceptual framework for detection of multifactor interactions underlying complex traits. The 63<sup>rd</sup> annual meeting of the American Society of Human Genetics (ASHG), Boston, Massachusetts, October 22–26, 2013.
- Lin WY, **Lou XY**, Gao GM, Liu NJ (2013). Weighted combination of truncated P-values for rare casual variants detection. The 63<sup>rd</sup> annual meeting of the American Society of Human Genetics (ASHG), Boston, Massachusetts, October 22–26, 2013.
- Cheng A, **Lou XY**, Xu HM, Lai CQ, Zhu J (2014). Physical activities on epistasis and ethnicity specific effects of factor viii level in the multiethnic study of atherosclerosis. The Genomics of Common Diseases 2014. Bolger Center, Potomac, MD, USA, September 17–20, 2014.
- Abdallah T, **Lou XY**, King W, Li JD, Jackson PL, Blalock JE, Gaggar A, Xu X (2016). Neutrophil chemo attractant peptide proline-glycine-proline is increased in acute respiratory distress syndrome. The 2<sup>nd</sup> Annual Vanderbilt-UAB Pulmonary Research Summit, Birmingham, AL, USA, June 24–25, 2016.

Mercer KE, Pack LM, **Lou XY**, Thyfault J, Campbell C, Fiehn O, Chandler CJ, Burnett DJ, Souza EC, Casazza GA, Keim NL, Newman JW, Hunter GR, Fernandez JR, Garvey WT, Harper ME, Hoppel CL, Adams SH (2019). Weight loss and fitness intervention increase markers of hepatic bile acid (BA) synthesis, while reducing serum total BA concentrations in sedentary, obese insulin resistant women. *Experimental Biology 2019*, Orlando, FL, USA, April 6–9, 2019.

Jin S, Cao J, **Lou XY**, Ma W, Zong H, Gaggar A, Ma J, Xu X, Li Z (2019). The matrikine proline-glycine-proline as a potential new biomarker in colorectal cancer. 2019 American Society of Clinical Oncology (ASCO) Annual Meeting, Chicago, IL, USA, May 31–June 4, 2019.

#### **MENTORSHIP OR CO-MENTORSHIP**

Postdoctoral Fellow: Guo-Bo Chen (2010–2011), Amrit B. Karki (2012–2012), Haiming Xu (2017–2017)

Ph.D. Students: Guo-Bo Chen (2006–2009), Xiao-Fei Chi (2006–2008), Erdal Cosgun (2010–2010), Ting Qi (2012–2015), Man-Chong Leong (2020–), Xinyu Yan (2020–)

Master Students: Xiwei Sun (2012–2014), Tingting Hou (2015–2018), Shouye Liu (2015–2018), Qile Li (2020–), Shuqian Chen (2020–), Sabrina Khuntia (2020–)

Summer Interns: Haijun Wang (2017–2017)

Faculty member: Runhua Liu, M.D., Ph.D., Assistant Professor (Department of Genetics at UAB, 2013–2015); Colleen Kays Gutman, M.D., Clinic Assistant Professor (Department of Emergency at UF, 2020–)

#### **PH.D. THESIS COMMITTEES:**

Yun-Guo Gong (Zhejiang University, 2009), Fei Xu (Zhejiang University, 2009), Guo-Bo Chen (Zhejiang University, 2009), Ruiqi Cen (UAMS, 2018–), Taiwo A. Famuyiwa (UALR, 2019–), Chang Jiang (UF, 2020–), Meilin Jiang (UF, 2020–), Quran Wu (UF, 2020–)

#### **TEACHING ACTIVITIES:**

- UF PHC6937: Frontiers in Biostatistics (Guest lectures; Spring 2020)
- UAMS Interprofessional Education Faculty Development Workgroup (2017–2019)
- UAB BST775: Statistical Methods for Genetic Analysis I (Fall 2013)
- UAB BST626 & Lab: Data Management & Reporting with SAS (Fall 2013)
- UAB BST795: Faculty Research Area Seminar (Fall 2011)
- “Linkage Studies of Nicotine Dependence” at the Short Course on the Genetics and Epigenetics of Addiction, National Institute on Drug Abuse, Bethesda, MD, March

31–April 4, 2008 (with Dr. Ming D. Li)

- Graduate Courses (Zhejiang University, China):  
Advanced Population Genetics (1997–2002)  
Linear Models and Statistical Analysis Methods (1997–2001)
- Undergraduate Courses (Zhejiang University, China):  
Plant Breeding (1999–2000)  
Biostatistics (1993–2000)
- High School Student Course (Shanglu High School, Dongyang, China):  
Biology (1985–1988)

#### **ADMINISTRATIVE ACTIVITIES:**

- UF PPHP Diversity, Equity, & Inclusion Committee (2019–)
- UF Biostatistics Diversity, Equity, & Inclusion Committee, Chair (2020–)
- UAB SSG Journal Club, Chair (2009–2014)
- UAB SSG-NORC Professional Development Workshop Series (2010)
- Faculty Mentoring Committee for Dr. Runhua Liu (UAB Department of Genetics), Member

#### **SOFTWARE DEVELOPED:**

**GMDR**, Generalized Multifactor Dimensionality Reduction (available at <http://www.soph.uab.edu/ssg/software> and <http://ibi.zju.edu.cn/software>)

#### **PATENTS:**

**GMDR-GPU** software, Registration Number: CN2012SR014341

**A Mixed Model-based Approach for Mapping Quantitative Trait Loci underlying Crop Seed Traits**, Application Number: CN201310549029

#### **CONTINUING EDUCATION AND TRAINING:**

Short Course on Statistical Analysis for Genetic Epidemiology (S.A.G.E.), University of Virginia, Charlottesville, Virginia, U.S., December 11–14, 2006

High Performance and Parallel Computing Bootcamp, The University of Virginia Alliance for Computational Science and Engineering, University of Virginia, Charlottesville, Virginia, U.S., January 7–11, 2008

Short Course on the Genetics and Epigenetics of Addiction, National Institute on Drug Abuse, Bethesda, Maryland, U.S., March 31–April 4, 2008

Genome-wide Association: Analyze This! The Genes, Environment, and Health Initiative, NIH, Bethesda, Maryland, U.S., August 4–5, 2008

The 5th Annual University of Washington Center for Mendelian Genomics (UW-CMG) Data Analysis Workshop, University of Washington, Seattle, Washington, U.S., August 14–18, 2017

**COMPUTER SKILLS:**

Languages: BASIC, C/C++, Fortran, Java++

Packages: SAS, SPLUS/R, MATLAB, MATHEMATICA, SIGMAPLOT, PERL, EXCEL, WORD, POWERPOINT, LATEX, and most statistical genetics software packages

Systems: MS-DOS/WINDOWS, LINUX/UNIX