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ACADEMIC TRAINING

BS (Forestry)	Nanjing Forestry University, China	1984
MS (Forest Genetics)	Nanjing Forestry University, China	1987
Ph.D. (Quantitative Genetics)	University of Washington	1995
Post-doc Associate (Genomic Mapping)	University of Washington	1996
Post-doc Associate (Biotechnology)	North Carolina State University	1999
Post-doc Associate (Statistical Genetics)	North Carolina State University	2000

PROFESSIONAL APPOINTMENTS

2008-	Professor of Public Health Sciences, Pennsylvania State University
2008-	Director, Center for Statistical Genetics, Department of Public Health Sciences, Pennsylvania State University
2008-	Professor of Statistics, Pennsylvania State University
2008-	Full Member, Penn State Hershey Cancer Institute
2008	Visiting Fellow, Princeton University (January-August)
2008-2010	Courtesy Professor of Statistics, University of Florida
2007-2008	University of Florida Research Foundation Professor
2006-2008	Member of Genetics Institute, University of Florida
2003-2008	Associate Professor of Statistics, University of Florida
2000-2003	Assistant Professor of Statistics, University of Florida
1987-1990	Assistant Professor of Forestry, Nanjing Forestry University

RESEARCH INTERESTS

- Statistical Genetics and Genomics
- Systems Biology
- Bioinformatics
- Functional Data Analysis, Longitudinal Data Analysis
- Population, Quantitative, Developmental and Evolutionary Genetics
- Computational and Mathematical Biology

HONORS AND AWARDS

- ◆ Changjiang Distinguished Professor, Beijing Forestry University (2009-)
- ◆ Reviewer Board for Mathematical Reviews (2009-)
- ◆ Board of Scientific Committee, International Conference of Mathematical Sciences, Istanbul, Turkey, 4–10 August 2009
- ◆ Session Organizer for Statistical and Computational Genetics, Bio-IT World Congress of Genes, Fosan, China 6–8 December 2008
- ◆ Invited Speaker and Discussion Organizer, Beyond Genomes–Applying Systems Biology, Cambridge Healthtech Institute (2008)
- ◆ Paper on mapping developmental instability, awarded the second place of the Liang Xi Prize by the Chinese Society of Forestry (2008)

- ◆ Nominated by graduate students for Distinguished Teaching Award, UF (2008)
- ◆ University of Florida Research Foundation Professorship Award (2007)
- ◆ Gamma Sigma Delta Junior Faculty Award, the Honor Society of Agriculture (2006)
- ◆ Appointed Adjunct Distinguished Professor, Nanjing Forestry University (2005-)
- ◆ Appointed Adjunct Distinguished Professor, Zhejiang Forestry University (2002-)
- ◆ Outstanding Young Investigator Abroad Award (National Science Foundation of China). This prestigious award is only conferred to talented young Chinese scientists working abroad (2001)
- ◆ Appointed Adjunct Professor, Research Institute of Tropical Forestry (2001-)
- ◆ The Best Paper Award by the World Chinese Science and Technology Organization (1999)
- ◆ Training Award on Mathematical and Statistical Genetics by National Science Foundation. Department of Mathematical Sciences, Michigan Technological University (1999)
- ◆ Training Award on the Genetics of Non-Linear Dynamic Systems by the National Center for Research Resources. Center for Developmental and Health Genetics, Pennsylvania State University (1998)
- ◆ Appointed Adjunct Professor, Chinese Academy of Forestry (1998-2001)
- ◆ Appointed Adjunct Professor, Nanjing Forestry University (2002-2005)
- ◆ Fourth-class Scientific Invention Prize for high-yielding poplar hybrids (State Science and Technology Commission of China) (1994)
- ◆ Second-class Scientific and Extension Prize for fast-growing poplar hybrids (Ministry of Forestry of China) (1991)
- ◆ Research Excellence Award (State Economy Commission of China and State Science and Technology Commission of China) (1990)

Bibliographic Listings

- International Scientist of the Year for 2006, International Biographic Center of Cambridge, England, 2006
- Selected Biographee, Marquis Who's Who in the World, 2001-2009
- Selected Biographee, Madison Who's Who in the World, 2005-2007
- Selected Biographee, Who's Who in Medicine and Health, 2003
- Selected Biographee, Marquis Who's Who in 20th Century America, 2002

PROFESSIONAL MEMBERSHIPS

- American Association for the Advancement of Science (1996-)
- American Statistical Association (2001-)
- The Institute of Mathematical Statistics (2008-)
- American Society of Human Genetics (2008-)
- The Honor Society of Agriculture Gamma Sigma Delta (2004-)
- International Biometric Society (2000-2002)
- New York Academy of Sciences (1996)
- Genetic Society of America (1996)
- Botanical Society of America (1996-1997)

PROFESSIONAL ACTIVITIES

Editorial Service

Journal	Role	Date
<i>BMC Genetics</i>	Editorial Editor	2009-
<i>Journal of Pharmaceutical Statistics</i>	Guest Editor	2008-2009
<i>Journal of Probability and Statistics</i>	Associate Editor	2008-
<i>Molecular Pain</i>	Associate Editor	2008-
<i>Theoretical Biology and Medical Modeling</i>	Associate Editor	2008-
<i>Sankhya B</i>	Co-Editor	2008-
<i>Frontiers in Bioscience: Encyclopedia of Bioscience</i>	Managing Editor	2008-
<i>Zoological Research</i>	Editorial Board	2008-
<i>Recent Patents on Nanotechnology</i>	Editorial Board	2006-
<i>Recent Patents on Biotechnology</i>	Editorial Board	2006-
<i>Recent Patents on DNA and Gene Sequences</i>	Editorial Board	2006-

Book Reviewer

Book Title	Publisher	Date
Multivariate Statistics	Marcel Dekker	2003
Statistical Genetics	Cambridge University Press	2004
Regression Analysis	World Scientific Publisher	2007
Molecular Quantitative Genetics	CRC	2007
Advanced Genetics	Jones & Bartlett Publishers	2008

Journal Reviewer

Statistics journals	
<i>Biometrics</i>	5
<i>Computational Statistics and Data Analysis</i>	2
<i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i>	5
<i>Journal of the American Statistical Association</i>	3
<i>Journal of Applied Statistics</i>	1
<i>Journal of Computational and Graphical Statistics</i>	2
<i>Korean Journal of Statistics</i>	1
<i>Pacific Symposium on Biocomputing</i>	3
<i>Statistical Applications in Genetics and Molecular Biology</i>	2
<i>International Journal of Biostatistics</i>	2
Genetics/Genomics/Bioinformatics journals	
<i>American Journal of Human Genetics</i> (abstracts)	20
<i>Bioinformatics</i>	9
<i>BioScience</i>	1
<i>Biotechnology Progress</i>	1
<i>BMC Bioinformatics</i>	13
<i>BMC Genetics</i>	23

<i>BMC Genomics</i>	5
<i>Current Genetics</i>	2
<i>Current Genomics</i>	1
<i>European Journal of Human Genetics</i>	1
<i>Gene</i>	1
<i>Genes and Immunity</i>	1
<i>Genetic Epidemiology</i>	3
<i>Genetica</i>	23
<i>Genetical Research</i>	3
<i>Genetics</i>	26
<i>Genetics, Selection and Evolution</i>	3
<i>Genomics, Proteomics and Bioinformatics</i>	1
<i>Hereditas</i>	3
<i>Heredity</i>	17
<i>Human Heredity</i>	9
<i>International Journal of Plant Genomics</i>	2
<i>Journal of Heredity</i>	2
<i>Journal of Genetics and Genomics</i>	5
<i>Molecular Systems Biology</i>	2
<i>Nature Review Genetics</i>	1
<i>Pharmacogenetics</i>	1
<i>PLoS Genetics</i>	6
<i>The Pharmacogenomics Journal</i>	6
<i>Theoretical and Applied Genetics</i>	12
Natural Science journals	
<i>American Journal of Botany</i>	1
<i>American Naturalist</i>	1
<i>Annals of Botany</i>	2
<i>CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources</i>	1
<i>Canadian Journal of Botany</i>	2
<i>China Science Bulletins</i>	2
<i>Ecological Applications</i>	1
<i>Evolution</i>	3
<i>Growth</i>	1
<i>Journal of Neotropical Entomology</i>	1
<i>Journal of Theoretical Biology</i>	3
<i>Journal of Mathematical Biology</i>	1
<i>Lab Animal</i>	1
<i>Medical Science Monitor (International Reviewers Panel)</i>	1
<i>Molecular Ecology</i>	2

<i>Nature</i>	1
<i>Nature Clinical Practice Cardiovascular Medicine</i>	2
<i>Plant Cell Reports</i>	1
<i>Proceedings of the Indian National Science Academy, Part B</i>	1
<i>Science in China</i>	15
Agricultural and Forestry journals	
<i>Agronomy Journal</i>	1
<i>Animal</i>	1
<i>Canadian Journal of Forest Research</i>	9
<i>Crop Science</i>	5
<i>Euphytica</i>	5
<i>Field Crop Research</i>	2
<i>Forest Science</i>	1
<i>Journal of the American Horticultural Science Association</i>	1
<i>Journal of Animal Breeding and Genetics</i>	1
<i>Journal of Nanjing Forestry University</i>	2
<i>Journal of Sustainable Forestry</i>	1
<i>Journal of Zhejiang University</i>	4
<i>Molecular Breeding</i>	1
<i>Plant Breeding</i>	1
<i>Silvae Genetica</i>	1
<i>Scientia Silvae Sinicae</i>	1
<i>Tree-Structure and Function</i>	2
<i>Tree Genetics and Genomics</i>	4
<i>Tree Physiology</i>	4
Total: 76	280

Grant Reviewer

Agency	Σ
NIH GO Grants	4
NSF Environmental Genomics	1
NSF Integrative Organismal Biology	8
The Israel Science Foundation	2
NSF Biological Infrastructure	1
USDA Host-Pathogen Association Program	1
Netherlands Science Foundation	1
German Research Foundation	1
Canine Research Foundation	1
NSF Molecular and Cellular Biosciences	2
USDA Entomology and Nematology Program	2

USDA Plant Genetic Mechanisms Program	1
USDA Plant Genetic Mechanisms Program	1
USDA Plant Genome Program	1
Total: 14	22

Grant Panelist

- ◆ NIH/CSR/DMCM/GGG Special Emphasis Review Panel (2009)
- ◆ NIH/NHLBI Special Emphasis Review Panel (2009)
- ◆ National Natural Science Foundation of China, Life Sciences Program, Beijing (2006)
- ◆ National Natural Science Foundation of China, Life Sciences Program, Beijing (2005)
- ◆ National Natural Science Foundation of China, Life Sciences Program, Beijing (2003)
- ◆ NSF Statistics and Probability Program (2003)
- ◆ Invited Scriber of the National Academy of Sciences Workshop on Dynamical Modeling of Complex Biomedical Systems (2001)

PUBLICATIONS

A. BOOKS

- [1] **Wu, R. L.**, C.-X. Ma and G. Casella, 2007 *Statistical Genetics of Quantitative Traits: Linkage, Maps, and QTL*. Springer-Verlag, New York.
- [2] **Wu, R. L.**, and M. Lin, 2008 *Statistical and Computational Pharmacogenomics*. Chapman & Hall/CRC, London.
- [3] **Wu, R. L.**, S. Wu, and J. S. Yap, 2008 *High-Dimensional Statistical Genetics in Plants*. Springer-Verlag, New York (in press) (~300 pages).

B. PEER-REVIEWED PAPERS

Submitted

212. He, Q. L., Z. Wang, Y. Li, Y. Q. Guo, M. R. Huang, M. X. Wang and R. L. Wu, 2009 How to detect genes for plant structure, development, and evolution: Functional mapping meets ontology. *Molecular Systems Biology*.
211. Liu, T., A. Thalamuthu, J. J. Liu, C. Chen, Y. Li and **R. L. Wu**, 2009 Testing epistatic interactions of complex diseases in case-control studies. *Biostatistics*.
210. Fu, G. F., A. Berg and **R. L. Wu**, 2009 Genetic mapping of biological shapes. *Theoretical Biology and Medical Modeling*.
209. Fu, G. F., Z. Wang, J. H. Li, K. Das and **R. L. Wu**, 2008 Integrating differential equations into functional mapping. *Biophysical Journal*.

208. Li, J. H., Y. Li and **R. L. Wu**, 2008 A statistical model for estimating the double reduction of quantitative trait loci in autotetraploids. *Genetics Research*.
207. Luo, J. T., W. W. Hager, Z. Wang and **R. L. Wu**, 2009 Modeling the genetic control of drug resistance dynamics. *Drug Discovery Today*.
206. Li, H. Y., and **R. L. Wu**, 2008 A pattern-mixture model for functional mapping of quantitative trait nucleotides with non-ignorable dropout data. Manuscript.
205. Berg, A., Q. L. He, Y. Shen, Y. Chen, M. R. Huang and **R. L. Wu**, 2008 Multilocus disequilibrium analysis of multiallelic markers in outcrossing populations. *Genetics*.
204. Wu, S., and **R. L. Wu**, 2008 Genetic mapping of growth curves by minimizing intergrated square errors. Manuscript.
203. Wu, S., and **R. L. Wu**, 2008 Genetic mapping of complex traits by minimizing intergrated square errors. Manuscript.
202. Wu, S., and **R. L. Wu**, 2008 Genetic mapping of quantitative trait loci in a non-equilibrium population. Manuscript.
201. Yap, J. S., S. Wu, Y. Li and **R. L. Wu**, 2008 Genetic mapping of high-order epistasis in the mouse. Manuscript.
200. Yap, J. S., and **R. L. Wu**, 2008 Nonparametric covariance estimation in functional mapping of reaction norms to two environmental signals. Manuscript.
199. Li, Y., A. Berg, M. N. Chang, P. Du, K. Ahn, D. Mauger, D. P. Liao and **R. L. Wu**, 2009 A statistical model for genetic mapping of viral infection by integrating epidemiological behavior. *Statistical Applications in Genetics and Molecular Biology*.
198. Li, Q., Z. W. Huang, C. G. Wang, A. Berg, J. Y. Gai, Y. J. Huang and **R. L. Wu**, 2008 Semiparametric functional mapping of quantitative trait loci stimulating genotype-environment interactions for growth trajectories. *New Phytologist*.
197. Kim, B. R., W. Zhao and **R. L. Wu**, 2009 Wavelet-based functional clustering for high-dimensional dynamic gene expression patterns. *BMC Genomics*.

Accepted

196. Huang, Z. W., H. Y. Li, **R. L. Wu** and J. Y. Gai, 2009 Identification of quantitative trait loci for plant height growth trajectories in Soybean (*Glycine max* L. Merr.) using functional mapping. *BMC Genetics*.

195. Pinedo, P. J., C. D. Buergelt, G. A. Donovan, P. Melendez, L. Morel, **R. L. Wu**, T. Y. Langaee and D. O. Rae, 2009 Candidate gene polymorphisms (BoIFNG, TLR4, SLC11A1) as risk factors for paratuberculosis infection in cattle. *Preventive Veterinary Medicine*, www.elsevier.com/locate/prevetmed.
194. Luo, J. T., W. W. Hager and **R. L. Wu**, 2009 A differential equation model for functional mapping of genes affecting short-term virus dynamics. *Journal of Mathematical Biology*.
193. Li Y, and **R. L. Wu**, 2009 Modeling host-cancer genetic interactions with multilocus sequence data. *Journal of Computer Sciences and Systems Biology* **2**: 24–43.
192. Li, N., K. Das and **R. L. Wu**, 2009 Functional mapping of human growth trajectories *Journal of Theoretical Biology* (accepted).
191. Wang, X. F., C. W., Xu, **R. L. Wu** and B. A. Larkins, 2009 Molecular dissection of endosperm traits. *Trends in Plant Science* (accepted).
190. Chang, S.-W., S. H. Choi, K. Li, R. S. Fleur, C. Huang, T. Shen, K. Ahn, D. Gordon, W. Kim, **R. L. Wu**, N. R. Mendell and S. J. Finch, 2009 Growth mixture modeling as an exploratory analysis tool in longitudinal QTL analysis. *BMC Proceedings* (accepted).
189. Wen, S., C. G. Wang, A. Berg, Y. Li, M. M. Chang, R. B. Fillingim, M. R. Wallace, R. Staud, L. Kaplan and **R. L. Wu**, 2008 Modeling genetic imprinting effects of DNA sequences with multilocus polymorphism data. *Algorithms for Molecular Biology* (accepted).
188. Li, Y., and **R. L. Wu**, 2009 Functional mapping of growth and development. *Biological Reviews* (accepted).
187. Wu, S., T. Liu, H. Y. Li, T. M. Yin, S. Wullschleger, G. A. Tuskan and **R. L. Wu**, 2009 An improved approach for mapping quantitative trait loci in a pseudo-testcross design: Revisiting a poplar genome study. *Bioinformatics and Biology Insights* (accepted) (invited).
186. Li, Y., W. Hou, W. Zhao, K. Ahn, and **R. L. Wu**, 2009 Predicting drug response with functional mapping. In: *Systems Biology in Drug Discovery and Development* (D. L. Young and S. Michelson, eds). John Wiley & Sons, Inc.
185. Cheng, Y., A. Berg, S. Wu, Y. Li and **R. L. Wu**, 2009 Computing genetic imprinting expressed by haplotypes. *Methods in Molecular Biology* (accepted).
184. Liu, T., and **R. L. Wu**, 2009 A Bayesian algorithm for functional mapping of dynamic traits. *Algorithms* **2**: 667–691.

183. Yap, J., J. Fan and **R. L. Wu**, 2009 Nonparametric modeling of covariance structure in functional mapping of quantitative trait loci. *Biometrics* **65**: 00-00.
182. Li, J. H., Q. Li, W. Hou, K. Han, Y. Li, S. Wu, Y. C. Li and **R. L. Wu**, 2009 An algorithmic model for constructing a linkage and linkage disequilibrium map in open-pollinated progeny populations. *Genetics Research* **91**: 9–21.
181. Yang, J., **R. L. Wu** and G. Casella, 2009 Nonparametric functional mapping of quantitative trait loci. *Biometrics* **65**: 30–39.
180. Hou, W., Q. Li, Y. Li, J. H. Li and **R. L. Wu**, 2009 Multilocus genomics of outcrossing populations. *Theoretical Population Genetics* **76**: 68–76.
179. Wang, Z. H., Y. Li and **R. L. Wu**, 2009 Joint functional mapping of quantitative trait loci for HIV-1 and CD4⁺ dynamics. *International Journal of Biostatistics* Vol. 5: Iss. 1, Article 9. **DOI**: 10.2202/1557-4679.1136
178. Zhang, B., C. F. Tong, T. M. Yin, X. Y. Zhang, Q. Zhuge, M. R. Huang, M. X. Wang and **R. L. Wu**, 2009 Detection of quantitative trait loci influencing growth trajectories of adventitious roots in *Populus* using functional mapping. *Tree Genetics and Genomics* **5**: 539–552.
177. Li, Y. C., J. S. Wu, Y. R. Zeng and R. L. Wu, 2009 A statistical model for mapping imprinted quantitative trait loci. *Journal of Genetics and Genomics* (accepted).
176. Li, Q., and **R. L. Wu**, 2009 A multilocus model for constructing a linkage disequilibrium map in human populations. *Statistical Applications in Genetics and Molecular Biology* Vol. 8: Iss. 1, Article 18. **DOI**: 10.2202/1544-6115.1419.
175. Lin, M., A. Berg and **R. L. Wu**, 2009 Modeling the genetic etiology of pharmacokinetic-pharmacodynamic links with the ARMA process. *Statistical Applications in Genetics and Molecular Biology* Vol. 8: Iss. 1, Article 1.
174. Chang, M. R., **R. L. Wu**, S. Wu and G. Casella, 2009 Score statistics of quantitative trait locus mapping. *Statistical Applications in Genetics and Molecular Biology* Vol. 8: Iss. 1, Article 16. **DOI**: 10.2202/1544-6115.1386.
173. Wu, S., J. S. Yap, Y. Li, Q. Li, G. F. Fu, J. Luo, K. Das, A. Berg and **R. L. Wu**, 2009 A systems biology approach for dissecting plant development via functional mapping. *Current Bioinformatics* (accepted).
172. Pinedo, P. J., C. G. Wang, D. O. Rae and **R. L. Wu**, 2009 Risk haplotype analysis for bovine paratuberculosis. *Mammalian Genome* **20**: 124–129.

171. Zeng, Y. R., J. H. Li, C. G. Wang, M. M. Chang, R. Yang and R. L. Wu, 2008 Genetic mapping of quantitative trait loci. In: *Principles and Practices of Plant Genomics. I. Genome Mapping* (C. Kole and A. G. Abbott, eds). Science Publishers, Northants, UK (invited).
170. Wu, R. L., A. Berg and Q. Li, 2008 Comment on Why do we test multiple traits in genetic association studies. *Journal of the Korean Statistical Society* **38**: 11–13.
169. Liu, T., A. Berg, J. S. Wu, B. Zhang, Y. H. Cui, J. Luo and **R. L. Wu**, 2008 Haplotype analysis of complex traits in outcrossing tree species: Allele discovery of quantitative trait loci. In: *Poplar Genomics* (S. Joshi and S. DiFazio, eds.) Science Publishers, Northants, UK. (invited).
168. Li, Y. C., C. M. Coelho, T. Liu, S. Wu, Y. R. Zeng, Y. Li, B. Hunter, R. A. Dante, B. A. Larkins and **R. L. Wu**, 2008 A statistical strategy to estimate maternal-zygotic interactions and parent-of-origin effects of QTLs for seed development. *PLoS ONE* 3(9): e3131. doi:10.1371/journal.pone.0003131.
167. Hou, W., H. Y. Li, B. Zhang, M. R. Huang and **R. L. Wu**, 2008 A nonlinear mixed-effect mixture model for functional mapping of longitudinal traits. *Heredity* **101**: 321–328.
166. Pinedo, P. J., C. D. Buergelt, G. A. Donovan, P. Melendez, L. Morel, **R. L. Wu**, T. Y. Langaee and D. O. Rae, 2008 Association between CARD15/NOD2 gene polymorphisms and paratuberculosis infection in cattle. *Journal of Veterinary Microbiology* 134: 346–352.
165. Chen, Y. M., G. F. Fu and **R. L. Wu**, 2008 Integration of functional mapping and delay differential equations to map the genes that regulate circadian rhythms. *Bioinformatics, Computational Biology, Genomics and Chemoinformatics* 1: 118–125.
164. He, Q. L., Y. Shen, Y. Chen, Y. Zhou, A. Berg, **R. L. Wu** and M. R. Huang, 2009 Development of 16 polymorphic simple sequence repeat markers for *Lycoris longituba* from expressed sequence tags. *Molecular Ecology Resources* 9: 278–280.
163. Kim, B.-R., L. Zhang, A. Berg, J. Fan and **R. L. Wu**, 2008 A computational approach to the functional clustering of periodic gene expression profiles. *Genetics* **180**: 821–834.
162. Ma, C.-X., Q. B. Yu, A. Berg, G. F. Fu, J. S. Yap, A. X. Tan, M. Kirst, Y. H. Cui and **R. L. Wu**, 2008 A statistical model for testing the pleiotropic control of phenotypic plasticity of a count trait. *Genetics* **179**: 627–636.

161. Das, K., and **R. L. Wu**, 2008 A statistical model for the identification of genes governing the incidence of cancer with age. *Theoretical Biology and Medical Modeling* **5**: 7.
160. Wang, C. G., Y. Cheng, T. Liu, Q. Li, R. Fillingim, P. Wallace, R. Staud, L. Kaplan and **R. L. Wu**, 2008 A computational model for sex-specific genetic architecture of complex traits in humans. *Molecular Pain* **4**: 13.
159. Zhao, W., and **R. L. Wu**, 2008 Wavelet-based nonparametric functional mapping of longitudinal curves. *Journal of the American Statistical Association* **103**: 714-725.
158. Ma, C.-X., Y. Li and **R. L. Wu**, 2008 Modeling the genetic control of HIV-1 dynamics after highly active antiretroviral therapy. *Current Genomics* **9**: 208-211.
157. Cui, Y. H., **R. L. Wu**, G. Casella and J. Zhu, 2008 Nonparametric functional mapping quantitative trait loci underlying programmed cell death. *Statistical Applications in Genetics and Molecular Biology* **7**: 1, Article 4 (<http://www.bepress.com/sagmb/vol7/iss1/art4>).

2007

156. Wu, S., J. Yang and **R. L. Wu**, 2007 Semiparametric functional mapping of quantitative trait loci governing long-term HIV dynamics. *Bioinformatics* **23**: i569-i576.
155. Yang, R. Q., H. J. Gao, X. Wang, J. Zhang, Z.-B. Zeng and R. L. Wu, 2007 A semiparametric model for composite functional mapping of dynamic quantitative traits. *Genetics* **177**: 1859-1870.
154. Coelho, C. M., S. Wu, Y. Li, B. Hunter, R. A. Dante, Y. H. Cui, **R. L. Wu** and B. A. Larkins, 2007 Identification of quantitative trait loci that affect endoreduplication in *Zea mays* endosperm. *Theoretical and Applied Genetics* **115**: 1147-1162.
153. Li, H. Y., Z. W. Huang, S. Wu, J. Y. Gai, Y. R. Zeng and **R. L. Wu**, 2007 A conceptual framework to mapping quantitative trait loci governing ontogenetic allometry. *PLoS ONE* **2**(8): e1245. doi:10.1371/journal.pone.0001245.
152. Hou, W., J. S. Yap, S. Wu, T. Liu, J. M. Cheverud and **R. L. Wu**, 2007 Mapping quantitative trait nucleotides underlying complex traits in a controlled cross. *PLoS ONE* **2**(8): e732. doi:10.1371/journal.pone.0000732 (a UF news release on this paper).
151. Li, Y. C., Y. Li, S. Wu, K. Han, Z. J. Wang, W. Hou, Y. R. Zeng and **R. L. Wu**, 2007 Estimation of linkage disequilibria in diploid populations with multilocus dominant markers. *Genetics* **176**: 1879-1892.

150. Cui, Y., K. L. Sun, X. Fan and **R. L. Wu**, 2007 Mapping nucleotide sequences that encode complex binary disease traits with HapMap. *Current Genomics* **8**: 307-322.
149. Yap, J. S., C. G. Wang and **R. L. Wu**, 2007 A simulation approach for functional mapping of quantitative trait loci that regulate thermal performance curves. *PLoS ONE* **2**(6): e554. doi:10.1371/journal.pone.0000554.
148. Liu, T., X. L. Liu, Y. M. Chen and **R. L. Wu**, 2007 A unifying differential equation model for functional genetic mapping of circadian rhythms. *Theoretical Biology and Medical Modeling* **4**: 5.
147. Wu, S., J. Yang, C. G. Wang and **R. L. Wu**, 2007 A general quantitative genetic model for haplotyping a complex trait in humans. *Current Genomics* **8**: 343-350.
146. Wu, J. S., J. Zhu, Y. R. Zeng and **R. L. Wu**, 2007 Functional mapping of norm reactions to environmental signals. *Genetical Research* **89**: 27-38.
145. Liu, T., R. J. Todhunter, S. Wu, W. Hou, R. Mateescu, Z. W. Zhang, N. I. Burton-Wurster, G. M. Acland, G. Lust and **R. L. Wu**, 2007 A random model for mapping imprinted quantitative trait loci in a structured pedigree: An implication for mapping canine hip dysplasia. *Genomics* **90**: 276-284 (selected as a feature article).
144. **Wu, R. L.**, W. Hou, Y. H. Cui, H. Y. Li, T. Liu, S. Wu, C.-X. Ma and Y. R. Zeng, 2007. Mapping the genetic architecture of complex traits with molecular markers. *Recent Patents on Nanotechnology* **1**: 41-49 (invited review article).
143. Zhao, W., H. Y. Li, W. Hou and **R. L. Wu**, 2007 Wavelet-based parametric functional mapping of developmental trajectories. *Genetics* **176**: 1811-1821.
142. Wu, J. S., B. Zhang, Y. H. Cui, W. Zhao, M. R. Huang, Y. R. Zeng, J. Zhu, and **R. L. Wu**, 2007 Genetic mapping of developmental instability: Design, model and algorithm. *Genetics* **176**: 1187-1196.
141. Lin, M., W. Hou, H. Y. Li, J. A. Johnson and **R. L. Wu**, 2007 Modeling interactive quantitative trait nucleotides for drug response. *Bioinformatics* **23**: 1251-1257.
140. Cui, Y. H., J. M. Cheverud and **R. L. Wu**, 2007 A statistical model for dissecting genomic imprinting through genetic mapping. *Genetica* **130**: 227-239.

2006

139. Lin, M., and **R. L. Wu**, 2006 Detecting sequence-sequence interactions for complex diseases. *Current Genomics* **7**: 59-72.
138. Zhang, L., B. Mukherjee, M. Ghosh and **R. L. Wu**, 2006 Accounting for population stratification in case-control studies of genetic associations: A Bayesian model. *Statistical Modeling* **6**: 352-372.

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10. **Wu, R. L.**, and M. X. Wang, 1991 Economical genetic analysis of yield breeding in *Populus*: Technique for multi-trait selection. *Scientia Silvae Sinicae* **27**(2): 20-25.
9. Wang, M. X., M. R. Huang and **R. L. Wu**, 1990 New advance in genetic improvement of poplars. *World Forestry Research* (Beijing) **4**: 10-20.
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C. NON-REFERRED PUBLICATIONS

1992

1. **Wu, R.**, P. Glackin and R. F. Stettler. Quantitative genetics of a three-generation *Populus trichocarpa* × *P. deltoides* hybrid pedigree. *Proceedings of the Western Forest Genetics Association Annual Meeting*. University of Colorado, Boulder, CO (27-30 July 1992), pp. 61.

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4. **Wu, R.**, and R. F. Stettler. Developmental genetics of growth and canopy structure in a three-generation hybrid pedigree of *Populus*. *The Proceedings of the First International Poplar Symposium*. University of Washington, Seattle, WA (20-25 August 1995), pp. 68.
5. Bradshaw, H. D., Jr, **R. Wu** and R. F. Stettler. Field trials to identify quantitative trait loci underlying growth, morphology, and stress response in *Populus*. *The Proceedings of the First International Poplar Symposium*. University of Washington, Seattle, WA (20-25 August 1995), pp. 106-109.

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9. **Wu, R. L.**, and D. M. O'Malley. Statistical model for mapping quantitative trait loci using megagametophytes in conifer. *The Proceedings of International Conference on Plant & Animal Genome VI*. University of California at San Diego, CA, 16-22 January 1998.

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11. Grissom, J. E., **R. L. Wu**, D. M. O'Malley and S. E. McKeand. Response of loblolly pine (*Pinus taeda*) seedlings from diverse families to controlled nutrient supply. *The 25th Biennial Meeting of the Southern Forestry Tree Improvement Conference*. Louisiana State University, New Orleans, LA, 10-14 July 1999.

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15. Li, B. and **R. Wu**. 2000. Hybrid vigor and genetic mechanism of heterosis in aspen hybrids. *Hybrid Breeding and Genetics* (Eds M. Dieter and H. Dungey). Queensland Forestry Institute, Australia.

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17. **Wu, R. L.**, C. X. Ma and G. Casella. Functional mapping of complex traits: A theoretical framework. *The Proceedings of International Conference on Plant, Animal & Microbe Genome X*. University of California at San Diego, CA, 16-22 January 2002.
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20. Zhang, L, K. C. M., Yang, J. Booth and **R. L. Wu**. A statistical approach for estimating maternal-offspring interaction effects on seed development in autogamous

- plants. Summer Research Conference in Statistics 2003, "*Statistics in Genetics, Molecular Biology and Bioinformatics*". The Southern Regional Council on Statistics and the American Statistical Association. Hosted by the University of Georgia Jekyll Island, Georgia June 8-11, 2003 (poster).
21. Zhao, W., G. Casella and **R. L. Wu**. A dynamic model for the genetic origin of ontogenetic growth. Summer Research Conference in Statistics 2003, "*Statistics in Genetics, Molecular Biology and Bioinformatics*". The Southern Regional Council on Statistics and the American Statistical Association. Hosted by the University of Georgia Jekyll Island, Georgia June 8-11, 2003 (poster).
 22. **Wu, R. L.**, C.-X. Ma, X.-Y. Lou and G. Casella. Mapping allometry and ontogeny: A genomic view of evo-devo. Summer Research Conference in Statistics, 2003 "*Statistics in Genetics, Molecular Biology and Bioinformatics*". The Southern Regional Council on Statistics and the American Statistical Association. Hosted by The University of Georgia Jekyll Island, Georgia June 8-11, 2003.
 23. Kubik, C., S. Bonos, R. Wu and W. Meyer. Creeping bentgrass (*Agrostis stolonifera* L.) cultivar identification using simple sequence repeats. *Molecular Breeding of Forage and Turf, 3rd International Symposium*, Dallas, TX, May 18-22, 2003, p.71 (poster).
 24. **Wu, R. L.**, M. Lin, W. Zhao and G. Casella. A conceptual framework for cancer gene identification. An AACR Special Conference in Cancer Research, "*SNPs, Haplotypes, and Cancer: Applications in Molecular Epidemiology*", Sonesta Beach Resort Key Biscayne, Key Biscayne, Florida, September 13-17, 2003.
 25. Wang, Z. H., W. Zhao and **R. L. Wu**. A dynamic model for fine mapping of cancer growth. An AACR Special Conference in Cancer Research, "*SNPs, Haplotypes, and Cancer: Applications in Molecular Epidemiology*", Sonesta Beach Resort Key Biscayne, Key Biscayne, Florida, September 13-17, 2003

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26. Lin, M., and **R. L. Wu**. A statistical genetic model for integrating growth and development. *Eastern North American Region (ENAR) of the International Biometric Society*, Pittsburgh, PA, March 28-31, 2004.
27. Wang, Z. H., and **R. L. Wu**. A unifying model for fine mapping of quantitative trait loci affecting CD4⁺ T cell and HIV-1 dynamics under highly active antiretroviral therapy. *Eastern North American Region (ENAR) of the International Biometric Society*, Pittsburgh, PA, March 28-31, 2004.
28. Cui, Y. H., G. Casella and **R. L. Wu**. A two-stage hierarchical model for detecting the epistatic control of maternal-offspring QTL over endosperm development. *Eastern North American Region (ENAR) of the International Biometric Society*, Pittsburgh, PA, March 28-31, 2004.

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29. Liu, T., F. Long and **R. L. Wu**. Statistical models for functional mapping of circadian rhythms. *Eastern North American Region (ENAR) of the International Biometric Society*, Austin, Texas, March 21, 2005.

30. Long, F., T. Liu and **R. L. Wu**. Statistical models for clustering gene expression profiles. *Eastern North American Region (ENAR) of the International Biometric Society*, Austin, Texas, March 21, 2005.
31. Hou, W., C. Garvin and **R. L. Wu**. Likelihood formulation for estimating parent-of-origin effects with a family-based pedigree. *Eastern North American Region (ENAR) of the International Biometric Society*, Austin, Texas, March 21, 2005.
32. Zhao, W., W. Hou, R. C. Littell and **R. L. Wu**. Structured antedependence model for functional mapping. *Eastern North American Region (ENAR) of the International Biometric Society*, Austin, Texas, March 21, 2005.
33. Liu, X. L., **R. L. Wu** and G. Casella. Detecting differentially-expressed time course gene expression profiles. *Joint Statistical Meeting*, Minneapolis, MN August, 2005.
34. Liu, T., and **R. L. Wu**. Statistical model for mapping imprinted quantitative trait loci. Conference on Environmental Genomics, Epigenetics and Genetic Imprinting. Duke University, November 2-4, 2005 (poster).
35. Li, H. Y., and **R. L. Wu**. Statistical models for detecting quantitative trait nucleotides that encode cancer growth. The First Florida Genetics Symposium, University of Florida, December 2005 (poster).

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36. Kim, B.-R., R. C. Littell and **R. L. Wu**. Cataloguing periodic gene expression profiles. *Eastern North American Region (ENAR) of the International Biometric Society*, Tampa, Florida, March 21, 2006.
37. Li, H. Y., R. C. Littell and **R. L. Wu**. Functional mapping of quantitative trait loci with non-ignorable dropouts. *Eastern North American Region (ENAR) of the International Biometric Society*, Tampa, Florida, March 21, 2006.
38. Wu, S., J. Yang and **R. L. Wu**. A nonparametric model for mapping quantitative trait loci that affect HIV dynamics. *Joint Statistical Meeting*, Seattle, Washington, August, 2006.
39. Hou, W., and **R. L. Wu**. Nonlinear mixed-effect mixture models for functional mapping of longitudinal traits. *Eastern North American Region (ENAR) of the International Biometric Society*, Tampa, Florida, March 21, 2006.
40. Cui, Y. H., and **R. L. Wu**. Genomewide Functional Mapping for Genetic Control of Programmed Cell Death: A Semiparametric Model. *Eastern North American Region (ENAR) of the International Biometric Society*, Tampa, Florida, March 21, 2006.

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41. Hou, W., and **R. L. Wu**. Covariate Model for Studying Pharmacogenomic Architecture of Drug Response. *Eastern North American Region (ENAR) of the International Biometric Society*, Atlanta, Georgia, March 11 – 14, 2007.
42. Yap, J. S., and **R. L. Wu**. Nonparametric Modeling of Covariance Structure in Functional Mapping. *Eastern North American Region (ENAR) of the International Biometric Society*, Atlanta, Georgia, March 11 – 14, 2007.
43. Lin, M., and **R. L. Wu**. Haplotyping a Complex Trait in a Nonequilibrium Population. *Eastern North American Region (ENAR) of the International Biometric Society*, Atlanta, Georgia, March 11 – 14, 2007.

44. Li, H. Y., R. C. Littell, and **R. L. Wu**. Functional Mapping of Longitudinal Binary Traits. *Eastern North American Region (ENAR) of the International Biometric Society*, Atlanta, Georgia, March 11 – 14, 2007.
45. Wang, C. G., Q. Li and **R. L. Wu**. Allometrical Scaling of Functional Mapping for Genetic Network. *Eastern North American Region (ENAR) of the International Biometric Society*, Atlanta, Georgia, March 11 – 14, 2007.
46. Berg, A., D. Drost, E. Novaes, M. Kirst and **R. L. Wu**. An Epistatic Model for Mapping Phenotypic Plasticity of a Count Trait. *The Third Florida Genetics Symposium*, University of Florida, Gainesville, FL, November 7 – 8, 2007 (**poster**).
47. Wang, C. G., A. Berg, Q. Li and **R. L. Wu**. A Statistical Strategy for Mapping Imprinted Quantitative Trait Loci: Implications for Genetic Mapping in Mice. *The Third Florida Genetics Symposium*, University of Florida, Gainesville, FL, November 7 – 8, 2007 (**poster**).
48. Li, Y., J. H. Li, G. Casella and **R. L. Wu**. A statistical model for characterizing *cis*- and *trans*-acting regulation by eQTL. *The Third Florida Genetics Symposium*, University of Florida, Gainesville, FL, November 7 – 8, 2007 (**poster**).
49. Huang, Y. J., Q. Li, A. Berg, Z. W. Huang, C. G. Wang, J. Y. Gai and **R. L. Wu**. Using Mechanistic Growth Models to Map Quantitative Traits Loci for Developmental Timing and Duration. *The Third Florida Genetics Symposium*, University of Florida, Gainesville, FL, November 7 – 8, 2007 (**poster**).
50. Li, Q., Z. W. Huang, C. G. Wang, A. Berg, J. Y. Gai, Y. J. Huang and **R. L. Wu**. Functional Mapping: How to Study Genotype by Environment Interactions for Growth Curves. *The Third Florida Genetics Symposium*, University of Florida, Gainesville, FL, November 7 – 8, 2007 (**poster**).
51. Wu, S., T. Liu, J. S. Yap, W. Hou and **R. L. Wu**. Mapping Quantitative Trait Loci of Complex Traits Based on Zygotic Linkage Disequilibrium. *The Third Florida Genetics Symposium*, University of Florida, Gainesville, FL, November 7 – 8, 2007 (**poster**).
52. Day, K., and **R. L. Wu**. A Genetic Model for Predicting the Incidence of Cancer with Age. *The Third Florida Genetics Symposium*, University of Florida, Gainesville, FL, November 7 – 8, 2007 (**poster**).
53. Pinedo, P. J., C. D. Buergelt, **R. L. Wu**, A. Donovan, P. Melendez, E. Williams, L. Morel and O. Rae. Genetic Resistance to Johne's Disease: a Candidate Gene Case Control Study, Preliminary Results. *Phi Zeta Research Emphasis Day*, University of Florida, Gainesville, FL, June 15, 2007 (**Contributed**).
54. Wu, S., T. Liu, J. Yang, J. S. Yap, W. Hou and **R. L. Wu**. Mapping Quantitative Trait Loci of Complex Traits Based on Zygotic Linkage Disequilibrium. *The American Society of Human Genetics (ASHG) 57th Annual Meeting*, San Diego, CA, October 2007 (**Peer-reviewed**).
55. Hou, W., S. Wu, T. Liu, J. Yang, J. S. Yap and **R. L. Wu**. Modeling Genetic Imprinting of Quantitative Traits in Humans. *The American Society of Human Genetics (ASHG) 57th Annual Meeting*, San Diego, CA, October 2007 (**Peer-reviewed**).

2008

56. Li, J. H., and **R. L. Wu**. Genetic Mapping of Quantitative Trait Loci in Autotetraploids. *Eastern North American Region (ENAR) of the International Biometric Society*, Washington, D. C., March 16 – 18, 2008.
57. Li, Q., A. Berg and **R. L. Wu**. Mapping Quantitative Trait Nucleotides Encoding Complex Diseases in a Natural Population with Family Structure. *Eastern North American Region (ENAR) of the International Biometric Society*, Washington, D. C., March 16 – 18, 2008.
58. Wu, S., G. F. Fu, Y. M. Chen and **R. L. Wu**. Genetic Mapping by Minimizing Integrated Square Errors. *Eastern North American Region (ENAR) of the International Biometric Society*, Washington, D. C., March 16 – 18, 2008.
59. Li, Y., J. H. Li and **R. L. Wu**. A Statistical Model for Characterizing Cis- and Trans-acting Regulation by eQTL. *Eastern North American Region (ENAR) of the International Biometric Society*, Washington, D. C., March 16 – 18, 2008.
60. Yap, J. S., and **R. L. Wu**. A spatiotemporal model for functional mapping. *Eastern North American Region (ENAR) of the International Biometric Society*, Washington, D. C., March 16 – 18, 2008.
61. Berg, A., and **R. L. Wu**. A Statistical Model for Testing the Epistatic Control of Phenotypic Plasticity for a Count Trait. *Eastern North American Region (ENAR) of the International Biometric Society*, Washington, D. C., March 16 – 18, 2008.
62. Liu, A. Thalamuthu, J. J. Liu, **R. L. Wu** and C. Chen. An Epistatic Model for Characterizing the Genetic Control of Complex Diseases in Case-Control Studies. *The American Society of Human Genetics (ASHG) 58th Annual Meeting*, Philadelphia, PA, November 11 to 15, 2008 (**Peer-reviewed**).

2009

63. Shen, L., J. Guo, Y. Li, Y. Li, A. Berg, **R. Wu** and Y. Zeng, 2008 Population Structure and Genetic Diversity in *Carya cathayensis* as Revealed by AFLP Analysis. Plant and Animal Genome XVII Conference, San Diego, California, January 10–14, 2009.

D. BOOK REVIEW

Quantitative Trait Loci: Protocols by Nicola J. Camp and Angela Cox. Xii + 359 pp. Totowa, NJ: Humana Press, 2002. *American Journal of Human Biology* **15**: 235-236 (2003).

GRANT SUPPORT

a. Funded Externally

Summary of external funding

<u>Funding Period</u>	<u>Grant Amount</u>	<u>Funding Agency/Title</u>	<u>Role</u>
08/2005-07/2010	\$3,631,453	NIH RO1/Sex-Related Genetic Influences on Pain and Analgesia	Co-PI
03/2006-02/2010	\$855,000	NSF/NIH/Statistical Models	PI

		for Studying the Genetic Architecture of Dynamic Traits	
09/2006-08/2011	\$2,480,200	NIH R21/R33/University of Florida Chemosensory Clinical Research Program	Co-PI
10/2008-09/2010	\$696,523	DOE/USDA/Linkage Analysis Appropriate for Comparative Genome Analysis and Trait Selection in Switchgrass	Co-PI
10/2003-09/2004	\$95,359	State of Florida/USF/Statistical models for unraveling and predicting genetic variation of anthrax pathogens: Implications for biodefense	PI
10/2001-09/2003	\$180,000	USDA/NRI QTL involved in suppression of Varroa mite reproduction on honey bees	Co-PI
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Total	\$7,942,535 (allocated to the Department Statistics: \$1,170,359)		

b. Funded Internally

Summary of internal funding

<u>Funding Period</u>	<u>Grant Amount</u>	<u>Funding Agency/Title</u>	<u>Role</u>
09/08-07/09	\$50,000	UF/IFAS Innovation Fund	Co-PI
09/07-08/08	\$7,000	Genetic Resistance to Johne's Disease: a Candidate Gene Case Control Study	Co-PI
06/07-05/10	\$3,000	University of Florida Research Foundation	PI
07/2006-06/2007	\$5,000	Hatch project/Theoretical genomics: Statistical models and applications	PI
07/2004-08/2005	\$30,000	IFAS Deans Fund/Statistical genetics	PI
08/2001-07/2005	\$80,000	Florida FIRST/Statistical genetics	PI
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Total	\$125,000		

INVITED PRESENTATIONS AND SEMINARS

1. “Statistical Methods for Estimating the Number of Genes Affecting a Quantitative Trait”. University of Washington/Washington State University Poplar Genetics Seminar Series, Seattle, WA, November, 1991
2. “Quantitative Genetics of Growth in Populus”. University of Washington/Washington State University Poplar Genetics Seminar Series, Seattle, WA, September 1992
3. “Quantitative Genetics of Leaf Variation in Populus”. University of Washington/Washington State University Poplar Genetics Seminar Series, Seattle, WA, December 1994
4. “Quantitative Genetics of Canopy Traits”. University of Washington/Washington State University Poplar Genetics Seminar Series, Seattle, WA, September 1995
5. “Genome Mapping of Growth and Development in Forest Trees”. University of Minnesota, St. Paul, MN, December 1995
6. “Quantitative Genetics of Growth and Development in Populus”. University of Washington/Washington State University Poplar Genetics Seminar Series, Seattle, WA, April 1996
7. “Genome Mapping of Growth and Development in Forest Trees”. North Carolina State University, Raleigh, NC, April 1996
8. “Statistical Methods for Mapping a Quantitative Trait”. Nanjing Forestry University, Nanjing, China, July 1997
9. “Phenotypic Plasticity of Root Architecture in Loblolly Pine”. Nanjing Forestry University, Nanjing, China, September 1998
10. “The Application of Molecular Markers to Population Genetics”. Nanjing Forestry University, Nanjing, China, September 1998
11. “Molecular Dissection of Quantitative Traits in Forest Trees”. Purdue University, West Lafayette, December 1998
12. “The Application of Marker-assisted Selection to Forest Tree Breeding”. Purdue University, West Lafayette, December 1998
13. “Allometry, Ontogeny and Pleiotropy”. Plant Breeding Seminar Series, North Carolina State University, Raleigh, NC, May 1999
14. “Genome Mapping of Growth, Development and Phenotypic Plasticity in Forest Trees”. Chinese Academy of Forestry, Beijing, China, July 1999
15. “Genome Mapping of Growth, Development and Phenotypic Plasticity in Forest Trees”. Nanjing Forestry University, Nanjing, China, July 1999
16. “A Maximum Likelihood Approach for Mining Genes Affecting a Quantitative Character”. Department of Agronomy, Iowa State University, Ames, IA, February 2000
17. “A Maximum Likelihood Approach for Mining Genes Affecting a Quantitative Character”. Department of Experimental Statistics, Louisiana State University, Baton Rouge, LA, April 2000
18. “New Strategies for Molecular Dissection of Quantitative Traits”. *First National Conference on Quantitative Genetics in Plant and Animal Breeding*, Yangzhou University, Yangzhou, China, May 2000

19. "Posterior Probability for Characterizing Linkage Phases in Outcrossing Species". Nanjing Forestry University, Nanjing, China, May 2000
20. "A Maximum Likelihood Approach for Mining Genes Affecting a Quantitative Character". Nanjing Forestry University, Nanjing, China, May 2000
21. "Posterior Probability for Characterizing Linkage Phases in Outcrossing Species". Department of Statistics, University of California, Riverside, CA, June 2000
22. "Functional Mapping of Complex Traits Based on Biological Laws". Department of Biostatistics, University of Alabama, Birmingham, AL, September 2001
23. "Functional Mapping of Quantitative Trait Loci Affecting Growth Trajectories". Department of Statistics, University of Florida, Gainesville, FL, September 2001
24. "A Systems Approach for Mapping Complex Traits". Department of Agronomy, Zhejiang University, Huanzhou, China, June 2001
25. "A Systems Approach for Mapping Complex Traits". Research Institute of Tropical Forestry, Fuyang, China, June 2001
26. "A Systems Approach for Mapping Complex Traits". Beijing Forestry University, Beijing, China, June 2001
27. "A Systems Approach for Mapping Complex Traits". Northwest University of Science and Technology, Yanglin, China, June 2001
28. "Statistical Methods for Genome Mapping in Polyploids". Polyploid Genome Workshop in the Plant, Animal & Microbe Genome Conference X, San Diego, CA, January 2002
29. "Functional Mapping of Quantitative Traits: A Theoretical Framework". Forest Tree Genome Workshop in the Plant, Animal & Microbe Genome Conference X, San Diego, CA, January 2002
30. "Statistical Methods for Genome Mapping in Polyploids". Distinguished Lecture Series of Genome Science, Rutgers University, New Brunswick, NJ, April 2002
31. "QTL Mapping". Invited lecture for ZOO 6927 - Graduate Evolutionary Quantitative Genetics (Dr. Wayne), University of Florida, April 2002
32. "Strategies to Uncover Genetic Loci Underlying Inherited Traits in Natural and Experimental Pedigrees". Cornell University, Ithaca, NY, September 2002
33. "The Discovery of Genetic Loci Underlying Canine Hip Dysplasia". Cornell University, Ithaca, NY, September 2002
34. "Statistical Methods for Mapping Quantitative Traits in Experimental and Natural Populations". Zhejiang University, October 2002
35. "Statistical Methods for Mapping Quantitative Traits in Experimental and Natural Populations". Nanjing Forestry University, October 2002
36. "Statistics Meets Genomics: Mapping Genes for Life". Zhejiang Forestry College, October 2002
37. "Statistical Methods for Mapping Quantitative Traits in Experimental and Natural Populations". Zhejiang Forestry College, October 2002
38. "Mechanistic Mapping of Developmental Interactions". Xiangshan Scientific Conference, Beijing, December 2002

39. "Mapping allometry and ontogeny: A genomic view of evo-devo". Summer Research Conference in Statistics, 2003 "*Statistics in Genetics, Molecular Biology and Bioinformatics*". The Southern Regional Council on Statistics and the American Statistical Association, Jekell Island, Georgia, June 2003
40. "Genes regulating HIV-1 dynamics: A search algorithm". The 1st Symposium of Science & Engineering in Biomedicine. Amelia Island, FL, August 2003
41. "Unraveling the genetic machinery of complex traits". A Plenary Lecture for the 45th Anniversary of Zhejiang Forestry University. Zhejiang Forestry University, October, 2003
42. "Genes regulating HIV-1 dynamics: A search algorithm". Zhejiang University, October 2003
43. "A unifying model for fine mapping of quantitative trait loci affecting CD4⁺ T cell and HIV-1 dynamics under highly active antiretroviral therapy". Brown Bag Lunch Seminar Series, Department of Statistics at the College of Medicine, University of Florida, November 2003
44. Collaborative research on statistical models for QTL mapping at the University of Arizona, invited by Prof. Brian Larkins (invited)
45. "Sequencing Complex Traits With HapMap". Sequencing Complex Traits With HapMap". Nanjing Forestry University, July 2004
46. "Sequencing Complex Traits With HapMap". Sequencing Complex Traits With HapMap". The Institute of Applied Mathematics, Chinese Academy of Sciences, July 2004
47. "Linkage and Linkage Disequilibrium Mapping in Experimental and Nature Populations". College of Dentistry, University of Florida, October 2004 (invited by Dr. Roger Fllingim)
48. "Functional Mapping: Towards High-Dimensional Biology". Department of Statistics, University of Florida, October 2004
49. "A Conceptual Framework for Cancer Gene Identification". Conference on System Analysis, Data Mining and Optimization in Biomedicine. University of Florida, February 2005
50. "Mathematical and Statistical Models for Identifying Genetic Variants That Encode Drug Response". Fred Hutchinson Cancer Research Center, Seattle, WA, March 2005
51. "Mathematical and Statistical Models for Identifying Genetic Variants That Encode Drug Response". Medical College of Georgia, April 2005
52. "Linkage analysis and linkage disequilibrium mapping". Department of Epidemiology and Health Policy Research, University of Florida (invited by Sharon Johnatty), April 2005
53. "Mathematical and Statistical Models for Identifying Genetic Variants That Encode Drug Response". University of British Columbia, Vancouver, BC, April 2005 (cancelled)
54. "Linkage Disequilibrium Mapping". College of Medicine, University of Florida (invited by Dr. Lei Zou), April 2005
55. "Modeling the Genetic Control of Drug Response: Does Size Matter?" Duke University, August 2005

56. "Modeling the Genetic Control of Drug Response: Does Size Matter?" Shanghai Jiaotong University, September 2005
57. "Modeling the Genetic Control of Drug Response: Does Size Matter?" Nanjing Forestry University, October 2005
58. "Statistical Models for Mapping Imprinted Quantitative Trait Loci" Nanjing Forestry University, October 2005
59. "Mapping Genome-Genome Interactions" Nanjing Forestry University, October 2005
60. "Functional Mapping: Towards High-dimensional Biology" The Third National Genetics Symposium, Nanjing, October 2005
61. "Statistical Models for Detecting Quantitative Trait Nucleotides That Encode Cancer Growth". Department of Statistics and Probability, Michigan State University, November 2005
62. "Statistical Models for Mapping Imprinted Quantitative Trait Loci". The First Florida Genetics Symposium, University of Florida, December 2005
63. "Functional Mapping: Towards High-dimensional Biology" Nanjing University, June 2006
64. "Functional Mapping: Towards High-dimensional Biology" Tropical Institute of Forestry, June 2006
65. "A Conceptual Framework for Studying the Genetic Architecture of Biomass Partitioning" The Third International Poplar Symposium, Nanjing, China, June 2006 (plenary lecture)
66. "Model for Gene Identification of Cancers" Department of Molecular Genetics and Microbiology, University of Florida, November 2006
67. "Statistical Issues for Functional Mapping of Quantitative Trait Loci Underlying Dynamic Traits" Plant Genome XV Statistical Genomics Workshop, January 2007
68. "Functional Mapping: How to Study Genotype by Environment Interactions for Growth Curves" North Carolina State University, April 2007
69. "Statistical and Computational Pharmacogenomics" Chinese Academy of Sciences and Max-Planck Society in German, October 2007
70. "Functional Mapping: How to Study Genotype by Environment Interactions for Growth Curves" Nanjing Forestry University, October 2007
71. "A Semiparametric Model for Functional Mapping of Quantitative Trait Loci Affecting Dynamic Traits", Cleveland Clinic Foundation, February 2008
72. "Statistical and Computational Pharmacogenomics: Haplotype Discovery and Modeling" Case Western Reserve University, February 2008
73. "Statistical and Computational Pharmacogenomics: Haplotype Discovery and Modeling" University of South Carolina, February 2008
74. "Statistical and Computational Pharmacogenomics: Haplotype Discovery and Modeling" Statistics Day of Princeton, Princeton University, April 4, 2008
75. "Statistical and Computational Pharmacogenomics: Haplotype Discovery and Modeling" Pennsylvania State University College of Medicine, May 2008
76. "Statistical Genetics: Current Status and Our Opportunities" State University of New York at Stony Brook, May 2008
77. "Statistical Genetics: Current Status and Our Opportunities" Vanderbilt University, June 2008

78. “Statistical and Computational Pharmacogenomics: Haplotype Discovery and Modeling” Cambridge Healthtech Institute (CHI) Conference Applying Systems Biology, San Francisco, CA, June 9–11, 2008
79. “A Statistical Design for Predicting Drug Response with Pharmacogenomic Data”, University of North Carolina at Chapel Hill, October, 2008
80. “A Statistical Design for Predicting Drug Response with Pharmacogenomic Data”, Colorado State University, October, 2008
81. “Statistical Genetics: Current Status and Our Opportunities” State University of Colorado State University, October, 2008
82. “Statistical and Computational Pharmacogenomics” The 64th Deming Workshop on Applied Statistics, Atlantic City, NJ, December 2008
83. “Modeling Host-Cancer Genetic Interactions with Multilocus Sequence Data” Department of Public Health Sciences, Pennsylvania State University, February, 2009.
84. “Network Mapping of a Complex System” Department of Statistics, Pennsylvania State University, February, 2009.
85. “Network Mapping of a Complex System” St. Jude Children’s Research Hospital, Memphis, TN, March, 2009.
86. “Modeling Host-Cancer Genetic Interactions with Multilocus Sequence Data” Department of Molecular Genetics and Microbiology, University of Florida, February, 2009.

TEACHING EXPERIENCE

- *Quantitative Genetics*, an undergraduate course (60 students), Nanjing Forestry University, Spring 1988
- *Statistical Methodology for Mapping Quantitative Traits*, a short graduate course (20 students), Nanjing Forestry University, Summer 1997
- *Statistical Molecular Genetics*, a national workshop (15 participants), Chinese Academy of Forestry, Summer 1998
- *Statistical Genetics*, a graduate course, University of Florida, Spring 2002 - future
- Guiding a dozen of graduate students for their independent studies of statistical genetics, University of Florida, Summer 2003
- *Quantitative Genetics: Advanced Genetics* (20 students), University of Florida, Fall 2003 <http://www.hos.ufl.edu/ctdcweb/pcb5065home.htm>
- *Population Genetics and Quantitative Genetics: Advanced Genetics*, University of Florida, Fall 2004 - future <http://www.hos.ufl.edu/ctdcweb/pcb5065home.htm>
- *Statistical Methodology for Mapping Quantitative Traits*, a short graduate course (30 students), Nanjing Forestry University, June 2006
- *Statistical Methodology for Mapping Quantitative Traits*, a short graduate course (15 students), Zhejiang Forestry University, August 2006
- *Statistical Methodology for Mapping Quantitative Traits*, a short graduate course (30 students), Nanjing Forestry University, October 2007
- *International Workshop on Statistical Genetics*, Beijing, China, August 2009

THESIS ADVISOR AND POSTGRADUATE-SCHOLAR SPONSOR

Thesis Advisor

The following abbreviations are used in this section:

- ABE (Agricultural & Biological Engineering)
- CAF (Chinese Academy of Forestry, Beijing)
- CISE (Computer and Information Science & Engineering)
- CVE (College of Veterinary Medicine)
- EE (Electronic Engineering)
- EV (Entomology/Nematology)
- ISE (Industrial and Systems Engineering)
- SFRC (School of Forest Resources & Conservation)
- ZFU (Zhejiang Forestry University, China)
- ZU (Zhejiang University, China)

Applicant's Role	Student	Research Topics	Home Department	Complete Date
Chair, PhD	Yao Li	eQTL mapping for developmental traits	UF-Statistics	2009 <i>exp.</i>
Chair, PhD	Qin Li	Model for constructing linkage disequilibrium map	UF-Statistics	2009 <i>exp.</i>
Chair, PhD	Song Wu	Generalized model for genetic mapping	UF-Statistics	2008 <i>exp.</i>
Chair, PhD	John Yap	Modeling of large covariance matrices	UF-Statistics	2008 <i>exp.</i>
Chair, PhD	Hongying Li ¹	Modeling non-ignorable dropouts	UF-Statistics	2007
Chair, PhD	Tian Liu ²	Bayesian machinery for functional mapping	UF-Statistics	2007
Chair, PhD	Wei Hou ³	Non-linear mixed effect model	UF-Statistics	2006
Chair, PhD	Bong-Rae Kim ⁴	Functional clustering	UF-Statistics	2006
Chair, PhD	Yuehua Cui ⁵	Modeling programmed cell death	UF-Statistics	2005
Chair, PhD	Min Lin ⁶	Computational pharmacogenomics	UF-Statistics	2005
Chair, PhD	Wei Zhao ⁷	Wavelet-based functional mapping	UF-Statistics	2005
Co-Chair, PhD (80%)	Yang Li	Statistical and computer algorithms	UF-CISE	2009 <i>exp.</i>
Co-Chair, PhD (50%)	Richard Lee	Microarray data analysis	UF-ABE	2009 <i>exp.</i>

Co-Chair, PhD (50%)	Guifang Fu	Differential equations for functional mapping	UF- Mathematics	2009 <i>exp.</i>
Co-Chair, PhD (50%)	Jiangtao Luo	Growth analysis	UF- Mathematics	2009 <i>exp.</i>
Co-Chair, PhD (80%)	Jiasheng Wu ⁸	Modeling environmental sensitivities	ZU- Agronomy	2006
Co-Chair, PhD (50%)	Jianjun Hu ⁹	Mapping genotype by environment interactions	CAF-Forestry	2002
Co-Chair, PhD (50%)	Jianjun Fang ¹⁰	Mapping resistance to insects in poplars	CAF-Forestry	1999
Chair, Masters	Shen Lin	Linkage disequilibrium mapping in forest trees	ZFU-Forestry	2009 <i>exp.</i>
Chair, Masters	Jiang Liu	Functional mapping of PK/PD	UF-Statistics	2008
Chair, Masters	Sheron Wen	Genetic imprinting	UF-Statistics	2008
Chair, Masters	Kun Han	Linkage mapping in an open-pollinated progeny	ZFU-Forestry	2008
Chair, Masters	Yun Cheng	Mapping imprinting nucleotides	UF-Statistics	2008
Chair, Masters	Yanchun Li ¹¹	Mapping imprinting quantitative trait loci	ZFU-Forestry	2007
Chair, Masters	Mei Tang ¹²	Modeling drug response	UF-Statistics	2006
Chair, Masters	Kelian Sun ¹³	Microarray data analysis	UF-Statistics	2005
Chair, Masters	Kai Wu ¹⁴	Population pharmacogenetics	UF-Statistics	2005
Chair, Masters	Song Wu ¹⁵	Semiparametric modeling of functional mapping	UF-Statistics	2005
Chair, Masters	Tian Liu ¹⁶	Haplotyping complex traits	UF-Statistics	2004
Chair, Masters	Fei Long ¹⁷	Allometric scaling	UF-Statistics	2004
Chair, Masters	Zuoheng Wang ¹⁸	Modelling HIV dynamics	UF-Statistics	2004
Chair, Masters	Yan Gong ¹⁹	Mapping pharmacodynamics	UF-Statistics	2003
Chair, Masters	Qing Lu ²⁰	Linkage analysis in outcrossing populations	UF-Statistics	2003
Chair, Masters	Lindsay Schoettinger ²¹	Zygotic linkage disequilibrium	UF-Statistics	2003
Chair, Masters	Zhaojie Wang ²²	Multivariate allometric scaling	UF-Statistics	2003

Co-Chair, Masters (50%)	Yunzhe Zhang ²³	Linkage map construction in poplar	CAF-Forestry	2001
Member, PhD	Karla Addesso	Genetic mapping in honey bees	UF-EN	2009 <i>exp.</i>
Member, PhD	Derek Drost	Genetic mapping in poplars	UF-SFRC	2009 <i>exp.</i>
Member, PhD	Jie Gao	Environmental monitoring	UF-ABE	2008 <i>exp.</i>
Member, PhD	Pablo Pinedo	Genetic mapping	UF-CVM	2008 <i>exp.</i>
Member, PhD	Zhen Li	Missing data analysis in genetics	UF-Statistics	2008 <i>exp.</i>
Member, PhD	Xumin Zhu	Signal transduction	UF-EE	2008 <i>exp.</i>
Member, PhD	Pengwen Chen	Differential equations	UF- Mathematics	2007
Member, PhD	Min Liu	Ecophysiology of crop growth	UF- Agronomy	2007
Member, PhD	Gogce Kayihhan	Genetic mapping in poplars	UF-SFRC	2006
Member, PhD	Hailong Meng	Bioinformatics	UF-CISE	2006
Member, PhD	Li'an Qi	Computational algorithms	UF-ISE	2006
Member, PhD	Bin Guo	Signal transduction	UF-EE	2006
Member, PhD	Luzhou Xu	Nonlinear analysis of growth	UF-EE	2006
Member, PhD	Jie Yang	Nonparametric functional mapping	UF-Statistics	2006
Member, PhD	Li Zhang	Modeling genotype- environment dependence	UF-Statistics	2006
Member, PhD	Brian Baltunis	Quantitative genetics of tree improvement	UF-SFRC	2005
Member, PhD	Salvador Gezan	Population genetics of tree improvement	UF-SFRC	2005
Member, PhD	Damaris Santana	Bayesian QTL mapping	UF-Statistics	2005
Member, PhD	Kelian Sun	Microarray analysis	UF-Botany	2005
Member, PhD	Jianhua Li	Signal transduction	UF-EE	2004

Member, PhD	Yongyi Min	Categorical data analysis	UF-Statistics	2003
Member, Masters	Karim Yaskoubd	Time series	UF-Statistics	2007
Member, Masters	Antara Roy	Genetics of circadian rhythms	UF-Statistics	2004
Member, Masters	Yuehua Cui	Microarray data analysis	UF-Statistics	2003
Member, Masters	Li Zhang	Genetics of seed development	UF-Statistics	2003
Member, Masters	Yun Zhu	Genetics of HIV dynamics	UF-Statistics	2003
<i>Member, Masters</i>	<i>Wei Zhao</i>	<i>Genetics of growth curves</i>	<i>UF-Statistics</i>	<i>2002</i>

PhD

¹Offered an Assistant Professor position, University of New Mexico

²Currently Research Staff (equivalent to Assistant Professor), Genome Institute of Singapore

³Currently Assistant Professor, University of Florida

⁴Currently Assistant Professor, Sookmyung Women's University, South Korea

⁵Currently Assistant Professor, Michigan State University

⁶Currently Assistant Professor, Duke University

⁷Currently Research Staff (equivalent to Assistant Professor), St. Jude Children's Research Hospital

⁸Currently Associate Professor, Zhejiang Forestry University, China

⁹Currently Associate Professor, Chinese Academy of Forestry, China

¹⁰Currently Associate Professor, Chinese Academy of Forestry, China

Masters

¹¹Currently Research Scientist, Fujian Academy of Agriculture and Forestry, China

¹²Currently Project Coordinator, Schering-Plough

¹³Currently Post-doctoral Research Associate, Michigan State University

¹⁴Currently PhD candidate, University of Florida

¹⁵Currently PhD candidate, University of Florida

¹⁶See 2

¹⁷Currently Project Coordinator, Capital One

¹⁸Currently PhD candidate, University of Chicago

¹⁹Research Assistant Professor, University of Florida

²⁰Currently PhD candidate, West Case Reserves University

²¹Currently Project Coordinator

²²Currently Research Scientist, Johns Hopkins University

²³Currently Research Scientist, Chinese Academy of Forestry, China

Postgraduate-Scholar Sponsor

1. Dr. Yang-Xiang Lou, University of Florida (2002-2004)
2. Jiasheng Wu, University of Florida (2004-2006)
3. Dr. Jie Yang, University of Florida (2007), co-sponsor
4. Youjun Huang, University of Florida (2007)
5. Zhong Wang, University of Florida (2008-)

Served 10 PhD Supervisory Committees at the Institute of Food and Agricultural Science and other colleges

Research Highlight

My groundbreaking work in **functional mapping** of complex traits was highlighted in *Nature Reviews Genetics* Vol 5 No 4 (2004)

DEPARTMENTAL COMMITTEES

Member, Merit Pay Committee, Department of Statistics, 2008
Chair, Search Committee for IFAS Statistics Assistant Professor, 2007
Graduate Search Committee for a biostatistician position (Chair, Linda Young), 2005
Steering Committee for new faculty, 2005-
Search Committee for a statistical geneticist position (Chair, Mark Yang), 2004
Search Committee for a forest biometrician position (Chair, Donald Rockwood), 2004
Search Committee for a quantitative geneticist position (Chair, John Davis), 2004
Curriculum Committee (Chair, Jim Booth), 2001
Search Committee for a statistical geneticist position (Chair, Mark Yang), 2001
Organizing Committee for University of Florida Fourth Annual Winter Workshop, 2001

MEDIA INTERVIEWS

- 2003 **“Summing Up the Genome: Statistical Genetics Group at the University of Florida”** Interviewed by reporter (Allyson A. Beutke) of the College of Liberal Art and Sciences at the University of Florida
- 2006 **“Gene Models for Predicting Human’s Health”**. Interviewed by journalists of Beijing Science and Technology Daily
- 2007 **“Whether Plant or Animal, UF’s New Genetic Model Can Predict Its Future”**. UF News, July 18, 2007
- 2007 **“Genetic Phonetics Could Be the Trick to Sounding Out DNA’s Meaning”**. UF News, August 16, 2007