# Curriculum Vitae

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Tenured Associate Professor
The Sir David Cox Endowed Professorship
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## EDUCATION AND TRAINING

- Postdoctoral Research Associate, Statistical genetics/genomics, University of California, Riverside, July 1998-December 2001. (With Prof. Shizhong Xu).
- Ph.D. July 1996. Quantitative and Population Genetics, Nanjing Forestry University, P. R. China.
- M.S. July 1988. Biostatistics, Zhejiang University, P. R. China.
- B.S. July 1983. Mathematics, Shaoyang Normal University, P. R. China.

## CONTINUING EDUCATION

- Short course on Bayesian Modeling, Inference and Prediction. Presenter: David Draper, University of California at Santa Cruz. March 18$^{th}$, 2005.
- Bayesian statistics and Markov chain Monte Carlo algorithms in genetics, Iowa State University, June 20-30, 2000.
- Advanced SAS course, Department of Statistics, Beijing University, P. R. China, July 20-August 2, 1995.
- Mathematics, Department of Mathematics, Hunan Teacher University, P. R. China, July 1985-July 1986.

CURRENT APPOINTMENTS

- The Sir David Cox Endowed Professorship in Biostatistics in the UAB Department of Biostatistics in the School of Public Health. April 2011 – present.
- Associate Professor (with tenure), the Section on Statistical Genetics, Department of Biostatistics, University of Alabama at Birmingham, August 2005 - present.
- Scientist of Nutrition Obesity Research Center (NORC), University of Alabama at Birmingham, June 2003 - present.
- Scientist of the UAB Comprehensive Cancer Center, the Cancer Control and Population Science Program, University of Alabama at Birmingham, 2009 - present

PREVIOUS APPOINTMENTS

- Assistant Professor of Statistical Genetics, the Section on Statistical Genetics, Department of Biostatistics, University of Alabama at Birmingham, July 2004-August 2005.
- Research Assistant Professor of Statistical Genetics, the Section on Statistical Genetics, Department of Biostatistics, University of Alabama at Birmingham, May 2002-July 2004.
- Assistant Professor of Statistical Genetics, Creighton University, January 2002-May 2002.
- Postdoctoral Research Associate, Statistical genetics/genomics, University of California, Riverside, July 1998-December 2001. (With Prof. Shizhong Xu).
- Associate Professor of Statistics and Genetics, Nanjing Forestry University, P. R. China, April 1996-June 1998.
- Assistant Professor of Mathematics, Nanjing Forestry University, P. R. China, August 1988-March 1996.
- Teacher of Mathematics, Chenbu High Shool, Hunan Province, P. R. China, August 1983-July 1985.

HONORS AND AWARDS

- The Sir David Cox Endowed Professorship in Biostatistics in the UAB Department of Biostatistics in the School of Public Health, appointed by The University of Alabama System Board of Trustees in April 8, 2011.
- The 2011 Graduate Dean's Award for Excellence in Mentorship, University of Alabama at Birmingham, USA.
- On the basis of my substantial service to peer review at the National Institutes of Health, I have been given special dispensation from NIH to submit grants at any time without respect to deadline from OCTOBER 01, 2010 to SEPTEMBER 30, 2011.
- CME Credit for JAMA Review. My peer review has met the criteria of quality and timeliness required to claim credit. 3/22/2010.
- Birmingham 2009 Top Ten Outstanding Chinese, Awarded by Birmingham Chinese Association.
- The 2007 recipient of the Distinguished Faculty Investigator Award, School of Public Health, University of Alabama at Birmingham, USA.
- 2004 Named New Investigator, Clinical Nutrition Research Center, University of Alabama at Birmingham, USA.
- 2004 Best Paper Award by Science Unbound Foundation, USA.
- Best Paper Award by Zhejiang science and technology commission, 1992.
- National Natural Science Foundation of China Grant "Statistical methods for mapping quantitative trait loci in forest trees", 1998-2000.
- National Natural Science Foundation of China Grant "Construction of genetic linkage map and mapping quantitative trait loci in Chinese Fir and Poplar", 1998-2000.
- National Natural Science Foundation of China Grant "Genetic analysis of forest germplasm resources for important trees species of *Castanopsis* special in China", 1998–2000.

PROFESSIONAL MEMBERSHIPS

- The American Society of Human Genetics, 2010-present.
- The American Statistical Association, 2005-present.

- NAASO, North American Association for the Study of Obesity, 2004-present.
- International Biometric Society, 2000-present.
- International Society for Bayesian Analysis, 2000-present.

## JOURNAL EDITORIAL BOARD

- Associate Editor for *BMC Genetics*, 2009 - present
- Associate Editor for *Genetics Research*, 2009 – present
- Associate Editor for *International Journal of Plant Genomics*, 2009 - present
- Associate Editor for *Journal of Biometrics & Biostatistics*, 2010 – present
- Review Editor for *Frontiers in Statistical Genetics and Methodology*, 2010- present

## RESEARCH AREAS

- Statistical methods of gene mapping for complex traits
- Bayesian Statistics and Markov chain Monte Carlo algorithms
- Bayesian model selection
- Hierarchical models
- Statistical analysis of genetic data
- High-dimensional statistical methods

## PEER-REVIEWED PUBLICATIONS

1. Yang, Y., H. Pei and **N. Yi**, 1991 Shortcut sampling inspection plans and their OC functions. J. Biomathematics, 6(4): 49-52.

2. **Yi, N.**, 1992 A study of precision of several sampling plans. J. Biomathematics, 7(1): 38-42.

3. **Yi, N.**, Y. Yang *et al*, 1992 Mean precision of multi-stage sampling. J. Biomathematics, 7(4): 169-171.

4. Yang, Y., H. Pei, **N. Yi**, and Y. Gao, 1994 Optimum allocations of sample size in two-stage sampling plan. J.App.Math., 9(4): 46-50.

5. **Yi, N.**, J. Shi and M. Wang, 1995 Multivariate analysis of genetic differentiation in forest populations. J. Nanjing For. Uni., 4: 7-14.

6. **Yi, N.**, 1995 Comparison of 3P sampling with PSWOR sampling. J.Nanjing For.Uni., 19(1): 89-102.

7. **Yi, N.** and Y. Yang, 1996 Mean precision of the ratio-type estimator in the two-stage sampling. J. Biomathematics, 11(1): 28-31.

8. **Yi, N.**, J. Shi and M. Wang, 1996 Genetic diversity and multilocus structure in forest trees. Chinese Biodiversity, 4(3): 153-159.

9. **Yi, N.** "A study on population genetic structure in forest trees", Ph.D. Dissertation, Nanjing Forestry University, 1996.

10. Yin, T, Y. Sun, **N. Yi**, X. Li, M. Huang and M. Wang,1998 Genome fingerprinting analysis in *Populus Deltoides*. Acta Botanica Sinica, 40(8):778-780.

11. **Yi, N.**, J. Shi and M. Wang, 1998 Estimation, variance and optimal sampling of multilocus gene diversity. J. Biomathematics, 14: 23-30.

12. **Yi, N.**, J. Shi and M. Wang, 1998 Linkage disequilibrium in populations of Cunninghamia lanceolate (Lamb.) Hook from The People's Republic of China. J. Biomathematics, 15: 11-19.

13. **Yi, N**., T. Yin, M. Huang, and L. Zhu, 1998 Mapping quantitative trait loci in forest trees. Progress in Biotechnology (Chinese), 18(3): 19-25.

14. **Yi, N.**, T. Yin, Z. Han, M. Huang, and H. Cao, 2000 Genetic variation of RAPD markers in a disease resistant seed orchard of Pinus Elliottii Engelm. Scientia Silvae Sinicae 36: 51-53.

15. **Yi, N.**, 2000 A random model approach to mapping quantitative trait loci using Megagametophte in Conifers. Scientia Silvae Sinicae. 37: 36-41.

16. Li Mei, Shi Jisen, Gan Siming, He Zhenxiang, Li Li, **N. Yi**, 2001 Correlation between RAPD based parental genetic distance and filial performance of Chinese fir, *Forest Research*. 14 (1):35-40 (Chinese)

17. Li Mei, Shi Jisen, He Zhenxiang, **N. Yi**, 2001 Study on molecular genetic variation of superior trees in Chinese fir, *SCIENTIA SILVAE SINICAE*. 37(4):137-141.

18. **Yi, N.** and S. Xu, 1999 Mapping quantitative trait loci for complex binary traits in outbred populations. Heredity 82: 668-676.

19. **Yi, N.** and S. Xu, 1999 A random approach to mapping quantitative trait loci for complex binary traits in outbred populations. Genetics 153: 1029-1040.

20. Xu, S. and **N. Yi**, 2000 Mixed model analysis of quantitative trait loci. *Proceedings of the National Academy of Sciences of the USA*. 97: 14542-14547.

21. **Yi, N.** and S. Xu, 2000 Bayesian mapping of quantitative trait loci for complex binary traits. Genetics 155: 1391-1403.

22. **Yi, N.** and S. Xu, 2000 Bayesian mapping of quantitative trait loci under the identity-by-descent-based variance component model. Genetics 156: 411-422.

23. **Yi, N.** and S. Xu, 2001 Bayesian mapping of quantitative trait loci under complicated mating designs. Genetics 157: 1759-1771.

24. Xu, S. and **Yi, N**., 2001 Genetic mapping for complex traits using Bayesian statistics. In "International symposium on mapping and identification of genes for complex polygenic traits and diseases and symposium on application of biological high technology and its products". Changsha, China.

25. **Yi, N.** and Xu, S., 2002 Mapping quantitative trait loci with epistatic effects. Genetical Research 79: 185-198.

26. **Yi, N.** and S. Xu, 2002 Linkage analysis of quantitative trait loci in multiple line crosses. Genetica 114: 217-320.

27. **Yi, N.**, V. George and D. B. Allison, 2003 Stochastic search variable selection for mapping multiple quantitative trait loci. Genetics 164: 1129-1138.

28. **Yi, N.**, S. Xu and D. B. Allison, 2003 Bayesian model choice and search strategies for mapping interacting quantitative trait loci. Genetics 165: 867-883.

29. Xu, S., **N. Yi**, D. Burke, A. Galeki and R. A. Miller, 2003 An EM algorithm for mapping binary disease loci: application to fibrosarcoma in a four-way cross mouse family. Genetical Research 82: 127-138.

30. Hsu, H., Zhang, H., Li, L., **N. Yi**, Yang, P., Wu, Q., Wu, Y., Sun, S., Renda, J., Xu, X., Yang, X., Lu, L., Van Zant, G., Williams, R. W., Allison, D. B., & Mountz, J. D., 2003 Age-related Thymic Involution in C57BL/6J X DBA/2J Recombinant Inbred Mice Fits A Negative Exponential Regression Model and Maps to Mouse Chromosome 9. Genes and Immunity 4: 402-10.

31. **Yi, N.** and Xu, S., 2003 Designs and methods to detect QTL for production traits based on random genetic models. In "*Poultry breeding and biotechnology*", edited by W. Muir and S. Aggrey. CABI Publishing, Wallingford, UK.

32. G. Churchill (**N. Yi** among many other authors), 2004 The collaborative cross, a community resource for the genetic analysis of complex traits. Nature Genetics 11: 1133-1137.

33. **Yi, N.**, 2004 A unified Markov chain Monte Carlo framework for mapping multiple quantitative trait loci. Genetics 167: 967-975. [PMID:15238545 PMCID: PMC1470906]

34. **Yi, N.**, A. Diament, S. Chiu, J. Fisler and C. Warden, 2004 Epistatic interaction between two nonstructural loci on chromosomes 7 and 3 influences hepatic lipase activity in BSB mice. *J Lipid Res* 2004; 45:2063-70.

35. **Yi, N.**, Adam Diament, Sally Chiu, Janis Fisler and Craig Warden, 2004 Characterization of Epistasis influencing complex spontaneous obesity in the BSB model. Genetics 167: 399-409.

36. **Yi, N.,** S. Xu, V. George and D. B. Allison, 2004 Mapping multiple quantitative trait loci for complex ordinal traits. Behavior Genetics 34: 3-15.

37. Warden, C., **N. Yi** and J. Fisler, 2004 Epistasis among genes is a universal phenomenon in obesity: evidence from rodent models. Nutrition 20: 74-77.

38. Huang-Ge Zhang, Hui-Chen Hsu, **N. Yi**, PingAr Yang, Qi Wu, David B. Allison and John D. Mountz, 2004 Identification of Multiple Genetic Loci that Regulate Adenovirus Gene Therapy. Gene Therapy 11: 4-14.

39. Beasley, T. M., D. Yang, **N. Yi**, D. C. Bullard, C. I. Amos, S. Xu, and D. B. Allison, 2004 A class of combined covariance-based and marginal-based tests for quantitative trait loci in experimental crosses. Genetics Selection Evolution 36: 601-619.

40. Farahani, P., J. S. Fisler, H. Wong, A. L. Diament, **N. Yi** and C. H. Warden, 2004 Reciprocal hemizygosity analysis of mouse hepatic lipase (Lipc) reveals influence on obesity. Obesity Research 2: 292-306.

41. C. Hansen, **N. Yi**, Y-M Zhang, S. Xu, Gavora J., and H. Chen, 2005 Identification of QTL for production traits in chicken. Animal Biotechnoloy 16: 67-79.

42. John D. Mountz, PingAr Yang, Qi Wu, Juling Zhou, Angela Fitgerald, Jennifer Allen, **N. Yi**, Lu Lu, Robert W. Williams, and Hui-Chen Hsu, 2005 Genetic segregation of spontaneous erosive arthritis and generalized autoimmune disease in BXD2 recombinant inbred strain of mice. Scand J Immunology 61: 128-138.

43. Huang-Ge Zhang, Katherine A. High, Qi Wu, PingAr Yang, Alex Schlachterman, Shaohua Yu, **N. Yi**, Hui-Chen Hsu, and John D. Mountz, 2005 Genetic Analysis of the Antibody Response to AAV2 and Factor IX. Molecular Therapy 11(6):866-74.

44. Maria De Luca, **N. Yi**, David B. Allison, Jeff Leips, and Douglas M. Ruden, 2005 Mapping Quantitative Trait Loci affecting variation in *Drosophila* triacylglycerol storage. Obesity Research 13: 1596-1606.

45. Joseph R. Vasselli, Richard Weindruch, Stephen B. Heymsfield, F. Xavier Pi-Sunyer, Carol N. Boozer, **N. Yi**, Chenxi Wang, and David B. Allison, 2005 'Intentional' Weight Loss Reduces Mortality Rate in a Rodent Model of Dietary Obesity. Obesity Research 13:693-702.

46. **Yi, N.**, B. Yandell, G. Churchill, D. Allison, E. J. Eisen and D. Pomp, 2005 Bayesian model selection for genome-wide epistatic analysis. Genetics 170: 1333-1344.

47. Ruth, J.H., Amin, M.A., Woods, J.M., He, X.,Samuel, S.L., **Yi, N.**, Haas, C.S., Koch, E.A., and Bullard, D.C., 2005 Accelerated Development of Arthritis in Mice Lacking Endothelial Selectins. Arthritis Research & Therapy 7: R959-R970.

48. Yang, R., **N. Yi** and S. Xu, 2006 Box-Cox transformation for QTL mapping. Genetica 128:133–143. [PMID: 17028946]

49. **Yi**, **N.**, Denise K. Zinniel, Kyoungmi Kim, Eugene J. Eisen, Alfred Bartolucci, David B. Allison and Daniel Pomp, 2006 Bayesian analysis of multiple epistatic QTL models for body weight and body composition in Mice. Genetical Research 87: 45-60. [PMID: 16545150]

50. Solomon K Musani, Huang-Ge Zhang, Hui-Chen Hsu, **N. Yi**, David B Allison, and John D. Mountz, 2006 Principal Component Analysis of Quantitative Trait Loci for Adenovirus. Hereditas 143: 189-197. [PMID: 17362354]

51. Daniel Shriner, Solomon K Musani, and **N. Yi**, 2007 Statistical methods for multiple QTL mapping in experimental cross. In "Current Topics in Human Genetics: studies in complex diseases" ed. Hong-Wen Deng. World Scientific Publishing Co. Pte. Ltd, Singopore.

52. Hui-Chen Hsu, Lu Lu, **N. Yi**, G. V. Zant, R. W. Williams and J. D. Mountz, 2007 Quantitative Trait Loci (QTL) Mapping in Aging Systems. In "Methods in Molecular Biology: Biological Aging: Methods and Protocols", edited by Tollefsbol, Trygve O.. Humana Press.

53. S. K. Musani, D. Shriner, N. Liu, R. Feng, C. S. Coffey, **N. Yi**, H. K. Tiwari, & D. B. Allison, 2007 Detection of Gene × Gene Interactions in Association Studies of Human Data. Human Heredity 63(2):67-84. [PMID: 17283436]

54. Brian S. Yandell, Tapan Mehta, Samprit Banerjee, Daniel Shriner, Ramprasad Venkataraman, Jee Young Moon, W. Whipple Neely, Hao Wu, Randy von Smith and **Nengjun Yi**, 2007 R/qtlbim: QTL with Bayesian Interval Mapping in Experimental Crosses. Bioinformatics 23: 641-634.

55. **Yi, N.**, D. Shriner, S. Banerjee, Tapan Mehta, D. Pomp, and Brian S. Yandell, 2007 An efficient Bayesian model selection approach for interacting QTL models with many effects. Genetics 176: 1865–1877. [PMID: 17483424 PMCID: PMC1931520]

56. **Yi, N.**, S. Banerjee, D. Pomp, and B. S. Yandell, 2007 Bayesian analysis of genome-wide interacting QTL for ordinal traits. Genetics 176: 1855–1864. [PMID: 17507680 PMCID: PMC1931535]

57. Hui-Chen Hsu, Lu Lu, **N. Yi**, G. V. Zant, R. W. Williams and J. D. Mountz, 2007 Quantitative Trait Loci (QTL) Mapping in Aging Systems. Methods Mol Biol. 371:321-48. [PMID: 17634591]

58. **Yi, N.** and D. Shriner, 2008 Advances in Bayesian multiple QTL mapping in experimental designs. Heredity 100: 240-252. [PMID: 17987056]

59. Shriner, D. and **N. Yi**, 2008 Deviance information criterion (DIC) in Bayesian multiple QTL mapping. Computational Statistics and Data Analysis. doi:10.1016/j.csda.2008.01.016.

60. **Yi, N.** and S. Xu, 2008 Bayesian LASSO for quantitative trait loci mapping. Genetics 179: 1045–1055. [PMID: 18505874 PMCID: PMC2429858]

61. Banerjee, S., B.S. Yandell, and **N Yi**, 2008 Bayesian QTL mapping for multiple traits. Genetics 179: 2275-2289. [PMID: 18689903 PMCID: PMC2516097]

62. **Yi, N**, S. Ding, S. W. Keith, C. S. Coffey, and D. B. Allison, 2008 Bayesian analysis of the effect of intentional weight loss on mortality rate. International Journal of Body Composition Research 6: 185-192.

63. Badu, G., D. Pomp, D. Shriner, D. B. Allison, and **N. Yi**, 2009 Genetic influences on growth and body composition in mice: multilocus interactions. International Journal of Obesity 33, 89–95. [PMID: 18982013 PMCID: PMC3206648]

64. **Yi, N.** and Banerjee, S. 2009 Hierarchical generalized linear models for genome-wide interacting QTL mapping. Genetics 181: 1101-1113. [PMID: 19139143 PMCID: PMC2651046]

65. Richard J. Reynolds, James M. Kelley, Laura B. Hughes, **N. Yi**, and S. Louis Bridges, Jr. 2009 Genetic association of htSNPs across the major histocompatibility complex with rheumatoid arthritis in an African American population. Genes and Immunity doi:10.1038/gene.2009.69

66. Boris Pasche, Kari B. Wisinski, Maureen Sadim, Virginia Kaklamani, Michael Pennison, Qinghua Zeng, Naresh Bellam, Jacquelyn Zimmerman, **Nengjun Yi**, Kui Zhang, John Baron, Daniel O. Stram, M. Geoffrey Hayes. 2010. Constitutively decreased *TGFBR1* allelic expression is a common finding in colorectal cancer and is associated with three *TGFBR1* SNPs. Journal of Experimental & Clinical Cancer Research **29:**57 doi:10.1186/1756-9966-29-57 [PMID: 20500843 PMCID: PMC2890549]

67. G. A. Ankra-Badu, D Shriner, E. LE Bihan-Duval, S. Mignon-Grasteau, F. Pitel, C. Beaumont, M. J. Duclos, J. Simon, T. E. Porter, A. Vignal, L. A. Cogburn, D. B. Allison, **N. Yi**, S. E. Aggrey. 2010. Mapping main, epistatic and sex-specific QTL for body composition in a chicken population divergently selected for low or high growth rate. *BMC Genomics* 2010, **11:**107. [PMID: 20149241 PMCID: PMC2830984]

68. Jun Li, Richard Renolds, Daniel Pomp, David B. Allison, **Nengjun Yi**. 2010. Mapping Interacting QTL for Count Phenotypes Using Hierarchical Poisson and Binomial Models: an Application to Reproductive Traits in Mice. Genetics Research 92: 13–23. [PMID: 20199696

PMCID: PMC2938180]

69. Boris Pasche, **N Yi** 2010 Candidate gene association studies: Successes and failures. Current Opinion in Genetics & Development 20: 257–261. [PMID: 20417090 PMCID: PMC2885524]

70. **Yi, N.,** Virginia Kaklamani, and Boris Pasche 2011 Bayesian Analysis of Genetic Interactions in Case-Control Studies, With Application to Adiponectin Genes and Colorectal Cancer Risk. Annals of Human Genetics 75: 90–104. (Article first published online: doi: 10.1111/j.1469-1809.2010.00605.x) [PMID: 20846215 PMCID: PMC3005151]

71. **Yi, N.** 2010 Statistical Analysis of Genetic Interactions. Genetics Research 92: 443-459. [PMID: 21429274 PMCID: PMC3203544]

72. **Yi, N.** and Degui Zhi 2011 Bayesian Analysis of Rare Variants in Genetic Association Studies. Genetic Epidemiology. 35: 57-69. [PMID: 21181897 PMCID: PMC3200544]

73. Banerjee, S. and **Yi, N.,** 2011 Identifying QTL for Multiple Complex Traits in Experimental Crosses. In "the Methods in Molecular Biology series" ed. Scott Rifkin. (in press).

74. Virginia Kaklamani, **N. Yi**, K. Zhang, Maureen Sadim, Kenneth Offit, Carole Oddoux, Harry Ostrer, Christos Mantzoros, Boris Pasche. 2011 Polymorphisms of *ADIPOQ* and *ADIPOR1* and prostate cancer risk. Metabolism 60(9):1234-43. [PMID: 21397927 PMCID: PMC3134585]

75. Jun Li, Kui Zhang, and **Nengjun Yi** 2011 A Bayesian hierarchical model for detecting haplotype-haplotype and haplotype-environment interactions in genetic association studies. Human Heredity 71(3): 148-60 (DOI: 10.1159/000324841). [PMID: 21778734 PMCID: PMC3153342]

76. Lin WY, Zhang B, **Yi N**, Gao G, Liu N 2011 Evaluation of Pooled Association Tests for Rare Variants Identification with the Genetic Analysis Workshop 17 Data. BMC Proceedings **5** (Suppl 9): S118.

77. Virginia Kaklamani, **Nengjun Yi**, Maureen Sadim, Kalliopi Siziopikou, Kui Zhang, Yianfei Xu, Sarah Tofilon, Surbhi Agarwal, Boris Pasche and Christos Mantzoros 2011 The role of the fat mass and obesity associated gene (FTO) in breast cancer risk. *BMC Medical Genetics*, **12:**52, doi:10.1186/1471-2350-12-52. [PMID: 21489227 PMCID: PMC3089782]

78. John J Arcaroli, Nianjun Liu, **Nengjun Yi**, and Edward Abraham 2011 Association between IL-32 and outcome in infection-associated acute lung injury. Critical Care 15:R138. [PMID: 21649914]

79. Wu G, **Yi N**, Absher D, Zhi D (2011) Statistical Quantification of Methylation Levels by Next-Generation Sequencing. PLoS ONE 6(6): e21034. doi:10.1371/journal.pone.0021034. [PMID: 21698242 PMCID: PMC3115964]

80. Chen, G. B., K. H. Ingram, G. de los Campos, **N. Yi**, X. Y. Lou, D. Pomp, D. B. Allison. (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 Supplements, S2:21.

81. **Yi, N.**, N. Liu, D. Zhi, J. Li 2011 Hierarchical Generalized Linear Models for Multiple Groups of Rare and Common Variants: Jointly Estimating Group and Individual-Variants Effects. PLoS

Genetics 7(12): e1002382. doi:10.1371/journal.pgen.1002382. [PMID: 22144906 PMCID: PMC3228815]

82. Reng-Yun Liu, Ping Chen, Zhe Lei, Jingcheng Miao, **Nengjun Yi**, Kui Zhang, Boris Pasche, Hong-Tao Zhang 2011 Association between *IL6* -174G>C and cancer: a meta-analysis of 103,827 individuals. Experimental and Therapeutic Medicine (in press).
83. Jacquelyn W. Zimmerman, Michael J. Pennison, Ivan Brezovich, **Nengjun Yi**, Celeste T. Yang, Ryne Ramaker, Devin Absher, Richard M. Myers, Niels Kuster, Frederico P. Costa, Alexandre Barbault, Boris Pasche 2012 Cancer cell proliferation is inhibited by specific modulation frequencies. British Journal of Cancer **106**, 307–313. doi:10.1038/bjc.2011.523.
84. Ma, Shuangge, Jian Huang, Yang Xie, **Nengjun Yi** 2011 Identification of Breast Cancer Prognosis Markers using Integrative Sparse Boosting. Methods of Information in Medicine (In press).

## BOOK CHAPTER

1. **Yi, N.** and Xu, S., 2003 Designs and methods to detect QTL for production traits based on random genetic models. In "*Poultry breeding and biotechnology*", edited by W. Muir and S. Aggrey. CABI Publishing, Wallingford, UK.

2. Hui-Chen Hsu, Lu Lu, **N. Yi**, G. V. Zant, R. W. Williams and J. D. Mountz, 2007 Quantitative Trait Loci (QTL) Mapping in Aging Systems. In "Methods in Molecular Biology: Biological Aging: Methods and Protocols", edited by Tollefsbol, Trygve O.. Humana Press.

3. Daniel Shriner, Solomon K Musani, and **N. Yi**, 2007 Statistical methods for multiple QTL mapping in experimental cross. In "Current Topics in Human Genetics: studies in complex diseases" ed. Hong-Wen Deng. World Scientific Publishing Co. Pte. Ltd, Singopore.

4. Banerjee, S. and **Yi, N.,** 2010 Identifying QTL for Multiple Complex Traits in Experimental Crosses. In "the Methods in Molecular Biology series" ed. Scott Rifkin. (in press)

## SOFTWARE RELEASES

1. **R/qtlbim:** QTL Bayesian interval mapping. (B.S. Yandell and **N. Yi**, free release on September 2006 through CRAN) (www.qtlbim.org)

R/qtlbim is an extensible, interactive environment for the Bayesian Interval Mapping of QTL, built on top of R/qtl (Broman *et al.* 2003), providing Bayesian analysis of multiple interacting quantitative trait loci (QTL) models for continuous, binary and ordinal traits in experimental crosses. It includes several efficient Markov chain Monte Carlo (MCMC) algorithms for evaluating the posterior of genetic architectures, *i.e.* the number and locations of QTL, their main and epistatic

effects, and gene-environment interactions. R/qtlbim provides extensive informative graphical and numerical summaries, and model selection and convergence diagnostics of the MCMC output, illustrated through the vignette, example and demo capabilities of R (R Development Core Team 2006). The package is freely available from cran.r-project.org.

2. **R/BhGLM:** Bayesian hierarchical GLMs, with application to genetic data analysis (http://www.ssg.uab.edu/bhglm/)

R/BhGLM provides functions for setting up and fitting Bayesian hierarchical GLMs, for numerically and graphically displaying the results, and for genetic association studies and QTL mapping. The Bayesian hierarchical GLMs include many models as special cases, e.g., classical GLMs, ridge regression, Bayesian lasso, and various adaptive lasso. These methods can be used not only for general data analysis but also for high-dimensional and correlated data. The functions are particularly useful for complicated genetic data analysis, for example, QTL mapping in experimental crosses, genetic association studies for rare and common variants, prediction of complex diseases and traits, gene-set and pathway analysis, haplotype association analysis, and gene-gene and gene-environment interactions.

MANUSCRIPTS UNDER REVIEW

- Costa, Frederico P., de Oliveira, André Cosme, Meirelles, Roberto, Machado, Marcel C.C., Zanesco, Tatiana, Surjan, Rodrigo, Chammas, Maria Cristina, Souza Rocha, Manoel, Morgan, Desiree, Cantor, Alan, **Yi, Nengjun**, Yang, Celeste T., Bottger, Brad, Bomholt, Fin, Kuster, Niels, Barbault, Alexandre, Pasche Boris. 2010 Treatment of advanced hepatocellular carcinoma with intrabuccally-administered amplitude-modulated electromagnetic fields. (in review)

- Yi, N. and S. Ma Hierarchical Shrinkage Priors and Model Fitting Algorithms for High-dimensional Generalized Linear Models (In review)

- Monique Hinchcliff, Michael J Pennison, Jacquelyn W. Zimmerman, Naresh Bellam, Qinghua Zeng, Chiang-Ching Huang, Richard Pope, Maureen Sadim, Wendy Wolf, Jeffrey Edberg, Robert Kimberly, Kui Zhang, Jun Li, **Nengjun Yi**, Maureen D. Mayes, John Varga, Boris Pasche 2011 Constitutively decreased *TGFBR1* signaling and risk for systemic sclerosis. JAMA (in review)

- Degui Zhi and Nengjun Yi 2011 Flexible variant combinations for analyzing rare variants with opposite effects in association studies. (in review)

- Ana I. Vazquez, M.S. Gustavo de los Campos, Yann C. Klimentidis, Guilherme J.M. Rosa, Daniel Gianola, Nengjun Yi, David B. Allison 2012 Whole Genome Enabled Prediction of Skin Cancer Liability. submitted to PLoS Genetics

- Wan-Yu Lin, Nengjun Yi, Degui Zhi, Kui Zhang, Nianjun Liu 2012 Haplotype-based methods for detecting low-frequency causal variants with GWAS genotyping platforms.

- Reng-Yun Liu, Zhe Lei, Nengjun Yi, Sha Zhu, Qian Qian, Jinxia Sun, Zeyi Liu, Xueying Zhao, Baohui Han, Jun Zhao, Xiao-Feng Chen, Wenxiang Wei, Jingcheng Miao, Yifeng Zhou, Kui Zhang, Boris Pasche, Daru Lu, Hong-Tao Zhang 2012 Association of *IL-6* Functional Haplotypes with Lung Cancer Risk.

RESEARCH GRANTS

**Active**

NIH 2 RO1 GM69430-07 (Yi) 06/01/10 – 05/30/2014 5.76 cal
NIH/NIGMS $ 231,057 (1st yr direct) $ 1233237 (total)
Bayesian Methods for Genome-Wide Interacting QTL Mapping (score 2.2, percentile 10%)
To develop and evaluate Bayesian hierarchical models and model selection methods for mapping interacting QTL.

2 R01 CA112520-06A2 (Pasche) 12/01/09 – 11/30/14 0.6 cal
NIH $1,967,476 (total direct)
TGF-beta polymorphisms and breast cancer in families
Role: Co-investigator

1 R01 CA137000-01A1 (Pasche) 12/01/09 – 11/30/14 0.36 cal
NIH $1,250,000 (total direct)
TGFBR1 Signaling in Colorectal Cancer
Role: Co-investigator

**Completed**

1R01 GM069430-01A2 (Yi) 06/01/05 – 05/30/2010 6.0 cal
NIH/NIGMS
Bayesian methods for mapping complex epistatic genes (score 130, percentile 0.7%)
This project is to develop Bayesian model selection methods and computer software for mapping epistatic genes in experimental crosses.
Total cost: $1,150,175
Role: Principal investigator

Pilot-feasibility study (Yi) 06/01/03 – 06/01/05 1.2 cal
Clinical Nutrition Research Center, UAB

Mapping complex epistatic genes for obesity in experimental designs
This study is to develop statistical methods and algorithms for mapping multiple and epistatic genes for obesity in experimental crosses.
Role: Principal investigator

NIH R01GM077490 (Allison) 9/01/07 - 08/31/11 3.48 cal
NIH/NIGMS
Genome-wide Structured Association Testing & Regional Admixture Mapping
Developing, evaluating, and applying enhanced SAT and RAM methods in the context of massive scale genome-wide association studies.
Role: Co-investigator

1R01 DK067487-01A1 (Allison) 01/01/2005 – 12/31/2008 1.8 cal
NIH
Effects of intentional weight loss on mortality rate
This project is to develop statistical methods for studying effects of intentional weight loss on mortality rate.
Role: Co-investigator

R01 HL80812-01 (Maria De Luca) 10/01/2004-09/30/2008 1.8 cal
NIH
QTL mapping age-related changes in lipid storage
This project is to identify QTL for age-related change in lipid storage in *Drosophila*.
Role: Co-investigator

R01 ES012933-01 (Douglas Ruden) 09/24/2004-08/31/2009 0.6 cal
NIH
QTL AND MICROARRAY MAPPING LEAD SENSITIVITY GENES
The major goals of this project are to use QTL mapping microarrays to identify lead sensitivity genes in Drosophila
Role: Co-investigator

VA Merit Review (John Mountz) 10/01/04-09/30/09 1.2 cal
Autoantibody Induced Arthritis and Autoimmune Disease in BXD2 Mice
The major goals of this project are to autoantibody induced arthritis and autoimmune disease using BXD2 mice.
Role: Co-investigator

R01 ES09912 (Amos) 7/1/02 – 6/30/07 1.2 cal
NIH
Positional Gene Identification of Complex Traits
This project is to develop statistical methods for mapping genes for complex traits in humans.
Role: Co-Investigator

R01 RR17009-01 (Bullard) 4/1/02 - 3/31/07
NIH
Genetic Mouse Models for Chronic Inflammatory Disease

This project will use the MRL/MpJ-Faslpr model system to further define the ICAM-1-dependent pathways responsible for mediating vasculitis.
Role: Co-Investigator

RO1 AG11653-08 (Mountz) 02/29/02 - 02/29/07
NIH
Defective Fas Apoptosis During Aging
This study foucuses on identification of populations of age-responder (A-R) and age non-responder (A-NR) T cells and apoptosis pathways.
Role: Co-Investigator

R21 ES 11751 (Douglas Ruden) 03/15/02 - 03/14/04
NIEHS
Developmental Toxicology of Lead, Mercury, and Cadmium
The major goals of this project are to use microarrays to identify protective genes induced by *Drosophila* larvae exposed to heavy metals.
Role: Co-Investigator

NIH R01 CA112520 (Pasche) 09/07/05-08/31/09
TGF-β polymorphisms and breast cancer in families
To assess the association between the *TGFBR1**6A and the *TGFB1* T29C variants and familial breast cancer in 5,357 discordant sibling case-control sets for whom DNA and high-quality breast cancer risk factor data are available.
Role: Co-Investigator

NIH R01 CA108741 (Pasche) 02/24/06-01/31/09
TGF-β polymorphisms and colon cancer risk
To assess the association between the *TGFBR1**6A and the *TGFB1* T29C variants and familial colorectal cancer in 4,208 sibling case-control pairs from the NCI-sponsored familial colon cancer registry for whom DNA and high-quality colorectal cancer risk factor data are available.
Role: Co-Investigator

## CURRENT TEACHING

- BST 740, Bayesian analysis. University of Alabama at Birmingham, Fall, 2004, 2006, 2008, 2010.
- BST 795, Special topics: Advanced Bayesian Analysis. University of Alabama at Birmingham, Fall, 2007, 2009.
- BST 741, Advanced Bayesian Analysis II. University of Alabama at Birmingham, Fall 2011.

## PREVIOUS TEACHING

- Faculty at the 1st Annual NSF-funded short course on statistical genetics & genomics. July 23, 2008.
- Guest Lecturer for HMG 703 "Quantitative Methods". University of Alabama at Birmingham, April 2008
- Guest Lecturer for HMG 703 "Quantitative Methods". University of Alabama at Birmingham, April 2007
- Guest Lecturer for MGE 702 "Advanced Human Genetics", Statistical Approaches to Genetic Crosses, May 3, 2005.
- Faculty at the 3th Annual NIH-funded Short Course on Statistical Genetics for Obesity and Nutrition Researchers, Birmingham, AL, February 6-9, 2003.
- Quantitative Genetics: Bayesian analysis of QTL mapping in line crosses. University of California, Riverside, January 2001. Organized by Prof. Xu.
- Quantitative Genetics: Bayesian analysis of QTL mapping in complex pedigrees. University of California, Riverside, January 2001. Organized by Prof. Xu.
- Applied Statistics, Population Genetics, Quantitative Genetics, Forest Genetics and Tree Breeding. Nanjing Forestry University, P. R. China, August 1996-June 1998.
- Mathematical statistics, Multivariate statistics. Nanjing Forestry University, P. R. China, August 1988-July 1993.

STUDENTS AND POST-DOCTORAL FELLOW:

Post-doctoral Fellow:

2003 – 2005, Kyoungmi Kim (Co-mentor with Grier Page) – Assistant Professor, UC David

2005 - 2008, Daniel Shriner (Co-mentor with David Allison) – Research Fellow, Center for Research on Genomics and Global Health, NIH

2007 - 2009, Georgina Badu (Co-mentor with David Allison) – Research Associate, Department of Twin Research and Genetic Epidemiology, King's College London

2008 – 2010, Richard Reynolds (Co-mentor with Lou Bridges) – Assistant Professor, Division of Clinical Immunology and Rheumatology, University of Alabama at Birmingham

2010 – present, Ana Vazquez (Co-mentor with David Allison)

2012 - present, Jun Li

Graduate Students:

2003 – 2008, Samprit Banerjee – Asst. Prof. at Divison of Biostatistics and Epidemiology, Department of Public Health, Weill Medical College of Cornell University

2008 – 2011, Jun Li – Post-doc fellow at the section on statistical genetics, University of Alabama at Birmingham

2008 – present, Tapan Metha

2011 – present, Himel Mallick

MASTER/PHD COMMITTEE MEMBERSHIP

Samprit Benerjee, PhD dissertation, Bayesian genome-wide QTL mapping for multiple traits, 2008

Jun Li, PhD dissertation, Bayesian Hierarchical Generalized Linear Models for Detecting (Rare) Haplotype-haplotype and Haplotype-environment Interactions in Genetic Association Analysis, 2011

Scott Keith, PhD dissertation, Free-knot splines and bootstrapping for nonlinear modeling in complex samples, 2008

Fenglong Xie, Master dissertation, Are SNPs in FCAR associated with SLE? 2008

Guodong Wu, Master dissertation, Statistical Quantification of Methylation Levels by Next Generation Sequencing, 2010

INVITED PRESENTATIONS

- Bayesian analysis of quantitative trait loci for complex traits in complicated mating designs. Pioneer Hi-Bred International, Inc. April 26, 2001.
- Bayesian analysis of quantitative trait loci for complex traits. Department of Biostatistics, the University of Alabama at Birmingham. July 12, 2001.
- Bayesian analysis of quantitative trait loci with epistatic effects. Plant and Animal Genome VIII, San Diego, California, January 2002.

- Mapping epistatic genes for complex traits. The conference "Statistical Integration of Genetic Information Across Data Domains: Biomedical, Agricultural, and Comparative Genomics", University of Alabama, Birmingham, AL. December 2nd, 2002.
- Bayesian Model Selection and Epistasis. Third Annual Short Course on Statistical Genetics for Obesity & Nutrition Researchers. University of Alabama, Birmingham, AL. February 6-9, 2003.
- Epistasis influences complex spontaneous obesity in the BSB model. NAASO 2003 Annual Scientific Meeting. Ft. Lauderdale, FL. October 11-15, 2003.
- The practical implementation of Bayesian model selection for identifying epistatic genes in experimental crosses. Plant and Animal Genome XII, San Diego, California, January 2004.
- Analysis of genome-wide epistasis via Bayesian model selection. Spring meeting of International Biometric Society, Eastern North American Region, Pittsburgh, PA, March 28-31, 2004.
- Bayesian model selection for mapping complex epistatic genes in experimental designs. Complex Trait Consortium, The Jackson Lab, July 6-9, 2004.
- Mapping complex epistatic genes for complex traits in experimental designs. Department of Biostatistics and Epidemiology, Florida International University, Feb 11, 2005.
- Mapping complex epistatic genes for obesity in experimental designs. Department of Nutrition, University of Alabama at Birmingham, March 15, 2005.
- Genetic Architecture of the Developmental Trajectory for Body Weight in a Cross of High Growth and Wild Strains of Mice. NAASO 2005 Annual Scientific Meeting. Vancouver, British Columbia, Canada. October 15-19, 2005.
- Bayesian Model selection for mapping interacting QTL. SCMA 2005 / FIM XII. Auburn University, Auburn, AL. December 3-4, 2005.
- Genome-wide interacting QTL analysis for complex traits in experimental crosses. Department of Biochemistry and Microbiology, Marshall University, December 2005.
- Efficient MCMC algorithms for mapping genome-wide interacting QTL. Spring meeting of International Biometric Society, Eastern North American Region, Tampa, FL, March 26-29, 2006.
- Bayesian multiple QTL analysis. Yangzhou University, China. June 26, 2006.
- Bayesian multiple QTL analysis. Nanjing Agricultural University, China. June 29, 2006.

- Bayesian multiple QTL analysis. Nanjing Forest University, China. July 3, 2006.
- Bayesian multiple QTL analysis. Shanghai Jiaotong University, China. July 29, 2006.
- Genome-wide interacting QTL analysis for obesity in experimental crosses. Monell Chemical Senses Center, Philadelphia. October 3, 2006.
- Bayesian multiple interacting QTL analysis. Department of Statistics and Bioinformatics Research Center, NCSU, Raleigh NC. March 29-30, 2007.
- Recent advances in Bayesian multiple QTL analysis. Lunch & Med Stat Seminar CCC Biostat & Bioinfo Unit & SOPH Biostat Dep, UAB. Feb 11, 2008.
- Large-scale hierarchical generalized linear models for interacting QTL mapping. Spring meeting of International Biometric Society, Eastern North American Region, Arlington, Virginia, March 16-19, 2008.
- Bayesian hierarchical generalized linear models for interacting QTL mapping. 1st Annual NSF-funded short course on statistical genetics & genomics. July 23, 2008.
- Hierarchical generalized linear models for multiple-SNP analysis. JSM Washington DC. Aug 2009.
- Detecting and characterizing multiple interacting genes in cancer case-control studies. 13th annual research retreat. UAB comprehensive cancer center. October 28, 2009.
- Statistical methods for finding the missing heritability of complex diseases. Genetics and Genomics Seminar Series, UAB school of medicine. Oct 8th, 2010.
- Hierarchical generalized linear models for finding the missing heritability of complex diseases/traits. Nanjing Agricultural University, China. July, 2011.
- Hierarchical generalized linear models for finding the missing heritability of complex diseases/traits. Yangzhou University, China. July, 2011.
- Hierarchical generalized linear models for finding the missing heritability of complex diseases/traits. Nanjing Forest University, China. July, 2011.

## PEER REVIEW ACTIVITIES

### Referee for Journals:

Genetics, American Journal of Human Genetics, Genetics Research, Genetica, Heredity, Trends in genetics, Human Heredity, Bioinformatics, Obesity Reviews, Genetics Selection Evolution, Genes

and Immunity, BMC genomics, BMC Medical Genetics, Mammalian Genome, PLoS Genetics, PLoS One, Theoretical and Applied Genetics, Nature Genetics, Journal of the Royal Statistical Society, Annals of Human Genetics, BMC Genetics, Journal of Heredity, Computational Statistics and Data Analysis, Annals of Applied Statistics, Biometrics, JAMA, Genetic Epidemiology, Journal of Biophamaceutical Statistics

Book review:

Springer (2006, 2007, 2008)
SAGE (2009)

NIH STUDY SECTION AND REVIEW OF GRANT PROPOSALS

- Genetic Variation and Evolution Study Section, NIH (July 2005)
- GCAT Study Section, NIH (March 2-3 2006)
- ZRG1 GGG-A, Center for Scientific Review Special Emphasis Panel, NIH (March 06-07,
- 2007)
- ZRG1 HOP-Q, Center for Scientific Review Special Emphasis Panel, NIH (May 16, 2008)
- ANR GENOPAT 2008, The French National Research Agency (ANR) (May 2008)
- ANR GENOMICS 2008, The French National Research Agency (ANR) (June 2008)
- ANR GENOPAT 2009, The French National Research Agency (ANR) (April 2009)
- ZRG1 PSE-03M, Center for Scientific Review Special Emphasis Panel, NIH (April 2009)
- ZRG1 PSE-02M, Center for Scientific Review Special Emphasis Panel, NIH (May 2009)
- ZRG1 GGG-F, Center for Scientific Review Special Emphasis Panel, NIH (June 2009)
- ZRG1 PSE-C, Challenge Grants Panel, NIH (June 2009)
- ZRG1 PSE-J, Challenge Grants Panel, NIH (June 2009)
- ZAT1 SM, Omics and Variable Responses to CAM (R21, R01), NIH (December 2009)
- External Peer Review, Cancer Research UK (Feb. 2010)
- ETMRC - CSO Research Grant, Scotland (Jan. 2010)
- RC4, Molecular Genetics A Study Section, NIH (May 2010)
- Morehouse School of Medicine/Tuskegee University/UAB Comprehensive Cancer Center Partnership, (June 2010)
- ZRG1 PSE-B 04 M, Genetics and Epidemiology of Chronic Diseases, NIH (Jan. 2011)

- ANR GEDA 2011, The French National Research Agency (ANR) (April 2011)
- ANR GWIS-AM 2011, The French National Research Agency (ANR) (April 2011)
- GCAT Study Section, NIH (October 6-7 2011)

LOCAL SERVICE

- Associate director of postdoctoral fellows in the Section on Statistical Genetics, department of Biostatistics, UAB, 2011-present.
- The graduate program committee's administrative subcommittee, 2006-2010.
- Organizing the monthly journal club meeting at the Section on Statistical Genetics, Department of Biostatistics at UAB, from 2003-2005.
- Judge, UAB Post-doctoral Research Day, 2005.
- Grader for qualify exams at Department of Biostatistics, 2005–2011.