

Papers in Refereed Journals

1. Ding, J., **Lin, S.** XMCPDT does have correct type I error rates. *American Journal of Human Genetics*, in press.
2. Cataland, S.R., Jin, M., **Lin, S.**, Kennedy, M.S., Kraut, E.H., George, J.N., Wu, H.M. (2007) A Prospective Study of Concurrent Cyclosporine and Plasma Exchange in Thrombotic Thrombocytopenic Purpura. *British Journal of Haematology*, **139**, 486-493.
3. **Lin, S.** (2007) Mixture Modeling of Progression Pathways of Heterogeneous Breast Tumors. *Journal of Theoretical Biology*, **249**, 254-261.
4. Licht, B.G., **Lin, S.**, Luo, Y., Hyson, L., Licht, M., Harper, K., Sullivan, S., Fernandez, S., Johnson, E. (2007) Familial Focal Epilepsy in Standard Poodles: Clinical Characteristics and Mode of Inheritance. *Journal of the American Veterinary Medical Association*, in press.
5. Trainor, B.C., **Lin, S.**, Rowland, M.R., Finy, M.S., Nelson, R.J. (2007) Environmental mediation of estrogen dependent aggressive behavior via genomic and non-genomic mechanisms. *Proceedings of the National Academy of Sciences (USA)*, **104**, 9840-9845.
6. Wan, S., and **Lin, S.** (2007) A Likelihood-based Procedure for obtaining Confidence Intervals of Disease Loci with General Pedigree Data. *BMC Genetics*, in press.
7. Biswas, S., **Lin, S.** (2007) Incorporating covariates in mapping heterogeneous traits - a hierarchical model using empirical Bayes estimation. *Genetic Epidemiology*, **31**, 684-696.
8. Papachristou, B., Ebeney, M., and **Lin, S.** (2007) Confidence intervals of QTLs - development and application of new linkage methods. *BMC Genetics*, in press.
9. Wang, L., **Lin, S.**, Rammoham, K., Liu, Z., Liu, J-Q., Liu, R-J., Guinther1, N., Lima1, J., Zhou, Q, Wang, T., Zheng, X, Birmingham, D., Rovin, B., Hebert, L., Wu, Y., Lynn, D., Cooke, G., Yu, C.Y., Zheng, P., Liu, Y. (2007) A Destabilizing Di-nucleotide Deletion in 3'-Untranslated Region of CD24 mRNA Confers Protection against both Systemic and Organ-specific Autoimmune Diseases. *PLoS Genetics*, **3**, e49.
10. Blower, P.E., Verducci, J.S., **Lin, S.**, Zhou, J., Chung, J.-H., Dai, Z., Liu, C.-G., Reinhold, W., Croce, C.M., Weinstein, J.N., Sadee W. (2007) MicroRNA microarray expression data for the NCI-60 cancer cell panel. *Molecular Cancer Therapeutics*, **6**, 1483-1491.
11. Wang, Z., Yan, P., Potter, D., Eng, C., Huang, T.H., and **Lin, S.** (2007) Heritable clustering and pathway discovery in breast cancer integrating epigenetic and phenotypic data. *BMC Bioinformatics*, **8**:38.
12. Popesco, M., **Lin, S.**, Wang, Z., Ma, Z., Friedman, L., Frosthholm, A., and Rotter, A. (2007) Serial Analysis of Gene Expression (SAGE) profiles in the adult and aged mouse cerebellum. *Neurobiology of Aging*, in press.

13. Khalili, A., Potter, D., Yan, P., Li, L., Gray, J., Huang, T., and **Lin, S.** (2007) Gamma-Normal-Gamma Mixture Model for Detecting Differentially Methylated Loci in Three Breast Cancer Cell Lines. *Cancer Informatics*, **2**, 43-54.
14. Wang, Z., **Lin, S.**, Popesco, M., and Rotter, A. (2007) Modeling and Analysis of Multi-library, Multi-group SAGE Data with Application to a Study of Mouse Cerebellum. *Biometrics*, **63**, 777-786.
15. Liu, Z., **Lin, S.** (2006) Classification Using Mass Spectrometry Proteomic Data with Kernel-Based Algorithms. *Engineering Letters*, **13**:3.
16. Liu, Z., **Lin, S.**, Tan, M. (2006) Genome-wide tagging SNPs with entropy-based Monte Carlo methods. *Journal of Computational Biology*, **13**, 1606-1614.
17. Ding, J., **Lin, S.**, Liu, Y. (2006) A Monte Carlo pedigree disequilibrium test for x-chromosome markers. *American Journal of Human Genetics*, **79**, 567-573.
18. Papachristou, C., **Lin, S.** (2006) A comparison of methods for intermediate fine mapping. *Genetic Epidemiology*, **30**, 677-689.
19. Biswas, S. and **Lin, S.** (2006) A Bayesian approach for incorporating variable rates of heterogeneity in linkage analysis. *Journal of the American Statistical Association*, **101**, 1341-1351.
20. Verducci, J.S., Melfi, V.F., **Lin, S.**, Wang, Z., Roy, S., and Sen, C.K. (2006) Microarray analysis of gene expression: considerations in data mining and statistical treatment. *Physiological Genomics*, **25**, 364-374.
21. Papachristou, C., **Lin, S.** (2006) A Two-Step Procedure for Constructing Confidence Intervals of Trait Loci with Application to a Rheumatoid Arthritis Dataset. *Genetic Epidemiology*, **30**, 18-29.
22. Papachristou, C., **Lin, S.** (2006) Microsatellites Versus Single-Nucleotide Polymorphisms in Confidence Interval Estimation of Disease Loci. *Genetic Epidemiology*, **30**, 3-17.
23. Liu, Z., **Lin, S.** (2005) Multilocus LD Measure and Tag SNP Selection with Generalized Mutual Information. *Genetic Epidemiology*, **29**, 353-364.
24. Papachristou, C., **Lin, S.** (2005) A confidence set inference procedure for gene mapping using markers with incomplete polymorphism. *Human Heredity*, **59**, 1-13.
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27. Biswas, S., **Lin, S.**, Berry, D.A. (2005) A new Bayesian Approach Incorporating Covariate Information for Heterogeneity and its comparison with HLOD. *BMC Genetics*, **6**, S138.

28. Alexandridis, R., **Lin, S.**, Irwin, M. (2004) Class discovery and classification of tumor samples using mixture modeling of gene expression data - a unified approach. *Bioinformatics*, **20**, 2545-2552.
29. **Lin, S.**, Biswas, S. (2004) On modelling locus heterogeneity using mixture distributions. *BMC Genetics*, 5:29.
30. Rogers, J.A., Hsu, J.C., **Lin, S.** (2004) Using the partitioning principle to construct confidence sets for the location of a disease gene. *Journal of Statistical Planning and Inference*, **125**, 101-118.
31. Biswas, S., **Lin, S.** (2004) Evaluations of maximization procedures for estimating linkage parameters under heterogeneity. *Genetic Epidemiology*, **26**, 206-217.
32. Zhou, Q.M., Rammonham, K., **Lin, S.**, Robinson, N., Li, Q., Liu, X., Bai, X.F., Yin, L., Brook, B. You, M., Guan, K., Zheng, P., and Liu, Y. (2003) CD24 is a significant modifier for risk and progression of multiple sclerosis. *Proceedings of the National Academy of Sciences (USA)*, **100**, 15041-15046.
33. Biswas, S., Papachristou, C., Irwin, M., **Lin, S.** (2003) Linkage analysis of the simulated data – evaluations and comparisons of methods. *BMC Genetics*, **4**, S70.
34. **Lin, S.**, Skrivanek, Z., Irwin, M. (2003) Haplotyping using SIMPLE - caution on ignoring interference. *Genetic Epidemiology*, **25**, 384-387.
35. Luo, Y., **Lin, S.** (2003) Information gain for genetic parameter estimation with incorporation of maker data. *Biometrics*, **59**, 393-401.
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38. Cheng, R., Ma, J.Z., Wright, F.A., **Lin, S.**, Gao, X., Wang, D., Elston, R.C., Li, M.D. (2003) Nonparametric disequilibrium mapping of functional sites using haplotypes of multiple tightly linked single-nucleotide polymorphism (SNP) markers. *Genetics*, **164**, 1175-1187.
39. Licht, B., Licht. M., Harper, K., **Lin, S.**, Curtin, J., Hyson L, and Willard, K. (2002) Clinical presentations of naturally occurring canine seizures: similarities to human seizures. *Epilepsy and Behavior*, **3**, 460-470.
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41. **Lin, S.** (2001) Sample size requirement for detecting interference under the Chi-square model. *Human Heredity*, **52**, 201-209.
42. Luo, Y., **Lin, S.**, and Irwin, M. (2001) Two-locus modeling of asthma in a Hutterite pedigree via Markov chain Monte Carlo. *Genetic Epidemiology*, **21**, S24-S29.

43. Wang, D., **Lin, S.**, Cheng, R., Gao, X., and Wright, F.A. (2001) Transformation of sib pair values for the Haseman-Elston method. *American Journal of Human Genetics*, **68**, 1238-1249.
44. **Lin, S.**, Rogers, J.A., and Hsu, J.C. (2001) A confidence set approach for finding tightly linked genomic regions. *American Journal of Human Genetics*, **68**, 1219-1228.
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52. **Lin, S.** and Speed, T. P. (1996b) A Note on the Combination of Estimates of a Recombination Fraction. *Annals of Human Genetics*, **60**, 251-257.
53. **Lin, S.** and Speed, T. P. (1996a) Incorporating crossover interference into pedigree analysis using the chi-square model. *Human Heredity*, **46**, 315-322.
54. **Lin, S.** (1995) A scheme for constructing an irreducible Markov chain for pedigree data. *Biometrics*, **51**, 318-322.
55. **Lin, S.**, Thompson E., and Wijsman E. (1994b) An algorithm for Monte Carlo estimation of genotype probabilities on complex pedigrees. *Annals of Human Genetics*, **58**, 343-357.
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Refereed Papers in Edited Books / Book Chapters

60. Siegmund, K., **Lin, S.** Epigenetics. In: *Handbook of Statistical Genetics (3rd Edition)*. Handbook in Statistical Genetics. Ed: David Balding, Martin Bishop and Chris Cannings. John Wiley & Sons.
61. **Lin, S.**, Alexandridis, R. (2003) Classification of Tissue Samples Using Mixture Modeling of Microarray Gene Expression Data. In: *Science and Statistics: A Festschrift for Terry Speed*. IMS Lecture Notes – Monograph Series, Volume 40. Ed: D. R. Goldstein. Beachwood: IMS. pp 419-435.
62. **Lin, S.** (1996) Monte Carlo methods in genetic analysis. In: *Genetic mapping and DNA sequencing*. IMA Volumes in Mathematics and its Applications. Eds: T. P. Speed and M. S. Waterman. New York: Springer-Verlag. pp 15-38.

Scholarly Articles in Popular Periodicals

63. Licht, B., Licht, M., Harper, K., Hyson, L., **Lin, S.** (2002) Poodle Epilepsy Project: What's New in 2002? *Poodle Variety*, February-March, 2002.
64. Licht, B., **Lin, S.**, Licht, M., Harper, K., Curtin, J. and Verona, E. (1999) What breeders should know about epilepsy: Part III, how can breeders control idiopathic epilepsy? *Poodle Variety*, June-July, 1999.
65. Licht, B., Licht, M., **Lin, S.**, Harper, K., Curtin, J., and Verona, E. (1999) What breeders should know about epilepsy: Part II, Is it inherited, due to the environment, or both? *Poodle Variety*, pp 31, 32, & 88, April-May, 1999.
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68. Ding, J., and **Lin, S.** Monte Carlo Pedigree Disequilibrium Test with Application to UK Rheumatoid Arthritis SNP Data. *Proceedings of the Genetic Analysis Workshop 15*, 2-11.
69. Wang, D., Gao, X., **Lin, S.**, Skrivanek, Z., Irwin, M., Wright, F. (2000) Comparison of several methods for linkage analysis. *Proceedings of the Genetic Analysis Workshop 12*, pp509-513.
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71. **Lin, S.** (1997) Monte Carlo Bayesian methods for quantitative traits. In *Proceedings of the Second World Conference of IASC*, Editors: E.J. Wegman and S.P. Azen, *Computing Science and Statistics* **29(2)**, pp240-249.
72. Wijsman, E. and **Lin, S.** (1995) Monte Carlo methods in genetic epidemiology: opportunities and problems. *American Statistical Association 1995 Proceedings of the Section on Epidemiology*, pp 38-47.
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75. Licht, B., Hyson, L. **Lin, S.**, Luo, Y., Fernandez, S., Licht, M., Harper, K. (2003) Benign familial partial epilepsy in poodles: naturally occurring animal models. *Journal of the International League Against Epilepsy*, **44**, S9, p215.
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