BIBLIOGRAPHY

Books

1. **Lin, S.**, Zhao, H. (2009) Handbook on Analyzing Human Genetics Data: Computational approaches and software. Springer, New York.

2. **Lin, S.**, Scholtens, D., Datta, S. (2022) Bioinformatics Methods: From Microarrays to Next-Generation Sequencing. CRC Press.

Refereed Papers in Edited Books / Book Chapters

3. Han, C., Park, J., **Lin, S.** (2022) BCurve: Bayesian Curve Credible Bands Approach for Detection of Differentially Methylated Regions. In *DNA Methylation* (Ed: Weihua Guan), *Methods in Molecular Biology*, **2432**,167-185.

4. Hansen, K., Siegmund, K., **Lin, S.** (2019) Chapter 33: DNA Methylation, 933-948. In: *Handbook of Statistical Genomics (4th Edition)*. Ed: David Balding, Ida Moltke, and John Marioni. John Wiley & Sons.

5. Liu, Z., and **Lin, S.** (2018) Sparse Treatment Effect Model for Taxa Identification with High Dimensional Metagenomics Data. In *Microbiome Analysis* (Methods in Molecular Biology), **1849**, 309-318. Ed: Robert G. BeikoWill HsiaoJohn Parkinson, Humana Press.

6. Park, J., **Lin, S.** (2015) Statistical Inference on Three-Dimensional Structure of Genome by Truncated Poisson Architecture Model. In *Ordered Data Analysis, Modeling, and Health Research Methods - In Honor of H. N. Nagaraja's 60th Birthday* Choudhary, P., Nagaraja, C., Ng, T. (Eds.) Springer Proceedings in Mathematics & Statistics, Pages 245-261, Springer, New York.

7. **Lin, S.** (2013) Assessing the Effects of Imprinting and Maternal Genotypes on Complex Genetic Traits. In *Risk Assessment and Evaluation of Predictions*. Lee, M.-L.T., Gail, M., Pfeiffer, R., Satten, G., Cai, T., Gandy, A. (Eds.) Lecture Notes in Statistics, Vol. 210, Pages 285-300, Springer, New York.

8. Taslim, C., Huang, K., Huang, T., **Lin, S.** (2012) Analyzing ChIP-seq data: preprocessing, normalization, differential identification and binding pattern characterization. (Methods in Molecular Biology). Vol 802, 275-291. Ed. J Wang, AC Tan, T Tian. Humana Press.

9. Deatherage, D.E., Potter, D., Yan, P., Huang, T.H.-M., **Lin, S.** (2009) Methylation analysis by microarray. Chapter 9, Microarray Analysis of the Physical Genome: Methods and Protocols (Methods in Molecular Biology). **556**, 117-139. Ed. Jonathan Pollack. Humana Press.

10. Igo, R., Luo, Y., **Lin, S.** (2010) Monte Carlo linkage analysis methods and software packages. In *Handbook on analyzing human genetic data: computational approaches and software*. Lin, S., and Zhao, H.Y. Eds. Springer, New York.

11. Yan, P., Potter, D., Deatherage, D.E., **Lin, S.**, Huang, T.H.-M. (2008) Differential methylation hybridization: profiling DNA methylation in a high-density CpG island microarray. Chapter 8, Methods in Molecular Biology for DNA Methylation Analysis, 2nd edition.

12. Siegmund, K., **Lin. S.** (2007) Chapter 40. Epigenetics. In: *Handbook of Statistical Genetics (3rd Edition).* Ed: David Balding, Martin Bishop and Chris Cannings. John Wiley & Sons.

13. **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.

14. **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.

Refereed Journal Papers - Methodological

15. Xie, Q., Han, C., Jin, V., **Lin, S.** (2022) HiCImpute: A Bayesian Hierarchical Model for Identifying Structural Zeros and Enhancing Single Cell Hi-C Data. *PLOS Computational Biology*, **18** (6), e1010129. doi.org/10.1371/journal.pcbi.1010129.

16. Chen, Q., Song, C., **Lin, S.** (2022) An Adaptive and Robust Test for Microbial Community Analysis. *Frontiers in Genetics*, 19 May 2022. https://doi.org/10.3389/fgene.2022.846258

17. Turkmen, A., **Lin, S.** (2021) Detecting X-linked common and rare variant effects in family-based sequencing studies. *Genetic Epidemiology*, **45**, 36-45.

18. Han, C., Xie, Q., **Lin, S.** (2021) Are dropout imputation methods for scRNA-seq effective for scHi-C data? *Briefings in Bioinformatics*, **22**(4): bbaa289. DOI: 10.1093/bib/bbaa289

19. Kim, M., **Lin, S.** (2020) Characterization of histone modification patterns and prediction of novel promoters using functional principal component analysis. *PLoS ONE*, 5(5):e0233630.

20. Zhou, X., Wang, M., **Lin, S.** (2020) Detecting Rare Haplotypes Associated with Complex Diseases Using Both Population and Family Data: Combined Logistic Bayesian Lasso. *Statistical Methods in Medical Research*, **29**, 3340-3350. https://doi.org/10.1177/0962280220927728

21. Zhang, F., **Lin, S.** (2020) Incorporating Information from Markers in LD with Test Locus for Detecting Imprinting and Maternal Effects. *European Journal of Human Genetics*, **28**, 1087-1097

22. Shokoohi, F., Khalili, A., Asgharian, M., and **Lin, S.** (2019) Capturing heterogeneity of covariate effects in hidden subpopulations in the presence of censoring and large number of covariates. *Annals of Applied Statistics*, **13**, 444-465.

23. Zhang, F., Khalili,A., and **Lin, S.** (2019) Imprinting and Maternal Effect Detection Using Partial Likelihood Based on Discordant Sibpair Data. *Statistica Sinica*, **29**, 1915-1937. doi:10.5705/ss.202016.0114

24. Datta, A., Biswas, S., and **Lin S.** (2019) A Family-Based Rare Haplotype Association Method for Quantitative Traits. *Human Heredity*, 83:175-195.

25. Park, J. and **Lin, S.** (2019) Evaluation and Comparison of Methods for Recapitulation of 3D Spatial Chromatin Structures. *Briefings in Bioinformatics*, **20**, 1205-1214.

26. Ma, V. L., **Lin, S.** (2019) Examining the rare disease assumption used to justify HWE testing with control samples. *Mathematical Biosciences and Engineering*, **17**, 73-91.

27. Chen, D.-P., Zhang, F., **Lin, S.** (2019) AIJ: Joint Test for Simultaneous Detection of Imprinting and Non-imprinting Allelic Expression Imbalance. *Mathematical Biosciences and Engineering*, **17**, 366-386.

28. Luo, H., **Lin, S.** (2018) Evaluation of Classical Statistical Methods for Analyzing BS-Seq Data. *OBM Genetics*, **2** Article 053; doi:10.21926/obm.genet.1804053.

29. Han, C., Tang, H., Lou, S., Goa, Y. Cho, M. H., **Lin, S.** (2018) Evaluation of Recent Statistical Methods for Detecting Differential Methylation Using BS-seq Data. *OBM Genetics*, **2** Article 041; doi:10.21926/obm.genet.1804041.

30. Li, L., Wang, C., Lu, T., **Lin, S.**, and Hu Y-Q. (2018) Indirect effect inference and application to GAW 20 data. *BMC Genetics*, **19**(Suppl 1): 67

31. Zhou, X., Wang, M., Stewart, W.C.L., and **Lin, S.** (2018) Logistic Bayesian LASSO for detecting association combining family and case-control data. *BMC Proceedings*, **12**(Suppl 9): 54.

32. Zhang, Y., Hofmann, J.N., Purdue, M.P., **Lin, S.**, Biswas, S. (2017) Logistic Bayesian LASSO for Genetic Association Analysis of Data from Complex Sampling Designs. *Journal of Human Genetics*, **62**, 819-829.

33. Turkmen, A. and **Lin, S.** (2017) Are Rare Variants Really Independent? *Genetic Epidemiology*, **41**, 363-371.

34. Park, J. and **Lin, S.** (2018) Detection of Differentially Methylated Regions Using Bayesian Curve Credible Bands. *Statistics in Biosciences*, **10**, 20-40.

35. Zhang, F., Ding, J. and **Lin, S.** (2017) Testing for Associations of Opposite Directionality in a Heterogeneous Population. *Statistics in Biosciences*, **9**, 137-159.

36. Zhang, Y., **Lin, S.**, and Biswas, S. (2017) Detecting rare haplotype-environment interaction under uncertainty of gene-environment independence assumption. *Biometrics*, **73**, 344-355.

37. Park, J., **Lin, S.** (2017) A Random Effect Model for Reconstruction of Spatial Chromatin Structure. *Biometrics*, **73**, 52-62.

38. Zhu, D., Hu, Y., and **Lin, S.** (2016) Block-Based Association Tests for Rare Variants Using Kullback-Leibler Divergence. *Journal of Human Genetics*, **61**, 965-975 .

39. Qin, Z. Li, B., Conneely, K.N., Wu, H., Hu, M., Ayyala, D., Park, Y., Jin, V.X., Zhang, F., Zhang, H., Li, L., **Lin, S.** (2016) Statistical challenges in analyzing methylation and long-range chromosomal interaction data. *Statistics in Biosciences*, **8**, 284-309.

40. Park, J., **Lin, S.** (2016) Impact of Data Resolution on Three-Dimensional Structure Inference Methods. *BMC Bioinformatics*, **17**:70.

41. Liu, Z.,**Lin, S.**, Deng, N., McGovern, D.P.B., Piantadosi, S. (2016) Sparse inverse covariance estimation with L0 Penalty for Network Construction with Omic Data. *Journal of Computational Biology*, 23, 192-202.

42. Liu, Z., **Lin, S.**, Piantadosi, S. (2015) Network Construction and Structure Detection with Metagenomic Count Data. *BioData Mining*, **8**, Article Number 40.

43. Ayyala, D.N., Frankhouser, D.E., Ganbat, J.O., Marcucci, G., Bundschuh, R., Yan, P., **Lin, S.** (2016) Statistical Methods for Detecting Differentially Methylated Regions Based on MethylCap-Seq Data. *Briefings in Bioinformatics*, **17**, 926-937.

44. Zhang, F., Khalili, A., **Lin, S.** (2016) Optimum study design for detecting imprinting and maternal effects based on part ial likelihood. *Biometrics*, **72**, 95-105.

45. Park, J., Taslim, C., **Lin, S.** (2015) BOG: R-package for Bacterium and Virus Analysis of Orthologous Groups. *Computational and Structural Biotechnology Journal*, **13**, 366-369.

46. Schimek, M.G., Budinska, E., Ding, J., Kugler, K.G., Svendova, V., **Lin, S.** (2015) TopKLists: a comprehensive R package for statistical inference, stochastic aggregation, and visualization of multiple omic ranked lists. *Statistical Applications in Genetics and Molecular Biology*, **14**, 311-316.

47. Ayyala, D., and **Lin, S.** (2015) GrammR: Graphical Representation and Modeling of Count Data with Application in Metagenomics. *Bioinformatics*, **31**, 1648-1654.

48. Wang, M., and **Lin, S.** (2015) Detecting Associations of Rare Variants with Common Diseases: Collapsing or Haplotyping? *Briefings in Bioinformatics*, **16**, 759-768.

49. Turkmen, A., Yan, Z., Hu, Y., and **Lin, S.** (2015) Kullback-Leibler Distance Methods for Detecting Disease Association with Rare Variants for Sequencing Data. *Annals of Human Genetics*, **79**, 199-208.

50. Niu, L., and **Lin, S.** (2015) A Bayesian mixture model for Chromatin Interaction Data. *Statistical Applications in Genetics and Molecular Biology*, **14**, 53-64.

51. **Lin, S.** (2015) Kullback-Leibler divergence for detection of rare haplotype common disease association. *European Journal of Human Genetics*, **23**, 1558-1565.

52. Frankhouser, D.E., Murphy, M., Blachly, J.S., Park, J., Zoller, M.W., Ganbat, J.-O., Curfman, J., Byrd, J.C., **Lin, S.**, Marcucci, G., Yan, P., Bundschuh, R. (2014) PrEMeR-CG: Inferring Nucleotide Level DNA Methylation Values from MethylCap-Seq Data. *Bioinformatics*, **30**, 3567-3574.

53. Zhang, F. and **Lin, S.** (2014) Nonparametric method for detecting imprinting effects using all members of general pedigrees with missing data. *Journal of Human Genetics*, **59**, 541-548.

54. Taslim, C., and **Lin, S.** (2014) A Mixture Modeling Framework for Differential Analysis of High-Throughput Data. *Computational and Mathematical Methods in Medicine*, **2014**, Article Number 758718. doi:10.1155/2014/758718.

55. Wang, M., and **Lin, S.** (2014) FamLBL: Detecting Rare Haplotype Disease Association Based on Common SNPs Using Case-Parent Triads. *Bioinformatics*, **30**, 2611-2618.

56. Niu, L., Li, G., and **Lin, S.** (2014) Statistical Models for Detecting Differential Chromatin Interactions Mediated by a Protein. *PLoS ONE*, **9**, e97560.

57. Turkmen, A., and **Lin, S.** (2014) Blocking Approach for Identification of Rare Variants in Family-based Association Studies. *PLoS ONE*, **9**, e86126.

58. Xia, S., **Lin, S.** (2014) Detecting longitudinal effects of haplotypes and smoking on hypertension using B-Splines and Logistic Bayesian Lasso. *BMC Proceedings*, **8**, S85.

59. Zhang, F., **Lin, S.** (2014) Detection of Imprinting Effects for Hypertension Based on General Pedigrees Utilizing All Affected and Unaffected Individuals. *BMC Proceedings*, **8**, S52.

60. Turkmen, A., **Lin, S.** (2014) Identifying Rare Variant Associations in Population-based and Family-based Designs. *BMC Proceedings*, **8**, S58.

61. Biswas, S., Xia, S., and **Lin, S.** (2014) Detecting Rare Haplotype-Environment Interaction with Logistic Bayesian LASSO. *Genetic Epidemiology*, **38**, 31-41.

62. Han, M., Hu, Y., **Lin, S.** (2013) Joint detection of association, imprinting and maternal effects using all children and their parents. *European Journal of Human Genetics*, **21**, 1449-1456.

63. Khalili, A., **Lin, S.** (2013) Regularization in finite mixture of regression models with diverging number of parameters. *Biometrics*, **69**, 436-446.

64. Yang, J. and **Lin, S.** (2013) Robust Partial Likelihood Approach for Detecting Imprinting and Maternal Effects Using Case-Control Families. *Annals of Applied Statistics*, **7**, 249-268.

65. Turkmen, A. and **Lin, S.** (2012) An Optimum Projection and Noise Reduction Approach for Detecting Rare and Common Variants Associated with Complex Diseases. *Human Heredity*, **74**, 51-60.

66. Taslim, C., **Lin, S.**, Huang, K., Huang, T. (2012) Integrative genome-wide chromatin signature analysis using finite mixture models. *BMC Genomics*, 13(Suppl 6):S3.

67. Papachristou, B., **Lin, S.** (2012) A confidence set inference method for identifying SNPs that regulate quantitative phenotypes. *Human Heredity*, **73**, 174-183.

68. Taslim, C., Chen, Z., Huang, K., Huang, T., Wang, Q., **Lin, S.** (2012) Integrated analysis identifies a class of androgen responsive genes regulated by short combinatorial long-range mechanism facilitated by CTCF. *Nucleic Acids Research*, **40**, 4754-4764.

69. Yang, J, and **Lin, S.** (2012) Likelihood Approach for Detecting Imprinting and Maternal Effect Using General Pedigrees from Prospective Family-Based Association Studies. *Biometrics*, **68**, 477-485.

70. Biswas, S., and **Lin, S.** (2012) Logistic Bayesian LASSO for identifying association with rare haplotypes and application to age-related macular degeneration. *Biometrics*, **68**, 587-597.

71. Sun, S., Huang, Y-W., Yan, P.S., Huang, T., **Lin, S.** (2011) Preprocessing differential methylation hybridization microarray data. *BioData Mining*, 4:13.

72. Taslim, C., Huang, T., **Lin, S.** (2011) DIME: R-package for Identifying Differential ChIP-seq Based on an Ensemble of Mixture Models. *Bioinformatics*, **27**, 1569-1570. DOI: 10.1093/bioinformatics/btr165

73. Turkmen, A., and **Lin, S.** (2011) Gene Based Partial Least Squares Approaches for Detecting Rare Variants Associations with Complex Traits. *BMC Proceedings*, 5(Suppl 9):S19.

74. Sun, S., Chen, Z., Yan, P.S., Huang, Y.W., Huang, T.H.M, **Lin, S.** (2011) Identifying hypermethylated CpG islands using a quantile regression model. *BMC Bioinformatics*, **12**, 54.

75. He, F, Zhou, J.Y., Hu, Y.Q., Sun, F., Yang, J., **Lin, S.**, Fung, W.K. (2011) Detection of Parent-of-Origin Effects for Quantitative Traits in Complete and Incomplete Nuclear Families With Multiple Children. *American Journal of Epidemiology*, **174**, 226-233. doi: 10.1093/aje/kwr056

76. Khalili, A., Chen, J., **Lin, S.** (2011) Feature selection in finite mixture of sparse normal linear models in high dimensional feature space. *Biostatistics*, **12**, 156-172. doi: 10.1093/biostatistics/kxq048

77. **Lin, S.** (2010) Space oriented rank-based data integration. *Statistical Applications in Genetics and Molecular Biology.* **9**, Article 20.

78. **Lin, S.** (2010) Rank Aggregation methods. *Wiley Interdisciplinary Reviews: Computational Statistics*, **2**, 555-570.

79. Liu, Z., **Lin, S.**, Tan, M. (2010) Sparse Support Vector Machines with L_p Penalty for Improved Biomarker Identification. *IEEE ACM Transactions on Computational Biology and Bioinformatics*, **7**, 100-107.

80. Zhou, J., Ding, J., Fung, W., **Lin, S.** (2010) Detection of Parent-of-Origin Effects Using General Pedigree Data. *Genetic Epidemiology*, **34**, 151-158.

81. Sun, S., Yan, P., Huang, T., **Lin, S.** (2009) Identifying differentially methylated genes using mixed effect and generalized least square models. *BMC Bioinformatics*, **10:**404.

82. Taslim, C., Wu, J., Yan, P., Singer, G., Ozer, G;, Parvin, J., Huang, T., **Lin, S.**, Huang, K. (2009) Comparative Study on ChIP-seq Data: Normalization and Binding Pattern Characterization. *Bioinformatics*, **25**, 2334-2340.

83. Guo, W., Liang, C.-Y., **Lin, S.** (2009) Haplotype association analysis of NARAC data using rGLM. *BMC Proceedings*, **3**, S32.

84. Yang, J., **Lin, S.** (2009) Detection of imprinting and heterogeneous maternal effects on high blood pressure using Framingham Heart Study data, *BMC Proceedings*, **3**, S125.

85. **Lin, S.**, Ding, J. (2009) Integration of Ranked Lists via Cross Entropy Monte Carlo with Applications to mRNA and microRNA Studies. *Biometrics*, **65**, 9-18.

86. Guo, W., **Lin, S.** (2009) Generalized Linear Modeling with Regularization for Detecting Common Disease Rare Haplotype Association. *Genetic Epidemiology*, **33**, 308-316.

87. Khalili, A., Huang, T., **Lin, S.** (2009) A Robust Unified Approach to Analyzing Methylation and Gene Expression Data. *Computational Statistics and Data Analysis*, **53**, 1701-1710.

88. Zhou, J., **Lin, S.**, Fung, W.K., Hu, Y.-Q. (2009) Detection of parent-of-origin effects in complete and incomplete nuclear families with multiple affected children using multiple tightly linked markers. *Human Heredity*, **67** , 116-127.

89. Zhou, J., Hu, Y.-Q., **Lin, S.**, Fung, W.K. (2009) Detection of Parent-of-Origin effects based on complete and incomplete nuclear families with multiple affected children. *Human Heredity*, **67**, 1-12.

90. Potter, D., Yan, P., Hung, T.H.-M., **Lin, S.** (2008) Probe signal correction for differential methylation hybridization experiments. *BMC Bioinformatics*, **9**:453.

91. Ding, J., **Lin, S.** (2008) XMCPDT does have correct type I error rates. *American Journal of Human Genetics*, **82**, 528-530.

92. **Lin, S.** (2007) Mixture Modeling of Progression Pathways of Heterogeneous Breast Tumors. *Journal of Theoretical Biology*, **249**, 254-261. DOI:10.1016/j.jtbi.2007.08.010

93. Wan, S., and **Lin, S.** (2007) A Likelihood-based Procedure for obtaining Confidence Intervals of Disease Loci with General Pedigree Data. *BMC Proceedings*, 1(Suppl 1):S106.

94. Biswas, S., **Lin, S.** (2007) Incorporating covariates in mapping heterogeneous traits - a hierarchical model using empirical Bayes estimation. *Genetic Epidemiology*, **31**, 684-696.

95. Papachristou, B., Abney, M., and **Lin, S.** (2007) Confidence intervals of QTLs - development and application of new linkage methods. *BMC Proceedings*, 1(Supp 1):S91.

96. 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.

97. 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.

98. Wang, Z., **Lin, S.**, Popesco, M., and Rotter, A. (2007) Modeling and Analysis of :q Multi-library, Multi-group SAGE Data with Application to a Study of Mouse Cerebellum. *Biometrics*, **63**, 777-786.

99. Liu, Z., **Lin, S.** (2006) Classification Using Mass Spectrometry Proteomic Data with Kernel-Based Algorithms. *Engineering Letters*, **13**:3.

100. Liu, Z., **Lin, S.**, Tan, M. (2006) Genome-wide tagging SNPs with entropy-based Monte Carlo methods. *Journal of Computational Biology*, **13**, 1606-1614.

101. 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.

102. Papachristou, C., **Lin, S.** (2006) A comparison of methods for intermediate fine mapping. *Genetic Epidemiology*, **30**, 677-689.

103. 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.

104. 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.

105. 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.

106. Papachristou, C., **Lin, S.** (2006) Microsatellites Versus Single-Nucleotide Polymorphisms in Confidence Interval Estimation of Disease Loci. *Genetic Epidemiology*, **30**, 3-17.

107. Liu, Z., **Lin, S.** (2005) Multilocus LD Measure and Tag SNP Selection with Generalized Mutual Information. *Genetic Epidemiology*, **29**, 353-364.

108. Papachristou, C., **Lin, S.** (2005) A confidence set inference procedure for gene mapping using markers with incomplete polymorphism. *Human Heredity*, **59**, 1-13.

109. Papachristou, C., **Lin, S.** (2005) Interval Estimation of Disease Loci - Development and Applications of New Linkage Methods. *BMC Genetics*, **6**, S21.

110. **Lin, S.**, Ding, J., Dong, C., Liu, Z., Ma, Z.J., Wan, S., and Xu, Y. (2005) Comparisons of methods for linkage analysis and haplotype reconstruction using extended pedigree data. *BMC Genetics*, **6**, S76.

111. 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.

112. 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.

113. **Lin, S.**, Biswas, S. (2004) On modelling locus heterogeneity using mixture distributions. *BMC Genetics*, 5:29.

114. 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.

115. Biswas, S., **Lin, S.** (2004) Evaluations of maximization procedures for estimating linkage parameters under heterogeneity. *Genetic Epidemiology*, **26**, 206-217.

116. Biswas, S., Papachristou, C., Irwin, M., **Lin, S.** (2003) Linkage analysis of the simulated data – evaluations and comparisons of methods. *BMC Genetics*, **4**, S70.

117. **Lin, S.**, Skrivanek, Z., Irwin, M. (2003) Haplotyping using SIMPLE - caution on ignoring interference. *Genetic Epidemiology*, **25**, 384-387.

118. Luo, Y., **Lin, S.** (2003) Information gain for genetic parameter estimation with incorporation of maker data. *Biometrics*, **59**, 393-401.

119. Luo, Y., **Lin, S.** (2003) Finding starting points for Markov chain Monte Carlo analysis of genetic data from large and complex pedigrees. *Genetic Epidemiology*, **25**, 14-24.

120. Skrivanek Z., **Lin, S.**, Irwin, M. (2003) Linkage analysis with sequential imputation. *Genetic Epidemiology*, **25**, 25-35.

121. 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.

122. **Lin, S.** (2002) Construction of a confidence set of markers for the location of a disease gene using affected-sib-pair data. *Human Heredity*, **53**, 103-112.

123. **Lin, S.** (2001) Sample size requirement for detecting interference under the chi-square model. *Human Heredity*, **52**, 201-209.

124. 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.

125. 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.

126. **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.

127. **Lin, S.**, Cheng, R., and Wright, F. (2001) Genetic crossover interference in the human genome. *Annals of Human Genetics*, **65**, 79-93.

128. **Lin, S.** (2000) Monte Carlo methods for linkage analysis of two-locus disease models. *Annals of Human Genetics*, **64**, 519-532.

129. **Lin, S.** (1999) Monte Carlo Bayesian methods for quantitative traits. *Computational Statistics and Data Analysis*, **31**, 89-108.

130. **Lin, S.** and Speed, T. P. (1999) Relative efficiencies of the chi-square recombination models for gene mapping with human pedigree data. *Annals of Human Genetics*, **63**, 81-95.

131. **Lin, S.**, Irwin, M. and Wright, F. (1999) A multiple locus analysis of the collaborative study on the genetics of alcoholism data set. *Genetic Epidemiology*, **17**, S229-S234.

132. **Lin, S.** and Speed, T. P. (1997) An algorithm for haplotype analysis. *Journal of Computational Biology*, **4**, 535-546.

133. **Lin, S.** (1996) Multipoint linkage analysis via Metropolis jumping kernels. *Biometrics*, **52**, 1417-1427.

134. **Lin, S.** and Speed, T. P. (1996) A note on the combination of estimates of a recombination fraction. *Annals of Human Genetics*, **60**, 251-257.

135. **Lin, S.** and Speed, T. P. (1996) Incorporating crossover interference into pedigree analysis using the chi-square model. *Human Heredity*, **46**, 315-322.

136. **Lin, S.** (1995) A scheme for constructing an irreducible Markov chain for pedigree data. *Biometrics*, **51**, 318-322.

137. **Lin, S.**, Thompson E., and Wijsman E. (1994) An algorithm for Monte Carlo estimation of genotype probabilities on complex pedigrees. *Annals of Human Genetics*, **58**, 343-357.

138. **Lin, S.**, Thompson E., and Wijsman E. (1994) Finding non-communicating sets for Markov chain Monte Carlo estimates on pedigrees. *American Journal of Human Genetics*, **54**, 695-704.

139. **Lin, S.**, and Thompson, E. (1993) Discussion on the Gibbs sampler and other Markov chain Monte Carlo methods. *Journal of the Royal Statistical Society B* **55**, 81-82.

140. **Lin, S.**, Thompson E., and Wijsman E. (1993) Achieving irreducibility of the Markov chain Monte Carlo method applied to/ pedigree data. *IMA Journal of Mathematics Applied in Medicine & Biology*, **10**, 1-17.

141. Thompson, E., **Lin, S.**, Olshen, A., and Wijsman, E. (1993) Monte Carlo analysis of a large hypercholesterolemia pedigree. *Genetic Epidemiology*, **10**, 677-682.

142. **Lin, S.** (1986) Several classes of curved surfaces in taxicab geometry. *Journal of the South China Normal University (Natural Science Edition), 1986, Number 1, 7-11.*

143. **Lin, S.** (1984) Some properties of semi-separable topological spaces. *Journal of the South China Normal University (Natural Science Edition), 1984, sum 33, 88-93.*

Papers in Refereed Journals - Applied

144. Yufan Zhou; Xiaolong Cheng; Yini Yang; Tian Li; Jingwei Li; Tim Huang; Junbai Wang; **Shili Lin**, Victor X. Jin. (2020) Modeling and analysis of Hi-C data by HiSIF identifies characteristic promoter-distal loops. *Genome Medicine*, Article number: 69.

145. Joseph, J., Zhou, X., Zilbermint, M., Stratakis , C., Faucz, F., Lodish, M., Berthon, A., Wilson, J., Hsueh, W., Golden, S., and **Lin, S.** (2020) The Association of ARMC5 with the Renin-Angiotensin-Aldosterone System, Blood Pressure and Glycemia in African Americans. *The Journal of Clinical Endocrinology and Metabolism*, **105**, 2625-2633. (featured in Endocrine eNews on May 27, 2020)

146. Wu, H., Jay, L., Masias, C., **Lin, S.**, Han, C., Yang, S., and Cataland, S.R. (2020) Interrelationship Between ADAMTS13 Activity, Von Willebrand Factor, and Complement Activation in Remission from Immune-Mediated TTP. *British Journal of Haematology*, **189**, e1-e30.

147. Zhou, Y., Gerrard, D., Wang, J., Li, T., Yang, Y., Fritz, A., Rajendran, M., **Lin, S.**, Frietze, S., Schiff, R., Jin, V. (2019) Temporal dynamic reorganization of 3D chromatin architecture in hormone-induced breast cancer and endocrine resistance. *Nature Communications*, **10**, Article number: 1522.

148. Gerrard, D.L, Wang, Y., Gaddis, M., Zhou, Y., Wang, J., Witt, H., **Lin, S.**, Farnham, P.J., Jin, V.X., Frietze, S.E. (2018) Three dimensional analysis reveals altered chromatin interaction by enhancer inhibitors harbors TCF7L2 regulated cancer gene signature. J Cell Biochem, **120**, 3056-3070.

149. Enquobahrie, D.A., Moore, A., Muhie, S., Tadesse, M., **Lin, S.**, Williams, M.A. (2015) Early Pregnancy Maternal Blood DNA Methylation in Repeat Pregnancies and Change in Gestational Diabetes Mellitus Status - A Pilot Study. *Reproductive Sciences*, **22**, 904-910.

150. Chen, Z., Lan, X., Thomas-Ahner, J.M., Liu, X., Ye, Z., Wu, D., Wang, L., Sunkel, B., Grenade, C., Chen, J., Zynger, D.L., Yan, P.S., Nephew, K.P., Huang, T.H.M., **Lin, S.**, Clinton, S.K., Jin, V.X., Li, W., Wang , Q. (2014). Agonist and Antagonist Switch DNA Motifs Recognized by Human Androgen Receptor in Prostate Cancer. *EMBO Journal*, **34**, 502-516.

151. Wood, K.L., Diaz, P.T., Rahmanian, S.D., King, M., Wu, H., Yang, S.B., **Lin, S.**, Horne, A. (2014) Gender Differences in Pulmonary Function, Respiratory Symptoms and Macrophage Proteomics among HIV-Infected Smokers. *Scientifica*, vol. 2014, Article ID 613689, 9 pages, 2014. doi:10.1155/2014/613689.

152. Shapiro, J.P., Biswis, S., Merchant, A.S., Satoskar, A., Taslim, C., **Lin, S.**, Rovin, B., Sen, C.K., Roy, S, Freitas, M.A. (2012) A quantitative proteome workflow for characterization of frozen clinical biopsies: laser capture microdissection coupled with label-free mass spectrometry. *Journal of Proteomics*, **2-12**, 433-440.

153. Wang, L., Liu, R., Li, D., **Lin, S.**, Fang, X, Backer, G., Kain, M., Rammoham, K., Zheng, P., Liu, Y. (2012) A hypermorphic SP1-binding CD24 Variant Associates with Risk and Progression of Multiple Sclerosis. *American Journal of Translational Research*, **4**, 347-356.

154. Yang, S., Jin, M., **Lin, S.**, Cataland, S., Wu, H. (2011) ADAMTS13 activity and antigen during therapy and follow-up of patients with idiopathic thrombotic thrombocytopenic purpura: correlation with clinical outcome. *Haematologica -THE HEMATOLOGY JOURNAL*, **96**, 1521-1527.

155. Cataland, S., Yang, S., Witkoff, L., Kraut, E., **Lin, S.**, George, J., Wu, H. (2009) Demographic and ADAMTS13 Biomarker Data as Predictors of Early Recurrences of Idiopathic Thrombotic Thrombocytpenic Purpura. European Journal of Haematology, **83**, 559-564.

156. Cataland, S.R., , M., **Lin, S.**, Kraut, E.H., George, J.N., Wu, H.M. (2008) Effect of prophylactic cyclosporine therapy on ADAMTS13 biomarkers in patients with idiopathic thrombotic thrombocytopenicc purpura. American Journal of Hematology, **83**, 911-915.

157. Lin, H.-J., Zuo, T., Lin, C.-H., Kuo, C.T., Liyanarachchi, S., Sun, S., Shen, R., Deatherage, D.E., Potter, D., Asamoto, L., **Lin, S.**, Yan, P.S., Cheng, A.-L., Ostrowski, M.C., Huang, T.H.-M. (2008) Breast Caner-associated Fibroblasts Confer AKT1-mediated Epigenetic Silencing of Cystatin M in Epithelial Cells. *Cancer Research*, **68**, 10257-10266.

158. Jin, M., Casper, T.C., Cataland, S.R., Rikabi, N.R., **Lin, S.**, Li, Y.J., Wu, H.M. (2008) Relationship between ADAMTS13 activity in clinical remission and the risk of TTP relapse. *British Journal of Haematology*, **141**, 651-658.

159. Popesco, M., **Lin, S.**, Wang, Z., Ma, Z., Friedman, L., Frostholm, A., and Rotter, A. (2008) Serial Analysis of Gene Expression (SAGE) profiles in the adult and aged mouse cerebellum. *Neurobiology of Aging*, **29**, 774-788.

160. Blower, P., Chung, J., Dai, Z., Verducci, J., **Lin, S.**, Liu, C., Reinhold, W., Croce, C., Weinstein, J., Sadee, W. (2008) MicroRNAs modulate the chemosensitivity of tumor cells. *Molecular Cancer Therapeutics*, **7**, 1-9.

161. Cataland, S.R., Jin, M., **Lin, S.**, Kennedy, M.S., Kraut, E.H., George, J.N., Wu, H.M. (2007) Ciclosporin and plasma exchange in thrombotic thrombocytopenic purpura: long-term follow-up with serial analysis of ADAMTS13 activity. *British Journal of Haematology*, **139**, 486-493.

162. 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*, **231**, 1520-1528.

163. Trainor, B.C., **Lin, S.**, Rowland, M.R., Finy, M.S., Nelson, R.J. (2007) Environmental mediation of estrogen dependent aggressive behavior via genomic an d non-genomic mechanisms. *Proceedings of the National Academy of Sciences (USA)*, **104**, 9840-9845.

164. 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 dinucleotide deletion in CD24 confers protection against autoimmune diseases. *PLoS Genetics*, **3**, e49.

165. Blower, P.E., Verducci, J.S., **Lin, S.**, Zhou, J., Chung, J.-H., Dai, Z., Li u, 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.

166. 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.

167. Licht, B., Licht. M., Harper, K., **Lin, S.**, Curtin, J., Hyson L, and Willard, K. (2002) Clinical characteristics and mode of inheritance of familial focal seizures in Standard Poodles. *Epilepsy and Behavior*, **3**, 460-470.

Scholarly Articles in Periodicals

168. Licht, B., Licht. M., Harper, K., Hyson, L., **Lin, S.** (2002) Poodle Epilepsy Project: What's new in 2002? *Poodle Variety*, February-March, 2002.

169. 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.

170. 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.

171. Licht, B., Harper, K., Licht. M., **Lin, S.** and Curtin, J. (1999) What breeders should know about epilepsy: Part I, what to tell a puppy buyer? *Poodle Variety*, pp 10 & 12, February-March, 1999.

172. Licht, B., **Lin, S.**, Licht, M., and Harper, K. (1998) Epilepsy in Dalmatians. *The Spotter*, Vol. 28, No. 4, pp 52 & 56.

173. **Lin, S.** (1984) The mappings of dual spaces and transposed matrices. *Teaching Mathematics at Normal Universities*, pp 23-28.

Selected Conference Proceeding Papers (not published elsewhere)

174. Masias, C., Yang, S., Sukumar, S., Flowers, A., Wu, H., Carter, K., Lin, S., Han, C., Cataland, S. (2020) Relapse Prediction Model for Immune-Mediated Thrombotic Thrombocytopenic Purpura. *Blood* **136** (Supplement 1): 8–9.

175. Schimek, G.S., Budinska, E., Kuglar, K., **Lin, S.** (2011) Package "TopKLists" for rank-based genomic data integration. Proceedings of the IASTED International Conference. on Computational Bioscience (CompBio 2011), 434-440 (refereed).

176. Sun, S., Potter, D., Yan, P., Huang, TH.-M., **Lin, S.** (2008) A quantile approach to analyzing differential methylation hybridization (DMH) microarrays. Poster proceedings of the 4th International Symposium on Bioinformatics Research and Applications (ISBRA): 87-90.

177. Wan, S., and **Lin, S.** Likelihood based confidence set procedures for disease localization with general pedigree data. *American Statistical Association 2007 Proceedings*.

178. 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.

179. 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.

180. Wright, F., Berry, C., Irwin, M. and **Lin, S.** (1998) Allele sharing: testing and modeling in a simulated dataset. *Proceedings of the Genetic Analysis Workshop 11*, pp 637-641.

181. **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. (Invited)

182. 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. (Invited)