Peng Liu

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Iowa State University   *pliu@iastate.edu*

EMPLOYMENT

Professor	**Department of Statistics**, Iowa State University	2020-present
Associate Professor	**Department of Statistics**, Iowa State University	2013-2020
Assistant Professor	**Department of Statistics**, Iowa State University	2006-2013

EDUCATION

Ph.D.   **Biological Statistics and Computational Biology**, Cornell University, 7/2006

M.S.   **Nutritional Sciences**, Cornell University, 8/2001

B. Med.   **Biomedical Sciences**, Peking University Health Science Center (previously known as Beijing Medical University), Beijing, China, 7/1998

RESEARCH INTERESTS

- Statistical Genomics, omics Data Analysis
- Microbiome Data Analysis
- Statistical Inference for High-dimensional Data
- Causal Inference
- Statistical Learning

HONORS AND AWARDS

- Iowa State University Plant Sciences Institute Scholar, 2018-present
- College of Liberal Arts and Sciences Award for Mid-Career Achievement in Research, 2018
- Iowa State University College of Agriculture and Life Sciences Team Award, 2015
- Iowa State University Award for Early Achievement in Research, 2013
- Graduate School Travel Award and Fellowship, Cornell University, 2005
- Student Research Grant Award, School of Industrial and Labor Relations, Cornell University, 2004
- Graduate School Travel Award and Fellowship, Cornell University, 2003
- Barns Fellowship, Cornell University, 2000
- Student Research Grant Award of Division of Nutritional Sciences, Cornell University, 2000

REFEREED JOURNAL ARTICLES (bold for Liu and her students, * for corresponding author)

1. **E. Goren,** C. Wang, Z. He, A. Sheflin, D. Chiniquy, J. Prenni, S. Tringe, D. Schachtman, **P. Liu***, Feature selection and causal analysis for microbiome studies in the presence of confounding using standardization. BMC Bioinformatics 22, 362 (2021). https://doi.org/10.1186/s12859-021-04232-2

2. J. Zhao, **Y. Qi, P. Liu**, A. Severin, M. Sayadi, I. Paetau-Robinson, W.S. White, (2021). Prebiotic Effects of a Cranberry Beverage in a Randomized, Placebo-Controlled, Crossover Clinical Trial. *Current Developments in Nutrition*, 5(2), 1190, https://doi.org/10.1093/cdn/nzab054_045

3. P. Kanodia, V. Paramasivan, R. Srivastava, **R. Bi**, **P. Liu**, W. A. Miller, S. H. Howell (2020), Control of translation during the unfolded protein response in maize seedlings: Life without PERKs, *Plant Direct*, https://doi.org/10.1002/pld3.241

4. J. Bao, Y. Yu, H. Li, J. Hawks, G. Szatkowski, B. Dade, **H. Wang, P. Liu**, T. Brutnell, B. Spehar, N. Tye-Murray (2020), Evidence for Independent Peripheral and Central Age-Related Hearing Impairment, *Journal of Neuroscience Research*, https://doi.org/10.1002/jnr.24639

5. L. A. Laboissonniere, J. J. Goetz, G. M. Martin, **R. Bi**, T. J.S. Lund, L. Ellson, M. R. Lynch, B. Mooney, H. Wickham, A. Mani, **P. Liu**, G. W. Schwartz, and J. M. Trimarchi (2019), Molecular signatures of retinal ganglion cells revealed through single cell profiling, *Scientific Reports,* 31;9(1):15778, doi: 10.1038/s41598-019-52215-4

6. A. Sheflin, D. Chiniquy, **C. Yuan, E. Goren**, I. Kumar, M. Braud, T. Brutnell, A. Eveland, S. Tringe, **P. Liu**, S. Kresovich, E. Marsh, D. Schachtman, and J. Prenni (2019), Metabolomics of sorghum roots during nitrogen stress reveals compromised metabolic capacity for defense response, *Plant Direct,* 3(3): e00122, https://doi.org/10.1002/pld3.122

7. M. He, K. Wimalanathan, **P. Liu**, C.J. Lawrence-Dill (2019), Compare Expression Profiles for Pre-defined Gene Groups with C-REx. Journal of Open Source Software, 4(37), 1255, http://joss.theoj.org/papers/10.21105/joss.01255

8. L. Dong, L. Qin, X.Dai, Z. Ding, **R. Bi**, **P. Liu**, Y. Chen, T. Brutnell, X. Wang, and P. Li (2019) Transcriptomic Analysis of Leaf Sheath Maturation in Maize, *International Journal of Molecular Sciences*, 20(10), 2472, https://doi.org/10.3390/ijms20102472

9. R.Srivastava, Z. Li, G. Russo, J. Tang, **R. Bi**, U. Muppirala, A. Severin, M. He, S. Vaitkevicius, C. Lawrence-Dill, **P. Liu**, A.E. Stapleton, D. Bassham, F. Brandizzi, S. Howell (2018), A multi-level analysis of the transition from cell survival to cell death in response to persistent ER stress in maize seedlings, *The Plant Cell*, 30, 1220-1242, http://www.plantcell.org/content/30/6/1220

10. **E. Goren**, **P. Liu*****,** C. Wang, and C. Wang (2018), BinQuasi: a peak detection method for ChIP-sequencing data with biological replicates, *Bioinformatics,* 34(17), 2909–2917, https://doi.org/10.1093/bioinformatics/bty227

11. Y. Zhang, R. Giuliani, Y. Zhang, W. L. Araujo, B. Wang, **P. Liu**, Qi Sun, A. Cousins, G. Edwards, A. Fernie, A. Barkan, T. Brutnell, P. Li (2018), Characterization of maize leaf Pyurvate Orthophosphate Dikinase using high throughput sequencing, *Journal of Integrative Plant Biology*, 60(8): 670-690, https://onlinelibrary.wiley.com/doi/full/10.1111/jipb.12656

12. M. He, **P. Liu**, C.J. Lawrence-Dill (2017), A hypothesis-driven approach assessing significance of differences in RNA expression levels among specific groups of genes, *Current Plant Biology,* 11-12, 46-51*,* https://doi.org/10.1016/j.cpb.2017.12.003

13. S. Hu, C. Wang, D. Sanchez, A. Lipka, **P. Liu**, Y. Yin, M. Blanco, T. Lubberstedt (2017), Gibberellins promote brassinosteroids action and both increase heterosis for plant height in maize (Zea mays L.), *Frontiers in Plant Science*, 8: 1039 doi: 10.3389/fpls.2017.01039

14. L. Laboissonniere, G. M. Martin, J. J Goetz, **R. Bi**, B. Pope, K. Weinand, L. Ellson, D. Fru, M. Lee, A. K Wester, **P. Liu**, and J. M Trimarchi (2017), Single cell transcriptome profiling of developing chick retinal cells, *The Journal of Comparative Neurology*, 2017, 525: 2735-2781 [doi: 10.1002/cne.24241](doi: 10.1002/cne.24241)

15. N. Cray, Y. Zhao, **Y. Fang, P. Liu**, L. Pollak, S. Duvick, D. F. Birt, and E. M. Whitley (2017), Effects of dietary resistant starch on the WNT signaling pathway and pre-neoplastic cells in the colons of azoxymethane-treated rats, *Nutrition and Cancer,* 69(4):632-642 [doi:10.1080/01635581.2017.1299875](doi:10.1080/01635581.2017.1299875)

16. C. Zhang, Z. Fei, **P. Liu**, J. Peng, D. Hannapel (2017). Transcriptome changes in response to cold acclimation in perennial ryegrass as revealed by a cross-species microarray analysis, *Crop Science*, 57:1-13 doi: 10.2135/cropsci2016.04.0252

17. **F. Liu,** C. Wang, Z. Wu, Q. Zhang, and **P. Liu*** (2016), A Zero-Inflated Poisson Model for Insertion Tolerance Analysis of Genes Based on Tn-seq Data, *Bioinformatics*, 32: 1701-1708, doi: 10.1093/bioinformatics/btw061

18. **R. Bi** and **P. Liu*** (2016), Sample size calculation for designing RNA-sequencing experiments, *BMC Bioinformatics,* **17** :146, [doi: 10.1186/s12859-016-0994-9](doi: 10.1186/s12859-016-0994-9)

19. Z. Ding, Y. Zhang, Y. Xiao, **F. Liu**, M. Wang, X. Zhu, **P. Liu**, Qi Sun, W. Wang, M. Peng, T. Brutnell, P. Li (2016), Transcriptome response of cassava leaves under natural shade, *Scientific Reports,* 6:31673, doi: 10.1038/srep31673

20. H. Sun, **R. Bi**, **P. Liu**, L. Nolan, and S. Lamont (2016), Combined Analysis of Primary Lymphoid Tissues' Transcriptomic Response to Extra-intestinal Escherichia coli (ExPEC) Infection, *Developmental & Comparative Immunology*, 57:99-106, [doi:10.1016/j.dci.2015.12.013](doi:10.1016/j.dci.2015.12.013)

21. B. Nelson, N. Cray, Y. Ai, **Y. Fang**, **P. Liu**, E. M. Whitley, D. Birt (2016), Effect of Dietary Resistant Starch on Inhibition of Colonic Preneoplasia and Wnt Signaling in Azoxymethane-Induced Rodent Models, *Nutrition and Cancer,* 68(6):1052-63, [doi:10.1080/01635581.2016.1192203](doi:10.1080/01635581.2016.1192203)

22. H. Sun, **P. Liu**, L. Nolan, and S. Lamont (2016), Thymus Transcriptome Reveals Novel Pathways in Response to Avian Pathogenic Escherichia coli (APEC) Infection, *Poultry Science,* 95(12): 2803-2814[doi: 10.3382/ps/pew202](doi: 10.3382/ps/pew202)

23. **F. Liu,** C. Wang, and **P. Liu*** (2015), A Semi-parametric Bayesian Approach for Differential Expression Analysis of RNA-seq Data, *Journal of Agricultural, Biological, and Environmental Statistics,* 20(4): 555-576, [doi: 10.1007/s13253-015-0227-0](doi: 10.1007/s13253-015-0227-0)

24. H. Sun, **P. Liu**, L. Nolan, and S. Lamont (2015), Novel Pathways Revealed in Bursa of Fabricius Transcriptome in Response to Extraintestinal Pathogenic Escherichia coli (ExPEC) Infection, *PLoS ONE*, 10(11): e0142570. doi:10.1371/journal.pone.0142570

25. H. Sun, **P. Liu**, L. Nolan, and S. Lamont (2015), Avian pathogenic *Escherichia coli* (APEC) infection alters the bone marrow transcriptome in chickens, *BMC Genomics*, 16: 690, [doi:10.1186/s12864-015-1850-4](doi:10.1186/s12864-015-1850-4)

26. J. E. Koltes, E. Fritz-Waters†, C. J. Eisley, I. Choi, H. Bao, A. Kommadath, N. V. L. Serão, N. J. Boddicker, S. M. Abrams, M. Schroyen, H. Loyd, C. K. Tuggle, G. S. Plastow, L. Guan, P. Stothard, J. K. Lunney, **P. Liu**, S. Carpenter, R. Rowland, J. C.M. Dellers, J. M. Reecy (2015), Identification of a putative quantitative trait nucleotide in Guanylate Binding Protein 5 for host response to PRRS virus infection, *BMC Genomics*, 16: 412, doi:10.1186/s12864-015-1635-9

27. L. Wang, Czedik-Eysenberg, A. Mertz, R. A., **Y. Si**, T. Tohge, A. Nunes-Nesi, S. Arrivault, L. K Dedow, D. W Bryant, **W. Zhou**, J. Xu, S. Weissmann, A. Studer, P. Li, C. Zhang, T. LaRue, Y. Shao, Z. Ding, Q. Sun, R. V Patel, R. Turgeon, X. Zhu, N. J Provart, T. C Mockler, A. R Fernie, M. Stitt, **P. Liu**, and T. P. Brutnell (2014), Exploring the mechanism of C_4 photosynthetic differentiation through a unified comparative analysis of maize and rice leaf transcriptomes, *Nature Biotechnology,* 32: 1158–1165, doi:10.1038/nbt.3019

28. **M. Orr**, **P. Liu** and D. Nettleton (2014), An Improved Method for Computing Q-values when the Distribution of Effect Sizes is Asymmetric, *Bioinformatics,* 30 (21) 3044-3053, doi:10.1093/bioinformatics/btu432

29. **T. Ji**, **P. Liu** and D. Nettleton (2014), Estimation and Testing of Gene Expression Heterosis, *Journal of Agricultural, Biological, and Environmental Statistics* 19(3): 319-337 doi:10.1007/s13253-014-0173-2

30. **Y. Du**, C. Wang and **P. Liu** (2014), A Permutation Test of Genetic Association between Salmonella Isolated On-farm and At-abattoir using Amplified Fragment Length Polymorphism, *Journal of Biometrics and Biostatistics,* 5:204 doi:10.4172/2155-6180.1000204

31. S. L. Taustra, P. Li, **Y. Si**, N. Gandotra, **P. Liu**, Q. Sun, T. P. Brutnell, and T. Nelson (2014) Developmental dynamics of Kranz cell transcriptional specificity in maize leaf reveals early onset of C4-related processes, *Journal of Experimental Botany*, 65(13):3543-55 doi:10.1093/jxb/eru152

32. **Y. Si**, **P. Liu***, P. Li and T. Brutnell (2014), Model-based clustering of RNA-seq data, *Bioinformatics,* 30(2): 197-205 doi: 10.1093/bioinformatics/btt632

33. **Y. Si** and **P. Liu*** (2013), An Optimal Test with Maximum Average Power While Controlling FDR with Application to RNA-seq Data, *Biometrics,* 69, 594-605. DOI: 10.1111/biom.12036

34. **W. Landau** and **P. Liu** (2013), Dispersion Estimation and Its Effect on Test Performance in RNA-seq Data Analysis: A Simulation-Based Comparison of Methods, *PLoS ONE,* 8(12): e81415. doi:10.1371/journal.pone.0081415

35. Q. Xia, W. T. Muraola, Z. Shen, O. Sahin, H. Wang, Z. Wu, **P. Liu**, and Q. Zhang (2013), Adaptive mechanisms of *Campylobacter jejuni* to erythromycin treatment, *BMC Microbiology*, 13:133. doi:10.1186/1471-2180-13-133

36. X. Chen, **P. Liu**, H-H. Chou (2013), Whole-genome thermodynamic analysis reduces siRNA off-target effects, *PLoS ONE* 8(3): e58326. doi:10.1371/journal.pone.0058326

37. Z. Wu, O. Sahin, Z. Shen, **P. Liu**, W. G. Miller and Q. Zhang (2013), Multi-omics approaches to deciphering a hypervirulent strain of *Campylobacter jejuni, Genome Biology and Evolution,* 5(11):2217-30, doi: 10.1093/gbe/evt172

38. H. Hao, Z. Yuan, Z. Shen, J. Han, O. Sahin, **P. Liu**, Q. Zhang (2013), Mutational and transcriptomic changes involved in the development of macrolide resistance in *Campylobacter jejuni*, *Antimicrobial Agents and Chemotherapy*, 57(3):1369, doi: 10.1128/AAC.01927-12

39. **M. Orr, P. Liu** and D. Nettleton (2012), Estimating the Number of Genes that are Differentially Expressed in Both of Two Independent Experiments, the *Journal of Agricultural, Biological, and Environmental Statistics*, 17(4): 583-600. doi: 10.1007/s13253-012-0108-8

40. **P. Liu*** and C. Wang (2012), An optimal semi-parametric testing procedure for normal means, *invited article for Journal of Probability and Statistics,* Volume 2012, Article ID 913560, doi:10.1155/2012/913560

41. H. Lin, C. Wang, **P. Liu**, D.J. Holtkamp (2012), Construction of Disease Risk Scoring Systems using Logistic Group Lasso: Application to Porcine Reproductive and Respiratory Syndrome Survey Data, *Journal of Applied Statistics,* 40(4): 736-746. doi:10.1080/02664763.2012.752449

42. W. Fang, **Y. Si**, S. Douglass, D.C. Diaz-Cano, S. Merchant, M. Pellegrini, **P. Liu** and M. Spalding (2012), Global Changes in *Chlamydomonas* Gene expression Regulated by Carbon Dioxide and CIA5/CCM1, *The Plant Cell, 24(5):1876-93,* doi/10.1105/tpc.112.097949

43. **T. Ji**, **P. Liu** and D. Nettleton (2012), Borrowing Information Across Genes and Experiments for Improved Residual Variance Estimation in Microarray Data Analysis, *Statistical Applications in Genetics and Molecular Biology,* 11: 3, Article 12, doi: 10.1515/1544-6115.1806

44. **V. M. Kvam, P. Liu*** **and Y. Si** (2012), A comparison of statistical methods for detecting differentially expressed genes from RNA-seq data, *invited article for American Journal of Botany*, 99(2): 248-256. doi/10.3732/ajb.1100340

45. E. E. Sandford, **M. Orr**, X. Li, H. Zhou, T. J. Johnson, S. Kariyawasam, **P. Liu**, L. K. Nolan and S. J. Lamont (2012), Strong Concordance Between Transcriptomic Patterns of Spleen and Peripheral Blood Leukocytes in Response to Avian Pathogenic *Escherichia coli*, *Avian Diseases,* 56(4):732-736, doi: 10.1637/10261-060512-Reg.1

46. T. Luangtongkum, Z. Shen, V. W. Seng, O. Sahin, B. Jeon, **P. Liu**, Q. Zhang (2012), Impaired fitness and transmission of macrolide-resistant *Campylobacter jejuni* in its natural host, *Antimicrobial Agents and Chemotherapy* 56(3): 1300-1308*,* doi: 10.1128/AAC.05516-11

47. E. E. Sandford, **M. Orr**, M Shelby, X. Li, H. Zhou, T. J. Johnson, S. Kariyawasam, **P. Liu**, L. K. Nolan and S. J. Lamont (2012), Leukocyte Transcriptome from Chickens Infected with Avian Pathogenic *Escherichia coli* Identifies Pathways Associated with Resistance, *Results in Immunology* 2: 44-53. doi:10.1016/j.rinim.2012.02.003

48. L. Wang, **Y. Si**, L. K. Dedow, Y. Shao, **P. Liu**, T. Brutnell (2011), A Low-Cost Library Construction Protocol and Data Analysis Pipeline for Illumina-Based Strand-Specific Multiplex RNA-Seq, *PLoS ONE* 6(10): e26426*.* doi:10.1371/journal.pone.0026426

49. E. E. Sandford, **M. Orr**, E. Balfanz, N. Bowerman, X. Li, H. Zhou, T. J. Johnson, S. Kariyawasam, **P. Liu**, L. K. Nolan and S. J. Lamont (2011) Spleen transcriptome response to infection with avian pathogenic *Escherichia coli* in broiler chickens, *BMC genomics*, 12:469 doi:10.1186/1471-2164-12-469

50. G. Li, K. Tivendale. **P. Liu**, Y. Feng, Y. Wannemuheler，W.Cai, P. Mangiamele, T. Johnson，C. Penn and L.K. Nolan (2011) Transcriptome Analysis of Avian Pathogenic *Escherichia coli* O1 in Chicken Serum Reveals Adaptive Responses to Systemic Infection, *Infection and Immunity*, 79: 1951-1960; doi:10.1128/IAI.01230-10

51. X. Yu, L. Li, J. Zola, M. Aluru, H. Ye, A. Foudree, H. Guo, S. Anderson, S. Aluru, **P. Liu**, S. Rodermel and Y. Yin (2011) A brassinosteroid transcriptional network revealed by genome-wide identification of *bes1* target genes in *Arabidopsis thaliana, The Plant Journal*, 65(4):634-46 doi: 10.1111/j.1365-313X.2010.04449.x

52. J. T. G. Hwang and **P. Liu** (2010) Optimal tests shrinking both means and variances applicable to microarray data analysis, *Statistical Applications in Genetics and Molecular Biology*, 9:1 article 36, doi: 10.2202/1544-6115.1587

53. P. Li, L. Ponnala, N. Gandotra, L. Wang, **Y. Si**, L. Tausta, T. Kebrom, N. Provart, R. Patel, C.R. Myers, E.J. Reidel, R. Turgeon, **P. Liu**, Q. Sun, T. Nelson, and T. Brutnell (2010) The developmental dynamics of the maize leaf transcriptome as revealed through ultra high-throughput sequencing, *Nature Genetics*, 42(12): 1060-1067, doi:10.1038/ng.703

54. **M. Orr** and **P. Liu*** (2009) Sample size estimation while controlling false discovery rate for microarray experiments using the ssize.fdr package, *R Journal*, 1(1) 47-53

55. S. Covshoff, W. Majeran, **P. Liu**, K. J. M. Kolkman, K. J. van Wijk, T. Brutnell (2008) De-regulation of maize C_4 photosynthetic development in a mesophyll cell defective, *Plant Physiology*, 146: 1469-1481, doi: 10.1104/pp.107.113423

56. **P. Liu*** and J. T. G. Hwang (2007) Quick estimation of sample size while controlling false discovery rate and application to microarray analysis, *Bioinformatics*, 23: 739-746, doi: 10.1093/bioinformatics/btl664

57. X. Zheng, H-C Huang, W. Li, **P. Liu,** Q-Z Li, Y. Liu (2007) Modeling nonlinearity in dilution design microarray data, *Bioinformatics*, 23: 1339-1347, doi:10.1093/bioinformatics/btm002

58. R. J. H. Sawers, **P. Liu**, K. Anufrikova, Q. Sun, G. Olsefski, J. T. G. Hwang, T. Brutnell (2007) A multi-treatment experimental system to examine photosynthetic differentiation in the maize leaf, *BMC genomics*, 8:12, doi:10.1186/1471-2164-8-12

59. S. A. Jesch, **P. Liu**, X. Zhao, M. T. Wells, and S. A. Henry (2006) Multiple endoplasmic reticulum-localized protein complexes respond to phospholipid metabolism and regulate gene expression by distinct mechanisms, *Journal of Biological Chemistry*, 281: 24070 – 24083, doi: 10.1074/jbc.M604541200

60. T. N. Soon, N. Shaw, N. Vinckenbosch, **P. Liu** (equally contributed first authors), et al., (2002) Selective cooperation between fatty acid-binding proteins and peroxisome proliferator-activated receptors in regulating transcription, *Molecular and Cellular Biology,* 22: 5114-5127, doi: 10.1128/MCB.22.14.5114-5127.2002

61. J. Ni, **P. Liu**, H. Jia (2000), Binding Properties of M-CAT Element in the Chicken Nicotinic Acetylcholine Receptor γ-Subunit Promoter, *Chinese Journal of Biochemistry and Molecular Biology*, 2000,V16(05): 580-585

BOOK CHAPTERS

62. **P. Liu** and **Y. Si**, Cluster analysis of RNA-sequencing data (2014), in the book of *Statistical Analysis of Next Generation Sequencing Data*, *Springer*

63. **P. Liu, E. Goren**, P. Morris, D. Walker, and C. Wang, Statistical Methods for Feature Selection in Microbiome Studies (2020), invited book chapter for *Statistical Analysis of Microbiome Data*, *Springer,* accepted

SUBMITTED PAPERS

64. M. I. Natukundaa, M. B. Mantilla-Pereza,b, M. A. Grahama,c, **P. Liu**, and M. G. Salas-Fernandez, Dissection of canopy layer-specific genetic control of leaf angle in Sorghum bicolor by RNA sequencing, *submitted*, 2020

65. M. Qi, J. C. Berry, K. Veley, L. O'Connor, O. M. Finkel, I. Salas-González, M. Kuhs, J. Jupe, E. Holcomb, T. Del Rio, C. Creech, **P. Liu**, S. Tringe, J. L. Dangl, D. Schachtman, R. S. Bart, Cross-system conservation of interacting beneficial and detrimental responses to drought in the sorghum microbiome, *submitted*, 2021

66. J. Wang, X. Li, T. Guo, M. Dzievit, X. Yu, **P. Liu**, J. Yu, Aerial Based High-throughput Phenotyping for Genetic Dissection of Seasonal Vegetation Index Dynamics in Maize, *revised and re-submitted*, 2021

67. **R. Bi** and **P. Liu**, A semi-parametric Bayesian methods for detection of gene expression with RNA-seq data, *revised and re-submitted*, 2021

68. J. C. Berry, M. Qi, B. V. Sonawane, A. Sheflin, A. B. Cousins, J. Prenni, D. P. Schachtman, **P. Liu**, R. S. Bart,Increased signal to noise ratios within experimental field trials by regressing spatially distributed soil properties as principal components, *submitted*, 2021

69. Qin, X. Wang, X. Tu, D. Tzeng, **R. Bi**, Z. Ding, **P. Liu**, G. Li, Y. Chen, T. Brutnell, S. Zhong, and P. Li, The LIGULELESS2 (LG2) regulatory network in the maize leaf, *revised and submitted to The Plant Journal*, 2019

PAPERS UNDER DEVELOPMENT

70. **C. Yuan, P. Liu**, and C. Wang, A Bayesian approach based on a hierarchical Poisson hurdle model for differential abundance analysis of microbiome data, *to be submitted*

71. **R. Bi** and **P. Liu**, RiboZIP, detection of differential translations based on a zero-inflated Poisson model for ribosome profiling data, *to be submitted*

72. **W. Zhao, P. Liu**, and C. Wang, Ranking differential abundant microbes using microbiome count data, *to be submitted*

73. J. Wang, X. Li, T. Guo, M. Dzievit, X. Yu, **P. Liu**, K. P. Price, J. Yu, Aerial Based High-throughput Phenotyping for Genetic Dissection of NDVI in Maize, *in preparation*

74. **H. Wang**, Y. Qiu, C. Wang, **P. Liu**, Gene Co-expression Network Reconstruction With Partial Correlation Graph, *in preparation*

75. Zhao, J., Qi, Y., Liu, P., Severin, A., Sayadi, M., Dubois, L., Thompson, W., Moseley, A., & White, W.S. (2021). Prebiotic Effects of a Cranberry Beverage in Healthy Adults: a Randomized, Placebo-Controlled, Crossover study. *in preparation*.

76. **C. Yuan, P. Liu**, and C. Wang, Causal mediation analysis with high-dimensional microbiome data, *in preparation*

77. M. Cao, **W. Zhou, P. Liu**, L. Wang, and T. B. Brutnell, A semiparametric approach for the study of circadian patterns using RNA-sequencing data, *in preparation*

78. **Y. Si**, **P. Liu**, L. Wang and T. Brutnell, Empirical Bayes methods to detect differential alternative splicing with RNA-seq data, *in preparation*

79. Y. Nguyen, **M. Orr, P. Liu** and D. Nettleton, A Histogram-based Method for False Discovery Rate Control in Two Independent Experiments, *in preparation*

80. L. Wang, A. Czedik-Eysenberg, **Y. Si**, L. Ponnala, A. Nunes-Nesi, T. Tohge, R. Mertz, P. Li, L. Dedow, T. Mockler, C. Myers, Q. Sun, **P. Liu**, A. Fernie, M. Stitt and T. P. Brutnell, Integration of maize leaf transcriptome and metabolome defines novel regulatory modules, *in preparation*

R PACKAGES FROM MY RESEARCH GROUP

1. `Ssize.fdr`: sample size calculation for t- and F-tests while controlling FDR
2. `AMAP.Seq`: empirical Bayes test to detect differentially expressed genes with RNA-seq data
3. `MBCluster.Seq`: model-based clustering with RNA-seq data
4. `ssizeRNA`: sample size calculation while controlling FDR for RNA-seq experiment
5. `BinQuasi`: Joint analysis of biological replicates for ChIP-sequencing data

GRANTS

1. **Co-PI** (sole statistician) for Systems Analysis of the Physiological and Molecular Mechanisms of Sorghum Nitrogen Use Efficiency, Water Use Efficiency, and Interactions with the Soil Microbiome, D. Schachtman (PI, University of Nebraska-Lincoln), with other co-PIs: M. Harrison (Boyce Thompson Institute), S. Kresovich (Clemson University); J. Prenni (Colorado State University), R. Bart, A. Eveland, and T. Mockler (Donald Danforth Plant Science Center), S. Tringe (Lawrence Berkeley National Laboratory–DOE Joint Genome Institute), I. Dweikat and A. Zygielbaum (University of Nebraska–Lincoln), J. Dangl (University of North Carolina at Chapel Hill), and A. Cousins (Washington State University)
   Source of Support: **DOE** (DE-SC0014395)
   Total Award Amount: $ 13,460,684
   My portion: $ 544,952
   Total Award Period Covered: 08/15/2015-07/31/2022

2. **PI** (sole PI) for Statistical Methods for 'omics Data Analysis
   Source of Support: Plant Science Institute, Iowa State University
   Total Award Amount: $ 225,000
   Total Award Period Covered: 2/1/2018-6/30/2024

3. **Co-investigator** (sole statistician) for Investigating Obesity-Induced Altered Ovarian Intracellular Signaling, together with Keating (PI)
   Source of Support: **NIH** (R01ES030341-01)
   Total Award Amount: $ 2,394,307
   Total Award Period Covered: 1/1/2020-10/31/2024

4. **Co-investigator** (sole statistician) for Global Effects of Flavivirus sfRNA on Translation Determined by Ribosome Profiling, together with W.A. Miller (PI, Iowa State University)
   Source of Support: **NIH**
   Total Award Amount: $ 391,104
   Total Award Period Covered: 6/04/2021 to 05/31/2023

5. **Co-investigator** (sole statistician) for Dietary Intervention Strategies to Support Methyl Group Metabolism in Polycystic Ovary Syndrome, together with K. Schalinske (PI, Iowa State University)
   Source of Support: **NIH**
   Total Award Amount: $ 146,551
   Total Award Period Covered: 02/25/2019 to 01/31/2020

6. **Co-PI** (sole statistician) for The molecular hallmark of epigenetic control in high-performing yeast, together with Z. Shao (PI, Iowa State University)
   Source of Support: Presidential Interdisciplinary Research Seed Grant Program (PIRS), Iowa State University
   Total Award Amount: $ 50,000
   Total Award Period Covered: 1/1/2018-12/31/2019

7. **Co-investigator** for Central Plains Research Data Center seed award, together with C. Wang (PI), Z. He, and D-K Lee (Iowa State University)
   Source of Support: Central Plains Research Data Center
   Total Award Period Covered: 08/16/2018-08/15/2019

8. **Co-investigator** for Hierarchical Modeling and Parallelized Bayesian Inference for the Analysis of RNAseq Data, together with D. Nettleton (PI), J. Niemi and P. Schnable (Iowa State University)
   Source of Support: **NIH**
   Total Award Amount: $ 1,173,287
   Total Award Period Covered: 09/01/2013-05/31/2018

9. **Co-PI** (sole statistician) for GEPR: A Systems Approach to the Development and Function of C4 Photosynthesis, T. Nelson (PI, Yale University), other co-PIs: T. Brutnell (Donald Danforth Plant Science Center) and K. van Wijk (Cornell University)
   Source of Support: **NSF**
   Total Award Amount: $ 8,386,495
   My portion: $ 372,843
   Total Award Period Covered: 02/15/2012-01/31/2017

10. **Co-PD** for Improving nutrient utilization and feed efficiency through research and extension to enhance pig industry sustainability and competitiveness, together with Patience (PD) and Anderson, Campbell, Dekkers, DeRouchey, Gabler, Gilbert, Johnson, Kerr, Lonergan, Lonergan, Mabry, Nettleton, Rothschild, Rowland, Tokach, Tuggle, van Kessel, Weber
    Source of Support: **USDA**

Total Award Amount: $ 4,999,158
Total Award Period Covered: 3/1/2011-2/29/2016

11. **Co-PI** (sole statistician) for GEPR: Comparative analysis of C3 and C4 leaf development in rice, sorghum and maize, T. Nelson (PI, Yale University), other co-PIs: T. Brutnell (Boyce Thompson Institute) and K. van Wijk (Cornell University)
Source of Support: **NSF**
Total Award Amount: $ 5,475,676
My portion: $ 280,484
Total Award Period Covered: 08/01/2007-07/31/2012

12. **Co-PI** (sole statistician) for Host:Pathogen Interactions in Avian Colibacillosis: a Systems-Based, Functional Genomics Approach**,** together with Nolan (PI), Johnson, Lamont, Kariyawasam and Trampel (Iowa State University)
Source of Support: **USDA**
Total Award Amount: $ 955,330
My portion: $ 96,744
Total Award Period Covered: 02/01/2008-01/31/2012

13. **Co-PI** (sole statistician) for Functional genomics analysis of a highly virulent *Campylobacter jejuni* clone causing sheep abortion, together with Zhang (PI), Yaeger and Sahin (Iowa State University)
Source of Support: **USDA**
Total Award Amount: $ 998,467
Total Award Period Covered: 12/15/09-12/14/12
14. **Co-investigator** for Integration of quantitative genetics, statistics, and computational biology for animal genetic improvement, together with Dekkers and Lamont (Iowa State University)
Source of Support: **USDA** CSREES
Total Award Amount: $ 258,000
Total Award Period Covered: 1/1/2010-12/31/2012

15. **Co-investigator** (sole statistician) for PSI Healthy Carbohydrate Project
Source of Support: Plant Sciences Institute, Iowa State University
Total Award Amount: $ 250,000
Total Award Period Covered: 2011-2012

16. **Co-PI** for Development of high-dimensional data analysis methods for the identification of differentially expressed gene sets, together with D. Nettleton (PI), S. X. Chen, J. Dekkers and C. Tuggle (Iowa State University)
Source of Support: **NSF**
Total Award Amount: $ 552,927
My portion: $ 46,950
Total Award Period Covered: 08/15/2007-08/14/2011

17. **Co-PI** (sole statistician) for Inorganic Carbon Transport and the CO2-concentrating Mechanism
18. f *Chlamydomonas*, together with Martin Spalding (PI, Iowa State University)
Source of Support: **USDA**
Total Award Amount: $ 351,000
Total Award Period Covered: 09/01/2007-08/31/2010

19. **Participant** for Approaching crops as ecosystems (ACE): Complex biotic interactions affecting plant health
> Source of Support: Plant Sciences Institute, Iowa State University
> Total Award Amount: $ 40,000
> Total Award Period Covered: 2011-2012

20. **Statistician** for Identification of Novel APEC Virulence Genes via Functional Genomics, together with Li (PI), Nolan, and Kariyawasam (Iowa State University)
> Source of Support: USDA Formula Funds Grant from Iowa State University
> Total Award Amount: $ 20,000
> Total Award Period Covered: 11/01/2007-10/31/2009

Pending:

21. **Co-investigator** for URoL:EN. Elucidation of the complex dynamic networks of conditional associations that emerge due to the interaction between root exudates and the rhizosphere microbiome, together with Schachtman (PI)
> Source of Support: **NSF**
> Total Award Amount: $ 2,462,905
> Total Award Period Covered: 12/01/2021-11/30/2026

22. **Co-investigator** (sole statistician) for Investigating Obesity-Induced Altered Ovarian Intracellular Signaling, together with Keating (PI)
> Source of Support: **NIH**
> Total Award Amount: $ 195,858
> Total Award Period Covered: 3/1/2021-2/29/2024

23. **Co-investigator** (sole statistician) for Targeting cerebral Pulsatility through Aerobic exercise Training in mIddLe agE (PulsATILE Trial), together with Wesley Lefferts (PI)
> Source of Support: **NIH**
> Total Award Amount: $2,822,667
> Total Award Period Covered: 4/1/2022-3/31/2027

STUDENT ADVISING

Graduate students:

♦ **Major/Co-Major Professor** for **26** graduate students (**20 graduated**)

PhD students (17):

Current:
1. *Yunhui Qi, Statistics*
2. *Zhili Qiao, Statistics*
3. *Amin Shiraz, Statistics*
4. *David Walker, Statistics*
5. *Hao Wang, Statistics*
6. *Wenting Zhao, Statistics*

Graduated:

7. *Emily Goren* (Co-Major Professor: Chong Wang), Statistics
PhD Dissertation (summer, 2019): Statistical methods for ChIP-seq and microbiome studies using next-generation sequencing data
currently working at the Institute for Health Metrics and Evaluation

8. *Ran Bi,* Statistics
PhD Dissertation (summer, 2018): Statistical methods for gene expression studies using next-generation sequencing experiments
currently working at FDA

9. *Chaohui Yuan* (Co-Major Professor: Chong Wang), Statistics
PhD Dissertation (summer, 2018): Statistical methods for microbiome data and antimicrobial resistance analysis
currently working at Eli Lily

10. *Haibo Liu* (Co-Major Professor: Chris Tuggle), Bioinformatics and Computational Biology
PhD Dissertation (spring, 2017): *The swine blood transcriptomics: Application and advancement*
currently working at Iowa State University

11. *Fangfang Liu* (Co-Major Professor: Chong Wang), Statistics
PhD Dissertation (spring, 2015): *Statistical methods in detecting differentially expressed genes, analyzing transposon insertion tolerance for gene, and group selection for survival data*
currently working at Pfizer Inc.

12. *Hye Jin Cho* (Co-Major Professor: Hui-Hsien Chou), Bioinformatics and Computational Biology
PhD Dissertation (summer, 2015): *Computational Prediction, Experiment Design and Statistical Validations of Non-Coding Regulatory RNA*

13. *Ali Berens* (Co-Major Professor: Amy Toth), Bioinformatics and Computational Biology
PhD Dissertation (summer, 2015): *Sociogenomics of social organization: Mechanistic and evolutionary underpinnings of caste development and facial recognition in paper wasps*

14. *Srihari Radhakrishnan* (Co-Major Professor: Nicole Valenzuela), Bioinformatics and Computational Biology
PhD Dissertation (fall, 2015): *On the causes and consequences of sex determination and sex-linkage*

15. *Yaqing Si*, Statistics
PhD Dissertation (summer, 2012): *Statistical analysis of RNA-seq data*
currently an Associate Professor at the School of Statistics, Southwestern University of Finance, Sichuan, China

16. *Megan Orr* (Co-Major Professor: Dan Nettleton), Statistics

PhD Dissertation (summer, 2012): *Assessing differential expression when the distribution of effect sizes is asymmetric and evaluating concordance of differential expression across multiple gene expression experiments*
currently a tenure-track Assistant Professor at the North Dakota State University

17. *Tieming Ji* (Co-Major Professor: Dan Nettleton, Pat Schnable), Statistics and Bioinformatics and Computational Biology
PhD Dissertation (summer, 2012): *Borrowing information across genes and experiments for improved error variance estimation in microarray data analysis and statistical inferences for gene expression heterosis*
currently a tenure-track Assistant Professor at the University of Missouri

MS students (9):

Current:
   None

Graduated:
18. *David Walker, Statistics*
   Master Creative Component (summer 2021): Developing variational Bayesian inference for applications to gene expression data

19. *Lauren McKeen (Co-major professor: Chong Wang), Statistics*
   Master Creative Component (fall 2020): *Simulation studies to assess the power of set testing methods for microbiome data*

20. Hao Wang (Co-major professor: Yumou Qiu), Statistics
   Master Creative Component (fall 2019): *Gene expression network based on partial correlations*

21. *Ran Bi,* Statistics
   Master Creative Component (fall 2014): *Sample size calculation while controlling false discovery rate for differential expression analysis with RNA-seq Data*

22. *Yingzhou Du (Co-Major Professor: Chong Wang), Statistics*
   Master Creative Component (spring 2014): *A Permutation Test of Genetic Association between Salmonella Isolated On-farm and At-abattoir using Amplified Fragment Length Polymorphism*

23. *William Landau*, Statistics
   Master Creative Component (spring 2013): *Dispersion Estimation and Its Effect on Test Performance in RNA-seq Data Analysis: A Comparison of Methods*

24. *Yanwen Xiong*, Statistics
   Master Creative Component (spring 2012): *Comparison of normalization methods for RNA-seq data analysis*

25. *Vanessa Kvam*, Statistics
   Master Creative Component (fall 2011): *A comparison of statistical methods for detecting differentially expressed genes from RNA-seq data*

26. *Hong Hua*, Statistics
    Master Creative Component (summer, 2009): *Microarray data analysis for a study of photosynthesis differentiation in maize*

♦ **Program of Study (POS) committee member** for another **100+** graduate students (70 completed)

♦ Rotation advisor for 3 students in the Program of Bioinformatics and Computational Biology, ISU

♦ **Research Assistants that I supported (11)**:

1. Megan Orr (05/08-12/10, and 05/11-07/12)
2. Yaqing Si (07/09-07/12)
3. Dason Kurkiewicz (05/11-12/12)
4. Wen Zhou (07/12-5/13, and 1/14-5/2014)
5. Fangfang Liu (01/13-5/13, and 8/13-12/13)
6. Yinan Fang (08/13-12/13)
7. Ran Bi (5/2014-8/2018)
8. Emily Goren (5/2015-5/2017, 1/18-4/2019)
9. Chaohui Yuan (8/2016-5/2017)
10. Wenting Zhao (5/18-present)
11. Hao Wang (5/19-present)
12. David Walker (8/19-present)
13. Lauren McKeen (8/19-5/2020)
14. Yunhui Qi (5/2020-8/2020, 1/2021-present)
15. Zhili Qiao (1/2021-present)

Other students
♦ Co-Mentor (with Dan Nettleton) for Alliance students Jared Mills and Katrina Williams, summer, 2010

INVITED TALKS

1. Hurdle Poisson Model-based Clustering for Microbiome Data, *ICSA*, Sep 2021

2. Feature selection for microbiome studies in the presence of confounding using standardization, *JSM*, Aug, 2021

3. A Semi-parametric Bayesian Approach for Detection of Gene Expression Heterosis with RNA-Seq Data, *University of Nebraska, Lincoln*, Oct, 2019

4. Feature selection for microbiome data, *Iowa State University*, Oct, 2019

5. Differential Abundance Analysis of Microbiome Data, *Purdue University*, Sep, 2019

6. Differential Abundance Analysis of Microbiome Data, *Colorado State University*, Sep, 2019

7. Development of Statistical Methods for `omics Data Analysis, PSI Predictive Phenomics Workshop, *Iowa State Universit*y, Apr, 2019

8. A Semi-Parametric Bayesian Approach for Detection of Gene Expression Heterosis with RNA-Seq Data, *University of Delaware*, Nov, 2018

9. Semi-parametric Bayesian approach for differential expression analysis with RNA-sequencing data, *ICSA China Conference*, Qingdao, China, July, 2018

10. Detection of Gene Expression Heterosis with RNA-Sequencing Data, *New York University School of Medicine*, May, 2018

11. Several statistical methods and models in plant genomics studies, PSI Predictive Phenomics Workshop, *Iowa State University*, Oct, 2014

12. Statistical Analysis of RNA-seq Data, Modern Views in Nutrition (MVN) 2014 seminar series, *Iowa State University*, Oct, 2014

13. Statistical Design and Analysis of RNA-seq Data, *Shandong Agricultural University, China*, Jul, 2014

14. An optimal test for detecting differential expression using RNA-seq data, *University of Missouri*, Columbia, Oct, 2012

15. An optimal test with maximum average power while controlling FDR with application to RNA-seq data, *ICSA 2012 Applied Statistics Symposium*, Boston, Jun 23-26, 2012

16. Model-Based Clustering for RNA-seq Data, *University of Maryland*, October, 2011

17. Model-Based Clustering for RNA-seq Data, *Conference on Statistical Analyses For Next Generation Sequencing*, *University of Alabama at Birmingham*, Sep 26-27, 2011

18. Optimal tests using shrinkage idea with application to high-dimensional gene expression data, *Symposium on Innovations in Design, Analysis, and Dissemination: Frontiers in Biostatistical Methods*, Kansas City, Missouri, April, 2011

19. Optimal tests using shrinkage idea with application to high-dimensional gene expression data, *Oklahoma State University*, October, 2010

20. Quick calculation of sample size while controlling false discovery rate with application to microarray, ABG seminar, *Iowa State University*, IA, 2006

21. Empirical Bayes test with application to microarray, *Rutgers University*, NJ, 2006

22. Empirical Bayes test with application to microarray, *University of Texas at Dallas*, TX, 2006

23. Empirical Bayes test with application to microarray, *Iowa State University*, IA, 2006

24. Empirical Bayes test with application to microarray, *Washington University at St. Louis*, MO, 2006

25. Quick calculation of sample size while controlling false discovery rate with application to microarray, *Mayo Clinic*, MN, 2006

INVITED LECTURES

26. Differential Expression Analysis of RNA-seq Data, STAT 598, Big Data for the Life Sciences and Engineering, *Purdue University*, 2019
27. Statistical analysis for RNA-seq data, BCB570, Bioinformatics IV: Functional Genomics and Systems Biology, *Iowa State University*, 2014
28. Statistical analysis for RNA-seq data, BCB570, Bioinformatics IV: Functional Genomics and Systems Biology, *Iowa State University*, 2013
29. Statistical analysis for RNA-seq data, BCB570, Bioinformatics IV: Functional Genomics and Systems Biology, *Iowa State University*, 2011
30. Experimental Design and statistical analysis of microarrays, NSF REU summer program on Bioinformatics, *Iowa State University*, 2010
31. Designing and Analyzing Microarray Experiment, Microbiology 604, *Iowa State University*, IA, 2007

SELECTED CONFERENCE PRESENTATIONS

1. **E. Goren**(presenter), **P. Liu**, C. Wang, and C. Wang, BinQuasi: a Peak Detection Method for ChIP-Sequencing Data with Biological Replicates, *Joint Statistical Meetings*, 2018

2. **R. Bi** (presenter), and **P. Liu**, A Semi-parametric Bayesian Approach for Detection of Gene Expression Heterosis with RNA-Seq Data, *Joint Statistical Meetings*, 2017

3. **R. Bi** (presenter), and **P. Liu**, Sample Size Calculation while Controlling False Discovery Rate for Differential Expression Analysis with RNA-Seq Experiment, *Joint Statistical Meetings*, 2015

4. **R. Bi** (presenter), and **P. Liu**, Sample Size Calculation while Controlling False Discovery Rate for Differential Expression Analysis with RNA-Seq Experiment, *Conference on Applied Statistics in Agriculture*, 2015

5. **F. Liu** (presenter), C. Wang and **P. Liu**, Zero-Inflated Poisson Regression for Identification of Essential Genes with Tn-seq data, *Joint Statistical Meetings*, 2014

6. **F. Liu**, **P. Liu** (presenter), and C. Wang, A novel Bayesian approach for differential gene expression analysis with RNA-seq data, topic-contributed session, *Joint Statistical Meetings*, 2013

7. **Y. Si** and **P. Liu** (presenter), Comparative analysis of RNA-seq data from different organisms, topic-contributed session, *Joint Statistical Meetings*, 2012

8. **Y. Si** (presenter) and **P. Liu**, An optimal test with maximum average power while controlling FDR with application to RNA-seq data, *Conference on New Statistical Methods for Next Generation Sequencing Data Analysis*, 2012

9. P. Li (presenter), R. Giuliani, W. L. Araujo, L. Dedow, Y. Si, C. Zhang, T. Slewinski, **P. Liu**, Q. Sun, G. E. Edwards, A. Fernie, R. Turgeon, A. Barkan, A. B. Cousins and T. P. Brutnell,

Defining the maize Pyurvate orthophosphate dikinase regulatory network, *Plant and Animal Genome conference*, 2012

10. E. Sandford, M. Orr, X. Li, H. Zhou, T.J. Johnson, S. Kariyawasam, **P. Liu**, L. Nolan, and S. J. Lamont (presenter), Multi-tissue, multi-time transcriptome analysis of host response to avian pathogenic *Escherichia coli*, the Avian Immunology Research Group (AIRG) meeting, 2012

11. **T. Ji** (presenter), **P. Liu**, and D. Nettleton, Estimation of Heterosis in Gene Expression, *Joint statistical meetings*, 2011

12. **Y. Si** (presenter) and **P. Liu**, Model-Based Clustering for RNA-Seq Data, *Joint statistical meetings*, 2011

13. L. Wang (presenter),**Y. Si** , L. K. Dedow, Y. Shao, **P. Liu**, T. Brutnell, A robust method of strand-specific multiplex RNA-seq to characterize plant transcriptomes, *Plant Biology 2011*

14. W. Fang (presenter), **Y. Si**, S. Douglass, D. Casero Diaz-Cano, S. Merchant, M. Pellegrini, **P. Liu** and M. Spalding, Global Changes in Chlamydomonas Gene expression Regulated by Carbon Dioxide and *CIA5/CCM1*, *Plant Biology 2011*

15. **Y. Si** (presenter) and **P. Liu**, Model-Based Clustering for RNA-Seq Data, *Statistical, Computational and Visualization Methods in Medical Informatics Conference,* Dubuque, Iowa 2011

16. E. Sandford (presenter), M. Orr, X. Li, H. Zhou, T.J. Johnson, S. Kariyawasam, **P. Liu**, L. Nolan, and S. J. Lamont, Whole Transcriptome Response of Peripheral Blood Leukocytes to Avian Pathogenic *Escherichia coli* Infection in Broiler Chickens, the 7th European Symposium on Poultry Genetics, 2011

17. **P. Liu** and Y. Si, A Weighted Average Likelihood Ratio Test with Application to RNAseq Data, topic-contributed session, *Joint Statistical Meetings*, Vancouver, Canada, 2010

18. **Y. Si** (presenter) and **P. Liu**, Model-Based Clustering for RNA-Seq Data, *Joint statistical meetings*, Vancouver, Canada, 2010

19. E. Sandford (presenter), M. Orr, X. Li, **P. Liu**, L. Nolan, H. Zhou and S. J. Lamont, Splenic gene expression after infection of broiler chickens with avian pathogenic *Escherichia coli*, *ISAG meeting*, 2010

20. G. Li (presenter), T. Johnson, **P. Liu**, and L. K. Nolan, Transcriptome Analysis of APEC in Serum Reveals Adaptive Responses to Systemic Infection. ASM, San Diego, May 2010

21. **T. Ji**, **P. Liu**, and D. Nettleton (presenter), Borrowing Information across Genes and across Experiments for Improved Residual Variance Estimation in Microarray Data Analysis, ENAR, New Orleans, March 2010

22. **Y. Si** (presenter) and **P. Liu**, Tests to Identify Differentially Expressed Genes from Next-Generation Sequencing Data, The Conference for Celebrating 75 Years of Statistics at Iowa State, 2009

23. **M. Orr** (presenter), **P. Liu** and D. Nettleton, Two methods of testing multivariate distributions and variable selection, The Conference for Celebrating 75 Years of Statistics at Iowa State, 2009

24. **T. Ji** (presenter), **P. Liu** and D. Nettleton, Borrowing Information across Genes and across Experiments for Improved Residual Variance Estimation, The Conference for Celebrating 75 Years of Statistics at Iowa State, 2009

25. L.K. Nolan (presenter), T. Johnson, S.J. Lamont, S. K. Kariyawasm, **P. Liu**, and D. Trampel, D. Host: Pathogen Interactions in Avian Colibacillosis: a Systems-Based, Functional Genomics Approach, USDA NRICGP Microbial Functional Genomics Awardees Program, August 2008

26. **P. Liu** (presenter) and C. Wang, An optimal semi-parametric testing procedure with application to microarray data, *ISU fall conference on statistics in biology*, 2008

27. **P. Liu** (presenter) and J. T. G. Optimal Tests Shrinking Both Means and Variances Applicable to Microarray Data Analysis, *Joint Statistical Meetings*, Salt Lake City, UT, 2007

28. **P. Liu** (presenter) and J. T. G. Hwang, Quick calculation of sample size while controlling false discovery rate with application to microarray, *Joint Statistical Meetings*, Seattle, WA, 2006

29. **P. Liu** (presenter) and J. T. G. Hwang, Why shrinking the variance estimates helps the multiple testing for a large number of populations such as genes? *Joint statistical meetings*, Minneapolis, MN, 2005

30. J. T. G. Hwang and **P. Liu** (presenter), Fast Estimation of Sample Size While Controlling for FDR in Multiple Testing, *ENAR spring meeting*, Austin, TX, 2005

31. **P. Liu** (presenter) et al, Hierarchical clustering analysis of 2-dimensional protein gel images: correlation with testicular toxicity in beagle dogs, *Annual meeting of Society of Toxicology*, Salt Lake City, 2003

DEPARTMENT TALKS

32. An optimal test to identify differentially expressed genes from RNA-seq data, Department of Statistics, *Iowa State University*, IA, 2012

33. Overview of RNA-seq data analysis and related research topics, the orientation seminar series for the first-year graduate students, Department of Statistics, *Iowa State University*, IA, 2011

34. Y. Si (presenter) and **P. Liu**, A Weighted Average Likelihood Ratio Test with Application to RNAseq Data, Biological Statistics group meeting, *Iowa State University*, 2011

35. Y. Si (presenter) and **P. Liu**, Model-Based Clustering for RNA-Seq Data, Biological Statistics group meeting, *Iowa State University*, 2010

36. T. Ji (presenter), **P. Liu** and D. Nettleton, Borrowing Information across Genes and across Experiments for Improved Residual Variance Estimation, Biological Statistics group meeting, *Iowa State University*, 2010

37. Overview of microarray data analysis and related research topics, the orientation seminar series for the first-year graduate students, Department of Statistics, *Iowa State University*, IA, 2008, 2010

38. Testing Significance of Gene Sets, Biological Statistics group meeting, *Iowa State University*, IA, 2007

39. Something about Academic Job Hunting, Survey/Social working group meeting, *Iowa State University*, IA, 2007

40. Quick calculation of sample size while controlling false discovery rate with application to microarray, VIGRE biostatistics meeting, *Iowa State University*, IA, 2006

TEACHING EXPERIENCES

♦ **Instructor for STAT 500**: Statistical Methods I, Iowa State University, Fall, 2018, 2019, 2020
  This is the 1st method core course for Statistics graduate students.
  Teaching evaluation: 4.5-4.6/5.0

♦ **Instructor for STAT 402**: Statistical Design and the Analysis of Experiments, Iowa State University, Spring of 2011, 2012, 2013, 2014, 2019, Fall of 2013, 2014, 2015, 2016, 2017
  This is a course of experimental design for graduate students outside of statistics.
  Teaching evaluation: 4.0-4.7/5.0

♦ **Instructor for STAT 416**: Statistical Design and Analysis for Gene Expression Experiments, Iowa State University, Spring of 2007, 2008, 2011, 2012, 2013, 2014, 2015, 2017, 2018
  This is a specialized method course for students outside of statistics.
  Teaching evaluation: 4.2-5.0/5.0

♦ **Instructor for STAT 516**: Statistical Design and Analysis for Microarray Experiments, Iowa State University, Spring, 2009
  This is a specialized method course for graduate students major in statistics.
  Teaching evaluation: 4.5/5.0

♦ **Instructor for STAT 104**: Introduction to Statistics, Iowa State University, Fall 2008, Spring 2010
  This is an introductory statistics course for undergraduates.
  Teaching evaluation: 3.8/5.0

EDITORIAL ACTIVITIES

♦ *Associate Editor of BMC Bioinformatics, Jan 2012 to present*

JOURNAL REFREEING

Animal Genetics, Annals of Applied Statistics, Bioinformatics, Biometrics, Biostatistics, BMC Bioinformatics, BMC Genomics, BMC Plant Biology, Journal of Applied Statistics, Journal of Nonparametric Statistics, Journal of Royal Statistical Society SC, Journal of Royal Society Interface, Journal of the American Statistical Association, Journal of Statistical Modeling,

Journal of Statistical Planning and Inference, PLoS Genetics, PLoS ONE, Statistics and Its Interface, Statistical Application in Genetics and Molecular Biology

OTHER PROFESSIONAL SERVICE

- External reviewer for tenure promotion cases, 2020
- Reviewer for French National Research Agency grant proposal, 2019
- Chair for a Statistics in Genomics and Genetics session in the *Joint Statistical Meeting*, July 2019, Denver
- Organizer for an invited session in the *ICSA International Conference*, December 2019, Hangzhou, China
- Chair for an invited session in the *ICSA International Conference*, December 2019, Hangzhou, China
- Chair for Zyskind Memorial Lecture for the Conference on Predictive Inference and Its Applications, May 2018, Iowa
- Organizer of a topic-contributed session, Novel statistical methods for RNA-seq data analysis, for Joint Statistical Meeting, July-August, 2012, San Diego
- Organizer and chair for an invited session, Shrinkage Ideas with Applications to Multiple Testing Problems, for International Chinese Statistical Association (ICSA) 2012 Applied Statistics Symposium, June 2012, Boston
- Co-organizer of Conference on New Statistical Methods for Next-Generation Sequencing Data Analysis, Iowa State University, May, 2012
- Program committee member for Statistical, Computational and Visualization Methods in Medical Informatics Conference, Clarke University, Dubuque, Iowa, 2011
- Reviewer for Louisiana Board of Regents Support Fund Research Competitiveness Program (RCS), 2011
- Organizer of a topic-contributed session, Statistical methods for next-generation sequencing data, for Joint Statistical Meeting, Vancouver, 2010
- Co-organizer and chair for an invited session in the conference celebrating 75 years of statistics at Iowa State, June 2009, Ames, IA
- Chair for sessions in the *ISU fall conference on statistics in biology*, Oct 2008, Ames, Iowa
- Panelist and reviewer for the Joint DMS(NSF)/NIGMS(NIH) Initiative to support research in the area of Mathematical Biology, fall, 2008
- Referee for *ISBRA*, 2008
- Reviewer for NSF grant proposal, 2008

PROFESSIONAL MEMBERSHIPs

- American Statistical Association (ASA)
- International Chinese Statistical Association (ICSA)

UNIVERSITY SERVICE

- Women and Minorities Committee (08-13)
- Graduate College Curriculum Committee (14-21)

DEPARTMENTAL SERVICE

- Computer Advisory Committee (06-07)

- Curriculum Committee (18-19)
- Diversity Committee (07-14, 20-21)
- Graduate Committee (12-13)
- Graduate Admission Committee (06-11)
- Honors and Awards Committee (17-18)
- Library Committee (12-14)
- Organizer, Group discussion for biological statistics (07-11)
- PhD/MS Exam Committee (10-11, 13-18, 19-21)
- Renovation Committee (07-09)
- Search Committee (14-15, 17-18, 19-20)
- Seminar Chair (Spring 2012, Fall 2018)
- Social Committee (06-07, 13-14)
- StatCom faculty advisor (16-17)