Peng Liu

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2117 Snedecor Hall   *Fax: 515-294-4040*
Iowa State University   *pliu@iastate.edu*

EMPLOYMENT

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

EDUCATION

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

M.S.   **Biological Statistics and Computational Biology**, Cornell University, 2/2004

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

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

RESEARCH INTERESTS

♦ Statistical Genomics, Bioinformatics, Biostatistics
♦ Statistical Inference for High-dimensional Data
♦ Bayesian Statistics

REFEREED JOURNAL PUBLICATIONS

1. **Y. Si**, **P. Liu**, P. Li and T. Brutnell (2013), Model-based clustering of RNA-seq data, *accepted by Bioinformatics*

2. **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

3. **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,* accepted

4. 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

5. 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

6. 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, accepted by Genome Biology and Evolution*

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

8. **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

9. 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,* doi:10.1080/02664763.2012.752449

10. 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, *published online before print, The Plant Cell, 24(5):1876-93,* doi/10.1105/tpc.112.097949

11. **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

12. **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

13. H. Hao, Z. Yuan, Z. Shen, J. Han, O. Sahin, **P. Liu**, Q. Zhang (2012), Mutational and transcriptomic changes involved in the development of macrolide resistance in *Campylobacter jejuni*, accepted by *Antimicrobial Agents and Chemotherapy*

14. 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*, accepted by *Avian Diseases*

15. 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

16. 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

17. 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

18. 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

19. 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

20. 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

21. 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

22. 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

23. **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

24. 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

25. **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

26. 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

27. 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

28. 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

29. 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

30. 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

SUBMITTED PAPERS

31. **T. Ji**, **P. Liu** and D. Nettleton, Estimation and Testing of Gene Expression Heterosis, *revised and re-submitted to JABES*, 2013

32. L. Wang, Czedik-Eysenberg, A. Mertz, R. A., **Y. Si**, …, **P. Liu**, and T. P. Brutnell, Exploring the mechanism of C_4 photosynthetic differentiation through a unified comparative analysis of maize and rice leaf transcriptomes, *under revision for Nature Biotechnology*, 2013

33. **M. Orr, P. Liu** and D. Nettleton, An Improved Method for Computing Q-Values When The Distribution of Effect Sizes Is Asymmetric, *submitted to Bioinformatics*, 2013

34. C. Zhang, S. Fei, **P. Liu**, T. Ji, J. Peng, D. Hannapel, Transcriptional changes in response to cold in perennial ryegrass as revealed by a cross-species microarray analysis, *submitted to Physiologia Plantarum*, 2012

35. **P. Liu**, C. Wang and J. T. G. Hwang, What if the probability density of p-values is not decreasing? A theory and its application to microarray data, *revised and re-submitted to Acta Mathematicae Applicatae Sinica, English Series*, 2013

BOOK CHAPTER UNDER DEVELOPMENT

36. **P. Liu**, Cluster analysis of RNA-sequencing data, *to be submitted*, 2013

PAPERS UNDER DEVELOPMENT

37. **Y. Si**, **P. Liu**, L. Wang and T. Brutnell, Empirical Bayes methods to detect differential alternative splicing with RNA-seq data, *in preparation*, 2012

38. **M. Orr, P. Liu** and D. Nettleton, Identifying Genes That Are Differentially Expressed in Both of Two Independent Experiments, *to be submitted*, 2012

39. **F. Liu, P. Liu**, and C. Wang, Non-parametric Bayesian method for detecting differentially expressed genes in RNA-sequencing data, *in preparation*, 2013

40. **F. Liu, P. Liu**, Z. Wu, and C. Wang, Mixture model analysis of Transposon-sequencing data to identify essential genes, *in preparation*, 201

41. S. Covshoff, …, **P. Liu**, and T. Brutnell, Study of C_4 photosynthetic development in the maize mutant bsd2, *in preparation*, 2012

42. L. Wang, **P. Liu,** and T. Brutnell, Selection of stably expression genes, *in preparation*, 2010

43. 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*, 2012

OTHER PUBLICATIONS

44. **P. Liu** and J. T. G. Hwang, Quick estimation of sample size while controlling false discovery rate for microarray experiments, *JSM proceedings [86] ASA Biometrics Session 270-274*, Seattle, WA, 2006

45. G. R. Warnes and **P. Liu**, Sample size estimation for microarray experiments, technical report 06-06, Department of Biostatistics and Computational Biology, University of Rochester, 2006

46. **P. Liu**, Fitting linear spline models to clustered time-course microarray data set, *Master thesis*, May 2004, Cornell, University

47. **P. Liu**, The role of intracellular fatty acid binding proteins (FABPS) in the gene regulation by peroxisome proliferator-activated receptors (PPARs), *Master thesis*, Aug, 2001, Cornell University

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

GRANTS

Awarded:

1. **PI** for GEPR: A Systems Approach to the Development and Function of C4 Photosynthesis, other PIs include T. Nelson (leading PI) from Yale University, T. Brutnell from Donald Danforth Plant Science Center and K. van Wijk from Cornell University
   Source of Support: NSF
   Total Award Amount: $ 8,386,495
   My portion: $ 372,843
   Total Award Period Covered: 02/15/2012-01/31/2016

2. **PI** for GEPR: Comparative analysis of C3 and C4 leaf development in rice, sorghum and maize, other PIs include T. Nelson (leading PI) from Yale University, T. Brutnell from Boyce Thompson Institute and K. van Wijk from 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

3. **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
   Source of Support: NIH
   Total Award Amount: $ 1,173,287

Total Award Period Covered: 09/01/2013-05/31/2017

4. **Co-investigator** 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 from 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

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

6. **Co-investigator** for Functional genomics analysis of a highly virulent Campylobacter jejuni clone causing sheep abortion, together with Zhang (PI), Yaeger and Sahin from Iowa State University
> Source of Support: USDA
> Total Award Amount: $ 998,467
> Total Award Period Covered: 12/15/09-12/14/12

7. **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

8. **Co-investigator** 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 AFRI
> Total Award Amount: $ 4,999,158
> Total Award Period Covered: 3/1/2011-2/29/2016

9. **Co-investigator** 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

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

11. **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 (1-year)

12. **Statistician** for Identification of Novel APEC Virulence Genes via Functional Genomics, together with Li (PI), Nolan, and Kariyawasam
> 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:

13. **Co-PI** for *BioSynCh*: Biomolecules and biomaterials synthesis based on plant surface lipid Chemistries, with B. Nikolau (PI), and E. Wurtele, M. Yandeau-Nelson and Y. Shao, submitted to DRAPA

14. **Co-PI** for Increasing protein composition in agronomic species, with E. Wurtele (PI) and L. Li, submitted to NSF

15. **Co-PI** for Systems-Based Approach to Understand the Cellular and Molecular Basis of Host Resistance and Vaccine Response to *Escherichia coli* in Chickens with S. Lamont (PI), and L. Nolan, submitted to USDA

16. **Co-PI** for Biological determinants of feed efficiency in lactating Holstein cows, with D. Spurlock (PI), and M. VandeHaar, submitted to USDA

17. **Co-PI** for Efficacy of Caffeic Acid and its Derivatives from Plant Foods in Improving Barrier Function in the Developing Intestine, with S. Hendrich (PI), J. Hostetter, G. Phillips, Q. Wang and M. Wannemuehler, submitted to USDA

STUDENT ADVISING

Graduate students:
♦ Advisor/co-advisor for **12** graduate students (**7 graduated**)

PhD students (7):

Current:
1. *Fangfang Liu,* Statistics
2. *Hye Jin Cho* (Co-Major Professor: Hui-Hsien Chou), Bioinformatics and Computational Biology
3. *Ali Berens* (Co-Major Professor: Amy Toth), Bioinformatics and Computational Biology
4. *Haibo Liu* (Co-Major Professor: Chris Tuggle), Bioinformatics and Computational Biology

Graduated:
5. *Yaqing Si*, Statistics
PhD Dissertation: *Statistical analysis of RNA-seq data*
currently working at the Union Bank

6. *Megan Orr* (Co-Major Professor: Dan Nettleton), Statistics
   PhD Dissertation: *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

7. *Tieming Ji* (Co-Major Professor: Dan Nettleton, Pat Schnable), Statistics and Bioinformatics and Computational Biology
   PhD Dissertation: *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 (5):

Current:
8. *Yingzhou Du* (Co-Major Professor: Chong Wang), Statistics

Graduated:
9. *William Landau*, Statistics
   Master Creative Component: *Dispersion Estimation and Its Effect on Test Performance in RNA-seq Data Analysis: A Comparison of Methods,* M.S. in Statistics, graduated in Spring 2013
   currently a PhD student at Iowa State University

10. *Yanwen Xiong*, Statistics
    Master Creative Component: *Comparison of normalization methods for RNA-seq data analysis,* M.S. in Statistics, graduated in Spring 2012
    currently a Senior Research Associate at the Pioneer Hi-Bred

11. *Vanessa Kvam*, Statistics
    Master Creative Component: *A comparison of statistical methods for detecting differentially expressed genes from RNA-seq data*, M.S. in Statistics, graduated in Fall 2011
    currently a biostatistician at AT Still University

12. *Hong Hua*, Statistics
    Master Creative Component: *Microarray data analysis for a study of photosynthesis differentiation in maize*, M.S. in Statistics, graduated in Summer, 2009
    currently a Senior Business analyst at Hewlett-Packard in China

♦ Program of Study (POS) committee member (not major professor) for another **60** graduate students (32 completed)

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

Research Assistants that I supported:

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)
5. Fangfang Liu (01/13-5/13, and 8/13-present)
6. Yinan Fang (08/13-present)

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

INVITED TALKS

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

2. 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

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

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

5. 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

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

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

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

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

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

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

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

INVITED LECTURES

13. Statistical analysis for RNA-seq data, BCB570, Bioinformatics IV: Functional Genomics and Systems Biology, *Iowa State University*, 2011
14. Experimental Design and statistical analysis of microarrays, NSF REU summer program on Bioinformatics, *Iowa State University,* 2010
15. Designing and Analyzing Microarray Experiment, Microbiology 604, *Iowa State University*, IA, 2007

SELECTED CONFERENCE PRESENTATIONS

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

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

3. 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

4. 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

5. 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

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

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

8. 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*

9. 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*

10. 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

11. 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

12. **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

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

14. 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

15. 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

16. 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

17. 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

18. 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

19. 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

20. 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

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

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

23. **P. Liu** 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

24. **P. Liu** 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

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

26. **P. Liu** 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

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

28. 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

29. 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

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

31. 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

32. 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

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

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

35. 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 516**: Statistical Design and Analysis for Microarray Experiments, Iowa State University, Spring, 2009
  Teach ~15 graduate students in statistics
  Responsibilities include: developing course materials, designing exams and class projects, giving lectures and labs
  Teaching evaluation; 4.5/5.0
- **Instructor for STAT 104**: Introduction to Statistics, Iowa State University, Fall 2008, Spring 2010
  Teach 50~90 undergraduate students in biological sciences
  Responsibilities include: developing course materials, designing exams and class projects, giving lectures and labs
  Teaching evaluation; 3.8/5.0
- **Instructor for STAT 402**: Statistical Design, Iowa State University, Spring of 2011, 2012, 2013, Fall 2012
  Taught 20-50 graduate students in biological sciences
  Responsibilities include: developing course materials, designing exams and class projects, giving lectures

Teaching evaluation: 4.2-4.5/5.0
♦ **Instructor for STAT 416**: Statistical Design and Analysis for Microarray Experiments, Iowa State University, Spring of 2007, 2008, 2011, 2012, 2013
Taught ~10 graduate students in biological sciences
Responsibilities include: developing course materials, designing exams and class projects, giving lectures
Teaching evaluation; 4.2-5.0/5.0

EDITORIAL ACTIVITIES

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

JOURNAL REFREEING

1. *Animal Genetics, 2007-2012*
2. *Annals of Applied Statistics, 2011*
3. *Bioinformatics*, 2006-2013
4. *Biometrics, 2013*
5. *Biostatistics, 2011*
6. *BMC Bioinformatics*, 2012
7. *BMC Genomics, 2011*
8. *BMC Plant Biology, 2011*
9. *JASA*, 2008
10. *Journal of Applied Statistics, 2011*
11. *Journal of Royal Society Interface, 2010*
12. *Journal of Statistical Modeling, 2009 - 2010*
13. *Journal of Statistical Planning and Inference, 2009- 2010*
14. *PLoS Genetics, 2009*
15. *PLoS ONE, 2012*
16. *Statistics and Its Interface, 2010*
17. *Statistical Application in Genetics and Molecular Biology, 2009 – 2011*

OTHER PROFESSIONAL SERVICE

♦ 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

HONORS AND AWARDS

- Iowa State University Award for Early Achievement in Research, 2013
- Graduate School Travel Award and Fellowship, Cornell University, 3/2005 and 8/2005
- Research Grant, 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

PROFESSIONAL MEMBERSHIPs

- American Statistical Association (ASA)
- Institute of Mathematical Statistics (IMS)
- International Chinese Statistical Association (ICSA)

UNIVERSITY SERVICE

- Women and Minorities Committee (08-13)

DEPARTMENTAL SERVICE

- Computer Advisory Committee (06-07)
- Diversity Committee (07-14)
- Graduate Committee (12-13)
- Graduate Admission Committee (06-11)
- Library Committee (12-14)
- Organizer, Group discussion for biological statistics (07-11)
- PhD/MS Exam Committee (10-11, 13-14)
- Renovation Committee (07-09)
- Seminar Chair (spring, 2012)
- Social Committee (06-07, 13-14)