UIC Epidemiology and Biostatistics Division
UNIVERSITY OF ILLINOIS AT CHICAGO
SCHOOL OF PUBLIC HEALTH

Jin Liu

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Research Interests

- Variable Selection and Dimension Reduction for Cancer -omics Data, Survival Analysis, Statistical Genetics, Mixed Models, Bioinformatics, Statistical Computing.

Education

- Ph.D. University of Iowa, Statistics, 2007-2011

    - *Dissertation Topic*: "Penalized Methods in Genome-Wide Association Studies"
    - *Advisor*: Professor Jian Huang,   *Co-advisor*: Associate Professor: Kai Wang
    - *Committee:* Jian Huang (Chair), Kai Wang(Co-chair), Kung-Sik Chan, Aixin Tan, Dale Zimmerman.

- M.S. University of Iowa, Statistics, 2005-2007

- B.A. Dalian University of Technology, Automatic Control, 2000-2004

Academic Experience

- **Assistant Professor**   **August 2013 - Present**

  Division of Epidemiology & Biostatistics, University of Illinois at Chicago, Chicago, IL

- **Postdoctoral Associate**   **August 2011 - July 2013**

  Department of Biostatistics, Yale University, New Haven, CT
  Advisor: Dr. Shuangge Ma

- **Graduate Student**   **August 2005 - July 2011**

  Department of Statistics & Actuarial Science, University of Iowa, Iowa City, IA
  Advisor: Dr. Jian Huang

Teaching

- **Assistant Professor**   **August 2013 - Present**

    - 594 Applied Statistical Genetics, January 2014 - May 2014.

- **Teaching Assistant**   **August 2005 - May 2009**

  Department of Statistics & Actuarial Science, University of Iowa, Iowa City, IA
  Led discussion sections and graded quizzes and homework for undergraduate students.

- 002 Statistics and Society, Fall 2005 to Spring 2007.
- 008 Statistics for Business, Spring 2008 and Fall 2009.
- 025 Elementary Statistics and Inference, Fall 2005 to Spring 2007.

Publications

1. **J.Liu**, J. Huang, Y. Zhan, Q. Lan, N. Rothma, T. Zheng and S. Ma. (2014) Integrative analysis of prognosis data on multiple cancer subtypes using compound group bridge. *Biometrics (Accepted)*.

2. **J.Liu**, J. Huang and S. Ma. (2014) Penalized multivariate linear mixed model for longitudinal genome-wide association studies. *BMC Proceedings (Accepted)*.

3. X. Shi, **J.Liu**, J. Huang, Y. Zhou Y. Xie and S. Ma. (2014) A penalized robust method for identifying geneenvironment interactions. *Genetic Epidemiology*. (In press)

4. **J.Liu**, J. Huang and S. Ma. (2014) Integrative analysis of multiple cancer diagnosis studies with composite penalization. *Scandinavian Journal of Statistics 41 (1), 87103*.

5. X. Shi, **J.Liu**, J. Huang, Y. Zhou and S. Ma. (2014) Integrative analysis of cancer prognosis data via contrasted group bridge penalization. *Genetic Epidemiology, 2014, 38(2), 144-151*.

6. **J.Liu**, J. Huang and S. Ma. (2013) Integrative analysis of multiple cancer genomic datasets under heterogeneity model. *Statistics in Medicine 32 (10), 3509-3521*.

7. **J.Liu***, J. Huang, S. Ma and K. Wang. (2013) Incorporating group correlations in genome-wide association studies using smoothed group Lasso. *Biostatistics 14 (2), 205-219*.

8. **J.Liu**, Huang J, Ma S. (2013) Integrative analysis of multiple cancer prognosis datasets under the heterogeneity model. *Topics in Applied Statistics. 2012 Symposium of the International Chinese Statistical Association Series: Springer Proceedings in Mathematics & Statistics, Vol. 55, Page 257-269. Eds: Mingxiu Hu, Yi Liu, Jianchang Lin*.

9. **J.Liu**, J. Huang, Y. Xie and S. Ma. (2013) Sparse group penalized integrative analysis of multiple cancer prognosis datasets genetics research. *Genetics Research, 2013, 95(2-3):68-77*.

10. **J.Liu**, J. Huang, Y. Zhan, Q. Lan, N. Rothma, T. Zheng and S. Ma. (2013) Identification of gene-environment interactions in cancer studies using penalization. *Genomics, 2013, 102(4), 189-194*.

11. X. Shi, S. Shen, **J.Liu**, J. Huang, Y. Zhou, S. Ma. (2013) Similarity of markers identified from cancer gene expression studies: observations from GEO. *Briefings in Bioinformatics. doi: 10.1093/bib/bbt044*.

12. **J.Liu***, K. Wang, S. Ma and J. Huang. (2013) Accounting for linkage disequilibrium in genome-wide association studies: a penalized regression method. *Statistics and Its Interface 6 (1), 99-115*.

13. **J.Liu**, J. Huang and S. Ma. (2013) Incorporating network structure in integrative analysis of cancer prognosis data. *Genetic Epidemiology 37 (2), 173183*.

14. **J.Liu***, J. Huang and S. Ma. (2012) Penalized methods for multiple outcome data in genome-wide association studies. *PLoS ONE 7(12): e51198.*.

15. **J.Liu***, K. Wang, S. Ma and J. Huang. (2011) Regularized regression method for genome-wide association studies. *BMC Proceedings, 5 (Suppl 9): S67*.

16. A. Thomas, H. Abel, Y. Di, L. Faye, J. Jin, **J.Liu**, Z. Wu and A. Paterson. (2011) Effect of linkage disequilibrium on the identification of functional variants. *Genetic Epidemiology, 35: S115-S119*.

Working Manuscripts

1. **J.Liu**, X. Shi, C. Yang, S. Ma and J. Huang. (2012) Semi-penalized inference with FDR control in generalized linear model.

2. **J.Liu**, F. Wang, X. Gao, H. Zhang and C. Yang. (2014) An integrative penalized regression method in genome-wide association studies.

3. **J.Liu**, F. Wang, X. Gao, H. Zhang and C. Yang. (2014) An empirical Bayesian approach to integrate GWAS with multiple tissue gene expressions.

4. **J.Liu**, C. Yang, X. Shi, C. Li, J. Huang, H. Zhao and S. Ma. (2013) A penalized multi-trait mixed model for association mapping in pedigree-based GWAS.

Invited Talks

1. Incorporating group correlations in genome-wide association studies using smoothed group Lasso. University of West Georgia, Carrollton, GA, March 28, 2012.

2. Integrative analysis of cancer prognosis data with sparse group penalization. ICSA applied statistical symposium, Boston, MA, June 24, 2012.

3. Incorporating group correlations in genome-wide association studies using smoothed group Lasso. Xiamen University, Xiamen, China, December 18, 2012.

4. Integrative analysis of prognosis data on multiple cancer subtypes using compound group bridge.

    - University of Louisville, Louisville, KY, January 24, 2013.
    - Kansas State University, Manhattan, KS, February 4, 2013.
    - Yale University, New Haven, CT, February 14, 2013.
    - New Jersey Institute of Technology, Newark, NJ, February 27, 2013.
    - Georgetown University, DC, March 4, 2013.
    - University of Northern Texas, Denton, TX, March 12, 2013.
    - University of Illinois at Chicago, Chicago, IL, March 19, 2013.
    - University of Texas at Dallas, Dallas, TX, March 25, 2013.

5. Integrative analysis of prognosis data on multiple cancer subtypes using compound group bridge. Joint Conference by ICSA and ISBS, Bethesda, MD, June 12, 2013.

6. A penalized multi-trait mixed model for association mapping in pedigree-based GWAS. Northwestern University, Chicago, IL, October 2, 2013.

Contributed Talks

1. A regularized regression method for genome-wide association Studies. Genetic Analysis Workshop 17, Boston, MA, October 16, 2010.

2. A penalized method accounting for linkage disequilibrium in genome-wide association studies. ENAR, Miami, FL, March 22, 2011.

3. Incorporating group correlations in genome-wide association studies using smoothed group Lasso. ENAR, Washington D.C., April 2, 2012.

4. Penalized multivariate linear mixed model for longitudinal genome-wide association studies. Genetic Analysis Workshop 18, Stevenson, OR, October 17, 2012.

5. Regularized integrative analysis of cancer prognosis studies. ENAR, Orlando FL, March 11, 2013.

6. A penalized multi-trait mixed model for association mapping in pedigree-based GWAS. ENAR, Baltimore MD, March 21, 2014.

Software and Package

- *SMCP*: an R package for computing smoothed MCP method in GWAS.
  `http://cran.r-project.org/web/packages/SMCP/index.html`

Honors & Awards

- Faculty Scholarship Support Fund   University of Illinois at Chicago 2014

Research Support

1. School of Public Health Seed Fund
   An integrative penalized regression method in Genome-Wide Association studies (pending).
   Role: PI

2. R03 Small Grant Program
   An integrative analysis of GWAS and gene-expression data using an empirical Bayesian approach (pending).
   Role: PI

Computer Skills

- Statistical Software: R, S-Plus, BUGS, PLINK, SAS.

- Languages: MATLAB, C, Linux shell scripts, PVM parallel processing.

- Operating Systems: Unix/Linux, Windows.

Academic Services

- MS Comprehensive Exam Committee   **Spring 2014 - Present**

Professional Activities

- Reviewer: BMC Bioinformatics, BMC Genetics, Communications in Statistics - Theory and Methods, Pharmacogenetics and Genomics, International Statistical Review, Statistics and Its Interface, Statistical Methodology, and Statistics in Medicine

- Membership: ENAR, ASA, ICSA