

## CURRICULUM VITAE

TIAN ZHENG

March 22, 2017

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### RESEARCH INTERESTS

Methodological research for exploring and analyzing interesting patterns in complex data from different application domains.

**Statistical genetics:** association mapping of complex traits using high-throughput genomic data. **Bioinformatics and Computational genomics:** Feature selection and classification for gene expression data, data mining of microarray data, hidden Markov models for DNA mutations and phylogenies inference, evaluation of protein regulatory network. **Statistics:** Nonparametric statistics, metric learning, sparse learning, modeling of (social) network structure, modeling of dynamic social interactions, design and analysis of sample surveys, dynamic latent space models for evolving relational data, models for high-dimensional spatial-temporal data, statistical education.

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### EDUCATION

- 09/1998–05/2002 Columbia University, New York, NY  
Ph.D. in Statistics (2002). M.A. in Statistics (2000).  
Thesis: Multiple-Marker Screening Approach Towards the Study of Complex Traits in Human Genetics. Advisor: Professor Shaw-Hwa Lo.
- 09/1994–07/1998 Tsinghua University, Beijing, China  
B.S. in Applied Mathematics (1998). Minor in Computer Science (1998). Thesis: Mathematical Modeling and Parametrization of a Class of Consonants.
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### EXPERIENCE

- 05/2012–present Associate professor (w./ tenure), Department of Statistics, Columbia University, New York, NY.
- 11/2012–present Chair and committee member, Center on Foundations of Data Science, Data Science Institute (DSI), Columbia University, New York, NY.
- 02/2015–present Affiliate member, Columbia Population Research Center (CPRC), Columbia University, New York, NY
- 09/2015–present Member, Data and Society Task Force, Columbia University
- 09/2014–present Member, Shared Research Computing Policy Advisory Committee (SRCPAC)
- 05/2013–present Member, Education Committee, Data Science Institute (DSI), Columbia University, New York, NY.

11/2012–present	Associate member, Herbert Irving Comprehensive Cancer Center (HICCC), Columbia University Medical Center, New York, NY.
09/2014–12/2014	Consulting researcher, Microsoft Research, New York, NY item[07/2007–05/2012] Associate professor (w/o tenure), Department of Statistics, Columbia University, New York, NY.
07/2002–06/2007	Assistant professor, Department of Statistics, Columbia University, New York, NY.

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## HONORS

2014	Elected fellow of American Statistical Association
2011	Elected member of International Statistical Institute.
2010	Google Research Award <sup>1</sup> , Google, Inc.
2009	JSM 2009 Poster Award, Section on Survey Research Methods (SRMS) of the American Statistical Association
2008	The Mitchell Prize <sup>2</sup> , Section on Bayesian Statistical Science (SBSS) of the American Statistical Association and the International Society for Bayesian Analysis (ISBA)
2008	Outstanding Statistical Application Award <sup>3</sup> , American Statistical Association
2007	Achievement award, WorldComp'07 (The 2007 World Congress in Computer Science, Computer Engineering and Applied Computing).
2007	Worldcomp'07 honorary first runner-up for best paper award in Bioinformatics and Computational Biology.
1998	Graduate of honors with distinction (awarded to top 2% of the graduating class), Tsinghua University.

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## RESEARCH GRANTS

Grants for which participating as senior investigator are listed.<sup>4</sup>

2016-2018	<i>Dissecting Spatiotemporal Brain Dynamics</i> . PIs: T Zheng and E Hillman. Data Science Interdisciplinary ROADS Grant, Columbia University
2016-2018	<i>Reproducible And Scalable Bayesian Modeling For Next-Generation Social Sciences</i> , PI: T Zheng. Defense Advanced Research Projects Agency (DARPA), two-month effort. Total projected award: \$1,501,742.00.
2015-2018	<i>A Novel Statistical Framework for Big Data Prediction</i> , PI: S-H Lo National Science Foundation (Role: co- <b>PI</b> , one-month effort. Total award: \$300,000.)

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<sup>1</sup>From Google Research University Awards website: “the Google Research Awards program aims to identify and support world-class, full-time faculty pursuing research in areas of mutual interest.”

<sup>2</sup>From ISBA website: “The Prize is awarded in recognition of an outstanding paper that describes how a Bayesian analysis has solved an important applied problem. The Prize is jointly sponsored by the Section on Bayesian Statistical Science (SBSS) of the ASA, the International Society for Bayesian Analysis (ISBA), and the Mitchell Prize Founders’ Committee.”

<sup>3</sup>From award website: “The Outstanding Statistical Application Award was established in 1986 to recognize the authors of papers that demonstrate an outstanding application of statistics in any substantive field.”

<sup>4</sup>Also participated in a number of training grants and center grants at Columbia University.

- 2010-2015 *Latent Space Models for Aggregated Relational Data in Social Sciences*, PI: T Zheng.  
National Science Foundation (Role: **PI**, Total award: \$350,000)
- 2010 *Dynamic Projection State-Space Model for Evolving Relational Data*, PI: T Zheng.  
Google Research Award, (Role: **PI**, unrestricted gift \$70,000).
- 2009-2010 *Latent Structure Models for Social Networks Using Aggregated Relational Data*,  
PI: T. Zheng.  
Columbia Population Research Center, (Role: **PI**, \$6,000.)
- 2009-2011 *Computational Discovery of Synergistic Mechanisms Responsible for Psychiatric Disorders*, PI: D Anastassiou and M Karayiorgou.  
National Institutes of Health, (Role: co-investigator, one-month effort.)
- 2009-2011 ARRA Administrative supplement to “*New Approach Towards Mapping of Complex Human Disorders*”, PI: S-H Lo.  
National Institutes of Health, (Role: co-**PI**, two-month effort. Total award: \$255,157.)
- 2007-2010 *A General Framework for High Throughput Biological Learning: Theory Development and Applications*, PI: S-H Lo.  
National Science Foundation (Role: co-**PI**, one-month effort. Total award: \$270,000.)
- 2006-2010 *Computer System for Functional Analysis of Genomic Data*, PI: A Rzhetsky.  
National Institutes of Health R01 grant, (Role: co-investigator, 10% effort.)
- 2005-2011 *New Approach Towards Mapping of Complex Human Disorders*, PI: S-H Lo.  
National Institutes of Health R01 grant, (Role: co-**PI**, 16.7% effort. Total award: \$795,703)
- 2005-2008 *Design and Analysis of “How many X’s do you know” surveys for the study of polarization in social networks*, PI: A Gelman.  
National Science Foundation (Role: co-**PI**, one-month effort. Total award: \$600,000.)

## PEER-REVIEWED PUBLICATIONS

(Note: Students are in *italic*.)

70. *Meng, L.* and *Zheng, T.* (2017+). Phase-Aligned Spectral Filtering for Decomposing Spatiotemporal Dynamics. *arXiv preprint*: arXiv:1604.04899. Under revision.
69. *Ma, Y.* and *Zheng, T.* (2017+). Stabilized Sparse Online Learning for Sparse Data. *arXiv preprint*: arXiv:1604.06498. Under revision.
68. *Liu Y., de la Pena, V.* and *Zheng T.*<sup>6</sup> (2017+) Kernel-based measures of association. Under preparation for *WIREs Computational Statistics*.
67. *Owczarek et. al.* (2017) ARF Confers a Context-dependent Response to Chemotherapy in Muscle-Invasive Bladder Cancer. *Cancer Research*. In press.
66. *Lo, A., Chernoff, H., Zheng, T., and Lo, S.-H.* (2016). Framework for making better predictions by directly estimating variables’ predictivity. *Proceedings of the National Academy of Sciences* **113**(50) 14277-14282.
65. *Kalinsky et al* (2016) Proteomic Modulation in Breast Tumors after Metformin Exposure: Results from a “Window of Opportunity” Trial. *Clinical and Translational Oncology*, 1-9.

64. He, R. and Zheng, T. (2016). Estimating exponential random graph models using sampled network data via graphon. *Advances in Social Networks Analysis and Mining (ASONAM), 2016 IEEE/ACM International Conference on*, IEEE.
63. Lo, A., Agne, M., Auerbach, J., Fan, R., Lo, S.-H., Wang, P. and Zheng, T.<sup>6</sup> (2016) Network-guided interaction mining for the blood pressure phenotype of unrelated individuals in GAW 19. *BMC Proceedings for GAW 19*. *BMC proceedings* **10** (7), 333.
62. Auerbach, J., Agne, M., Fan, R., Lo, A., Lo, S.-H., Zheng, T. and Wang, P. (2016) Identification regions of disease related variants in admixed populations with summation partition approach. *BMC Proceedings for GAW 19*. *BMC proceedings* **10** (7), 131.
61. Zhang et al. (2016) Nkx3.1 Controls the DNA Repair Response in the Mouse Prostate. *Prostate* **76** (4): 402-8.
60. Ma Y., and Zheng T.<sup>6</sup> (2015+) sDist: Adaptive Sparse Distance Metric Learning. *Statistical Data Analysis and Mining*. In press.
59. Tan, L.S.L, Chan, A. H., and Zheng T.<sup>6</sup> (2015) Topic-adjusted visibility metric for scientific articles. *Annals of Applied Statistics* **10**(1): 1-31.
58. Davis, R.A., Zang, P., and Zheng, T. (2015+) Sparse vector autoregressive modeling. *Journal of Computational and Graphical Statistics*. In press.
57. Lo, A., Chernoff, H., Zheng, T. and Lo, S.-H. (2015) Why aren't significant variables automatically good predictors. *Proc Natl Acad Sci U S A* **112** (45):13892-13897.
56. Liu, Y., Gelman, A. and Zheng, T. (2015) Simulation-Efficient Shortest Probability Intervals. *Statistics and Computing*.**25**(4): 809-819.
55. Cai, B., Zheng, T. and Gelmann E. P. (2015) NKX3.1 Suppresses Tmprss2-ERG Gene Rearrangement and Mediates Repair of Androgen Receptor-Induced DNA Damage. *Cancer Research* **75**(13): 2686-2698.
54. He R. and Zheng T.<sup>6</sup> (2015) GLMLE: Graph-limit Enabled Fast Computation for Fitting Exponential Random Graph Models to Large Social Networks. *Social network analysis and mining*, **5** (1): 1:19.
53. McCormick, T. H. and Zheng, T. (2015) Latent space models for aggregated relational data. *Journal of American Statistical Association*. **110** (512): 1684-1695.
52. Avagyan S. *et al.* (2014) Hematopoietic stem cell dysfunction underlies the progressive lymphocytopenia in XLF/Cernunnos deficiency. *Blood*, **124** (10): 1622-1625.
51. Ou Yang, T.-H., Cheng, W.-Y., Zheng, T., Maurer, M. A., and Anastassiou, D. (2014) Breast cancer prognostic biomarker using attractor metagenes and the FGD3-SUSD3 Metagene. *Cancer Epidemiology Biomarkers & Prevention* 0399.2014.
50. Aytes A., Mitrofanova A., Lefebvre C., Alvarez M. J., Castillo-Martin M., Zheng T., Eastham J. A., Gopalan A., Pienta K. J., Shen M. M., Califano A. and Abate-Shen C. (2014) Global analyses of cross-species regulatory networks identifies FOXM1 and CENPF as synergistic master regulators of prostate cancer malignancy. *Cancer Cell* **25**(5): 638-651.
49. McCormick, T. H. and Zheng, T. (2014) Network-based methods for accessing hard-to-reach populations using standard surveys. In *Handbook on Hard-to-Survey Populations*. (ed. Tourangeau, R., Edwards, E., Johnson, T. P., Wolter, K. M., and Bates, N.) Cambridge University Press.
48. He R. and Zheng T.<sup>6</sup> (2013) Estimation of exponential random graph models for large social networks via graph limit. *Proceedings of The 2013 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining (ASONAM 2013)*. pp248-255. Accepted as "Full Paper." (13% acceptance rate).

47. Agne M., Huang C.-H., Hu I., Wang H., Zheng T. and Lo S.-H. (2013) Considering interactive effects in the identification of influential regions in extremely rare variants via fixed bin approach. *BMC Proceedings*, **8**(S1): S7.
46. Wang H., Huang C.-H., Zheng T., Lo S.-H. and Hu I. (2013) Discovering pure gene-environment association in blood pressure GWAS data: a two-step approach incorporating a new statistic. *BMC Proceedings*, **8**(S1): S62.
45. Fan R., Huang C. H., Hu I., Wang H., Zheng T., Lo S.-H. (2013) A partition-based approach to identify gene-environmental interactions in Genome-Wide Association Studies. *BMC Proceedings* **8**(S1): S60.
44. Liu Y., Huang C. H., Hu I., Lo S.-H., and Zheng, T.<sup>6</sup> (2013) A dual clustering framework for association screening with whole genome sequencing data and functional traits. *BMC Proceedings* **8**(S1): S47 (correction S112).
43. Irshad, S., Bansal, M., Castillo-Martin, M., Zheng, T., Aytes, A., Wenske, S., Magnen, C.L., Guarnieri, P., Sumazin, P., Benson M.C., Shen, M.M., Califano, A., and Abate-Shen, C. (2013) A molecular signature predictive of indolent prostate cancer. *Science Translational Medicine* **5** (202): 202ra122.
42. Zhou, H., Zheng, T.<sup>6</sup> (2013) Bayesian Hierarchical Graph-Structured Model for Pathway Analysis Using Gene Expression Data. *Statistical Applications in Genetics and Molecular Biology* **12**(3):. 393-412
41. McCormick, T. H., Moussa, A., Ruf, J., DiPrete, T. A., Gelman, A., Teitler, J., Zheng, T.<sup>6</sup> (2013) Measuring social distance using indirectly observed network data. *Journal of Statistical Theory and Practice* **7**(1): 120-132.
40. Wang, H. Lo, S.-H., Zheng, T. and Hu, I. (2012) Interaction-based feature selection and classification for high-dimensional biological data. *Bioinformatics* **28**(21)2834-2842.
39. McCormick, T. H., and Zheng, T. (2012) Latent demographic profile estimation in at-risk populations. *Annals of Applied Statistics* **6**(4):1795-1813.
38. McCormick, T. H., He, R., Kolaczyk, E. D. and Zheng, T.<sup>6</sup> (2012) Surveying hard-to-reach groups through sampled respondents in a social network. *Statistics in Biosciences* **4**(1):177-195
37. McCormick, T. H., Zheng, T. and Salganick, M. J. (2011). B: ORGANIZATIONAL BEHAVIOR-How Many People Do You Know? Efficiently Estimating Personal Network Size Bb: 140. *Operations Research Management Science***51**(1): 49.
36. Wang, H., Huang, C.-H., Lo, S.-H., Zheng, T., and Hu, I. (2011) New insights on old methods in identifying causal rare variants. *BMC Proceedings for the Genetic Analysis Workshop 17* (Boston, MA) **5**(s9):s50.
35. Agne, M., Huang, C.-H., Hu, I., Wang, H., Zheng, T., and Lo, S.-H. (2011) Identifying Influential Regions in Extremely Rare Variants using a Fixed-Bin Approach. *BMC Proceedings for the Genetic Analysis Workshop 17* (Boston, MA) **5**(s9):s3.
34. Liu, Y., Huang, C.-H., Hu, I., Lo, S.-H., and Zheng, T.<sup>6</sup> (2011) Association Screening for Genes with Multiple Potentially Rare Variants: an Inverse-Probability Weighted Clustering Approach. *BMC Proceedings for the Genetic Analysis Workshop 17* (Boston, MA) **5**(s9):s106.
33. Fan, R., Huang, C.-H., Lo, S.-H., Zheng, T., and Ionita-Laza, I. (2011) Identifying Rare Disease Variants in the Genetic Analysis Workshop 17 Simulated Data: A Comparison of Several Statistical Approaches. *BMC Proceedings for the Genetic Analysis Workshop 17* (Boston, MA) **5**(s9):s17.
32. Zheng, T., Chernoff, H., Hu, I., Ionita-Laza, I., Lo, S.-H. (2011) Discovering influential variables: a general computer intensive method for common genetic disorders. In Lu, H.H.S., Schölkopf, B., Zhao, H. (Eds.) (2011) *Handbook of Statistical Bioinformatics*, Springer-Verlag, New York. MS Link.

31. DiPrete, T. A., *McCormick, T. H.*, Gelman, A., Teitler, J., Zheng, T. (2011) Segregation in social networks based on acquaintanceship and trust. *American Journal of Sociology* **116** (4):1234-83
30. Kim, S., Singh, P., Park, J., Park, S., Friedman, A., Zheng, T., Sun, Q., Lee, Y.-H. and Lee, K. (2011) Fungal photoreceptor MGWC-1-mediated disease suppression in rice. *Fungal Genetics and Biology* **48**(4):400-407.
29. Zheng, T. and Gastwirth, J. L. (2011) On Bootstrap Tests of Symmetry About an Unknown Median. *Journal of Data Science* **8**(3): 397-412
28. Chernoff, H., Lo, S. H. and Zheng, T. (2009) Discovering influential variables: a method of partitions. *Annals of Applied Statistics* **3** (4):1335-1369.
27. *McCormick, T. H.*, Salganik, M. J., and Zheng, T. (2010) How many people do you know?: efficiently estimating personal network size. *Journal of the American Statistical Association* **105**(489):59-70 (Highlighted in the April 2010 issue of Amstat News, the official membership magazine of the American Statistical Association.)
26. Wang, S., Zheng, T., Chanock, S., Jedrychowski, W. and Perera, F. P. (2010) Methods for detecting interactions between genetic polymorphisms and prenatal environment exposure with a mother-child design. *Genetic Epidemiology* **34**(2) 172-180.
25. An, P., Mukherjee, O., Chanda, P., Yao, L., Engelman, C. D., Huang, C.-H., Zheng, T., Kovac, I. P., Dube, M.-P., Liang, X., Li, J., de Andrade, M., Culverhouse, R., Malzahn, D., Manning, A. K., Clarke, G. M., Jung, J., Province, M. A. (2009) The challenge of detecting epistasis (GxG interactions): Genetic Analysis Workshop 16. *Genetic Epidemiology* **33**(s1) s58-s67.
24. *Qiao, B.*, *Huang, C.-H.*, *Cong, L.*, Xie, J., Lo, S.-H., Zheng, T.<sup>5</sup> (2009) Genome-Wide Gene-Based Analysis of Rheumatoid Arthritis-Associated Interaction with PTPN22 and HLA-DRB1. *BMC Proceedings for the Genetic Analysis Workshop 16* **3**(s7):s132.
23. *Huang, C.-H.*, *Cong, L.*, Xie, J., *Qiao, B.*, Lo, S.-H., Zheng, T.<sup>5</sup> (2009) Rheumatoid Arthritis-Associated Gene-Gene Interaction Network for Rheumatoid Arthritis Candidate Genes. *BMC Proceedings for the Genetic Analysis Workshop 16* **3**(s7):s75.
22. Salicru, M., Vives, S. and Zheng, T.<sup>5</sup> (2009) Inferential clustering approach for two-color spotted microarray experiments. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* **6**(4):594-604. (Featured article from the October-December 2009 issue).
21. *Watkinson, J.*, Liang, K.C., Wang, X., Zheng, T., and Anastassiou, D. (2008) Inference of regulatory gene interactions from expression data using three-way mutual information. *The Annals of New York Academy of Sciences* **1158**:302-313.
20. Lo, S.-H., Chernoff, H., *Cong, L.*, *Ding, Y.* and Zheng, T. (2008) Discovering interactions among BRCA1 and other candidate genes involved in Sporadic Breast Cancer. *Proc Natl Acad Sci U S A* **105**: 12387-12392.
19. *Iossifov, I.*, Zheng, T., Baron, M., Gilliam, T.C. and Rzhetsky, A. (2008) Genetic-linkage mapping of complex hereditary disorders to a whole-genome molecular-interaction network. *Genome Research* **18**:1150-1162.
18. *Watkinson, J.*, Wang, X., Zheng, T. and Anastassiou, D. (2008) Identification of gene-gene interactions associated with disease from gene expression data. *BMC Systems Biology* **2**:10.
17. *Yan, X.* and Zheng, T.<sup>6</sup> (2008) Selecting informative genes for discriminant analysis using multigene expression profiles. *BMC Genomics* **9**(S2):S14.

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<sup>5</sup>Joint correspondence author.

16. Chen, G. K., Zheng, T., Witte, J. S. and Goode, E. L. (2007) Genome-wide association analyses of expression phenotypes. *Genetic Epidemiology* **31**(S1):S7-S11.
15. Woo, J.H., Zheng, T.<sup>7</sup> and Kim, J.H. (2007) Identifying genomic regulators of set-wise co-expression. *Proceedings of IEEE 7th International Conference on Bioinformatics and BioEngineering*. paper URL. (Acceptance for regular research papers is 65 out of  $\sim 500$ .) Extended paper published in *International Journal of Functional Informatics and Personalised Medicine* **1**:407-418.
14. Yan, X. and Zheng, T.<sup>6</sup> (2007) Discriminant Analysis using multigene profiles in classification of breast cancer. *Proceedings of the 2007 International Conference on Bioinformatics and Computational Biology*. (Acceptance rate: 30%. Worldcomp'07 Honorary First Runner-Up for Best Paper Award in Bioinformatics and Computational Biology.) Ms file.
13. Zheng, T., Wang, S., Cong, L., Ding, Y., Ionita-Laza, I. and Lo, S.H. (2007) Joint study of genetic regulators for expression traits related to breast cancer. In "Genetic Analysis Workshop 15: Gene Expression Analysis and Approaches to Detecting Multiple Functional Loci." *BMC Proceedings* **1** S1:S10.
12. Wang, S., Zheng, T. and Wang, Y. (2007) Transcription activity hotspot, is it real or an artifact? In "Genetic Analysis Workshop 15: Gene Expression Analysis and Approaches to Detecting Multiple Functional Loci." *BMC Proceedings* **1** S1:S94.
11. Li, Z., Zheng, T., Califano, A. and Floratos, A. (2007) Pattern-based mining strategy for multi-Locus association analysis on GAW15 problem 2 chromosome 18 dataset. In "Genetic Analysis Workshop 15: Gene Expression Analysis and Approaches to Detecting Multiple Functional Loci." *BMC Proceedings* **1** S1:S16.
10. Ding, Y., Cong, L., Ionita-Laza, I., Lo, S.H. and Zheng, T.<sup>6</sup> (2007) Constructing gene association network for rheumatoid arthritis using the backward genotype-trait association (BGTA) Algorithm. In "Genetic Analysis Workshop 15: Gene Expression Analysis and Approaches to Detecting Multiple Functional Loci." *BMC Proceedings* **1** S1:S13.
9. Rzhetsky, A., Wajngurt, D., Park, N. and Zheng, T. (2007) Probing genetic overlap among complex human phenotypes, *Proc Natl Acad Sci U S A* **104**, 11694-11699.
8. Zheng, T., Ichiba, T. and Morton, B.R. (2007) Assessing substitution variation across sites in grass chloroplast DNA, *Journal of Molecular Evolution*, **64**, 605-613.
7. Kerman, J., Gelman, A., Zheng, T. and Ding, Y. (2007) Visualization in Bayesian data analysis. In Chen, C.-H., Hardle, W. and Unwin, A. (eds), *Handbook of Computational Statistics (Volume III) Data Visualization*. Springer-Verlag, Heidelberg. Paper URL.
6. Zheng, T. and Lo, S.H. (2007) A modified Kendall rank-order association test for evaluating the repeatability of two studies with a large number of objects. In Nair, V. (ed), *Advances in Statistical Modeling and Inference—Essays in Honor of Kjell A. Doksum*. World Scientific, Hackensack, NJ. Ms file.
5. Rzhetsky, A., Zheng, T.<sup>7</sup> and Weinreb, C. (2006) Self-correcting maps of molecular pathways, *PLoS One*, **1**, e61.
4. Zheng, T., Wang, H. and Lo, S.H. (2006) Backward genotype-trait association (BGTA)-based dissection of complex traits in case-control designs, *Hum Hered*, **62**, 196-212.
3. Zheng, T., Salganik, M.J. and Gelman, A. (2006) How many people do you know in prison?: Using overdispersion in count data to estimate social structure in networks, *Journal of the American Statistical Association*, **101**, 409-423.

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<sup>6</sup>Correspondence author.

<sup>7</sup>Joint first author.

2. Lo, S.H. and Zheng, T. (2004) A demonstration and findings of a statistical approach through reanalysis of inflammatory bowel disease data, *Proc Natl Acad Sci U S A*, **101**, 10386-10391.
  1. Lo, S.H. and Zheng, T. (2002) Backward haplotype transmission association (BHTA) algorithm—a fast multiple-marker screening method, *Hum Hered*, **53**, 197-215.
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## OTHER PUBLICATIONS

(Note: Students are in *italic*.)

71. Zheng, T. (2002) Multiple-marker screening approach towards the mapping of complex traits in human genetics. Columbia University Doctoral Dissertation.
  72. Ding, Y. and Zheng, T. (2006) Tree-Based Integration of One-versus-Some (OVS) Classifiers for Multiclass Classification, *Proceedings of the joint statistical meeting 2006*. Preprint URL.
  73. Rosner, E. and Zheng T. (2006) Helpfulness of the genders—a student project. STATS. (This is a magazine style article on Teaching Statistics)
  74. McCormick, T. H. and Zheng, T. (2007) Adjusting for recall bias in “how many X’s do you know?” surveys, *Proceedings of the joint statistical meeting 2007*. Preprint URL.
  75. Zheng, T. and Lo, S.-H. (2008) Discussion on “Quantifying the Fraction of Missing Information for Hypothesis Testing in Statistical and Genetic Studies by Nicolae, Meng and Kong.” *Statistical Science*. **23**(3):321-324.
  76. McCormick, T. H., Zheng, T. (2009) Towards a unified framework for inference with aggregated relational data. *Proceedings of the joint statistical meeting 2009*. Link
  77. McCormick, T. H., Moussa, A., Ruf, J., DiPrete, T. A., Gelman, A., Teitler, J., Zheng, T. (2009) Comparing two methods for predicting opinions using social structure. *Proceedings of the joint statistical meeting 2009*. (Manuscript #33 above is an extended journal paper version of this report.)
  78. McCormick, T. H., and Zheng, T. (2010) A latent space representation of overdispersion in “How many X’s do you know?” data. *Proceedings of the joint statistical meeting 2010*.
  79. Huang, C.-H., Agne, M., Hu, I., Ionita-Laza, I., Zheng, T., and Lo, S.-H. (2011) GAW 17-Identifying Influential Variables on Unrelated Individual Data. Genetic Analysis Workshop 17 (Boston, MA).
  80. Zheng, T. and Ying, Z. (2013) Columbia University Statistics. In Agresti, A. and Meng, X.-L. (eds) “*Strength in Numbers: The Rising of Academic Statistics Departments in the U. S.*”, Springer, New York.
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## UNPUBLISHED TECHNICAL REPORTS AND WORKING PAPERS

(Note: Students are in *italic*.)

81. Zheng, T., Wang, H. and Lo, S.H. (2004) Rank-based generalized genotype-trait association algorithm for the mapping of quantitative trait loci. Technical report. Department of Statistics, Columbia University.
82. Zheng, T., Lo, S.H., Reilly, C. and Blumenthal, M.N. (2005) Genetic Analysis of Asthma Data Using the Backward Haplotype Transmission Association (BHTA) method. Technical report. Department of Statistics, Columbia University.
83. Ionita-Laza, I., Ding, Y., Cong, L., Lo, S.H. and Zheng, T. (2007) Combined Linkage and Association Analysis of the NARAC Dataset. Technical report. Department of Statistics, Columbia University.



84. Zheng, T. and Lo, S.-H. (2008) Constructing gene association networks for complex human disorders using the backward genotype-trait association (BGTA) algorithm. Technical report, Department of Statistics, Columbia University.
85. Ding, Y. and Zheng, T. (2008) Feature Selection and Classification Based on K-Nearest Neighbor Patterns. Working paper. Department of Statistics, Columbia University.
86. Chen, J., McCormick, T. H., Zheng, T., Gelman, A., DiPrete, T. A. and Teitler, J. (2009) The cube model for social structure in acquaintances subnetworks. Work in progress.
87. Huang, C.-H., Qiao, B., Cong, L., Zheng, T. and Lo, S.-H. (2009) Genomewide analysis of genetic interactions with BRCA1 associated with the risk of sporadic breast cancer. Work in progress.
88. Ding, Y., Lo, S.-H. and Zheng, T. (2009) Sum of Squared Local Sums (SSLS): a nonparametric association measure. Work in progress.
89. Wu, X., Ying, Z. and Zheng, T. (2011) Nonparametric weighted log-rank tests for comparing multivariate distributions. In revision.
90. Zhou, H., Wang, S., Zheng, T. (2014+) Penalized conditional logistic regression for high-dimensional matched case-control DNA methylation data. Under revision.
91. Davis, R.A., Zang, P., and Zheng, T. (2015) Reduced-Rank Covariance Estimation in Vector Autoregressive Modeling. *arXiv preprint*: <https://arxiv.org/abs/1412.2183>

#### INVITED SEMINAR TALKS

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|----------------|---|
| September 2016 | Undergraduate Statistics Seminar, Columbia University   |
| September 2016 | Science Research Fellow seminar, Columbia University  |
| July 2016      | Tsinghua University Statistics Summer Camp  |
| February 2016  | Center for the Promotion of Research Involving Innovative Statistical Methodology (PRIISM), New York University |
| July 2015      | Institute of System Sciences, Chinese Academy of Sciences   |
| Oct 2014       | Department of Biostatistics, Yale University  |
| April 2014     | Microsoft Research NYC  |
| April 2014     | Department of Psychiatry, Columbia University   |
| Oct 2012       | Johnson Research Labs   |
| Oct 2011       | Department of Statistics, University of Illinois at Urbana-Champaign  |
| Oct 2011       | Department of Statistics, University of Illinois at Chicago   |
| Nov 2010       | Department of Statistics, University of Michigan  |
| Oct 2010       | Department of Mathematics and Statistics, Boston University   |
| April 2009     | Department of Statistics, Rutgers University  |
| April 2008     | Department of Statistics, George Washington University  |
| Feb 2008       | Division of Biostatistics, New York University  |
| Dec 2007       | Department of Statistics, University of Minnesota   |

Nov 2007	Department of Statistics, Purdue University
Oct 2007	Department of Biostatistics, University of Pennsylvania
June 2007	Bioinformatics Division, Department of Automation, Institute of Information Processing, Tsinghua University (Beijing, China)
November 2006	Department of Statistics, Yale University.
November 2006	Department of Statistics, Harvard University.
November 2005	University seminar on Genetic Epidemiology, Columbia University.
April 2005	Department of Biostatistics, Yale University.
November 2004	Department of Statistics, Columbia University.
November 2003	Department of Biostatistics, University of Alabama at Birmingham.
October 2002	International Center for Health Outcomes and Innovation Research, Columbia University.
February 2002	Department of Statistics, University of Wisconsin at Madison.
February 2002	Department of Statistics, University of California at Riverside.
February 2002	Department of Statistics, University of California at Davis.
February 2002	Department of Statistics, University of North Carolina at Chapel Hill.
February 2002	Department of Statistics, Pennsylvania State University.
February 2002	Department of Statistics, Columbia University.
February 2002	Department of Statistics, Ohio State University.

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#### INVITED CONFERENCE PRESENTATIONS

August 2017	JSM 2017
July 2017	Program on Quantitative Methods for Drug Discovery and Development, National Singapore University
June 2017	The third annual flagship conference on the Theory of Big Data, University College London, UK.
February 2017	Women in Data Science (WiDS) 2017
August 2016	JSM 2016 "Phase-aligned spectral filtering for spatiotemporal dynamics"
July 2016	Third Taihu International Statistics Forum (Shanghai) "Phase-aligned spectral filtering for spatiotemporal dynamics"
June 2016	Workshop on Big Data Learning for Prediction, National Sun Yat-sen University, Taiwan
June 2016	Workshop on Big Data Learning for Prediction, National Tsinghua University, Taiwan.
June 2016	IMS-APRM 2016 "Adaptive sparse non-linear metric learning via boosting"
June 2016	ASA SLDM annual meeting "Adaptive sparse non-linear metric learning via boosting"
April 2016	Columbia Data Science day.
August 2015	JSM 2015 Discussion "The fifth V for big data"

- July 2015 “Latent Space Model for Aggregated Relational Data,” 2015 Workshop on Network Data Analysis at Northeast Normal University, Changchun, Jilin, China.
- June 2015 “Latent Space Model for Aggregated Relational Data,” Tsinghua workshop on Modern Statistics, 2015, Beijing, China.
- Nov 2013 “Estimation of Exponential Random Graph Models for Large Social Networks via Graph Limits” DIMACS Workshop on Statistical Analysis of Network Dynamics and Interactions, New Brunswick, NJ.
- Oct 2013 “A general framework of association measures, with applications to genetics.” The 2013 Rao Prize Conference, Penn State University, University Park, PA.
- August 2013 Discussion on “social network analysis.” ISI World Statistical Congress 2013, Hong Kong
- July 2013 “Bayesian Hierarchical Graph-Structured Model with Application to Pathway Analysis Using Gene Expression Data”, IMS-China 2013, Chengdu, China.
- August 2012 “Social network analysis through randomly sampled respondents.” SAMSI computational advertising workshop.
- April 2012 “Bayesian Hierarchical Graph-Structured Model with Application to Pathway Analysis Using Gene Expression Data” ENAR 2012, Washington, DC.
- March 2011 “Statistical methods for studying social networks using aggregated relational data”. ENAR 2011, Miami, FL.
- October 2010 “Statistical methods for studying social networks using aggregated relational data”. SAMSI complex networks modeling workshop.
- August 2010 “Discovering Influential Variables: A Partition-Based Learning Method to Identify Susceptible Genetic Risk Factors in Common Human Disorders,” Joint Statistical Meeting 2010, Vancouver, BC, Canada.
- July 2010 “Constructing Gene Association Networks for Complex Human Disorders Using the BGTA Algorithm,” NCTS Workshop on “Statistics and Probability with Applications for Biology”, Hsin-Chu, Taiwan.
- June 2010 “Studying co-regulation and inter-regulation of genes via eQTL mapping,” ICSA Applied Statistics Symposium, Indianapolis, IN.
- May 2010 Workshop on “Statistical Issues in Analyzing Data from Diverse Sources”, CCICADA (a Department of Homeland Security Center of Excellence), New Brunswick, NJ.
- April 2010 “Latent space model for aggregated relational data,” New England Statistics Symposium, Harvard University, Cambridge, MA.
- March 2010 “Latent space model for aggregated relational data in the study of high-risk population for HIV+ and AIDS.” ENAR 2010, New Orleans, LA.
- August 2009 (**Poster award**) “Latent Structural Models for Aggregated Relational Data”, Joint Statistical Meeting 2009, Washington, DC.
- July 2009 “Constructing Gene Association Networks for Complex Human Disorders Using the BGTA Algorithm,” IMS-APRM 1st meeting, Seoul, Korea.
- June 2009 “Constructing Gene Association Networks for Complex Human Disorders Using the BGTA Algorithm, Workshop on Detecting Influential Variables in High-Dimensional Data, Taida Institute of Mathematical Science, National Taiwan University, Taipei, Taiwan.

- Nov 2008      **(Peer reviewed)** “Immunohistochemical evaluation of uteri from female rhesus monkeys (Macaca Mulatta) after cyclic intramuscular estrogen treatment,” American Society of Reproductive Medicine 64th Annual Meeting. (As co-author)
- June 2008      “Feature selection and classification based on k-nearest-neighbor patterns,” Beijing International Conference on Machine Learning and Data Mining.
- June 2008      “Constructing Gene Association Networks for Complex Human Disorders Using the BGTA Algorithm,” ICSA 2008 applied statistics symposium.
- Oct 2007      “Studying co-regulation and inter-regulation of genes via eQTL mapping,” IEEE 2007 International Conference on Bioinformatics and BioEngineering.
- Oct 2007      “Evaluating the repeatability of two studies of a large number of objects: modified Kendall rank-order association test,” Current and Future Trends in Nonparametrics.
- August 2007    “Studying co-regulation and inter-regulation of genes via eQTL mapping,” Joint Statistical Meeting 2007
- June 2007      **(Peer-reviewed)** “Discriminant analysis using multigene expression profiles in classification of breast Cancer,” BioComp’07.
- June 2007      “Studying co-regulation and inter-regulation of genes via eQTL mapping,” NSF Sponsored International Conference on Bioinformatics, Hangzhou, China.
- August 2006    Discussion on “Statistical models for networks,” Joint Statistical Meeting 2006.
- August 2006    “Design and analysis of ‘how many X’ surveys,” Joint Statistical Meeting 2006.
- June 2006      “Evaluating the repeatability of two studies of a large number of objects: modified Kendall rank-order association test,” ICSA 2006 applied statistics symposium.
- August 2005    “A nonparametric multipoint screening method for QTL mapping,” Joint Statistical Meeting 2005.
- June 2005      “A nonparametric multipoint screening method for QTL mapping,” International Conference on Statistics in Honour of Professor Kai-Tai Fang’s 65th Birthday.
- March 2004     “Information-driven marker selection for large scale genomic studies on complex traits,” International Biometric Society, Eastern North American Region (ENAR), Spring Meeting 2004.

## TEACHING AND MENTORING

### — Courses taught

- STAT W1111      Introduction to statistics—an introductory level course (aver. enroll.: 120 students). Teaching innovation—**Statistics Projected website:**  
<http://www.stat.columbia.edu/~tzheng/teaching/ProjectSave/>.
- STAT W4315/3315    Linear Regression Models—core requirement for M.A. in statistics program or undergraduate majors (aver. enroll.: 65 students).
- STAT W4335      Sample Surveys (aver. enroll.: 45 students)
- STAT W8325      Topics in Advanced Statistics—topics including relational data; network analysis; modern statistical learning and computing, with applications to biology, a topic course for PHD students (aver. enroll.: 10 students).

STAT G6101	Statistical Modeling/Data Analysis I (Core curriculum for PHD program; aver. enroll.: 25 students)
STAT G6102	Statistical Modeling/Data Analysis II (Core curriculum for PHD program; aver. enroll.: 20 students)
STAT G6103	Statistical Modeling/Data Analysis III (Core curriculum for PHD program, aver. enroll.: 15 students).
STAT/CS W4242	Introduction to Data Science. (Re-structured and designed a new course on data science for students in non-quantitative degree programs.)
STAT GU5243	Applied Data Science. Project-based learning course in data science for statistics students.

— **Doctoral Theses supervised**

2004	Xin Yan, “ <i>Discriminant analysis using multi-gene profiles in molecular classification of breast cancer</i> ,” Department of Statistics, Columbia University (jointly with Professor Shaw-Hwa Lo)
2004	Hui Wang, “ <i>A new approach of detecting influential markers for complex phenotypes with genotype data</i> ,” Department of Statistics, Columbia University (jointly with Professor Shaw-Hwa Lo)
2008	Yuejing Ding, “ <i>On feature selection and classification in high dimensions</i> ,” Department of Statistics, Columbia University
2011	Tyler McCormick, “ <i>Statistical methods for aggregated relational data</i> ,” Department of Statistics, Columbia University
2012	Pengfei Zang, “ <i>Sparse Vector Autoregressive Model for high dimensional time series</i> ,” Department of Statistics, Columbia University (Jointly with Professor Richard Davis)
2013	Ying Liu, “ <i>Kernel-based association measures</i> ,” Department of Statistics, Columbia University
2014	Hui Zhou, “ <i>Graph structured inference for high-throughput genomic data</i> ,” Department of Biostatistics, Columbia University (Jointly with Professor Shuang Wang)
2015	Ran He, “ <i>A Graphon-based Framework for Modeling Large Networks</i> ,” Department of Statistics, Columbia University
2016	Lu Meng, “ <i>Spectral Filtering for Spatio-temporal Dynamics and Multivariate Forecasts</i> ,” Department of Statistics, Columbia University
2016	Yuting Ma, “ <i>Flexible Sparse Learning of Feature Subspaces</i> ,” Department of Statistics, Columbia University
In progress	Swupnil Sahai (4th year), Department of Statistics, Columbia University (Jointly with Professor Andrew Gelman)
In progress	Tim Jones (4th year), Department of Statistics, Columbia University
In progress	Jing Wu (3rd year), Department of Statistics, Columbia University
In progress	Chengliang Tang (1st year), Department of Statistics, Columbia University

— **Postdoctoral researchers mentored.**

2014-2015	Linda Tan, Department of Statistics, Columbia University
2015-2016	Shirin Golchi, Department of Statistics, Columbia University
2016-present	Mohammad Khabbazian, Department of Statistics, Columbia University

— **Other mentoring**

2002-present	Mentored master students, undergraduate and high school students on research projects.
2015-present	As faculty advisor of the Columbia Statistics Club, helped organizing hackathons with industry sponsors.
2015-present	Mentored student instructors who taught a new data science course in the Columbia Science Honor Program for high school students.
2016-present	Mentored postdoctoral fellows in the Columbia Collaboratory Program for designing data science bootcamp.

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**CONSULTING PROJECTS**

2014-present	Consultant to Drs. Edward Gelmann and Shan Zha, HICCC, Columbia University Medical Center
2013-present	Consultant to Dr. Kevin Kalinsky, HICCC, Columbia University Medical Center
2011-present	Consultant to Dr. Cory Abate-Shen, HICCC, Columbia University Medical Center
2011-2013	Consultant to Bureau of Epidemiology Services, New York City Department of Health and Mental Hygiene
2010	Consultant to Drs. Alex Carballo-Dièguez and Ivan Balan at HIV Center for Clinical and Behavioral Studies, New York State Psychiatric Institute and Columbia University.
May 2008	Consultant to Dr. Jian Tang at Mount Sinai School of Medicine.
2007-present	Consultant to Dr. Andrew Joe at the Department of Medicine, The Medical Center of Columbia University on Microarray data analysis.
2005-2006	Consultant to Dr. Doris Chang at the Department of Psychology, New School University on “Chinese immigrant women: domestic abuse and help seeking.”
Summer 2004	Consultant to Dr. Kwangwon Lee at the Department of Plant Pathology, Cornell University on “Characterization of the roles of light in plant-microbe interactions.”
Summer 2003	Consultant to Dr. Steven Schinke of the School of Social Work, Columbia University on clinical trials evaluating the effects of intervention approaches on alcohol use among adolescents.
Summer 2003	Consultant to Intersystems Inc on the Prevention Program Outcomes Monitoring System survey evaluating science-based prevention programs identified and disseminated by the Center for Substance Abuse Prevention (CSAP) of the Substance Abuse and Mental Health Services Administration (SAMHSA).
2002-2003	Consultant to International Center for Health Outcomes and Innovation Research (IN-CHOIR), Columbia University on “Randomized Evaluation of Mechanical Assistance for Treatment of Congestive Heart Failure (REMATCH).”

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**PROFESSIONAL SERVICE**

- 2014-present Board of directors, International Chinese Statistical Association (ICSA)  
 2016-present Advisory board member, Stats.org

**— Editorial and review service**

- 2007-2013 Associate editor, Journal of the American Statistical Association, Applications and Case Studies.  
 2011-2014 Review editor, Frontiers in Genetic Architecture—a specialty of Frontiers in Genetics.  
 2011-2012 Guest editor, for a special issue on networks, Statistics and its Interface.  
 2011-2012 JASA ACS editor search committee.  
 2013-2014 ASA Forensic Science Advisory Committee (FSAC) GAO group  
 2015 Panel member, National Science Foundation  
 2016 Panel member, National Science Foundation  
 2013-present Associate editor, Statistical analysis and data mining (SAM).  
 2013-present Faculty member, F1000 Prime.  
 2015-present Associate editor, Statistics in Biosciences (SIBS)

**— Referee**

| ASA SLDM student paper competition 2015, 2016, 2017 | BioComp'07 | Behavior Genetics | Bioinformatics | BMC Genomics | Communications in Statistics | Human Heredity | IEEE BIBE 07 | IEEE transactions on signal processing | Journal of Official Statistics | Journal of Statistical Planning and Inference | Journal of the American Statistical Association | National Security Agency | New Media and Society | NSF | PLoS genetics | Sociological Methodology | PNAS | Statistical Applications in Genetics and Molecular Biology | Statistical Methodology | Statistics in Bioscience | Prentice Hall | The American Statistician | U.S. Army Research | Wiley | American Medical Informatics Association Symposium 2005 |

**— Conference/invited sessions organizers and chairs**

- 2016-2017 Chair, committee on student paper competition for JSM 2017, section on Statistical Learning and Data Mining, ASA.  
 2016 Organized special session on “Statistical Learning for Data Science” in ASA sponsored 2016 IEEE Conference on Data Science and Applied Analytics.  
 2015-2016 Chair, committee on student paper competition for JSM 2016, section on Statistical Learning and Data Mining, ASA.  
 2015 Organized topic-contributed sessions for JSM 2015: “Statistical methods for observational health studies,” and “Scalable Bayesian learning and computing.”  
 2014-2015 Co-chair, committee on student paper competition for JSM 2015, section on Statistical Learning and Data Mining, ASA.

2012-2014	Organizing committee, member, SAMSI 2013-2014 program on Computational Methods in Social Sciences.
2011-2013	Scientific program committee vice-chair, ISI World Statistics Congress 2013, Hong Kong.
2009-2011	Executive committee, Program Chair, ICSA Applied Statistics Symposium 2011, New York
2010	Organized invited session for JSM 2010 “Latent space models for network analysis”
2010	Organized IMS sponsored invited session for ENAR 2010 “Studying genetic and environmental risk factors of complex human disorders and their interactions”
2007	Program committee, IEEE 2007 International Conference on Bioinformatics and BioEngineering.
2007	Organized invited session JSM 2007: <i>Statistical methods for gene regulatory networks</i> .
2006–present	Organized invited sessions for ICSA applied statistics symposium 2006: <i>Recent contributions to nonparametric methodologies in biomedical research</i> ; 2008: <i>Designs and analyses of genome-wide association studies</i> .
2005	Organized topic contributed session JSM 2005: <i>Recent statistical contributions to Genetics and Epidemiology</i> .
2003–present	Chaired sessions for Joint Statistical Meetings: 2003, 2005 and 2007.

— **University/Departmental service**

2012-present	chair, center on Foundations of Data Science, Data Science Institute, Columbia University
2013-present	member, Education committee, Data Science Institute, Columbia University
2014-present	member, HPC Yeti OC Executive committee
2014-present	member, Shared Research Computing Policy Advisory Committee (SRCPAC), Columbia University
2015-present	faculty advisor, Columbia Statistics Club
2015-present	member, data and society task force, Columbia University
2017-present	department representative, Equality committee, Arts & Sciences, Columbia University
2017-present	member, EPPC subcommittee on Coordination of Instructional Staffing and Scheduling, Arts & Sciences, Columbia University
2017	chair, faculty search committee for open-rank position, Department of Statistics, Columbia University
2016-2017	member, hiring committee for lecturer in discipline, Department of Statistics, Columbia University
2016	chair, hiring committee for term assistant professors, Department of Statistics, Columbia University
2015-2016	series creator, ColumbiaX series on “data science and analytics” on edX.
2015	Lenfest junior faculty grant review committee, Columbia University
2015	Review committee, ROADS grant, Data Science Institute, Columbia University



- 2013-2014 member, hiring committee for lecturer of Analytics, School of Continuing Education, Columbia University
- 2007-2008 director of graduate study (Ph.D. program), Department of Statistics, Columbia University.
- 2006-07, 2002-03 seminar chair, Department of Statistics, Columbia University.
- 2004–present doctoral students mentoring: Yuejing Ding (2004), Jiayi Chen (2005), Xiaoru Wu (2006), Li Song (2006), Tyler McCormick (2007), Ying Liu (2009), Lu Meng (2011), Yuanjun Gao (2012), Shuaiwen Wang (2013), Yixin Wang (2014), Chengliang Tang (2016) Department of Statistics, Columbia University.
- 2002–present Computing committee, committee on curriculum, committee on junior search (2002-2003), committee on PhD admissions, Department of Statistics, Columbia University.

— **Doctoral Defense Committees**

- 2016 (Oral Exam) Feihan Lu, Department of Statistics, Columbia University  
Yuting Ma, Department of Statistics, Columbia University  
Adeline Lo, Department of Sociology, University of California at San Diego  
Lu Meng, Department of Statistics, Columbia University  
Diego Franco Saldana, Department of Statistics, Columbia University  
(Oral Exam) Jing Wu, Department of Statistics, Columbia University
- 2015 Michael Agne, Department of Statistics, Columbia University  
(Oral Exam) Haolei Weng, Department of Statistics, Columbia University  
Ran He, Department of Statistics, Columbia University  
(Oral Exam) Adeline Lo, Department of Political Science, University of California at San Diego  
(Oral Exam) Lu Meng, Department of Statistics, Columbia University
- 2014 (Oral Exam) Diego Franco, Department of Statistics, Columbia University  
Mengqian Lu, Department of Earth and Environmental Engineering, SEAS, Columbia University  
Ruixue Fan, Department of Statistics, Columbia University  
Hui Zhou, Department of Biostatistics, Columbia University  
(Oral Exam) Michael Agne, Department of Statistics, Columbia University  
(Oral Exam) Ruixue Fan, Department of Statistics, Columbia University  
(Oral Exam) Ran He, Department of Statistics, Columbia University
- 2013 (Oral Exam) Hui Zhou, Department of Biostatistics, Columbia University  
Ying Liu, Department of Statistics, Columbia University  
Chien Hsun Huang, Department of Statistics, Columbia University  
Vincent Dorie, Department of Statistics, Columbia University

- Bo Qian, Department of Statistics, Columbia University
- 2012 (Oral Exam) Ying Liu, Department of Statistics, Columbia University  
 (Oral Exam) Chien Hsun Huang, Department of Statistics, Columbia University  
 (Oral Exam) Vincent Dorie, Department of Statistics, Columbia University  
 Pengfei Zang, Department of Statistics, Columbia University
- 2011 (Oral Exam) Pengfei Zang, Department of Statistics, Columbia University  
 Xiaoru Wu, Department of Statistics, Columbia University  
 Amal Moussa, Department of Statistics, Columbia University  
 Tyler McCormick, Department of Statistics, Columbia University  
 (Oral Exam) Gongjun Xu, Department of Statistics, Columbia University
- 2010 (Oral Exam) Tyler McCormick, Department of Statistics, Columbia University
- 2008 (Oral Exam) Xiaoru Wu, Department of Statistics, Columbia University  
 Yuejing Ding, Department of Statistics, Columbia University  
 Ivan Iossifov, Department of Medical Informatics, Columbia University
- 2006 (Oral Exam) Yihong Zhao, Department of Biostatistics, Columbia University  
 Iuliana Ionita, Department of Computer Science, New York University  
 (Oral Exam) Shouhao Zhou, Department of Statistics, Columbia University  
 Jouni Kerman, Department of Statistics, Columbia University
- 2005 (Oral Exam) Jouni Kerman, Department of Statistics, Columbia University  
 Jing Han, Division of Biostatistics, New York University
- 2004 (Thesis outline defense) Jing Han, Division of Biostatistics, New York University  
 Hui Wang, Department of Statistics, Columbia University  
 Xin Yan, Department of Statistics, Columbia University
- 2003 Cristian Pasarica, Department of Statistics, Columbia University  
 Zaiying Huang, Department of Statistics, Columbia University
- 2002 Yuhang Xing, Department of Finance, Columbia University

## MEMBERSHIPS

- American Statistical Association (elected fellow)  
 Royal Statistical Society  
 Institute of Mathematical Statistics  
 International Chinese Statistical Association  
 International Statistical Institute (elected)