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School of Computer Science

Carnegie Mellon University

Pittsburgh, PA 15213

Positions

- **Professor**, Machine Learning Department & Language Technology Institute & Computer Science Department, School of Computer Science, *Carnegie Mellon University*. (June, 2014 –)
- **Associate Professor with tenure**, Machine Learning Department & Language Technology Institute & Computer Science Department, School of Computer Science, *Carnegie Mellon University*. (June, 2011 – June 2014)
- **Visiting Associate Professor**, Department of Statistics, *Stanford University*. (Aug, 2010 – Aug 2011)
- **Visiting Research Professor**, *Facebook Inc.*. (Aug, 2010 – Aug 2011)
- **Associate Professor**, Machine Learning Department & Language Technology Institute & Computer Science Department, School of Computer Science, *Carnegie Mellon University*. (June, 2009 – 2011)
- **Assistant Professor**, Machine Learning Department & Language Technology Institute & Computer Science Department, School of Computer Science, *Carnegie Mellon University*. (September 1, 2004 – June, 2009)

Education

- **University of California, Berkeley**, Ph.D. in Computer Science (1999–2004).
  Research advisors: Profs. Richard Karp, Michael Jordan and Stuart Russell
- **Rutgers University**, Ph.D. in Molecular Biology and Biochemistry (1994–1999).
  Research advisor: Prof. Chung S. Yang
- **Rutgers University**, M.Sc. in Computer Science (1996–1998).
  Research advisor: Prof. Casimir Kulikowski
- **Tsinghua University**, B.Sc. in Physics (1988–1993).
  Research advisor: Prof. Jun Zhao

Awards and Honors

- Member of the DARPA Information Science and Technology (ISAT) Advisory Group, 2011-2014.
- IBM Open Collaborative Research Faculty Award, IBM, 2012-2014.
- Young Investigator Award, United States Air Force Office of Scientific Research, 2010-2015.
- Alfred P. Sloan Research Fellowship in Computer Science, 2008-2010.
- Career Award, National Science Foundation, 2006-2011.
- Best Paper Award, The 1st IEEE Workshop on Large Scale Visual Commerce, 2013.
- Best Paper Award, International Conference on Intelligence Systems for Molecular Biology, 2011.
- Best Paper Award, Association for Computational Linguistics (ACL), 2009.
- Best Paper Award, SIAM International Conference on Data Mining, 2007.
- John Van Ryzin Award for best paper, International Biometric Society-ENAR Annual Meetings, 2006.
- Runner-up Best Student Paper Award, 18th Conference on Uncertainty in Artificial Intelligence, 2003.
- Regents Fellowship, UC Berkeley, 1999.
- *Anthony Lu* Best Paper Award, Rutgers University, 1999.

Principal External Grants and Awards

1. Commonwealth of Pennsylvania Tobacco Settlement Grant (co-PI): "Computational Analysis of Integrated Multivariate Protein Data", Sep 1, 2004 – Jun 30, 2006, $237,443.

2. Glaxo-Smith-Kline (PI): Gift for Discretionary Project, Nov 1, 2005 – Dec 31, 2015, $ 150,000.

3. NSF CCF-0523757 (PI): "Nonparametric Bayesian Models for Genetic Variations and Their Associations to Diseases and Population Demography", Aug 1, 2005 – Jul 31, 2008, $ 300,000.

4. NSF DBI-0546594, Career Award (PI): "CAREER: Uncovering the Process and Mechanism of Regulatory Evolution – Novel Statistical Models and Computational Algorithms for Evolutionary Genomics", Mar 1, 2006 – Feb 28, 2011, $1,312,321.

5. NIH 1 R01 GM078622-01 (co-PI, with R. Murphy and W. Cohen): "Probabilistic Modeling of Information from Images and Text in Online Journals", Jul 1, 2006 – Jun 30, 2009, $791,891.

6. NSF DBI- 0640543 (PI, with co-PI Christos Faloutsos): "Indexing, Mining and Modeling Spatio-Temporal Patterns of Gene Expressions", Aug 15, 2007 – July 30, 2010, $1,331,995.

7. NSF IIS-0713379 (PI): "Novel Statistical Models and Algorithms for Network Modeling, Mining, and Reverse Engineering", Sep 15, 2007 – Aug 30, 2010, $429,000.

8. DARPA NBCH1080007 (PI): "Computer Science Futures II-Engaging Young Scholars in Computer Science", July 1, 2008 – July 1, 2010, $360,000.

9. Alfred P. Sloan Foundation: "2008 Sloan Research Fellowship in Computer Science", Sep 16, 2008 – Sep 15, 2010, $50,000.

10. ONR N000140910758 (PI): "Toward a Unified Theory of Real-time Dynamic Network Analysis", Apr 1, 2009 – Mar 31, 2012, $630,207.

11. NIH 1R01GM087694 (PI): "Genome-Transcriptome-Phenome-Wide Association: a new paradigm for association studies of complex diseases", May 15, 2009 – Mar 31, 2015, $3,169,089.

12. NIH 1RC2HL101487-01 (co-PI): "Linking Genetics, Genomics and Phenomics to better understand Asthma Severity", Sep 1, 2009 – Aug 31, 2011, $214,520.

13. AFOSR FA95501010247 (PI): "SocioScape: Real-time Analysis and Mining of Dynamic Heterogeneous Networks in Complex Socio-Cultural Systems", June 1, 2010 – June 1, 2015, $600,000.

14. NIH 1R01GM093156 (PI): "Time/Space-Varying Networks of Molecular Interactions: A New Paradigm for Studying Dynamic Biological Regulation and Pathways", July 1, 2010 – Jun 30, 2015, $2,237,288.

15. NSF IIS-1111142 (PI, with Scott Kiesling): "Collaborative Research: Discovering and Exploiting Latent Communities in Social Media", Aug 1, 2011 – July 31, 2014, $547,805.

16. NSF IIS-1115313 (PI, with Fei-Fei Li): "Collaborative Research: Using Large-Scale Image Data for Online Social Media Analysis", Sep 15, 2011 – Aug 30, 2014, $204,202.

17. IBM (PI): Open Collaborative Faculty Award, an IBM grant challenge. Apr 2012 – Apr, 2014, $300,000.

18. NSF RI-1218749 (PI, with Le Song): "Collaborative Research: Efficient, Nonparametric and Local-Minimum-Free Latent Variable Models: with application to large-scale computer vision and genomics", Sep 15, 2012 – Aug 30, 2015, $200,000.

19. DARPA XDATA (with Jeff Schneider). 2012 – 2015, $600,000.

20. Facebook: Faculty Award, $25,000.

Research Interests

Core Machine learning, with emphasis on theory and algorithms for learning complex probabilistic models, learning with prior knowledge, and reasoning and decision-making in open, evolving and uncertain possible worlds. Of particular interest are:

- Theory and algorithms for learning time/space varying-coefficient models with evolving structures
- Theory and algorithms for learning sparse structured input/output models and multi-task models in ultra high-dimensional space
- Nonparametric Bayesian methods, infinite mixture models, algorithms and applications of Bayesian nonparametrics for data mining and object/topic/event tracking in open, evolving possible worlds
- Nonparametric graphical models, RKHS embedding and spectrum algorithm for general graph models
- Distributed and online algorithms for optimization, approximate inference, and Monte Carlo sampling on Tara-scale data

Architecture for Large Scale Machine Learning, with emphasize on developing general purpose systems for machine learning on massive data with massive model on industrial-scale multicore and distributed systems. Of particular interest are:

- Design and implementation of parameter server system for data parallelism
- Design and implementation of partitioning and scheduling system for model parallelism
- Global and local protocols for consistency in inference and learning
- Programming model and interface for Big Learning on parallel systems
- Theoretical analysis of various machine learning algorithms under data parallelism and model parallelism

Information & Intelligent Systems, with emphasis on developing web-scale, multi-core, and on-line machine learning systems for social media, computer vision, and HCI applications. Of particular interest are:

- Multi-view latent space models, topics models, sparse coding methods for image/text/relational information retrieval
- Evolving structure, stable metrics, and prediction for large-scale dynamic social networks; goal-driven network design/modification/optimization
- Web-scale image understanding, search, annotation, and retrieval; photo storyline; analysis of video and multimedia
- User modeling and personalization, computational advertising, and temporal analysis based on image, text, and activities
- Information visualization, indexing and storage, web and mobile app development

Computational biology, with emphasis on developing probabilistic models and algorithms that address problems of practical biological and medical concerns. Problems of primary focus include:

- Modeling evolution of gene expression, cis-regulatory code and transcriptional regulatory network in metazoan organisms
- Modeling genome-microenvironment interactions in cancer development and embryogenesis via joint analysis of genomic, proteomic, cytogenetic and pathway signaling data
- Statistical inference on genetic fingerprints, pedigrees, and their associations to diseases and other complex traits; application to clinical diagnosis and forensic analysis
- Modeling substitution, recombination, selection and genome rearrangement for comparative genomic analysis

- Biological image and text mining

Teaching

- **Instructor**, *Machine Learning* (15-781/10-701).
  CMU, Fall 2006, Spring 2008, Fall 2008, Spring 2010, Fall 2011, Fall 2012
  This is a core-curriculum course for SCS graduate students, focusing on fundamental algorithms and theory for statistical machine learning, pattern recognition and information retrieval.
- **Co-Instructor**, *Machine Learning* (10-601).
  CMU, Fall 2013
  This is a master-level course for SCS graduate and undergraduate students, focusing on algorithms and practice of statistical machine learning, and popular applications.
- **Co-Instructor**, *Computational Genomics* (10-810) (formally known as Computational Molecular Biology: a Machine Learning Approach).
  CMU, Spring 2005, 2006, 2007, 2009.
  This course focuses on modern machine learning methodologies for computational problems in molecular biology and genetics. This is a core-curriculum course for CMU-Pitt computational biology Ph.D. program.
- **Instructor**, *Probabilistic Graphical Models* (10-708).
  CMU, Fall 2005, Fall 2007, Fall 2009, Spring 2012, Spring 2013, Spring 2014.
  This is an advanced machine learning course covering probabilistic graphical models for efficient inference, decision-making and learning in problems with a very large number of attributes, complex stochastic dependencies, and huge datasets.
- **Instructor**, *Advanced Topics in Graphical Models* (10-801).
  CMU, Spring 2007.
  This course covers advanced topics in approximate inference, model selection, Bayesian nonparametrics, and their applications.

Papers and Publications

Journal Papers

Published

[1] **E. P. Xing**, R. Curtis, G. Schoenherr, S. Lee, J. Yin, K. Puniyani, W. Wu, P. Kinnaird, *GWAS in a Box: Statistical and Visual Analytics of Structured Associations via GenAMap*.
PLoS One, in press, 2014.

[2] A. Parikh, R. Curtis, I. Kuhn, S. Becker, M. Bissell, **E. P. Xing**, and Wei Wu *Network Analysis of Breast Cancer Progression and Reversal Using a Tree-evolving Network Algorithm*.
PLoS Computational Biology, in press, 2014.

[3] S. Shringarpure and **E. P. Xing**, *Effects of Sample Selection Bias on the Accuracy of Population Structure and Ancestry Inference*.
Genes, Genomes, Genetics, 2014.

[4] D. Yogatama, C. Wang, B.R. Routledge, N.A. Smith, and **E. P. Xing**, *Dynamic Language Models for Streaming Text*.
Transactions of the Association for Computational Linguistics, 2014.

[5] M. Kolar, H. Liu and **E. P. Xing**, *Graph Estimation From Multi-attribute Data*.
Journal of Machine Learning Research, in press, 2014.

[6] J. Zhu, N. Chen and **E. P. Xing**, *Bayesian Inference with Posterior Regularization, and applications to Infinite Latent SVMs*.
Journal of Machine Learning Research, in press, 2014.

[7] A. Martins, M. Figueiredo, P. Aguiar, N.A. Smith, and **E. P. Xing**, AD^3*: Alternating Directions Dual Decomposition for MAP Inference in Graphical Models*.
Journal of Machine Learning Research, in press, 2014.

[8] K. Puniyani and **E. P. Xing**, *GINI : From ISH images to Gene Interaction Networks*.
PLoS Computational Biology, 9(10): e1003227, 2013.

[9] K. Puniyani and **E. P. Xing**, *NP-MuScL: Unsupervised global prediction of interaction networks from multiple data sources*.
Journal of Computational Biology, 20(11):892-904, 2013.

[10] M. Yamada, W. Jitkrittum, L. Sigal, **E. P. Xing**, and M. Sugiyama, *High-Dimensional Feature Selection by Feature-Wise Kernelized Lasso*.
Neural Computation, Vol. 26, No. 1, Pages 185-20, 2013.

[11] R. Curtis, S. Kim, J. L. Woolford, W. Xu, and **E. P. Xing**, *Structured association analysis leads to insight into Saccharomyces cerevisiae gene regulation by finding multiple contributing eQTL hotspots associated with functional gene modules*.
BMC Genomics, vol. 14, no. 196, 2013.

[12] M. Kolar, and **E. P. Xing**, *Estimating Time-Varying Networks With Jumps*.
Electronic Journal of Statistics Vol. 6 (2012) 2069-2106 (arXiv:1012.3795).

[13] K. Sohn, Z. Ghahramani and **E. P. Xing**, *Robust estimation of local genetic ancestry in admixed populations using a non-parametric Bayesian approach*.
Genetics, vol 191, no. 4, 2012.

[14] J. Zhu, A. Ahmed, and **E. P. Xing** *MedLDA: Maximum Margin Supervised Topic Models*.
Journal of Machine Learning Research, 13 (2012) 2237-2278.

[15] R. Curtis, J. Xiang, A. Parikh, P. Kinnaird, and **E. P. Xing**, *Enabling dynamic network analysis through visualization in TVNViewer*.
BMC Bioinformatics, vol. 13, no. 204, 2012.

[16] R. Curtis, A. Goyal and **E. P. Xing**, *Enhancing the usability and performance of structured association mapping algorithms using automation, parallelization, and visualization in the GenAMap software system*.
BMC Genetics, vol. 13, no. 24, 2012.

[17] S. Kim, and **E. P. Xing**, *Tree-Guided Group Lasso for Multi-Response Regression with Structured Sparsity, with applications to eQTL Mapping*.
Annals of Applied Statistics, Vol. 6, No. 3, 1095-1117, 2012.

[18] N. Chen, J. Zhu, F. Sun and **E. P. Xing** *Large-margin Predictive Latent Subspace Learning for Multi-view Data Analysis*.
IEEE Transaction on Pattern Analysis and Machine Intelligence, 34(12): 2365-2378, 2012

[19] Q. Ho, A. Parikh and **E. P. Xing**, *Multiscale Community Blockmodel for Network Exploration*.
Journal of American Statistical Association, Volume 107, Issue 499, 916-934, 2012

[20] X. Chen, Q. Lin, S. Kim, J. Carbonell and **E. P. Xing**, *A Smoothing Proximal Gradient Method for General Structured Sparse Learning*.
Annals of Applied Statistics, Vol. 6, No. 2, 719-752, 2012

[21] R.E. Curtis, A. Yuen, L. Song, A. Goyal, and **E. P. Xing**, *TVNViewer: An interactive visualization tool for exploring networks that change over time or space*.
Bioinformatics, doi: 10.1093/bioinformatics/btr273.

[22] S. Kim and **E. P. Xing**, *Exploiting Genome Structure in Association Analysis*.
Journal of Computational Biology, Vol 18, 1-16, 2011.

[23] S. Hanneke, W. Fu and **E. P. Xing**, *Discrete Temporal Models of Social Networks*.
Electronic Journal of Statistics, Vol. 4, 585 – 605, 2010. (arXiv:0908.1258).

[24] **E. P. Xing**, W. Fu, L. Song, *A State-Space Mixed Membership Blockmodel for Dynamic Network Tomography*.
Annals of Applied Statistics Vol. 4, No. 2, 535 – 566, 2010 (arXiv:0901.0138).

[25] M. Kolar, L. Song, A. Ahmed, and **E. P. Xing**, *Estimating Time-Varying Networks*.
Annals of Applied Statistics, Vol. 4, No. 1, 94 – 123, 2010 (arXiv:0812.5087).

[26] J. Zhu and **E. P. Xing** *Maximum Entropy Discrimination Markov Network*.
Journal of Machine Learning Research, 10(Nov):2531-2569, 2009.

[27] S. Kim and **E. P. Xing**, *Statistical Estimation of Correlated Genome Associations to a Quantitative Trait Network*.
PLoS Genetics, 5(8):e1000587, 2009.

[28] A. Ahmed and **E. P. Xing**, *Recovering Time-Varying Networks of Dependencies in Social and Biological Studies*.
Proc. Natl. Acad. Sci., vol. 106, no. 29, 11878-11883, 2009.

[29] S. Shringarpure and **E. P. Xing**, *mStruct: Inference of Population Structure in Light of Both Genetic Admixing and Allele Mutations*.
Genetics, Vol 182, Issue 2, 2009. (Journal version of [166].)

[30] A. Martins, M. Figueiredo, P. Aguiar, N.A. Smith, and **E. P. Xing**, *Nonextensive Entropic Kernels*.
Journal of Machine Learning Research, Vol 10, pp935-975, 2009. (Journal version of [165].)

[31] K-A Sohn and **E. P. Xing**, *A Hierarchical Dirichlet Process Mixture Model For Haplotype Reconstruction From Multi-Population Data*.
Annals of Applied Statistics, Vol. 3, No. 2, 791821, 2009.

[32] E. Airodi, D. Blei, S. Fienberg and **E. P. Xing**, *Mixed Membership Stochastic Blockmodels*.
Journal of Machine Learning Research, Vol 9:1981–2014, 2008. (Journal version of [160].)

[33] P. Ray, S. Shringarpure, M. Kolar and **E. P. Xing**, *CSMET: Comparative Genomic Motif Detection via Multi-Resolution Phylogenetic Shadowing*.
PLoS Computational Biology, vol. 4, issue 6, p1-20, 2008.

[34] H. Kamisetty, **E. P. Xing** and C. J. Langmead, *Free Energy Estimates of All-Atom Protein Structures Using Generalized Belief Propagation*.
Journal of Computational Biology, 15(7): 755-766, 2008.

[35] J. Yang, R. Yan, Y. Liu, and **E. P. Xing**, *Harmonium Models for Video Classification*.
Statistical Analysis and Data Mining, vol. 1, issue 1, p23-37, 2008. (Journal version of [180].)

[36] K-A Sohn and **E. P. Xing**, *Spectrum: Joint Bayesian Inference of Population Structure and Recombination Event*.
Bioinformatics, 23: i479-i489, 2007. (Journal version of [174].)

[37] **E. P. Xing**, M. Jordan and R. Sharan, *Bayesian Haplotype Inference via the Dirichlet Process*.
Journal of Computational Biology, Volume 14, Number 3, Pp. 267-284, 2007. (Journal version of [198].)

[38] **E. P. Xing** and K-A Sohn *Hidden Markov Dirichlet Process: Modeling Genetic Recombination in Open Ancestral Space.*
Journal of Bayesian Analysis, vol. 2, Number 2, 2007. (Journal version of [184].)

[39] T. Lin, E.W. Myers and **E. P. Xing**, *Interpreting Anonymous DNA Samples From Mass Disasters — probabilistic forensic inference using genetic markers.*
Bioinformatics, 22(14): e298-e306, 2006. (Journal version of [185].)

[40] W. Wu, N. Dave, G.C. Tseng, T. Richards, **E. P. Xing**, and N. Kaminski, *Comparison of normalization methods for CodeLink Bioarray data.*
BMC Bioinformatics, vol. 6, no. 309, 2005.

[41] W. Wu, **E. P. Xing**, C. Myers, I. Mian and M. Bissell, *Evaluation of normalization methods for cDNA microarray data by k-NN classification.*
BMC Bioinformatics, vol. 6, no. 191, 2005.

[42] **E. P. Xing** and R. Karp *MotifPrototyper: a profile Bayesian model for motif family.*
Proc. Natl. Acad. Sci., vol. 101, no. 29, 10523-10528, 2004.

[43] **E. P. Xing**, D. Wolf, I. Dubchak, S. Spengler, M. Zorn, I. Muchnik and C. Kulikowski, *Automatic discovery of sub-molecular sequence domains in multi-aligned sequences: a dynamic programming algorithm for multiple alignment segmentation.*
J Theor Biol, 212(2):129-39, 2001.

[44] **E. P. Xing** and R. Karp, *CLIFF: clustering of high-dimensional microarray data via iterative feature filtering using normalized cuts.*
Bioinformatics, 17 Suppl 1:S306-15, 2001. (Journal version of [205].)

[45] Y. Cai, G. Yang, Y. Nie, L. Wang, X. Zhao, Y. Song, D. Seril, J. Liao, **E. P. Xing** and C. Yang, *Molecular alterations of $p73$ in human esophageal squamous cell carcinomas: loss of heterozygosity occurs frequently; loss of imprinting and elevation of $p73$ expression may be related to defective $p53$.*
Carcinogenesis, 21(4):683-9, 2000.

[46] **E. P. Xing**, Y. Nie, Y. Song, G. Yang, Y. Cai, L. Wang and S. Yang, *Mechanisms of inactivation of $p14^{ARF}$, $p15^{INK4b}$, and $p16^{INK4a}$ genes in human esophageal squamous cell carcinoma.*
Clin Cancer Res, 5(10):2704-13, 1999.

[47] **E. P. Xing**, G. Yang, L. Wang, S. Shi and S. Yang, *Loss of heterozygosity of the Rb gene correlates with pRb protein expression and associates with $p53$ alteration in human esophageal cancer.*
Clin Cancer Res, 5(5):1231-40, 1999.

[48] T. Shi, G. Yang, L. Wang, Z. Xue, B. Feng, W. Ding, **E. P. Xing** and S. Yang, *Role of $p53$ gene mutations in human esophageal carcinogenesis: results from immunohistochemical and mutation analyses of carcinomas and nearby non-cancerous lesions.*
Carcinogenesis, 20(4):591-7, 1999.

[49] **E. P. Xing**, Y. Nie, L. Wang, G. Yang, and S. Yang, *Aberrant methylation of $p16^{INK4a}$ and deletion of $p15^{INK4b}$ are frequent events in human esophageal cancer in Linxian, China.*
Carcinogenesis, 20(1):77-84, 1999.

Invited

[50] **E. P. Xing**, W. Wu, M. Jordan and R. Karp, *LOGOS: A modular Bayesian model for de novo motif detection .*
Journal of Bioinformatics and Computational Biology, 2(1), 127-154, 2004. Invited to a special issue devoted to CSB2003 (expanded from [200] and peer reviewed again).

Submitted

[51] M. Kolar, and **E. P. Xing**, *Sparsistent Estimation of Time-Varying Discrete Markov Random Fields*.
Electronic Journal of Statistics, under review, 2013 (arXiv:0907.2337).

[52] S. Kim, J. Howrylak, B. Raby, S. Weiss, and **E. P. Xing**, *Association Analysis of Dynamic-Traits via Temporally-Smoothed Lasso*.
PLoS Computational Biology (under review), 2013.

[53] L. Song, H. Liu, A. Parikh and **E. P. Xing**, *Nonparametric Latent Tree Graphical Models: Inference, Estimation, and Structure Learning*.
Journal of Machine Learning Research, under review, 2014.

Books and Book Chapters

[54] **E. P. Xing**, M. Kolar, S. Kim, X. Chen, High-Dimensional Sparse Structured Input-Output Models, with applications to GWA Analysis. In I. Rish, G. Cechi, A. Lozano, and A. Niculescu-Mizil ed., *Practical Applications of Sparse Modeling*, p43-79, MIT Press, 2014.

[55] W. Wu and **E. P. Xing**, A Survey of cDNA Microarray Normalization and a Comparison by k-NN Classification, in S. Phillip ed., *Methods in Microarray Normalization*, p81-120, CRC Press, 2008.

[56] E. Airodi, D. Blei, S. Fienberg, A. Goldenberg, **E. P. Xing**, and A. Zheng, Eds. *Statistical Network Analysis: Models, Issues & New Directions*, Lecture Notes in Computer Science, volume no. 4503. Springer-Verlag, 2007.

[57] **E. P. Xing**, Feature Selection in Microarray Analysis, in D. Berrar, W. Dubitzky and M. Granzow eds., *A Practical Approach to Microarray Data Analysis*, Kluwer, 2002.

Refereed Conference Papers

Published

[58] A. Parikh, S. Cohen and **E. P. Xing**, *Spectral Unsupervised Parsing with Additive Tree Metrics*.
Proceedings of The 52nd Annual Meeting of the Association for Computational Linguistics, 2014. (ACL '14)

[59] G. Kim and **E. P. Xing**, *Reconstructing Storyline Graphs for Image Recommendation from Web Community Photos*.
Proceedings of the 26th IEEE Conference on Computer Vision and Pattern Recognition, 2014. (CVPR '14)

[60] G. Kim, L. Sigal and **E. P. Xing**, *Jointly Summarizing Large-Scale Web Images and Videos for the Storyline Reconstruction*.
Proceedings of the 26th IEEE Conference on Computer Vision and Pattern Recognition, 2014. (CVPR '14)

[61] B. Zhao and **E. P. Xing**, *Quasi Real-Time Summarization for Consumer Videos*.
Proceedings of the 26th IEEE Conference on Computer Vision and Pattern Recognition, 2014. (CVPR '14)

[62] B. Zhao and **E. P. Xing**, *Hierarchical Feature Hashing for Fast Dimensionality Reduction*.
Proceedings of the 26th IEEE Conference on Computer Vision and Pattern Recognition, 2014. (CVPR '14)

[63] A. Kumar, A. Beutel, Q. Ho and and **E. P. Xing**, *Slow-Worker-Agnostic Distributed Learning for Big Models on Big Data*.
Proceedings of the 17th International Conference on Artificial Intelligence and Statistics, 2014. (AISTATS '14)

[64] J. B. Oliva, W. Neiswanger, B. Poczos, J. Schneider and and **E. P. Xing**, *Fast Distribution To Real Regression*.
Proceedings of the 17th International Conference on Artificial Intelligence and Statistics, 2014.
(AISTATS '14)

[65] W. Neiswanger, F. Wood and **E. P. Xing**, *The Dependent Dirichlet Process Mixture of Objects for Detection-free Tracking and Object Modeling*.
Proceedings of the 17th International Conference on Artificial Intelligence and Statistics, 2014.
(AISTATS '14)

[66] A. Beutel, A. Kumar, E. E. Papalexakis, P. P. Talukdar, C. Faloutsos and **E. P. Xing**, *FlexiFaCT: Scalable Flexible Factorization of Coupled Tensors on Hadoop*.
Proceedings of The Fourteenth SIAM International Conference on Data Mining, 2014. (SDM '14)

[67] G. Kim and **E. P. Xing**, *Visualizing Brand Associations from Web Community Photos*.
Proceedings of The 7th ACM International Conference on Web Search and Data Mining, 2014.
(WSDM '14).

[68] M. Sachan, A. Dubey, S. Srivastava, **E. P. Xing**, and Eduard Hovy
Spatial Compactness meets Topical Consistency: Jointly modeling Links and Content for Community Detection.
Proceedings of The 7th ACM International Conference on Web Search and Data Mining, 2014.
(WSDM '14).

[69] A. P. Parikh, W. Wu, and **E. P. Xing**, *Robust Reverse Engineering of Dynamic Gene Networks under Sample Heterogeneity*.
Pacific Symposium on Biocomputing 2014, (PSB '14).

[70] G. Kim and **E. P. Xing**, *Discovering Pictorial Brand Associations from Large-Scale Online Image Data*.
The 1st IEEE Workshop on Large Scale Visual Commerce, 2013. (lsviscom2013). Recipient of the BEST PAPER Award.

[71] Q. Ho, J. Cipar, H. Cui, J.-K. Kim, S. Lee, P. B. Gibbons, G. Gibson, G. R. Ganger and **E. P. Xing**, *More Effective Distributed ML via a Stale Synchronous Parallel Parameter Server*.
Advances in Neural Information Processing Systems 27 (eds. Zoubin Ghahramani and Max Welling), MIT Press, Cambridge, MA, 2013. (NIPS '13).

[72] S. Williamson, S. N. MacEachern and **E. P. Xing**, *Restricting exchangeable nonparametric distributions*.
Advances in Neural Information Processing Systems 27 (eds. Zoubin Ghahramani and Max Welling), MIT Press, Cambridge, MA, 2013. (NIPS '13).

[73] J. Yin, Q. Ho and **E. P. Xing**, *A Scalable Approach to Probabilistic Latent Space Inference of Large-Scale Networks*.
Advances in Neural Information Processing Systems 27 (eds. Zoubin Ghahramani and Max Welling), MIT Press, Cambridge, MA, 2013. (NIPS '13).

[74] C. Wang, X. Chen, A. Smola and **E. P. Xing**, *Variance Reduction for Stochastic Gradient Optimization*.
Advances in Neural Information Processing Systems 27 (eds. Zoubin Ghahramani and Max Welling), MIT Press, Cambridge, MA, 2013. (NIPS '13).

[75] P. Xie and **E. P. Xing**, *Integrating Document Clustering and Topic Modeling*.
Proceedings of the 29th International Conference on Conference on Uncertainty in Artificial Intelligence, 2013. (UAI '13).

[76] T. Bahadori, Y. Liu, and **E. P. Xing**, *Fast Structure Learning in Generalized Stochastic Processes*

with Latent Factors.
Proceedings of The 19th ACM SIGKDD Conference on knowledge Discovery and Data Mining, 2013. (KDD '13)

[77] A. Ahmed and **E. P. Xing**, *Scalable Dynamic Nonparametric Bayesian Models of Content and Users*. 23rd International Joint Conference on Artificial Intelligence (IJCAI '13), 2013. Invited to Sister Conference Best Papers Track, based on KDD12 best Ph.D. dissertation award.

[78] P. Xie and **E. P. Xing**, *Multi-Modal Distance Metric Learning*. 23rd International Joint Conference on Artificial Intelligence (IJCAI '13), 2013.

[79] J. Cipar, Q. Ho, J. K. Kim, S. Lee, G. R. Ganger, G. Gibson, K. Keeton and **E. P. Xing**, *Solving the straggler problem with bounded staleness*. 14th Workshop on Hot Topics in Operating Systems (HotOS XIV), 2013. Santa Ana Pueblo.

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An earlier version of this paper also appeared as a book chapter in Lecture Notes in Bioinformatics, Special issue for 2nd RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotypes, 2004.

[199] **E. P. Xing**, M. Jordan and S. Russell, *Graph partition strategies for generalized mean field inference.*.
Proceedings of the 20th Annual Conference on Uncertainty in Artificial Intelligence (eds. M. Chickering and J. Halpern), AUAI Press, Arlington, Virginia, 602–611, 2004. (UAI '04)

[200] **E. P. Xing**, W. Wu, M. Jordan and R. Karp, *LOGOS: A modular Bayesian model for de novo motif detection*.
Proceedings of the 2nd IEEE Computer Society Bioinformatics Conference, IEEE Computer Society, Washington, DC, USA, 2:266–76, 2003. (CSB '03)

[201] **E. P. Xing**, M. Jordan and S. Russell, *A generalized mean field algorithm for variational inference in exponential families*.
Proceedings of the 19th Annual Conference on Uncertainty in Artificial Intelligence (eds. Meek and Kjælff), Morgan Kaufmann Publishers, San Francisco, CA, 583–591, 2003. (UAI '03). Recipient of the Runner-up Best Student Paper Award.

[202] **E. P. Xing**, *An expressive modular probabilistic model for de novo motif detection*.
Workshop on Learning Graphical Models for Computational Genomics, 18th International Joint Conference on Artificial Intelligence (IJCAI '03), 2003.

[203] **E. P. Xing**, A. Ng, M. Jordan and S. Russell, *Distance Metric Learning, with application to Clustering with side-information*.
Advances in Neural Information Processing Systems 15 (eds. S. Becker, S. Thrun and K. Obermayer), MIT Press, Cambridge, MA, 505–512, 2003. (NIPS 02)

[204] **E. P. Xing**, M. Jordan, R. Karp and S. Russell, *A Hierarchical Bayesian Markovian Model for Motifs in Biopolymer Sequences*.
Advances in Neural Information Processing Systems 15 (eds. S. Becker, S. Thrun and K. Obermayer), MIT Press, Cambridge, MA, 1489–1496, 2003. (NIPS 02)

[205] **E. P. Xing** and R. Karp, *CLIFF: clustering of high-dimensional microarray data via iterative feature filtering using normalized cuts*.
Proceedings of the Ninth International Conference on Intelligent Systems for Molecular Biology, 2001. (ISMB '01)

[206] **E. P. Xing**, M. Jordan and R. Karp,K, *Feature selection for high-dimensional genomic microarray data*.
Proceedings of the Eighteenth International Conference on Machine Learning (eds. C. E. Brodley and A. P. Danyluk), Morgan Kaufmann Publishers Inc., San Francisco, CA, USA, 601–608, 2001. (ICML '01)

[207] **E. P. Xing**, C. Kulikowski, I. Muchnik, I. Dubchak, D. Wolf, S. Spengler and M. Zorn, *Analysis of ribosomal RNA sequences by combinatorial clustering*.
Proceedings of the Seventh International Conference on Intelligent Systems for Molecular Biology, AAAI Press, 287–296, 1999. (ISMB '99)

Submitted

Unrefereed Technical Reports

[208] **E. P. Xing** and M. Jordan, *On semidefinite relaxation for normalized k-cut and connections to spectral clustering*.
Technical Report CSD-03-1265, Computer Science Division, UC Berkeley, 2003.

[209] **E. P. Xing**, *Dynamic Nonparametric Bayesian Models and the Birth-Death Process.*.
Technical Report CMU-CALD-05-114, Carnegie Mellon University, 2005.

[210] **E. P. Xing**, *On Topic Evolution*.
Technical Report CMU-CALD-05-115, Carnegie Mellon University, 2005.

[211] F. Guo and **E. P. Xing**, *Bayesian Exponential Family Harmoniums*.
Technical Report CMU-ML-06-103, Carnegie Mellon University, 2006.

[212] F. Li, Y-M. Yang and **E. P. Xing**, *Inferring regulatory networks using a hierarchical Bayesian graphical Gaussian model*.
Technical Report CMU-ML-06-117, Carnegie Mellon University, 2006.

Invited Talks

[1] *Feature Selection for High-Dimensional Genomic Microarray Data in Concept Learning and Clustering Analysis,*
Statistics in Functional Genomics, Joint Summer Research Conference of AMS/IMS/SIAM, Mount Holyoke, June 10-14, 2001.

[2] *Feature Selection for High-Dimensional Genomic Microarray Data,*
NIPS 2001 Workshop on Machine Learning Techniques for Bioinformatics, Whistler, Dec 8, 2001.

[3] *Expressive Statistical Models for Motifs,*
Intel Workshop on Machine Learning and Life Sciences, Berkeley, Nov 3-4, 2003.

[4] *Application of nonparametric Bayesian methods in genetic inference*
NIPS 2003 Workshop on Nonparametric Bayesian Methods and Infinite Models, Whistler, Dec 13, 2003.

[5] *Generalized Mean Field Inference in Graphical Models,*
The 2004 joint WNAR/IMS meeting, Albuquerque, June 27-30, 2004.

[6] *Generalized mean field inference in graphical models, and applications to computational biology,*
AI Seminar, Carnegie Mellon University, Pittsburgh, PA, February 3, 2004.

[7] *Mining Associated Text and Images with Dual-Wing Harmoniums,*
UC BERKELEY CIS (Center for Intelligent Systems) SEMINAR, Berkeley, CA, April 20, 2005.

[8] *In silico motif detection under complex genomic and evolutionary context - new Bayesian models motivated from biological principles,*
UC Irvine ICS Seminar CIS, Irvine, CA, April 22, 2005.

[9] *Probabilistic Graphical Models and Algorithms for Genomic Analysis,*
Department of Molecular and Computational Biology, University of Southern California, Los Angeles, CA, April 23, 2005.

[10] *Variational methods for inference in graphical models,*
Workshop on Random Graphs & Stochastic Computation, Statistical and Applied Mathematical Sciences Institute, Research Triangle Park, NC, June 13-14, 2005.

[11] *Nonparametric Bayesian Models for Haplotype Inference,*
Section on Bayesian Statistical Science, The Joint Statistical Meetings, Minneapolis, Aug 6-11, 2005.

[12] *Combinatorial and Statistical Approaches to Analyzing Biological Networks,*
Tutorial Program, 2005 IEEE Computational Systems Bioinformatics Conference, Stanford, Aug 8-11, 2005.

[13] *Mining Associated Text and Images with Dual-Wing Harmoniums and A Latent Mixed Membership Model for Relational Data,*
Computer Science Department, Stanford University, Stanford, CA, Aug 12, 2005.

[14] *In silico detection of cis-regulatory elements under complex genomic and evolutionary context: a probabilistic graphical model approach,*
DIMACS Workshop on Machine Learning Approaches for Understanding Gene Regulation, Rutgers University, Aug 15-17, 2005.

[15] *How many founders shall we assume for haplotype reconstruction?*
Center for Information Theory and Its Applications, Inaugural Workshop, University of California, San Diego, February 6-10, 2006.

[16] *How many founders shall we assume for haplotype reconstruction? — on coalescence, Dirichlet processes, and nonparametric Bayes,*
Invited Lecture (hosted by Prof. Andrew Yao), Computer Science Department, Tsinghua University, Beijing, China, April 25, 2006.

[17] *Machine Learning, and the Role of Machine Learning in Computational Biology*
Keynote, Symposium of the 80th Anniversary Of the Physics Department, Tsinghua University, Beijing, China, April 29, 2006.

[18] *How many founders shall we assume for haplotype reconstruction? — on coalescence, Dirichlet processes, and nonparametric Bayes,*
Invited Lecture, Workshop on Learning with Nonparametric Bayesian Methods, International Conference on Machine Learning, Pittsburgh, Pennsylvania, 25-29 June, 2006.

[19] *Reasoning in open possible worlds: on A New Class of Nonparametric Bayesian Models for Haplotype Phasing, LD Modeling and Demographic Inference in Open Ancestral Space,*
Department of Computer Science, National University of Singapore, Singapore, 16 November, 2006.

[20] *A New Class of Nonparametric Bayesian Models for Haplotype Phasing, LD Modeling and Demographic Inference in Open Ancestral Space,*
College of Life Sciences, Fudan University, Shanghai, China, 12 November, 2006.

[21] *Modeling and reasoning the temporal evolution of networks*
The 2007 Information Theory and Applications Workshop, University of California, San Diego, Jan 29- Feb 2, 2007.

[22] *A Hidden Markov Dirichlet Process Model for Joint Inference of Population Structure, Linkage Disequilibrium, and Recombination Hotspots,*
Invited talk, International Biometric Society-ENAR Annual Meetings, Atlanta, Georgia, 2007.

[23] *Statistical network analysis and inference: methods and applications,*
UC BERKELEY CIS (Center for Intelligent Systems) SEMINAR, Berkeley, CA, April 19, 2007.

[24] *Probabilistic Graphical Models and Algorithms for Integrative Bioinformatics,*
Keynote, Workshop on Bioinformatics, Graybill Conference (on Statistics and Probability) VI, Colorado State University, Fort Collins, Colorado, June 12-13, 2007.

[25] *Probabilistic Graphical Models and Algorithms for Integrative Bioinformatics,*
Computational Biology Seminar, Department of Molecular and Computational Biology, University of Southern California, Los Angeles, California, October 4, 2007.

[26] *Statistical network analysis and inference,*

Invited talk, Workshop on Gene Co-Expression Network Analysis and its Applications in Systems Biology, 8th International Conference on Systems Biology, Long Beach, California, October 5, 2007.

[27] *Probabilistic Graphical Models and Algorithms for Integrative Bioinformatics,*
Computer Science Department Colloquia, Princeton University, Princeton, New Jersey, October 10, 2007.

[28] *Statistical Network Analysis and Inference: Methods and Applications,*
Invited talk, Workshop III: Social Data Mining and Knowledge Building, Institute for Pure and Applied Mathematics (IPAM), Los Angeles, California, November 5-9, 2007.

[29] *Nonparametric Bayesian Methods for Genetic Inference,*
Computational Biology Seminar, Department of Integrative Biology, UC Berkeley, Berkeley, California, November 7, 2007.

[30] *Nonparametric Bayesian Methods for Genetic Inference,*
Biostatistics Seminar, Department of Statistics, Stanford University, Stanford, California, November 8, 2007.

[31] *Probabilistic Graphical Models — theory, algorithm, and application,*
Keynote, The Sixth International Conference on Machine Learning and Applications (ICMLA'07), Cincinnati, Ohio, USA, December 13-15, 2007 .

[32] *Nonparametric Bayesian Methods for Genetic Inference,*
Statistics Seminar, Department of Statistics, University of Chicago, Chicago, Illinois, USA, March 10, 2008.

[33] *Computational analysis of eukaryotic transcriptional regulatory sequence and its evolution,*
Natural History Seminars, Department of Ecology and Evolution, University of Chicago, Chicago, Illinois, USA, March 11, 2008.

[34] *Statistical Network Analysis and Inference: Methods and Applications,*
Yahoo!-Dais Seminar, Department of Computer Science, University of Illinois, Urbana-Champaign, Illinois, USA, March 12, 2008.

[35] *Nonparametric Bayesian Methods for Genetic Inference,*
Computational Biology Seminar, Department of Computer Science, University of Illinois, Urbana-Champaign, Illinois, USA, March 13, 2008.

[36] *Nonparametric Bayesian Methods for Genetic Inference,*
Bioinformatics Seminar Series, CSAIL, MIT, Boston, Massachusetts, USA, April 9, 2008.

[37] *Discrete Temporal Models for Evolving Graphs,*
Invited Speaker, Workshop on Future Directions in High-Dimensional Data Analysis: New Methodologies: New Data Types and New Applications, Isaac Newton Institute for Mathematical Sciences, Cambridge University, Cambridge, UK, June 23-27, 2008.

[38] *Genome-Phenome Association: Computational Challenges and new Algorithms,*
Invited Speaker, DIMACS Workshop on Computational Issues in Genetic Epidemiology, DIMACS Center, Rutgers University, Piscatawy, NJ, Aug 21-22, 2008.

[39] *Bayesian Methods for Genetic Inference,*
Invited Speaker, Program of Population Genetics and Genomics, Kavli Institute for Theoretical Physics, UC Santa Barbara, CA, Sep 15 - Dec 12 (talk took place on 9/23), 2008.

[40] *Fitting Stochastic Models to Empirical Data,*
Plenary Talk, Workshop on Statistical Inference for Complex Networks, Santa Fe Institute, Santa Fe, NM, Dec 3-5, 2008.

[41] *Time (and Space)-Varying Networks: Reverse engineering rewiring social and genetic interactions,*

Invited Speaker, Workshop on Statistical Inference for Complex Networks, Santa Fe Institute, Santa Fe, NM, Dec 3-5, 2008.

[42] *Recent Advances in Learning Sparse Structured Input/Output Model: Models, Algorithms, and Applications,*
Keynote, NIPS 2008 Workshop on "Structured Input, Structured Output", Vancouver, BC, Canada, Dec 8-14, 2008.

[43] *A State-Space Mixed Membership Blockmodel for Dynamic Network Tomography,*
Invited Speaker, Workshop on Statistical Methods for the Analysis of Network Data in Practice, University College Dublin", Dublin, Ireland, June 15-17, 2009.

[44] *Estimating Time-Varying Networks,*
Invited Speaker, Workshop on Statistical Methods for the Analysis of Network Data in Practice", University College Dublin, Dublin, Ireland, June 15-17, 2009.

[45] *On the Primal and Dual Sparsity of Structured Input/Output Models,*
Invited Speaker, Sino-USA Summer School in Vision, Learning, and Pattern Recognition", Peking University, Beijing, China, July 20-27, 2009.

[46] *On the Primal and Dual Sparsity of Structured Input/Output Models,*
Invited Speaker, Joint Statistics Meeting (JSM)", Washington D. C., Aug 1-6, 2009.

[47] *Time Varying Networks: reverse engineering and analyzing rewiring social and genetic interactions,*
Center for Statistics and the Social Sciences Seminar, Department of Statistics, University of Washington, Seattle, WA, Sep 28, 2009.

[48] *Time Varying Networks: reverse engineering and analyzing rewiring genetic interactions,*
Neyman Seminar, Department of Statistics, University of California, Berkeley, CA, Oct 14, 2009.

[49] *Jointly Maximum Margin and Maximum Entropy Learning of Graphical Models,*
Distinguished Seminar, NEC Research, CA, Oct 16, 2009.

[50] *Time Varying Graphical Models: reverse engineering and analyzing rewiring networks,*
Keynote, NIPS 2009 Mini-Symposium on "Machine Learning in Computational Biology", Vancouver, BC, Canada, Dec 10, 2009.

[51] *Jointly Maximum Margin and Maximum Entropy Learning of Graphical Models,*
Invited Speaker, NIPS 2009 Workshop on "Approximate Learning of Large Scale Graphical Models", Vancouver, BC, Canada, Dec 11-12, 2009.

[52] *Modeling Dynamic Network Tomography,*
Invited Speaker, NIPS 2009 Workshop on "Applications for Topic Models: Text and Beyond", Vancouver, BC, Canada, Dec 11-12, 2009.

[53] *Dynamic Network Tomography,*
Invited Speaker, NIPS 2009 Workshop on "Analyzing Networks and Learning with Graphs", Vancouver, BC, Canada, Dec 11, 2009.

[54] *Time Varying Graphical Models: Reverse engineering and analyzing evolving genetic and social networks,*
BME Departmental Seminar, Department of Biomedical Engineering, Johns Hopkins University, MD, Jan 25, 2010.

[55] *Dynamic Network Tomography,*
Computer Science Colloquia, Department of Computer Science, Purdue University, IN, Feb 11, 2010.

[56] *Dynamic Network Tomography,*
2009/2010 EPSRC Symposium on the Mathematics of Complexity Science and Systems Biology, Systems Biology Centre, The University of Warwick, UK, Mar 9, 2010.

[57] *Dynamic Network Tomography: Model, Algorithm, Theory, and Application,*
Machine Learning Seminar, Department of Engineering, Cambridge University, UK, Mar 11, 2010.

[58] *Structured Sparse Regression and Genome-Phenome Association Analysis In Complex Diseases,*
Statistics Seminar, Department of Statistics, Oxford University, UK, Mar 12, 2010.

[59] *Dynamic Network Tomography: Model, Algorithm, Theory, and Application,*
Machine Learning Seminar, Gatsby Computational Neuroscience Unit, University College London, UK, Mar 12, 2010.

[60] *Time Varying Networks: Reverse Engineering and Analyzing Rewiring Social and Genetic Interactions,*
Invited talk, International Biometric Society-ENAR Annual Meetings, New Orleans, LA, Mar 22, 2010.

[61] *Dynamic Network Analysis: Model, Algorithm, Theory, and Application,*
CSAIL Seminar, CSAIL, MIT, MA, Apr 14, 2010.

[62] *Dynamic Network Analysis: Model, Algorithm, Theory, and Application,*
Statistics Colloquium, Department of Statistics, Harvard University, MA, Apr 15, 2010.

[63] *Genome-Phenome Association Analysis of Complex Diseases – a Structured Sparse Regression Approach,*
BioStatistics Seminar, Department of BioStatistics, Harvard University, MA, Apr 16, 2010.

[64] *Genome-Phenome Association Analysis of Complex Diseases – a Structured Sparse Regression Approach,*
Bioinformatics Seminar, University of California, Los Angeles, CA, May 10, 2010.

[65] *Dynamic Network Analysis: Model, Algorithm, Theory, and Application,*
Invited talk, International Conference on Statistics and Society, Beijing, China, July 10-12, 2010.

[66] *Dynamic Network Analysis: Model, Algorithm, Theory, and Application,*
Keynote, Eighth Workshop on Mining and Learning with Graphs 2010 (MLG-2010), Washington DC, July 24-25, 2010.

[67] *Genome-Phenome Association Analysis of Complex Diseases – a Structured Sparse Regression Approach,*
Keynote: The Tenth Annual International Workshop on Bioinformatics and Systems Biology, Kyoto, Japan, 26-28 July 2010.

[68] *Statistical Analysis of Complex Networks: A SAMSI Preview,*
Invited talk, Joint Statistics Meeting, Vancouver, Canada, Aug 1-5, 2010.

[69] *Statistical Analysis of Complex Networks*
Invited talk, Opening Workshop for the SAMSI program on Complex Networks, Research Triangle Park, NC, August 29-September 1, 2010.

[70] *Dynamic Network Analysis: Model, Algorithm, Theory, and Application,*
Columbia Statistics Seminar, Columbia University, New York, October 11, 2010.

[71] *Genome-Phenome Association Analysis of Complex Diseases a Structured Sparse Regression Approach,*
Distinguished speaker, 4th Annual Program in Quantitative Genomics (PQG) Conference, Harvard University, Boston, November 15-16, 2010.

[72] *Reverse Engineering Tree-Evolving Gene Networks Underlying Developing Breast Cancer Cell Lineages,*
Stanford CCSB Seminar, Center for Cancer Systems Biology, Stanford University, Palo Alto, CA, November 20, 2010.

[73] *Learning varying coefficient varying structure models: Reverse engineering rewiring networks underlying dynamics processes,*
Stanford Statistics Seminar, Department of Statistics, Stanford University, Palo Alto, CA, January 18, 2011.

[74] *Probabilistic Graphical Models: Theory, Algorithms and Application,*
Compact Course, Universität Heidelberg, Germany, February 7-11, 2011.

[75] *On High-Dimensional Sparse Structured Input-Output Models, with Applications to Genome-Phenome Association Analysis of Complex Diseases,*
Workshop in Biostatistics, Department of Statistics, Stanford University, Palo Alto, CA, February 24, 2011.

[76] *Sparsity and Learning Large Scale Models,*
Keynote: CVPR 2011 Workshop on Large Scale Learning for Vision, Colorado Springs, June 20, 2011.

[77] *Modern Statistical Methods for Genetic Association Study: Structured Genome-Transcriptome-Phenome Association Analysis,*
Tutorial: Nineteenth International Conference on Intelligence Systems for Molecular Biology (ISMB 2011), Vienna, Austria, July 17-19, 2011.

[78] *Smoothing Proximal Gradient Method for General Structured Sparse Regression,*
Invited talk, Duke Workshop on Sensing and Analysis of High-Dimensional Data, Duke University, NC, July 26-28, 2011.

[79] *Jointly Maximum Margin and Maximum Entropy Learning of Graphical Models,*
Computer Science Department Colloquia, Princeton University, Princeton, New Jersey, October 6, 2011.

[80] *On Learning High-Dimensional Sparse Structured Input-Output Models, with Applications to Genome-Phenome Association Analysis of Complex Diseases and Web-Scale Image Understanding,*
Applied Mathematics (APPM) Colloquium, University of Colorado at Boulder, Boulder, Colorado, April 5, 2012.

[81] *Topic Models, Latent Space Models, Sparse Coding, and All That: A systematic understanding of probabilistic semantic extraction in large corpus,*
Tutorial: The 50th Annual Meeting of the Association for Computational Linguistics, (ACL 2012), Jeju , Korea, July 8-11, 2012.

[82] *On Learning Sparse Structured Input-Output Models,*
Invited Keynote Talk: EMNLP-CoNLL 2012, Jeju , Korea, July 12-14, 2012.

[83] *Jointly Maximum Margin and Maximum Entropy Learning of Graphical Models,*
Applied Mathematics Seminar, Yale University, New Haven, Connecticut, November 27, 2012.

[84] *Reverse Engineering Evolving Gene Networks Underlying Developing Biological Systems: a principled statistical machine learning approach,*
ISCB-Asia/SCCG 2012 Keynote Address, Shenzhen, China, December 18, 2012.

[85] *Reverse Engineering Evolving Gene Networks Underlying Developing Biological Systems: A Principled Statistical Machine Learning Approach,*
Correlated and High-Dimensional Data Seminar, Department of Biostatistics, Harvard University, Boston, Massachusetts, March 14, 2013.

[86] *Machine Learning Approaches to Network and Social Media,*
Distinguished Lecture Series, George Mason University, Washington DC, April 19, 2013.

[87] *Big Data, Big Model, and Big Learning,*

CS Distinguished Lecture, University of Southern California, Los Angeles, May 22, 2013.

[88] *An All-Inclusive New Paradigm of Learning of Graphical Models,*
Keynote, 26th Canadian Conference on Artificial Intelligence, Regina, Saskatchewan, Canada, May 28-31, 2013.

[89] *Reverse Engineering Evolving Gene Networks Underlying Developing Biological Systems: A Statistical Machine Learning Approach,*
Workshop of "Dynamics of biological networks: from nodes' dynamics to network evolution" University of Edinburgh, Edinburgh, UK, June 25-26, 2013.

[90] *Genome-Phenome Association Analysis under Complex Structures,*
Workshop of "Heritability Analysis and Genetic Trait Prediction", Twenty-first International Conference on Intelligence Systems for Molecular Biology (ISMB 2013), Berlin, Germany, July 18-23, 2013.

[91] *Genome-Phenome Association Analysis under Complex Structures,*
Keynote, The 7th International Conference on Systems Biology (ISB 2013), Huangshan, China, August 22-24, 2013.

[92] *Big Data, Big Model, Big Learning*
CS Distinguished Lecture, Georgia Institute of Technology, Atlanta, October 3, 2013.

[93] *The Algorithmic and System Interface of Big Learning*
SSC Seminar Series, University of Texas at Austin, Austin, October 18, 2013.

[94] *Petuum: A New Algorithmic and System Framework for Big Learning*
Invited Talk, Microsoft Research, Redmond, February 6, 2014.

Professional Service

- **Invited or Guest Lecturer**
  - The "Dragon Star Lecture" on Machine learning, 2009 (Tsinghua/Pekin University) and 2010 (Shanghai Jiaoto/Fudan University). Delivered a week-long 20 lecture series at the invitation of the Chinese Academic of Science.
  - Invited Lecturer on Probabilistic Graphical Models at University of Heidelberg, 2011. Delivered a week long lecture series at the invitation of University of Heidelberg.

- **Editorial Board** of
  - *Journal of the American Statistical Association* (associate editor)
  - *Annals of Applied Statistics* (associate editor)
  - *Journal of Machine Learning Research* (action editor)
  - *Machine Learning* Journal (action editor)
  - *IEEE Transactions on Pattern Analysis and Machine Intelligence* (associate editor)
  - *PLoS Computational Biology* (guest associate editor)

- **Member** of
  - DARPA Information Science and Technology (ISAT) Advisory Group
  - NIH Biodata Management and Analysis (BDMA) Study Section

- **Invited panelist/participant** of
  - DARPA CS Futures II, 2007-2008.
  - International Expert Review Committee of the Doctoral Plus Program (DK-plus) Population Genetics of University of Vienna (October 22nd, 2008, and November 5, 2009), invited by the

Austrian Science Fund (FWF) Board of Trustees.

- **Organizer or Co-Organizer** for
  - Workshop on "Divergence Methods for Probabilistic Inference, ICML 2014
  - Workshop on "Spectral Learning", NIPS 2012
  - Workshop on Structured Sparsity: Learning and Inference, ICML 2011
  - Workshop on Analyzing Graphs: Theories and Applications. Advances in Neural Information Processing Systems 22, NIPS-08 (2008)
  - Workshop on Statistical Models of Networks. Advances in Neural Information Processing Systems 21, NIPS-07 (2007)
  - Workshop on Learning in Structured Output Spaces. The 24th International Conference on Machine Learning, ICML-07 (2007)
  - Institute of Mathematical Statistics (IMS) Session on Dynamic Network Models. International Biometric Society-ENAR Annual Meetings, Atlanta, Georgia, 2007
  - Workshop on Learning in Structured Output Spaces. The 23rd International Conference on Machine Learning, ICML-06 (2006)
  - Workshop on Statistical Network Analysis: Models, Issues and New Directions. The 23rd International Conference on Machine Learning, ICML-06 (2006)

- **Chair, co-Chair**, or **Senior Program Committee** member for
  - Program Committee Chair, The Thirtieth International Conference on Machine Learning, ICML-14 (2014)
  - Area Chair: Advances in Neural Information Processing Systems 26 NIPS-12, (2012).
  - Area Chair: Advances in Neural Information Processing Systems 25 NIPS-11, (2011).
  - Area Chair: The 28th International Conference on Machine Learning ICML-11, (2011).
  - Area Chair: The 19th International Conference on Intelligent Systems for Molecular Biology ISMB-11, (2011).
  - SPC: The Seventeenth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining, KDD-11 (2011).
  - Area Chair: The 18th International Conference on Intelligent Systems for Molecular Biology ISMB-10, (2010).
  - Tutorial Chair: The 7th Asia Pacific Bioinformatics Conference, APBC09 (2009)
  - Publication Chair, and SPC, The Twenty-Fifth International Conference on Conference on Uncertainty in Artificial Intelligence, UAI'09 (2009)
  - SPC, The Fourteenth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining, KDD-08 (2008)
  - SPC, The Fourteenth Annual International Conference on Research in Computational Molecular Biology, RECOMB-10 (2010).
  - SPC, The Thirteenth Annual International Conference on Research in Computational Molecular Biology, RECOMB-09 (2009).
  - SPC, The Twelfth Annual International Conference on Research in Computational Molecular Biology, RECOMB-08 (2008).
  - SPC, The Twenty-Fourth International Conference on Machine Learning, ICML-07 (2007)

- **Program Committee** member for

- The 24th International Conference on Conference on Uncertainty in Artificial Intelligence, UAI'08 (2008)

- European Conference on Computer Vision, ECCV-08 (2008)

- The NIPS workshop on Machine Learning in Computational Biology, NIPS (2007)

- Joint Conference on Empirical Methods in Natural Language Processing and Computational Natural Language Learning, EMNLP-CoNLL (2007)

- The 11th IEEE International Conference on Computer Vision, ICCV (2007)

- IEEE Conference on Computer Vision and Pattern Recognition Program, CVPR (2007, 2008)

- SIAM International Conference on Data Mining, SDM (2007)

- Workshop on Multimodal Information Retrieval. The Twentieth International Joint Conference of Artificial Intelligence, IJCAI (2007)

- Workshop on Learning with Nonparametric Bayesian Mothods. The Twenty-Third International Conference on Machine Learning, ICML (2006)

- The Twenty-Third International Conference on Machine Learning, ICML (2006)

- The Twenty-First, Twenty-Third, National Conference on Artificial Intelligence, AAAI (2006, 2008), and and AAAI-08 Nectar track (2008)

- The Fourth and Seventh Asia-Pacific Bioinformatics Conference, APBC (2006, 2009)

- The Sixteenth, Seventeenth and Eighteenth International Conference on Genome Informatics (2005, 2006, 2007)

- The Tenth and Eleventh International Conference on Artificial Intelligence and Statistics, AIS-TAT (2005, 2007)

- The First, Second, Third, and Fifth Annual RECOMB Satellite Workshop on Regulatory Genomics (2004, 2005, 2006, 2008)

- **Reviewer** for
  - *American Journal of Human Genetics*,

  - *Annals of Applied Statistics*,

  - *Proc. Natl. Acad. Sci.*,

  - *PLOS Computational Biology*,

  - *PLOS Genetics*,

  - *ACM Transactions on Knowledge Discovery from Data*,

  - *Bioinformatics*,

  - *BMC Bioinformatics*,

  - *International Journal of Computer Vision*,

  - *Journal of American Statistical Association*,

  - *Journal of Computational Biology*,

  - *Journal of Machine Learning Research*,

  - *Journal of Artificial Intelligence Research*,

  - *IEEE Transactions on Information Theory*,

  - *Genome Research*,

  - *Knowledge and Information Systems*,

- *Machine Learning*,
- *Nature, Methods*,
- *Nucleic Acid Research*,
- *Social Networks*,
- *Statistica Sinica*,
- Annual Conference on Advances in Neural Information Processing Systems (*NIPS*),
- Annual Conference on Uncertainty in Artificial Intelligence (*UAI*),
- Annual Conference on International Conference on Machine Learning (*ICML*),
- Annual IEEE Conference on Computer Vision and Pattern Recognition (*CVPR*),
- Annual Conference on Research in Computational Molecular Biology (*RECOMB*),
- Annual Conference on Intelligent Systems for Molecular Biology (*ISMB*),
- Annual Pacific Symposium on Biocomputing (*PSB*),
- National Conference on Artificial Intelligence (*AAAI*).

- **Grant Panelist** (domestic) for
  - Biological Databases & Informatics, National Science Foundation
  - Information & Knowledge Management panel, IIS, National Science Foundation
  - Plant Genome Research Program, National Science Foundation
  - NSF Career Panel
  - NSF RI/IIS Panel
  - NIH BDMA study section
  - NIH Special Emphasis Panel
  - NIH Directors New Innovator Award Panel

- **Grant and Award Reviewer/Panelist** (international) for
  - Austrian Science Fund (FWF)
  - British Computer Society (BCS), Distinguished Dissertation Award
  - Canada Foundation for Innovation (CFI)
  - Israel Science Foundation
  - The Research Grants Council (RGC) of Hong Kong
  - The Wellcome Trust

- **Professional organizations:**
  - Institute of Mathematical Statistics (IMS),
  - Association for Computing Machinery (ACM),
  - Institute of Electrical and Electronics Engineers (IEEE),
  - International Society for Bayesian Analysis (ISBA),
  - American Association for Artificial Intelligence (AAAI),
  - American Association for Cancer Research (AACR),
  - International Society for Computational Biology (ISCB).

University Services (A partial listing)

- Annual Machine Learning Summer School, co-organizer (2005, 2006), Machine Learning Department, CMU.
- Faculty Search Committee, member (2006, 2007, 2008, 2012, 2013), chair (2013), Machine Learning Department, CMU.
- Admissions Committee, member (2006), Machine Learning Department, CMU.
- Admissions Committee, member (2005), Language Technology Institute, CMU.
- Admissions Committee, member (2006), chair (2007, 2008), Joint CMU-Pitt Ph.D. Program in Computational Biology.
- Curriculum Committee, member (2006, 2007), Joint CMU-Pitt Ph.D. Program in Computational Biology.
- ACM Doctoral Dissertation Award and SCS Best Thesis Award Committee, member (2007), chair (2008), SCS, CMU.
- New Collaborations Competition, Reviewer (2007), Language Technology Institute, CMU.

Advising

Current students, Postdocs, and Research Scientists:

Graduate Student:

Advising 10 Ph.D. students: Micol Marchetti-Bowick (MLD), Wei Dai (MLD), Kumar Avinava Dubey (MLD), Qirong Ho (MLD), Seunghak Lee (CSD), Willie Neiswanger (MLD), Ankur Parikh (MLD), Veeranjaneyulu Sadhanala (MLD), Georg Schoenherr (CSD), Bin Zhao (MLD);

co-advising 2 Ph.D. students: Jin Kyu Kim (CSD), Jinliang Wei (CSD);

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