

Curriculum Vitae

Qing Zhou

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Education

- BS/MS, Engineering, Tsinghua University, 2001.
- PhD, Statistics, Harvard University, 2006.

Appointment

- Assistant Professor of Statistics, UCLA, since 2006.

Honors and Awards

- UCLA Faculty Career Development Award, 2008.
- NSF CAREER Award, 2011.

Publications

A. Refereed Journal Articles

1. Ji, H.K.*, Zhou, Q.*, Wen, F., Xia, H.Y., Lu, X., and Li, Y.D. (2001). AsMamDB: An alternative splice database of mammals. *Nucleic Acids Research*, 29: 260-263. (*Joint first authors.)
2. Zhou, Q. and Li, Y.D. (2003). Directed variation in evolution strategies. *IEEE Transactions on Evolutionary Computation*, 7: 356-366.
3. Jensen, S.T., Liu, X.S., Zhou, Q., and Liu, J.S. (2004). Computational discovery of gene regulatory binding motifs: A Bayesian perspective. *Statistical Science*, 19: 188-204.
4. Zhou, Q. and Liu, J.S. (2004). Modeling within-motif dependence for transcription factor binding site predictions. *Bioinformatics*, 20: 909-916.
5. Zhou, Q. and Wong, W.H. (2004). CisModule: De novo discovery of cis-regulatory modules by hierarchical mixture modeling. *Proceedings of the National Academy of Sciences of USA*, 101: 12114-12119.

6. Hong, P., Liu, X.S., Zhou, Q., Lu, X., Liu, J.S., and Wong, W.H. (2005). A boosting approach for motif modeling using ChIP-chip data. *Bioinformatics*, 21: 2636-2643.
7. Johnson, D.S., Zhou, Q., Yagi, K., Satoh, N., Wong, W., and Sidow, A. (2005). De novo discovery of a tissue-specific gene regulatory module in a chordate. *Genome Research*, 15: 1315-1324.
8. Kou, S.C.*, Zhou, Q.*, and Wong, W.H. (2006). Equi-energy sampler with applications in statistical inference and statistical mechanics (with discussion). *Annals of Statistics*, 34: 1581-1652. (*Equally contributed authors.)
9. Zhou, Q. and Wong, W.H. (2007). Coupling hidden Markov models for the discovery of cis-regulatory modules in multiple species. *Annals of Applied Statistics*, 1: 36-65.
10. Zhou, Q., Chipperfield, H., Melton, D.A., and Wong, W.H. (2007). A gene regulatory network in mouse embryonic stem cells. *Proceedings of the National Academy of Sciences of USA*, 104: 16438-16443.
11. Zhou, Q. and Liu, J.S. (2008). Extracting sequence features to predict protein-DNA interactions: A comparative study. *Nucleic Acids Research*, 36: 4137-4148.
12. Zhou, Q. and Wong, W.H. (2008). Reconstructing the energy landscape of a distribution from Monte Carlo samples. *Annals of Applied Statistics*, 2: 1307-1331.
13. Sridharan, R., Tchieu, J., Mason, M.J., Yachechko, R., Kuoy, E., Horvath, S., Zhou, Q., and Plath, K. (2009). Role of the murine reprogramming factors in the induction of pluripotency. *Cell*, 136: 364-377.
14. Zhou, Q. and Wong, W.H. (2009). Energy landscape of a spin glass model: Exploration and characterization. *Physical Review E*, 79: 051117.
15. Gao, K., Zhou, H., Zhang, L., Lee, J.W., Zhou, Q., Hu, S., Wolinsky, L.E., Farrell, J., Eibl, G., and Wong, D.T. (2009). Systemic disease-induced salivary biomarker profiles in mouse models of melanoma and non-small cell lung cancer. *PLoS ONE*, 4: e5875.
16. Mason, M.J., Fan, G., Plath, K., Zhou, Q.*, and Horvath, S.* (2009). Signed weighted gene co-expression network analysis of transcriptional regulation in murine embryonic stem cells. *BMC Genomics*, 10: 327. (*Co-corresponding authors.)
17. Ouyang, Z., Zhou, Q., and Wong, W.H. (2009). ChIP-seq of transcription factors predicts absolute and differential gene expression in embryonic stem cells. *Proceedings of the National Academy of Sciences of USA*, 106: 21521-21526.
18. Chen, G. and Zhou, Q. (2010). Heterogeneity in DNA multiple alignments: Modeling, inference, and applications in motif finding. *Biometrics*, 66: 694-704.
19. Mason, M.J., Plath, K., and Zhou, Q. (2010). Identification of context-dependent motifs by contrasting ChIP binding data. *Bioinformatics*, 26: 2826-2832.

20. Zhou, Q. (2010). On weight matrix and free energy models for sequence motif detection. *Journal of Computational Biology*, 17: 1621-1638.
21. Zhou, Q. (2011). Random walk over basins of attraction to construct Ising energy landscapes. *Physical Review Letters*, 106: 180602.
22. Zhou, Q. (2011). Multi-domain sampling with applications to structural inference of Bayesian networks. *Journal of the American Statistical Association*, in press.

B. Work in Progress

1. Chen, G. and Zhou, Q. (2011). Searching ChIP-seq genomic islands for combinatorial regulatory codes in mouse embryonic stem cells. *BMC Genomics*, revision.

C. Other Publications

1. Zhou, Q. (2006). Detecting cis-regulatory modules by modeling correlated structures in genomic sequences. *PhD Dissertation*, Statistics, Harvard University.
2. Zhou, Q. and Gupta, M. (2009). Regulatory motif discovery: From decoding to meta-analysis. *New Developments in Biostatistics and Bioinformatics*, Chapter 8: 179-208, World Scientific.
3. Zhou, Q. (2010). Review of “A Guide to QTL Mapping with R/qtl” by Broman and Sen. *Journal of Statistical Software*, 32: Book Review 5.
4. Liu, J.S. and Zhou, Q. (2011). Predictive modeling approaches for studying protein-DNA binding. *Proceedings of the 4th International Congress of Chinese Mathematicians*, Vol. 4: 151-167, Higher Education Press and International Press.

Research Grants

A. Independent Grants (as sole PI)

- Statistical methods for integrated gene regulation analyses. NSF DMS-0805491, 2008-2012, \$138,767.
- CAREER: Sparse modeling driven by large-scale genomic data. NSF DMS-1055286, 2011-2016, \$400,000.

B. Collaborative Grants (as co-investigator)

- Telomere and its bio-regulators as predictors for clinical diabetes in women. NIH R21 DK084452 (PI: Simin Liu), 2009-2011.

Teaching

Average instructor rating 8.5/9.0 in 2010-2011.

- Stats 201C: Advanced Modeling and Inference (graduate course).
- Stats M254: Statistical Methods in Computational Biology (graduate course).
- Stats 102C: Introduction to Monte Carlo Methods (undergraduate course).
- Stats 102B: Computation and Optimization for Statistics (undergraduate course).

Advising Graduate Students

A. PhD Students (year of graduation, current status)

- Michael J. Mason (2010), Bioinformatician, Benaroya Research Institute.
- Gong Chen (2010), Research Statistician, Abbott Laboratories.
- Fei Fu (current), advanced to candidacy.
- Matthew D. Levinson (current), advanced to candidacy.
- Maria Cha (current).

B. MS Students (year of graduation)

- Haiqiang Wang (2009), Jin Wook Lee (2009), Jung In Kim (2010), Yuju Lee (current).

C. Other Thesis Committees

- I have served and am serving as a committee member for 14 PhD and 10 MS students in addition to my students listed above.

University and Departmental Services

- Executive committee member, Interdepartmental Program in Bioinformatics, since 2007.
- Core faculty member, Interdepartmental Program in Bioinformatics, since 2007.
- Faculty member, BWF Inter-school Training Program in Metabolic Diseases, since 2009.
- Steering committee member, BWF Inter-school Training Program in Metabolic Diseases, since 2010.
- Director, Center for Statistical Research in Computational Biology, Department of Statistics, since 2010.

Professional Services

A. Referee Service

- Reviewer for NSF grants.
- Reviewer for academic journals: PNAS, Annals of Statistics, Journal of the American Statistical Association, Annals of Applied Statistics, Biometrics, Cell Stem Cell, Molecular Systems Biology, Nucleic Acids Research, PLoS Computational Biology, Bioinformatics, Physics Letters A, IEEE Transactions on Pattern Analysis and Machine Intelligence, etc.

B. Conference Organization

- Organizer: *Workshop on Computational Biology and Statistics*, Los Angeles, CA, USA, October 2008.
- Program Committee: *The Seventh Asia Pacific Bioinformatics Conference (APBC2009)*, Beijing, China, January 2009.
- Program Committee: *International Conference on Bioinformatics: Models, Methods, and Algorithms – Bioinformatics 2011*, Rome, Italy, January 2011.