

Note: in Computer Science, top conference papers have lower acceptance rate than many top journals and are highly regarded. RECOMB and ISMB are two flagship computational biology conferences with acceptance rate <20% and in total accept ~80 regular papers each year. My group has published 14 RECOMB and ISMB main conference papers since 2005. RECOMB and ISMB also have some satellite conferences, which are not as competitive as the main conferences. NIPS and AISTATS are two top machine learning conferences.

### **Peer-reviewed conference papers** (\* indicates corresponding author.)

1. Jianzhu Ma, Sheng Wang and **Jinbo Xu\***. *MRFalign: protein remote homology detection through alignment of Markov Random Fields*. RECOMB2014. (accepted, to also appear at PLOS Computational Biology)
2. Fan Yang, **Jinbo Xu** and Jianyang Zeng. *Drug-target interaction prediction by integrating chemical, genomic, functional and pharmacological data*. Pacific Symposium on Biocomputing (PSB). The Big Island of Hawaii. January 3-7, 2014.
3. Zhiyong Wang, **Jinbo Xu\*** and Xinghua Shi. *Finding alternative eQTLs by exploring sparse model space*. In Proceedings of the RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges (RECOMB/ISCB RegSys 2013), Toronto, Canada, November 2013.
4. Zhiyong Wang and **Jinbo Xu\***. *Predicting protein contact map using evolutionary and physical constraints by integer programming*. ISMB2013, also appears in *Bioinformatics* (2013) 29 (13):i266-i273.
5. Jianzhu Ma, Sheng Wang, Feng Zhao and **Jinbo Xu\***. *Protein threading using context-specific alignment potential*. ISMB2013, also appears in *Bioinformatics* (2013) 29 (13):i257-i265.
6. Jianzhu Ma, Jian Peng, Sheng Wang and **Jinbo Xu\***. *Estimating the partition function of graphical models using Langevin importance sampling*. AI and Statistics (AISTATS) 2013.
7. Jianzhu Ma, Jian Peng, Sheng Wang and **Jinbo Xu\***. *A conditional neural fields model for protein threading*. ISMB2012, also appears in *Bioinformatics* (2012) 28 (12):i59-i66.
8. Xiaohui Chen, Xinghua Shi, Zhiyong Wang, Xing Xu and **Jinbo Xu\***. *A Two-Graph Guided Multi-task Lasso Approach for eQTL Mapping*. AI and Statistics (AISTATS) 2012.
9. Jian Peng, Nathan Srebro, Tamir Hazan and **Jinbo Xu**. *Approximate Inference with Intersected Outer Bounds and Rounding Schemes*. AI and Statistics (AISTATS), 2012.
10. Zhiyong Wang and **Jinbo Xu\***. *A Conditional Random Fields method for RNA sequence-structure relationship modeling and conformation sampling*. ISMB2011, also appears in *Bioinformatics* (2011) 27 (13):i102-i110.
11. Feng Zhao, Jian Peng and **Jinbo Xu\***. *Fragment-free approach to protein folding using conditional neural fields*. ISMB2010, also appears in *Bioinformatics* (2010) 26 (12):i310-i317.
12. Jian Peng and **Jinbo Xu\***. *Low-homology protein threading*. ISMB2010, also appears in *Bioinformatics* (2010) 26 (12):i294-i300.
13. Jian Peng, Liefeng Bo and **Jinbo Xu**. *Conditional Neural Fields*. NIPS 2009.
14. Jian Peng and **Jinbo Xu\***. *Boosting protein threading accuracy*. In the Proceedings of the 13th International Conference on Research in Computational Molecular Biology (RECOMB), Lecture Notes in Computer Science, Vol. 5541, pp. 31-45, 2009. (**This paper also won the best poster award**)

15. Feng Zhao, Jian Peng, Joe DeBartolo, Karl F. Freed, Tobin R. Sosnick and **Jinbo Xu\***. *A probabilistic graphical model for ab initio folding*. In the Proceedings of the 13th International Conference on Research in Computational Molecular Biology (RECOMB), Lecture Notes in Computer Science, Vol. 5541, pp. 59-73, 2009.
16. Shuaicheng Li, Dongbo Bu, Xin Gao, **Jinbo Xu\*** and Ming Li. *Designing protein structural alphabets*. ISMB2008, also appears at Bioinformatics (2008) 24 (13):i182-i189.
17. Jing Zhang, Xin Gao, **Jinbo Xu\*** and Ming Li. *Rapid Protein Side-Chain Packing Using Local Backbone Information*. In the Proceedings of the 11th International Conference on Research in Computational Molecular Biology (RECOMB), 285-299. Lecture Notes in Computer Science 4955, 2008.
18. Bonnie Berger, Rohit Singh and **Jinbo Xu**. *Graph Algorithms for Biological Systems Analysis*. In the Proceedings of the nineteenth annual ACM-SIAM Symposium on Discrete Algorithms (SODA), 2008. (**invited paper, authors ranked alphabetically**)
19. Rohit Singh, **Jinbo Xu** and Bonnie Berger. *Global Alignment of Multiple Protein Interaction Networks*. In the Proceedings of Pacific Symposium in Biocomputing (PSB) 13:303-314, 2008. Hawaii, USA.
20. **Jinbo Xu**. *Solving the Contact Map Overlap Problem via Tree Decomposition and a DEE-Like Pruning Strategy*. In the Proceedings of the 46th IEEE Conference on Decision and Control, December 2007. Orlando, USA. (**invited paper**)
21. Xin Gao, Dongbo Bu, Shuai Cheng Li, **Jinbo Xu\*** and Ming Li. *FragQA: predicting local fragment quality of a sequence-structure alignment*. In the Proceedings of the 17th International Conference on Genome Informatics (GIW), December 2007. (**best paper award**)
22. Xin Gao, Dongbo Bu, ShuaiCheng Li, Ming Li, and **Jinbo Xu\***. *Consensus Contact Prediction by Linear Programming*. Life Science Society Computational Systems Conference (CSB), August 2007. Stanford, USA.
23. Jianbo Qian, Shuai Cheng Li, Dongbo Bu, Ming Li and **Jinbo Xu**. *Finding Compact Structural Motifs in Many Proteins*. Combinatorial Pattern Matching (CPM), July 2007. London, Canada.
24. Rohit Singh, **Jinbo Xu** and Bonnie Berger. *Pairwise Global Alignment of Protein Interaction Networks By Matching Neighborhood Topology*. In the Proceedings of the 11th International Conference on Research in Computational Molecular Biology (RECOMB), 16-31. Lecture Notes in Computer Science 4453, 2007.
25. Feng Jiao, **Jinbo Xu\***, Libo Yu and Dale Schuurmans. *Protein Fold Recognition Using the Gradient Boost Algorithm*. Life Science Society Computational Systems Bioinformatics (CSB), 2006. Stanford, USA.
26. **Jinbo Xu\***, Feng Jiao and Bonnie Berger. *A Parameterized Algorithm for Protein Structure Alignment*. In the Proceedings of the 10th International Conference on Research in Computational Molecular Biology (RECOMB), Lecture Notes in Bioinformatics 3909, 488-499. Springer 2006.
27. Rohit Singh, **Jinbo Xu** and Bonnie Berger. *Struct2Net: Integrating Structure into Protein-Protein Interaction Prediction*. Pacific Symposium on Biocomputing (PSB) 2006:403-414, Hawaii, USA.
28. **Jinbo Xu**, Feng Jiao and Bonnie Berger. *A Tree-Decomposition Approach to Protein Structure Prediction*. Computational Systems Bioinformatics (CSB), 2005. Stanford, USA.

29. **Jinbo Xu**. *Rapid Protein Side-Chain Packing via Tree Decomposition*. In the Proceedings of the 9th International Conference on Research in Computational Molecular Biology (RECOMB), Lecture Notes in Computer Science, Vol. 3500, pp. 423-439, 2005. Springer. (**An extended version invited to the Journal of the ACM.**)
30. **Jinbo Xu**, Libo Yu and Ming Li. *Consensus Fold Recognition by Predicted Model Quality*. Asia-Pacific Bioinformatics Conference (APBC) 2005:73-83, Singapore.
31. Thomas Tang, **Jinbo Xu** and Ming Li. *Discovery of Sequence-Structure Motifs from Protein Segments and Two Applications*. Pacific Symposium on Biocomputing (PSB) 2005. Hawaii, USA.
32. **Jinbo Xu**, Daniel Brown, Ming Li and Bin Ma. *Optimizing multiple spaced seeds for homology search*. Combinatorial Pattern Matching (CPM) 2004, Istanbul, Turkey.
33. **Jinbo Xu**, Ying Xu, Guohui Lin, Dongsup Kim and Ming Li. *Protein Structure Prediction by Linear Programming*. Pacific Symposium on Biocomputing (PSB) 2003: 264-275, Hawaii, USA.
34. **Jinbo Xu**. *Speed up LP Approach to Protein Threading via Graph Reduction*. in the Proceedings of the 3<sup>rd</sup> International Workshop on Algorithms in Bioinformatics (WABI), Lecture Notes in Computer Science Vol. 2812, pp. 374-388, 2003.