

# *Jinbo Xu*

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## **EDUCATION & TRAINING**

Department of Mathematics, Massachusetts Institute of Technology  
Postdoctoral Fellow, 2004–2005 (Supervisor: Bonnie Berger)

School of Computer Science, University of Waterloo, Canada  
Ph.D. in Computer Science, 1999–2003 (Supervisor: Ming Li, Prabhakar Ragde)

Institute of Computing Technology, Chinese Academy of Sciences, China  
Master of Science in Computer Science, 1996–1999

Department of Computer Science, China University of Science and Technology  
Bachelor of Science in Computer Science, 1991–1996

## **EMPLOYMENT & AFFILIATIONS**

Toyota Technological Institute at Chicago	Assistant Professor	10/2005–present
University of Chicago	Assistant Professor (Part Time)	10/2005–present
Massachusetts Institute of Technology	Research Affiliate	10/2006–present
University of Waterloo	Adjunct Assistant Professor	10/2005–present

## **CURRENT RESEARCH ACTIVITIES**

Developing mathematical models (e.g., probabilistic graphical model) and computer algorithms (e.g., linear programming, graph tree-decomposition, Monte Carlo sampling) for the protein folding problem.

## **GRANTS AND FELLOWSHIPS**

1. NIH grant (1R01GM081642-01) for “Protein structure refinement using novel move set”, 08/2007-08/2010, with Tobin Sosnick (PI) and Karl Feed.
2. NIH grant for “Prediction of protein interactome”, 12/2007-12/2012, with Bonnie Berger (PI) and Jadwiga Bienkowska.
3. BWF (Burroughs Wellcome Fund) Postdoctoral Fellowship, 10/2004-10/2005, supervised by Prof. Bonnie Berger, the Department of Mathematics, MIT.

## **REFEREED CONFERENCE PUBLICATIONS**

An asterisk indicates that I am the corresponding or co-corresponding author.

1. Jian Peng and Jinbo Xu\*. Boosting Protein Threading Accuracy. RECOMB 2009. In Press.
2. Feng Zhao, Jian Peng, Joe DeBartolo, Karl F. Freed, Tobin R. Sosnick and Jinbo Xu\*. A probabilistic graphical model for ab initio folding. RECOMB 2009. In Press.
3. Shuaicheng Li, Dongbo Bu, Xin Gao, Jinbo Xu\* and Ming Li. Designing Protein Structural Alphabets, ISMB 2008. Also appears at the Bioinformatics Journal.
4. Jing Zhang, Xin Gao, Jinbo Xu\* and Ming Li. Rapid Protein Side-Chain Packing Using Local Backbone Information. RECOMB 2008.

5. 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)**
6. Rohit Singh, Jinbo Xu and Bonnie Berger. Global Alignment of Multiple Protein Interaction Networks. PSB, Jan 2008.
7. Jinbo Xu. Solving the Contact Map Overlap Problem via Tree Decomposition and a DEE-Like Pruning Strategy, accepted by the 46th IEEE Conference on Decision and Control, December 2007. **(invited paper)**
8. 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 Springer 2007.
9. Xin Gao, Dongbo Bu, Shuai Cheng Li, Jinbo Xu\* and Ming Li. FragQA: predicting local fragment quality of a sequence-structure alignment, the 17th International Conference on Genome Informatics (GIW), December 2007. **(best paper award)**
10. Xin Gao, Dongbo Bu, ShuaiCheng Li, Ming Li, and Jinbo Xu. Consensus Contact Prediction by Linear Programming, Computational System Bioinformatics (CSB), August 2007.
11. 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.
12. Feng Jiao, Jinbo Xu\*, Libo Yu and Dale Schuurmans. Protein Fold Recognition Using the Gradient Boost Algorithm. Computational Systems Bioinformatics (CSB), 2006.
13. Jinbo Xu, Feng Jiao and Bonnie Berger. A Parameterized Algorithm for Protein Structure Alignment. In the Proceedings of the 10th Annual International Conference on Research in Computational Molecular Biology (RECOMB), 488-499. Lecture Notes in Computer Science 3909 Springer 2006.
14. Rohit Singh, Jinbo Xu and Bonnie Berger. Struct2Net: Integrating Structure Into Protein-Protein Interaction Prediction. Proceedings of the Pacific Symposium on Biocomputation (PSB), 2006. **(The first two authors contribute equally to the paper.)**
15. Jinbo Xu, Feng Jiao and Bonnie Berger. A Tree-Decomposition Approach to Protein Structure Prediction. In Proceedings of the 2005 IEEE Computational Systems Bioinformatics Conference (CSB'05), 247-256, 2005.
16. Jinbo Xu. Rapid Protein Side-Chain Packing via Tree Decomposition. In Proceedings of the 9th Annual International Conference on Research in Computational Molecular Biology RECOMB (2005), 423-439.
17. Jinbo Xu, Libo Yu and Ming Li. Consensus Fold Recognition by Predicted Model Quality. Third Asia-Pacific Bioinformatics Conference, Singapore, 2005.
18. Thomas Tang, Jinbo Xu and Ming Li. Discovering Sequence-Structure Motifs from Protein Segments and Two Applications. Pacific Symposium on Biocomputing (PSB), Hawaii, USA, 2005.
19. Jinbo Xu, Daniel Brown, Ming Li, and Bin Ma. Optimizing Multiple Spaced Seeds for Homology Search. Combinatorial Pattern Matching (CPM), Istanbul, Turkey, July 2004.
20. Jinbo Xu. Speed up LP Approach to Protein Threading via Graph Reduction. In G. Benson, R. Page, ed., Algorithms and Bioinformatics: 3rd International Workshop (WABI), 2812 volume of Lecture Notes in Bioinformatics, pp. 374-388, Budapest, Hungary, September 2003. Springer.
21. Jinbo Xu, Ming Li, Guohui Lin, Dongsup Kim and Ying Xu. Protein Threading By Linear Programming. Pacific Symposium in Biocomputing (PSB), pp. 264-275, Hawaii, January 3-7, 2003.

## REFEREED JOURNAL PUBLICATIONS

1. Jian Peng and Jinbo Xu\*. Improving protein profile-profile alignment using non-evolutionary/structure information. *Bioinformatics*, 2009. (submitted)
2. Jinbo Xu\*, Jian Peng and Feng Zhao. Template-based and template-free modeling by new RAPTOR in CASP8. *PROTEINS*, 2009. (**invited paper**)
3. Rohit Singh, Jinbo Xu and Bonnie Berger. Global Alignment of Multiple Protein-Protein Interaction Networks. *Proceedings of National Academy of Sciences*, 2008.
4. Shuaicheng Li, Dongbo Bu, Jinbo Xu\* and Ming Li. Fragment-HMM: A New Approach To Protein Structure Prediction. *Protein Science*, 2008.
5. Ben Boyerinas, Sun-Mi Park, Noam Shomron, Cydney B. Nielsen, Christine Feig, Jinbo Xu, Christopher B. Burge and Marcus E. Peter. Let-7-regulated Oncofetal Genes for Human Cancer. *Cancer Research*, 2008.
6. Feng Zhao, ShuaiCheng Li, Beckett W. Sterner and Jinbo Xu\*. Discriminative Learning for Protein Conformation Sampling. *PROTEINS: Structure, Function and Bioinformatics*, 2008.
7. Jinbo Xu, Feng Jiao and Bonnie Berger. A Parameterized Algorithm for Protein Structure Alignment. *Journal of Computational Biology*, Vol. 14, No. 5, pp.564-577, 2007. Early version appears at RECOMB 2006.
8. Jinbo Xu\*, Bonnie Berger. Fast and Accurate Algorithms for Protein Side-Chain Packing. *The Journal of the ACM*, 53(4):1-25, 2006. (**invited paper**)
9. Jinbo Xu, Daniel Brown, Ming Li, Bin Ma. Optimizing multiple spaced seeds for homology search. *Journal of Computational Biology*, 13(7):1355-1368, 2006.
10. Jinbo Xu. Protein Fold Recognition by Predicted Alignment Accuracy. *IEEE/ACM Trans. on Computational Biology and Bioinformatics*, 2(2):157-165, 2005.
11. Jinbo Xu, Ming Li, and Ying Xu. Protein Threading by Linear Programming: Theoretical Analysis and Computational Results. *Journal of Combinatorial Optimization*. 8(4):403-418, December 2004.
12. Jinbo Xu, Ming Li, Dongsup Kim and Ying Xu. RAPTOR: Optimal Protein Threading by Linear Programming. *Journal of Bioinformatics and Computational Biology*, 1(1):95-117, April 2003. (**invited paper**)
13. Jinbo Xu and Ming Li. Assessment of RAPTOR's Linear Programming Approach in CAFASP3. *Proteins: Structure, Function and Genetics*, 53(S6):579-584, October 2003. (**invited paper**)
14. Zhi-Zhong Chen, Tao Jiang, Guohui Lin, Jianjun Wen, Dong Xu, Jinbo Xu and Ying Xu. Approximation Algorithms for *NMR* Spectral Peak Assignment. *Theoretical Computer Science*, 299:211-229, 2002.
15. Jie Lin, Jinbo Xu, Naijie Gu and Guoliang Chen. Parallel String Matching Algorithm on Distributed Systems. (Chinese) *Journal of Software*, 11(6):771-778, 2000.
16. Jinbo Xu and Guoliang Chen. Design and Analysis of Parallel *FFT* Algorithm On *CCC* Model, (Chinese) *Journal of Computer Research & Development*, 34:59-63, 1998.
17. Guoliang Chen and Jinbo Xu. Communication Strategy of Parallel *FFT* Algorithm On *LogP* Model, (Chinese) *Journal of Computer Science*, 8:702-710, 1997.

## BOOK CHAPTER

1. Dongbo Bu, Shuaicheng Li, Xin Gao, Libo Yu, Jinbo Xu and Ming Li. Consensus Approaches to Protein Structure Prediction. Book Chapter in *Machine Learning in Bioinformatics*, Eds: Yan-Qing Zhang and Jagath C. Rajapakse, John Wiley & Sons, 2007.
2. Jinbo Xu, Feng Jiao and Libo Yu. Protein Structure Prediction Using Threading. Book Chapter in *Protein Structure Prediction: Methods and Protocols*. Humana Press. 2006.

## INVITED TALKS

1. Protein threading by nonlinearly combining evolutionary and non-evolutionary information. The University of Minnesota, 2009.
2. Protein threading by nonlinearly combining evolutionary and non-evolutionary information. MIT, 2009.
3. Linear programming approach to protein structure prediction. INFORMS Annual Meeting, October 2008.
4. Graph Algorithms for Biological Systems Analysis. SIAM on Discrete Mathematics, June 2008.
5. Global Alignment of Multiple Protein Interaction Networks. The University of Illinois at Chicago, 2008.
6. Protein Conformation Sampling Using Conditional Random Fields, MIT, 2008.
7. Graph Algorithms for Protein Structure Alignment. The 46th IEEE Conference on Decision and Control, December 2007.
8. Knowledge-based Protein Structure Prediction. Institute of Computing Technology, Chinese Academy of Sciences, March 2007. (Distinguished Lecture)
9. Knowledge-based Protein Structure Prediction. Tsinghua University, March 2007.
10. Knowledge-based Protein Structure Prediction. Microsoft Research in Asia, March 2007.
11. Knowledge-based Protein Structure Prediction. Toyota Technological Institute at Japan, April 2007.
12. Protein Side Chain Packing via Tree Decomposition. University of Waterloo, August 2006.
13. A Parameterized Algorithm for Protein Structure Alignment. University of Waterloo, July 2006.
14. A Parameterized Algorithm for Protein Structure Alignment. Massachusetts Institute of Technology, May 2006.
15. Knowledge-based Protein Structure Prediction. Northwestern University, May 2006.
16. A Parameterized Algorithm for Protein Structure Alignment. University of Illinois at Chicago, November 2005.
17. Fast and Accurate Algorithms for Protein Side-Chain Packing. Boston University, October 2005.
18. Rapid Protein Side-Chain Packing via Tree Decomposition. DIMACS Workshop on Information Processing by Protein Structures in Molecular Recognition. June 13-14, 2005.
19. RAPTOR: protein threading by linear programming. SIAM mini-symposium, SIAM Conference on Control and Its Applications. New Orleans, LA, July 11-14, 2005.
20. ACE: consensus method to fold recognition. CASP6, Italy. December 2004. **(an invitation to our ACE group)**
21. Protein Structure Prediction by Linear Programming. School of Medicine, University of Western Ontario, 2004.
22. Protein Structure Prediction. The Interdisciplinary Coffee Talk Society, University of Waterloo, 2003.

## HONORS & AWARDS

1. My program RAPTOR ranked second in CASP8 (Critical Assessment of Protein Structure Prediction), 2008.
2. BWF Program in Mathematical Molecular Biology Fellowship, 2004–2005.
3. My program RAPTOR-ACE ranked second in CASP6, 2004.
4. PhD thesis nominated for ACM Doctoral Dissertation Award and NSERC Doctoral Prize, 2003.
5. My program RAPTOR ranked first in CAFASP3/CASP5, 2002.
6. 1999-2003 International Student Scholarship, University of Waterloo.
7. 1996 China Computer World Prize.
8. 1995 Second Prize of China Collegiate Mathematical Contest of Modeling.
9. 1990 First Prize of China High School Mathematical Contest, No.1 in Jiangxi Province.

**PATENT**

Jinbo Xu and Ming Li. Protein Threading by Linear Programming. Filed on January 2, 2003 for Canadian Patent and on January 2, 2004 for US Patent.

**SERVICE**

1. Referee for the following international journals and conferences: Journal of Proteome, Protein Engineering, Journal of Bioinformatics and Computational Biology, Bioinformatics Journal, Journal of Computational Biology, Algorithmica, Pattern Recognition Letter, Mathematical Biosciences, Journal of Mathematical Biology, IEEE/ACM Trans. on Computational Biology and Bioinformatics, BMC Bioinformatics, SIAM Journal of Computing, ACM-SIAM Symposium on Discrete Algorithms (SODA 2007), Journal of Molecular Biology

2. Service to workshops and conferences:

IEEE Bioinformatics and Biomedicine 2008

International Workshop on Biological Data Management (BIDM) 2007

IEEE 7th International Symposium on Bioinformatics & Bioengineering (IEEE BIBE 2007)

The Sixth IEEE International Conference on Machine Learning and Applications, 2007

Co-chair of the Bioinformatics and Computational Biology workshop, the Eighth International Conference on High-Performance Computing in Asia-Pacific Region (HPC-Asia 2005)