

Department of Bioinformatics and Genomics
College of Computing and Informatics
The University of North Carolina at Charlotte
9201 University City Blvd
Charlotte, NC 28223-0001

Phone: (704) 687-7492
Fax: (704) 687-8667
Email: jguo4@uncc.edu

Research Interests

Structural Bioinformatics: protein structure prediction and modeling, protein-DNA docking and structure-based transcription factor binding site prediction

Education

Ph.D. Molecular and Cellular Biochemistry, University of Kentucky, 1995-2001

M.S. Computer Science, University of Kentucky, 2000-2002

M.S. Biochemistry, Nankai University, China, 1990-1993

B.S. Biochemistry, Nankai University, China, 1986-1990

Professional Experience

- *Assistant Professor*, Department of Bioinformatics and Genomics, Department of Computer Science, University of North Carolina at Charlotte (UNCC), 2007-present
- *Assistant Research Scientist*, Department of Biochemistry and Molecular Biology and Institute of Bioinformatics, University of Georgia, 2004-2007
- *Group Leader*, Computational Structure Biology Group, Computational Systems Biology Laboratory, BCMB, University of Georgia, 2003-2007
- *Postdoctoral Research Associate*, Protein Informatics Group, Life Sciences Division, Oak Ridge National Lab (ORNL) (2001-2003) and University of Tennessee and Department of Biochemistry and Molecular Biology, University of Georgia (2003-2004)*
*Advisor (Ying Xu)'s lab moved from ORNL to the University of Georgia in September, 2003.
- *Research Assistant*, Department of Molecular and Cellular Biochemistry, University of Kentucky, 1995-2001
- *Lecturer*, Department of Biochemistry and Molecular Biology, Nankai University, 1993-95
- *Research Assistant*, Department of Biology, Nankai University, 1991-1993

Research Funding

1. "CAREER: A Structure-Based Approach to Transcription Factor-binding Site Prediction via Protein-DNA docking",
PI, National Science Foundation (NSF), 2009-2014
2. "An Integrative Approach to Study the Transcriptional Regulation of ALAS1 by Heme",
Co-PI, CMC-UNC Charlotte Collaborative Grants Program, 2009-2010

Publications

A. Journal papers

1. Kim, R. and **Guo, J-T.***, “PDA: an automatic and comprehensive analysis program for protein-DNA complex structures”, *BMC Genomics*, 10(Suppl 1):S13, 2009, (*corresponding author)
2. Liu, Z*. **Guo, J-T.*** Li, T. and Xu, Y. “Structure-based recognition of binding sites of transcription factors using an efficient protein-DNA docking approach”, *Proteins: Structure, Function, and Bioinformatics*, 72(4):1114-1124, 2008, *co-first authors
3. **Guo, J-T.*** Xu, Y. “Towards modeling of amyloid fibril structures”, *Frontiers in Bioscience*, 13:4039-4050, 2008 (*corresponding author)
4. Ellrott, K. **Guo, J-T.** Olman, V. Xu, Y. "Improvement in Protein Sequence Structure Alignment using Insertion/Deletion Frequency Array", *Journal of Bioinformatics and Computational Biology*, 6(3):585-602, 2008
5. **Guo, J-T.** Ellrott, K. Xu, Y. “A historical perspective of protein structure prediction”, *Methods Mol Biol.* 413:3-42, 2008
6. **Guo, J-T.** Jaromczyk, JW. Xu, Y. “Analysis of Chameleon Sequences and Their Implications in Biological Processes”, *Proteins: Structure, Function, and Bioinformatics*, 67(3):548-58, 2007
7. Li, G. Liu, Z. **Guo, J-T.** Xu, Y. “An Algorithm for Simultaneous Backbone Threading and Side-Chain Packing”, *Algorithmica*, 48(4):329-342, 2007
8. **Guo, J-T.** Xu, Y. “Amyloid Fibril Structure Modeling Using Protein Threading and Molecular Dynamics Simulations”. *Method in Enzymology*, 412:300-314, 2006
9. Wang, P. B. Yan, **J-T. Guo**, C. Hicks, Xu, Y. "Structural genomics analysis of alternative splicing and its application in modeling structures of alternatively spliced variants", *Proc Natl Acad Sci USA*, 102(52):18920-18925, 2005.
10. Sharp, J.S. **Guo, J-T.** Uchiki, T. Xu, Y. Dealwis, C. Hettich, R. “Application of Photochemical Surface Mapping of C16S Sml1p to Constrained Computational Modeling”. *Analytical Biochemistry*, 340(2):201-212, 2005
11. Liu, Z. Mao, F. **Guo J-T.** Yan, B. Wang, P. Qu, Y. Xu, Y. "Quantitative Validation of Protein-DNA Interaction using an Optimized Knowledge-based Potential", *Nucleic Acids Research*, 33(2):546-558, 2005
12. **Guo, J-T.** Wetzal, R. Xu, Y. "Molecular Modeling of the Core of Abeta Amyloid Fibrils", *Proteins: Structure, Function, and Bioinformatics*, 57(2):357-364, 2004.
13. **Guo, J-T.** Ellrott, K. Chung, WJ. Xu, D. Passovets, S. Xu, Y. "PROSPECT-PSPP: An Automatic Computational Pipeline for Protein Structure Prediction", *Nucleic Acids Res.*, 32:W522-5, 2004

14. Gupta, V. Peterson, C.B. Dice, L. Uchiki, T. **Guo, J-T.** Xu, Y. Hettich, R. Dealwis, C. "Sml1p Protein is a Dimer in Solution: Characterization of Denaturation and Renaturation of Recombinant Sml1p". *Biochemistry*, 43(26):8568-8578, 2004
15. Qu, Y. **Guo, J-T.** Olman, V. and Xu, Y. "Protein structure prediction using sparse dipolar coupling data", *Nucleic Acids Research*, 32(2):551-561, 2004.
16. Williams, A. Portelius, E. Kheterpal, **Guo, J-T.** Xu, Y. Cook, K. Wetzel, R. "Mapping Abeta Amyloid Fibril Secondary Structure Using Scanning Proline Mutagenesis". *J. Mol. Biol.* 335:833-842, 2004
17. Kim, D. Xu, D. **Guo, J-T.** Ellrott, K. Xu, Y. "PROSPECT II: Protein Structure Prediction Program for the Genome-scale Application". *Protein Eng.* 16(9), 641-650, 2003
18. **Guo, J-T.** Xu, D. Kim, D. Xu, Y. "Improving the Performance of DomainParser for Structural Domain Partition Using Neural Networks". *Nucleic Acids Research.* 31(3), 944-952, 2003
19. **Guo, J-T.** Yu, J. Grass, D. de Beer, F.C. Kindy, M.S. "Inflammation Dependent Cerebral Deposition of Serum Amyloid A Protein in a Mouse Model of Amyloidosis". *J. Neurosci.* 22(14), 5900-5909, 2002
20. Xie, C. Lovell, M. Xiong, S. Kindy, M. **Guo, J-T.** Xie, J. Amaranth, V. Montine, T.J. Marksbery, W. "Expression of Glutathione-S-Transferase isozyme in the SY5Y neuroblastoma Cell Line Increases Resistance to Oxidative Stress". *Free Radical Biology and Medicine*, 31(1):73-81, 2001
21. Yu, J. Zhu, H. **Guo, J-T.** de Beer, F.C. Kindy, M.S. "Expression of Mouse Apolipoprotein SAA1.1 in CE/J Mice: Isoform-specific Effects on Amyloidogenesis". *Laboratory Investigation*, 80(12), 1797-1806, 2000
22. De villiers, W.J.S. Varilek, G.W. de Beer, M.C. **Guo, J-T.** Kindy, M.S. "Increased Serum Amyloid A Levels Reflect Colitis severity and Precede Amyloid Formation in IL-2 Deficient Mice". *Cytokine*, 12(9):1337-1347, 2000
23. Yu, J. **Guo, J-T.** Zhu, H. Kindy, M.S. "Amyloid Formation in the Rat: Adenoviral Expression of Mouse Serum Amyloid A Proteins". *Amyloid*, 7(1):32-40, 2000
24. Kindy, M.S. Yu, J. **Guo, J-T.** Zhu, H. "Apolipoprotein Serum Amyloid A in Alzheimer's Disease". *J. Alzheimer's Disease*, 1:155-167, 1999

B. Referred full conference papers

25. Kim, R. McCafferty, J. and **Guo, J-T.*** "A Systematic Study of Homologous Protein Structures with Insertions/Deletions", *Comput Syst Bioinformatics Conf.* 103-113, 2009 (*corresponding author)
26. Ellrott, K. **Guo, J-T.** Olman, V. Xu, Y. "Improvement in Protein Sequence Structure Alignment using Insertion/Deletion Frequency Array", *Comput Syst Bioinformatics Conf.* 6:335-42, 2007
27. Ellrott, K. **Guo, J-T.** Olman, V. Xu, Y. "A Generalized Threading Model using Integer Programming with Secondary Structure Element Deletion", *Genome Informatics*, 17(2), 248-258, 2006

28. Qu, Y. **Guo, J-T**, Olman, V. and Xu, Y. "Protein Fold Recognition Through Application of Residual Dipolar Coupling Data", *Proceedings of the 9th Pacific Symposium on Biocomputing (PSB)*, 9:459-470, 2004

C. Book chapters

29. **Guo, J-T**, Hall, C. Xu, Y. Wetzel R. "Modeling Protein Aggregate Assembly and Structure", In *Computational Methods for Protein Structure Prediction and Modeling*, Springer, 279-317, 2006

Invited Talks

1. "A Systematic Study of Homologous Protein Structures with Insertions/Deletions", 8th International Conference on Computational Systems Bioinformatics (CSB2009), Stanford University, August 11, 2009
2. "A Systematic Analysis of Indels-Toward Alternatively Spliced Protein Isoform Structure Prediction", College of Computer Science and Technology, Jilin University, Dec.19, 2008
3. "Structural Bioinformatics: From Sequences to Biological Complexity", Department of Computer Science, University of Missouri-Columbia, April 10, 2007
4. "Structural Bioinformatics: From Sequences to Biological Complexity". The College of Natural and Agricultural Sciences, University of California, Riverside, March 26, 2007
5. "Structural Bioinformatics: From Sequences to Biological Complexity". Department of Computer Science, University of Nebraska at Omaha, February 5, 2007
6. "Structural Bioinformatics: From Sequences to Biological Complexity". Bioinformatics Research Center (BRC), University of North Carolina at Charlotte, February 1, 2007
7. "Protein structure prediction and its application in modeling AS isoform structures", Emory University, December 8, 2006.
8. "Structure prediction and modeling of alternatively spliced protein variants and applications". 2nd Annual UK-Southeast USA Symposium on Structural Genomics and Proteomics of Membrane and Metalloproteins, University of St. Andrews, St. Andrews, Scotland, August 27-29, 2006.
9. "Protein structure prediction". Computational Biology Institute, Oak Ridge National Laboratory, Oak Ridge, TN, June 24, 2004
10. "Protein structure prediction using threading techniques". Southeast Collaborative Alliance Biocomputing Center (SECABC) Symposium, May 24-25, 2004 Atlanta, GA
11. "PROSPECT, a threading-based protein structure prediction system". Division of Developmental and Clinical Immunology, Department of Medicine, University of Alabama at Birmingham. March 24, 2004
12. "Genome-scale protein structure prediction using PROSPECT". Department of Computer Science, University of Georgia, November 21, 2003

13. “*Genome-scale protein structure prediction*”. The third annual EITC conference, Princeton, NJ, October 31-November 1, 2003
14. “*Solving biological problems computationally*”. Oak Ridge National Lab, Oak Ridge, TN, October 9, 2002
15. “*Protein domain decomposition using network flow algorithms and neural networks*”. SIAM Conference, San Diego, CA, August 11-14, 2002
16. “*Inflammation dependent cerebral amyloid deposition in transgenic mouse models*”. New York University, August 29, 2001

Professional Activities

1. Program Committee Member for Conferences:

- ❖ *The IEEE International Conference on Bioinformatics and Biomedicine 2009 (BIBM 2009)*, Nov. 1-4, 2009, Washington DC, USA
- ❖ *ISIBM International Joint Conference on Bioinformatics, Systems Biology and Intelligent Computing (IJCBS 2009)*, August 3-6, 2009, Shanghai, China
- ❖ *The IEEE International Conference on Bioinformatics and Biomedicine 2008 (BIBM 2008)*, November 7-9, Philadelphia, PA, USA
- ❖ *International Conference on Biocomputation, Bioinformatics, and Biomedical Technologies, (BIOTECHNO 2008)*, June 29 - July 5, 2008, Bucharest, Romania
- ❖ *2008 International Symposium on Bioinformatics Research and Applications (ISBRA 2008)*, May 6-8, Atlanta, GA, USA.
- ❖ *The IEEE International Conference on Bioinformatics and Biomedicine 2007 (BIBM 2007)*, November 2-4, Silicon Valley, CA, USA.
- ❖ *The IEEE 7th International Symposium on Bioinformatics and Bioengineering (BIBE2007)*, October 15-17, Cambridge - Boston, Massachusetts, USA.
- ❖ *2007 International Symposium on Bioinformatics Research and Applications (ISBRA 2007)*, May 6-9, Atlanta, GA, USA.
- ❖ *2nd International Workshop on Bioinformatics Research and Applications (IWBRA 2006)*, May 28-31, University of Reading, UK
- ❖ *1st International Workshop on Bioinformatics Research and Applications (IWBRA 2005)*, May 22-25, Atlanta, GA, USA

2. Other Conference Activities

- ❖ Co-organizer, *CSB 2007 Workshop on Alternative Splicing*, August 17, 2007, University of California at San Diego, San Diego, CA, USA
- ❖ Travel Fellowship Program Committee, *15th Annual International Conference on Intelligent Systems for Molecular Biology and 6th European Conference on Computational Biology, (ISMB/ECCB 2007)*, July 19-25, Vienna, Austria.
- ❖ “*From sequence to structure: protein structure prediction*”, tutorial, 2004 IEEE Computational Systems Bioinformatics Conference (CSB2004)

3. Reviewer for scientific journals and conferences

A: Journals

Current Protein and Peptide Science, Bioinformatics, FASEB Journal,
Frontiers in Bioscience, Journal of Bioinformatics and Computational Biology,
Journal of Molecular Biology, Protein Engineering, Design, and Selection
Mathematical Biosciences

B: Bioinformatics conferences

IEEE Bioinformatics Conference, CSB 2003-06
International Workshop on Bioinformatics Research and Applications, IWBRA 2005-06
International Symposium on Bioinformatics Research and Applications, ISBRA 2007-08
The Fifth International Bioinformatics Workshop (IBW2007)
The 18th International Conference on Genome Informatics (GIW2007)
The 7th International Symposium on Bioinformatics and Bioengineering (BIBE2007)
The IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2007-09)
International Conference on Biocomputation, Bioinformatics, and Biomedical
Technologies, (BIOTECHNO 2008)

4. Internal activities

- ❖ Ph.D. Admission Committee, University of North Carolina at Charlotte, 2009-
- ❖ Graduate Faculty, University of North Carolina at Charlotte, 2007-
- ❖ Bioinformatics Faculty Search Committee, University of North Carolina at Charlotte, 2007-2008
- ❖ Graduate Faculty Representative, Doctoral Committee of Kevin Hammond, Department of Electrical and Computer Engineering, University of North Carolina at Charlotte, 2007-
- ❖ Course Committee, Bioinformatics Research Center (BRC), University of North Carolina at Charlotte, 2007-2008
- ❖ Seminar Series Committee, Bioinformatics Research Center (BRC), University of North Carolina at Charlotte, 2007-2008

Honors and Awards

2009-2014	NSF CAREER award
1998-2001	Research Assistantship, University of Kentucky
1997-1998	Graduate School Academic Year Fellowship, University of Kentucky
1995-1997	Research Assistantship, University of Kentucky
1991-1993	GuangHua Graduate Fellowship, Nankai University, China

Teaching

- ❖ “*Computational Structural Biology*”, BINF6202/ITSC8202, UNC Charlotte, (Spring, 2009)
- ❖ “*Statistics for Bioinformatics*”, BINF6200/ITSC8200, UNC Charlotte, (Spring, Fall, 2008)

- ❖ “*Advanced High-Throughput Biological Data Analyses*”, (team taught), BCMB/MIBO 8211, University of Georgia, 2007
- ❖ “*Computational Methods in Bioinformatics*”, (team taught), BCMB8210, University of Georgia, 2004-06
- ❖ “*Protein Structure Prediction*”, Institute of Bioinformatics Summer School, University of Georgia, 2005, 2007

Postdocs and Student

Dr. RyangGuk Kim, (2007-) postdoctoral research associate, UNC Charlotte
 Jon McCafferty, (2008) rotation graduate student, UNC Charlotte
 Kyle Ellrott, (2002-2007) graduate student, University of Tennessee/University of Georgia
 Tayiba Robinson, (2006) UGA NSF/REU summer undergraduate research program
 James Mcguire, (2004) UGA NSF/REU summer undergraduate research program
 Shiming Dong (2003-2004) graduate student, CS Department, University of Georgia

Software/Webserver Developed

1. **PDA** (for Protein-DNA complex structure Analyzer) is a comprehensive protein-DNA complex structure analysis program. PDA takes PDB files as inputs and performs structural analysis that includes 1) whole protein-DNA complex structure restoration, especially the reconstruction of double-stranded DNA structures; 2) an efficient new approach for DNA base-pair detection; 3) systematic annotation of protein-DNA interactions; and 4) extraction of DNA subsequences involved in protein-DNA interactions and identification of protein-DNA binding units. WebPDA (<http://bioinfozen.uncc.edu/webpda>) is a web interface for using PDA and for data retrieval.
2. **DomainParser2** is a computer program for partitioning a solved protein structure into structural domains. The domain decomposition problem is formulated as a network flow model and neural network is applied for the prediction. DomainParser2 was ranked the best in three out of five categories from a recent large-scale comparative study of automatic protein domain partition programs. (“Partitioning protein structures into domains: why is it so difficult?”, Holland, TA, Veretnik, S, Shindyalov, IN., and Bourne, PE. *J. Mol. Biol.*, 2006, 361:562-90). Domainparser2 has also been used in CASP6 for evaluation of protein domain prediction (“Domain definition and target classification for CASP6”, Tress, M. *et. al. Proteins-Structure Function and Bioinformatics*, 2005, 61:8-18).
3. **PROSPECT-PSPP** (http://csbl.bmb.uga.edu/protein_pipeline/login.php) is an automatic computational pipeline for protein structure prediction. It is an integration of multiple computational tools, for fully automated protein structure prediction. The pipeline consists of tools for (a) preprocessing of protein sequences, which includes signal peptide prediction, protein type prediction (membrane or soluble), protein domain partition, (b) secondary structure prediction, (c) fold recognition, and (d) atomic structural model generation. The centerpiece of the pipeline is our threading-based program PROSPECT. The pipeline is implemented using SOAP (Simple Object Access Protocol), which makes it easier for sharing our tools and resources. The pipeline has an easy-to-use user interface and can be used for genome scale protein structure prediction.