

Jinfeng Zhang

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CONTACT INFORMATION

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EDUCATION

University of Illinois at Chicago, Chicago, Illinois USA

Ph.D., Bioinformatics, August 2004
M.S., Mathematics & Computer Science, May 2002
M.S., Chemistry, Dec 2000

Peking University, Beijing, P.R. China

B.A., Chemistry, June 1997

PROFESSIONAL EXPERIENCE

Florida State University, 2007/8.
Associate Professor, Department of Statistics.

Harvard University, 2004/11 – 2007/7.
Postdoc fellow, Department of Statistics.

RESEARCH INTERESTS

Bioinformatics, Computational Biology, Data Mining, Text Mining, Computational Statistics.

PEER-REVIEWED JOURNAL PUBLICATIONS

IF: Impact factor; *: corresponding author; †: equal contributions.

1. Yan Li, Albert Steppi, Yidong Zhou, Feng Mao, Philip Craig Miller, Max M. He, Tingting Zhao, Qiang Sun, Jinfeng Zhang*. Tumoral expression of drug and xenobiotic metabolizing enzymes in breast cancer patients of different ethnicities with implications to personalized medicine. *Scientific Reports*, accepted.
2. Kaixian Yu*, Qing-Xiang Amy Sang, Pei-Yau Lung, Winston Tan, Ty Lively, Cedric Sheffield, Mayassa Bou Dargham, Jun S. Liu*, Jinfeng Zhang*. Personalized chemotherapy selection for breast cancer using gene expression profiles. *Scientific Reports*, 2017 3;7:43294. doi: 10.1038/srep43294.

3. Y Shi*, A Steppi, Y Cao, J Wang, MM He, L Li*, J Zhang*. Integrative comparison of mRNA expression patterns in breast cancers from Caucasian and Asian Americans with implications for precision medicine, *Cancer Research* 2017, 77(2):423-433. .
4. P Zou, L Liu, L Zheng, K Payne, M H. Manjili, M O. Idowu, J Zhang, E M Schmelz and Z Cheng. Coordinated upregulation of mitochondrial biogenesis and turnover in breast cancer cells: the role of dynamin related protein-1 and implication for breast cancer treatment. *Oxidative Medicine and Cellular Longevity*, 2016, 4085727.
5. K Tang, J Zhang, J Liang. Distance-Guided Forward and Backward Chain-Growth Monte Carlo Method for Conformational Sampling and Structural Prediction of Antibody CDR-H3 Loops. *J Chem Theory Comput* 2017, 13(1):380-388.
6. Ke Tang, Samuel Wong, Jun S. Liu, Jinfeng Zhang, Jie Liang, Conformational sampling and structure prediction of multiple interacting loops in soluble and beta-barrel membrane proteins using multi-loop distance-guided chain-growth Monte Carlo method. *Bioinformatics*, (2015) 31 (16): 2646-2652.
7. Daniel L. Vera, Thelma F. Madzima, Jonathan D. Labonne, Mohammad P. Alam, Gregg G. Hoffman, S.B. Girimurugan, Jinfeng Zhang, Karen M. McGinnis, Jonathan H. Dennis and Hank W. Bass. *The Plant Cell*, 2014, 26(10):3883-93. IF: 10.66.
8. G He, A Steppi, J Laborde, A Srivastava, P Zhao, J Zhang*, (2014) RASS: A webserver for RNA alignment in the joint sequence-structure space. *Nucleic Acids Research*, W377-81. IF: 8.38.
9. K Tang, J Zhang*, J Liang*. (2014) Fast Protein Loop Sampling and Structure Prediction Using Distance-Guided Sequential Chain-Growth Monte Carlo Method. *PLoS Computational Biology*, 10(4): e1003539. doi:10.1371/journal.pcbi.1003539. IF: 4.87.
10. Sexton, B.S., Avey, D., Druliner, B. R., Fincher, J. A., Grau, D. J., Borowsky, M. L., Gupta, S., Girimurugan, S., Chicken, E., Zhang, J., Noble, W.S., Zhu, F., Kingston, R. E., and Dennis, J. H. (2013) The spring-loaded genome: Nucleosome redistributions are widespread, transient, and DNA-directed. *Genome Research*, 10.1101/gr.160150.113. IF: 14.397.
11. Paul A. Stewart, Jennifer Luks, Mark D. Roycik, Qing-Xiang Amy Sang*, and Jinfeng Zhang* (2013) Differentially Expressed Transcripts and Dysregulated Signaling Pathways and Networks in African American Breast Cancer. *PLoS One*, 8(12): e82460. IF: 3.73.
12. Wei Wu, Anuj Srivastava, Jose Laborde, Jinfeng Zhang*, An Efficient Multiple Protein Structure Comparison Method and its Application to Structure Clustering and Outlier Detection, *IEEE, BIBM*, 2013, 69-73.

13. Jose Laborde, Daniel Robinson, Anuj Srivastava, Eric Klassen and Jinfeng Zhang*, RNA global alignment in the joint sequence-structure space using Elastic Shape Analysis, *Nucl. Acids Res.* (2013) 41 (11): e114. doi: 10.1093/nar/gkt187. IF: 8.278.
14. Rajesh Chowdhary, Jinfeng Zhang, Sin Lam Tan, Daniel Osborne, Vladimir B Bajic, Jun S Liu, PIMiner: a web tool for extraction of protein interactions from biomedical literature, *IJDMB*, (2013) 7 (4): 450-462. IF: 0.39.
15. Leif Ellingson, Jinfeng Zhang*, Protein Surface Matching by Combining Local and Global Geometric Information , *PLoS ONE*, 2012, 7(7): e40540. IF: 4.41.
16. Tingting Zhao, Lindsey Bell, Mark W. Horner, John Sulik, Jinfeng Zhang, Consumer Responses towards Home Energy Financial Incentives: A Survey-Based Study, *Energy policy*, (2012), 47:291-297. IF: 2.44.
17. Rajesh Chowdhary, Sin Lam Tan, Jinfeng Zhang, Vladimir B. Bajic and Jun S. Liu, Context-specific Protein Network Miner - an online system for exploring context-specific protein interaction networks from the literature *PLoS One*, 2012, 7(4): e34480., IF: 4.41.
18. Sentil Balaji, Charles McClendon, Rajesh Chowdhary, Jun S Liu and Jinfeng Zhang*, IMID: Integrated molecular interaction database, *Bioinformatics*, 2012, 28 (5): 747-749. IF: 4.93
19. Rajesh Chowdhary*, Jinfeng Zhang*, Sin Lam Tan, Daniel Osborne, Vladimir B Bajic, Jun S Liu*, PIMiner: a web tool for extraction of protein interactions from biomedical literature, *IJDMB*, 2012, accepted. IF: 0.68
20. Tyrone Ryba, Ichiro Hiratani, Dana Battaglia, Micheal Kulik, Jinfeng Zhang, Stephen Dalton, and David M Gilbert. Replication timing: a fingerprint for cell identity and pluripotency, *PLoS Computational Biology*, 2011, 7(10): e1002225. IF: 5.76
21. Wei Liu, Anuj Srivastava*, Jinfeng Zhang*. A mathematical framework for protein structure comparison, *PLoS Computational Biology*, 2011, 7(2), e1001075. IF: 5.76
22. L Bell, R Chowdhary, JS Liu, X Niu, J Zhang*. Integrated bio-entity network: a system for biological knowledge discovery. *PLoS ONE*, 2011, 6(6), e21474. IF: 4.41
23. Zhiyong Cheng, Jinfeng Zhang, David P Ballou, Charles H Williams. On the reactivity of thioredoxin as a disulfide oxidoreductase, *Chemical Review*, 2011, 111(9), 5768-5783. IF: 33.03
24. Tyrone Ryba, Ichiro Hiratani, Junjie Lu, Mari Itoh, Michael Kulik, Jinfeng Zhang, Stephen Dalton, David M. Gilbert. Evolutionarily conserved replication timing profiles distinguish closely related cell types and predict long range chromatin interactions, *Genome Research*, 2010, 20(6):761-70. IF: 13.59
25. Rajesh Chowdhary[†], Jinfeng Zhang[†], Jun S Liu. Bayesian Inference of Protein-protein Interactions from Biological Literature , *Bioinformatics*, 2009, 25(12), 1536-1542. IF: 4.93

26. Jinfeng Zhang, Sam C. Kou, Jun S. Liu, Polymer structure simulation and optimization via a fragment re-growth Monte Carlo. *J. Chem. Phys.* 2007, 126, 225101. IF: 2.93
27. Jinfeng Zhang, Ming Lin, Rong Chen, Jie Liang, Jun S. Liu, Monte Carlo sampling of near-native structures of proteins with applications. *Proteins*, 2007, 66, 61-68. IF: 2.81
28. Jinfeng Zhang, Jun S. Liu, On side-chain conformational entropy of proteins. *PLoS Computational Biology*, 2006, 2(12): e168. doi:10.1371/journal.pcbi.0020168. IF: 5.76
29. Jinfeng Zhang, Rong Chen, Jie Liang, Empirical potential function for simplified protein models: combining contact and local sequence-structure descriptors. *Proteins* 2006, 63, 949-960. IF: 2.81
30. Jinfeng Zhang, Yu Chen, Rong Chen, Jie Liang, Importance of chirality and reduced flexibility of protein side chains: A study with square and tetrahedral lattice models. *J. Chem. Phys.* 2004, 121, 592-603. IF: 2.93
31. Jinfeng Zhang, Rong Chen, Chao Tang, Jie Liang, Origin of scaling behavior of protein packing density: A Sequential Monte Carlo study of compact long chain polymers. *J. Chem. Phys.* 2003, 118, 13, 6102-6109. IF: 2.93
32. Jie Liang, Jinfeng Zhang, Rong Chen, Statistical geometry of packing defects of lattice chain polymer from enumeration and sequential Monte Carlo method. *J. Chem. Phys.* 2002, 117, 3511-3521. IF: 2.93

PEER-REVIEWED CONFERENCE PAPERS

AR: acceptance rate; *: corresponding author.

1. Chi Zhang, Rajesh Chowdhary, Jinfeng Zhang, Biological pathway discovery through text mining and data integration, *IEEE-EMBS*, 2012, accepted.
2. Shreyas Karnik, Sin Lam Tan, Bess Berg, Ingrid Glurich, Humberto J Vidaillet, C. David Page, Jinfeng Zhang, Rajesh Chowdhary, Predicting Atrial Fibrillation and Flutter using Electronic Health Records, *IEEE-EMBS*, 2012, accepted.
3. Jose Laborde, Anuj Srivastava*, Jinfeng Zhang*. Structure-based RNA function prediction using elastic shape analysis, *IEEE-BIBM*, 2011, 16-21. AR: 19%
4. Lindsey Bell, Jinfeng Zhang*, Xufeng Niu. Mixture of logistic models and an ensemble approach for extracting protein-protein interactions. *ACM-BCB*, 371-375, (2011). AR: 30%
5. Leif Ellingson, Jinfeng Zhang*. An efficient algorithm for matching protein binding sites for protein function prediction. *ACM-BCB*, 289-293, (2011). AR: 30%
6. Yue Li, Gary Tyson, Jinfeng Zhang*. Effect of sequences on the shape of protein energy landscapes, *ACM-BCB*, 35-42, (2010). AR: 30%

7. Wei Liu, Anuj Srivastava*, Jinfeng Zhang*. Protein structure alignment using elastic shape analysis, ACM-BCB, 62-70, (2010). AR: 30%

PATENTS

1. Automatic extraction of Bio-entity relationships from literature, USPTO, 8,886,522, Jinfeng Zhang, 2014. USPTO No. 9,542,528, 2017.
2. Fingerprint for cell identity and pluripotency, USPTO, 9,245,090, David Gilbert, Tyrone Ryba, Jinfeng Zhang, 2016.
3. Chemotherapy regimen selection, Jinfeng Zhang, Kaixian Yu, Amy Sang, USPTO, 61/950,498, pending.
4. Detection and Segmentation of Differently Expressed Genetic And Epigenetic Features from Genome Wide Measurements, USPTO, 14/216,416, Jinfeng Zhang, Sentil Girimurugan, Jonathan Dennis, Pending.

BOOK CHAPTERS

1. Jie Liang, Sema Kachalo, Xiang Li, Zheng Ouyang, Yan-Yuan Tseng, Jinfeng Zhang. Geometric structures of proteins for understanding folding, discriminating natives and predicting biochemical functions . The World Is a Jigsaw (Ed. Rien van de Weygaert), 2009, Springer.

PRESENTATIONS AND TALKS

1. Elastic shape analysis for protein structure comparison. Institute of Molecular Biophysics, FSU, 2011.
2. A mathematical framework for protein structure comparison. University of Georgia, Department of Biochemistry and Molecular Biology, 2011.
3. An ensemble approach for extracting protein-protein interaction information from literature, Lindey Bell, Xufeng Niu, Jinfeng Zhang, 2011, ACM-BCB, Chicago.
4. Integrated bio-entity network and its applications in automatic knowledge discovery, school of medicine, FSU, 2011.
5. A mathematical framework for protein structure comparison, Department of Bioengineering, UIC, 2011.
6. A fragment closure method for protein structure simulations, Kevin Bartz, Daniel Fernandez, Sam Wong, Sam Kou, Jun Liu, Jinfeng Zhang. CASP9 2010.
7. Jinfeng Zhang, Yue Li, Sam C. Kou, Gary Tyson, Jun S. Liu, FRESS: an Efficient Monte Carlo Method for Biopolymer Structure Simulation, Biophysical Journal, Volume 96, Issue 3, Supplement 1, February 2009, Page 653a

8. Automatic extraction of protein-protein interaction information from literature, 2009, Harbin Institute of Technology.
9. Novel Monte Carlo method for protein structure analysis, 2009, Department of Statistics, University of Florida.

PROFESSIONAL AFFILIATIONS

American Statistical Association 2007 -
Biophysical Society, 2002 -
American Chemical Society, 1998 - 2000

FUNDING

As PI:

Collaborative Research: Mathematical Framework for Biomolecules: From Protein to RNA to Chromosomes, NIH 1R01GM126558, \$1,542,978, 07/2017-06/2022. Co-PIs: Dr. Jie Liang, University of Illinois at Chicago; Dr. Anuj Srivastava, Florida State University; Dr. Wei Wu, Florida State University.

An Innovative Approach for Peer Review, NIH SBIR, \$225,000. 08/2017-01/2018.

A platform for the extraction, integration and mining of biological information, NSF STTR, #1416949, \$225,000. 07/01/2014 - 06/30/2015.

Elastic shape analysis for protein structure comparison, NIH/NIGMS, 1R21GM101552, \$381,206, 07/01/2012 -04/30/2014. Co-PI: Dr. Anuj Srivastava, Department of Statistics, FSU.

GAP award, FSU, 2014, \$50,000.

COFRS, FSU, \$16,000, 2010.

FYAP, FSU, \$16,000, 2008.

As Co- PI:

Nuclease Profiling as an Integrative Resource for Maize Epigenomics, NSF PGRP, \$ 2,133,825, 08/2015 – 07/2019, Lead PI: HW Bass, FSU.

Chromatin structural changes linking drugs of abuse with HIV reactivation, NIH 1R01DA033775-01, \$1,769,229, 04/01/2012 – 03/31/2017. PI: Dr. Jonathan Dennis, Department of Biology, FSU.