

Curriculum Vitae

Tao Jiang

Date of Birth: May 6, 1963.

Citizenship: Canadian. Permanent resident of USA.

Work Address:

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Educational Background:

Ph.D. Computer Science (November, 1988)
University of Minnesota, Twin Cities
B.S. Computer Science (August, 1984)
University of Science and Technology of China, Hefei, P.R.China

Research Interest:

Design and Analysis of Algorithms (especially approximation algorithms and average-case analysis), Computational Molecular Biology (especially sequence annotation and comparison, comparative genomics, haplotype inference, and pedigree analysis), Information Gathering and Retrieval, Computational Complexity in Automata Theory, and Machine Learning.

Employment History:

Presidential Chair Professor, Dept. of Computer Science, Univ. of California, Riverside, CA, July 2007 - June 2010.
Professor, Dept. of Computer Science, Univ. of California, Riverside, CA, July 1999 - .
Cheung Kong (Changjiang) Visiting Prof., Dept. of Computer Science, Tsinghua University, Beijing, China, Feb. 2006 - .
Visiting Prof., Dept. of Computer Science, Tsinghua University, Beijing, China, August 2003 - 2006.
Principal Scientist, Shanghai Center for Bioinformation Technology, Shanghai, China, August 2002 - .
Visiting Professor, Center for Theoretical Biology, Beijing University, Beijing, China, Sept. 2002 - 2005.
Faculty member, Genetics Graduate Program, Univ. of California, Riverside, CA, July 2000 - .

Cooperating faculty, Dept. of Elec. Eng., Univ. of California, Riverside, CA, July 2001 - .
Professor, Dept. of Computing and Software, McMaster Univ., Hamilton, Ontario,
Canada, July 1998 - June 2001.
Visiting Professor, Dept. of Computer Science, City Univ. of Hong Kong, May - August, 1999.
Associate Prof., Dept. of Comp. Sci. and Syst., McMaster Univ., July 1993 - July 1998.
Associate Member, Dept. of Elec. and Comp. Eng., McMaster Univ., Mar. 1990 - August 2001.
Adjunct Professor, Dept. of Comp. Sci., Beijing Univ. of Aeronautics and Astronautics,
Beijing, China, Aug. 1995 - 2007.
Visiting Associate Professor, Dept. of Comp. Sci. and Eng., University of Washington,
Sept. 1995 - May 1996.
Assistant Prof., Dept. of Comp. Sci. and Syst., McMaster Univ., Jan. 1989 - July 1993.
Research and Teaching Assistants, Dept. of Comp. Sci., Univ. of Minnesota,
Sept. 1985 - Dec. 1988.

Courses Taught:

Introduction to Computer Programming, Data Structures and Algorithms, Automata Theory and Formal Languages, Design and Analysis of Algorithms, Algorithmic Techniques in Computational Biology, Discrete Mathematics, Theory of Computation, Computer Systems and Architecture.

Supervisoryships:

I have supervised seven postdocs, ten Ph.D's, three M.Eng's, and nine M.Sc's.

Professional Activities:

Program committee member of many international conferences and workshops including ICYCS'93, COCOON'95,97,99-01, IEEE FOCS'97, ISAAC'98,01,03,09, RECOMB'99,04,05,08,09, CPM'99,02,06,08, IEEE BIBE'01,04, ICS'02, HiPC BCB'02, CIAA'03, IEEE CSB'03,04,06,07, IEEE ICTAI'03, APPROX'00, ICALP'04, FCT'05, ISMB'05-09, RECOMB-CG'06-08, AAIM'06, TAMC'07, APBC'07, etc.
Program committee co-chair of COCOON'97 and APBC'06, and organizing committee co-chair of IEEE FOCS'2000.
Guest editor for *Theoretical Computer Science: Special Issue for COCOON'97*, 1997.
Guest editor for *International Journal of Foundations of Computer Science: Special Issue in Algorithmic Aspects of Computational Biology*, 1995.
Editorial board, *International Journal of Foundations of Computer Science (IJFCS)*, 1999 - 2005.
Editorial board, *Journal of Computer Science and Technology (JCST)*, 2000 - .
Editorial board, *Journal of Combinatorial Optimization (JOCO)*, 2000 - .
Editorial board, *BMC Bioinformatics*, 2001 - .
Editorial board, *Journal Bioinformatics and Computational Biology (JBCB)*, 2002 - .
Editorial board, *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, 2004 - .
Editorial board, *Algorithmica*, 2004 - .
Editorial board, *Journal of Computer and System Sciences (JCSS)*, 2007 - 08.
Area editor, *Journal of Computer and System Sciences (JCSS)*, 2008 - .

Selection panel member for Ontario Graduate Scholarship (OGS) program, 1996-98.
Member of Online Science Advisory Board (SAB) on new technologies in research and clinical applications, 1997 - .
NSF DBI Computational Biology Review Panelist, 1999.
NSF CISE Major Research Instrumentation (MRI) Review Panelist, 2000.
NSF CISE Advanced Computational Research (ACR) Algorithms Review Panelist, 2002.
NSF CISE Research Infrastructure Review Panelist, 2003.
NSF CISE CCR Theory of Computing Career Review Panelist, 2003.
NSF CISE CCF Theory of Computing Review Panelist, 2004.
University of California Life Science Informatics (LSI) Program Task Force, 2000-02.
Reviewers for various scientific journals and funding agencies.
Member of ACM, SIGACT, IEEE (senior member grade), and Computer Society.

Honors:

Fellow of the Association for Computing Machinery (ACM), 2007 - .
Fellow of the American Association for the Advancement of Science (AAAS), 2006 - .
The Best Paper Award, *15th International Conference on Genome Informatics (GIW)*, Yokohama, Japan, Dec., 2004.
The Best Poster Award, *7th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Berlin, Germany, 2003.
Japan Society for the Promotion of Science Research Fellowship, 1996.
Guo Muo-Ruo Prize, University of Science and Technology of China, 1982.

Research Grants:

1. "Identifying Microorganisms involved in Human Health and Disease Processes" (PI: J. Borneman; co-PIs: M. Chrobak, X. Cui, D. Jeske, and T. Jiang), \$1.42M (my appropriation is about \$300K), 7/2008 - 6/2012, *NIH/NIAID Research Grant (R01) in Biodata Management and Analysis (BMDA)*.
2. "Development of a High Throughput Assay for Transcription Factor Binding Sites" (PI: F.M. Sladek; co-PI: T. Jiang), 11/2007 - 12/2008, \$50k, *Institute of Integrative Genome Biology, UCR*.
3. "III-CXT: Collaborative Research: A High-Throughput Approach to the Assignment of Orthologous Genes Based on Genome Rearrangement" (PI: T. Jiang; co-PI: L. Zhang/Virginia Tech), 9/2007 - 8/2010, \$450K (UCR appropriation: \$260k), *NSF IIS Research Grant*.
4. "Efficient Analysis of SNPs and Haplotypes with Applications in Gene Mapping" (PI: J. Li/CWRU; co-PIs: T. Chen/USC and T. Jiang), \$1.2M (UCR appropriation: \$410K), 3/2006 - 2/2009, *NIH/NLM Research Grant in Biomedical Informatics and Bioinformatics (R01)*.
5. "IGERT in Chemical Genomics: Forging Complementation at the Interface of Chemistry, Engineering, Computational Sciences and Cell Biology" (PI: J. Bailey-Serres; co-PIs: T. Jiang, N. Raikhel, M. Pirrung, and J. Schultz), \$2.9M, 2005-2010, *NSF Integrative Graduate Education and Research Traineeship Program (IGERT)*.

6. "Bioinformatics Research in Drug Target Identification" (PI: T. Jiang; co-PI: Y. Zhong), 3 million RMB (\approx \$400k), 2003-08, a subproject of *Chinese National Key Project for Basic Research (973 Project)*.
7. "Algorithmic Problems in Haplotyping, Oligonucleotide Fingerprinting, and NMR Peak Assignment", \$200k, 2003-07, *NSF CCF Research Grant*.
8. "Coupling Expressed Sequences and Bacterial Artificial Chromosome Resources to Access the Barley Genome" (PI: T. Close; co-PIs: T. Jiang and S. Lonardi), \$2.4M, 2003-07, *NSF Plant Genome Project*.
9. "A Comparative Genomics Approach to the Search for Operons in Microbial Genomes", \$243,750, 2002-05, *DOE Genomics:GTL Program*, subcontract from Sandia National Labs.
10. "Analysis of Microbial Communities Using a DNA Array Approach" (PI: J. Borneman; co-PIs: M. Chrobak, D. Crowley, T. Jiang, and J. Press), \$584,907, 2002-06, *NSF DBI Research Grant*.
11. "ITR/ACS: Computational Techniques for Applied Bioinformatics" (co-PIs: M. Clegg and M. Li), \$785k, 2000-04, *NSF Information Technology Research (ITR) Grant*.
12. "Efficient Algorithms for Molecular Sequences, Evolutionary Trees, and Physical Maps", \$267k, 2000-04, *NSF CCR Research Grant*.
13. "Life Sciences Informatics Program Opportunity Award", \$15k, 2000-01, *UC Life Science Informatics*.
14. "Average-Case Analysis by the Incompressibility Method", \$1300, 2000-01, *UCR Academic Senate Research Funds*.
15. "Approximation Algorithms for Sequences, Trees and Maps, and Average-Case Analysis by Incompressibility", \$42k/year, 2000-03, *NSERC Research Grant*.
16. "Computational Techniques for Industrial Bioinformatics" (with M. LI, et al.), \$120k/year, 1998-2000, *Communication and Information Technology Ontario (CITO) Research Grant*.
17. "Algorithms for Some Combinatorial Problems Arising in Computational Biology" (with L. WANG and M. Li), \$322k (HKD), 1997, *Hong Kong UGC Research Grant*.
18. "Computer Equipment for a Computational Molecular Biology Laboratory" (with S. Qiao and W.F.S. Smyth), \$65.5k, 1997, *NSERC Equipment Grant*.
19. "Approximation Algorithms for Sequences, Average-Case Analysis, and State Complexity of Two-Way Finite Automata", \$33.3k/year, 1995-99, *NSERC Research Grant*.
20. "Computational Issues in Alignment and Sequencing" (with D. WOOD, et al.), \$100k/year, 1994-1997, *MRC/NSERC Canadian Genome Analysis and Technology Research Grant*.
21. "Efficient Algorithms and Complexity Theory for Biological Sequences, Shortest Common Supersequences, and Succinct Finite Automata", \$26k/year, 1992-95, *NSERC Research Grant*.
22. "Expansion of Parallel Computing System" (with S. QIAO), \$36.7k, 1994, *NSERC Equipment Grant*.
23. "Transputer Multiprocessor System" (with S. QIAO), \$40k, 1991, *NSERC Equipment Grant*.

24. "Networks of Finite-State Machines: Algorithms, Simulation, Complexity, and Synchronization", \$20k/year, 1990-92, *NSERC Operating Grant*.
25. "Iterative/Cellular Arrays: Simulations, Algorithms and Complexity", \$19k, 1989-90, *McMaster University Junior Faculty Operating and Equipment Grant*.

Invited Lectures and Seminars in Recent Years:

1. Approximation Algorithms for Multiple Sequence Alignment
 - (a) 1st World Congress on Medicine, Health and Biotechnology, Austin, TX, April, 1994
 - (b) DIMACS Workshop on Sequence Alignment, Princeton, NJ, Nov 12-14, 1994
 - (c) University of Washington, CSE Dept, April, 1996
 - (d) Univ of Tokyo, Human Genome Center, July, 1996
 - (e) University of Waterloo, Jan, 1999
 - (f) UC Riverside, Feb, 1999
 - (g) University of Arizona, April, 1999
 - (h) Beijing Workshop on Comp Biol, June 29, 1999
2. Algorithmic Approaches to Multiple Complete Digest Mapping
 - (a) 2nd Sandia Workshop on Computational Biology, Feb, 1996
 - (b) University of Washington, Industrial Affiliates Meeting, March, 1996
 - (c) DIMACS Workshop on Graph Algorithms, July 14-15, 1999
3. Average-Case Analysis by the Incompressibility Method
 - (a) Gunma University, Japan, July, 1996
 - (b) Tokyo Institute of Technology, July, 1996
 - (c) Providence University, Taiwan, Dec, 1998
 - (d) University of Arizona, April, 1999
 - (e) Harvey Mudd College, CA, Dec. 2, 1999
 - (f) UCSB, CS Dept, March 1, 2000
 - (g) USC, CS Dept, March 23, 2000
 - (h) UCR, CSE Dept Colloquium, Nov. 20, 2000
 - (i) Kyoto Univ, Applied Math Dept, July 1, 2002
 - (j) Tokyo Denki Univ, Math Sci, July 8, 2002
 - (k) Summer School on Basic Studies in Computer Science (BASICS), MoGan Mountain, China, July 14, 2002
 - (l) Univ of Milano - Bicocca, Dept of Comp Sci, July 15, 2003
 - (m) Tsinghua University, June, 2005
4. A Gibbs Sampling Approach to Drug Target Search
 - (a) DIMACS Workshop on Discrete Mathematical Problems with Medical Applications, Rutgers, Dec. 8-10, 1999
 - (b) UCR College of Engineering Industry Day, 2000
5. Approximation of Shortest Common Superstrings

- (a) Penn State University, 1993
 - (b) University of Washington, CSE Dept, May, 1996
 - (c) Gunma University, Japan, June, 1996
 - (d) Tohoku University, July, 1996
 - (e) University of Tokyo, July, 1996
6. Efficient Gathering of Information on the Internet
- (a) Gunma University, Japan, June, 1996
 - (b) 1st Tianyuan Meeting in Mathematics, Berkeley, 1997
7. Quartet Cleaning: A New Technique for Reconstructing Evolutionary Trees
- (a) City Univ of HK, July, 1999
 - (b) CMS Winter Meeting, Dec. 11-13, 1999, Montreal, Quebec
 - (c) Dept of Statistics, UCR, Feb. 29, 2000
8. Matching and Comparing Sequences in Molecular Biology
- (a) 1st COCOON (plenary talk), Xian, China, August, 1995
 - (b) International Computer Symposium (keynote speech), Taiwan, Dec. 1998
 - (c) Dept of Physics, UCR, Feb. 17, 2000
 - (d) Institute of Information Sciences, Academia Sinica, Taipei, Taiwan, Aug. 8-10, 2001
 - (e) Beijing Univ of Aeronautics and Astronautics, CS Dept, July 17, 2002
9. Comparing Annotated Sequences
- (a) MSI, San Diego, Sept. 19, 2000
 - (b) CWRU Mini Symposium on Computational Genetics, Oct. 20, 2000
 - (c) USC, Dept of Math, Oct. 26, 2000
 - (d) Celera AgGen, Davis, CA, May 2, 2001
10. Searching for Promoters in the Human Genome
- (a) Bioengineering Center, Industrial Technology Research Institute, Taiwan, Aug 7, 2001
 - (b) Bioinformatics Forum, National Taiwan Univ, Taiwan, Aug. 11, 2001
 - (c) Genomics and Bioinformatics Institute, Chinese Academy of Sciences, Hangzhou, China, August 14, 2001
11. Probe Selection Algorithm with Applications in the Analysis of Microbial Communities
- (a) Post-Genome Knowledge Discovery Workshop on Sequence and Gene Expression Analysis, Singapore, Jan 17, 2002
 - (b) Kyoto University, Bioinformatics Center, July 1, 2002
 - (c) Genomics and Bioinformatics Institute, Chinese Academy of Sciences, Hangzhou, China, July 15, 2002
 - (d) Society of Chinese Bioscientists in America Annual Meeting, UC Irvine, Oct. 19, 2002
12. Identifying Transcription Factor Binding Sites through Markov Chain Optimization
- (a) UCSD, Dept of Computer Science, May 8, 2002
 - (b) Kyoto Univ, Bioinformatics Center, July 1, 2002
 - (c) Univ of Tokyo, Human Genome Center, July 9, 2002

- (d) Tsinghua Univ, CS Dept, Beijing, China, July 16, 2002
 - (e) Tsinghua Univ, Bioinformatics Institute, Beijing China, July 17, 2002
 - (f) Fudan Univ, Bioinformatics Center, Shanghai, China, July 18, 2002
13. Efficient Haplotyping Algorithms on Pedigrees and Applications
- (a) Univ of Milano - Bicocca, Dept of Comp Sci, Italy, July 16, 2003
 - (b) Fudan University, College of Life Sciences, Shanghai, China, August 22, 2003
 - (c) Fudan International Bioinformatics Workshop, Dec. 18-19, 2003
 - (d) School of Comp Sci, Harbin Institute of Technology, Dec. 27, 2003
 - (e) Arizona State Univ, CS Dept seminar, March 23, 2004
 - (f) CS Dept, Univ of Illinois, Chicago, May 3, 2004
 - (g) UC Riverside, Genetics Program, May 10, 2004
 - (h) Math Dept, Tsinghua Univ, July, 2004
 - (i) CS Dept, Tsinghua Univ, July, 2004
 - (j) Inst. for Computing Tech., Academia Sinica, July, 2004
 - (k) Dept of Biological Sciences, University of Nevada at Las Vegas, Feb. 18, 2005
 - (l) Workshop on New Horizons in Computing (NHC) – Recent Trends in Theoretical Computer Science, Feb 28 - Mar 3, 2005, Kyoto, Japan
 - (m) Dept of Computer Science, Tamkang University, Taiwan, May 24, 2006
14. Computing Phylogenetic Roots of Graphs
- (a) SIAM Discrete Mathematics Conference, August 11-14, 2002, San Diego. (The talk had to be given by my former postdoc Dr. Guohui Lin due to a last minute time conflict.)
15. A Class of Edit Kernels for SVMs to Predict Translation Initiation Sites in Eukaryotic mRNAs
- (a) Beijing University Bioinformatics Center, July 2004
 - (b) Shanghai Center for Bioinformatics Technology, April 2005
 - (c) Dept of Computer Science, Tamkang University, Taiwan, May 23, 2006
16. Computing the Assignment of Orthologous Genes via Genome Rearrangement
- (a) Keynote speech at *Third Asia-Pacific Bioinformatics Conference (APBC2005)*, Jan 17-21, 2005, Singapore
 - (b) Dept of Computer Science, Tsinghua University, March 3, 2005
 - (c) Dept of Computer Science, University of Texas at Dallas, May 6, 2005
 - (d) 2nd Annual Conference on Computation and Logic (ACCL'05), Kunming, China, 17-20 May, 2005.
 - (e) 3rd Annual Bioinformatics Workshop, Jilin University, Changchun, China, July 5-7, 2005
 - (f) Eastern Forum of Science and Technology: Advances in Computational Biology, Shanghai, July 2, 2005
 - (g) Dept of Computer Science, University of Science and Technology of China, Hefei, China, Aug 24, 2005
 - (h) Dept of Computer Science, University of Milan - Bicocca, Italy, April 6, 2006
 - (i) Invited lecture at *Workshop on Molecular Evolution*, Shanghai, China, April 19-21, 2006.
 - (j) Dept of Computer Science, Tamkang University, Taiwan, May 23, 2006
 - (k) Institute of Information, Academia Sinica, Taipei, Taiwan, May 25, 2006

- (l) Dept of Computer Science, National Taiwan University, Taipei, Taiwan, May 26, 2006
 - (m) Keynote speech at *Workshop on BioAlgorithmics*, July 12-15, 2006, Singapore
 - (n) Invited speech at the *4th RECOMB Comparative Genomics Satellite Workshop*, Montreal, Canada, September, 24-26, 2006
 - (o) Dept of Computer Science, National Tsinghua University, Hsinchu, Taiwan, Dec. 7, 2006
 - (p) Joint Program in Computational Biology, Carnegie Mellon University, Feb. 9, 2007
 - (q) Keynote speech at the 1st *IEEE International Conference on Bioinformatics and Biomedical Engineering (ICBBE)*, Wuhan, China, July 7-8, 2007. (declined due to logistics)
 - (r) Invited speech at the *18th Annual Symposium on Combinatorial Pattern Matching (CPM)*, July 9-11, 2007, London, Ontario, Canada.
17. An Improved Gibbs Sampling Method for Motif Discovery via Sequence Weighting
 - (a) Invited speech at the *3rd RECOMB Satellite Workshop in Regulatory Genomics*, July 17-18, 2006, Singapore
 - (b) Shanghai Center for Bioinformation Technology, Sept. 5, 2006
 - (c) Bioinformatics Institute, Tsinghua University, Sept. 14, 2006
 - (d) Chemical Genomics Program, UC Rievrside, Oct. 18, 2007
 - (e) Department of Clinical and Molecular Pharmacology, City of Hope, Oct. 22, 2007
 18. A Max-Flow Based Approach to Identify Protein Complexes Using Protein Interaction and Microarray Data
 - (a) Invited talk at Tsinghua-USC Workshop on Emerging Information Technologies, Los Angeles, CA, April 30 - May 2, 2008
 - (b) Frontiers in Bioinformatics and Systems Biology Colloquium, UCSD, Oct. 2, 2008
 19. Searching and Predicting Drug-like Compounds using Maximum Common Substructure
 - (a) Shanghai Center for Bioinformation Technology, Aug. 26, 2008
 - (b) Bioinformatics Division, TNLIST, Tsinghua University, Sept. 1, 2008.
 20. Introduction to Computational Biology and Genomics
 - (a) Tsinghua University, Dept. of Comp. Sci. grad student orientation, Sept. 2005
 - (b) Institute of Software, Chinese Academy of Sciences, Dec. 14, 2005
 - (c) St. John's University, Taipei, Taiwan, May 24, 2006

Journal Publications:

1. J. Xiao, L. Liu, L. Xia, and T. Jiang. Efficient algorithms for reconstructing zero-recombinant haplotypes on a pedigree based on fast elimination of redundant linear equations. *SIAM Journal on Computing*, to appear.
2. J. Xiao, L. Wang, X. Liu, and T. Jiang. An efficient voting algorithm for finding additive biclusters with random background. *Journal of Computational Biology (JCB)*, to appear.
3. L. Liu and T. Jiang. Linear-time reconstruction of zero-recombinant Mendelian inheritance on pedigrees without mating loops. *Journal of Combinatorial Optimization*, to appear.
4. X. Chen, L. Liu, Z. Liu and T. Jiang. On the minimum common integer partition problem. *ACM Transactions on Algorithms (TALG)*, accepted May 2008.

5. Y. Cao, A. Charasi, L.C. Cheng, T. Jiang, and T. Girke. ChemmineR: A compound mining framework for R. *Bioinformatics* 24(15): 1733-1734, 2008.
6. Z. Fu and T. Jiang. Clustering of main orthologs for multiple genomes. *Journal of Bioinformatics and Computational Biology (JBCB)* 6(3):573-84, 2008.
7. X. Chen, L. Guo, Z. Fan, and T. Jiang. W-AlignACE: An improved Gibbs sampling algorithm based on more accurate position weight matrices. *Bioinformatics* 24(9), pp. 1121-1128, 2008.
8. J. Li and T. Jiang. A survey on haplotyping algorithms for tightly linked markers. *Journal of Bioinformatics and Computational Biology (JBCB)* 6(1), pp. 241-259, 2008.
9. P. Bonizzoni, G. Della Vedova, R. Dondi, and T. Jiang. On the approximation of correlation clustering and consensus clustering. *Journal of Computer and System Sciences (JCSS)* 74(5), pp. 671-696, 2008.
10. A. Figueroa, A. Goldstein, T. Jiang, M. Kurowski, A. Lingas, and M. Persson. Approximate clustering of incomplete fingerprints. *Journal of Discrete Algorithms* 6(1), pp. 103-108, 2008.
11. Z. Fu, X. Chen, V. Vacic, P. Nan, Y. Zhong, and T. Jiang. MSOAR: A high-throughput ortholog assignment system based on genome rearrangement. *Journal of Computational Biology* 14(9), pp. 1160-1175, 2007.
12. Z. Fu and T. Jiang. Computing the breakpoint distance between partially ordered genomes. *Journal of Bioinformatics and Computational Biology (JBCB)* 5(5), pp. 1087-1101, 2007.
13. B. Lucier, T. Jiang, and M. Li. Average-case analysis of quicksort and binary insertion tree height using incompressibility. *Information Processing Letters (IPL)* 103(2), pp. 45-51, 2007.
14. L. Liu, X. Chen, J. Xiao, T. Jiang. Complexity and approximation of the minimum recombination haplotype configuration problem. *Theoretical Computer Science* 378, pp. 316-330, 2007.
15. Z. Liu, S.F. Yan, J.R. Walker, T.A. Zwingman, T. Jiang, J. Li, and Y. Zhou. Study of gene function based on spatial co-expression in a high-resolution mouse brain atlas. *BMC Systems Biology* 1:19, 2007.
16. C. Yang, E. Bolotin, T. Jiang, F.M. Sladek, and E. Martinez. Prevalence of the initiator over the TATA box in human and yeast genes and identification of DNA motifs enriched in human TATA-less core promoters. *Gene* 389, pp. 52-65, 2007.
17. W. Zhao, P. Zhang, and T. Jiang. A network flow approach to the minimum common integer partition problem. *Theoretical Computer Science* 369, pp. 456-462, 2006.
18. H. Li, X. Chen, and T. Jiang. A general framework for biclustering gene expression data. *Journal of Bioinformatics and Computational Biology (JBCB)* 4(4):911-923, 2006.
19. E. Bent, B. Yin, A. Figueroa, J. Ye, Q. Fu, Z. Liu, V. McDonald, D. Jeske, T. Jiang, and J. Borneman. Development of a 9,600-clone procedure for oligonucleotide fingerprinting of rRNA genes: utilization to identify soil bacterial rRNA genes that correlate in abundance with the development of avocado root rot. *Journal of Microbiological Methods* 67:171-180, 2006.
20. J. Zheng, J.T. Svensson, T.J. Close, T. Jiang, and S. Lonardi. OligoSpawn: a software tool for the design of overgo probes from large unigene datasets. *BMC Bioinformatics* 2006, 7:7.

21. H. Li, K. Zhang, and T. Jiang. Efficient and robust feature extraction by maximum margin criterion. *IEEE Transactions on Neural Networks* 17(1):157-65, 2006.
22. J. Li and T. Jiang. Haplotype-based linkage disequilibrium mapping via direct data mining. *Bioinformatics* 21(24):4384-4393, 2005.
23. X. Chen, J. Zheng, Z. Fu, P. Nan, Y. Zhong, S. Lonardi, and T. Jiang. Assignment of orthologous genes via genome rearrangement. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)* 2-4, pp. 302-315, 2005
24. Z. Liu, J. Borneman, and T. Jiang. A software system for gene sequence database construction based on fast approximate string matching. *International Journal of Bioinformatics Research and Applications* 1(3):273-291, 2005.
25. J. Li and T. Jiang. Computing the minimum recombinant haplotype configuration from incomplete genotype data on a pedigree by integer linear programming. *Journal of Computational Biology* special issue for RECOMB'04, 12(6):719-739, 2005.
26. H. Li and T. Jiang. A class of edit kernels for SVMs to predict translation initiation sites in Eukaryotic mRNAs. *Journal of Computational Biology* special issue for RECOMB'04, 12(6):702-718, 2005.
27. Z. Chen, G. Lin, R. Rizzi, J. Wen, D. Xu, Y. Xu., and T. Jiang. More reliable protein NMR peak assignment via improved 2-interval scheduling. *Journal of Computational Biology* 12-2, 129-146, 2005.
28. A. Figueroa, J. Borneman, and T. Jiang. Clustering binary fingerprint vectors with missing values for DNA array data analysis. *Journal of Computational Biology* 11-5, 887-901, 2004.
29. G. Lin and T. Jiang. A further improved approximation algorithm for breakpoint graph decomposition. *Journal of Combinatorial Optimization* 8-2, 2004, 183-194.
30. J. Zheng, T. Close, T. Jiang, and S. Lonardi. Efficient selection of unique and popular oligos for large EST databases. *Bioinformatics* 20, 2004, 2101-2112.
31. T. Jiang, G. Lin, B. Ma, and K. Zhang. The longest common subsequence problem for arc-annotated sequences. *Journal of Discrete Algorithms* 2-2, June 2004, 257-270 (invited).
32. X. Chen, Z. Su, P. Dam, B. Palenik, Y. Xu, and T. Jiang. Operon prediction by comparative genomics: an application to the *Synechococcus sp.* WH8102 genome. *Nucleic Acids Research* 32-7, 2147-2157, 2004.
33. P. Keraney, J. Badger, M. Li, J. Tsang, and T. Jiang. Selecting the branches for an evolutionary tree: a polynomial-time approximation scheme. *Journal of Algorithms* 51(1), 1-14, 2004.
34. L. Jia, M. Clegg, and T. Jiang. Evolutionary dynamics of the DNA-binding domains in putative R2R3-MYB genes identified from *Oryza sativa ssp. indica* and *japonica* genomes. *Plant Physiology* 134(2), 575-585, 2004.
35. Z. Chen, T. Jiang, and G. Lin. Computing phylogenetic roots with bounded degrees and errors. *SIAM Journal on Computing* 32-4, 864-879, 2003.

36. L. Jia, M. Clegg, and T. Jiang. Excess nonsynonymous substitutions suggest that positive selection episodes operated in the DNA-binding domain evolution of *Arabidopsis* R2R3-MYB genes. *Plant Molecular Biology* 52(3), 627-642, 2003.
37. G. Lin, D. Xu, Z. Chen, T. Jiang, J. Wen, and Y. Xu. Computational assignment of protein backbone NMR peaks by efficient bounding and filtering. *Journal of Bioinformatics and Computational Biology* 2-1, 387-410, 2003.
38. Z. Chen, G. Lin, T. Jiang, J. Wen, D. Xu, J. Xu, and Y. Xu. Approximation algorithms for NMR spectral peak assignment. *Theoretical Computer Science* 299(1-3), 211-229, 2003.
39. E. Bach, J. Boyar, L. Epstein, L. Favrholt, T. Jiang, K.S. Larsen, G. Lin, and R. van Stee. Tight bounds on the competitive ratio on accommodating sequences for the seat reservation problem. *Journal of Scheduling* 6, 131-147, 2003.
40. J. Li and T. Jiang. Efficient inference of haplotypes from genotypes on a pedigree. *Journal of Bioinformatics and Computational Biology* 1(1):41-69, 2003.
41. C. Vogl, J. Badger, P. Kearney, M. Li, M. Clegg, and T. Jiang. Probabilistic analysis indicates discordant gene trees in chloroplast evolution. *Journal of Molecular Evolution* 56(3):330-340, 2003.
42. Yaw-Ling Lin, Xiaoqiu Huang, T. Jiang, and Kun-Mao Chao. MAVG: Locating CpG islands in a genomic sequence. *Bioinformatics* 19-1, 151-152, 2003.
43. Kyle Ellrott, Julie Kasarjian, T. Jiang, and Junichi Ryu. RMsearch: a DNA recognition sequence search program. *BioTechniques* 33-6, 1322-1326, 2002.
44. Y.L. Lin, T. Jiang and K.M. Chao. Efficient algorithms for locating the length-constrained heaviest segments, with applications to biomolecular sequence analysis. *Journal of Computer and System Sciences* 65-3 (special issue on computational molecular biology), pp. 570-586, 2002.
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Submitted for Publication:

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2. L. Liu, Y. Wu, S. Lonardi, and T. Jiang. Efficient genome-wide tagSNP selection across populations via the linkage disequilibrium criterion. *Journal of Computational Biology (JCB)*, revised Aug. 2008.

Peer-Reviewed Conference Publications:

(Note: Polished forms of many of the following papers have appeared or will appear in journals listed above.)

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