

Curriculum Vitae

Tao Jiang

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 and Bioinformatics (especially sequence analysis, comparative genomics, haplotype inference, alternative splicing, etc.), Information Gathering and Retrieval, Computational Complexity in Automata Theory, and Machine Learning.

Employment History:

Distinguished Professor, Dept. of Computer Science, Univ. of California, Riverside, CA, July 2019 - .
Professor, Dept. of Computer Science, Univ. of California, Riverside, CA, July 1999 - June 2019.
Visiting Chair Prof., Beijing National Research Center for Information Science and Technology,
Tsinghua University, Beijing, China, June 2014 - .
Presidential Chair Professor, Dept. of Computer Science, Univ. of California, Riverside, CA, July 2007 -
June 2010.
Visiting Chair Prof., School of Information Science and Technology, Tsinghua University, Beijing, China,
May 2008 - May 2014.
Cheung Kong (Changjiang) Visiting Prof., Dept. of Computer Science, Tsinghua University, Beijing, China,
March 2006 - Feb. 2009.
Visiting Chair 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.

Supervisorship:

I have supervised nine postdocs, 24 Ph.D's (including six co-advised), three M.Eng's, and 11 M.Sc's.

Professional Activities:

Program committee member of many international conferences and workshops including ICYCS'93, COCOON'95,97,99-01, FOCS'97, ISAAC'98,01,03,09-10,12 RECOMB'99,04-05,08-11,14-23 IEEE BIBE'01,04, ICS'02, HiPC BCB'02, CIAA'03, CSB'03,04,06,07, IEEE ICTAI'03, APPROX'00, ICALP'04, FCT'05, ISMB'05-22, RECOMB-CG'06-08, AAIM'06, TAMC'07, SPIRE'10, ESA'2011, CPM'99,02,06,08, APBC'07,09,11, MFCS'13, etc.

Program committee co-chair of COCOON'97, APBC'06 and RECOMB-Seq'13, 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 - 2011.

Editorial board, *Journal of Combinatorial Optimization (JOCO)*, 2000 - .

Editorial advisory board, *BMC Bioinformatics*, 2001 - .

Editorial board, *Journal Bioinformatics and Computational Biology (JBCB)*, 2002 - 2015.

Editorial board, *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, 2004 - 2012.

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 - 2014.

Steering committee member, *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, 2009 - 2012.

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.

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, the *13th Asia Pacific Bioinformatics Conference (APBC)*, Hsinchu, Taiwan, Jan., 2015.

The Best Paper Award, the *9th LSS Computational Systems Bioinformatics Conference (CSB)*, Stanford, CA, August, 2010.

The Best Paper Award, the *19th International Conference on Genome Informatics (GIW)*, Gold Coast, Australia, Dec., 2008.

The Best Paper Award, the *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 Moruo Scholarship, University of Science and Technology of China, 1982.

Research Grants:

1. “RNA Regulatory Networks in Neuronal Cell Type Diversity and Function” (PI: C. Zhang; co-PIs: E. Au, N. Harrison and T. Jiang), \$3.07M (my appropriation is \$243K), 12/1/2021 - 11/30/2026, *NIH R01 Grant*.
2. “EAGER: Transcript-Based Differential Expression Analysis for Population Data Without Predefined Conditions” (PI: T. Jiang), \$200K, 9/2016 - 8/2019, *NSF IIS Research Grant*.
3. “Incorporation of Genetic Variation Data into Transcriptome” (PI: F. Sladek; co-PI: T. Jiang), \$150K, 9/2016 - 8/2018, *NIH NURSA NDSP Grant via Baylor College of Medicine*.

4. “Novel Bacteria Affect DNA Damage in Mice” (PI: J. Borneman; co-PIs: T. Jiang and D. McCole), \$73K, 7/2014 - 6/2015, *UCR Seed Grant*.
5. “Collaborative Research: ABI Innovation: Genome-Wide Inference of mRNA Isoforms and Abundance Estimation from Biased RNA-Seq Reads” (PI: T. Jiang; coPI: X. Xiao/UCLA), \$770K (UCR appropriation is about \$570K), 9/2013 - 8/2017, *NSF ABI Research Grant*.
6. “Dietary Effects on the Gut-Brain Axis” (PI: F. Sladek; co-PIs: J. Borneman, M. Curras-Collazo, T. Jiang, and C. Lytle), \$70K, 9/2013 - 6/2014, *UCR Seed Grant*.
7. “Nuclear Receptor DNA Binding in Human Physiology and Disease” (PI: F. Sladek; co-PI: T. Jiang), \$1.51M (my appropriation is about \$370K), 3/2012 - 6/2017, *NIH R01 Grant*.
8. “Multi-Point and Multi-Locus Analysis of Genomic Data”, \$167.2K, 8/1/2009 - 12/31/2012, subcontract from CWRU via an *NIH/NLM R01 Grant* with the same title.
9. “Nuclear Receptor Networks in Human Disease” (PI: F. Sladek; co-PI: T. Jiang), \$760K (my appropriation is about \$220K), 7/13/2009 - 4/30/2012, *NIH/NIMH Exploratory/Developmental (R21) Grant*.
10. “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 - 6/2013, *NIH/NIAID Research (R01) Grant*.
11. “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*.
12. “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 - 8/2011, \$450K (UCR appropriation: \$260K), *NSF IIS Research Grant*.
13. “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 - 3/13/2010, *NIH/NLM Research (R01) Grant in Biomedical Informatics and Bioinformatics*.
14. “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, 9/2005 - 8/2012, *NSF Integrative Graduate Education and Research Traineeship Program (IGERT)*.
15. “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)*.
16. “Algorithmic Problems in Haplotyping, Oligonucleotide Fingerprinting, and NMR Peak Assignment”, \$200K, 2003-07, *NSF CCF Research Grant*.
17. “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*.
18. “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.

19. "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*.
20. "ITR/ACS: Computational Techniques for Applied Bioinformatics" (co-PIs: M. Clegg and M. Li), \$785K, 2000-04, *NSF Information Technology Research (ITR) Grant (large)*.
21. "Efficient Algorithms for Molecular Sequences, Evolutionary Trees, and Physical Maps", \$267K, 2000-04, *NSF CCR Research Grant*.
22. "Life Sciences Informatics Program Opportunity Award", \$15K, 2000-01, *UC Life Science Informatics*.
23. "Average-Case Analysis by the Incompressibility Method", \$1300, 2000-01, *UCR Academic Senate Research Funds*.
24. "Approximation Algorithms for Sequences, Trees and Maps, and Average-Case Analysis by Incompressibility", \$42K/year, 2000-03, *NSERC Research Grant*.
25. "Computational Techniques for Industrial Bioinformatics" (with M. Li, et al.), \$120K/year, 1998-2000, *Communication and Information Technology Ontario (CITO) Research Grant*.
26. "Algorithms for Some Combinatorial Problems Arising in Computational Biology" (with L. WANG and M. Li), \$322K (HKD), 1997, *Hong Kong UGC Research Grant*.
27. "Computer Equipment for a Computational Molecular Biology Laboratory" (with S. Qiao and W.F.S. Smyth), \$65.5K, 1997, *NSERC Equipment Grant*.
28. "Approximation Algorithms for Sequences, Average-Case Analysis, and State Complexity of Two-Way Finite Automata", \$33.3K/year, 1995-99, *NSERC Research Grant*.
29. "Computational Issues in Alignment and Sequencing" (with D. WOOD, et al.), \$100K/year, 1994-1997, *MRC/NSERC Canadian Genome Analysis and Technology Research Grant*.
30. "Efficient Algorithms and Complexity Theory for Biological Sequences, Shortest Common Supersequences, and Succinct Finite Automata", \$26K/year, 1992-95, *NSERC Research Grant*.
31. "Expansion of Parallel Computing System" (with S. QIAO), \$36.7K, 1994, *NSERC Equipment Grant*.
32. "Transputer Multiprocessor System" (with S. QIAO), \$40K, 1991, *NSERC Equipment Grant*.
33. "Networks of Finite-State Machines: Algorithms, Simulation, Complexity, and Synchronization", \$20K/year, 1990-92, *NSERC Operating Grant*.
34. "Iterative/Cellular Arrays: Simulations, Algorithms and Complexity", \$19K, 1989-90, *McMaster University Junior Faculty Operating and Equipment Grant*.

Invited Lectures and Seminars Since 1994:

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) Dept of Computer Science, University of Waterloo, Jan, 1999
 - (f) Dept of Computer Science, UCR, Feb, 1999
 - (g) Dept of Computer Science, 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
 - (n) Invited short course (6 hours) at International Fall School in Formal Languages and Applications (FSFLA), Tarragona, Spain, Oct. 31 - 4 Nov. 4, 2011.
 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 Insititute, 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 Insititute, Chinese Academy of Sciences, Hangzhou, China, July 15, 2002
 - (d) Society of Chinese Bioscientists in America Annual Meeting, UC Irvine, Oct. 19, 2002
 - (e) Institute of Microbiology, Chinese Academy of Sciences, Beijing, Aug. 5, 2010
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) UCR, 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 Hew 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 Phylogentic 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 Bioinformatiion 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.
 - (s) Distinguished colloquium, School of Informatics and Computing, Indiana University, Bloomington, IN, April 9, 2010.
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, Shanghai, Sept. 5, 2006
 - (c) Bioinformatics Institute, Tsinghua University, Beijing, 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
 - (f) Invited speech at *Information Processing - Modern Perspectives*, May 25, Turku, Finland, 2009.
 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.
 - (c) Keynote speech at *Ohio Collaborative Conference on Bioinformatics (OCCBI)*, Cleveland, Ohio, Jun 15-17, 2009.
 20. A New Model of Multi-Marker Correlation for Genome-Wide Tag SNP Selection
 - (a) Bioinformatics Division, TNLIST, Tsinghua University, March 20, 2009.
 - (b) Invited talk at Workshop on Network-based Genome-wide Association Studies with Massively Parallel Implementation, Tsinghua University, June 24, 2009.
 21. Inference of Isoforms from Short Sequence Reads
 - (a) Bioinformatics Division, TNLIST, Tsinghua University, Beijng, Nov. 12, 2009.
 - (b) Invited talk at Bioinformatics Workshop, Xining, Qinghai, China, July 24-25, 2010.
 - (c) Institute of Mathematics and Systems Science, Chinese Academy of Scienes, Beijing, August 31, 2010
 - (d) Dept of Computer and Information Science, Indiana University, Indianapolis, Nov. 5, 2010
 - (e) School of Computer Science, Jilin University, Changchun, China, Dec. 9, 2010.
 - (f) Bioinformatics IDP Seminar Series, UCLA, Jan. 24, 2011.
 - (g) Computer Science Department Distinguished Lecture Series, UC Davis, May 19, 2011.
 - (h) Invited talk at International Bioinformatics Workshop (IBW), Xi'an, China, July 11-12, 2011.
 - (i) Qingdao Institute of BioEnergy and Bioprocess Technology (CAS-QIBEBT), Chinese Academy of Sciences, Qingdao, China, August, 2011.
 - (j) Invited talk at IPAM Workshop II: Transcriptomics and Epigenomics, UCLA, October 25 - 28, 2011.

- (k) Department of Computer Science, Technical University of Catalonia, Barcelona, Spain, Nov. 4, 2011.
 - (l) Korean Bioinformation Center (KOBIC), Daejeon, Korea, Dec. 13, 2011.
 - (m) Department of Computer Science, Seoul National University, Seoul, Korea, Dec. 14, 2011.
 - (n) School of Mathematics, Shandong University, Jinan, China, March 26, 2012
 - (o) Invited talk at FAW-AAIM' 12, Beijing, China, May 14-16, 2012.
 - (p) Department of Computer Science, Fudan University, Dec. 9, 2012.
 - (q) Shenzhen Institute of Advanced Technology, Chinese Academy of Sciences, Dec. 11, 2012.
22. Accurate HLA Type Inference Using a Weighted Similarity Graph
- (a) Bioinformatics Division, TNLIST, Tsinghua University, Beijing, Dec. 23, 2010.
23. Separating metagenomic short reads into genomes via clustering
- (a) Bioinformatics Division, TNLIST, Tsinghua University, Beijing, Sept. 15, 2011.
 - (b) Models and Algorithms for Genome Evolution (MAGE), Montreal, Canada, August 24-26, 2013.
24. Differential gene expression analysis using coexpression and RNA-Seq data
- (a) Bioinformatics Division, TNLIST, Tsinghua University, Beijing, Oct. 17, 2013.
 - (b) College of Information Engineering, Shanghai Maritime University, Shanghai, Dec. 3, 2013.
 - (c) Division of Mathematical Sciences, Nanyang Technological University, Singapore, Dec. 26, 2013
 - (d) Department of Computer Science, University of Hong Kong, Oct. 21, 2014
 - (e) Department of Computer Science Colloquium, Michigan State University, Nov. 7, 2014
 - (f) School of Mathematics, Shandong University, Jinan, China, Dec. 2, 2014
 - (g) Dept of Statistics, UCR, Jan. 20, 2015
 - (h) Invited talk at *5th Southern California Systems Biology Conference*, UCI, Jan. 31, 2015
 - (i) Institute of Mathematics and Systems Science, Chinese Academy of Sciences, Beijing, July 1, 2016.
25. Phylogeny-based classification of microbial communities
- (a) Bioinformatics Division, TNLIST, Tsinghua University, Beijing, China, Dec. 4, 2014
26. Transcript-Based Differential Expression Analysis on Population RNA-Seq Data
- (a) Invited talk at *Stochastic Biological Big Data and Data Mining Workshop*, Beijing, China, June 25-26, 2016.
 - (b) Plenary talk at the *10th International Conference on Systems Biology*, Weihai, China, August 19-21, 2016.
27. Toward More Sensitive Differential Expression Analysis on RNA-Seq Data
- (a) College of Computer and Control Engineering, Nankai University, Tianjin, China, Nov. 23, 2016.
 - (b) Invited talk at *KAUST Research Conference: Computational Systems Biology in Biomedicine*, KAUST, Saudi Arabia, Dec. 5-7, 2016.
 - (c) Invited talk at *International Workshop on Mathematical Issues in Information Sciences (MIIS)*, Shenzhen, China, Dec. 17-20, 2016.

- (d) College of Physics and Information Science, Hunan Normal University, Changsha, China, Nov. 30, 2017
 - (e) School of Computer Science, Jilin University, Changchun, China, Dec. 14, 2017.
 - (f) Department of Systems Biology, City of Hope, March 1, 2018.
 - (g) School of Informatics and Computing, Indiana University, Indianapolis, May 21, 2018 (canceled at the last minute due to a canceled connecting flight).
28. Alignment-free Estimation of Exon-inclusion Ratios without a Reference Transcriptome
 - (a) School of Medicine, Jilin University, Changchun, China, Dec. 14, 2018.
 - (b) School of Mathematics, Shandong University, Jinan, China, June 20, 2019.
 29. Prediction of Isoform Functions from Sequences and Expression Profiles via Deep Learning
 - (a) Invited talk at *Annual ShanghaiTech Symposium on Information Science and Technology (AS-SIST)*, Shanghai, China, June 30 - July 2, 2019.
 - (b) School of Mathematics, Shandong University, Jinan, China, July 16, 2019.
 30. Predicting Isoform Functions via Deep Learning and Refinement of Interaction Networks
 - (a) Invited talk, College of Artificial Intelligence, Dalian Maritime University, Dalian, China, Nov. 11, 2022 (virtual).
 - (b) Invited talk at the *Powertalk Seminar Series*, Informatics Institute, Heersink School of Medicine, University of Alabama at Birmingham, April 7, 2022 (virtual).
 31. Bioinformatics from the Perspectives of Combinatorial Algorithms: A Few Examples
 - (a) Invited guest lecture at the *Freshman Seminar Series*, the Bioinformatics Program, Huazhong University of Science and Technology, Wuhan, China, Oct. 12, 2016.
 - (b) Invited guest lecture for freshmen, the Institute of Interdisciplinary Information Science, Tsinghua University, Beijing, China, Nov. 22, 2016.
 32. 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. Y. Xiong, X. He, D. Zhao, T. Jiang, and J. Zeng. DeepRCI: Predicting RNA-chromatin interactions via deep learning with multi-omics data. *Quantitative Biology*, accepted 11/24/2022.
2. D. Hao*, H. Chen, P. Xiao, and T. Jiang*. A global analysis of alternative splicing of *Dichocarpum* medicinal plants, Ranunculales. *Current Genomics* 23(3), pp. 207-216, 2022.
3. A. De Francesco, A. Lovelace, D. Shaw, M. Qiu, Y. Wang, F. Gurung, V. Ancona, C. Wang, A. Levy, T. Jiang, and W. Ma. Transcriptome profiling of *Candidatus Liberibacter asiaticus* in citrus and psyllids. *Phytopathology* 112(1):116-130, 2022.
4. X. He, S. Zhang, Y. Zhang, Z. Lei, T. Jiang, and J. Zeng. Characterizing RNA pseudouridylation by convolutional neural networks. *Genomics, Proteomics and Bioinformatics* 19(5), pp. 815-833, 2021.

5. H. Chen, D. Shaw, B. Bu, and T. Jiang. FINER: enhancing the prediction of tissue-specific functions of isoforms by refining isoform interaction networks. *NAR Genomics and Bioinformatics* 3(2), 2021.
6. Y. Xiong, X. He, D. Zhao, T. Tian, L. Hong, T. Jiang*, and J. Zeng*. Modeling multi-species RNA modification through multi-task curriculum learning. *Nucleic Acids Research* 49(7), pp. 3719-3734, 2021.
7. H. Hu, X. Liu, A. Xiao, Y. Li, C. Zhang, T. Jiang, D. Zhao, S. Song, and J. Zeng. Riboexp: an interpretable reinforcement learning framework for ribosome density modeling. *Briefings in Bioinformatics* 22(5), bbaa412, 2021.
8. D. Shaw, H. Chen, M. Xie, and T. Jiang. DeepLPI: a multimodal deep learning method for predicting the interactions between lncRNAs and protein isoforms. *BMC Bioinformatics* 22:24, 2021.
9. J. Zhou, W. Zeng, R. Jiang, W. Ma, Q. Zhang, and T. Jiang. IRIS: A method for predicting in vivo RNA secondary structures using PARIS data. *Quantitative Biology* 8(4), pp 369381, 2020.
10. L. Hong, J. Lin, S. Li, F. Wan, H. Yang, T. Jiang, D. Zhao, and J. Zeng. A novel machine learning framework for automated biomedical relation extraction from large-scale literature repositories. *Nature Machine Intelligence* 2, pp. 347355, 2020.
11. W. Pan, T. Jiang, S. Lonardi. OMGS: Optical Map-based Genome Scaffolding. *Journal of Computational Biology* 27(4), pp. 519533, 2020.
12. C. Li, W. Xie, J. Rosenblum, J. Zhou, J. Guo, Y. Miao, Y. Shen, H. Wang, L. Gong, M. Li, S. Zhao, S. Cheng, H. Zhu, T. Jiang, S. Ling, F. Wang, H. Zhang, M. Zhang, Y. Qu, Q. Zhang, G. Li, J. Wang, J. Ma, Z. Zhuang, and Y. Zhang. Somatic SF3B1 hotspot mutation in prolactinomas. *Nature Communications* 11, No. 2506, 2020.
13. P. Deol, E. Kozlova, M. Valdez, C. Ho, E. Yang, G. Gonzalez, H. Richardson, E. Truong, J. Reid, J. Valdez, J. Deans, J. Martinez-Lomeli, J. Evans, T. Jiang, F. Sladek, M. Curras-Collazo. Dysregulation of hypothalamic gene expression and the oxytocinergic system by soybean oil diets in male mice. *Endocrinology* 161(2), bqz044, 2020.
14. J. Shi, X. Zeng, R. Jiang, T. Jiang, M. Xu. A simulated annealing approach for resolution guided homogeneous cryo electron microscopy image selection. *Quantitative Biology* 8, pp. 51-63, 2020.
15. S. Li, F. Wan, H. Shu, T. Jiang, D. Zhao, and J. Zeng. MONN: a Multi-objective neural network for predicting compound-protein interactions and affinities. *Cell Systems* 10(4), pp. 308-322, 2020.
16. C. Xu, Q. Liu, J. Zhou, M. Xie, J. Feng, and T. Jiang. Quantifying functional impact of noncoding variants with multi-task Bayesian neural network. *Bioinformatics* 36(5), pp. 1397-1404, 2020.
17. L. Xiong, K. Xu, K. Tian, Y. Shao, L. Tang, G. Gao, M. Zhang, T. Jiang, and Q. Zhang SCALE: method for single-cell ATAC-seq analysis via latent feature extraction. *Nature Communications* 10, No. 4576, 2019.
18. A. Arefeen, X. Xiao, and T. Jiang. DeepPASTA: Deep neural network based polyadenylation site analysis. *Bioinformatics* 35(22), pp. 45774585, 2019.

19. H. Chen, D. Shaw, J. Zeng, D. Bu, and T. Jiang. DIFFUSE: Predicting isoform functions from sequences and expression profiles via deep learning. *Bioinformatics* 35(4), pp. i284i294, 2019; also presented at the *27th Annual International Conference on Intelligent Systems for Molecular Biology and 17th European Conference on Computational Biology (ISMB/ECCB)*, Basel, Switzerland, July 21-25, 2019.
20. D. Shaw, H. Chen and T. Jiang. DeepIsoFun: A deep domain adaptation approach to predict isoform functions. *Bioinformatics* 35(15), pp. 2535-2644, 2019.
21. H. Hu, A. Xiao, S. Zhang, Y. Li, X. Shi, T. Jiang, L. Zhang, L. Zhang, and J. Zeng. DeepHINT: Understanding HIV-1 integration via deep learning with attention. *Bioinformatics* 35(10), pp. 1660-1667, 2019.
22. F. Wan, L. Hong, A. Xiao, T. Jiang, and J. Zeng. NeoDTI: Neural integration of neighbor information from a heterogeneous network for discovering new drug-target interactions. *Bioinformatics* 35(1), pp. 104-111, 2019.
23. S. Ma, T. Jiang and R. Jiang. Constructing tissue-specific transcriptional regulatory networks via a Markov random field. *BMC Genomics* 2018, 19 (Suppl 10):884; also presented at the *29th International Conference on Genome Informatics (GIW)*, December 3-5, 2018, Kunming, China.
24. P. Li, Y. Wei, M. Mei, L. Tang, L. Sun, W. Huang, J. Zhou, C. Zou, S. Zhang, C. Qin, T. Jiang, J. Dai, X. Tan, and Q. Zhang. Integrative analysis of Zika virus genome RNA structure reveals critical determinants of viral infectivity. *Cell Host and Microbe* 24(6), pp. 875-886, 2018.
25. A. Arefeen, J. Liu, X. Xiao, and T. Jiang. TAPAS: Tool for alternative polyadenylation site analysis. *Bioinformatics* 34(15), pp. 2521-2529, 2018.
26. J. Zhou, S. Ma, D. Wang, J. Zeng, T. Jiang. FreePSI: an alignment-free approach to estimating exon-inclusion ratios without a reference transcriptome. *Nucleic Acids Research* 46(2), pp. e11, 2018.
27. P. Zhang, Y. Xu, T. Jiang, A. Li, G. Lin, and E. Miyano. Improved approximation algorithms for the maximum happy vertices and edges problems. *Algorithmica* 80, pp. 1412-1438, 2017.
28. S. Zhang, H. Hu, J. Zhou, X. He, T. Jiang, and J. Zeng. Analysis of ribosome stalling and translation elongation dynamics by deep learning. *Cell Systems* 5, pp. 212-220, 2017.
29. S. Li, D. Dong, Y. Wu, S. Zhang, C. Zhang, X. Liu, T. Jiang, J. Zeng. A deep boosting based approach for capturing the sequence binding preferences of RNA-binding proteins from high-throughput CLIP-Seq data. *Nucleic Acids Research* 45(14), pp. e129, 2017.
30. S. Zhang, H. Hu, T. Jiang, L. Zhang and J. Zeng. TITER: predicting translation initiation sites by deep learning. *Bioinformatics* 33(14):i234-i242, 2017; also presented at the *25th Annual International Conference on Intelligent Systems for Molecular Biology and 16th European Conference on Computational Biology (ISMB/ECCB)*, July 21-25, 2017, Prague, Czech Republic.
31. J. Liu, T. Yu, T. Jiang, and G. Li. TransComb: Genome-guided transcriptome assembly via combing junctions in splicing graphs. *Genome Biology* 17:213, 2016. doi: 10.1186/s13059-016-1074-1.
32. M. Xie, Q. Wu, J. Wang, and T. Jiang. H-PoP and H-PoPG: Heuristic partitioning algorithms for single individual haplotyping of polyploids. *Bioinformatics* 32(24):3735-3744, 2016; doi: 10.1093/bioinformatics/btw537.

33. E.W. Yang and T. Jiang. SDEAP: A splice graph based differential transcript expression analysis tool for population data. *Bioinformatics* 32(23):3593-3602, 2016; doi: 10.1093/bioinformatics/btw513.
34. Munoz-Amatriain, Maria; Lonardi, Stefano; Luo, Ming-Cheng; Madishetty, Kavitha; Svensson, Jan; Moscou, Matthew; Wanamaker, Steve; Jiang, Tao; Kleinhofs, Andris; Muehlbauer, Gary; Wise, Roger; Stein, Nils; Ma, Yaqin; Rodriguez, Edmundo; Kudrna, David; Bhat, Prasanna; Chao, Shiao-man; Condamine, Pascal; Heinen, Shane; Resnik, Josh; Wing, Rod; Witt, Heather; Alpert, Matthew; Beccuti, Marco; Bozdogan, Serdar; Cordero, Francesca; Mirebrahim, Hamid; Ounit, Rachid; Wu, Yonghui; You, Frank; Zheng, Jie; Simkova, Hana; Dolezel, Jaroslav; Grimwood, Jane; Schmutz, Jeremy; Duma, Denisa; Altschmied, Lothar; Blake, Tom; Bregitzer, Phil; Cooper, Laurel; Dilbirligi, Muharrem; Falk, Anders; Feiz, Leila; Graner, Andreas; Gustafson, Perry; Hayes, Patrick; Lemaux, Peggy; Mammadov, Jafar; Close, Timothy. Sequencing of 15,622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. *Plant Journal* 84(1):216-27, 2015.
35. O. Tanaseichuk, A. Khodabakshi, D. Petrov, J. Che, T. Jiang, B. Zhou, A. Santrosyan, and Y. Zhou. An efficient hierarchical clustering algorithm for large datasets. *Austin Journal of Proteomics, Bioinformatics & Genomics*, 2015;2(1):1008.
36. S. Ma, T. Jiang and R. Jiang. Differential regulation enrichment analysis via the integration of transcriptional regulatory network and gene expression data. *Bioinformatics* 31(4):563-571, 2015.
37. M. Tasnim, S. Ma., E.W. Yang, T. Jiang, and W. Li. Accurate inference of isoforms from multiple sample RNA-Seq data. *BMC Genomics* 16(Suppl 2):S15, 2015; also presented at the *13th Asia Pacific Bioinformatics Conference (APBC)*, Hsinchu, Taiwan, Jan., 2015 (the best paper award).
38. C. Xu*, X. Ju*, D. Song*, F. Huang*, D. Tang, Z. Zou, C. Zhang, T. Joshi, L. Jia, W. Xu, K.-F. Xu, Q. Wang, Y. Xiong, Z. Guo, X. Chen, F. Huang, J. Xu, Y. Zhong, Y. Zhu, Y. Peng, L. Wang, X. Zhang, R. Jiang, D. Li, T. Jiang, D. Xu, and C. Jiang. An association analysis between psychophysical characteristics and genome-wide gene expression changes in human adaptation to the extreme climate at the Antarctic Dome Argus. *Molecular Psychiatry* 20:536544, 2015.
39. E. Bao, T. Jiang and T. Girke. AlignGraph: algorithm for secondary *de novo* genome assembly guided by closely related references. *Bioinformatics* 30(12) pp. i319-i328, 2014; also presented at the *22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, July, 2014, Boston, MA.
40. O. Tanaseichuk, J. Borneman and T. Jiang. Phylogeny-based classification of microbial communities. *Bioinformatics* 30(4):449-456, 2014.
41. Y. Chen, J. Hao, W. Jiang, T. He, X. Zhang, T. Jiang, and R. Jiang. Identifying potential cancer driver genes by genomic data integration. *Scientific Reports* 3(3538), Dec. 18, 2013. doi:10.1038/srep03538.
42. W.B. Wang, T. Jiang and S. Gardner. Detection of homologous recombination events in bacterial genomes. *PLoS ONE* 8(10): e75230, 2013. doi:10.1371/journal.pone.0075230.
43. E.W. Yang, T. Girke and T. Jiang. Differential gene expression analysis using coexpression and RNA-Seq data. *Bioinformatics* 29(17):2153-2161, 2013.
44. S. Roy, L. Poidevin, T. Jiang, and H.S. Judelson. Novel core promoter elements in the oomycete pathogen *Phytophthora infestans* and their influence on expression detected by genome-wide analysis. *BMC Genomics* 14:106, 2013.

45. E. Bao, T. Jiang and T. Girke. BRANCH: boosting RNA-Seq assemblies with partial or related genomic sequences. *Bioinformatics* 29(10):1250-1259, 2013.
46. M. Xie, J. Wang and T. Jiang. A fast and accurate algorithm for single individual haplotyping. *BMC Systems Biology* 6(Suppl 2):S8, 2012; also presented at the *23rd International Conference on Genome Informatics (GIW)*, Tainan, Taiwan, Dec. 2012.
47. E.Y. Lai, W.B. Wang, T. Jiang, and K.P. Wu. A linear time algorithm for reconstructing zero-recombinant haplotype configuration on a pedigree. *BMC Bioinformatics* 13(Suppl 17):S19; also presented at the *11th International Conference on Bioinformatics (InCoB)*, Bangkok, Thailand, Oct. 2012.
48. P. Ruegger, E. Bent, W. Li, D. Jeske, X. Cui, J. Braun, T. Jiang, and J. Borneman. Improving oligonucleotide fingerprinting of rRNA genes by implementation of polony microarray technology. *Journal of Microbiological Methods* 90:235-240, 2012.
49. O. Tanaseichuk, J. Borneman and T. Jiang. Separating metagenomic short reads into genomes via clustering. *Algorithms for Molecular Biology* 7(1):27, 2012.
50. W. Li and T. Jiang. Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. *Bioinformatics* 28(22):2914-21, 2012.
51. B. Fang, D. Mane-Padros, E. Bolotin, T. Jiang, and F. Sladek. Identification of a binding motif specific to HNF4 by comparative analysis of multiple nuclear receptors. *Nucleic Acids Research* 40(12):5343-5356, 2012.
52. M. Xie, J. Li and T. Jiang. Detecting genome-wide epistases based on the clustering of relatively frequent items. *Bioinformatics* 28(1), pp. 5-12, 2012.
53. Y. Pirola, P. Bonizzoni and T. Jiang. An efficient algorithm for haplotype inference on pedigrees with recombinations and mutations. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)* 9(1), pp. 12-25, 2012.
54. J. Xiao, T. Lou and T. Jiang. An efficient algorithm for haplotype inference on pedigrees with a small number of recombinants. *Algorithmica* 62(3-4), pp. 951-981, 2012.
55. P.M. Ruegger, G. Della Vedova, T. Jiang, and J. Borneman. Improving probe set selection for microbial community analysis by leveraging taxonomic information of training sequences. *BMC Bioinformatics* 12:394, 2011.
56. E. Bao, T. Jiang, I. Kaloshian, and T. Girke. SEED: Efficient clustering of next generation sequences. *Bioinformatics* 27, 2502-2509, 2011.
57. W. Li, J. Feng and T. Jiang. IsoLasso: A LASSO regression approach to RNA-Seq based transcriptome assembly. *Journal of Computational Biology* 18(11), pp. 1693-1707, 2011.
58. Y. Chen, T. Jiang and R. Jiang. Uncover disease genes by maximizing information flow in the phenome-interactome network. *Bioinformatics* 27(13), pp. i167-i176, 2011; also presented at the *19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, 2011, Vienna, Austria.

59. W.B. Wang and T. Jiang. Inferring haplotypes from genotypes on a pedigree with mutations, genotyping errors and missing alleles. *Journal of Bioinformatics and Computational Biology (JBCB)* special issue for *CSB'2010*, 9(2), pp. 339-365, 2011.
60. G. Shi, M.C. Peng and T. Jiang. MultiMSOAR 2.0: An accurate tool to identify ortholog groups among multiple genomes. *PLoS ONE* 6(6):e20892, 2011.
61. J. Feng, W. Li and T. Jiang. Inference of isoforms from short sequence reads. *Journal of Computational Biology* 18(3), pp. 305-321, 2011.
62. J. Feng, R. Jiang and T. Jiang. A max-flow based approach to the identification of protein complexes using protein interaction and microarray data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)* 8(3), pp. 621-634, 2011.
63. M. Xie, J. Li and T. Jiang. Accurate HLA type inference using a weighted similarity graph. *BMC Bioinformatics* 11 (Suppl 11): S10, 2010; also presented at the *21st International Conference on Genome Informatics (GIW)*, Shanghai, China, Dec. 16-18, 2010.
64. Y. Cao, T. Jiang and T. Girke. Accelerated similarity searching and clustering of large compound sets by geometric embedding and locality sensitive hashing. *Bioinformatics* 26(7), pp. 953-959, 2010.
65. L. Liu and T. Jiang. Linear-time reconstruction of zero-recombinant Mendelian inheritance on pedigrees without mating loops. *Journal of Combinatorial Optimization* 19(2), pp. 217-240, 2010.
66. E. Bolotin, H. Liao, T. Ta, C. Yang, W. Hwang-Verslues, J. Evans, T. Jiang, and F. Sladek. Integrated approach for identification of Human HNF4 target genes using protein binding microarrays. *Hepatology* 51(2):642-53, 2010. (Selected for Faculty of 1000 Biology.)
67. T. Jiang. Some algorithmic challenges in genome-wide ortholog assignment. *Journal of Computer Science and Technology* 25(1):42-52, 2010.
68. 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)* 17(1):21-37, 2010.
69. G. Shi, L. Zhang and T. Jiang. MSOAR 2.0: Incorporating tandem duplications into ortholog assignment based on genome rearrangement. *BMC Bioinformatics* 2010, 11:10.
70. Y. Yang, J. Zhao, R. Morgan, W. Ma, and T. Jiang. Computational prediction of type III secreted proteins from gram-negative bacteria. *BMC Bioinformatics* 11(Suppl 1):S47, 2010; also presented at the *8th Asia Pacific Bioinformatics Conference (APBC)*, Bangalore, India, January, 2010.
71. G. Della Vedova, R. Dondi, T. Jiang, G. Pavesi, Y. Pirola, and L. Wang. Beyond Evolutionary Trees. *Natural Computing* (special issue to commemorate the 60th birthday of Prof. G. Mauri), Sept., 2009, DOI 10.1007/s11047-009-9156-6.
72. 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* 38(6), pp. 2198-2219, 2009.
73. D. Song, Y. Yang, B. Yu, B. Zheng, Z. Deng, B. Lu, X. Chen, and T. Jiang. Computational prediction of novel non-coding RNAs in Arabidopsis thaliana, *BMC Bioinformatics* 10 (Suppl 1):S36, 2009 (special issue for selected papers presented at the *Seventh Asia-Pacific Bioinformatics Conference (APBC)*, Jan. 2009, Beijing).

74. Y. Cao, T. Jiang and T. Girke. A maximum common substructure-based algorithm for searching and predicting drug-like compounds. *Bioinformatics* 28(13), i366-i374, 2008; also presented at the *16th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, 2008, Toronto, Canada.
75. X. Chen, L. Liu, Z. Liu and T. Jiang. On the minimum common integer partition problem. *ACM Transactions on Algorithms (TALG)* 5(1), article 12, 2008.
76. 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)* 15(10):1275-93, 2008.
77. 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.
78. Z. Fu and T. Jiang. Clustering of main orthologs for multiple genomes. *Journal of Bioinformatics and Computational Biology (JBCB)* 6(3):573-84, 2008.
79. 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.
80. 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.
81. 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.
82. 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.
83. 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.
84. 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.
85. 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.
86. 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.
87. 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.
88. 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.
89. 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.

90. 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.
91. 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.
92. 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.
93. 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.
94. J. Li and T. Jiang. Haplotype-based linkage disequilibrium mapping via direct data mining. *Bioinformatics* 21(24):4384-4393, 2005.
95. 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.
96. 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.
97. 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.
98. 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.
99. 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.
100. 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.
101. G. Lin and T. Jiang. A further improved approximation algorithm for breakpoint graph decomposition. *Journal of Combinatorial Optimization* 8-2, 2004, 183-194.
102. 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.
103. 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).
104. 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.

105. P. Kearney, 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.
106. 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.
107. Z. Chen, T. Jiang, and G. Lin. Computing phylogenetic roots with bounded degrees and errors. *SIAM Journal on Computing* 32-4, 864-879, 2003.
108. 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.
109. 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.
110. 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.
111. 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.
112. 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.
113. 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.
114. Y.L. Lin, X. Huang, T. Jiang, and K.M. Chao. MAVG: Locating CpG islands in a genomic sequence. *Bioinformatics* 19-1, 151-152, 2003.
115. K. Ellrott, J. Kasarjian, T. Jiang, and J. Ryu. RMsearch: a DNA recombination sequence search program. *BioTechniques* 33-6, 1322-1326, 2002.
116. 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.
117. G. Lin, Z. Chen, T. Jiang, and J. Wen. The longest common subsequence problem for sequences with nested arc annotations. *Journal of Computer and System Sciences* 65-3 (special issue on computational molecular biology), pp. 465-480, 2002.
118. L. Valinsky, G. Della Vedova, T. Jiang, and J. Borneman. Oligonucleotide fingerprinting of ribosomal RNA genes for analysis of fungal community composition. *Applied and Environmental Microbiology* 68-12, pp. 5999-6004, 2002.
119. K. Ellrott, C. Yang, F.M. Sladek, and T. Jiang. Identifying transcription factor binding sites through Markov chain optimization. *Bioinformatics* 18, pp. 100S-109S, 2002; also presented at the *First European Conference on Computational Biology (ECCB)*, Oct., 2002, Saarbrücken, Germany.

120. L. Valinsky, G. Della Vedova, A. Scupham, S. Alvey, A. Figueroa, B. Yin, R.J. Hartin, M. Chrobak, D. Crowley, T. Jiang, and J. Borneman. Analysis of microbial community composition using oligonucleotide fingerprinting of rRNA genes. *Applied and Environmental Microbiology* 68-7, pp. 3243-3250, 2002.
121. T. Jiang, G. Lin, B. Ma and K. Zhang. A general edit distance between RNA structures. *Journal of Computational Biology* 9(2), 371-388, 2002.
122. T. Jiang, M. Li and P. Vitanyi. The average-case area of Heilbronn-type triangles. *Random Structures and Algorithms* 20(2), 206-219, 2002.
123. Y. Xu, D. Xu, D. Kim, V. Olman, J. Razumovskaya, and T. Jiang. Automated assignment of backbone NMR peaks using constrained bipartite matching. *IEEE Computational Science and Engineering* (feature article), Feb., 50-62, 2002.
124. E.F. Adebisi, T. Jiang and M. Kaufmann. An efficient algorithm for finding short approximate non-tandem repeats. *Bioinformatics* Vol. 17, pp. S5-S12, 2001; also presented at the *9th International Conference on Intelligent Systems for Molecular Biology (ISMB)*, July, 2001, Copenhagen, Denmark.
125. J. Borneman, M. Chrobak, G. Della Vedova, A. Figueroa, and T. Jiang. Probe selection algorithms with applications in the analysis of microbial communities. *Bioinformatics* Vol. 17, pp. S39-S46, 2001; also presented at the *9th International Conference on Intelligent Systems for Molecular Biology (ISMB)*, July, 2001, Copenhagen, Denmark.
126. T. Jiang, P. Kearney and M. Li. A polynomial time approximation scheme for inferring evolutionary trees from quartet topologies and its application. *SIAM Journal on Computing* 30(6), 1942-1961, 2001.
127. P. Zhao and T. Jiang. A heuristic algorithm for multiple sequence alignment based on blocks. *Journal of Combinatorial Optimization: special issue on Discrete Mathematical Problems with Medical Applications* 5, 95-115, 2001.
128. T. Jiang, M. Li and P. Vitanyi. A lower bound on the average-case complexity of Shellsort. *Journal of the ACM*, 47:5 (2000), 905-911.
129. H. Buhrman, T. Jiang, M. Li, and P. Vitanyi. New applications of the incompressibility method: Part II. *Theoretical Computer Science* special issue in honor of Manuel Blum's 60th birthday (invited) 235 (1), 59-70, 2000.
130. T. Jiang, M. Li and P. Vitanyi. Average-case analysis of algorithms using Kolmogorov complexity. *Journal of Computer Science and Technology* 15-5 (by invitation), pp. 402-408, 2000.
131. L. Wang, D. Gusfield, and T. Jiang. A more efficient approximation scheme for tree alignment. *SIAM Journal on Computing* 30-1, 283-299, 2000.
132. O. Etzioni, S. Hanks, T. Jiang, and O. Madani. Optimal information gathering on the Internet with cost and time constraints. *SIAM Journal on Computing* 29-5, pp. 1596-1620, 2000.
133. T. Jiang, P. Kearney, and M. Li. Some open problems in computational molecular biology. *Journal of Algorithms* 34-1, pp. 194-201, 2000 (invited); also in *SIGACT News*, Sept., 1999.

134. T. Jiang, M. Li, and P. Vitanyi. New applications of the incompressibility method. *Computer Journal* (invited) 42-4, pp. 287-293, 1999.
135. D. Fasulo, T. Jiang, R. Karp, R. Settergren, and E. Thayer. An algorithmic approach to multiple complete digest mapping. *Journal of Computational Biology* 6(2), 1999, 187-208.
136. B. DasGupta, X. He, T. Jiang, M. Li, and J. Tromp. On the linear-cost subtree-transfer distance between phylogenetic trees. *Algorithmica* special issue on computational biology 25, 176-195, 1999.
137. Y. Hua, T. Jiang, and B. Wu. Aligning DNA sequences to minimize the change in protein. *Journal of Combinatorial Optimization: Special Issue on Computational Molecular Biology* 3, 227-245, 1999.
138. B. DasGupta, T. Jiang, S. Kannan, M. Li and Z. Sweedyk. On the complexity and approximation of syntenic distance. *Discrete Applied Mathematics* special issue on computational biology, Vol. 88, No. 1-3, 59-82, 1998.
139. T. Jiang and R. Karp. Mapping clones with a given ordering or interleaving. *Algorithmica* 21, 262-284, 1998.
140. D. Breslauer, T. Jiang, and Z. Jiang. Rotation of periodic strings and short superstrings. *Journal of Algorithms* 24, 340-353, 1997.
141. T. Jiang, J. Seiferas and P. Vitanyi. Two heads are better than two tapes. *Journal of the ACM* 44(2), 237-256, March 1997.
142. J. Hein, T. Jiang, L. Wang and K. Zhang. On the complexity of comparing evolutionary trees. *Discrete Applied Mathematics* 71, 153-169, 1996.
143. T. Jiang and M. Li. k one-way heads cannot do string-matching. *Journal of Computer and System Sciences* 53(3), 513-524, 1996.
144. L. Wang and T. Jiang. An approximation scheme for some Steiner tree problems in the plane. *Networks* 28, 187-193, 1996.
145. L. Wang, T. Jiang and E. Lawler. Approximation algorithms for tree alignment with a given phylogeny. *Algorithmica* 16, 302-315, 1996.
146. T. Hancock, T. Jiang, M. Li, and J. Tromp. Lower bounds on learning decision lists and trees. *Information and Computation* 126-2, 114-122, 1996.
147. T. Jiang and M. Li. DNA sequencing and string learning. *Mathematical Systems Theory* 29-4, 387-405, 1996.
148. T. Jiang and M. Li. On the approximation of shortest common supersequences and longest common subsequences. *SIAM Journal on Computing*, 1122-1139, 1995.
149. O. Ibarra, T. Jiang, N. Tran, and H. Wang. New decidability results concerning two-way counter machines. *SIAM Journal on Computing* 24-1, 123-137, 1995.
150. T. Jiang, L. Wang and K. Zhang. Alignment of trees - an alternative to tree edit. *Theoretical Computer Science* 143-1, 137-148, 1995.

151. T. Jiang and V. Timkovsky. Shortest consistent superstrings computable in polynomial time. *Theoretical Computer Science* 143-1, 113-122, 1995.
152. T. Jiang, A. Salomaa, K. Salomaa, and S. Yu. Decision problems for patterns. *Journal of Computer and System Sciences* 50-1, 53-63, 1995.
153. A. Blum, T. Jiang, M. Li, J. Tromp, and M. Yannakakis. Linear approximation of shortest superstrings. *Journal of the ACM* 41-4, 630-647, 1994.
154. T. Jiang and M. Li. Approximating shortest superstrings with constraints. *Theoretical Computer Science* 134, 473-491, 1994.
155. L. Wang and T. Jiang. On the complexity of multiple sequence alignment. *Journal of Computational Biology* 1-4, 337-348, 1994.
156. K. Zhang and T. Jiang. Some MAX SNP-hard results concerning unordered, labeled trees. *Information Processing Letters* 49, 249-254, 1994.
157. E. Kinber, T. Jiang, A. Salomaa, K. Salomaa, and S. Yu. Pattern languages with and without erasing. *International Journal of Computer Mathematics*, vol. 50, 147-163, 1994.
158. O. Ibarra, T. Jiang, and H. Wang. Some results concerning 2-D on-line tessellation acceptors and 2-D alternating finite automata. *Theoretical Computer Science* 125, 243-257, 1994.
159. O. Ibarra, T. Jiang and H. Wang. On efficient parallel algorithms for solving set recurrence equations. *Journal of Algorithms* 14, 1993, 244-257.
160. T. Jiang and M. Li. On the complexity of learning strings and sequences. *Theoretical Computer Science* 119, 1993, 363-371.
161. T. Jiang and B. Ravikumar. Minimal NFA problems are hard. *SIAM Journal on Computing* 22-6, 1993, 1117-1141.
162. O. Ibarra, T. Jiang, N. Tran, and H. Wang. On the equivalence of two-way pushdown automata and counter machines over bounded languages. *International Journal of Foundations of Computer Science* 4-2, 135-146, 1993.
163. O. Ibarra, T. Jiang and H. Wang. String editing on a one-way linear array of finite-state machines. *IEEE Transactions on Computers* 41-1, 1992, 112-118.
164. T. Jiang. The synchronization of nonuniform networks of finite automata, *Information and Computation* 97-2, 1992, 234-261.
165. O. Ibarra, T. Jiang, H. Wang, and Q. Zheng. A hierarchy result for 2-dimensional TM's operating in small space. *Information Sciences* 64, 1992, 9-56.
166. O. Ibarra, T. Jiang and H. Wang. A characterization of exponential-time languages by alternating context-free grammars. *Theoretical Computer Science* 99, 1992, 301-313
167. T. Jiang, M. Li and D. Du. A note on shortest superstrings with flipping. *Information Processing Letters* 44-4, 1992, 195-200.

168. J. Chang, O. Ibarra, T. Jiang, and B. Ravikumar. Some classes of languages in NC^1 . *Information and Computation* 90, 1991, 86-106.
169. O. Ibarra and T. Jiang. The power of alternating one-reversal counters and stacks. *SIAM Journal on Computing* 20, 1991, 278-290.
170. O. Ibarra, T. Jiang, and H. Wang. Parallel parsing on a one-way linear array of finite-state machines. *Theoretical Computer Science* 85, 1991, 53-74.
171. O. Ibarra and T. Jiang. Learning regular languages from counterexamples. *Journal of Computer and System Sciences* 43, 1991, 299-316.
172. T. Jiang and B. Ravikumar. A note on the space complexity of some decision problems for finite automata. *Information Processing Letters* 40-1, 1991, 25-31.
173. T. Jiang, E. McDowell and B. Ravikumar. The structure and complexity of minimal NFA's over a unary alphabet. *International Journal of Foundations of Computer Science* 2-2, 1991, 163-182.
174. J. Chang, O. Ibarra, T. Jiang, and M. Palis. Systolic algorithms for some scheduling and graph problems. *Journal of VLSI Signal Processing* 1-4, 1990, 307-320.
175. T. Jiang. On the complexity of 1-tape ATMs and off-line 1-tape ATMs running in constant reversals, *Theoretical Computer Science* 76, 1990, 323-330.
176. J. Chang, O. Ibarra, and T. Jiang. On iterative and cellular tree arrays. *Journal of Computer and System Sciences* 38, 1989, 52-473.
177. O. Ibarra and T. Jiang. Optimal simulation of tree arrays by linear arrays. *Information Processing Letters* 30, 1989, 295-302.
178. O. Ibarra, T. Jiang, and B. Ravikumar. Some subclasses of context-free languages in NC^1 . *Information Processing Letters* 29, 1988, 111-117.
179. O. Ibarra and T. Jiang. Relating the power of cellular arrays to their closure properties. *Theoretical Computer Science* 57, 1988, 225-238.
180. O. Ibarra and T. Jiang. On one-way cellular arrays. *SIAM Journal on Computing* 16-6, 1987, 1135-1154.
181. T. Jiang. Hajos conjecture is true for planar graphs. *Journal of China University of Science and Technology* 14-4, 1984, 585-592.

Peer-Reviewed Conference Publications:

(Note: Polished forms of many of the following papers have appeared or will appear in journals listed above. For conferences that publish proceedings in journals as special issues, I list their papers only as journal publications.)

1. Z. Hong, J. Feng and T. Jiang. Truly unsupervised image-to-image translation with contrastive representation learning. Proc. *16th Asian Conference on Computer Vision (ACCV)*, pp. 2646-2662, Macau SAR, China, Dec 4-8, 2022.

2. C. Xu, Z. Hong, M. Huang, and T. Jiang. Acceleration of federated learning with alleviated forgetting in local training. *Proc. 10th International Conference on Learning Representations (ICLR)*, April 25, 2022 (virtual).
3. C. Xu, Q. Lu, M. Huang, and T. Jiang. Reinforced molecular optimization with neighborhood-controlled grammars. *Proc. 34th Conference on Neural Information Processing Systems (NeurIPS)*, Dec. 6-12, 2020, Vancouver, Canada (virtual).
4. S. Li, F. Wan, H. Shu, T. Jiang, D. Zhao, and J. Zeng. MONN: a multi-objective neural network for predicting pairwise non-covalent interactions and binding affinities between compounds and proteins. *Proc. 24th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Padova, Italy, May 10-13, 2020.
5. Z. Hong, X. Fan, T. Jiang, and J. Feng. End-to-end unpaired image denoising with conditional adversarial networks. *Proc. 34th AAAI Conference on Artificial Intelligence (AAAI)* 34(04), pp. 4140-4149, New York, NY, Feb. 7-12, 2020.
6. W. Pan, T. Jiang and S. Lonardi. OMGS: Optical map-based genome scaffolding. *Proc. 23rd Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, pp. 190-207, Washington DC, May 5-8, 2019.
7. S. Zhang, H. Hu, J. Zhou, X. He, T. Jiang, and J. Zeng. ROSE: a deep learning based framework for predicting ribosome stalling. *Proc. 21st Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Hong Kong, May, 2017, pp. 402-403. (Oral presentation.)
8. P. Zhang, T. Jiang and A. Li. Improved approximation algorithms for the maximum happy vertices and edges Problems. *Proc. 21st International Computing and Combinatorics Conference (COCOON)*, Beijing, China, August, 2015, pp. 159-170.
9. E. Yang and T. Jiang. GDNorm: An improved Poisson regression model for reducing biases in Hi-C data. *Proc. 14th Workshop on Algorithms in Bioinformatics (WABI)*, Wroclaw, Poland, Sept., 2014, pp. 263-280.
10. O. Tanaseichuk, J. Borneman and T. Jiang. A probabilistic approach to accurate abundance-based binning of metagenomic reads. *Proc. 12th Workshop on Algorithms in Bioinformatics (WABI)*, Ljubljana, Slovenia, Sept. 2012, pp. 404-416.
11. O. Tanaseichuk, J. Borneman and T. Jiang. Separating metagenomic short reads into genomes via clustering (extended abstract). *Proc. 11th Workshop on Algorithms in Bioinformatics (WABI)*, Saarbrücken, Germany, Sept., 2011, pp. 298-313.
12. W. Li, J. Feng and T. Jiang. IsoLasso: A LASSO regression approach to RNA-Seq based transcriptome assembly (extended abstract). *Proc. 15th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Vancouver, BC, Canada, March, 2011, pp. 168-188.
13. Y. Pirola and T. Jiang. Haplotype inference on pedigrees with recombinations and mutations. *Proc. 10th Workshop on Algorithms in Bioinformatics (WABI)*, Sept., 2010, Liverpool, UK, pp. 148-161.
14. G. Shi, M.C. Peng and T. Jiang. Accurate identification of ortholog groups for multiple genomes. *Proc. 9th LSS Computational Systems Bioinformatics Conference (CSB)*, Stanford, CA, August, 2010, pp. 166-179.

15. W.B. Wang and T. Jiang. Inferring haplotypes from genotypes on a pedigree with mutations, genotyping errors and missing alleles. *Proc. 9th LSS Computational Systems Bioinformatics Conference (CSB)*, Stanford, CA, August, 2010, pp. 192-203. The best paper award.
16. W. Li, P. Ruedger, J. Borneman, and T. Jiang. Polony identification using the EM algorithm based on a Gaussian mixture model *Proc. 10th IEEE International Conference on Bioinformatics and Bioengineering (BIBE)*, Philadelphia, PA, May 31 - June 3, 2010, pp. 220-225.
17. J. Feng, W. Li and T. Jiang. Inference of isoforms from short sequence reads (extended abstract). *Proc. 14th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Lisbon, Portugal, April, 2010, pp. 138-157.
18. J. Xiao, T. Lou and T. Jiang. An efficient algorithm for haplotype inference on pedigrees with a small number of recombinants (extended abstract). *Proc. 17th Annual European Symposium on Algorithms (ESA)*, September, 2009, Copenhagen, Denmark, pp. 325-336.
19. G. Shi, L. Zhang and T. Jiang. MSOAR 2.0: Incorporating tandem duplications into ortholog assignment based on genome rearrangement. *Proc. 8th LSS Computational Systems Bioinformatics Conference (CSB)*, Stanford, August, 2009, pp. 1-12.
20. W.B. Wang and T. Jiang. Efficient inference of haplotypes from genotypes on a pedigree with mutations and missing alleles. *Proc. 20th Symposium on Combinatorial Pattern Matching (CPM)*, Lille, France, June, 2009, pp. 353-367.
21. W.B. Wang and T. Jiang. A new model of multi-marker correlation for genome-wide tag SNP selection. *Proc. 19th International Conference on Genome Informatics (GIW)*, Gold Coast, Australia, Dec., 2008, pp. 27-41. The best paper award.
22. J. Feng, R. Jiang and T. Jiang. A max-flow based approach to the identification of protein complexes using protein interaction and microarray data (extended abstract). *Proc. 7th LSS Computational Systems Bioinformatics Conference (CSB)*, Stanford, August, 2008, pp. 51-62.
23. J. Xiao, L. Wang, X. Liu, and T. Jiang. Finding additive biclusters with random background. *Proc. 19th Symposium on Combinatorial Pattern Matching (CPM)*, Pisa, Italy, 2008, pp. 263-276.
24. L. Liu and T. Jiang. Linear-time reconstruction of zero-recombinant Mendelian inheritance on pedigrees without mating loops. *Proc. 18th International Conference on Genome Informatics (GIW)*, pp. 95-106, Singapore, Dec. 2007.
25. Z. Fu and T. Jiang. Clustering of main orthologs for multiple genomes. *Proc. LSS Computational Systems Bioinformatics Conference (CSB)*, San Diego, August, 2007, pp. 195-202.
26. L. Liu, Y. Wu, S. Lonardi, and T. Jiang. Efficient algorithms for genome-wide tagSNP selection across populations via the linkage disequilibrium criterion. *Proc. LSS Computational Systems Bioinformatics Conference (CSB)*, San Diego, August, 2007, pp. 67-78.
27. X. Chen, L. Guo, Z. Fan, and T. Jiang. Learning position weight matrices from sequence and expression data. *Proc. LSS Computational Systems Bioinformatics Conference (CSB)*, San Diego, August, 2007, pp. 249-261.
28. Z. Fu and T. Jiang. Computing the Breakpoint Distance between Partially Ordered Genomes. *Proc. Fifth Asia-Pacific Bioinformatics Conference (APBC)*, Jan., 2007, Hong Kong, pp. 237-246.

29. J. Xiao, L. Liu, L. Xia, and T. Jiang. Fast elimination of redundant linear equations and reconstruction of recombination-free Mendelian inheritance on a pedigree. *Proc. 18th ACM-SIAM Symposium on Discrete Algorithms (SODA)*, 2007, New Orleans, LA, pp. 655-664.
30. X. Chen and T. Jiang. An improved Gibbs sampling method for motif discovery via sequence weighting. *Proc. LSS Computational Systems Bioinformatics Conference (CSB)*, August, 2006, Stanford, CA, pp. 239-247.
31. X. Chen, L. Liu, Z. Liu and T. Jiang. On the Minimum Common Integer Partition Problem. *Proc. Intern. Conf. on Algorithms and Complexity (CIAC)*, May, 2006, Rome, Italy, pp. 236-247.
32. Z. Fu, X. Chen, V. Vacic, P. Nan, Y. Zhong, and T. Jiang. A parsimony approach to genome-wide ortholog assignment. *Proc. 10th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Venice, Italy, April, 2006, 578-594.
33. P. Bonizzoni, G. Della Vedova, R. Dondi, and T. Jiang. Correlation clustering and consensus clustering. *Proc. 16th International Symposium on Algorithms and Computation (ISAAC)*, Hainan, China, December, 2005, LNCS 3827, pp. 226-235.
34. L. Liu, X. Chen, J. Xiao, T. Jiang. Complexity and approximation of the minimum recombination haplotype configuration problem. *Proc. 16th International Symposium on Algorithms and Computation (ISAAC)*, Hainan, China, December, 2005, LNCS 3827, pp. 370-379. Best paper nomination (top 5.35%).
35. H. Li, K. Zhang, and T. Jiang. Robust and accurate cancer classification with gene expression. *Proc. IEEE Computational Systems Bioinformatics Conference (CSB)*, Aug., 2005, Stanford, CA, pp. 310-321.
36. H. Li, K. Zhang, and T. Jiang. The regularized EM algorithm and applications to mixture models. *Proc. 20th National Conference on Artificial Intelligence (AAAI'05)*, Pittsburgh, PA, July, 2005, pp. 807-812.
37. Z. Liu, X. Chen, J. Borneman, and T. Jiang. A fast algorithm for approximate string matching on gene sequences. *Proc. 16th Symposium on Combinatorial Pattern Matching (CPM)*, Jeju Island, Korea, June, 2005, pp. 79-90.
38. A. Figueroa, A. Goldstein, T. Jiang, M. Kurowski, A. Lingas, and M. Persson. Approximate clustering of fingerprint vectors with missing values. *Proc. Computing: The Australasian Theory Symposium (CATS)*, Newcastle, Australia, Jan. 30 - Feb. 3, 2005, pp. 57-60.
39. X. Chen, J. Zheng, Z. Fu, P. Nan, Y. Zhong, S. Lonardi, and T. Jiang. Computing the assignment of orthologous genes via genome rearrangement. *Proc. Third Asia-Pacific Bioinformatics Conference (APBC)*, Jan., 2005, Singapore (invited keynote speech), pp. 363-378.
40. X. Chen, Z. Su, Y. Xu, and T. Jiang. Computational prediction of operons in *Synechococcus* sp. WH8102. *Proc. 15th International Conference on Genome Informatics (GIW)*, Yokohama, Japan, Dec., 2004, pp. 211-222. (The best paper award)
41. A. Figueroa, Z. Liu, J. Borneman, and T. Jiang. Building phylogenetic trees from binary oligonucleotide fingerprint vectors. *Proc. 26th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBS)*, September, 2004, San Francisco, CA, pp. 2844-2847.

42. Z. Liu, J. Borneman and T. Jiang. A software system for gene sequence database construction. *Proc. 26th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBS)*, September, 2004, San Francisco, CA, pp. 2797-2800.
43. H. Li, K. Zhang and T. Jiang. Clustering gene expression data by minimizing structural α -entropy. *Proc. IEEE Computer Society Bioinformatics Conference (CSB)*, August, 2004, Stanford, CA, pp. 142-151.
44. J. Li and T. Jiang. Haplotype association mapping by density-based clustering in case-control studies. *Proc. 2nd RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotypes*, CMU, Pittsburgh, PA, 2004, 47-57.
45. H. Li and T. Jiang. A class of edit kernels for SVMs to predic translation initiation sites in Eukaryotic mRNAs. *Proc. 8th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, San Diego, CA, March, 2004, 262-271.
46. J. Li and T. Jiang. An exact solution for finding minimum recombinant haplotype configurations on pedigrees with missing data by integer linear programming. *Proc. 8th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, San Diego, CA, March, 2004, 20-29.
47. Z. Su, P. Dam, X. Chen, V. Olman, T. Jiang, B. Palenik and Y. Xu. Computational Inference of Regulatory Pathways in Microbes: An application to phosphorus assimilation pathways in *Synechococcus* WH8102. *Proc. 14th International Conference on Genome Informatics (GIW)* (eds: M. Gribskov, M. Kanehisa, S. Miyano, and T. Takagi), pp. 3-13, Universal Academy Press Inc., Tokyo, Japan, 2003.
48. H. Li, T. Jiang, and K. Zhang. Efficient and robust feature extraction by maximum margin criterion. *Advances in Neural Information Processing Systems (NIPS)*, Vol. 17, Vancouver, Canada, Dec. 9-11, 2003.
49. K. Doi, J. Li and T. Jiang. Minimum recombinant haplotype configuration on tree pedigrees. *Proc. Workshop on Algorithms in Bioinformatics (WABI)*, Sept. 2003, Budapest, Hungary, pp. 339-353.
50. Z. Chen, T. Jiang, G. Lin, R. Rizzi, J. Wen, D. Xu, and Y. Xu. More reliable protein NMR peak assignment via improved 2-interval scheduling. *Proc. 11th Annual European Symposium on Algorithms (ESA)*, Sept. 2003, Budapest, Hungary, pp. 580-592.
51. A. Figueroa, J. Borneman, and T. Jiang. Clustering binary fingerprint vectors with missing values for DNA array data analysis. *Proc. IEEE Computer Society Bioinformatics Conference (CSB)*, Stanford, CA, Sept. 2003, pp. 38-47.
52. J. Li, C. Benner, T. Jiang, and Y. Zhou. Statistical validation of compound-structure selectivity relationship using NCI cancer database. *Proc. International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS)*, June, 2003, Las Vegas, Nevada, pp. 146-151.
53. J. Zheng, T. Close, T. Jiang, and S. Lonardi. Efficient selection of unique and popular oligos for large EST databases. *Proc. 14th Annual Symposium on Combinatorial Pattern Matching (CPM)*, Morelia, Mexico, June, 2003, pp. 384-401.

54. J. Li and T. Jiang. Efficient rule-based haplotyping algorithms for pedigree data. *Proc. 7th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Berlin, Germany, April, 2003, pp. 197-206.
55. Z. Chen, T. Jiang, G. Lin, J. Wen, D. Xu, and Y. Xu. Approximation algorithms for NMR spectral peak assignment. *Proc. 2nd Workshop on Algorithms in Bioinformatics (WABI)*, Rome, Italy, Sept., 2002, pp. 82-96.
56. G. Lin, D. Xu, Z. Chen, T. Jiang, and Y. Xu. An efficient branch-and-bound algorithm for the assignment of protein backbone NMR peaks. *Proc. First IEEE Computer Society Bioinformatics Conference (CSB)*, Palo Alto, CA, Aug. 2002, pp. 165-174.
57. L.Y. Lin, T. Jiang and K.M. Chao. Efficient algorithms for locating the length-constrained heaviest segments, with applications to biomolecular sequence analysis. *Proc. 27th International Symposium on Mathematical Foundations of Computer Science (MFCS)* August, 2002, Warszawa-Otwock, Poland, pp. 459-470.
58. G. Della Vedova, T. Jiang, J. Li, and J. Wen. Approximating minimum quartet inconsistency. *Proc. 13th ACM-SIAM Symposium on Discrete Algorithms (SODA)*, Jan., 2002, San Francisco, CA, pp. 894-895.
59. Z. Chen, T. Jiang, and G. Lin. Computing phylogenetic roots with bounded degrees and errors. *Proc. 7th WADS*, pp. 377-388, August, 2001, Providence, RI.
60. G. Lin, Z. Chen, T. Jiang, and J. Wen. The longest common subsequence problem for sequences with nested arc annotations. *Proc. ICALP'2001*, pp. 444-455, July 8-12, Crete, Greece.
61. T. Jiang, M. Li and P. Vitanyi. The incompressibility method. *Proc. 27th Annual Conference on Current Trends in Theory and Practice of Informatics (SOFSEM)* (invited), pp. 36-53, Dec. 2000, Milovy, Czech Republic.
62. T. Jiang, P. Kearney and G. Lin. Phylogenetic k-root and Steiner k-root problems. *Proc. 11th International Symposium on Algorithms and Computation (ISAAC)*, Taiwan, Dec. 2000, pp. 539-551.
63. T. Jiang and P. Zhao. A heuristic algorithm for blocked multiple sequence alignment. *Proc. IEEE International Symposium on Bio-Informatics & Biomedical Engineering (BIBE)*, Nov., 2000, pp. 176-183, VA.
64. E. Bach, J. Boyar, T. Jiang, K.S. Larsen and G. Lin. Better bounds on the accommodating ratio for the seat reservation problem. in *Proc. 6th International Computing and Combinatorics Conference (COCOON)*, Sydney, Australia, 2000, pp. 221-231.
65. T. Jiang, G. Lin, B. Ma and K. Zhang. The longest common subsequence problem for arc-annotated sequences. *Proc. 11th Annual Symposium on Combinatorial Pattern Matching (CPM)*, Montreal, Quebec, 2000, LNCS 1848, pp. 154-165.
66. D. Bryant, V. Berry, T. Jiang, P. Kearney, M. Li, T. Wareham, and H. Zhang. A practical algorithm for recovering the best supported edges in an evolutionary tree. *Proc. ACM-SIAM SODA'2000*, 287-296, San Francisco, CA.

67. C. Trendall, T. Wareham, X. Zhang, and T. Jiang. Stochastic heuristic algorithms for drug target identification. in *Proc. Pacific Symposium on Bioinformatics (PSB)*, pp. 392-403, 2000, Honolulu, Hawaii.
68. V. Berry, T. Jiang, P. Kearney, M. Li and T. Wareham. Quartet cleaning: Improved algorithms and simulations. *Proc. 7th Annual European Symposium on Algorithms (ESA)*, pp. 313-324, 1999, Prague, Czech Republic.
69. T. Jiang, M. Li and P. Vitanyi. Average-case complexity of Shellsort. *Proc. 26th International Colloquium on Automata, Languages, and Programming (ICALP)*, 1999, Prague, Czech Republic.
70. H. Buhrman, T. Jiang, M. Li and P. Vitanyi. New applications of the incompressibility method. *Proc. 26th International Colloquium on Automata, Languages, and Programming (ICALP)*, pp. 453-462, 1999, Prague, Czech Republic.
71. T. Jiang, M. Li and P. Vitanyi. The expected size of Heilbronn's triangles. *Proc. 14th Annual IEEE Conference on Computational Complexity*, 1999.
72. P. Kearney, M. Li, J. Tsang, and T. Jiang. Recovering branches on the tree of life: An approximation algorithm. In *Proc. 10th Annual ACM-SIAM Symposium on Discrete Algorithms (SODA)*, Jan. 1999.
73. T. Jiang, P. Kearney and M. Li. Orchestrating quartets: approximation and data correction. in *Proc. 39th IEEE Symposium on Foundations of Computer Science (FOCS)*, 1998, Palo Alto, CA, 416-425.
74. Y. Hua, T. Jiang and B. Wu. Aligning DNA sequences to minimize the change in protein. In *Proc. 8th Combinatorial Pattern Matching Conference (CPM)*, 1998, Rutgers Univ, NJ.
75. D. Fasulo, T. Jiang, R. Karp, and N. Sharma. Constructing maps using the span and inclusion relations. In *Proc. Second Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, 1998, New York City, NY.
76. D. Fasulo, T. Jiang, R. Karp, R. Settegren, and E. Thayer. An algorithmic approach to multiple complete digest mapping. In *Proc. First Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, 1997, Santa Fe, NM.
77. L. Wang, D. Gusfield, and T. Jiang. A more efficient approximation scheme for tree alignment. In *Proc. First Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, 1997, Santa Fe, NM.
78. B. DasGupta, T. Jiang, S. Kannan, M. Li and Z. Sweedyk. On the complexity and approximation of syntenic distance. In *Proc. First Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, 1997, Santa Fe, NM.
79. B. DasGupta, X. He, T. Jiang, M. Li, J. Tromp, and L. Zhang. On distances between phylogenies. In *Proc. 8th Annual ACM-SIAM Symposium on Discrete Algorithms (SODA)*, 1997, New Orleans.
80. T. Jiang and R. Karp. Mapping clones with a given ordering or interleaving. In *Proc. 8th Annual ACM-SIAM Symposium on Discrete Algorithms (SODA)*, 1997, New Orleans.
81. O. Etzioni, S. Hanks, T. Jiang, R. Karp, O. Madani, and O. Waarts. Efficient information gathering on the Internet. in *Proc. 37th IEEE Symposium on Foundations of Computer Science (FOCS)*, 1996, Burlington, Vermont, 234-243.

82. T. Jiang, Z. Jiang and D. Breslauer. Rotation of periodic strings and short superstrings. *Proc. Third South American Workshop on String Processing*, Recife, Brazil, 1996.
83. T. Hancock, T. Jiang, M. Li, and J. Tromp. Lower bounds on learning decision lists and trees. *Proc. 12th Symp. on Theoretical Aspects of Comp. Sci. (STACS)*, Munich, Germany, 1995.
84. J. Hein, T. Jiang, L. Wang and K. Zhang. On the complexity of comparing evolutionary trees. *Proc. 6th Combinatorial Pattern Matching Conference (CPM)*. Helsinki, Finland, 1995.
85. T. Jiang, E. Lawler and L. Wang. Aligning sequences via an evolutionary tree: complexity and approximation. *Proc. 26th ACM Symposium on Theory of Computing (STOC)*, 1994, Montreal, Canada, 760-769.
86. T. Jiang, J. Seiferas and P. Vitanyi. Two heads are better than two tapes. *Proc. 26th ACM Symposium on Theory of Computing (STOC)*, 1994, Montreal, Canada, 668-677.
87. T. Jiang, L. Wang and K. Zhang. Alignment of trees - an alternative to tree edit. *Proc. 5th Combinatorial Pattern Matching Conference (CPM)*, 1994, Asilomar, California, USA, 75-86.
88. T. Jiang and M. Li. On the approximation of shortest common supersequences and longest common subsequences. *Proc. 21st International Colloquium on Automata, Languages, and Programming (ICALP)*, 1994, Jerusalem, Israel.
89. T. Jiang and L. Wang. An approximation scheme for some Steiner tree problems in the plane. *Proc. 5th International Symposium on Algorithms and Computation (ISAAC)*, 1994, Beijing, P.R. China.
90. O. Ibarra, T. Jiang, N. Tran, and H. Wang. On the equivalence of two-way pushdown automata and counter machines over bounded languages. *Proc. 10th Symposium on Theoretical Aspects of Computer Science (STACS)*, 1993, Wurzburg, Germany.
91. T. Jiang and M. Li. k one-way heads cannot do string-matching. *Proc. 25th ACM Symposium on Theory of Computing (STOC)*, 1993, San Diego, California.
92. T. Jiang, A. Salomaa, K. Salomaa, and S. Yu. Inclusion is undecidable for pattern languages. *Proc. 20th International Colloquium on Automata, Languages, and Programming (ICALP)*, 1993, Lund, Sweden.
93. O. Ibarra, T. Jiang, N. Tran, and H. Wang. New decidability results concerning two-way counter machines and applications. *Proc. 20th International Colloquium on Automata, Languages, and Programming (ICALP)*, 1993, Lund, Sweden.
94. T. Jiang and M. Li. Approximating shortest superstrings with constraints. *Proc. 3rd Workshop on Algorithms and Data Structures (WADS)*, 1993, Montreal, Canada.
95. A. Blum, T. Jiang, M. Li, J. Tromp, and M. Yannakakis. Linear approximation of shortest superstrings. *Proc. 23rd ACM Symposium on Theory of Computing (STOC)*, 1991, New Orleans, Louisiana, USA, 328-336.
96. T. Jiang and B. Ravikumar. Minimal NFA problems are hard. *Proc. 18th International Colloquium on Automata, Languages, and Programming (ICALP)*, 1991, Madrid, Spain, *Lecture Notes in Computer Science* 510, Springer-Verlag, 629-638.

97. T. Jiang and M. Li. On the complexity of learning strings and sequences. *Proc. th Workshop on Computational Learning Theory (COLT)*, 1991, Santa Cruz, California, USA.
98. O. Ibarra, T. Jiang and H. Wang. Some results concerning 2-D on-line tessellation acceptors and 2-D alternating finite automata. *Proc. 16th International Symposium on Mathematical Foundations of Computer Science (MFCS)*, 1991, Warsaw, Poland.
99. T. Jiang, E. McDowell and B. Ravikumar. The structure and complexity of minimal NFA's over a unary alphabet. *Proc. 11th Conference on Foundations of Software Technology and Theoretical Computer Science (FTSTCS)*, 1991, New Delhi, India.
100. T. Jiang. On the complexity of (off-line) 1-tape Alternating TM's running in constant reversals, *Proc. 2nd International Conference on Computing and Information (ICCI)*, 1990, Niagara Falls, Canada, *Lecture Notes in Computer Science*, Springer-Verlag, 92-99.
101. O. Ibarra, T. Jiang and H. Wang. String editing on a one-way linear array of finite-state machines. *Proc. 19th International Conference on Parallel Processing (ICPP)*, 1990, St. Charles, IL, USA.
102. O. Ibarra, T. Jiang and H. Wang. Efficient parallel algorithms for solving set recurrence equations and applications. *Proc. 2nd IEEE Symposium on Parallel and Distributed Processing*, 1990, Dallas, Texas, USA.
103. T. Jiang. The synchronization of nonuniform networks of finite automata, *Proc. 30th IEEE Symposium on Foundations of Computer Science (FOCS)*, 1989, Research Triangle, North Carolina, 376-381.
104. O. Ibarra, T. Jiang and H. Wang. Parallel parsing on a one-way linear array of finite-state machines. *Proc. 9th Conference on Foundations of Software Technology and Theoretical Computer Science (FSTTCS)*, 1989, Bangalore, India, *Lecture Notes in Computer Science*, Springer-Verlag.
105. O. Ibarra and T. Jiang. Trading reversals for alternation. *Proc. IEEE Structure in Complexity Theory 3rd Annual Conference*, 1988, Washington DC, 70-77.
106. J. Chang, O. Ibarra, T. Jiang, and B. Ravikumar. Some languages in NC^1 . *Proc. 1988 Aegean Workshop on Computing: 3rd International Workshop on Parallel Computation and VLSI Theory*, Corfu Island, Greece, *Lecture Notes in Computer Science* 319, Springer-Verlag, 64-73.
107. J. Chang, O. Ibarra, T. Jiang, and M. Palis. Systolic algorithms for some scheduling and graph problems. *Proc. International Conference on Systolic Arrays*, 1988, San Diego, CA.
108. O. Ibarra and T. Jiang. Learning regular languages from counterexamples. *Proc. First Workshop on Computational Learning Theory (COLT)*, 1988, MIT, 371-385.
109. O. Ibarra and T. Jiang. On the computing power of one-way cellular arrays. *Proc. 14th International Colloquium on Automata, Languages and Programming (ICALP)*, 1987, Karlsruhe, F.R.Germany, *Lecture Notes in Computer Science* 267, Springer-Verlag, 550-562.

Conference Abstracts and Posters (not peer-reviewed):

1. C. Yang, H. Liao, T. Jiang, and F. Sladek. Comparison of HNF4 binding sites in the human and mouse genomes. *Keystone Meeting on Molecular Biology*, 2004.

2. A. Figueroa, J. Borneman, and T. Jiang. Clustering binary fingerprint vectors with missing values for DNA array data analysis. The best poster award at *RECOMB'2003*, Berlin, Germany, 2003.
3. C. Yang, T. Jiang, and F. Sladek. Analysis of nuclear receptor HNF4 binding sites in the human genome. *Genomic Approaches to Gene Regulation*, Cold Spring Harbor, March, 2003.
4. Lea Valinsky, Gianluca Della Vedova, Marek Chrobak, Tao Jiang, James Borneman, Analysis of fungal community composition using an array-based oligonucleotide fingerprinting approach, *Annual of American Society for Microbiology (ASM)*, 2002.
5. Francey Sladek, Kyle Ellrott, Chuhu Yang, and Tao Jiang, Searching the human genome for HNF4 α binding sites using computational methods and experimental verification. *Keystone Meeting on Molecular Biology*, April, 2002.
6. Li Jia, Michael Clegg, and Tao Jiang, Analysis of the AtMyb gene family evolutionary dynamics on the Arabidopsis genome. Poster session at *Gorden Conference on Molecular Evolution*, Ventura, CA, Jan. 13-18, 2002; Poster at *RECOMB'2002*, DC, April, 2002.
7. Y. Xu, D. Xu, D. Kim, Z. Chen, G. Lin, J. Wen, and T. Jiang, Combinatorial optimization algorithms for assignment of protein backbone NMR peaks. Poster (PS-109) at *RECOMB'2002*, DC, April, 2002.
8. Lea Valinsky, Lexa Scupham, Gianluca Della Vedova, Marek Chrobak, Tao Jiang, Andres Figueroa, Jack Hartin, Bei Yin, James Borneman. A DNA array approach for analysis of microbial communities using oligonucleotide fingerprinting of ribosomal RNA genes. *Annual Meeting of the American Phytopathological Society*, Salt Lake City, Utah, USA, August 25-29, 2001; *Phytopathology* June, 2001. 91 (6 Supplement):S90.

Books and Book Chapters:

1. Kun-Mao Chao and Tao Jiang. Computational methods for biomolecular sequence comparison. *Frontiers in Biostatistics and Bioinformatics: University of Science and Technology of China 50th Anniversary Special Series*, 2009, pp. 154-161.
2. Bhaskar DasGupta, Xin He, Tao Jiang, Ming Li, John Tromp and Louxin Zhang. Nearest Neighbor Interchange and Related Distances. *Encyclopedia of Algorithms*, Ming-Yang Kao (editor), Springer-Verlag, 2008.
3. Lea Valinsky, Alexandra J Scupham, Gianluca Della Vedova, Zheng Liu, Andres Figueroa, Katechan Jampachaisri, Bei Yin, Elizabeth Bent, Robert Mancini-Jones, James Press, Tao Jiang and James Borneman. 2004. Oligonucleotide Fingerprinting of Ribosomal RNA Genes (OFRG), pp. 569-585. In G. A. Kowalchuk, F. J. de Bruijn, I. M. Head, A. D. L. Akkermans, J. D. van Elsas (ed.) *Molecular Microbial Ecology Manual* (2nd ed). Kluwer Academic Publishers, Dordrecht, The Netherlands.
4. T. Jiang and L. Wang. Methods for multiple sequence alignment and applications. *Current Topics in Computational Molecular Biology* (eds. T. Jiang, Y. Xu and M.Q. Zhang), the *MIT Press Series on Computational Molecular Biology*, MIT Press, Feb. 2002, 71-110.
5. Tao Jiang, Ying Xu and Michael Zhang (eds). *Current Topics in Computational Molecular Biology*. the *MIT Press Series on Computational Molecular Biology*, MIT Press, Feb. 2002.

6. B. DasGupta, X. He, T. Jiang, M. Li, J. Tromp, and L. Zhang. On computing the nearest neighbor interchange distance. *DIMACS volume on Discrete Mathematical Problems with Medical Applications*, Vol. 55, pp. 125-143, 2000.
7. L. Wang and T. Jiang. Computing shortest networks with fixed topologies. *Advances in Steiner Trees*, D.Z. Du, J.M. Smith and J.H. Rubinstein (eds.), Kluwer Academic Publishers, 2000, pp. 39-62.
8. T. Jiang, M. Li and P. Vitanyi. Some examples of average-case analysis by the incompressibility method. in *Jewels are Forever: Contributions on Theoretical Computer Science in Honor of Arto Salomaa*, J. Karhumaki, H. Maurer, G. Paun, and G. Rozenberg (eds.), Springer, 1999, pp. 250-261.
9. B. DasGupta, X. He, T. Jiang, M. Li, J. Tromp, and L. Zhang. Computing distances between evolutionary trees. in *Handbook in Combinatorial Optimization*, D.Z. Du and P. Pardalos (eds.), Vol. 2, Kluwer Academic Publishers, 1998.
10. T. Jiang, M. Li and B. Ravikumar. Basic notions in computational complexity. In *Algorithms and Theory of Computation Handbook*, Mikhail Atallah (ed.), CRC Press, 1998.
11. T. Jiang, M. Li, B. Ravikumar and K. Regan. Formal grammars and languages. In *Algorithms and Theory of Computation Handbook*, Mikhail Atallah (ed.), CRC Press, 1998.
12. T. Jiang, M. Li, B. Ravikumar and K. Regan. Computability. In *Algorithms and Theory of Computation Handbook*, Mikhail Atallah (ed.), CRC Press, 1998.
13. T. Jiang and D.T. Lee (eds). *Computing and Combinatorics, Proceedings of the Third Annual International Conference*. LNCS 1276, Springer, August 1997, 522 pp.
14. T. Jiang and M. Li. Shortest common superstrings. In *Pattern Matching Algorithms*, A. Apostolico and Z. Galil (eds.), Oxford University Press, 1997, 237-265.
15. T. Jiang, M. Li and B. Ravikumar. Formal models and computability. In *Handbook for Computer Science and Engineering*, A. Tucker (ed.), CRC Press, 1996, 31-63.
16. T. Jiang and M. Li. Optimization problems in molecular biology. in *Advances in Optimization and Approximation*, D.Z. Du and J. Sun (eds.), Kluwer Academic Publishers, MA, 1994, 195-216.
17. O. Ibarra and T. Jiang. On some open problems concerning the complexity of cellular arrays. In *Results and Trends in Theoretical Computer Science*, J. Karhumaki, H. Maurer, G. Rozenberg (eds.), Springer-Verlag, LNCS 812, 1994, 183-196.