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 (especially sequence annotation and comparison, comparative genomics, haplotype inference, and pedigree analysis), Information Gathering and Retrieval, Computational Complexity in Automata Theory, and Machine Learning.

Employment History:

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.
Visting 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, fifteen Ph.D's, three M.Eng's, and eleven 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'99,04-05,08-11,14-21
    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'05-20, 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. "EAGER: Transcript-Based Differential Expression Analysis for Population Data Without Predefined Conditions" (PI: T. Jiang), $200K, 9/2016 - 8/2019, *NSF IIS Research Grant*.

2. "Incorporation of Genetic Variation Data into Transcriptomine" (PI: F. Sladek; co-PI: T. Jiang), $150K, 9/2016 - 8/2018, *NIH NURSA NDSP Grant via Baylor College of Medicine*.

3. "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*.

4. "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*.

5. "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*.

6. "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*.

7. "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.

8. "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*.

9. "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*.

10. "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 Integative Genome Biology*, UCR.

11. "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*.

12. "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*.

13. "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)*.

14. "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)*.

15. "Algorithmic Problems in Haplotyping, Oligonucleotide Fingerprinting, and NMR Peak Assignment", $200K, 2003-07, *NSF CCF Research Grant*.

16. "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*.

17. "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.

18. "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*.

19. "ITR/ACS: Computational Techniques for Applied Bioinformatics" (co-PIs: M. Clegg and M. Li), $785K, 2000-04, *NSF Inoformation Technology Research (ITR) Grant (large)*.

20. "Efficient Algorithms for Molecular Sequences, Evolutionary Trees, and Physical Maps", $267K, 2000-04, *NSF CCR Research Grant*.

21. "Life Sciences Informatics Program Opportunity Award", $15K, 2000-01, *UC Life Science Informatics*.

22. "Average-Case Analysis by the Incompressibility Method", $1300, 2000-01, *UCR Academic Senate Research Funds*.

23. "Approximation Algorithms for Sequences, Trees and Maps, and Average-Case Analysis by Incompressibility", $42K/year, 2000-03, *NSERC Research Grant*.

24. "Computational Techniques for Industrial Bioinformatics" (with M. Li, et al.), $120K/year, 1998-2000, *Communication and Information Technology Ontario (CITO) Research Grant*.

25. "Algorithms for Some Combinatorial Problems Arising in Computational Biology" (with L. WANG and M. Li), $322K (HKD), 1997, *Hong Kong UGC Research Grant*.

26. "Computer Equipment for a Computational Molecular Biology Laboratory" (with S. Qiao and W.F.S. Smyth), $65.5K, 1997, *NSERC Equipment Grant*.

27. "Approximation Algorithms for Sequences, Average-Case Analysis, and State Complexity of Two-Way Finite Automata", $33.3K/year, 1995-99, *NSERC Research Grant*.

28. "Computational Issues in Alignment and Sequencing" (with D. WOOD, et al.), $100K/year, 1994-1997, *MRC/NSERC Canadian Genome Analysis and Technology Research Grant*.

29. "Efficient Algorithms and Complexity Theory for Biological Sequences, Shortest Common Supersequences, and Succinct Finite Automata", $26K/year, 1992-95, *NSERC Research Grant*.

30. "Expansion of Parallel Computing System" (with S. QIAO), $36.7K, 1994, *NSERC Equipment Grant*.

31. "Transputer Multiprocessor System" (with S. QIAO), $40K, 1991, *NSERC Equipment Grant*.

32. "Networks of Finite-State Machines: Algorithms, Simulation, Complexity, and Synchronization", $20K/year, 1990-92, *NSERC Operating Grant*.

33. "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) Uinversity 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) Uinversity 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) Uinversity 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 Promotors 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, Carnagie 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 logisitics)

(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 Infromatics 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 Informatcs 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. 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.

31. Introduction to Computational Biology and Genomics

    (a) Tsinghua University, Dept. of Comp. Sci. grad student orientation, Sept. 2005
    (b) Institute of Software, Chinese Academy of Sciences, Dec. 14, 2005
    (c) St. John's University, Taipei, Taiwan, May 24, 2006

Journal Publications:

1. J. 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*, accepted 6/30, 2020.

2. 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*, accepted 4/17/2020.

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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. 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. To be presented at the *24th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Padova, Italy, May 10-13, 2020.

2. 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)*, New York, NY, Feb. 7-12, 2020.

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