

# Tao Jiang

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

79  
papers

1,573  
citations

22  
h-index

37  
g-index

81  
ext. papers

2,010  
ext. citations

4.5  
avg, IF

4.91  
L-index

| #  | Paper   | IF   | Citations |
|----|---|------|-----------|
| 79 | Assignment of orthologous genes via genome rearrangement. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2005</b> , 2, 302-15  | 3    | 101       |
| 78 | IsoLasso: a LASSO regression approach to RNA-Seq based transcriptome assembly. <i>Journal of Computational Biology</i> , <b>2011</b> , 18, 1693-707   | 1.7  | 100       |
| 77 | NeoDTI: neural integration of neighbor information from a heterogeneous network for discovering new drug-target interactions. <i>Bioinformatics</i> , <b>2019</b> , 35, 104-111                         | 7.2  | 97        |
| 76 | SCALE method for single-cell ATAC-seq analysis via latent feature extraction. <i>Nature Communications</i> , <b>2019</b> , 10, 4576   | 17.4 | 70        |
| 75 | Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. <i>Bioinformatics</i> , <b>2012</b> , 28, 2914-21   | 7.2  | 68        |
| 74 | Computing the minimum recombinant haplotype configuration from incomplete genotype data on a pedigree by integer linear programming. <i>Journal of Computational Biology</i> , <b>2005</b> , 12, 719-39 | 1.7  | 62        |
| 73 | Efficient inference of haplotypes from genotypes on a pedigree. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2003</b> , 1, 41-69   | 1    | 61        |
| 72 | MSOAR: a high-throughput ortholog assignment system based on genome rearrangement. <i>Journal of Computational Biology</i> , <b>2007</b> , 14, 1160-75  | 1.7  | 60        |
| 71 | MSOAR 2.0: Incorporating tandem duplications into ortholog assignment based on genome rearrangement. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 10   | 3.6  | 46        |
| 70 | TITER: predicting translation initiation sites by deep learning. <i>Bioinformatics</i> , <b>2017</b> , 33, i234-i242  | 7.2  | 44        |
| 69 | Pattern languages with and without erasing. <i>International Journal of Computer Mathematics</i> , <b>1994</b> , 50, 147-163  | 1.2  | 44        |
| 68 | Inference of isoforms from short sequence reads. <i>Journal of Computational Biology</i> , <b>2011</b> , 18, 305-21   | 1.7  | 41        |
| 67 | A class of edit kernels for SVMs to predict translation initiation sites in eukaryotic mRNAs. <i>Journal of Computational Biology</i> , <b>2005</b> , 12, 702-18  | 1.7  | 41        |
| 66 | TransComb: genome-guided transcriptome assembly via combing junctions in splicing graphs. <i>Genome Biology</i> , <b>2016</b> , 17, 213   | 18.3 | 40        |
| 65 | Analysis of Ribosome Stalling and Translation Elongation Dynamics by Deep Learning. <i>Cell Systems</i> , <b>2017</b> , 5, 212-220.e6   | 10.6 | 39        |
| 64 | Approximation algorithms for tree alignment with a given phylogeny. <i>Algorithmica</i> , <b>1996</b> , 16, 302-315   | 0.9  | 39        |
| 63 | The longest common subsequence problem for sequences with nested arc annotations. <i>Journal of Computer and System Sciences</i> , <b>2002</b> , 65, 465-480  | 1    | 36        |

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|----|--|------|----|
| 62 | The longest common subsequence problem for arc-annotated sequences. <i>Journal of Discrete Algorithms</i> , <b>2004</b> , 2, 257-270   |      | 32 |
| 61 | TAPAS: tool for alternative polyadenylation site analysis. <i>Bioinformatics</i> , <b>2018</b> , 34, 2521-2529   | 7.2  | 30 |
| 60 | THE STRUCTURE AND COMPLEXITY OF MINIMAL NFAB OVER A UNARY ALPHABET. <i>International Journal of Foundations of Computer Science</i> , <b>1991</b> , 02, 163-182                                  | 0.6  | 29 |
| 59 | Efficient rule-based haplotyping algorithms for pedigree data <b>2003</b> ,  |      | 27 |
| 58 | DeepHINT: understanding HIV-1 integration via deep learning with attention. <i>Bioinformatics</i> , <b>2019</b> , 35, 1660-1667  | 7.2  | 26 |
| 57 | An exact solution for finding minimum recombinant haplotype configurations on pedigrees with missing data by integer linear programming <b>2004</b> ,  |      | 20 |
| 56 | Differential gene expression analysis using coexpression and RNA-Seq data. <i>Bioinformatics</i> , <b>2013</b> , 29, 2153-61   | 7.2  | 19 |
| 55 | Minimum Recombinant Haplotype Configuration on Tree Pedigrees. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 339-353  | 0.9  | 18 |
| 54 | A deep boosting based approach for capturing the sequence binding preferences of RNA-binding proteins from high-throughput CLIP-seq data. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e129 | 20.1 | 17 |
| 53 | A Further Improved Approximation Algorithm for Breakpoint Graph Decomposition. <i>Journal of Combinatorial Optimization</i> , <b>2004</b> , 8, 183-194   | 0.9  | 17 |
| 52 | Approximation algorithms for NMR spectral peak assignment. <i>Theoretical Computer Science</i> , <b>2003</b> , 299, 211-229  | 1.1  | 16 |
| 51 | . <i>Computing in Science and Engineering</i> , <b>2002</b> , 4, 50-62   | 1.5  | 16 |
| 50 | Differential regulation enrichment analysis via the integration of transcriptional regulatory network and gene expression data. <i>Bioinformatics</i> , <b>2015</b> , 31, 563-71                 | 7.2  | 15 |
| 49 | Improved Approximation Algorithms for the Maximum Happy Vertices and Edges Problems. <i>Algorithmica</i> , <b>2018</b> , 80, 1412-1438   | 0.9  | 15 |
| 48 | An approximation scheme for some Steiner tree problems in the plane. <i>Networks</i> , <b>1996</b> , 28, 187-193   | 1.6  | 15 |
| 47 | DIFFUSE: predicting isoform functions from sequences and expression profiles via deep learning. <i>Bioinformatics</i> , <b>2019</b> , 35, i284-i294  | 7.2  | 14 |
| 46 | A survey on haplotyping algorithms for tightly linked markers. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2008</b> , 6, 241-59  | 1    | 14 |
| 45 | The average-case area of Heilbronn-type triangles*. <i>Random Structures and Algorithms</i> , <b>2002</b> , 20, 206-219.   | 0.8  | 14 |

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|----|---|------|----|
| 44 | DeepPASTA: deep neural network based polyadenylation site analysis. <i>Bioinformatics</i> , <b>2019</b> , 35, 4577-4585   |      | 13 |
| 43 | Complexity and approximation of the minimum recombinant haplotype configuration problem. <i>Theoretical Computer Science</i> , <b>2007</b> , 378, 316-330   | 1.1  | 13 |
| 42 | New applications of the incompressibility method: Part II. <i>Theoretical Computer Science</i> , <b>2000</b> , 235, 59-70   | 1.1  | 13 |
| 41 | A lower bound on the average-case complexity of shellsort. <i>Journal of the ACM</i> , <b>2000</b> , 47, 905-911  | 2    | 12 |
| 40 | Improved Approximation Algorithms for the Maximum Happy Vertices and Edges Problems. <i>Lecture Notes in Computer Science</i> , <b>2015</b> , 159-170   | 0.9  | 12 |
| 39 | DeepIsoFun: a deep domain adaptation approach to predict isoform functions. <i>Bioinformatics</i> , <b>2019</b> , 35, 2535-2544   | 7.2  | 12 |
| 38 | DNA sequencing and string learning. <i>Mathematical Systems Theory</i> , <b>1996</b> , 29, 387-405  |      | 11 |
| 37 | Orchestrating quartets: approximation and data correction   |      | 10 |
| 36 | Clustering of main orthologs for multiple genomes. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2008</b> , 6, 573-84   | 1    | 9  |
| 35 | A novel machine learning framework for automated biomedical relation extraction from large-scale literature repositories. <i>Nature Machine Intelligence</i> , <b>2020</b> , 2, 347-355                   | 22.5 | 8  |
| 34 | An efficient algorithm for haplotype inference on pedigrees with recombinations and mutations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2012</b> , 9, 12-25          | 3    | 8  |
| 33 | Some Algorithmic Challenges in Genome-Wide Ortholog Assignment. <i>Journal of Computer Science and Technology</i> , <b>2010</b> , 25, 42-52   | 1.7  | 8  |
| 32 | A Parsimony Approach to Genome-Wide Ortholog Assignment. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 578-594   | 0.9  | 8  |
| 31 | Efficient Algorithms for Reconstructing Zero-Recombinant Haplotypes on a Pedigree Based on Fast Elimination of Redundant Linear Equations. <i>SIAM Journal on Computing</i> , <b>2009</b> , 38, 2198-2219 | 1.1  | 7  |
| 30 | Average-case analysis of algorithms using Kolmogorov complexity. <i>Journal of Computer Science and Technology</i> , <b>2000</b> , 15, 402-408  | 1.7  | 7  |
| 29 | DeepLPI: a multimodal deep learning method for predicting the interactions between lncRNAs and protein isoforms. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 24   | 3.6  | 7  |
| 28 | Two heads are better than two tapes. <i>Journal of the ACM</i> , <b>1997</b> , 44, 237-256  | 2    | 6  |
| 27 | A linear-time algorithm for reconstructing zero-recombinant haplotype configuration on pedigrees without mating loops. <i>Journal of Combinatorial Optimization</i> , <b>2010</b> , 19, 217-240           | 0.9  | 5  |

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|----|---|------|---|
| 26 | Mapping Clones with a Given Ordering or Interleaving. <i>Algorithmica</i> , <b>1998</b> , 21, 262-284   | 0.9  | 5 |
| 25 | Constructing tissue-specific transcriptional regulatory networks via a Markov random field. <i>BMC Genomics</i> , <b>2018</b> , 19, 884   | 4.5  | 5 |
| 24 | Inferring haplotypes from genotypes on a pedigree with mutations, genotyping errors and missing alleles. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2011</b> , 9, 339-65 | 1    | 4 |
| 23 | Computational assignment of protein backbone NMR peaks by efficient bounding and filtering. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2003</b> , 1, 387-409             | 1    | 4 |
| 22 | More reliable protein NMR peak assignment via improved 2-interval scheduling. <i>Journal of Computational Biology</i> , <b>2005</b> , 12, 129-46  | 1.7  | 4 |
| 21 | Modeling multi-species RNA modification through multi-task curriculum learning. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 3719-3734   | 20.1 | 4 |
| 20 | A linear-time algorithm for reconstructing zero-recombinant haplotype configuration on a pedigree. <i>BMC Bioinformatics</i> , <b>2012</b> , 13 Suppl 17, S19                                 | 3.6  | 3 |
| 19 | Average-case analysis of QuickSort and Binary Insertion Tree height using incompressibility. <i>Information Processing Letters</i> , <b>2007</b> , 103, 45-51                                 | 0.8  | 3 |
| 18 | A New Model of Multi-Marker Correlation for Genome-Wide Tag SNP Selection <b>2008</b> ,   |      | 3 |
| 17 | LEARNING POSITION WEIGHT MATRICES FROM SEQUENCE AND EXPRESSION DATA <b>2007</b> ,   |      | 3 |
| 16 | Dysregulation of Hypothalamic Gene Expression and the Oxytocinergic System by Soybean Oil Diets in Male Mice. <i>Endocrinology</i> , <b>2020</b> , 161,                                       | 4.8  | 3 |
| 15 | SDEAP: a splice graph based differential transcript expression analysis tool for population data. <i>Bioinformatics</i> , <b>2016</b> , 32, 3593-3602   | 7.2  | 2 |
| 14 | An Efficient Algorithm for Haplotype Inference on Pedigrees with a Small Number of Recombinants. <i>Algorithmica</i> , <b>2012</b> , 62, 951-981  | 0.9  | 2 |
| 13 | Workshop: Transcriptome assembly from RNA-Seq data: Objectives, algorithms and challenges <b>2011</b> ,   |      | 2 |
| 12 | AN IMPROVED GIBBS SAMPLING METHOD FOR MOTIF DISCOVERY VIA SEQUENCE WEIGHTING <b>2006</b> ,  |      | 2 |
| 11 | CLUSTERING OF MAIN ORTHOLOGS FOR MULTIPLE GENOMES <b>2007</b> ,   |      | 2 |
| 10 | DeepHINT: Understanding HIV-1 integration via deep learning with attention  |      | 2 |
| 9  | Facile Fabrication of Multilayer Stretchable Electronics via a Two-mode Mechanical Cutting Process.. <i>ACS Nano</i> , <b>2021</b> ,  | 16.7 | 2 |

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|---|--|------|---|
| 8 | A simulated annealing approach for resolution guided homogeneous cryo-electron microscopy image selection. <i>Quantitative Biology</i> , <b>2020</b> , 8, 51-63                      | 3.9  | 1 |
| 7 | FreePSI: an alignment-free approach to estimating exon-inclusion ratios without a reference transcriptome. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e11                     | 20.1 | 1 |
| 6 | More Reliable Protein NMR Peak Assignment via Improved 2-Interval Scheduling. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 580-592                                       | 0.9  | 1 |
| 5 | Enhancement and Imputation of Peak Signal Enables Accurate Cell-Type Classification in scATAC-seq. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 658352                           | 4.5  | 1 |
| 4 | Riboexp: an interpretable reinforcement learning framework for ribosome density modeling. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,                                     | 13.4 | 1 |
| 3 | Beyond evolutionary trees. <i>Natural Computing</i> , <b>2010</b> , 9, 421-435   | 1.3  | 0 |
| 2 | FINER: enhancing the prediction of tissue-specific functions of isoforms by refining isoform interaction networks. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqab057 | 3.7  | 0 |
| 1 | The Incompressibility Method. <i>Lecture Notes in Computer Science</i> , <b>2000</b> , 36-53   | 0.9  |   |