

Louxin Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

125
papers

2,797
citations

279798

23
h-index

214800

47
g-index

133
all docs

133
docs citations

133
times ranked

2718
citing authors

#	ARTICLE	IF	CITATIONS
1	How much can deep learning improve prediction of the responses to drugs in cancer cell lines?. Briefings in Bioinformatics, 2022, 23, .	6.5	12
2	Detecting molecular subtypes from multi-omics datasets using SUMO. Cell Reports Methods, 2022, 2, 100152.	2.9	6
3	Asymptotic enumeration and distributional properties of galled networks. Journal of Combinatorial Theory - Series A, 2022, 189, 105599.	0.8	4
4	A survey and systematic assessment of computational methods for drug response prediction. Briefings in Bioinformatics, 2021, 22, 232-246.	6.5	42
5	On the asymptotic growth of the number of tree-child networks. European Journal of Combinatorics, 2021, 93, 103278.	0.8	11
6	The Bourque distances for mutation trees of cancers. Algorithms for Molecular Biology, 2021, 16, 9.	1.2	6
7	Guest Editorial for the 17th Asia Pacific Bioinformatics Conference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2123-2124.	3.0	0
8	Introduction to the Special Issue of the 18th Annual International RECOMB Satellite Workshop on Comparative Genomics. Journal of Bioinformatics and Computational Biology, 2021, 19, 2102003.	0.8	0
9	Stage-specific protein-domain mutational profile of invasive ductal breast cancer. BMC Medical Genomics, 2020, 13, 150.	1.5	0
10	Counting and enumerating tree-child networks and their subclasses. Journal of Computer and System Sciences, 2020, 114, 84-104.	1.2	16
11	Counting and enumerating galled networks. Discrete Applied Mathematics, 2020, 283, 644-654.	0.9	10
12	Evidence for transmission of COVID-19 prior to symptom onset. ELife, 2020, 9, .	6.0	259
13	Recent Progresses in the Combinatorial and Algorithmic Study of Rooted Phylogenetic Networks. Lecture Notes in Computer Science, 2020, , 22-27.	1.3	0
14	Clusters, Trees, and Phylogenetic Network Classes. Computational Biology, 2019, , 277-315.	0.2	10
15	ZDOG: zooming in on dominating genes with mutations in cancer pathways. BMC Bioinformatics, 2019, 20, 740.	2.6	1
16	Generating normal networks via leaf insertion and nearest neighbor interchange. BMC Bioinformatics, 2019, 20, 642.	2.6	4
17	Compression of Phylogenetic Networks and Algorithm for the Tree Containment Problem. Journal of Computational Biology, 2019, 26, 285-294.	1.6	5
18	Online buffer management for transmitting packets with processing cycles. Theoretical Computer Science, 2018, 723, 73-83.	0.9	0

#	ARTICLE	IF	CITATIONS
19	Solving the tree containment problem in linear time for nearly stable phylogenetic networks. <i>Discrete Applied Mathematics</i> , 2018, 246, 62-79.	0.9	13
20	S-Cluster++: a fast program for solving the cluster containment problem for phylogenetic networks. <i>Bioinformatics</i> , 2018, 34, i680-i686.	4.1	6
21	RecPhyloXML: a format for reconciled gene trees. <i>Bioinformatics</i> , 2018, 34, 3646-3652.	4.1	22
22	A decomposition theorem and two algorithms for reticulation-visible networks. <i>Information and Computation</i> , 2017, 252, 161-175.	0.7	21
23	Reconciliation With Nonbinary Gene Trees Revisited. <i>Journal of the ACM</i> , 2017, 64, 1-28.	2.2	2
24	A program to compute the soft Robinson-Foulds distance between phylogenetic networks. <i>BMC Genomics</i> , 2017, 18, 111.	2.8	11
25	Improved anticancer drug response prediction in cell lines using matrix factorization with similarity regularization. <i>BMC Cancer</i> , 2017, 17, 513.	2.6	118
26	Predicting chemotherapeutic drug combinations through gene network profiling. <i>Scientific Reports</i> , 2016, 6, 18658.	3.3	24
27	On Tree-Based Phylogenetic Networks. <i>Journal of Computational Biology</i> , 2016, 23, 553-565.	1.6	41
28	A program for verification of phylogenetic network models. <i>Bioinformatics</i> , 2016, 32, i503-i510.	4.1	12
29	Superiority and Complexity of the Spaced Seeds. , 2016, , 2166-2170.		2
30	Fitness Profiling Links Topoisomerase II Regulation of Centromeric Integrity to Doxorubicin Resistance in Fission Yeast. <i>Scientific Reports</i> , 2015, 5, 8400.	3.3	21
31	Locating a Tree in a Phylogenetic Network in Quadratic Time. <i>Lecture Notes in Computer Science</i> , 2015, , 96-107.	1.3	15
32	Superiority and Complexity of the Spaced Seeds. , 2015, , 1-5.		0
33	Are the Duplication Cost and Robinson-Foulds Distance Equivalent?. <i>Journal of Computational Biology</i> , 2014, 21, 578-590.	1.6	5
34	Profiling the transcription factor regulatory networks of human cell types. <i>Nucleic Acids Research</i> , 2014, 42, 12380-12387.	14.5	19
35	Effect of Incomplete Lineage Sorting On Tree-Reconciliation-Based Inference of Gene Duplication. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 477-485.	3.0	6
36	Reconciliation with Non-binary Gene Trees Revisited. <i>Lecture Notes in Computer Science</i> , 2014, , 418-432.	1.3	14

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37	Maximum Likelihood Inference of the Evolutionary History of a PPI Network from the Duplication History of Its Proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1412-1421.	3.0	9
38	MOTIF DISCOVERY WITH DATA MINING IN 3D PROTEIN STRUCTURE DATABASES: DISCOVERY, VALIDATION AND PREDICTION OF THE U-SHAPE ZINC BINDING ("HUF-ZINC") MOTIF. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340008.	0.8	3
39	Counting motifs in the human interactome. <i>Nature Communications</i> , 2013, 4, 2241.	12.8	52
40	Inverted Expression Profiles of Sex-Biased Genes in Response to Toxicant Perturbations and Diseases. <i>PLoS ONE</i> , 2013, 8, e56668.	2.5	5
41	A Linear-Time Algorithm for Reconciliation of Non-binary Gene Tree and Binary Species Tree. <i>Lecture Notes in Computer Science</i> , 2013, , 190-201.	1.3	4
42	Computing Distances Between Evolutionary Trees. , 2013, , 747-781.		1
43	A Tool for Non-binary Tree Reconciliation. <i>Lecture Notes in Computer Science</i> , 2013, , 40-51.	1.3	0
44	Effect of Incomplete Lineage Sorting on Tree-Reconciliation-Based Inference of Gene Duplication. <i>Lecture Notes in Computer Science</i> , 2013, , 261-272.	1.3	2
45	APPROXIMATING THE SPANNING k -TREE FOREST PROBLEM. <i>International Journal of Foundations of Computer Science</i> , 2012, 23, 1543-1554.	1.1	1
46	Two combinatorial optimization problems for SNP discovery using base-specific cleavage and mass spectrometry. <i>BMC Systems Biology</i> , 2012, 6, S5.	3.0	1
47	Revealing Mammalian Evolutionary Relationships by Comparative Analysis of Gene Clusters. <i>Genome Biology and Evolution</i> , 2012, 4, 586-601.	2.5	9
48	Toxicogenomic Analysis Suggests Chemical-Induced Sexual Dimorphism in the Expression of Metabolic Genes in Zebrafish Liver. <i>PLoS ONE</i> , 2012, 7, e51971.	2.5	4
49	Network model and efficient method for detecting relative duplications or horizontal gene transfers. , 2011, , .		4
50	From Gene Trees to Species Trees II: Species Tree Inference by Minimizing Deep Coalescence Events. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1685-1691.	3.0	48
51	Efficient estimation of the accuracy of the maximum likelihood method for ancestral state reconstruction. <i>Journal of Combinatorial Optimization</i> , 2011, 21, 409-422.	1.3	6
52	Structural properties of the reconciliation space and their applications in enumerating nearly-optimal reconciliations between a gene tree and a species tree. <i>BMC Bioinformatics</i> , 2011, 12, S7.	2.6	16
53	Conversion events in gene clusters. <i>BMC Evolutionary Biology</i> , 2011, 11, 226.	3.2	12
54	A Polynomial Algebra Method for Computing Exemplar Breakpoint Distance. <i>Lecture Notes in Computer Science</i> , 2011, , 297-305.	1.3	7

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55	Existence of Inverted Profile in Chemically Responsive Molecular Pathways in the Zebrafish Liver. PLoS ONE, 2011, 6, e27819.	2.5	11
56	Analyzing the Fitch Method for Reconstructing Ancestral States on Ultrametric Phylogenetic Trees. Bulletin of Mathematical Biology, 2010, 72, 1760-1782.	1.9	8
57	Greedy Selection of Species for Ancestral State Reconstruction on Phylogenies: Elimination Is Better than Insertion. PLoS ONE, 2010, 5, e8985.	2.5	9
58	CAGE: Combinatorial Analysis of Gene-Cluster Evolution. Journal of Computational Biology, 2010, 17, 1227-1242.	1.6	10
59	An Efficient Method for DNA-Based Species Assignment via Gene Tree and Species Tree Reconciliation. Lecture Notes in Computer Science, 2010, , 300-311.	1.3	6
60	Positive correlation between gene coexpression and positional clustering in the zebrafish genome. BMC Genomics, 2009, 10, 42.	2.8	26
61	Inferring the Recent Duplication History of a Gene Cluster. Lecture Notes in Computer Science, 2009, , 111-125.	1.3	1
62	A stable iterative method for refining discriminative gene clusters. BMC Genomics, 2008, 9, S18.	2.8	3
63	Approximating the Spanning Star Forest Problem and Its Application to Genomic Sequence Alignment. SIAM Journal on Computing, 2008, 38, 946-962.	1.0	32
64	Run Probabilities of Seed-Like Patterns and Identifying Good Transition Seeds. Journal of Computational Biology, 2008, 15, 1295-1313.	1.6	16
65	Spectrum-Based <i>De Novo</i> Repeat Detection in Genomic Sequences. Journal of Computational Biology, 2008, 15, 469-488.	1.6	3
66	More Taxa Are Not Necessarily Better for the Reconstruction of Ancestral Character States. Systematic Biology, 2008, 57, 647-653.	5.6	53
67	DUPCAR: Reconstructing Contiguous Ancestral Regions with Duplications. Journal of Computational Biology, 2008, 15, 1007-1027.	1.6	51
68	A PTAS For The k -Consensus Structures Problem Under Squared Euclidean Distance. Algorithms, 2008, 1, 43-51.	2.1	2
69	A PTAS for the k -Consensus Structures Problem Under Euclidean Squared Distance. , 2008, , 35-44.		0
70	Transcriptome Analysis of Cold Syndrome Using Microarray. The American Journal of Chinese Medicine, 2007, 35, 609-620.	3.8	19
71	Expression Profile of Immunogenes in Cold Constitution. , 2007, , .		0
72	A Robust Method for Generating Discriminative Gene Clusters. , 2007, , .		0

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73	Reconstructing Recombination Network from Sequence Data: The Small Parsimony Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 394-402.	3.0	9
74	Superiority of Spaced Seeds for Homology Search. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 496-505.	3.0	13
75	Algorithmic and Complexity Issues of Three Clustering Methods in Microarray Data Analysis. Algorithmica, 2007, 48, 203-219.	1.3	7
76	The Consecutive Ones Submatrix Problem for Sparse Matrices. Algorithmica, 2007, 48, 287-299.	1.3	15
77	A Heuristic Algorithm for Reconstructing Ancestral Gene Orders with Duplications. Lecture Notes in Computer Science, 2007, , 122-135.	1.3	1
78	Selecting Genomes for Reconstruction of Ancestral Genomes. Lecture Notes in Computer Science, 2007, , 110-121.	1.3	1
79	RUN PROBABILITY OF HIGH-ORDER SEED PATTERNS AND ITS APPLICATIONS TO FINDING GOOD TRANSITION SEEDS. , 2007, , .		0
80	Reconstructing contiguous regions of an ancestral genome. Genome Research, 2006, 16, 1557-1565.	5.5	246
81	Models and Methods in Comparative Genomics. Advances in Computers, 2006, 68, 59-104.	1.6	1
82	Controlling Size When Aligning Multiple Genomic Sequences with Duplications. Lecture Notes in Computer Science, 2006, , 138-149.	1.3	4
83	Superiority and complexity of the spaced seeds. , 2006, , .		24
84	Genome-scale analysis of positional clustering of mouse testis-specific genes. BMC Genomics, 2005, 6, 7.	2.8	47
85	Divide-and-conquer approach for the exemplar breakpoint distance. Bioinformatics, 2005, 21, 2171-2176.	4.1	42
86	ANALYSIS OF SPACED SEED TECHNIQUE IN SEQUENCE ALIGNMENT. Cosmos, 2005, 01, 57-73.	0.4	1
87	Quick, Practical Selection of Effective Seeds for Homology Search. Journal of Computational Biology, 2005, 12, 1137-1152.	1.6	13
88	A post-processing method for optimizing synthesis strategy for oligonucleotide microarrays. Nucleic Acids Research, 2005, 33, e144-e144.	14.5	10
89	Translation initiation sites prediction with mixture Gaussian models in human cDNA sequences. IEEE Transactions on Knowledge and Data Engineering, 2005, 17, 1152-1160.	5.7	23
90	On Counting Tandem Duplication Trees. Molecular Biology and Evolution, 2004, 21, 1160-1163.	8.9	6

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91	Good spaced seeds for homology search. <i>Bioinformatics</i> , 2004, 20, 1053-1059.	4.1	69
92	COMPUTING AND COMBINATORICS CONFERENCE " COCOON'02. <i>International Journal of Foundations of Computer Science</i> , 2004, 15, 1-1.	1.1	0
93	Sensitivity analysis and efficient method for identifying optimal spaced seeds. <i>Journal of Computer and System Sciences</i> , 2004, 68, 22-40.	1.2	66
94	Recent Applications of Hidden Markov Models in Computational Biology. <i>Genomics, Proteomics and Bioinformatics</i> , 2004, 2, 84-96.	6.9	41
95	Translation Initiation Sites Prediction with Mixture Gaussian Models. <i>Lecture Notes in Computer Science</i> , 2004, , 338-349.	1.3	3
96	Approximation Algorithms for the Consecutive Ones Submatrix Problem on Sparse Matrices. <i>Lecture Notes in Computer Science</i> , 2004, , 835-846.	1.3	3
97	Distinguishing string selection problems. <i>Information and Computation</i> , 2003, 185, 41-55.	0.7	198
98	Greedy method for inferring tandem duplication history. <i>Bioinformatics</i> , 2003, 19, 1497-1504.	4.1	33
99	Efficient Methods for Inferring Tandem Duplication History. <i>Lecture Notes in Computer Science</i> , 2002, , 97-111.	1.3	3
100	A new clustering method for microarray data analysis. <i>Proceedings</i> , 2002, 1, 268-75.	0.1	0
101	Perfect Phylogenetic Networks with Recombination. <i>Journal of Computational Biology</i> , 2001, 8, 69-78.	1.6	187
102	SEPARATING AUXILIARY ARITY HIERARCHY OF FIRST-ORDER INCREMENTAL EVALUATION SYSTEMS USING (3K+1)-ary INPUT RELATIONS. <i>International Journal of Foundations of Computer Science</i> , 2000, 11, 573-578.	1.1	6
103	From Gene Trees to Species Trees. <i>SIAM Journal on Computing</i> , 2000, 30, 729-752.	1.0	153
104	Optimal Bounds for Matching Routing on Trees. <i>SIAM Journal on Discrete Mathematics</i> , 1999, 12, 64-77.	0.8	8
105	Fitting Distances by Tree Metrics with Increment Error. <i>Journal of Combinatorial Optimization</i> , 1999, 3, 213-225.	1.3	12
106	Twist"Rotation Transformations of Binary Trees and Arithmetic Expressions. <i>Journal of Algorithms</i> , 1999, 32, 155-166.	0.9	12
107	Addition in $\log_2 n + O(1)$ steps on average a simple analysis. <i>Theoretical Computer Science</i> , 1998, 191, 245-248.	0.9	3
108	On reconstructing species trees from gene trees in term of duplications and losses. , 1998, ,		28

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109	Computing Distances between Evolutionary Trees. , 1998, , 781-822.		5
110	On a Mirkin-Muchnik-Smith Conjecture for Comparing Molecular Phylogenies. Journal of Computational Biology, 1997, 4, 177-187.	1.6	120
111	Many-to-one packet routing via matchings. Lecture Notes in Computer Science, 1997, , 11-17.	1.3	6
112	Small weight bases for hamming codes. Theoretical Computer Science, 1997, 181, 337-345.	0.9	3
113	On the descriptive power of special Thue systems. Discrete Mathematics, 1996, 160, 291-297.	0.7	1
114	On the Nearest Neighbour Interchange Distance Between Evolutionary Trees. Journal of Theoretical Biology, 1996, 182, 463-467.	1.7	76
115	On the approximation of longest common nonsupersequences and shortest common nonsubsequences. Theoretical Computer Science, 1995, 143, 353-362.	0.9	4
116	Routing on trees via matchings. Lecture Notes in Computer Science, 1995, , 251-262.	1.3	6
117	Applying rewriting methods to special monoids. Mathematical Proceedings of the Cambridge Philosophical Society, 1992, 112, 495-505.	0.4	14
118	ON THE CONJUGACY PROBLEM FOR ONE-RELATOR MONOIDS WITH ELEMENTS OF FINITE ORDER. International Journal of Algebra and Computation, 1992, 02, 209-220.	0.5	11
119	Some properties of finite special string-rewriting systems. Journal of Symbolic Computation, 1992, 14, 359-369.	0.8	2
120	The pre-NTS property is undecidable for context-free grammars. Information Processing Letters, 1992, 44, 181-184.	0.6	2
121	A short proof of a theorem of Adjan. Proceedings of the American Mathematical Society, 1992, 116, 1-1.	0.8	13
122	Conjugacy in special monoids. Journal of Algebra, 1991, 143, 487-497.	0.7	25
123	Decision problems for finite special string-rewriting systems that are confluent on some congruence class. Acta Informatica, 1991, 28, 477-510.	0.5	20
124	Rational strong codes and structure of rational group languages. Semigroup Forum, 1986, 35, 181-193.	0.6	3
125	A new clustering method for microarray data analysis. , 0, , .		3