Kun-Mao Chao

List of Publications by Year
in descending order

100 papers	1,852 citations	304743 22 h-index	315739 38 g-index
106 all docs	106 docs citations	106 times ranked	1764 citing authors

#	Article	IF	Citations
1	Proof of a Conjecture About Minimum Spanning Tree Cycle Intersection. Discrete Applied Mathematics, 2022, 321, 19-23.	0.9	3
2	Strontium ranelate-laden near-infrared photothermal-inspired methylcellulose hydrogel for arthritis treatment. Materials Science and Engineering C, 2021, 123, 111980.	7.3	25
3	Facilitated and Controlled Strontium Ranelate Delivery Using GCS-HA Nanocarriers Embedded into PEGDA Coupled with Decortication Driven Spinal Regeneration. International Journal of Nanomedicine, 2021, Volume 16, 4209-4224.	6.7	11
4	On the influenza vaccination policy through mathematical modeling. International Journal of Infectious Diseases, 2020, 98, 71-79.	3.3	4
5	Data-driven interdisciplinary mathematical modelling quantitatively unveils competition dynamics of co-circulating influenza strains. Journal of Translational Medicine, 2017, 15, 163.	4.4	2
6	A Takagi-Sugeno fuzzy neural network-based algorithm with single-channel EEG signal for the discrimination between light and deep sleep stages. , 2016, , .		4
7	SMART: Statistical Metabolomics Analysisâ€"An R Tool. Analytical Chemistry, 2016, 88, 6334-6341.	6.5	24
8	Maximum-Sum Segments. , 2016, , 1242-1244.		0
9	Maximum-Average Segments. , 2016, , 1241-1242.		0
10	<scp><i>M</i></scp><i>ycobacterium tuberculosis</i> nucleic acid amplification tests reduce nosocomial tuberculosis exposure in intensive care units: A nationwide cohort study. Respirology, 2015, 20, 1233-1240.	2.3	9
11	Optimal Duration of Anti-TB Treatment in Patients With Diabetes. Chest, 2015, 147, 520-528.	0.8	60
12	Maximum-Average Segments. , 2015, , 1-3.		0
13	Maximum-Sum Segments. , 2015, , 1-3.		0
14	Forming Plurality at Minimum Cost. Lecture Notes in Computer Science, 2015, , 77-88.	1.3	2
15	A Fixed-Parameter Algorithm for Detecting a Singleton Attractor in an AND/OR Boolean Network with Bounded Treewidth. IEICE Transactions on Fundamentals of Electronics, Communications and Computer Sciences, 2015, E98.A, 384-390.	0.3	1
16	Preface Algorithms and Computation (ISAAC 2012). Algorithmica, 2014, 70, 694-695.	1.3	0
17	A fault-tolerant method for HLA typing with PacBio data. BMC Bioinformatics, 2014, 15, 296.	2.6	18
18	The Generalized Popular Condensation Problem. Lecture Notes in Computer Science, 2014, , 606-617.	1.3	4

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19	Locating Valid SLCAs for XML Keyword Search with NOT Semantics. SIGMOD Record, 2014, 43, 29-34.	1.2	1
20	Risk factors for pulmonary tuberculosis in patients with chronic obstructive airway disease in Taiwan: a nationwide cohort study. BMC Infectious Diseases, 2013, 13, 194.	2.9	69
21	A Fully Compressed Algorithm for Computing the Edit Distance of Run-Length Encoded Strings. Algorithmica, 2013, 65, 354-370.	1.3	4
22	In-silico drug screening and potential target identification for hepatocellular carcinoma using Support Vector Machines based on drug screening result. Gene, 2013, 518, 201-208.	2.2	9
23	A linear-time algorithm for finding an edge-partition with max-min ratio at most two. Discrete Applied Mathematics, 2013, 161, 932-943.	0.9	1
24	The impact of diabetes mellitus and its control on the development of tuberculosis: a nationwide longitudinal study in Taiwan. Pharmacoepidemiology and Drug Safety, 2013, 22, 995-1003.	1.9	5
25	GUEST EDITORS' FOREWORD. International Journal of Computational Geometry and Applications, 2013, 23, 425-426.	0.5	0
26	Urinary tuberculosis is associated with the development of urothelial carcinoma but not renal cell carcinoma: a nationwide cohort study in Taiwan. British Journal of Cancer, 2013, 109, 2933-2940.	6.4	13
27	A Compact and Efficient Labeling Scheme for XML Documents. Lecture Notes in Computer Science, 2013, , 269-283.	1.3	6
28	Pulmonary Tuberculosis and Delay in Anti-Tuberculous Treatment Are Important Risk Factors for Chronic Obstructive Pulmonary Disease. PLoS ONE, 2012, 7, e37978.	2.5	89
29	Efficient algorithms for local ranking. Information Processing Letters, 2012, 112, 517-522.	0.6	1
30	Efficient retrieval of approximate palindromes in a run-length encoded string. Theoretical Computer Science, 2012, 432, 28-37.	0.9	2
31	Asymptotic Limits of a New Type of Maximization Recurrence with an Application to Bioinformatics. Lecture Notes in Computer Science, 2012, , 177-188.	1.3	2
32	Preserving Inversion Phylogeny Reconstruction. Lecture Notes in Computer Science, 2012, , 1-13.	1.3	2
33	Linear-Time Algorithms for the Multiple Gene Duplication Problems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 260-265.	3.0	15
34	Influence of Pressure Control Levels on the Pulse Pressure Variations. Shock, 2011, 36, 628-632.	2.1	2
35	The Extent of Linkage Disequilibrium and Computational Challenges of Single Nucleotide Polymorphisms in Genome-Wide Association Studies. Current Drug Metabolism, 2011, 12, 498-506.	1.2	5
36	On the generalized constrained longest common subsequence problems. Journal of Combinatorial Optimization, 2011, 21, 383-392.	1.3	56

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37	Finding all sorting tandem duplication random loss operations. Journal of Discrete Algorithms, 2011, 9, 32-48.	0.7	14
38	MINKOWSKI SUM SELECTION AND FINDING. International Journal of Computational Geometry and Applications, 2011, 21, 283-311.	0.5	1
39	Improving the performance of identifying contributors for XML keyword search. SIGMOD Record, 2011, 40, 5-10.	1.2	8
40	Gene Expression-Based Chemical Genomics Identifies Potential Therapeutic Drugs in Hepatocellular Carcinoma. PLoS ONE, 2011, 6, e27186.	2.5	58
41	Hardness of comparing two run-length encoded strings. Journal of Complexity, 2010, 26, 364-374.	1.3	10
42	A tight bound on the min-ratio edge-partitioning problem of a tree. Discrete Applied Mathematics, 2010, 158, 1471-1478.	0.9	2
43	FINDING ALL APPROXIMATE GAPPED PALINDROMES. International Journal of Foundations of Computer Science, 2010, 21, 925-939.	1.1	10
44	Identifying Approximate Palindromes in Run-Length Encoded Strings. Lecture Notes in Computer Science, 2010, , 339-350.	1.3	2
45	Faster Algorithms for Searching Relevant Matches in XML Databases. Lecture Notes in Computer Science, 2010, , 290-297.	1.3	1
46	A Fully Compressed Algorithm for Computing the Edit Distance of Run-Length Encoded Strings. Lecture Notes in Computer Science, 2010, , 415-426.	1.3	2
47	The backup 2â€center and backup 2â€median problems on trees. Networks, 2009, 53, 39-49.	2.7	11
48	On Locating Disjoint Segments with Maximum Sum of Densities. Algorithmica, 2009, 54, 107-117.	1.3	0
49	Optimal algorithms for the average-constrained maximum-sum segment problem. Information Processing Letters, 2009, 109, 171-174.	0.6	3
50	Finding All Approximate Gapped Palindromes. Lecture Notes in Computer Science, 2009, , 1084-1093.	1.3	14
51	Finding All Sorting Tandem Duplication Random Loss Operations. Lecture Notes in Computer Science, 2009, , 301-313.	1.3	0
52	Approximate Matching for Run-Length Encoded Strings Is 3sum-Hard. Lecture Notes in Computer Science, 2009, , 168-179.	1.3	5
53	The Swap Edges of a Multiple-Sources Routing Tree. Algorithmica, 2008, 50, 299-311.	1.3	16
54	Algorithms for finding the weight-constrained k longest paths in a tree and the length-constrained k maximum-sum segments of a sequence. Theoretical Computer Science, 2008, 407, 349-358.	0.9	13

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55	The 2-radius and 2-radiian problems on trees. Theoretical Computer Science, 2008, 407, 524-531.	0.9	0
56	A new framework for the selection of tag SNPs by multimarker haplotypes. Journal of Biomedical Informatics, 2008, 41, 953-961.	4.3	4
57	PhosphoPOINT: a comprehensive human kinase interactome and phospho-protein database. Bioinformatics, 2008, 24, i14-i20.	4.1	88
58	CNVDetector: locating copy number variations using array CGH data. Bioinformatics, 2008, 24, 2773-2775.	4.1	10
59	Maximum-scoring Segment with Length Restrictions. , 2008, , 506-507.		0
60	Maximum-Density Segment. , 2008, , 502-504.		0
61	Minkowski Sum Selection and Finding. Lecture Notes in Computer Science, 2008, , 460-471.	1.3	1
62	A tight analysis of the Katrielâ€"Bodlaender algorithm for online topological ordering. Theoretical Computer Science, 2007, 389, 182-189.	0.9	8
63	On the range maximum-sum segment query problem. Discrete Applied Mathematics, 2007, 155, 2043-2052.	0.9	15
64	On the uniform edge-partition of a tree. Discrete Applied Mathematics, 2007, 155, 1213-1223.	0.9	6
65	Algorithms for Computing the Length-Constrained Max-Score Segments with Applications to DNA Copy Number Data Analysis. , 2007, , 834-845.		0
66	Improved algorithms for the <mml:math altimg="si1.gif" overflow="scroll" xmlns:xocs="http://www.elsevier.com/xml/xocs/dtd" xmlns:xs="http://www.w3.org/2001/XMLSchema" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns="http://www.elsevier.com/xml/ja/dtd" xmlns:ja="http://www.elsevier.com/xml/ja/dtd" xmlns:mml="http://www.w3.org/1998/Math/MathML" xmlns:tb="http://www.elsevier.com/xml/common/table/dtd" xmlns:sb="http://www.elsevier.com/xml/common/struct-bib/dtd" xmlns:ce="http://www.elsevier.com/x	0.9	15
67	A greedier approach for finding tag SNPs. Bioinformatics, 2006, 22, 685-691.	4.1	21
68	Distant HNF1 Site as a Master Control for the Human Class I Alcohol Dehydrogenase Gene Expression*. Journal of Biological Chemistry, 2006, 281, 19809-19821.	3.4	17
69	On Locating Disjoint Segments with Maximum Sum of Densities. Lecture Notes in Computer Science, 2006, , 300-307.	1.3	3
70	A fast algorithm for computing a longest common increasing subsequence. Information Processing Letters, 2005, 93, 249-253.	0.6	38
71	Optimal algorithms for locating the longest and shortest segments satisfying a sum or an average constraint. Information Processing Letters, 2005, 96, 197-201.	0.6	19
72	Selecting additional tag SNPs for tolerating missing data in genotyping. BMC Bioinformatics, 2005, 6, 263.	2.6	17

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73	Finding a Length-Constrained Maximum-Density Path in a Tree. Journal of Combinatorial Optimization, 2005, 9, 147-156.	1.3	11
74	An Approximation Algorithm for Haplotype Inference by Maximum Parsimony. Journal of Computational Biology, 2005, 12, 1261-1274.	1.6	32
75	Efficient combination of multiple word models for improved sequence comparison. Bioinformatics, 2004, 20, 2529-2533.	4.1	12
76	An optimal algorithm for querying tree structures and its applications in bioinformatics. SIGMOD Record, 2004, 33, 21-26.	1.2	1
77	On the Range Maximum-Sum Segment Query Problem. Lecture Notes in Computer Science, 2004, , 294-305.	1.3	13
78	DYNAMIC PROGRAMMING STRATEGIES FOR ANALYZING BIOMOLECULAR SEQUENCES. Lecture Notes Series, Institute for Mathematical Sciences, 2004, , 1-23.	0.2	0
79	MAVG: locating non-overlapping maximum average segments in a given sequence. Bioinformatics, 2003, 19, 151-152.	4.1	36
80	Constrained Multiple Sequence Alignment Tool Development and Its Application to RNase Family Alignment. Journal of Bioinformatics and Computational Biology, 2003, 01, 267-287.	0.8	44
81	A generalized global alignment algorithm. Bioinformatics, 2003, 19, 228-233.	4.1	77
82	Finding a Length-Constrained Maximum-Density Path in a Tree. Lecture Notes in Computer Science, 2003, , 78-87.	1.3	0
83	Light graphs with small routing cost. Networks, 2002, 39, 130-138.	2.7	23
84	Efficient algorithms for locating the length-constrained heaviest segments with applications to biomolecular sequence analysis. Journal of Computer and System Sciences, 2002, 65, 570-586.	1.2	78
85	A Polynomial Time Approximation Scheme for Optimal Product-Requirement Communication Spanning Trees. Journal of Algorithms, 2000, 36, 182-204.	0.9	21
86	Approximation algorithms for some optimum communication spanning tree problems. Discrete Applied Mathematics, 2000, 102, 245-266.	0.9	51
87	A Polynomial-Time Approximation Scheme for Minimum Routing Cost Spanning Trees. SIAM Journal on Computing, 2000, 29, 761-778.	1.0	103
88	Title is missing!. Journal of Combinatorial Optimization, 1999, 3, 199-211.	1.3	30
89	On computing all suboptimal alignments. Information Sciences, 1998, 105, 189-207.	6.9	7
90	Fast algorithms for aligning sequences with restricted affine gap penalties. Lecture Notes in Computer Science, 1997, , 264-273.	1.3	0

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91	Linear-space algorithms that build local alignments from fragments. Algorithmica, 1995, 13, 106-134.	1.3	33
92	Globin Gene Server: A Prototype E-Mail Database Server Featuring Extensive Multiple Alignments and Data Compilation for Electronic Genetic Analysis. Genomics, 1994, 21, 344-353.	2.9	35
93	Recent Developments in Linear-Space Alignment Methods: A Survey. Journal of Computational Biology, 1994, 1, 271-291.	1.6	51
94	Constrained sequence alignment. Bulletin of Mathematical Biology, 1993, 55, 503-524.	1.9	19
95	Positive and negative regulatory elements of the rabbit embryonic Ïµ-globin gene revealed by an improved multiple alignment program and functional analysis. DNA Sequence, 1993, 4, 163-176.	0.7	26
96	Locating well-conserved regions within a pairwise alignment. Bioinformatics, 1993, 9, 387-396.	4.1	17
97	Aligning two sequences within a specified diagonal band. Bioinformatics, 1992, 8, 481-487.	4.1	94
98	Efficient methods for generating optimal single and multiple spaced seeds. , 0, , .		13
99	Approximation algorithms for the optimization problems of SNPs and haplotypes. , 0, , .		0
100	Pattern identification in a haplotype block. , 0, , 23-35.		0