

Matteo Comin

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

626
citations

687363

13
h-index

677142

22
g-index

45
all docs

45
docs citations

45
times ranked

403
citing authors

#	ARTICLE	IF	CITATIONS
1	Benchmarking of alignment-free sequence comparison methods. <i>Genome Biology</i> , 2019, 20, 144.	8.8	147
2	MetaProb: accurate metagenomic reads binning based on probabilistic sequence signatures. <i>Bioinformatics</i> , 2016, 32, i567-i575.	4.1	58
3	Alignment-free phylogeny of whole genomes using underlying subwords. <i>Algorithms for Molecular Biology</i> , 2012, 7, 34.	1.2	51
4	PROuST: A Comparison Method of Three-Dimensional Structures of Proteins Using Indexing Techniques. <i>Journal of Computational Biology</i> , 2004, 11, 1061-1072.	1.6	28
5	Clustering of reads with alignment-free measures and quality values. <i>Algorithms for Molecular Biology</i> , 2015, 10, 4.	1.2	26
6	The Irredundant Class Method for Remote Homology Detection of Protein Sequences. <i>Journal of Computational Biology</i> , 2011, 18, 1819-1829.	1.6	22
7	Better quality score compression through sequence-based quality smoothing. <i>BMC Bioinformatics</i> , 2019, 20, 302.	2.6	19
8	Assembly-free genome comparison based on next-generation sequencing reads and variable length patterns. <i>BMC Bioinformatics</i> , 2014, 15, S1.	2.6	18
9	Beyond Fixed-Resolution Alignment-Free Measures for Mammalian Enhancers Sequence Comparison. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 628-637.	3.0	17
10	Comparison of microbiome samples: methods and computational challenges. <i>Briefings in Bioinformatics</i> , 2021, 22, 88-95.	6.5	17
11	Fast Entropic Profiler: An Information Theoretic Approach for the Discovery of Patterns in Genomes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 500-509.	3.0	16
12	Classification of protein sequences by means of irredundant patterns. <i>BMC Bioinformatics</i> , 2010, 11, S16.	2.6	15
13	Higher recall in metagenomic sequence classification exploiting overlapping reads. <i>BMC Genomics</i> , 2017, 18, 917.	2.8	14
14	Whole-Genome Phylogeny by Virtue of Unic Subwords. , 2012, , .		13
15	Metagenomic reads binning with spaced seeds. <i>Theoretical Computer Science</i> , 2017, 698, 88-99.	0.9	13
16	On the comparison of regulatory sequences with multiple resolution Entropic Profiles. <i>BMC Bioinformatics</i> , 2016, 17, 130.	2.6	12
17	MetaCon: unsupervised clustering of metagenomic contigs with probabilistic k-mers statistics and coverage. <i>BMC Bioinformatics</i> , 2019, 20, 367.	2.6	12
18	Efficient computation of spaced seed hashing with block indexing. <i>BMC Bioinformatics</i> , 2018, 19, 441.	2.6	11

#	ARTICLE	IF	CITATIONS
19	SKraken: Fast and Sensitive Classification of Short Metagenomic Reads based on Filtering Uninformative k-mers. , 2017, , .		10
20	Fast and Sensitive Classification of Short Metagenomic Reads with SKraken. Communications in Computer and Information Science, 2018, , 212-226.	0.5	9
21	Iterative Spaced Seed Hashing: Closing the Gap Between Spaced Seed Hashing and <i>k</i> -mer Hashing. Journal of Computational Biology, 2020, 27, 223-233.	1.6	8
22	FSH: fast spaced seed hashing exploiting adjacent hashes. Algorithms for Molecular Biology, 2018, 13, 8.	1.2	7
23	SUBTLE MOTIF DISCOVERY FOR DETECTION OF DNA REGULATORY SITES. , 2007, , .		7
24	K2Mem: Discovering Discriminative K-mers From Sequencing Data for Metagenomic Reads Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 220-229.	3.0	7
25	Binding Balls: Fast Detection of Binding Sites Using a Property of Spherical Fourier Transform. Journal of Computational Biology, 2009, 16, 1577-1591.	1.6	6
26	Filtering Degenerate Patterns with Application to Protein Sequence Analysis. Algorithms, 2013, 6, 352-370.	2.1	6
27	Fast comparison of genomic and meta-genomic reads with alignment-free measures based on quality values. BMC Medical Genomics, 2016, 9, 36.	1.5	6
28	Bridging Lossy and Lossless Compression by Motif Pattern Discovery. Electronic Notes in Discrete Mathematics, 2005, 21, 219-225.	0.4	5
29	MetaProb 2: Metagenomic Reads Binning Based on Assembly Using Minimizers and K-Mers Statistics. Journal of Computational Biology, 2021, 28, 1052-1062.	1.6	5
30	Improving Metagenomic Classification Using Discriminative k-mers from Sequencing Data. Lecture Notes in Computer Science, 2020, , 68-81.	1.3	5
31	GRID DEPLOYMENT OF BIOINFORMATICS APPLICATIONS: A CASE STUDY IN PROTEIN SIMILARITY DETERMINATION. Parallel Processing Letters, 2004, 14, 163-176.	0.6	4
32	Parallel Continuous Flow: A Parallel Suffix Tree Construction Tool for Whole Genomes. Journal of Computational Biology, 2014, 21, 330-344.	1.6	3
33	Indexing <i>k</i> -mers in linear space for quality value compression. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940011.	0.8	3
34	Indexing k-mers in Linear-space for Quality Value Compression. , 2019, , .		3
35	Fast alignment of reads to a variation graph with application to SNP detection. Journal of Integrative Bioinformatics, 2021, .	1.5	3
36	Special Issue of the 1st International Applied Bioinformatics Conference (iABC'21). Journal of Integrative Bioinformatics, 2021, 18, .	1.5	2

#	ARTICLE	IF	CITATIONS
37	SPRISS: approximating frequent <i>k</i> -mers by sampling reads, and applications. <i>Bioinformatics</i> , 2022, 38, 3343-3350.	4.1	2
38	MINING OVERREPRESENTED 3D PATTERNS OF SECONDARY STRUCTURES IN PROTEINS. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 1067-1087.	0.8	1
39	Binning metagenomic reads with probabilistic sequence signatures based on spaced seeds. , 2017, , .		1
40	Efficient <i>k</i> -mer Indexing with Application to Mapping-free SNP Genotyping. , 2022, , .		1
41	Reducing the Space of Degenerate Patterns in Protein Remote Homology Detection. , 2013, , .		0
42	Higher recall in metagenomic sequence classification exploiting Overlapping Reads. , 2016, , .		0