Matteo Comin

List of Publications by Year
in descending order

42 papers	626 citations

687363

13 h-index	22 g-index

677142

45 all docs	45 docs citations
45 times ranked	403 citing authors

#	Article	IF	Citations
1	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
2	Efficient k-mer Indexing with Application to Mapping-free SNP Genotyping. , 2022, , .		1
3	SPRISS: approximating frequent *k*-mers by sampling reads, and applications. Bioinformatics, 2022, 38, 3343-3350.	4.1	2
4	Comparison of microbiome samples: methods and computational challenges. Briefings in Bioinformatics, 2021, 22, 88-95.	6.5	17
5	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
6	Fast alignment of reads to a variation graph with application to SNP detection. Journal of Integrative Bioinformatics, 2021, .	1.5	3
7	Special Issue of the 1st International Applied Bioinformatics Conference (iABC'21). Journal of Integrative Bioinformatics, 2021, 18, .	1.5	2
8	Iterative Spaced Seed Hashing: Closing the Gap Between Spaced Seed Hashing and *k*-mer Hashing. Journal of Computational Biology, 2020, 27, 223-233.	1.6	8
9	Improving Metagenomic Classification Using Discriminative k-mers from Sequencing Data. Lecture Notes in Computer Science, 2020, , 68-81.	1.3	5
10	Benchmarking of alignment-free sequence comparison methods. Genome Biology, 2019, 20, 144.	8.8	147
11	Indexing *k*-mers in linear space for quality value compression. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940011.	0.8	3
12	Better quality score compression through sequence-based quality smoothing. BMC Bioinformatics, 2019, 20, 302.	2.6	19
13	MetaCon: unsupervised clustering of metagenomic contigs with probabilistic k-mers statistics and coverage. BMC Bioinformatics, 2019, 20, 367.	2.6	12
14	Indexing k-mers in Linear-space for Quality Value Compression. , 2019, , .		3
15	Efficient computation of spaced seed hashing with block indexing. BMC Bioinformatics, 2018, 19, 441.	2.6	11
16	Fast and Sensitive Classification of Short Metagenomic Reads with SKraken. Communications in Computer and Information Science, 2018, , 212-226.	0.5	9
17	FSH: fast spaced seed hashing exploiting adjacent hashes. Algorithms for Molecular Biology, 2018, 13, 8.	1.2	7
18	Metagenomic reads binning with spaced seeds. Theoretical Computer Science, 2017, 698, 88-99.	0.9	13

#	Article	IF	Citations
19	Binning metagenomic reads with probabilistic sequence signatures based on spaced seeds. , 2017, , .		1
20	Higher recall in metagenomic sequence classification exploiting overlapping reads. BMC Genomics, 2017, 18, 917.	2.8	14
21	SKraken: Fast and Sensitive Classification of Short Metagenomic Reads based on Filtering Uninformative k-mers. , 2017, , .		10
22	Higher recall in metagenomic sequence classification exploiting Overlapping Reads. , 2016, , .		0
23	MetaProb: accurate metagenomic reads binning based on probabilistic sequence signatures. Bioinformatics, 2016, 32, i567-i575.	4.1	58
24	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
25	On the comparison of regulatory sequences with multiple resolution Entropic Profiles. BMC Bioinformatics, 2016, 17, 130.	2.6	12
26	Clustering of reads with alignment-free measures and quality values. Algorithms for Molecular Biology, 2015, 10, 4.	1.2	26
27	Beyond Fixed-Resolution Alignment-Free Measures for Mammalian Enhancers Sequence Comparison. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 628-637.	3.0	17
28	Parallel Continuous Flow: A Parallel Suffix Tree Construction Tool for Whole Genomes. Journal of Computational Biology, 2014, 21, 330-344.	1.6	3
29	Fast Entropic Profiler: An Information Theoretic Approach for the Discovery of Patterns in Genomes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 500-509.	3.0	16
30	Assembly-free genome comparison based on next-generation sequencing reads and variable length patterns. BMC Bioinformatics, 2014, 15, S1.	2.6	18
31	Reducing the Space of Degenerate Patterns in Protein Remote Homology Detection. , 2013, , .		0
32	Filtering Degenerate Patterns with Application to Protein Sequence Analysis. Algorithms, 2013, 6, 352-370.	2.1	6
33	Whole-Genome Phylogeny by Virtue of Unic Subwords. , 2012, , .		13
34	Alignment-free phylogeny of whole genomes using underlying subwords. Algorithms for Molecular Biology, 2012, 7, 34.	1.2	51
35	The Irredundant Class Method for Remote Homology Detection of Protein Sequences. Journal of Computational Biology, 2011, 18, 1819-1829.	1.6	22
36	Classification of protein sequences by means of irredundant patterns. BMC Bioinformatics, 2010, 11, S16.	2.6	15

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37	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
38	MINING OVERREPRESENTED 3D PATTERNS OF SECONDARY STRUCTURES IN PROTEINS. Journal of Bioinformatics and Computational Biology, 2008, 06, 1067-1087.	0.8	1
39	SUBTLE MOTIF DISCOVERY FOR DETECTION OF DNA REGULATORY SITES. , 2007, , .		7
40	Bridging Lossy and Lossless Compression by Motif Pattern Discovery. Electronic Notes in Discrete Mathematics, 2005, 21, 219-225.	0.4	5
41	PROuST: A Comparison Method of Three-Dimensional Structures of Proteins Using Indexing Techniques. Journal of Computational Biology, 2004, 11, 1061-1072.	1.6	28
42	GRID DEPLOYMENT OF BIOINFORMATICS APPLICATIONS: A CASE STUDY IN PROTEIN SIMILARITY DETERMINATION. Parallel Processing Letters, 2004, 14, 163-176.	0.6	4