

# Yuri Pirola

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

1,200  
citations

759233

12  
h-index

454955

30  
g-index

54  
all docs

54  
docs citations

54  
times ranked

2985  
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational graph pangenomics: a tutorial on data structures and their applications. <i>Natural Computing</i> , 2022, 21, 81-108.	3.0	22
2	Shark: fishing relevant reads in an RNA-Seq sample. <i>Bioinformatics</i> , 2021, 37, 464-472.	4.1	8
3	Computing the multi-string BWT and LCP array in external memory. <i>Theoretical Computer Science</i> , 2021, 862, 42-58.	0.9	3
4	MALVIRUS: an integrated application for viral variant analysis. <i>BMC Bioinformatics</i> , 2021, 22, 625.	2.6	4
5	Î <sup>3</sup> -TRIS: a graph-algorithm for comprehensive identification of vector genomic insertion sites. <i>Bioinformatics</i> , 2020, 36, 1622-1624.	4.1	7
6	Multithread Multistring Burrowsâ€“Wheeler Transform and Longest Common Prefix Array. <i>Journal of Computational Biology</i> , 2019, 26, 948-961.	1.6	8
7	Overlap graphs and <i>de Bruijn</i> graphs: data structures for <i>de novo</i> genome assembly in the big data era. <i>Quantitative Biology</i> , 2019, 7, 278-292.	0.5	30
8	Bioconda: sustainable and comprehensive software distribution for the life sciences. <i>Nature Methods</i> , 2018, 15, 475-476.	19.0	714
9	FSG: Fast String Graph Construction for De Novo Assembly. <i>Journal of Computational Biology</i> , 2017, 24, 953-968.	1.6	12
10	An External-Memory Algorithm for String Graph Construction. <i>Algorithmica</i> , 2017, 78, 394-424.	1.3	9
11	Use of SNP genotypes to identify carriers of harmful recessive mutations in cattle populations. <i>BMC Genomics</i> , 2016, 17, 857.	2.8	10
12	FSG: Fast String Graph Construction for De Novo Assembly of Reads Data. <i>Lecture Notes in Computer Science</i> , 2016, , 27-39.	1.3	1
13	Transcriptional profiling of immortalized and K-ras-transformed mouse fibroblasts upon PKA stimulation by forskolin in low glucose availability. <i>Genomics Data</i> , 2016, 9, 100-104.	1.3	3
14	On the Minimum Error Correction Problem for Haplotype Assembly in Diploid and Polyploid Genomes. <i>Journal of Computational Biology</i> , 2016, 23, 718-736.	1.6	29
15	LSG: An External-Memory Tool to Compute String Graphs for Next-Generation Sequencing Data Assembly. <i>Journal of Computational Biology</i> , 2016, 23, 137-149.	1.6	14
16	H <sub>ap</sub> C <sub>ol</sub> : accurate and memory-efficient haplotype assembly from long reads. <i>Bioinformatics</i> , 2016, 32, 1610-1617.	4.1	40
17	Protein Kinase A Activation Promotes Cancer Cell Resistance to Glucose Starvation and Anoikis. <i>PLoS Genetics</i> , 2016, 12, e1005931.	3.5	61
18	Beyond Evolutionary Trees. , 2016, , 183-189.		0

#	ARTICLE	IF	CITATIONS
19	Covering Pairs in Directed Acyclic Graphs. Computer Journal, 2015, 58, 1673-1686.	2.4	6
20	A Clustering Algorithm for Planning the Integration Process of a Large Number of Conceptual Schemas. Journal of Computer Science and Technology, 2015, 30, 214-224.	1.5	4
21	On the Fixed Parameter Tractability and Approximability of the Minimum Error Correction Problem. Lecture Notes in Computer Science, 2015, , 100-113.	1.3	8
22	Transcriptome Assembly and Alternative Splicing Analysis. Methods in Molecular Biology, 2015, 1269, 173-188.	0.9	1
23	Modeling Alternative Splicing Variants from RNA-Seq Data with Isoform Graphs. Journal of Computational Biology, 2014, 21, 16-40.	1.6	22
24	Constructing String Graphs in External Memory. Lecture Notes in Computer Science, 2014, , 311-325.	1.3	5
25	Covering Pairs in Directed Acyclic Graphs. Lecture Notes in Computer Science, 2014, , 126-137.	1.3	0
26	Parameterized complexity of k-anonymity: hardness and tractability. Journal of Combinatorial Optimization, 2013, 26, 19-43.	1.3	5
27	Haplotype-based prediction of gene alleles using pedigrees and SNP genotypes. , 2013, , .		6
28	Maximum Disjoint Paths on Edge-Colored Graphs: Approximability and Tractability. Algorithms, 2013, 6, 1-11.	2.1	10
29	A fast and practical approach to genotype phasing and imputation on a pedigree with erroneous and incomplete information. , 2012, , .		0
30	A fast and practical approach to genotype phasing and imputation on a pedigree with erroneous and incomplete information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1582-1594.	3.0	1
31	An Efficient Algorithm for Haplotype Inference on Pedigrees with Recombinations and Mutations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 12-25.	3.0	9
32	A study of the neutrality of Boolean function landscapes in genetic programming. Theoretical Computer Science, 2012, 425, 34-57.	0.9	13
33	Plntron: a fast method for detecting the gene structure due to alternative splicing via maximal pairings of a pattern and a text. BMC Bioinformatics, 2012, 13, S2.	2.6	8
34	Plntron: A fast method for gene structure prediction via maximal pairings of a pattern and a text. , 2011, , .		0
35	Beyond evolutionary trees. Natural Computing, 2010, 9, 421-435.	3.0	2
36	Variants of constrained longest common subsequence. Information Processing Letters, 2010, 110, 877-881.	0.6	33

#	ARTICLE	IF	CITATIONS
37	Pure Parsimony Xor Haplotyping. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 598-610.	3.0	4
38	Haplotype Inference on Pedigrees with Recombinations and Mutations. Lecture Notes in Computer Science, 2010, , 148-161.	1.3	0
39	Detecting Alternative Gene Structures from Spliced ESTs: A Computational Approach. Journal of Computational Biology, 2009, 16, 43-66.	1.6	23
40	Pure Parsimony Xor Haplotyping. Lecture Notes in Computer Science, 2009, , 186-197.	1.3	0
41	A Comprehensive View of Fitness Landscapes with Neutrality and Fitness Clouds. Lecture Notes in Computer Science, 2007, , 241-250.	1.3	16
42	A quantitative study of neutrality in GP boolean landscapes. , 2006, , .		15