# Paola Bonizzoni

List of Publications by Year
in descending order

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|---|---|---|---|
| 99<br>papers | 1,475<br>citations | 361413<br>20<br>h-index | 434195<br>31<br>g-index |
| 125<br>all docs | 125<br>docs citations | 125<br>times ranked | 1039<br>citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Finding Maximal Exact Matches Using the r-Index. Journal of Computational Biology, 2022, 29, 188-194. | 1.6 | 4 |
| 2 | Computational graph pangenomics: a tutorial on data structures and their applications. Natural Computing, 2022, 21, 81-108. | 3.0 | 22 |
| 3 | On the longest common prefix of suffixes in an inverse Lyndon factorization and other properties. Theoretical Computer Science, 2021, 862, 24-41. | 0.9 | 5 |
| 4 | Shark: fishing relevant reads in an RNA-Seq sample. Bioinformatics, 2021, 37, 464-472. | 4.1 | 8 |
| 5 | Inferring cancer progression from Single-Cell Sequencing while allowing mutation losses. Bioinformatics, 2021, 37, 326-333. | 4.1 | 35 |
| 6 | Triplet-based similarity score for fully multilabeled trees with poly-occurring labels. Bioinformatics, 2021, 37, 178-184. | 4.1 | 13 |
| 7 | Effective Clustering for Single Cell Sequencing Cancer Data. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 4068-4078. | 6.3 | 8 |
| 8 | Incomplete Directed Perfect Phylogeny inÂLinear Time. Lecture Notes in Computer Science, 2021, , 172-185. | 1.3 | 0 |
| 9 | Comparative genome analysis using sample-specific string detection in accurate long reads. Bioinformatics Advances, 2021, 1, . | 2.4 | 5 |
| 10 | Computing the multi-string BWT and LCP array in external memory. Theoretical Computer Science, 2021, 862, 42-58. | 0.9 | 3 |
| 11 | gpps: an ILP-based approach for inferring cancer progression with mutation losses from single cell data. BMC Bioinformatics, 2020, 21, 413. | 2.6 | 10 |
| 12 | Does Relaxing the Infinite Sites Assumption Give Better Tumor Phylogenies? An ILP-Based Comparative Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1410-1423. | 3.0 | 14 |
| 13 | MALVA: Genotyping by Mapping-free ALlele Detection of Known VAriants. IScience, 2019, 18, 20-27. | 4.1 | 27 |
| 14 | Multithread Multistring Burrowsâ€"Wheeler Transform and Longest Common Prefix Array. Journal of Computational Biology, 2019, 26, 948-961. | 1.6 | 8 |
| 15 | Overlap graphs and <i><b>de Bruijn</b></i> graphs: data structures for <i><b>de novo</b></i>genome assembly in the big data era. Quantitative Biology, 2019, 7, 278-292. | 0.5 | 30 |
| 16 | ASGAL: aligning RNA-Seq data to a splicing graph to detect novel alternative splicing events. BMC Bioinformatics, 2018, 19, 444. | 2.6 | 26 |
| 17 | GPPS: an ILP-based approach for inferring cancer progression with mutation losses from single cell data. , 2018, , . |  | 3 |
| 18 | Inverse Lyndon words and inverse Lyndon factorizations of words. Advances in Applied Mathematics, 2018, 101, 281-319. | 0.7 | 14 |

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| 19 | HapCHAT: adaptive haplotype assembly for efficiently leveraging high coverage in long reads. BMC Bioinformatics, 2018, 19, 252. | 2.6 | 8 |
| 20 | FSG: Fast String Graph Construction for De Novo Assembly. Journal of Computational Biology, 2017, 24, 953-968. | 1.6 | 12 |
| 21 | Species-Driven Persistent Phylogeny. Fundamenta Informaticae, 2017, 154, 47-63. | 0.4 | 0 |
| 22 | An External-Memory Algorithm for String Graph Construction. Algorithmica, 2017, 78, 394-424. | 1.3 | 9 |
| 23 | A colored graph approach to perfect phylogeny with persistent characters. Theoretical Computer Science, 2017, 658, 60-73. | 0.9 | 12 |
| 24 | Beyond Perfect Phylogeny. , 2017, , . | | 42 |
| 25 | FSG: Fast String Graph Construction for De Novo Assembly of Reads Data. Lecture Notes in Computer Science, 2016, , 27-39. | 1.3 | 1 |
| 26 | On the Minimum Error Correction Problem for Haplotype Assembly in Diploid and Polyploid Genomes. Journal of Computational Biology, 2016, 23, 718-736. | 1.6 | 29 |
| 27 | LSG: An External-Memory Tool to Compute String Graphs for Next-Generation Sequencing Data Assembly. Journal of Computational Biology, 2016, 23, 137-149. | 1.6 | 14 |
| 28 | H<scp>ap</scp>C<scp>ol</scp>: accurate and memory-efficient haplotype assembly from long reads. Bioinformatics, 2016, 32, 1610-1617. | 4.1 | 40 |
| 29 | Covering Pairs in Directed Acyclic Graphs. Computer Journal, 2015, 58, 1673-1686. | 2.4 | 6 |
| 30 | 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 |
| 31 | Existence of constants in regular splicing languages. Information and Computation, 2015, 242, 340-353. | 0.7 | 10 |
| 32 | On the Fixed Parameter Tractability and Approximability of the Minimum Error Correction Problem. Lecture Notes in Computer Science, 2015, , 100-113. | 1.3 | 8 |
| 33 | Restricted and Swap Common Superstring: A Multivariate Algorithmic Perspective. Algorithmica, 2015, 72, 914-939. | 1.3 | 1 |
| 34 | Transcriptome Assembly and Alternative Splicing Analysis. Methods in Molecular Biology, 2015, 1269, 173-188. | 0.9 | 1 |
| 35 | Modeling Alternative Splicing Variants from RNA-Seq Data with Isoform Graphs. Journal of Computational Biology, 2014, 21, 16-40. | 1.6 | 22 |
| 36 | Complexity insights of the Minimum Duplication problem. Theoretical Computer Science, 2014, 530, 66-79. | 0.9 | 5 |

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| 37 | Further Steps in TANGO: improved taxonomic assignment in metagenomics. Bioinformatics, 2014, 30, 17-23. | 4.1 | 22 |
| 38 | Explaining evolution via constrained persistent perfect phylogeny. BMC Genomics, 2014, 15, S10. | 2.8 | 40 |
| 39 | Constructing String Graphs in External Memory. Lecture Notes in Computer Science, 2014, , 311-325. | 1.3 | 5 |
| 40 | Covering Pairs in Directed Acyclic Graphs. Lecture Notes in Computer Science, 2014, , 126-137. | 1.3 | 0 |
| 41 | Parameterized complexity of k-anonymity: hardness and tractability. Journal of Combinatorial Optimization, 2013, 26, 19-43. | 1.3 | 5 |
| 42 | Haplotype-based prediction of gene alleles using pedigrees and SNP genotypes. , 2013, , . | | 6 |
| 43 | Maximum Disjoint Paths on Edge-Colored Graphs: Approximability and Tractability. Algorithms, 2013, 6, 1-11. | 2.1 | 10 |
| 44 | Reconstructing isoform graphs from RNA-Seq data. , 2012, , . | | 1 |
| 45 | A fast and practical approach to genotype phasing and imputation on a pedigree with erroneous and incomplete information. , 2012, , . | | 0 |
| 46 | 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 |
| 47 | 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 |
| 48 | The binary perfect phylogeny with persistent characters. Theoretical Computer Science, 2012, 454, 51-63. | 0.9 | 57 |
| 49 | On the parameterized complexity of the repetition free longest common subsequence problem. Information Processing Letters, 2012, 112, 272-276. | 0.6 | 19 |
| 50 | A randomized PTAS for the minimum Consensus Clustering with a fixed number of clusters. Theoretical Computer Science, 2012, 429, 36-45. | 0.9 | 1 |
| 51 | PIntron: 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 |
| 52 | Restricted and Swap Common Superstring: A Parameterized View. Lecture Notes in Computer Science, 2012, , 49-60. | 1.3 | 1 |
| 53 | Complexity Insights of the Minimum Duplication Problem. Lecture Notes in Computer Science, 2012, , 153-164. | 1.3 | 5 |
| 54 | PIntron: A fast method for gene structure prediction via maximal pairings of a pattern and a text. , 2011, , . | | 0 |

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| 55 | Picture Languages Generated by Assembling Tiles. Fundamenta Informaticae, 2011, 110, 77-93. | 0.4 | 0 |
| 56 | Anonymizing binary and small tables isÂhardÂtoÂapproximate. Journal of Combinatorial Optimization, 2011, 22, 97-119. | 1.3 | 14 |
| 57 | ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. Nucleic Acids Research, 2011, 39, D80-D85. | 14.5 | 38 |
| 58 | Regular Splicing Languages Must Have a Constant. Lecture Notes in Computer Science, 2011, , 82-92. | 1.3 | 7 |
| 59 | Constants and label-equivalence: A decision procedure for reflexive regular splicing languages. Theoretical Computer Science, 2010, 411, 865-877. | 0.9 | 4 |
| 60 | A characterization of (regular) circular languages generated by monotone complete splicing systems. Theoretical Computer Science, 2010, 411, 4149-4161. | 0.9 | 10 |
| 61 | Fingerprint Clustering with Bounded Number ofÂMissing Values. Algorithmica, 2010, 58, 282-303. | 1.3 | 1 |
| 62 | On the regularity of circular splicing languages: a survey and new developments. Natural Computing, 2010, 9, 397-420. | 3.0 | 8 |
| 63 | Variants of constrained longest common subsequence. Information Processing Letters, 2010, 110, 877-881. | 0.6 | 33 |
| 64 | Pure Parsimony Xor Haplotyping. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 598-610. | 3.0 | 4 |
| 65 | Haplotype Inference on Pedigrees with Recombinations and Mutations. Lecture Notes in Computer Science, 2010, , 148-161. | 1.3 | 0 |
| 66 | Detecting Alternative Gene Structures from Spliced ESTs: A Computational Approach. Journal of Computational Biology, 2009, 16, 43-66. | 1.6 | 23 |
| 67 | Picture Languages Generated by Assembling Tiles. Lecture Notes in Computer Science, 2009, , 224-235. | 1.3 | 2 |
| 68 | Finite Splicing: Generative Capacity, NewÂModels and Complexity Aspects. Natural Computing Series, 2009, , 313-329. | 2.2 | 0 |
| 69 | Pure Parsimony Xor Haplotyping. Lecture Notes in Computer Science, 2009, , 186-197. | 1.3 | 0 |
| 70 | On the Approximation of Correlation Clustering and Consensus Clustering. Journal of Computer and System Sciences, 2008, 74, 671-696. | 1.2 | 28 |
| 71 | Exemplar Longest Common Subsequence. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 535-543. | 3.0 | 30 |
| 72 | A Linear-Time Algorithm for the Perfect Phylogeny Haplotype Problem. Algorithmica, 2007, 48, 267-285. | 1.3 | 22 |

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| 73 | Linear splicing and syntactic monoid. Discrete Applied Mathematics, 2006, 154, 452-470. | 0.9 | 4 |
| 74 | ASPIC: a web resource for alternative splicing prediction and transcript isoforms characterization. Nucleic Acids Research, 2006, 34, W440-W443. | 14.5 | 27 |
| 75 | Computational methods for alternative splicing prediction. Briefings in Functional Genomics & Proteomics, 2006, 5, 46-51. | 3.8 | 16 |
| 76 | Exemplar Longest Common Subsequence. Lecture Notes in Computer Science, 2006, , 622-629. | 1.3 | 1 |
| 77 | Fingerprint Clustering with Bounded Number of Missing Values. Lecture Notes in Computer Science, 2006, , 106-116. | 1.3 | 0 |
| 78 | A Decision Procedure for Reflexive Regular Splicing Languages. Lecture Notes in Computer Science, 2006, , 315-326. | 1.3 | 3 |
| 79 | On the power of circular splicing. Discrete Applied Mathematics, 2005, 150, 51-66. | 0.9 | 11 |
| 80 | ASPIC: a novel method to predict the exon-intron structure of a gene that is optimally compatible to a set of transcript sequences. BMC Bioinformatics, 2005, 6, 244. | 2.6 | 32 |
| 81 | The structure of reflexive regular splicing languages via Schützenberger constants. Theoretical Computer Science, 2005, 334, 71-98. | 0.9 | 22 |
| 82 | Regular splicing languages and subclasses. Theoretical Computer Science, 2005, 340, 349-363. | 0.9 | 16 |
| 83 | Reconciling a gene tree to a species tree under the duplication cost model. Theoretical Computer Science, 2005, 347, 36-53. | 0.9 | 71 |
| 84 | Correlation Clustering and Consensus Clustering. Lecture Notes in Computer Science, 2005, , 226-235. | 1.3 | 14 |
| 85 | Recombinant DNA ,Gene Splicing as Generative Devices of Formal Languages. Lecture Notes in Computer Science, 2005, , 65-67. | 1.3 | 1 |
| 86 | Circular splicing and regularity. RAIRO - Theoretical Informatics and Applications, 2004, 38, 189-228. | 0.5 | 12 |
| 87 | The Haplotyping problem: An overview of computational models and solutions. Journal of Computer Science and Technology, 2003, 18, 675-688. | 1.5 | 104 |
| 88 | Decision Problems for Linear and Circular Splicing Systems. Lecture Notes in Computer Science, 2003, , 78-92. | 1.3 | 11 |
| 89 | Regular Languages Generated by Reflexive Finite Splicing Systems. Lecture Notes in Computer Science, 2003, , 134-145. | 1.3 | 6 |
| 90 | Experimenting an approximation algorithm for the LCS. Discrete Applied Mathematics, 2001, 110, 13-24. | 0.9 | 23 |

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| 91 | Nesting of prime substructures in k-ary relations. Theoretical Computer Science, 2001, 259, 341-357. | 0.9 | 0 |
| 92 | The complexity of multiple sequence alignment with SP-score that is a metric. Theoretical Computer Science, 2001, 259, 63-79. | 0.9 | 91 |
| 93 | Separating some splicing models. Information Processing Letters, 2001, 79, 255-259. | 0.6 | 25 |
| 94 | An approximation algorithm for the shortest common supersequence problem. , 2001, , . | | 22 |
| 95 | DNA and circular splicing?. Lecture Notes in Computer Science, 2001, , 117-129. | 1.3 | 10 |
| 96 | APPROXIMATING THE MAXIMUM ISOMORPHIC AGREEMENT SUBTREE IS HARD. International Journal of Foundations of Computer Science, 2000, 11, 579-590. | 1.1 | 4 |
| 97 | Primitive 2-structures with the (n âˆ' 2)-property. Theoretical Computer Science, 1994, 132, 151-178. | 0.9 | 9 |
| 98 | Circular Languages Generated by Complete Splicing Systems and Pure Unitary Languages. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 9, 22-31. | 0.8 | 1 |
| 99 | Automata and Formal Languages for Next Generation Sequencing Data. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 252, 1-2. | 0.8 | 0 |