

Arlindo L Oliveira

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

3,877
citations

331538

21
h-index

133188

59
g-index

93
all docs

93
docs citations

93
times ranked

3529
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | A blueprint for conscious machines. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 3.3 | 1 |
| 2 | Using Soft Labels to Model Uncertainty in Medical Image Segmentation. Lecture Notes in Computer Science, 2022, , 585-596. | 1.0 | 3 |
| 3 | Artificial Intelligence Applications in Stroke. , 2021, , 261-273. | | 0 |
| 4 | Biotechnology, Big Data and Artificial Intelligence. Biotechnology Journal, 2019, 14, e1800613. | 1.8 | 81 |
| 5 | Using Machine Learning to Improve the Prediction of Functional Outcome in Ischemic Stroke Patients. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1953-1959. | 1.9 | 79 |
| 6 | Computational Approach to the Discovery of Phytochemical Molecules with Therapeutic Potential Targets to the PKCZ protein. Letters in Drug Design and Discovery, 2018, 15, 488-499. | 0.4 | 19 |
| 7 | DegreeCox “ a network-based regularization method for survival analysis. BMC Bioinformatics, 2016, 17, 449. | 1.2 | 22 |
| 8 | The YEASTRACT database: an upgraded information system for the analysis of gene and genomic transcription regulation in <i>Saccharomyces cerevisiae</i> . Nucleic Acids Research, 2014, 42, D161-D166. | 6.5 | 215 |
| 9 | Using Information Interaction to Discover Epistatic Effects in Complex Diseases. PLoS ONE, 2013, 8, e76300. | 1.1 | 9 |
| 10 | Mining query log graphs towards a query folksonomy. Concurrency Computation Practice and Experience, 2012, 24, 2179-2192. | 1.4 | 9 |
| 11 | Efficient and Accurate Haplotype Inference by Combining Parsimony and Pedigree Information. Lecture Notes in Computer Science, 2012, , 38-56. | 1.0 | 13 |
| 12 | Quantitative Modeling the <i>Saccharomyces cerevisiae</i> FLR1 Regulatory Network Using an S-System Formalism. , 2011, , . | | 0 |
| 13 | Using systems biology approaches to study a multidrug resistance network. , 2011, , . | | 0 |
| 14 | Efficient alignment of pyrosequencing reads for re-sequencing applications. BMC Bioinformatics, 2011, 12, 163. | 1.2 | 9 |
| 15 | Qualitative modelling and formal verification of the FLR1 gene mancozeb response in <i>Saccharomyces cerevisiae</i> . IET Systems Biology, 2011, 5, 308-316. | 0.8 | 7 |
| 16 | Fully Generalized Graph Cores. Communications in Computer and Information Science, 2011, , 22-34. | 0.4 | 2 |
| 17 | Haplotype inference with pseudo-Boolean optimization. Annals of Operations Research, 2011, 184, 137-162. | 2.6 | 13 |
| 18 | GRISOTTO: A greedy approach to improve combinatorial algorithms for motif discovery with prior knowledge. Algorithms for Molecular Biology, 2011, 6, 13. | 0.3 | 3 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | YEASTRACT: providing a programmatic access to curated transcriptional regulatory associations in <i>Saccharomyces cerevisiae</i> through a web services interface. <i>Nucleic Acids Research</i> , 2011, 39, D136-D140. | 6.5 | 171 |
| 20 | Fully compressed suffix trees. <i>ACM Transactions on Algorithms</i> , 2011, 7, 1-34. | 0.9 | 39 |
| 21 | Sliding Window Update Using Suffix Arrays. , 2011, , . | | 3 |
| 22 | QUANTITATIVE MODELING OF THE <i>SACCHAROMYCES CEREVISIAE</i> FLR1 REGULATORY NETWORK USING AN S-SYSTEM FORMALISM. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 613-630. | 0.3 | 3 |
| 23 | TFRank: network-based prioritization of regulatory associations underlying transcriptional responses. <i>Bioinformatics</i> , 2011, 27, 3149-3157. | 1.8 | 17 |
| 24 | On Community Detection in Very Large Networks. <i>Communications in Computer and Information Science</i> , 2011, , 208-216. | 0.4 | 4 |
| 25 | A Data Mining Approach for the Detection of High-Risk Breast Cancer Groups. <i>Advances in Intelligent and Soft Computing</i> , 2010, , 43-51. | 0.2 | 27 |
| 26 | Using graph modularity analysis to identify transcription factor binding sites. , 2010, , . | | 0 |
| 27 | Haplotype Inference by Pure Parsimony: A Survey. <i>Journal of Computational Biology</i> , 2010, 17, 969-992. | 0.8 | 9 |
| 28 | Apt-pbo. , 2010, , . | | 21 |
| 29 | Refining current knowledge on the yeast FLR1 regulatory network by combined experimental and computational approaches. <i>Molecular BioSystems</i> , 2010, 6, 2471. | 2.9 | 22 |
| 30 | Identification of Regulatory Modules in Time Series Gene Expression Data Using a Linear Time Biclustering Algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 153-165. | 1.9 | 86 |
| 31 | Mining Large Query Induced Graphs towards a Hierarchical Query Folksonomy. <i>Lecture Notes in Computer Science</i> , 2010, , 237-242. | 1.0 | 3 |
| 32 | Parallel and Distributed Compressed Indexes. <i>Lecture Notes in Computer Science</i> , 2010, , 348-360. | 1.0 | 2 |
| 33 | Approximate String Matching with Compressed Indexes. <i>Algorithms</i> , 2009, 2, 1105-1136. | 1.2 | 25 |
| 34 | CONSTANT TIME CLASH DETECTION IN PROTEIN FOLDING. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 55-74. | 0.3 | 2 |
| 35 | BiGGEsTS: integrated environment for biclustering analysis of time series gene expression data. <i>BMC Research Notes</i> , 2009, 2, 124. | 0.6 | 57 |
| 36 | A polynomial time biclustering algorithm for finding approximate expression patterns in gene expression time series. <i>Algorithms for Molecular Biology</i> , 2009, 4, 8. | 0.3 | 47 |

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|----|--|-----|-----------|
| 37 | Efficient Biclustering Algorithms for Time Series Gene Expression Data Analysis. Lecture Notes in Computer Science, 2009, , 1013-1019. | 1.0 | 6 |
| 38 | On the Suitability of Suffix Arrays for Lempel-Ziv Data Compression. Communications in Computer and Information Science, 2009, , 267-280. | 0.4 | 3 |
| 39 | A compressed self-index using a Ziv-Lempel dictionary. Information Retrieval, 2008, 11, 359-388. | 1.6 | 19 |
| 40 | An analysis of the positional distribution of DNA motifs in promoter regions and its biological relevance. BMC Bioinformatics, 2008, 9, 89. | 1.2 | 14 |
| 41 | ccrB typing tool: an online resource for staphylococci ccrB sequence typing. Journal of Antimicrobial Chemotherapy, 2008, 61, 959-960. | 1.3 | 16 |
| 42 | USING GRAMMATICAL INFERENCE TECHNIQUES TO LEARN ONTOLOGIES THAT DESCRIBE THE STRUCTURE OF DOMAIN INSTANCES. Applied Artificial Intelligence, 2008, 22, 139-167. | 2.0 | 0 |
| 43 | Haplotype Inference with Boolean Constraint Solving: An Overview. , 2008, , . | | 3 |
| 44 | Efficient Haplotype Inference with Combined CP and OR Techniques. , 2008, , 308-312. | | 11 |
| 45 | Dynamic Fully-Compressed Suffix Trees. , 2008, , 191-203. | | 13 |
| 46 | Ontology Design Principles and Normalization Techniques in the Web. Lecture Notes in Computer Science, 2008, , 28-43. | 1.0 | 2 |
| 47 | Fully-Compressed Suffix Trees. , 2008, , 362-373. | | 19 |
| 48 | Clique Analysis of Query Log Graphs. Lecture Notes in Computer Science, 2008, , 188-199. | 1.0 | 7 |
| 49 | Indexed Hierarchical Approximate String Matching. Lecture Notes in Computer Science, 2008, , 144-154. | 1.0 | 1 |
| 50 | Identification of Transcription Factor Binding Sites in Promoter Regions by Modularity Analysis of the Motif Co-occurrence Graph. , 2008, , 220-231. | | 0 |
| 51 | Semi-supervised single-label text categorization using centroid-based classifiers. , 2007, , . | | 27 |
| 52 | YEASTRACT-DISCOVERER: new tools to improve the analysis of transcriptional regulatory associations in Saccharomyces cerevisiae. Nucleic Acids Research, 2007, 36, D132-D136. | 6.5 | 140 |
| 53 | Learning bayesian networks consistent with the optimal branching. , 2007, , . | | 6 |
| 54 | Efficient generation of super condensed neighborhoods. Journal of Discrete Algorithms, 2007, 5, 501-513. | 0.7 | 0 |

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|----|--|-----|-----------|
| 55 | Efficient Haplotype Inference with Pseudo-boolean Optimization. Lecture Notes in Computer Science, 2007, , 125-139. | 1.0 | 24 |
| 56 | Approximate String Matching with Lempel-Ziv Compressed Indexes. , 2007, , 264-275. | | 3 |
| 57 | AN EFFICIENT BICLUSTERING ALGORITHM FOR FINDING GENES WITH SIMILAR PATTERNS IN TIME-SERIES EXPRESSION DATA. , 2007, , . | | 11 |
| 58 | Bioinformatics: A New Approach for the Challenges of Molecular Biology. , 2007, , 295-309. | | 0 |
| 59 | Efficient and Tight Upper Bounds for Haplotype Inference by Pure Parsimony Using Delayed Haplotype Selection. , 2007, , 621-632. | | 3 |
| 60 | An Efficient Algorithm for the Identification of Structured Motifs in DNA Promoter Sequences. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 126-140. | 1.9 | 51 |
| 61 | The YEASTRACT database: a tool for the analysis of transcription regulatory associations in Saccharomyces cerevisiae. Nucleic Acids Research, 2006, 34, D446-D451. | 6.5 | 421 |
| 62 | MUSA: a parameter free algorithm for the identification of biologically significant motifs. Bioinformatics, 2006, 22, 2996-3002. | 1.8 | 26 |
| 63 | DFT and Probabilistic Testability Analysis at RTL. , 2006, , . | | 4 |
| 64 | A Compressed Self-index Using a Ziv-Lempel Dictionary. Lecture Notes in Computer Science, 2006, , 163-180. | 1.0 | 6 |
| 65 | Inference of regular languages using state merging algorithms with search. Pattern Recognition, 2005, 38, 1457-1467. | 5.1 | 32 |
| 66 | A Linear Time Biclustering Algorithm for Time Series Gene Expression Data. Lecture Notes in Computer Science, 2005, , 39-52. | 1.0 | 29 |
| 67 | Using a More Powerful Teacher to Reduce the Number of Queries of the L* Algorithm in Practical Applications. Lecture Notes in Computer Science, 2005, , 325-336. | 1.0 | 3 |
| 68 | Constraint Relaxations for Discovering Unknown Sequential Patterns. Lecture Notes in Computer Science, 2005, , 11-32. | 1.0 | 8 |
| 69 | Faster Generation of Super Condensed Neighbourhoods Using Finite Automata. Lecture Notes in Computer Science, 2005, , 246-255. | 1.0 | 1 |
| 70 | Biclustering algorithms for biological data analysis: a survey. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 24-45. | 1.9 | 1,588 |
| 71 | Metrics for Grid Applicability: A Distributed Elliptic Curve Platform Assessment. Lecture Notes in Computer Science, 2004, , 864-871. | 1.0 | 1 |
| 72 | On the problem of gate assignment under different rise and fall delays. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2003, 22, 807-814. | 1.9 | 1 |

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|----|--|-----|-----------|
| 73 | Generalization of Pattern-Growth Methods for Sequential Pattern Mining with Gap Constraints. , 2003, , 239-251. | | 35 |
| 74 | A Data Mining Approach to Credit Risk Evaluation and Behaviour Scoring. Lecture Notes in Computer Science, 2003, , 184-188. | 1.0 | 2 |
| 75 | An Empirical Comparison of Text Categorization Methods. Lecture Notes in Computer Science, 2003, , 183-196. | 1.0 | 28 |
| 76 | Implicit FSM decomposition applied to low-power design. IEEE Transactions on Very Large Scale Integration (VLSI) Systems, 2002, 10, 560-565. | 2.1 | 21 |
| 77 | Inference of Sequential Association Rules Guided by Context-Free Grammars. Lecture Notes in Computer Science, 2002, , 1-13. | 1.0 | 5 |
| 78 | Techniques for the creation of digital watermarks in sequential circuit designs. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2001, 20, 1101-1117. | 1.9 | 118 |
| 79 | Efficient Algorithms for the Inference of Minimum Size DFAs. , 2001, 44, 93-119. | | 28 |
| 80 | FSM decomposition by direct circuit manipulation applied to low power design. , 2000, , . | | 7 |
| 81 | A new algorithm for exact reduction of incompletely specified finite state machines. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 1999, 18, 1619-1632. | 1.9 | 26 |
| 82 | Exact minimization of binary decision diagrams using implicit techniques. IEEE Transactions on Computers, 1998, 47, 1282-1296. | 2.4 | 18 |
| 83 | Using the Minimum Description Length Principle to Infer Reduced Ordered Decision Graphs. Machine Learning, 1996, 25, 23-50. | 3.4 | 4 |
| 84 | Using the minimum description length principle to infer reduced ordered decision graphs. Machine Learning, 1996, 25, 23-50. | 3.4 | 15 |
| 85 | Limits of exact algorithms for inference of minimum size finite state machines. Lecture Notes in Computer Science, 1996, , 59-66. | 1.0 | 9 |
| 86 | Learning Concepts by Synthesizing Minimal Threshold Gate Networks. , 1991, , 193-197. | | 0 |
| 87 | A probabilistic method for the computation of testability of RTL constructs. , 0, , . | | 7 |
| 88 | Probabilistic Testability Analysis and DFT Methods at RTL. , 0, , . | | 4 |