

# Arlindo L Oliveira

## List of Publications by Year in descending order

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Version: 2024-02-01

88  
papers

3,877  
citations

331259

21  
h-index

133063

59  
g-index

93  
all docs

93  
docs citations

93  
times ranked

3529  
citing authors

#	ARTICLE	IF	CITATIONS
1	Biclustering algorithms for biological data analysis: a survey. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 24-45.	1.9	1,588
2	The YEASTRACT database: a tool for the analysis of transcription regulatory associations in <i>Saccharomyces cerevisiae</i> . Nucleic Acids Research, 2006, 34, D446-D451.	6.5	421
3	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
4	YEASTRACT: providing a programmatic access to curated transcriptional regulatory associations in <i>Saccharomyces cerevisiae</i> through a web services interface. Nucleic Acids Research, 2011, 39, D136-D140.	6.5	171
5	YEASTRACT-DISCOVERER: new tools to improve the analysis of transcriptional regulatory associations in <i>Saccharomyces cerevisiae</i> . Nucleic Acids Research, 2007, 36, D132-D136.	6.5	140
6	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
7	Identification of Regulatory Modules in Time Series Gene Expression Data Using a Linear Time Biclustering Algorithm. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 153-165.	1.9	86
8	Biotechnology, Big Data and Artificial Intelligence. Biotechnology Journal, 2019, 14, e1800613.	1.8	81
9	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
10	BIGGEsTS: integrated environment for biclustering analysis of time series gene expression data. BMC Research Notes, 2009, 2, 124.	0.6	57
11	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
12	A polynomial time biclustering algorithm for finding approximate expression patterns in gene expression time series. Algorithms for Molecular Biology, 2009, 4, 8.	0.3	47
13	Fully compressed suffix trees. ACM Transactions on Algorithms, 2011, 7, 1-34.	0.9	39
14	Generalization of Pattern-Growth Methods for Sequential Pattern Mining with Gap Constraints. , 2003, , 239-251.		35
15	Inference of regular languages using state merging algorithms with search. Pattern Recognition, 2005, 38, 1457-1467.	5.1	32
16	A Linear Time Biclustering Algorithm for Time Series Gene Expression Data. Lecture Notes in Computer Science, 2005, , 39-52.	1.0	29
17	Efficient Algorithms for the Inference of Minimum Size DFAs. , 2001, 44, 93-119.		28
18	An Empirical Comparison of Text Categorization Methods. Lecture Notes in Computer Science, 2003, , 183-196.	1.0	28

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19	Semi-supervised single-label text categorization using centroid-based classifiers. , 2007, , .		27
20	A Data Mining Approach for the Detection of High-Risk Breast Cancer Groups. Advances in Intelligent and Soft Computing, 2010, , 43-51.	0.2	27
21	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
22	MUSA: a parameter free algorithm for the identification of biologically significant motifs. Bioinformatics, 2006, 22, 2996-3002.	1.8	26
23	Approximate String Matching with Compressed Indexes. Algorithms, 2009, 2, 1105-1136.	1.2	25
24	Efficient Haplotype Inference with Pseudo-boolean Optimization. Lecture Notes in Computer Science, 2007, , 125-139.	1.0	24
25	Refining current knowledge on the yeast FLR1 regulatory network by combined experimental and computational approaches. Molecular BioSystems, 2010, 6, 2471.	2.9	22
26	DegreeCox “ a network-based regularization method for survival analysis. BMC Bioinformatics, 2016, 17, 449.	1.2	22
27	Implicit FSM decomposition applied to low-power design. IEEE Transactions on Very Large Scale Integration (VLSI) Systems, 2002, 10, 560-565.	2.1	21
28	Apt-pbo. , 2010, , .		21
29	A compressed self-index using a Ziv“Lempel dictionary. Information Retrieval, 2008, 11, 359-388.	1.6	19
30	Fully-Compressed Suffix Trees. , 2008, , 362-373.		19
31	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
32	Exact minimization of binary decision diagrams using implicit techniques. IEEE Transactions on Computers, 1998, 47, 1282-1296.	2.4	18
33	TFRank: network-based prioritization of regulatory associations underlying transcriptional responses. Bioinformatics, 2011, 27, 3149-3157.	1.8	17
34	ccrB typing tool: an online resource for staphylococci ccrB sequence typing. Journal of Antimicrobial Chemotherapy, 2008, 61, 959-960.	1.3	16
35	Using the minimum description length principle to infer reduced ordered decision graphs. Machine Learning, 1996, 25, 23-50.	3.4	15
36	An analysis of the positional distribution of DNA motifs in promoter regions and its biological relevance. BMC Bioinformatics, 2008, 9, 89.	1.2	14

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37	Haplotype inference with pseudo-Boolean optimization. <i>Annals of Operations Research</i> , 2011, 184, 137-162.	2.6	13
38	Dynamic Fully-Compressed Suffix Trees. , 2008, , 191-203.		13
39	Efficient and Accurate Haplotype Inference by Combining Parsimony and Pedigree Information. <i>Lecture Notes in Computer Science</i> , 2012, , 38-56.	1.0	13
40	Efficient Haplotype Inference with Combined CP and OR Techniques. , 2008, , 308-312.		11
41	AN EFFICIENT BICLUSTERING ALGORITHM FOR FINDING GENES WITH SIMILAR PATTERNS IN TIME-SERIES EXPRESSION DATA. , 2007, , .		11
42	Haplotype Inference by Pure Parsimony: A Survey. <i>Journal of Computational Biology</i> , 2010, 17, 969-992.	0.8	9
43	Efficient alignment of pyrosequencing reads for re-sequencing applications. <i>BMC Bioinformatics</i> , 2011, 12, 163.	1.2	9
44	Mining query log graphs towards a query folksonomy. <i>Concurrency Computation Practice and Experience</i> , 2012, 24, 2179-2192.	1.4	9
45	Using Information Interaction to Discover Epistatic Effects in Complex Diseases. <i>PLoS ONE</i> , 2013, 8, e76300.	1.1	9
46	Limits of exact algorithms for inference of minimum size finite state machines. <i>Lecture Notes in Computer Science</i> , 1996, , 59-66.	1.0	9
47	Constraint Relaxations for Discovering Unknown Sequential Patterns. <i>Lecture Notes in Computer Science</i> , 2005, , 11-32.	1.0	8
48	FSM decomposition by direct circuit manipulation applied to low power design. , 2000, , .		7
49	A probabilistic method for the computation of testability of RTL constructs. , 0, , .		7
50	Qualitative modelling and formal verification of the FLR1 gene mancozeb response in <i>Saccharomyces cerevisiae</i> . <i>IET Systems Biology</i> , 2011, 5, 308-316.	0.8	7
51	Clique Analysis of Query Log Graphs. <i>Lecture Notes in Computer Science</i> , 2008, , 188-199.	1.0	7
52	Learning bayesian networks consistent with the optimal branching. , 2007, , .		6
53	A Compressed Self-index Using a Ziv-Lempel Dictionary. <i>Lecture Notes in Computer Science</i> , 2006, , 163-180.	1.0	6
54	Efficient Biclustering Algorithms for Time Series Gene Expression Data Analysis. <i>Lecture Notes in Computer Science</i> , 2009, , 1013-1019.	1.0	6

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55	Inference of Sequential Association Rules Guided by Context-Free Grammars. Lecture Notes in Computer Science, 2002, , 1-13.	1.0	5
56	Using the Minimum Description Length Principle to Infer Reduced Ordered Decision Graphs. Machine Learning, 1996, 25, 23-50.	3.4	4
57	Probabilistic Testability Analysis and DFT Methods at RTL. , 0, , .		4
58	DFT and Probabilistic Testability Analysis at RTL. , 2006, , .		4
59	On Community Detection in Very Large Networks. Communications in Computer and Information Science, 2011, , 208-216.	0.4	4
60	Haplotype Inference with Boolean Constraint Solving: An Overview. , 2008, , .		3
61	GRISOTTO: A greedy approach to improve combinatorial algorithms for motif discovery with prior knowledge. Algorithms for Molecular Biology, 2011, 6, 13.	0.3	3
62	Sliding Window Update Using Suffix Arrays. , 2011, , .		3
63	QUANTITATIVE MODELING OF THE<i>SACCHAROMYCES CEREVISIAE</i>FLR1 REGULATORY NETWORK USING AN S-SYSTEM FORMALISM. Journal of Bioinformatics and Computational Biology, 2011, 09, 613-630.	0.3	3
64	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
65	Approximate String Matching with Lempel-Ziv Compressed Indexes. , 2007, , 264-275.		3
66	Mining Large Query Induced Graphs towards a Hierarchical Query Folksonomy. Lecture Notes in Computer Science, 2010, , 237-242.	1.0	3
67	On the Suitability of Suffix Arrays for Lempel-Ziv Data Compression. Communications in Computer and Information Science, 2009, , 267-280.	0.4	3
68	Efficient and Tight Upper Bounds for Haplotype Inference by Pure Parsimony Using Delayed Haplotype Selection. , 2007, , 621-632.		3
69	Using Soft Labels to Model Uncertainty in Medical Image Segmentation. Lecture Notes in Computer Science, 2022, , 585-596.	1.0	3
70	A Data Mining Approach to Credit Risk Evaluation and Behaviour Scoring. Lecture Notes in Computer Science, 2003, , 184-188.	1.0	2
71	CONSTANT TIME CLASH DETECTION IN PROTEIN FOLDING. Journal of Bioinformatics and Computational Biology, 2009, 07, 55-74.	0.3	2
72	Fully Generalized Graph Cores. Communications in Computer and Information Science, 2011, , 22-34.	0.4	2

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73	Ontology Design Principles and Normalization Techniques in the Web. Lecture Notes in Computer Science, 2008, , 28-43.	1.0	2
74	Parallel and Distributed Compressed Indexes. Lecture Notes in Computer Science, 2010, , 348-360.	1.0	2
75	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
76	Metrics for Grid Applicability: A Distributed Elliptic Curve Platform Assessment. Lecture Notes in Computer Science, 2004, , 864-871.	1.0	1
77	Faster Generation of Super Condensed Neighbourhoods Using Finite Automata. Lecture Notes in Computer Science, 2005, , 246-255.	1.0	1
78	Indexed Hierarchical Approximate String Matching. Lecture Notes in Computer Science, 2008, , 144-154.	1.0	1
79	A blueprint for conscious machines. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	1
80	Efficient generation of super condensed neighborhoods. Journal of Discrete Algorithms, 2007, 5, 501-513.	0.7	0
81	USING GRAMMATICAL INFERENCE TECHNIQUES TO LEARN ONTOLOGIES THAT DESCRIBE THE STRUCTURE OF DOMAIN INSTANCES. Applied Artificial Intelligence, 2008, 22, 139-167.	2.0	0
82	Using graph modularity analysis to identify transcription factor binding sites. , 2010, , .		0
83	Quantitative Modeling the Saccharomyces cerevisiae FLR1 Regulatory Network Using an S-System Formalism. , 2011, , .		0
84	Using systems biology approaches to study a multidrug resistance network. , 2011, , .		0
85	Artificial Intelligence Applications in Stroke. , 2021, , 261-273.		0
86	Learning Concepts by Synthesizing Minimal Threshold Gate Networks. , 1991, , 193-197.		0
87	Bioinformatics: A New Approach for the Challenges of Molecular Biology. , 2007, , 295-309.		0
88	Identification of Transcription Factor Binding Sites in Promoter Regions by Modularity Analysis of the Motif Co-occurrence Graph. , 2008, , 220-231.		0