

Srinivas Aluru

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

5,616
citations

489802

18
h-index

721071

23
g-index

51
all docs

51
docs citations

51
times ranked

9049
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequential and parallel algorithms for all-pair k-mismatch maximal common substrings. Journal of Parallel and Distributed Computing, 2020, 144, 68-79.	2.7	0
2	A comprehensive evaluation of long read error correction methods. BMC Genomics, 2020, 21, 889.	1.2	58
3	Accelerating Sequence Alignment to Graphs. , 2019, , .		16
4	RD26 mediates crosstalk between drought and brassinosteroid signalling pathways. Nature Communications, 2017, 8, 14573.	5.8	202
5	A Memory and Time Scalable Parallelization of the Reptile Error-Correction Code. , 2016, , .		1
6	A Parallel Algorithm for Finding All Pairs $\hat{\rho}$ -Mismatch Maximal Common Substrings. , 2016, , .		2
7	Text Indexing. , 2016, , 2226-2231.		0
8	In search of perfect reads. BMC Bioinformatics, 2015, 16, S7.	1.2	3
9	Parallel Read Error Correction for Big Genomic Datasets. , 2015, , .		2
10	Fast and Accurate Construction of Ultra-Dense Consensus Genetic Maps Using Evolution Strategy Optimization. PLoS ONE, 2015, 10, e0122485.	1.1	9
11	Parallel Bayesian Network Structure Learning for Genome-Scale Gene Networks. , 2014, , .		12
12	In search of perfect reads. , 2014, , .		0
13	A Review of Hardware Acceleration for Computational Genomics. IEEE Design and Test, 2014, 31, 19-30.	1.1	59
14	A survey of error-correction methods for next-generation sequencing. Briefings in Bioinformatics, 2013, 14, 56-66.	3.2	205
15	Large-scale metagenomic clustering via quasi clique enumeration and read assignment ambiguity resolution. , 2013, , .		0
16	A Parallel Algorithm for Spectrum-based Short Read Error Correction. , 2012, , .		8
17	Parallel Bayesian network structure learning with application to gene networks. , 2012, , .		9
18	Workshop: Taxonomic clustering of large-scale metagenomic data. , 2012, , .		0

#	ARTICLE	IF	CITATIONS
19	Accelerating Pairwise Computations on Cell Processors. IEEE Transactions on Parallel and Distributed Systems, 2011, 22, 69-77.	4.0	10
20	Parallel Metagenomic Sequence Clustering Via Sketching and Maximal Quasi-clique Enumeration on Map-Reduce Clouds. , 2011, , .		15
21	An improved maximum likelihood formulation for accurate genome assembly. , 2011, , .		4
22	Parallel Discovery of Direct Causal Relations and Markov Boundaries with Applications to Gene Networks. , 2011, , .		8
23	A brassinosteroid transcriptional network revealed by genome-wide identification of BES1 target genes in <i>Arabidopsis thaliana</i> . Plant Journal, 2011, 65, 634-646.	2.8	565
24	Repeat-aware modeling and correction of short read errors. BMC Bioinformatics, 2011, 12, S52.	1.2	22
25	Reptile: representative tiling for short read error correction. Bioinformatics, 2010, 26, 2526-2533.	1.8	132
26	Parallel applications employing pairwise computations on emerging architectures. , 2010, , .		0
27	A MapReduce Style Framework for Computations on Trees. , 2010, , .		4
28	Parallel Information-Theory-Based Construction of Genome-Wide Gene Regulatory Networks. IEEE Transactions on Parallel and Distributed Systems, 2010, 21, 1721-1733.	4.0	36
29	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. PLoS Genetics, 2009, 5, e1000728.	1.5	39
30	The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, 2009, 326, 1112-1115.	6.0	3,612
31	Parallel Genomic Alignments on the Cell Broadband Engine. IEEE Transactions on Parallel and Distributed Systems, 2009, 20, 1600-1610.	4.0	21
32	A parallel algorithm for exact Bayesian network inference. , 2009, , .		4
33	Constructing Gene Regulatory Networks on Clusters of Cell Processors. , 2009, , .		6
34	Parallel Construction of Bidirected String Graphs for Genome Assembly. , 2008, , .		16
35	Parallel biological sequence alignments on the Cell Broadband Engine. Parallel and Distributed Processing Symposium (IPDPS), Proceedings of the International Conference on, 2008, , .	1.0	17
36	Large-Scale Phylogenetic Analysis on Current HPC Architectures. Scientific Programming, 2008, 16, 255-270.	0.5	14

#	ARTICLE	IF	CITATIONS
37	Text Indexing. , 2008, , 950-954.		0
38	Nearly Identical Paralogs: Implications for Maize (<i>Zea mays</i> L.) Genome Evolution. <i>Genetics</i> , 2007, 175, 429-439.	1.2	60
39	Space efficient linear time construction of suffix arrays. <i>Journal of Discrete Algorithms</i> , 2005, 3, 143-156.	0.7	145
40	Quality assessment of maize assembled genomic islands (MAGIs) and large-scale experimental verification of predicted genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12282-12287.	3.3	67
41	A strategy for assembling the maize (<i>Zea mays</i> L.) genome. <i>Bioinformatics</i> , 2004, 20, 140-147.	1.8	55
42	Parallel biological sequence comparison using prefix computations. <i>Journal of Parallel and Distributed Computing</i> , 2003, 63, 264-272.	2.7	64
43	Space and time efficient parallel algorithms and software for EST clustering. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2003, 14, 1209-1221.	4.0	26
44	Efficient clustering of large EST data sets on parallel computers. <i>Nucleic Acids Research</i> , 2003, 31, 2963-2974.	6.5	69
45	Computational biology on parallel computers. , 2003, , .		0
46	A Formal Analysis of Space Filling Curves for Parallel Domain Decomposition. , 0, , .		7