

# Michael A Langston

## List of Publications by Year in descending order

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75  
papers

2,543  
citations

236925

25  
h-index

206112

48  
g-index

78  
all docs

78  
docs citations

78  
times ranked

3315  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular Subtyping and Outlier Detection in Human Disease Using the Paraclique Algorithm. Algorithms, 2021, 14, 63.	2.1	1
2	Association of Cardiovascular Disease and Long-Term Exposure to Fine Particulate Matter (PM2.5) in the Southeastern United States. Atmosphere, 2021, 12, 947.	2.3	4
3	Examining the Drivers of Racial/Ethnic Disparities in Non-Adherence to Antihypertensive Medications and Mortality Due to Heart Disease and Stroke: A County-Level Analysis. International Journal of Environmental Research and Public Health, 2021, 18, 12702.	2.6	1
4	Structural and Social Determinants of Health Factors Associated with County-Level Variation in Non-Adherence to Antihypertensive Medication Treatment. International Journal of Environmental Research and Public Health, 2020, 17, 6684.	2.6	13
5	Biclique: an R package for maximal biclique enumeration in bipartite graphs. BMC Research Notes, 2020, 13, 88.	1.4	9
6	MicroRNA Profiling in Adipose Before and After Weight Loss Highlights the Role of miR-223-3p and the NLRP3 Inflammasome. Obesity, 2020, 28, 570-580.	3.0	11
7	The Effects of Social, Personal, and Behavioral Risk Factors and PM2.5 on Cardio-Metabolic Disparities in a Cohort of Community Health Center Patients. International Journal of Environmental Research and Public Health, 2020, 17, 3561.	2.6	14
8	Compound Analytics using Combinatorics for Feature Selection: A Case Study in Biomarker Detection. , 2019, , .		0
9	On Finding and Enumerating Maximal and Maximum k-Partite Cliques in k-Partite Graphs. Algorithms, 2019, 12, 23.	2.1	10
10	A robustness metric for biological data clustering algorithms. BMC Bioinformatics, 2019, 20, 503.	2.6	13
11	Molecular Subtyping in Human Disease Using the Paraclique Algorithm. Communications in Computer and Information Science, 2019, , 54-58.	0.5	0
12	Graph Theoretical Analysis of Genome-Scale Data: Examination of Gene Activation Occurring in the Setting of Community-Acquired Pneumonia. Shock, 2018, 50, 53-59.	2.1	9
13	Classification and Anomaly Detection in Traffic Patterns of New York City Taxis: A Case Study in Compound Analytics. , 2018, , .		1
14	A multifactorial obesity model developed from nationwide public health exposome data and modern computational analyses. Obesity Research and Clinical Practice, 2017, 11, 522-533.	1.8	15
15	Integrative Functional Genomics for Systems Genetics in GeneWeaver.org. Methods in Molecular Biology, 2017, 1488, 131-152.	0.9	6
16	Infant Deaths and Mortality from Gun Violence: Causal or Casual?. Journal of the National Medical Association, 2017, 109, 246-251.	0.8	1
17	Genome-wide DNA methylation analysis reveals loci that distinguish different types of adipose tissue in obese individuals. Clinical Epigenetics, 2017, 9, 48.	4.1	32
18	Compound Analytics: Templates for Integrating Graph Algorithms and Machine Learning. , 2017, , .		2

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19	Multiscale graph theoretical tools reveal subtle patterns in big geospatial data. , 2017, , .		2
20	Robust Inference of Genetic Exchange Communities from Microbial Genomes Using TF-IDF. <i>Frontiers in Microbiology</i> , 2017, 8, 21.	3.5	14
21	Graph Algorithm Alternatives via Polynomial-Time Transformations: An Empirical Study Using Boolean Satisfiability and Integer Linear Programming. , 2017, , .		0
22	A novel approach to analyzing lung cancer mortality disparities: Using the exposome and a graph-theoretical toolchain. <i>Environmental Disease</i> , 2017, 2, 33-44.	0.1	10
23	Cross-Species Integrative Functional Genomics in GeneWeaver Reveals a Role for Pafah1b1 in Altered Response to Alcohol. <i>Frontiers in Behavioral Neuroscience</i> , 2016, 10, 1.	2.0	123
24	Validation of research trajectory 1 of an Exposome framework: Exposure to benzo(a)pyrene confers enhanced susceptibility to bacterial infection. <i>Environmental Research</i> , 2016, 146, 173-184.	7.5	15
25	Lower bounds on paraclique density. <i>Discrete Applied Mathematics</i> , 2016, 204, 208-212.	0.9	17
26	GeneWeaver: data driven alignment of cross-species genomics in biology and disease. <i>Nucleic Acids Research</i> , 2016, 44, D555-D559.	14.5	30
27	Scalable multipartite subgraph enumeration for integrative analysis of heterogeneous experimental functional genomics data. , 2015, , .		3
28	EntropyExplorer: an R package for computing and comparing differential Shannon entropy, differential coefficient of variation and differential expression. <i>BMC Research Notes</i> , 2015, 8, 832.	1.4	21
29	Rural congestive heart failure mortality among US elderly, 1999â€2013: Identifying counties with promising outcomes and opportunities for implementation research. <i>Family Medicine and Community Health</i> , 2015, 3, 27-38.	1.6	1
30	GeneWeaver: finding consilience in heterogeneous cross-species functional genomics data. <i>Mammalian Genome</i> , 2015, 26, 556-566.	2.2	12
31	Exploration of Preterm Birth Rates Using the Public Health Exposome Database and Computational Analysis Methods. <i>International Journal of Environmental Research and Public Health</i> , 2014, 11, 12346-12366.	2.6	25
32	Efficient prediction of human protein-protein interactions at a global scale. <i>BMC Bioinformatics</i> , 2014, 15, 383.	2.6	32
33	DNA Methylation Changes Separate Allergic Patients from Healthy Controls and May Reflect Altered CD4+ T-Cell Population Structure. <i>PLoS Genetics</i> , 2014, 10, e1004059.	3.5	70
34	Toward an efficient, highly scalable maximum clique solver for massive graphs. , 2014, , .		2
35	On finding bicliques in bipartite graphs: a novel algorithm and its application to the integration of diverse biological data types. <i>BMC Bioinformatics</i> , 2014, 15, 110.	2.6	131
36	The Public Health Exposome: A Population-Based, Exposure Science Approach to Health Disparities Research. <i>International Journal of Environmental Research and Public Health</i> , 2014, 11, 12866-12895.	2.6	137

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37	Scalable Combinatorial Tools for Health Disparities Research. <i>International Journal of Environmental Research and Public Health</i> , 2014, 11, 10419-10443.	2.6	22
38	Differential Shannon entropy and differential coefficient of variation: alternatives and augmentations to differential expression in the search for disease-related genes. <i>International Journal of Computational Biology and Drug Design</i> , 2014, 7, 183.	0.3	12
39	Social Determinants and the Classification of Disease: Descriptive Epidemiology of Selected Socially Mediated Disease Constellations. <i>PLoS ONE</i> , 2014, 9, e110271.	2.5	12
40	GeneWeaver: a web-based system for integrative functional genomics. <i>Nucleic Acids Research</i> , 2012, 40, D1067-D1076.	14.5	112
41	Genetic Dissection of Acute Ethanol Responsive Gene Networks in Prefrontal Cortex: Functional and Mechanistic Implications. <i>PLoS ONE</i> , 2012, 7, e33575.	2.5	109
42	A systematic comparison of genome-scale clustering algorithms. <i>BMC Bioinformatics</i> , 2012, 13, S7.	2.6	55
43	Genetic analysis of BDNF expression cliques and adult neurogenesis in the hippocampus. , 2010, , .		1
44	Threshold selection in gene co-expression networks using spectral graph theory techniques. <i>BMC Bioinformatics</i> , 2009, 10, S4.	2.6	71
45	Comparison of threshold selection methods for microarray gene co-expression matrices. <i>BMC Research Notes</i> , 2009, 2, 240.	1.4	37
46	Ontological discovery environment: A system for integrating gene-phenotype associations. <i>Genomics</i> , 2009, 94, 377-387.	2.9	35
47	Using out-of-core techniques to produce exact solutions to the maximum clique problem on extremely large graphs. , 2009, , .		2
48	Graph Algorithms for Integrated Biological Analysis, with Applications to Type 1 Diabetes Data. , 2009, , 207-222.		7
49	The Maximum Common Subgraph Problem: Faster Solutions via Vertex Cover. , 2007, , .		25
50	Genome-level analysis of genetic regulation of liver gene expression networks. <i>Hepatology</i> , 2007, 46, 548-557.	7.3	49
51	Crown Structures for Vertex Cover Kernelization. <i>Theory of Computing Systems</i> , 2007, 41, 411-430.	1.1	97
52	Extracting Gene Networks for Low-Dose Radiation Using Graph Theoretical Algorithms. <i>PLoS Computational Biology</i> , 2006, 2, e89.	3.2	86
53	A network-based analysis of the late-phase reaction of the skin. <i>Journal of Allergy and Clinical Immunology</i> , 2006, 118, 220-225.	2.9	27
54	Detecting Differential and Correlated Protein Expression in Label-Free Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2006, 5, 2909-2918.	3.7	361

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55	Scalable Parallel Algorithms for FPT Problems. <i>Algorithmica</i> , 2006, 45, 269-284.	1.3	62
56	Computational, Integrative, and Comparative Methods for the Elucidation of Genetic Coexpression Networks. <i>Journal of Biomedicine and Biotechnology</i> , 2005, 2005, 172-180.	3.0	29
57	Combinatorial Genetic Regulatory Network Analysis Tools for High Throughput Transcriptomic Data. , 2005, , 150-165.		27
58	Fast Algorithms for K-Immersion Testing. <i>Journal of Algorithms</i> , 1999, 30, 344-378.	0.9	9
59	Approximating the pathwidth of outerplanar graphs. <i>Information Processing Letters</i> , 1998, 68, 17-23.	0.6	15
60	On algorithmic applications of the immersion order. <i>Discrete Mathematics</i> , 1998, 182, 191-196.	0.7	13
61	AN INTRODUCTION TO THE SPECIAL ISSUE. <i>International Journal of Parallel, Emergent and Distributed Systems</i> , 1996, 8, 1-2.	0.4	0
62	Chapter 8 Algorithmic implications of the graph minor theorem. <i>Handbooks in Operations Research and Management Science</i> , 1995, 7, 481-502.	0.6	14
63	On search, decision, and the efficiency of polynomial-time algorithms. <i>Journal of Computer and System Sciences</i> , 1994, 49, 769-779.	1.2	67
64	Obstruction set isolation for the gate matrix layout problem. <i>Discrete Applied Mathematics</i> , 1994, 54, 169-213.	0.9	44
65	MIMD VERSUS SIMD COMPUTATION: EXPERIENCE WITH NON-NUMERIC PARALLEL ALGORITHMS. <i>International Journal of Parallel, Emergent and Distributed Systems</i> , 1994, 2, 123-138.	0.4	0
66	On Well-Partial-Order Theory and Its Application to Combinatorial Problems of VLSI Design. <i>SIAM Journal on Discrete Mathematics</i> , 1992, 5, 117-126.	0.8	69
67	Analysis of a Compound Bin Packing Algorithm. <i>SIAM Journal on Discrete Mathematics</i> , 1991, 4, 61-79.	0.8	27
68	Polynomial-time self-reducibility: theoretical motivations and practical results. <i>International Journal of Computer Mathematics</i> , 1989, 31, 1-9.	1.8	15
69	Stable duplicate-key extraction with optimal time and space bounds. <i>Acta Informatica</i> , 1989, 26, 473-484.	0.5	12
70	Online variable-sized bin packing. <i>Discrete Applied Mathematics</i> , 1988, 22, 143-148.	0.9	29
71	Practical in-place merging. <i>Communications of the ACM</i> , 1988, 31, 348-352.	4.5	50
72	Interstage Transportation Planning in the Deterministic Flow-Shop Environment. <i>Operations Research</i> , 1987, 35, 556-564.	1.9	62

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73	A Study of Composite Heuristic Algorithms. Journal of the Operational Research Society, 1987, 38, 539.	3.4	0
74	Nonconstructive advances in polynomial-time complexity. Information Processing Letters, 1987, 26, 157-162.	0.6	72
75	Improved 0/1-interchange scheduling. BIT Numerical Mathematics, 1982, 22, 282-290.	2.0	17