

Alexander Statnikov

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

3,338
citations

361413

20
h-index

395702

33
g-index

36
all docs

36
docs citations

36
times ranked

5199
citing authors

#	ARTICLE	IF	CITATIONS
1	Methods for computational causal discovery in biomedicine. <i>Behaviormetrika</i> , 2017, 44, 165-191.	1.3	11
2	An Evaluation of Active Learning Causal Discovery Methods for Reverse-Engineering Local Causal Pathways of Gene Regulation. <i>Scientific Reports</i> , 2016, 6, 22558.	3.3	4
3	A Complex Systems Approach to Causal Discovery in Psychiatry. <i>PLoS ONE</i> , 2016, 11, e0151174.	2.5	29
4	Low-Grade Inflammation in Symptomatic Knee Osteoarthritis: Prognostic Value of Inflammatory Plasma Lipids and Peripheral Blood Leukocyte Biomarkers. <i>Arthritis and Rheumatology</i> , 2015, 67, 2905-2915.	5.6	93
5	Early identification of posttraumatic stress following military deployment: Application of machine learning methods to a prospective study of Danish soldiers. <i>Journal of Affective Disorders</i> , 2015, 184, 170-175.	4.1	57
6	Bridging a translational gap: using machine learning to improve the prediction of PTSD. <i>BMC Psychiatry</i> , 2015, 15, 30.	2.6	126
7	Molecular Characterization of the Peripheral Airway Field of Cancerization in Lung Adenocarcinoma. <i>PLoS ONE</i> , 2015, 10, e0118132.	2.5	21
8	Computational Methods for Unraveling Temporal Brain Connectivity Data. <i>AMIA ... Annual Symposium proceedings</i> , 2015, 2015, 2043-52.	0.2	0
9	De-Novo Learning of Genome-Scale Regulatory Networks in <i>S. cerevisiae</i> . <i>PLoS ONE</i> , 2014, 9, e106479.	2.5	18
10	Quantitative forecasting of PTSD from early trauma responses: A Machine Learning application. <i>Journal of Psychiatric Research</i> , 2014, 59, 68-76.	3.1	199
11	A comprehensive empirical comparison of modern supervised classification and feature selection methods for text categorization. <i>Journal of the Association for Information Science and Technology</i> , 2014, 65, 1964-1987.	2.9	50
12	Information content and analysis methods for Multi-Modal High-Throughput Biomedical Data. <i>Scientific Reports</i> , 2014, 4, 4411.	3.3	30
13	Computational Prediction of Neutralization Epitopes Targeted by Human Anti-V3 HIV Monoclonal Antibodies. <i>PLoS ONE</i> , 2014, 9, e89987.	2.5	8
14	A comprehensive evaluation of multcategory classification methods for microbiomic data. <i>Microbiome</i> , 2013, 1, 11.	11.1	169
15	Co-expression network analysis identifies Spleen Tyrosine Kinase (SYK) as a candidate oncogenic driver in a subset of small-cell lung cancer. <i>BMC Systems Biology</i> , 2013, 7, S1.	3.0	83
16	Microbiomic Signatures of Psoriasis: Feasibility and Methodology Comparison. <i>Scientific Reports</i> , 2013, 3, 2620.	3.3	71
17	New methods for separating causes from effects in genomics data. <i>BMC Genomics</i> , 2012, 13, S22.	2.8	20
18	Regression of Atherosclerosis Is Characterized by Broad Changes in the Plaque Macrophage Transcriptome. <i>PLoS ONE</i> , 2012, 7, e39790.	2.5	96

#	ARTICLE	IF	CITATIONS
19	Multicriteria Engineering Optimization Problems: Statement, Solution and Applications. Journal of Optimization Theory and Applications, 2012, 155, 355-375.	1.5	16
20	Assessing quality and completeness of human transcriptional regulatory pathways on a genome-wide scale. Biology Direct, 2011, 6, 15.	4.6	56
21	Causal graph-based analysis of genome-wide association data in rheumatoid arthritis. Biology Direct, 2011, 6, 25.	4.6	22
22	Using gene expression profiles from peripheral blood to identify asymptomatic responses to acute respiratory viral infections. BMC Research Notes, 2010, 3, 264.	1.4	9
23	The Notch/Hes1 Pathway Sustains NF- κ B Activation through CYLD Repression in T Cell Leukemia. Cancer Cell, 2010, 18, 268-281.	16.8	261
24	Analysis and Computational Dissection of Molecular Signature Multiplicity. PLoS Computational Biology, 2010, 6, e1000790.	3.2	57
25	The FAST-AIMS Clinical Mass Spectrometry Analysis System. Advances in Bioinformatics, 2009, 2009, 1-4.	5.7	0
26	Factors Influencing the Statistical Power of Complex Data Analysis Protocols for Molecular Signature Development from Microarray Data. PLoS ONE, 2009, 4, e4922.	2.5	20
27	A comprehensive comparison of random forests and support vector machines for microarray-based cancer classification. BMC Bioinformatics, 2008, 9, 319.	2.6	504
28	Are random forests better than support vector machines for microarray-based cancer classification?. AMIA ... Annual Symposium proceedings, 2007, , 686-90.	0.2	20
29	Challenges in the analysis of mass-throughput data: a technical commentary from the statistical machine learning perspective. Cancer Informatics, 2007, 2, 133-62.	1.9	15
30	Challenges in the Analysis of Mass-Throughput Data: A Technical Commentary from the Statistical Machine Learning Perspective. Cancer Informatics, 2006, 2, 117693510600200.	1.9	19
31	A Comparison of Citation Metrics to Machine Learning Filters for the Identification of High Quality MEDLINE Documents. Journal of the American Medical Informatics Association: JAMIA, 2006, 13, 446-455.	4.4	22
32	GEMS: A system for automated cancer diagnosis and biomarker discovery from microarray gene expression data. International Journal of Medical Informatics, 2005, 74, 491-503.	3.3	161
33	A comprehensive evaluation of multiclassification methods for microarray gene expression cancer diagnosis. Bioinformatics, 2005, 21, 631-643.	4.1	750
34	Extracting drug-drug interaction articles from MEDLINE to improve the content of drug databases. AMIA ... Annual Symposium proceedings, 2005, , 216-20.	0.2	12
35	Text Categorization Models for High-Quality Article Retrieval in Internal Medicine. Journal of the American Medical Informatics Association: JAMIA, 2004, 12, 207-216.	4.4	133
36	Time and sample efficient discovery of Markov blankets and direct causal relations. , 2003, , .		176