

Ioannis Tsamardinos

List of Publications by Year in descending order

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Version: 2024-02-01

86
papers

4,754
citations

257101

24
h-index

110170

64
g-index

97
all docs

97
docs citations

97
times ranked

5445
citing authors

#	ARTICLE	IF	CITATIONS
1	The max-min hill-climbing Bayesian network structure learning algorithm. <i>Machine Learning</i> , 2006, 65, 31-78.	3.4	1,145
2	A comprehensive evaluation of multiclass classification methods for microarray gene expression cancer diagnosis. <i>Bioinformatics</i> , 2005, 21, 631-643.	1.8	750
3	Autominder: an intelligent cognitive orthotic system for people with memory impairment. <i>Robotics and Autonomous Systems</i> , 2003, 44, 273-282.	3.0	288
4	Time and sample efficient discovery of Markov blankets and direct causal relations. , 2003, , .		176
5	GEMS: A system for automated cancer diagnosis and biomarker discovery from microarray gene expression data. <i>International Journal of Medical Informatics</i> , 2005, 74, 491-503.	1.6	161
6	Applications of Machine Learning in Human Microbiome Studies: A Review on Feature Selection, Biomarker Identification, Disease Prediction and Treatment. <i>Frontiers in Microbiology</i> , 2021, 12, 634511.	1.5	157
7	Text Categorization Models for High-Quality Article Retrieval in Internal Medicine. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2004, 12, 207-216.	2.2	133
8	MatureBayes: A Probabilistic Algorithm for Identifying the Mature miRNA within Novel Precursors. <i>PLoS ONE</i> , 2010, 5, e11843.	1.1	132
9	Bootstrapping the out-of-sample predictions for efficient and accurate cross-validation. <i>Machine Learning</i> , 2018, 107, 1895-1922.	3.4	124
10	Circulating cell-free DNA in breast cancer: size profiling, levels, and methylation patterns lead to prognostic and predictive classifiers. <i>Oncogene</i> , 2019, 38, 3387-3401.	2.6	109
11	Chemically intuited, large-scale screening of MOFs by machine learning techniques. <i>Npj Computational Materials</i> , 2017, 3, .	3.5	107
12	Feature Selection with the <i>R</i> Package <i>MXM</i> : Discovering Statistically Equivalent Feature Subsets. <i>Journal of Statistical Software</i> , 2017, 80, .	1.8	88
13	CTP: A New Constraint-Based Formalism for Conditional, Temporal Planning. <i>Constraints</i> , 2003, 8, 365-388.	0.4	74
14	A vision and strategy for the virtual physiological human: 2012 update. <i>Interface Focus</i> , 2013, 3, 20130004.	1.5	74
15	On User-Centric Modular QoE Prediction for VoIP Based on Machine-Learning Algorithms. <i>IEEE Transactions on Mobile Computing</i> , 2016, 15, 1443-1456.	3.9	58
16	Development and validation of risk assessment models for diabetes-related complications based on the DCCT/EDIC data. <i>Journal of Diabetes and Its Complications</i> , 2015, 29, 479-487.	1.2	54
17	A systematic review of predictive risk models for diabetes complications based on large scale clinical studies. <i>Journal of Diabetes and Its Complications</i> , 2013, 27, 407-413.	1.2	50
18	Performance-Estimation Properties of Cross-Validation-Based Protocols with Simultaneous Hyper-Parameter Optimization. <i>International Journal on Artificial Intelligence Tools</i> , 2015, 24, 1540023.	0.7	49

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19	A greedy feature selection algorithm for Big Data of high dimensionality. <i>Machine Learning</i> , 2019, 108, 149-202.	3.4	46
20	Combining evidence from four immune cell types identifies DNA methylation patterns that implicate functionally distinct pathways during Multiple Sclerosis progression. <i>EBioMedicine</i> , 2019, 43, 411-423.	2.7	45
21	A Validated Clinical Risk Prediction Model for Lung Cancer in Smokers of All Ages and Exposure Types: A HUNT Study. <i>EBioMedicine</i> , 2018, 31, 36-46.	2.7	43
22	An Automated Machine Learning architecture for the accelerated prediction of Metal-Organic Frameworks performance in energy and environmental applications. <i>Microporous and Mesoporous Materials</i> , 2020, 300, 110160.	2.2	40
23	Feature selection for high-dimensional temporal data. <i>BMC Bioinformatics</i> , 2018, 19, 17.	1.2	35
24	MatureP: prediction of secreted proteins with exclusive information from their mature regions. <i>Scientific Reports</i> , 2017, 7, 3263.	1.6	33
25	Accurate Blood-Based Diagnostic Biosignatures for Alzheimer's Disease via Automated Machine Learning. <i>Journal of Clinical Medicine</i> , 2020, 9, 3016.	1.0	31
26	Probabilistic Computational Causal Discovery for Systems Biology. <i>Studies in Mechanobiology, Tissue Engineering and Biomaterials</i> , 2016, , 33-73.	0.7	27
27	Toward Automatic Risk Assessment to Support Suicide Prevention. <i>Crisis</i> , 2019, 40, 249-256.	0.9	27
28	Realization of a service for the long-term risk assessment of diabetes-related complications. <i>Journal of Diabetes and Its Complications</i> , 2015, 29, 691-698.	1.2	25
29	Constraint-based causal discovery with mixed data. <i>International Journal of Data Science and Analytics</i> , 2018, 6, 19-30.	2.4	25
30	BioDataome: a collection of uniformly preprocessed and automatically annotated datasets for data-driven biology. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	25
31	Structural Basis of the Subcellular Topology Landscape of Escherichia coli. <i>Frontiers in Microbiology</i> , 2019, 10, 1670.	1.5	25
32	Structure-based variable selection for survival data. <i>Bioinformatics</i> , 2010, 26, 1887-1894.	1.8	24
33	GATA-1 genome-wide occupancy associates with distinct epigenetic profiles in mouse fetal liver erythropoiesis. <i>Nucleic Acids Research</i> , 2013, 41, 4938-4948.	6.5	24
34	STATegra: Multi-Omics Data Integration – A Conceptual Scheme With a Bioinformatics Pipeline. <i>Frontiers in Genetics</i> , 2021, 12, 620453.	1.1	24
35	Deciphering the Methylation Landscape in Breast Cancer: Diagnostic and Prognostic Biosignatures through Automated Machine Learning. <i>Cancers</i> , 2021, 13, 1677.	1.7	24
36	Predicting Causal Relationships from Biological Data: Applying Automated Causal Discovery on Mass Cytometry Data of Human Immune Cells. <i>Scientific Reports</i> , 2017, 7, 12724.	1.6	21

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37	Factors Influencing the Statistical Power of Complex Data Analysis Protocols for Molecular Signature Development from Microarray Data. <i>PLoS ONE</i> , 2009, 4, e4922.	1.1	20
38	MiRduplexSVM: A High-Performing MiRNA-Duplex Prediction and Evaluation Methodology. <i>PLoS ONE</i> , 2015, 10, e0126151.	1.1	20
39	Prediction of outcome in patients with non-small cell lung cancer treated with second line PD-1/PDL-1 inhibitors based on clinical parameters: Results from a prospective, single institution study. <i>PLoS ONE</i> , 2021, 16, e0252537.	1.1	20
40	Automated machine learning optimizes and accelerates predictive modeling from COVID-19 high throughput datasets. <i>Scientific Reports</i> , 2021, 11, 15107.	1.6	20
41	Just Add Data: automated predictive modeling for knowledge discovery and feature selection. <i>Npj Precision Oncology</i> , 2022, 6, .	2.3	20
42	BIOMARKER SIGNATURE IDENTIFICATION IN ðœOMICSð€•DATA WITH MULTI-CLASS OUTCOME. <i>Computational and Structural Biotechnology Journal</i> , 2013, 6, e201303004.	1.9	18
43	An AutoML application to forecasting bank failures. <i>Applied Economics Letters</i> , 2021, 28, 5-9.	1.0	18
44	A unified approach for sparse dynamical system inference from temporal measurements. <i>Bioinformatics</i> , 2019, 35, 3387-3396.	1.8	17
45	A comparative evaluation of data-merging and meta-analysis methods for reconstructing gene-gene interactions. <i>BMC Bioinformatics</i> , 2016, 17, 194.	1.2	16
46	Hidden Treasures in ðœAncientð€•Microarrays: Gene-Expression Portrays Biology and Potential Resistance Pathways of Major Lung Cancer Subtypes and Normal Tissue. <i>Frontiers in Oncology</i> , 2014, 4, 251.	1.3	15
47	Non-parametric combination analysis of multiple data types enables detection of novel regulatory mechanisms in T cells of multiple sclerosis patients. <i>Scientific Reports</i> , 2019, 9, 11996.	1.6	13
48	Scanning of Genetic Variants and Genetic Mapping of Phenotypic Traits in Gilthead Sea Bream Through ddRAD Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 675.	1.1	13
49	Discovering and Exploiting Deterministic Label Relationships in Multi-Label Learning. , 2015, , .		13
50	On scoring Maximal Ancestral Graphs with the MaxðœMin Hill Climbing algorithm. <i>International Journal of Approximate Reasoning</i> , 2018, 102, 74-85.	1.9	12
51	Challenges in the Multivariate Analysis of Mass Cytometry Data: The Effect of Randomization. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2019, 95, 1178-1190.	1.1	12
52	T-ReCS: stable selection of dynamically formed groups of features with application to prediction of clinical outcomes. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015, , 431-42.	0.7	12
53	omicsNPC: Applying the Non-Parametric Combination Methodology to the Integrative Analysis of Heterogeneous Omics Data. <i>PLoS ONE</i> , 2016, 11, e0165545.	1.1	11
54	A data driven approach reveals disease similarity on a molecular level. <i>Npj Systems Biology and Applications</i> , 2019, 5, 39.	1.4	11

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55	Extending greedy feature selection algorithms to multiple solutions. <i>Data Mining and Knowledge Discovery</i> , 2021, 35, 1393-1434.	2.4	11
56	Feature selection with the R package MXM. <i>F1000Research</i> , 2018, 7, 1505.	0.8	11
57	The Essentials of Multiomics. <i>Oncologist</i> , 2022, 27, 272-284.	1.9	11
58	Liquid Biopsy in Type 2 Diabetes Mellitus Management: Building Specific Biosignatures via Machine Learning. <i>Journal of Clinical Medicine</i> , 2022, 11, 1045.	1.0	10
59	SCENERY: a web application for (causal) network reconstruction from cytometry data. <i>Nucleic Acids Research</i> , 2017, 45, W270-W275.	6.5	9
60	Mining Free-Text Medical Notes for Suicide Risk Assessment. , 2018, , .		9
61	Feedforward regulation of Myc coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. <i>PLoS Biology</i> , 2019, 17, e2006506.	2.6	8
62	Forecasting military mental health in a complete sample of Danish military personnel deployed between 1992-2013. <i>Journal of Affective Disorders</i> , 2021, 288, 167-174.	2.0	7
63	T-RECS: STABLE SELECTION OF DYNAMICALLY FORMED GROUPS OF FEATURES WITH APPLICATION TO PREDICTION OF CLINICAL OUTCOMES. , 2014, , .		7
64	Feature selection with the R package MXM. <i>F1000Research</i> , 2018, 7, 1505.	0.8	7
65	Applicability of an Automated Model and Parameter Selection in the Prediction of Screening-Level PTSD in Danish Soldiers Following Deployment: Development Study of Transferable Predictive Models Using Automated Machine Learning. <i>JMIR Medical Informatics</i> , 2020, 8, e17119.	1.3	7
66	“Reduced” HUNT model outperforms NLST and NELSON study criteria in predicting lung cancer in the Danish screening trial. <i>BMJ Open Respiratory Research</i> , 2019, 6, e000512.	1.2	6
67	Somatic copy number aberrations detected in circulating tumor DNA can hold diagnostic value for early detection of hepatocellular carcinoma. <i>EBioMedicine</i> , 2020, 57, 102851.	2.7	6
68	Tissue-Specific Methylation Biosignatures for Monitoring Diseases: An In Silico Approach. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2959.	1.8	6
69	Towards Robust and Versatile Causal Discovery for Business Applications. , 2016, , .		5
70	The morphological classification of heartbeats as dominant and non-dominant in ECG signals. <i>Physiological Measurement</i> , 2010, 31, 611-631.	1.2	4
71	Pathway Activity Score Learning for Dimensionality Reduction of Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2020, , 246-261.	1.0	4
72	Heart Rate Classification Using ECG Signal Processing and Machine Learning Methods. , 2021, , .		4

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73	Translating vitamin D transcriptomics to clinical evidence: Analysis of data in asthma and chronic obstructive pulmonary disease, followed by clinical data meta-analysis. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2020, 197, 105505.	1.2	3
74	Learning Pathway Dynamics from Single-Cell Proteomic Data: A Comparative Study. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 241-252.	1.1	3
75	PROTEUS: Predictive Explanation of Anomalies. , 2021, , .		3
76	Multi-Source Causal Analysis: Learning Bayesian Networks from Multiple Datasets. <i>IFIP Advances in Information and Communication Technology</i> , 2009, , 479-490.	0.5	3
77	Credit Card Fraud Detection with Automated Machine Learning Systems. <i>Applied Artificial Intelligence</i> , 2022, 36, .	2.0	3
78	To feature space and back: Identifying top-weighted features in polynomial Support Vector Machine models. <i>Intelligent Data Analysis</i> , 2012, 16, 551-579.	0.4	2
79	The \hat{l}^3 -OMP algorithm for feature selection with application to gene expression data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	1.9	2
80	Latent Feature Representations for Human Gene Expression Data Improve Phenotypic Predictions. , 2020, , .		2
81	Learning biologically-interpretable latent representations for gene expression data. <i>Machine Learning</i> , 2023, 112, 4257-4287.	3.4	2
82	A bioinformatics approach for investigating the determinants of Drosha processing. , 2013, , .		1
83	Improvement of lung cancer risk prediction adding SNPs to the HUNT Lung Cancer Model: A HUNT Study.. <i>Journal of Clinical Oncology</i> , 2019, 37, e20696-e20696.	0.8	1
84	Out-of-Sample Tuning for Causal Discovery. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2024, , 1-11.	7.2	1
85	Serum microRNAs/enriched pathways in lung cancer 1-4 years before diagnosis: A pilot study from the HUNT Biobank, Norway.. <i>Journal of Clinical Oncology</i> , 2016, 34, 11539-11539.	0.8	0
86	Proteomics analysis discovers biomarkers in serum months to years before small cell lung cancer: The HUNT study.. <i>Journal of Clinical Oncology</i> , 2019, 37, e20095-e20095.	0.8	0