Ioannis Tsamardinos

List of Publications by Year in descending order

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	Out-of-Sample Tuning for Causal Discovery. IEEE Transactions on Neural Networks and Learning Systems, 2024, , 1-11.	7.2	1
2	Learning biologically-interpretable latent representations for gene expression data. Machine Learning, 2023, 112, 4257-4287.	3.4	2
3	The Essentials of Multiomics. Oncologist, 2022, 27, 272-284.	1.9	11
4	Liquid Biopsy in Type 2 Diabetes Mellitus Management: Building Specific Biosignatures via Machine Learning. Journal of Clinical Medicine, 2022, 11, 1045.	1.0	10
5	Tissue-Specific Methylation Biosignatures for Monitoring Diseases: An In Silico Approach. International Journal of Molecular Sciences, 2022, 23, 2959.	1.8	6
6	Just Add Data: automated predictive modeling for knowledge discovery and feature selection. Npj Precision Oncology, 2022, 6, .	2.3	20
7	Credit Card Fraud Detection with Automated Machine Learning Systems. Applied Artificial Intelligence, 2022, 36, .	2.0	3
8	Applications of Machine Learning in Human Microbiome Studies: A Review on Feature Selection, Biomarker Identification, Disease Prediction and Treatment. Frontiers in Microbiology, 2021, 12, 634511.	1.5	157
9	STATegra: Multi-Omics Data Integration â€" A Conceptual Scheme With a Bioinformatics Pipeline. Frontiers in Genetics, 2021, 12, 620453.	1.1	24
10	PROTEUS: Predictive Explanation of Anomalies. , 2021, , .		3
11	Deciphering the Methylation Landscape in Breast Cancer: Diagnostic and Prognostic Biosignatures through Automated Machine Learning. Cancers, 2021, 13, 1677.	1.7	24
12	Extending greedy feature selection algorithms to multiple solutions. Data Mining and Knowledge Discovery, 2021, 35, 1393-1434.	2.4	11
13	Forecasting military mental health in a complete sample of Danish military personnel deployed between 1992-2013. Journal of Affective Disorders, 2021, 288, 167-174.	2.0	7
14	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. PLoS ONE, 2021, 16, e0252537.	1.1	20
15	Automated machine learning optimizes and accelerates predictive modeling from COVID-19 high throughput datasets. Scientific Reports, 2021, 11, 15107.	1.6	20
16	An AutoML application to forecasting bank failures. Applied Economics Letters, 2021, 28, 5-9.	1.0	18
17	Heart Rate Classification Using ECG Signal Processing and Machine Learning Methods. , 2021, , .		4
18	Translating vitamin D transcriptomics to clinical evidence: Analysis of data in asthma and chronic obstructive pulmonary disease, followed by clinical data meta-analysis. Journal of Steroid Biochemistry and Molecular Biology, 2020, 197, 105505.	1.2	3

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19	The Î³-OMP algorithm for feature selection with application to gene expression data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	1.9	2
20	Somatic copy number aberrations detected in circulating tumor DNA can hold diagnostic value for early detection of hepatocellular carcinoma. EBioMedicine, 2020, 57, 102851.	2.7	6
21	Accurate Blood-Based Diagnostic Biosignatures for Alzheimerâ€™s Disease via Automated Machine Learning. Journal of Clinical Medicine, 2020, 9, 3016.	1.0	31
22	An Automated Machine Learning architecture for the accelerated prediction of Metal-Organic Frameworks performance in energy and environmental applications. Microporous and Mesoporous Materials, 2020, 300, 110160.	2.2	40
23	Learning Pathway Dynamics from Singleâ€Cell Proteomic Data: A Comparative Study. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 241-252.	1.1	3
24	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. JMIR Medical Informatics, 2020, 8, e17119.	1.3	7
25	Latent Feature Representations for Human Gene Expression Data Improve Phenotypic Predictions. , 2020, , .		2
26	Pathway Activity Score Learning for Dimensionality Reduction of Gene Expression Data. Lecture Notes in Computer Science, 2020, , 246-261.	1.0	4
27	A greedy feature selection algorithm for Big Data of high dimensionality. Machine Learning, 2019, 108, 149-202.	3.4	46
28	Non-parametric combination analysis of multiple data types enables detection of novel regulatory mechanisms in T cells of multiple sclerosis patients. Scientific Reports, 2019, 9, 11996.	1.6	13
29	A data driven approach reveals disease similarity on a molecular level. Npj Systems Biology and Applications, 2019, 5, 39.	1.4	11
30	Challenges in the Multivariate Analysis of Mass Cytometry Data: The Effect of Randomization. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2019, 95, 1178-1190.	1.1	12
31	Scanning of Genetic Variants and Genetic Mapping of Phenotypic Traits in Gilthead Sea Bream Through ddRAD Sequencing. Frontiers in Genetics, 2019, 10, 675.	1.1	13
32	Structural Basis of the Subcellular Topology Landscape of Escherichia coli. Frontiers in Microbiology, 2019, 10, 1670.	1.5	25
33	Combining evidence from four immune cell types identifies DNA methylation patterns that implicate functionally distinct pathways during Multiple Sclerosis progression. EBioMedicine, 2019, 43, 411-423.	2.7	45
34	Feedforward regulation of Myc coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. PLoS Biology, 2019, 17, e2006506.	2.6	8
35	A unified approach for sparse dynamical system inference from temporal measurements. Bioinformatics, 2019, 35, 3387-3396.	1.8	17
36	â€˜Reducedâ€™ HUNT model outperforms NLST and NELSON study criteria in predicting lung cancer in the Danish screening trial. BMJ Open Respiratory Research, 2019, 6, e000512.	1.2	6

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37	Circulating cell-free DNA in breast cancer: size profiling, levels, and methylation patterns lead to prognostic and predictive classifiers. Oncogene, 2019, 38, 3387-3401.	2.6	109
38	Toward Automatic Risk Assessment to Support Suicide Prevention. Crisis, 2019, 40, 249-256.	0.9	27
39	Improvement of lung cancer risk prediction adding SNPs to the HUNT Lung Cancer Model: A HUNT Study.. Journal of Clinical Oncology, 2019, 37, e20696-e20696.	0.8	1
40	Proteomics analysis discovers biomarkers in serum months to years before small cell lung cancer: The HUNT study.. Journal of Clinical Oncology, 2019, 37, e20095-e20095.	0.8	0
41	A Validated Clinical Risk Prediction Model for Lung Cancer in Smokers of All Ages and Exposure Types: A HUNT Study. EBioMedicine, 2018, 31, 36-46.	2.7	43
42	Mining Free-Text Medical Notes for Suicide Risk Assessment. , 2018, , .		9
43	Bootstrapping the out-of-sample predictions for efficient and accurate cross-validation. Machine Learning, 2018, 107, 1895-1922.	3.4	124
44	Constraint-based causal discovery with mixed data. International Journal of Data Science and Analytics, 2018, 6, 19-30.	2.4	25
45	Feature selection for high-dimensional temporal data. BMC Bioinformatics, 2018, 19, 17.	1.2	35
46	BioDataome: a collection of uniformly preprocessed and automatically annotated datasets for data-driven biology. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	25
47	On scoring Maximal Ancestral Graphs with the Maxâ€"Min Hill Climbing algorithm. International Journal of Approximate Reasoning, 2018, 102, 74-85.	1.9	12
48	Feature selection with the R package MXM. F1000Research, 2018, 7, 1505.	0.8	7
49	Feature selection with the R package MXM. F1000Research, 2018, 7, 1505.	0.8	11
50	SCENERY: a web application for (causal) network reconstruction from cytometry data. Nucleic Acids Research, 2017, 45, W270-W275.	6.5	9
51	Chemically intuited, large-scale screening of MOFs by machine learning techniques. Npj Computational Materials, 2017, 3, .	3.5	107
52	Predicting Causal Relationships from Biological Data: Applying Automated Causal Discovery on Mass Cytometry Data of Human Immune Cells. Scientific Reports, 2017, 7, 12724.	1.6	21
53	MatureP: prediction of secreted proteins with exclusive information from their mature regions. Scientific Reports, 2017, 7, 3263.	1.6	33
54	Feature Selection with the <i>R</i> Package MXM: Discovering Statistically Equivalent Feature Subsets. Journal of Statistical Software, 2017, 80, .	1.8	88

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55	omicsNPC: Applying the Non-Parametric Combination Methodology to the Integrative Analysis of Heterogeneous Omics Data. PLoS ONE, 2016, 11, e0165545.	1.1	11
56	Towards Robust and Versatile Causal Discovery for Business Applications. , 2016, , .		5
57	A comparative evaluation of data-merging and meta-analysis methods for reconstructing gene-gene interactions. BMC Bioinformatics, 2016, 17, 194.	1.2	16
58	On User-Centric Modular QoE Prediction for VoIP Based on Machine-Learning Algorithms. IEEE Transactions on Mobile Computing, 2016, 15, 1443-1456.	3.9	58
59	Probabilistic Computational Causal Discovery for Systems Biology. Studies in Mechanobiology, Tissue Engineering and Biomaterials, 2016, , 33-73.	0.7	27
60	Serum microRNAs/enriched pathways in lung cancer 1-4 years before diagnosis: A pilot study from the HUNT Biobank, Norway.. Journal of Clinical Oncology, 2016, 34, 11539-11539.	0.8	0
61	MiRduplexSVM: A High-Performing MiRNA-Duplex Prediction and Evaluation Methodology. PLoS ONE, 2015, 10, e0126151.	1.1	20
62	Realization of a service for the long-term risk assessment of diabetes-related complications. Journal of Diabetes and Its Complications, 2015, 29, 691-698.	1.2	25
63	Development and validation of risk assessment models for diabetes-related complications based on the DCCT/EDIC data. Journal of Diabetes and Its Complications, 2015, 29, 479-487.	1.2	54
64	Performance-Estimation Properties of Cross-Validation-Based Protocols with Simultaneous Hyper-Parameter Optimization. International Journal on Artificial Intelligence Tools, 2015, 24, 1540023.	0.7	49
65	Discovering and Exploiting Deterministic Label Relationships in Multi-Label Learning. , 2015, , .		13
66	T-ReCS: stable selection of dynamically formed groups of features with application to prediction of clinical outcomes. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 431-42.	0.7	12
67	Hidden Treasures in Ã¢â‚¬Å"AncientÃ¢â‚¬Â•Microarrays: Gene-Expression Portrays Biology and Potential Resistance Pathways of Major Lung Cancer Subtypes and Normal Tissue. Frontiers in Oncology, 2014, 4, 251.	1.3	15
68	T-RECS: STABLE SELECTION OF DYNAMICALLY FORMED GROUPS OF FEATURES WITH APPLICATION TO PREDICTION OF CLINICAL OUTCOMES. , 2014, , .		7
69	A systematic review of predictive risk models for diabetes complications based on large scale clinical studies. Journal of Diabetes and Its Complications, 2013, 27, 407-413.	1.2	50
70	A vision and strategy for the virtual physiological human: 2012 update. Interface Focus, 2013, 3, 20130004.	1.5	74
71	A bioinformatics approach for investigating the determinants of Drosha processing. , 2013, , .		1
72	BIOMARKER SIGNATURE IDENTIFICATION IN â€œOMICSâ€•DATA WITH MULTI-CLASS OUTCOME. Computational and Structural Biotechnology Journal, 2013, 6, e201303004.	1.9	18

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73	GATA-1 genome-wide occupancy associates with distinct epigenetic profiles in mouse fetal liver erythropoiesis. Nucleic Acids Research, 2013, 41, 4938-4948.	6.5	24
74	To feature space and back: Identifying top-weighted features in polynomial Support Vector Machine models. Intelligent Data Analysis, 2012, 16, 551-579.	0.4	2
75	The morphological classification of heartbeats as dominant and non-dominant in ECG signals. Physiological Measurement, 2010, 31, 611-631.	1.2	4
76	Structure-based variable selection for survival data. Bioinformatics, 2010, 26, 1887-1894.	1.8	24
77	MatureBayes: A Probabilistic Algorithm for Identifying the Mature miRNA within Novel Precursors. PLoS ONE, 2010, 5, e11843.	1.1	132
78	Factors Influencing the Statistical Power of Complex Data Analysis Protocols for Molecular Signature Development from Microarray Data. PLoS ONE, 2009, 4, e4922.	1.1	20
79	Multi-Source Causal Analysis: Learning Bayesian Networks from Multiple Datasets. IFIP Advances in Information and Communication Technology, 2009, , 479-490.	0.5	3
80	The max-min hill-climbing Bayesian network structure learning algorithm. Machine Learning, 2006, 65, 31-78.	3.4	1,145
81	GEMS: A system for automated cancer diagnosis and biomarker discovery from microarray gene expression data. International Journal of Medical Informatics, 2005, 74, 491-503.	1.6	161
82	A comprehensive evaluation of multicategory classification methods for microarray gene expression cancer diagnosis. Bioinformatics, 2005, 21, 631-643.	1.8	750
83	Text Categorization Models for High-Quality Article Retrieval in Internal Medicine. Journal of the American Medical Informatics Association: JAMIA, 2004, 12, 207-216.	2.2	133
84	CTP: A New Constraint-Based Formalism for Conditional, Temporal Planning. Constraints, 2003, 8, 365-388.	0.4	74
85	Autominder: an intelligent cognitive orthotic system for people with memory impairment. Robotics and Autonomous Systems, 2003, 44, 273-282.	3.0	288
86	Time and sample efficient discovery of Markov blankets and direct causal relations. , 2003, , .		176