

Ulisses M Braga-Neto

List of Publications by Year in descending order

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62
papers

1,484
citations

567281

15
h-index

414414

32
g-index

64
all docs

64
docs citations

64
times ranked

1414
citing authors

#	ARTICLE	IF	CITATIONS
1	Is cross-validation valid for small-sample microarray classification?. <i>Bioinformatics</i> , 2004, 20, 374-380.	4.1	546
2	Maximum-Likelihood Adaptive Filter for Partially Observed Boolean Dynamical Systems. <i>IEEE Transactions on Signal Processing</i> , 2017, 65, 359-371.	5.3	93
3	Is cross-validation better than resubstitution for ranking genes?. <i>Bioinformatics</i> , 2004, 20, 253-258.	4.1	73
4	A Theoretical Tour of Connectivity in Image Processing and Analysis. <i>Journal of Mathematical Imaging and Vision</i> , 2003, 19, 5-31.	1.3	58
5	Particle filters for partially-observed Boolean dynamical systems. <i>Automatica</i> , 2018, 87, 238-250.	5.0	53
6	Control of Gene Regulatory Networks Using Bayesian Inverse Reinforcement Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1250-1261.	3.0	43
7	Intrinsically Multivariate Predictive Genes. <i>IEEE Journal on Selected Topics in Signal Processing</i> , 2008, 2, 424-439.	10.8	41
8	Boolean Kalman filter and smoother under model uncertainty. <i>Automatica</i> , 2020, 111, 108609.	5.0	40
9	Control of Gene Regulatory Networks With Noisy Measurements and Uncertain Inputs. <i>IEEE Transactions on Control of Network Systems</i> , 2018, 5, 760-769.	3.7	35
10	Joint Sampling Distribution Between Actual and Estimated Classification Errors for Linear Discriminant Analysis. <i>IEEE Transactions on Information Theory</i> , 2010, 56, 784-804.	2.4	33
11	Grayscale Level Connectivity: Theory and Applications. <i>IEEE Transactions on Image Processing</i> , 2004, 13, 1567-1580.	9.8	32
12	Finite-horizon LQR controller for partially-observed Boolean dynamical systems. <i>Automatica</i> , 2018, 95, 172-179.	5.0	31
13	Optimal state estimation for boolean dynamical systems using a boolean Kalman smoother. , 2015, , .		27
14	Optimal gene regulatory network inference using the Boolean Kalman filter and multiple model adaptive estimation. , 2015, , .		25
15	Cross-validation under separate sampling: strong bias and how to correct it. <i>Bioinformatics</i> , 2014, 30, 3349-3355.	4.1	24
16	Point-Based Methodology to Monitor and Control Gene Regulatory Networks via Noisy Measurements. <i>IEEE Transactions on Control Systems Technology</i> , 2019, 27, 1023-1035.	5.2	23
17	Nonstationary linear discriminant analysis. , 2017, , .		21
18	Maximum-Likelihood Estimation of the Discrete Coefficient of Determination in Stochastic Boolean Systems. <i>IEEE Transactions on Signal Processing</i> , 2013, 61, 3880-3894.	5.3	18

#	ARTICLE	IF	CITATIONS
19	Multiple Model Adaptive controller for Partially-Observed Boolean Dynamical Systems. , 2017, , .		17
20	A Machine-Learning-Based IoT System for Optimizing Nutrient Supply in Commercial Aquaponic Operations. Sensors, 2022, 22, 3510.	3.8	17
21	State-feedback control of Partially-Observed Boolean Dynamical Systems using RNA-seq time series data. , 2016, , .		16
22	Optimal finite-horizon sensor selection for Boolean Kalman Filter. , 2017, , .		16
23	Optimal Fault Detection and Diagnosis in Transcriptional Circuits Using Next-Generation Sequencing. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 516-525.	3.0	16
24	Scalable optimal Bayesian classification of single-cell trajectories under regulatory model uncertainty. BMC Genomics, 2019, 20, 435.	2.8	16
25	Gene regulatory network state estimation from arbitrary correlated measurements. Eurasip Journal on Advances in Signal Processing, 2018, 2018, .	1.7	15
26	Sequential Experimental Design for Optimal Structural Intervention in Gene Regulatory Networks Based on the Mean Objective Cost of Uncertainty. Cancer Informatics, 2018, 17, 117693511879024.	1.9	15
27	Point-based value iteration for partially-observed Boolean dynamical systems with finite observation space. , 2016, , .		14
28	Boolean Kalman Filter with correlated observation noise. , 2017, , .		13
29	Optimal Control of Gene Regulatory Networks with Unknown Cost Function. , 2018, , .		13
30	Contribution of Coronavirus-Specific Immunoglobulin G Responses to Complement Overactivation in Patients with Severe Coronavirus Disease 2019. Journal of Infectious Diseases, 2022, 226, 766-777.	4.0	12
31	Intrinsically Bayesian robust classifier for single-cell gene expression trajectories in gene regulatory networks. BMC Systems Biology, 2018, 12, 23.	3.0	11
32	Classification of Single-Cell Gene Expression Trajectories from Incomplete and Noisy Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 193-207.	3.0	10
33	Classification and Error Estimation for Discrete Data. Current Genomics, 2009, 10, 446-462.	1.6	9
34	Bayesian estimation of the discrete coefficient of determination. Eurasip Journal on Bioinformatics and Systems Biology, 2016, 2016, 1.	1.4	6
35	Classification of Gaussian trajectories with missing data in Boolean gene regulatory networks. , 2017, , .		6
36	Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	6

#	ARTICLE	IF	CITATIONS
37	Particle filtering approach to state estimation in Boolean dynamical systems. , 2013, , .		5
38	Joint state and parameter estimation for Boolean dynamical systems. , 2012, , .		4
39	Modeling and systematic analysis of biomarker validation using selected reaction monitoring. Eurasip Journal on Bioinformatics and Systems Biology, 2014, 2014, 17.	1.4	4
40	Unbiased bootstrap error estimation for linear discriminant analysis. Eurasip Journal on Bioinformatics and Systems Biology, 2014, 2014, 15.	1.4	4
41	A Naive-Bayes approach to Bolstered error estimation in high-dimensional spaces. , 2014, , .		3
42	Bayesian top scoring pairs for feature selection. , 2017, , .		3
43	An asymptotically-exact expression for the variance of classification error for the discrete histogram rule. , 2008, , .		2
44	Bayesian ABC-MCMC Classification of Liquid Chromatographyâ€“Mass Spectrometry Data. Cancer Informatics, 2015, 14s5, CIN.S30798.	1.9	2
45	A Bayesian approach to Top-Scoring Pairs classification. , 2017, , .		2
46	Bayesian Classification of Proteomics Biomarkers from Selected Reaction Monitoring Data using an Approximate Bayesian Computation-Markov Chain Monte Carlo Approach. Cancer Informatics, 2018, 17, 117693511878692.	1.9	2
47	Bayesian Classification of Genomic Big Data. , 2018, , 411-427.		2
48	PALLAS: Penalized mAXimum Likelihood and pArticle Swarms for Inference of Gene Regulatory Networks From Time Series Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1807-1816.	3.0	2
49	Modeling and systematic analysis of LC-MS proteomics pipeline. , 2011, , .		1
50	A statistical test for intrinsically multivariate predictive genes. , 2012, , .		1
51	On the Bias of Precision Estimation Under Separate Sampling. Cancer Informatics, 2019, 18, 117693511986082.	1.9	1
52	Bolstered error estimator with feature selection. , 2009, , .		0
53	Sample size calculation from specified RMS of the resubstitution error for linear classifiers. , 2009, , .		0
54	Bagging degrades the performance of linear discriminant classifiers. , 2009, , .		0

#	ARTICLE	IF	CITATIONS
55	Approximate expressions for the variances of non-randomized error estimators and CoD estimators for the discrete histogram rule. , 2010, , .		0
56	RMS bounds and sample size considerations for error estimation in linear discriminant analysis. , 2010, , .		0
57	Multiple reaction monitoring: Modeling and systematic analysis. , 2011, , .		0
58	Relationship between the accuracy of classifier error estimation and distribution complexity. , 2011, , .		0
59	A parallel programming framework with Markovian messaging for LC-MS peptide detection. , 2011, , .		0
60	Improved branch-and-bound algorithm for U-curve optimization. , 2013, , .		0
61	Machine Learning Requires Probability and Statistics [Perspectives]. IEEE Signal Processing Magazine, 2020, 37, 118-122.	5.6	0
62	A stochastic metapopulation state-space approach to modeling and estimating COVID-19 spread. Mathematical Biosciences and Engineering, 2021, 18, 7685-7710.	1.9	0