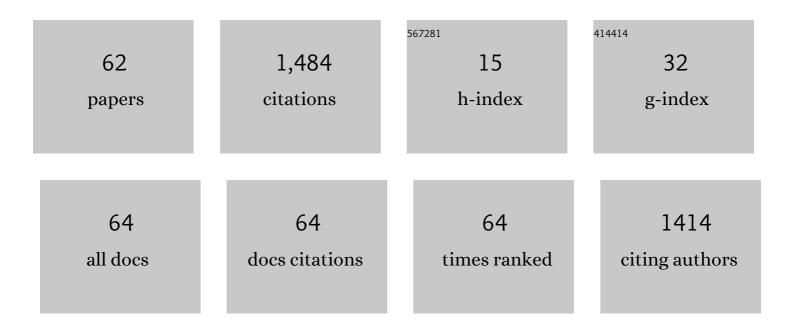
Ulisses M Braga-Neto

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	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
2	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
3	A Machine-Learning-Based IoT System for Optimizing Nutrient Supply in Commercial Aquaponic Operations. Sensors, 2022, 22, 3510.	3.8	17
4	A stochastic metapopulation state-space approach to modeling and estimating COVID-19 spread. Mathematical Biosciences and Engineering, 2021, 18, 7685-7710.	1.9	0
5	Boolean Kalman filter and smoother under model uncertainty. Automatica, 2020, 111, 108609.	5.0	40
6	Machine Learning Requires Probability and Statistics [Perspectives]. IEEE Signal Processing Magazine, 2020, 37, 118-122.	5.6	0
7	On the Bias of Precision Estimation Under Separate Sampling. Cancer Informatics, 2019, 18, 117693511986082.	1.9	1
8	Scalable optimal Bayesian classification of single-cell trajectories under regulatory model uncertainty. BMC Genomics, 2019, 20, 435.	2.8	16
9	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
10	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
11	Point-Based Methodology to Monitor and Control Gene Regulatory Networks via Noisy Measurements. IEEE Transactions on Control Systems Technology, 2019, 27, 1023-1035.	5.2	23
12	Control of Gene Regulatory Networks Using Bayesian Inverse Reinforcement Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1250-1261.	3.0	43
13	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
14	Gene regulatory network state estimation from arbitrary correlated measurements. Eurasip Journal on Advances in Signal Processing, 2018, 2018, .	1.7	15
15	Control of Gene Regulatory Networks With Noisy Measurements and Uncertain Inputs. IEEE Transactions on Control of Network Systems, 2018, 5, 760-769.	3.7	35
16	Particle filters for partially-observed Boolean dynamical systems. Automatica, 2018, 87, 238-250.	5.0	53
17	Optimal Control of Gene Regulatory Networks with Unknown Cost Function. , 2018, , .		13
18	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

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19	Intrinsically Bayesian robust classifier for single-cell gene expression trajectories in gene regulatory networks. BMC Systems Biology, 2018, 12, 23.	3.0	11
20	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
21	Finite-horizon LQR controller for partially-observed Boolean dynamical systems. Automatica, 2018, 95, 172-179.	5.0	31
22	Bayesian Classification of Genomic Big Data. , 2018, , 411-427.		2
23	Boolean Kalman Filter with correlated observation noise. , 2017, , .		13
24	Multiple Model Adaptive controller for Partially-Observed Boolean Dynamical Systems. , 2017, , .		17
25	Classification of Gaussian trajectories with missing data in Boolean gene regulatory networks. , 2017, , .		6
26	A Bayesian approach to Top-Scoring Pairs classification. , 2017, , .		2
27	Maximum-Likelihood Adaptive Filter for Partially Observed Boolean Dynamical Systems. IEEE Transactions on Signal Processing, 2017, 65, 359-371.	5.3	93
28	Bayesian top scoring pairs for feature selection. , 2017, , .		3
29	Optimal finite-horizon sensor selection for Boolean Kalman Filter. , 2017, , .		16
30	Nonstationary linear discriminant analysis. , 2017, , .		21
31	Point-based value iteration for partially-observed Boolean dynamical systems with finite observation space. , 2016, , .		14
32	State-feedback control of Partially-Observed Boolean Dynamical Systems using RNA-seq time series data. , 2016, , .		16
33	Bayesian estimation of the discrete coefficient of determination. Eurasip Journal on Bioinformatics and Systems Biology, 2016, 2016, 1.	1.4	6
34	Bayesian ABC-MCMC Classification of Liquid Chromatography–Mass Spectrometry Data. Cancer Informatics, 2015, 14s5, CIN.S30798.	1.9	2
35	Optimal gene regulatory network inference using the Boolean Kalman filter and multiple model adaptive estimation. , 2015, , .		25
36	Optimal state estimation for boolean dynamical systems using a boolean Kalman smoother. , 2015, , .		27

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37	Modeling and systematic analysis of biomarker validation using selected reaction monitoring. Eurasip Journal on Bioinformatics and Systems Biology, 2014, 2014, 17.	1.4	4
38	Unbiased bootstrap error estimation for linear discriminant analysis. Eurasip Journal on Bioinformatics and Systems Biology, 2014, 2014, 15.	1.4	4
39	A Naive-Bayes approach to Bolstered error estimation in high-dimensional spaces. , 2014, , .		3
40	Cross-validation under separate sampling: strong bias and how to correct it. Bioinformatics, 2014, 30, 3349-3355.	4.1	24
41	Particle filtering approach to state estimation in Boolean dynamical systems. , 2013, , .		5
42	Maximum-Likelihood Estimation of the Discrete Coefficient of Determination in Stochastic Boolean Systems. IEEE Transactions on Signal Processing, 2013, 61, 3880-3894.	5.3	18
43	Improved branch-and-bound algorithm for U-curve optimization. , 2013, , .		Ο
44	Joint state and parameter estimation for Boolean dynamical systems. , 2012, , .		4
45	A statistical test for intrinsically multivariate predictive genes. , 2012, , .		1
46	Multiple reaction monitoring: Modeling and systematic analysis. , 2011, , .		0
47	Relationship between the accuracy of classifier error estimation and distribution complexity. , 2011, , .		Ο
48	A parallel programming framework with Markovian messaging for LC-MS peptide detection. , 2011, , .		0
49	Modeling and systematic analysis of LC-MS proteomics pipeline. , 2011, , .		1
50	Joint Sampling Distribution Between Actual and Estimated Classification Errors for Linear Discriminant Analysis. IEEE Transactions on Information Theory, 2010, 56, 784-804.	2.4	33
51	Approximate expressions for the variances of non-randomized error estimators and CoD estimators for the discrete histogram rule. , 2010, , .		Ο
52	RMS bounds and sample size considerations for error estimation in linear discriminant analysis. , 2010, , .		0
53	Bolstered error estimator with feature selection. , 2009, , .		0
54	Sample size calculation from specified RMS of the resubstitution error for linear classifiers. , 2009, , .		0

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55	Bagging degrades the performance of linear discriminant classifiers. , 2009, , .		0
56	Classification and Error Estimation for Discrete Data. Current Genomics, 2009, 10, 446-462.	1.6	9
5 7	Intrinsically Multivariate Predictive Genes. IEEE Journal on Selected Topics in Signal Processing, 2008, 2, 424-439.	10.8	41
58	An asymptotically-exact expression for the variance of classification error for the discrete histogram rule. , 2008, , .		2
59	Is cross-validation valid for small-sample microarray classification?. Bioinformatics, 2004, 20, 374-380.	4.1	546
60	Is cross-validation better than resubstitution for ranking genes?. Bioinformatics, 2004, 20, 253-258.	4.1	73
61	Grayscale Level Connectivity: Theory and Applications. IEEE Transactions on Image Processing, 2004, 13, 1567-1580.	9.8	32
62	A Theoretical Tour of Connectivity in Image Processing and Analysis. Journal of Mathematical Imaging and Vision, 2003, 19, 5-31.	1.3	58