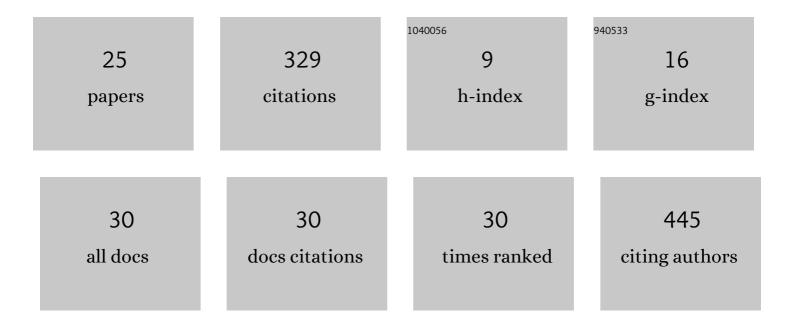
Hilario Navarro

List of Publications by Year in descending order

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ΗΠΑΡΙΟ ΝΑΥΑΡΡΟ

#	Article	IF	CITATIONS
1	Skewness-Kurtosis Model-Based Projection Pursuit with Application to Summarizing Gene Expression Data. Mathematics, 2021, 9, 954.	2.2	6
2	Skewness-Based Projection Pursuit as an Eigenvector Problem in Scale Mixtures of Skew-Normal Distributions. Symmetry, 2021, 13, 1056.	2.2	2
3	Data projections by skewness maximization under scale mixtures of skew-normal vectors. Advances in Data Analysis and Classification, 2020, 14, 435-461.	1.4	5
4	Bayesian networks established functional differences between breast cancer subtypes. PLoS ONE, 2020, 15, e0234752.	2.5	5
5	Computational models applied to metabolomics data hints at the relevance of glutamine metabolism in breast cancer. BMC Cancer, 2020, 20, 307.	2.6	9
6	A stochastic ordering based on the canonical transformation of skew-normal vectors. Test, 2019, 28, 475-498.	1.1	10
7	Biological molecular layer classification of muscle-invasive bladder cancer opens new treatment opportunities. BMC Cancer, 2019, 19, 636.	2.6	15
8	A novel approach to triple-negative breast cancer molecular classification reveals a luminal immune-positive subgroup with good prognoses. Scientific Reports, 2019, 9, 1538.	3.3	46
9	Molecular characterization of breast cancer cell response to metabolic drugs. Oncotarget, 2018, 9, 9645-9660.	1.8	22
10	Probabilistic graphical models relate immune status with response to neoadjuvant chemotherapy in breast cancer. Oncotarget, 2018, 9, 27586-27594.	1.8	8
11	Functional proteomics outlines the complexity of breast cancer molecular subtypes. Scientific Reports, 2017, 7, 10100.	3.3	50
12	Urothelial cancer proteomics provides both prognostic and functional information. Scientific Reports, 2017, 7, 15819.	3.3	20
13	A note on the direction maximizing skewness in multivariate skew-t vectors. Statistics and Probability Letters, 2015, 96, 328-332.	0.7	11
14	Combined Label-Free Quantitative Proteomics and microRNA Expression Analysis of Breast Cancer Unravel Molecular Differences with Clinical Implications. Cancer Research, 2015, 75, 2243-2253.	0.9	62
15	Exploring correlations in gene expression microarray data for maximum predictive–minimum redundancy biomarker selection and classification. Computers in Biology and Medicine, 2013, 43, 1437-1443.	7.0	11
16	A study of the effect of kurtosis on discriminant analysis under elliptical populations. Journal of Multivariate Analysis, 2012, 107, 53-63.	1.0	14
17	Uncovering Bivariate Interactions in High Dimensional Data Using Random Forests with Data Augmentation. Fundamenta Informaticae, 2011, 113, 97-115.	0.4	1
18	A new method for identifying bivariate differential expression in high dimensional microarray data using quadratic discriminant analysis. BMC Bioinformatics, 2011, 12, S6.	2.6	9

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#	Article	IF	CITATIONS
19	Evaluating the difference between graph structures in Gaussian Bayesian networks. Expert Systems With Applications, 2011, 38, 12409-12414.	7.6	8
20	The Effect of Non-normality in the Power Exponential Distributions. Understanding Complex Systems, 2011, , 119-129.	0.6	5
21	Relative Sensitivity of Conditional Distributions to Kurtosis Deviations in the Joint Model. Procedia, Social and Behavioral Sciences, 2010, 2, 7664-7665.	0.5	1
22	Conditional Specification with Exponential Power Distributions. Communications in Statistics - Theory and Methods, 2010, 39, 2231-2240.	1.0	0
23	Using random forests to uncover bivariate interactions in high dimensional small data sets. , 2009, , .		1
24	Asymptotic relationships between posterior probabilities and p-values using the hazard rate. Statistics and Probability Letters, 2004, 66, 59-66.	0.7	5
25	Local effect of asymmetry deviations from Gaussianity using information-based measures. , 0, , .		1