

# A Perera

## List of Publications by Year in descending order

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99  
papers

2,019  
citations

257450

24  
h-index

265206

42  
g-index

104  
all docs

104  
docs citations

104  
times ranked

3341  
citing authors

#	ARTICLE	IF	CITATIONS
1	Drift compensation of gas sensor array data by Orthogonal Signal Correction. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2010, 100, 28-35.	3.5	189
2	Drift compensation of gas sensor array data by common principal component analysis. <i>Sensors and Actuators B: Chemical</i> , 2010, 146, 460-465.	7.8	167
3	Dynamic Trajectories of Left Ventricular Ejection Fraction in Heart Failure. <i>Journal of the American College of Cardiology</i> , 2018, 72, 591-601.	2.8	132
4	eRah: A Computational Tool Integrating Spectral Deconvolution and Alignment with Quantification and Identification of Metabolites in GC/MS-Based Metabolomics. <i>Analytical Chemistry</i> , 2016, 88, 9821-9829.	6.5	101
5	Aberrant DNA methylation in non-small cell lung cancer-associated fibroblasts. <i>Carcinogenesis</i> , 2015, 36, bgv146.	2.8	84
6	Validity of the Polar V800 monitor for measuring heart rate variability in mountain running route conditions. <i>European Journal of Applied Physiology</i> , 2018, 118, 669-677.	2.5	84
7	An R package to analyse LC/MS metabolomic data: MAIT (Metabolite Automatic Identification Toolkit). <i>Bioinformatics</i> , 2014, 30, 1937-1939.	4.1	62
8	FELLA: an R package to enrich metabolomics data. <i>BMC Bioinformatics</i> , 2018, 19, 538.	2.6	61
9	Intensity drift removal in LC/MS metabolomics by common variance compensation. <i>Bioinformatics</i> , 2014, 30, 2899-2905.	4.1	56
10	Clinical phenotype clustering in cardiovascular risk patients for the identification of responsive metabolotypes after red wine polyphenol intake. <i>Journal of Nutritional Biochemistry</i> , 2016, 28, 114-120.	4.2	53
11	Heart Failure With Preserved Ejection Fraction Infrequently Evolves Toward a Reduced Phenotype in Long-Term Survivors. <i>Circulation: Heart Failure</i> , 2019, 12, e005652.	3.9	53
12	Applying learning analytics to students' interaction in business simulation games. The usefulness of learning analytics to know what students really learn. <i>Computers in Human Behavior</i> , 2019, 92, 600-612.	8.5	53
13	An intelligent detector based on temperature modulation of a gas sensor with a digital signal processor. <i>Sensors and Actuators B: Chemical</i> , 2001, 78, 32-39.	7.8	52
14	On-line novelty detection by recursive dynamic principal component analysis and gas sensor arrays under drift conditions. <i>IEEE Sensors Journal</i> , 2006, 6, 770-783.	4.7	46
15	A portable electronic nose based on embedded PC technology and GNU/Linux: hardware, software and applications. <i>IEEE Sensors Journal</i> , 2002, 2, 235-246.	4.7	39
16	Non-targeted metabolomics reveals alterations in liver and plasma of gilt-head bream exposed to oxybenzone. <i>Chemosphere</i> , 2018, 211, 624-631.	8.2	39
17	MISS: a non-linear methodology based on mutual information for genetic association studies in both population and sib-pairs analysis. <i>Bioinformatics</i> , 2010, 26, 1811-1818.	4.1	36
18	A biomimetic approach to machine olfaction, featuring a very large-scale chemical sensor array and embedded neuro-bio-inspired computation. <i>Microsystem Technologies</i> , 2014, 20, 729-742.	2.0	36

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19	Multiview and multifeature spectral clustering using common eigenvectors. <i>Pattern Recognition Letters</i> , 2018, 102, 30-36.	4.2	34
20	Bioinspired early detection through gas flow modulation in chemo-sensory systems. <i>Sensors and Actuators B: Chemical</i> , 2015, 206, 538-547.	7.8	33
21	MMP1 drives tumor progression in large cell carcinoma of the lung through fibroblast senescence. <i>Cancer Letters</i> , 2021, 507, 1-12.	7.2	33
22	Benchmarking network propagation methods for disease gene identification. <i>PLoS Computational Biology</i> , 2019, 15, e1007276.	3.2	30
23	Null diffusion-based enrichment for metabolomics data. <i>PLoS ONE</i> , 2017, 12, e0189012.	2.5	29
24	Early Prediction of Alzheimer's Disease Using Null Longitudinal Model-Based Classifiers. <i>PLoS ONE</i> , 2017, 12, e0168011.	2.5	28
25	Compound identification in gas chromatography/mass spectrometry-based metabolomics by blind source separation. <i>Journal of Chromatography A</i> , 2015, 1409, 226-233.	3.7	26
26	Evaluation of Cross-Validation Strategies in Sequence-Based Binding Prediction Using Deep Learning. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 1645-1657.	5.4	26
27	Clinical Validation of Eye Vergence as an Objective Marker for Diagnosis of ADHD in Children. <i>Journal of Attention Disorders</i> , 2019, 23, 599-614.	2.6	25
28	solaris: an R interface to SOLAR for variance component analysis in pedigrees. <i>Bioinformatics</i> , 2016, 32, 1901-1902.	4.1	24
29	A dimensionality-reduction technique inspired by receptor convergence in the olfactory system. <i>Sensors and Actuators B: Chemical</i> , 2006, 116, 17-22.	7.8	23
30	Evaluation of fish spoilage by means of a single metal oxide sensor under temperature modulation. <i>Sensors and Actuators B: Chemical</i> , 2010, 146, 477-482.	7.8	23
31	diffuStats: an R package to compute diffusion-based scores on biological networks. <i>Bioinformatics</i> , 2018, 34, 533-534.	4.1	23
32	Feature extraction on three way enose signals. <i>Sensors and Actuators B: Chemical</i> , 2006, 116, 145-150.	7.8	21
33	Gas measurement systems based on IEEE1451.2 standard. <i>Sensors and Actuators B: Chemical</i> , 2006, 116, 11-16.	7.8	21
34	Fuzzy inference system for sensor array calibration: prediction of CO and CH4 levels in variable humidity conditions. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2002, 64, 103-122.	3.5	20
35	A new gene-based association test for genome-wide association studies. <i>BMC Proceedings</i> , 2009, 3, S130.	1.6	19
36	Predictability of gene ontology slim-terms from primary structure information in Embryophyta plant proteins. <i>BMC Bioinformatics</i> , 2013, 14, 68.	2.6	14

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37	Dimensionality Reduction Oriented Toward the Feature Visualization for Ischemia Detection. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 590-598.	3.2	13
38	Fault detection, identification, and reconstruction of faulty chemical gas sensors under drift conditions, using Principal Component Analysis and Multiscale-PCA. , 2010, , .		10
39	Common Principal Component Analysis For Drift Compensation Of Gas Sensor Array Data. , 2009, , .		9
40	Data Simulation in Machine Olfaction with the R Package Chemosensors. PLoS ONE, 2014, 9, e88839.	2.5	9
41	Peak Aggregation as an Innovative Strategy for Improving the Predictive Power of LC-MS Metabolomic Profiles. Analytical Chemistry, 2014, 86, 2320-2325.	6.5	9
42	Automated resolution of chromatographic signals by independent component analysisâ€œorthogonal signal deconvolution in comprehensive gas chromatography/mass spectrometry-based metabolomics. Computer Methods and Programs in Biomedicine, 2016, 130, 135-141.	4.7	9
43	Principal discriminants analysis for small-sample-size problems: application to chemical sensing. , 0, , .		8
44	A software tool for large-scale synthetic experiments based on polymeric sensor arrays. Sensors and Actuators B: Chemical, 2013, 177, 596-604.	7.8	8
45	Eye Vergence Responses During an Attention Task in Adults With ADHD and Clinical Controls. Journal of Attention Disorders, 2021, 25, 1302-1310.	2.6	8
46	The Central Role of KNG1 Gene as a Genetic Determinant of Coagulation Pathway-Related Traits: Exploring Metaphenotypes. PLoS ONE, 2016, 11, e0167187.	2.5	8
47	Biologically Inspired Computation for Chemical Sensing. Procedia Computer Science, 2011, 7, 226-227.	2.0	7
48	Automatic capacitor bank identification in power distribution systems. Electric Power Systems Research, 2014, 111, 96-102.	3.6	7
49	Baitmet, a computational approach for GCâ€œMS library-driven metabolite profiling. Metabolomics, 2017, 13, 1.	3.0	7
50	Assessment of Heart Rate Variability during an Endurance Mountain Trail Race by Multi-Scale Entropy Analysis. Entropy, 2017, 19, 658.	2.2	7
51	Affected pathways and transcriptional regulators in gene expression response to an ultra-marathon trail: Global and independent activity approaches. PLoS ONE, 2017, 12, e0180322.	2.5	7
52	Computational Detection of Transcription Factor Binding Sites Through Differential RÃ©nyi Entropy. IEEE Transactions on Information Theory, 2010, 56, 734-741.	2.4	6
53	Predictability of protein subcellular locations by pattern recognition techniques. , 2010, 2010, 5512-5.		6
54	A subspace method for the detection of transcription factor binding sites. Bioinformatics, 2012, 28, 1328-1335.	4.1	6

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55	Avoiding hard chromatographic segmentation: A moving window approach for the automated resolution of gas chromatography–mass spectrometry-based metabolomics signals by multivariate methods. <i>Journal of Chromatography A</i> , 2016, 1474, 145-151.	3.7	6
56	Global Collaborative Social Network (Share4Rare) to Promote Citizen Science in Rare Disease Research: Platform Development Study. <i>JMIR Formative Research</i> , 2021, 5, e22695.	1.4	6
57	On-line event detection by recursive Dynamic Principal Component Analysis and gas sensor arrays under drift conditions. , 0, , .		5
58	Balancing Data on Deep Learning-Based Proteochemometric Activity Classification. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 1657-1669.	5.4	5
59	mWISE: An Algorithm for Context-Based Annotation of Liquid Chromatography–Mass Spectrometry Features through Diffusion in Graphs. <i>Analytical Chemistry</i> , 2021, 93, 10772-10778.	6.5	5
60	Game learning analytics of instant messaging and online discussion forums in higher education. <i>Education and Training</i> , 2021, 63, 1288-1308.	3.1	5
61	Finding the best calibration points for a gas sensor array with support vector regression. , 0, , .		4
62	DNA Binding Site Characterization by Means of Rényi Entropy Measures on Nucleotide Transitions. <i>IEEE Transactions on Nanobioscience</i> , 2008, 7, 133-141.	3.3	4
63	SNP sets selection under mutual information criterion, application to F7/FVII dataset. , 2008, 2008, 3783-6.		3
64	Search of phenotype related candidate genes using gene ontology-based semantic similarity and protein interaction information: Application to Brugada syndrome. , 2009, 2009, 7079-82.		3
65	Graph theory-based measures as predictors of gene morbidity. , 2010, 2010, 803-6.		3
66	Multiview: a software package for multiview pattern recognition methods. <i>Bioinformatics</i> , 2019, 35, 2877-2879.	4.1	3
67	MultiPaths: a Python framework for analyzing multi-layer biological networks using diffusion algorithms. <i>Bioinformatics</i> , 2021, 37, 137-139.	4.1	3
68	Mapping layperson medical terminology into the Human Phenotype Ontology using neural machine translation models. <i>Expert Systems With Applications</i> , 2022, 204, 117446.	7.6	3
69	A bio-inspired nonlinear algorithm to integrate carbon monoxide concentration aiming to fulfil international standards. <i>Sensors and Actuators B: Chemical</i> , 2000, 69, 308-313.	7.8	2
70	Machine olfaction: pattern recognition for the identification of aromas. , 0, , .		2
71	Clustering of individuals given SNPs similarity based on normalized mutual information: F7 SNPs in the GAIT sample. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2007, 2007, 123-6.	0.5	2
72	Data set from gas sensor array under flow modulation. <i>Data in Brief</i> , 2015, 3, 131-136.	1.0	2

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73	The effect of statistical normalization on network propagation scores. <i>Bioinformatics</i> , 2021, 37, 845-852.	4.1	2
74	Detection of transcription factor binding sites using R�nyi entropy. , 2008, , .		1
75	Transcription factor binding site detection through position cross-mutual information variability analysis. , 2009, 2009, 7087-90.		1
76	Improving Drift Correction by Double Projection Preprocessing in Gas Sensor Arrays. , 2009, , .		1
77	An information theory-based tool for characterizing the interaction environment of a protein. , 2010, 2010, 5529-32.		1
78	MEET: Motif elements estimation toolkit. , 2011, 2011, 6483-6.		1
79	A Large Scale Virtual Gas Sensor Array. , 2011, , .		1
80	Biologically inspired large scale chemical sensor arrays and embedded data processing. <i>Proceedings of SPIE</i> , 2013, , .	0.8	1
81	Sequence information gain based motif analysis. <i>BMC Bioinformatics</i> , 2015, 16, 377.	2.6	1
82	Applicability of semi-supervised learning assumptions for gene ontology terms prediction. <i>Revista Facultad De Ingenier�a</i> , 2016, , .	0.5	1
83	Machine-Learning QSAR Model for Predicting Activity against Malaria Parasite�s Ion Pump PfATP4 and In Silico Binding Assay Validation. <i>Proceedings (mdpi)</i> , 2017, 1, 652.	0.2	1
84	Title is missing!. <i>Journal of Medical and Biological Engineering</i> , 2013, 33, 504.	1.8	1
85	Potato creams recognition from electronic nose and tongue signals: feature extraction/selection and RBF neural networks classifiers. , 0, , .		0
86	DNA Binding Sites Characterization by Means of R�nyi Entropy Measures on Nucleotide Transitions. , 2006, 2006, 5783-6.		0
87	Use of Gene Ontology semantic information in protein interaction data visualization. , 2008, , .		0
88	Floating Feature Selection for multiloci association of quantitative traits in sib-pairs analysis. , 2008, , .		0
89	Total solvent amount and human panel test predictions using gas sensor fast chromatography and multivariate linear and non-linear processing. , 2009, , .		0
90	Exons and introns characterization in nucleic acid sequences by time-frequency analysis. , 2010, 2010, 1783-6.		0

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91	Analysis of incomplete gene expression dataset through protein-protein interaction information. , 2011, 2011, 6845-8.		0
92	Odour Mapping Under Strong Backgrounds With a Metal Oxide Sensor Array. , 2011, , .		0
93	Multiview approach to spectral clustering. , 2012, 2012, 1254-7.		0
94	Network-based enrichment analysis of gene expression through protein-protein interaction data. , 2012, 2012, 6317-20.		0
95	Effect of genetic regions on the correlation between single point mutation variability and morbidity. Computers in Biology and Medicine, 2013, 43, 594-599.	7.0	0
96	Training-induced gene expression plasticity in cardiac function and neural regulation for ultra-trail runners. , 2015, , .		0
97	Synthetic benchmarks for machine olfaction: Classification, segmentation and sensor damage. Data in Brief, 2015, 3, 126-130.	1.0	0
98	Compound Identification in Comprehensive Gas Chromatographyâ€”Mass Spectrometry-Based Metabolomics by Blind Source Separation. Advances in Intelligent Systems and Computing, 2015, , 49-57.	0.6	0
99	DNA Binding Sites Characterization by Means of RÃ©nyi Entropy Measures on Nucleotide Transitions. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	0