Daniel GonzÃ¡lez Glez-PeÃ±a

List of Publications by Year
in descending order

81 papers	1,414 citations	448610 19 h-index	406436 35 g-index
89 all docs	89 docs citations	89 times ranked	2386 citing authors

#	Article	IF	Citations
1	Real-time polyp detection model using convolutional neural networks. Neural Computing and Applications, 2022, 34, 10375-10396.	3.2	29
2	Enhancing sepsis management through machine learning techniques: A review. Medicina Intensiva, 2022, 46, 140-156.	0.4	9
3	Performance of Convolutional Neural Networks for Polyp Localization on Public Colonoscopy Image Datasets. Diagnostics, 2022, 12, 898.	1.3	13
4	Deep Neural Networks approaches for detecting and classifying colorectal polyps. Neurocomputing, 2021, 423, 721-734.	3.5	65
5	Improving the bed movement physics of inclined grate biomass CFD simulations. Applied Thermal Engineering, 2021, 182, 116043.	3.0	6
6	DREIMT: a drug repositioning database and prioritization tool for immunomodulation. Bioinformatics, 2021, 37, 578-579.	1.8	9
7	Are There Benefits from Thermal Bacteria for Health? The Hydrogenome Role. Water (Switzerland), 2021, 13, 1439.	1.2	1
8	Compi: a framework for portable and reproducible pipelines. PeerJ Computer Science, 2021, 7, e593.	2.7	8
9	An RNA-seq Based Machine Learning Approach Identifies Latent Tuberculosis Patients With an Active Tuberculosis Profile. Frontiers in Immunology, 2020, 11, 1470.	2.2	25
10	Metatax: Metataxonomics with a Compi-Based Pipeline for Precision Medicine. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 252-257.	2.2	2
11	CHAPTER 5. Statistics, Data Mining and Modeling. New Developments in Mass Spectrometry, 2020, , 120-200.	0.2	0
12	Gold Standard Evaluation of an Automatic HAIs Surveillance System. BioMed Research International, 2019, 2019, 1-10.	0.9	5
13	Perceptions of the use of intelligent information access systems in university level active learning activities among teachers of biomedical subjects. International Journal of Medical Informatics, 2018, 112, 21-33.	1.6	23
14	Bicycle: a bioinformatics pipeline to analyze bisulfite sequencing data. Bioinformatics, 2018, 34, 1414-1415.	1.8	21
15	S2P: A software tool to quickly carry out reproducible biomedical research projects involving 2D-gel and MALDI-TOF MS protein data. Computer Methods and Programs in Biomedicine, 2018, 155, 1-9.	2.6	5
16	GC4S: A bioinformatics-oriented Java software library of reusable graphical user interface components. PLoS ONE, 2018, 13, e0204474.	1.1	5
17	PanDrugs: a novel method to prioritize anticancer drug treatments according to individual genomic data. Genome Medicine, 2018, 10, 41.	3.6	63
18	S2P: A Desktop Application for Fast and Easy Processing of 2D-Gel and MALDI-Based Mass Spectrometry Protein Data. Advances in Intelligent Systems and Computing, 2017, , 1-8.	0.5	1

#	Article	IF	Citations
19	RUbioSeq+: A multiplatform application that executes parallelized pipelines to analyse next-generation sequencing data. Computer Methods and Programs in Biomedicine, 2017, 138, 73-81.	2.6	11
20	Implementing effective machine learning-based workflows for the analysis of mass spectrometry data. Journal of Integrated OMICS, 2016, 6, .	0.5	3
21	LA-iMageS: a software for elemental distribution bioimaging using LAâ€"ICPâ€"MS data. Journal of Cheminformatics, 2016, 8, 65.	2.8	35
22	RUbioSeq+: An Application that Executes Parallelized Pipelines to Analyse Next-Generation Sequencing Data. Advances in Intelligent Systems and Computing, 2016, , 141-149.	0.5	0
23	Laser ablation and inductively coupled plasma mass spectrometry focusing on bioimaging from elemental distribution using MatLab software: a practical guide. Journal of Analytical Atomic Spectrometry, 2016, 31, 832-840.	1.6	22
24	Mass-Up: an all-in-one open software application for MALDI-TOF mass spectrometry knowledge discovery. BMC Bioinformatics, 2015, 16, 318.	1.2	86
25	miRGate: a curated database of human, mouse and rat miRNAâ€"mRNA targets. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav035.	1.4	87
26	Agent-Based Spatiotemporal Simulation of Biomolecular Systems within the Open Source MASON Framework. BioMed Research International, 2015, 2015, 1-12.	0.9	6
27	A New Bioinformatic Pipeline to Address the Most Common Requirements in RNA-seq Data Analysis. Advances in Intelligent Systems and Computing, 2015, , 117-125.	0.5	0
28	Enabling systematic, harmonised and large-scale biofilms data computation: The Biofilms Experiment Workbench. Computer Methods and Programs in Biomedicine, 2015, 118, 309-321.	2.6	7
29	Marky: A tool supporting annotation consistency in multi-user and iterative document annotation projects. Computer Methods and Programs in Biomedicine, 2015, 118, 242-251.	2.6	21
30	A novel ensemble of classifiers that use biological relevant gene sets for microarray classification. Applied Soft Computing Journal, 2014, 17, 117-126.	4.1	21
31	A comprehensive analysis about the influence of low-level preprocessing techniques on mass spectrometry data for sample classification. International Journal of Data Mining and Bioinformatics, 2014, 10, 455.	0.1	3
32	Web scraping technologies in an API world. Briefings in Bioinformatics, 2014, 15, 788-797.	3.2	84
33	Marky: A Lightweight Web Tracking Tool for Document Annotation. Advances in Intelligent Systems and Computing, 2014, , 269-276.	0.5	2
34	BEW: Bioinformatics Workbench for Analysis of Biofilms Experimental Data. Advances in Intelligent Systems and Computing, 2014, , 49-56.	0.5	2
35	A Workflow for the Application of Biclustering to Mass Spectrometry Data. Advances in Intelligent Systems and Computing, 2013, , 145-153.	0.5	2
36	Speeding up the screening of steroids in urine: Development of a user-friendly library. Steroids, 2013, 78, 1226-1232.	0.8	9

#	Article	IF	Citations
37	genEnsemble: A new model for the combination of classifiers and integration of biological knowledge applied to genomic data. Expert Systems With Applications, 2013, 40, 52-63.	4.4	6
38	BioAnnote: A software platform for annotating biomedical documents with application in medical learning environments. Computer Methods and Programs in Biomedicine, 2013, 111, 139-147.	2.6	26
39	A novel ensemble approach for multicategory classification of DNA microarray data using biological relevant gene sets. International Journal of Data Mining and Bioinformatics, 2012, 6, 602.	0.1	7
40	Fast human serum profiling through chemical depletion coupled to gold-nanoparticle-assisted protein separation. Talanta, 2012, 100, 239-245.	2.9	28
41	A JAVA application framework for scientific software development. Software - Practice and Experience, 2012, 42, 1015-1036.	2.5	10
42	Applying AIBench Framework to Develop Rich User Interfaces in NGS Studies. Advances in Intelligent and Soft Computing, 2012, , 189-196.	0.2	0
43	Biological Knowledge Integration in DNA Microarray Gene Expression Classification Based on Rough Set Theory. Advances in Intelligent and Soft Computing, 2012, , 53-61.	0.2	3
44	Using variable precision rough set for selection and classification of biological knowledge integrated in DNA gene expression. Journal of Integrative Bioinformatics, 2012, 9, 199.	1.0	4
45	A simulated annealing-based algorithm for iterative class discovery using fuzzy logic for informative gene selection. Journal of Integrated OMICS, 2011, 1, .	0.5	0
46	Rapid development of proteomic applications with the AIBench framework. Journal of Integrative Bioinformatics, 2011, 8, 16-30.	1.0	5
47	PileLine: a toolbox to handle genome position information in next-generation sequencing studies. BMC Bioinformatics, 2011, 12, 31.	1.2	10
48	Using inductive learning to assess compound feed production in cooperative poultry farms. Expert Systems With Applications, 2011, , .	4.4	1
49	Building a GATK-Based Tool for Methylation Analysis in Next-Generation Bisulfite Sequencing Experiments. Advances in Intelligent and Soft Computing, 2011, , 87-91.	0.2	0
50	PileLineGUI: a desktop environment for handling genome position files in next-generation sequencing studies. Nucleic Acids Research, 2011, 39, W562-W566.	6.5	6
51	Building Proteomics Applications with the AIBench Application Framework. Advances in Intelligent and Soft Computing, 2011, , 99-107.	0.2	2
52	Rapid development of Proteomic applications with the AIBench framework. Journal of Integrative Bioinformatics, 2011, 8, 171.	1.0	4
53	ALTER: program-oriented conversion of DNA and protein alignments. Nucleic Acids Research, 2010, 38, W14-W18.	6.5	367
54	AIBench: A rapid application development framework for translational research in biomedicine. Computer Methods and Programs in Biomedicine, 2010, 98, 191-203.	2.6	41

#	Article	IF	Citations
55	A novel ^{18}O inverse labelingâ€based workflow for accurate bottomâ€up mass spectrometry quantification of proteins separated by gel electrophoresis. Electrophoresis, 2010, 31, 3407-3419.	1.3	9
56	BioDR: Semantic indexing networks for biomedical document retrieval. Expert Systems With Applications, 2010, 37, 3444-3453.	4.4	14
57	PathJam: a new service for integrating biological pathway information. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	3
58	Incorporating biological knowledge to microarray data classification through genomic data fusion. , 2010, , .		2
59	Indirect ultrasonication for protein quantification and peptide mass mapping through mass spectrometry-based techniques. Talanta, 2010, 82, 587-593.	2.9	5
60	Decision peptide-driven: A free software tool for accurate protein quantification using gel electrophoresis and matrix assisted laser desorption ionization time of flight mass spectrometry. Talanta, 2010, 82, 1412-1420.	2.9	12
61	An Experimental Evaluation of a Novel Stochastic Method for Iterative Class Discovery on Real Microarray Datasets. Advances in Intelligent and Soft Computing, 2010, , 9-16.	0.2	0
62	PathAgent: Multi-agent System for Updated Pathway Information Integration. Advances in Intelligent and Soft Computing, 2010, , 77-85.	0.2	0
63	A Comparative Study of Microarray Data Classification Methods Based on Ensemble Biological Relevant Gene Sets. Advances in Intelligent and Soft Computing, 2010, , 25-32.	0.2	1
64	PathJam: a new service for integrating biological pathway information. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	4
65	WhichGenes: a web-based tool for gathering, building, storing and exporting gene sets with application in gene set enrichment analysis. Nucleic Acids Research, 2009, 37, W329-W334.	6.5	30
66	geneCBR: a translational tool for multiple-microarray analysis and integrative information retrieval for aiding diagnosis in cancer research. BMC Bioinformatics, 2009, 10, 187.	1.2	31
67	DFP: a Bioconductor package for fuzzy profile identification and gene reduction of microarray data. BMC Bioinformatics, 2009, 10, 37.	1.2	12
68	@Note: A workbench for Biomedical Text Mining. Journal of Biomedical Informatics, 2009, 42, 710-720.	2.5	34
69	Managing irrelevant knowledge in CBR models for unsolicited e-mail classification. Expert Systems With Applications, 2009, 36, 1601-1614.	4.4	11
70	geneSetFinder: A Multiagent Architecture for Gathering Biological Information. Advances in Intelligent and Soft Computing, 2009, , 50-59.	0.2	0
71	Current Efforts to Integrate Biological Pathway Information. Lecture Notes in Computer Science, 2009, , 1092-1096.	1.0	0
72	Classification of MedLine Documents Using MeSH Terms. Lecture Notes in Computer Science, 2009, , 926-929.	1.0	1

#	Article	IF	Citations
73	Biomedical Text Mining Applied to Document Retrieval and Semantic Indexing. Lecture Notes in Computer Science, 2009, , 954-963.	1.0	1
74	An Evolutionary Approach for Sample-Based Clustering on Microarray Data. Lecture Notes in Computer Science, 2009, , 972-978.	1.0	0
75	A framework for the development of Biomedical Text Mining software tools. , 2008, , .		1
76	The Impact of Noise in Spam Filtering: A Case Study. Lecture Notes in Computer Science, 2008, , 228-241.	1.0	3
77	Assessing Classification Accuracy in the Revision Stage of a CBR Spam Filtering System. Lecture Notes in Computer Science, 2007, , 374-388.	1.0	4
78	Using Fuzzy Patterns for Gene Selection and Data Reduction on Microarray Data. Lecture Notes in Computer Science, 2006, , 1087-1094.	1.0	4
79	Applying GCS Networks to Fuzzy Discretized Microarray Data for Tumour Diagnosis. Lecture Notes in Computer Science, 2006, , 1095-1102.	1.0	5
80	Multiple-Microarray Analysis and Internet Gathering Information with Application for Aiding Medical Diagnosis in Cancer Research. Advances in Soft Computing, 0, , 112-117.	0.4	0
81	Beds and Bits: The Challenge of Translational Bioinformatics. Advances in Soft Computing, 0, , 128-136.	0.4	0