

# Cesare Furlanello

## List of Publications by Year in descending order

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Version: 2024-02-01

94  
papers

8,240  
citations

101384

36  
h-index

53109

85  
g-index

103  
all docs

103  
docs citations

103  
times ranked

16672  
citing authors

#	ARTICLE	IF	CITATIONS
1	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
2	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	9.4	795
3	Gut microbiota profiling of pediatric nonalcoholic fatty liver disease and obese patients unveiled by an integrated meta-omics-based approach. <i>Hepatology</i> , 2017, 65, 451-464.	3.6	572
4	Repeatability of published microarray gene expression analyses. <i>Nature Genetics</i> , 2009, 41, 149-155.	9.4	477
5	Recursive feature elimination with random forest for PTR-MS analysis of agroindustrial products. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2006, 83, 83-90.	1.8	452
6	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. <i>Nature Biotechnology</i> , 2014, 32, 926-932.	9.4	420
7	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, 133.	3.8	325
8	A Comparison of MCC and CEN Error Measures in Multi-Class Prediction. <i>PLoS ONE</i> , 2012, 7, e41882.	1.1	286
9	minerva and minepy: a C engine for the MINE suite and its R, Python and MATLAB wrappers. <i>Bioinformatics</i> , 2013, 29, 407-408.	1.8	174
10	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
11	Predicting habitat suitability with machine learning models: The potential area of <i>Pinus sylvestris</i> L. in the Iberian Peninsula. <i>Ecological Modelling</i> , 2006, 197, 383-393.	1.2	154
12	Mitigation Measures for Pandemic Influenza in Italy: An Individual Based Model Considering Different Scenarios. <i>PLoS ONE</i> , 2008, 3, e1790.	1.1	143
13	Entropy-based gene ranking without selection bias for the predictive classification of microarray data. <i>BMC Bioinformatics</i> , 2003, 4, 54.	1.2	116
14	Tumor-infiltrating T lymphocytes improve clinical outcome of therapy-resistant neuroblastoma. <i>Oncotarget</i> , 2015, 6, e1019981.	2.1	105
15	LPS-induced TNF- $\alpha$ factor mediates pro-inflammatory and pro-fibrogenic pattern in non-alcoholic fatty liver disease. <i>Oncotarget</i> , 2015, 6, 41434-41452.	0.8	100
16	Deep representation learning of electronic health records to unlock patient stratification at scale. <i>Npj Digital Medicine</i> , 2020, 3, 96.	5.7	90
17	Cellular and gene signatures of tumor-infiltrating dendritic cells and natural-killer cells predict prognosis of neuroblastoma. <i>Nature Communications</i> , 2020, 11, 5992.	5.8	87
18	Algebraic stability indicators for ranked lists in molecular profiling. <i>Bioinformatics</i> , 2008, 24, 258-264.	1.8	85

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19	PD-L1 Is a Therapeutic Target of the Bromodomain Inhibitor JQ1 and, Combined with HLA Class I, a Promising Prognostic Biomarker in Neuroblastoma. <i>Clinical Cancer Research</i> , 2017, 23, 4462-4472.	3.2	85
20	Clinical Value of Prognosis Gene Expression Signatures in Colorectal Cancer: A Systematic Review. <i>PLoS ONE</i> , 2012, 7, e48877.	1.1	79
21	Phylogenetic convolutional neural networks in metagenomics. <i>BMC Bioinformatics</i> , 2018, 19, 49.	1.2	75
22	Machine learning methods for predictive proteomics. <i>Briefings in Bioinformatics</i> , 2007, 9, 119-128.	3.2	65
23	Geographical Information Systems and Bootstrap Aggregation (Bagging) of Tree-Based Classifiers for Lyme Disease Risk Prediction in Trentino, Italian Alps. <i>Journal of Medical Entomology</i> , 2002, 39, 485-492.	0.9	61
24	Rapid and non-destructive identification of strawberry cultivars by direct PTR-MS headspace analysis and data mining techniques. <i>Sensors and Actuators B: Chemical</i> , 2007, 121, 379-385.	4.0	61
25	Deep learning for automatic stereotypical motor movement detection using wearable sensors in autism spectrum disorders. <i>Signal Processing</i> , 2018, 144, 180-191.	2.1	60
26	Focal adhesion kinase depletion reduces human hepatocellular carcinoma growth by repressing enhancer of zeste homolog 2. <i>Cell Death and Differentiation</i> , 2017, 24, 889-902.	5.0	53
27	The impact of climate change on grapevine phenology and the influence of altitude: A regional study. <i>Agricultural and Forest Meteorology</i> , 2019, 271, 73-82.	1.9	52
28	Evaluating reproducibility of AI algorithms in digital pathology with DAPPER. <i>PLoS Computational Biology</i> , 2019, 15, e1006269.	1.5	49
29	Gene expression profiling identifies potential relevant genes in alveolar rhabdomyosarcoma pathogenesis and discriminates PAX3-FKHR positive and negative tumors. <i>International Journal of Cancer</i> , 2006, 118, 2772-2781.	2.3	48
30	Modern data mining tools in descriptive sensory analysis: A case study with a Random forest approach. <i>Food Quality and Preference</i> , 2007, 18, 681-689.	2.3	48
31	Novelty Detection using Deep Normative Modeling for IMU-Based Abnormal Movement Monitoring in Parkinson's Disease and Autism Spectrum Disorders. <i>Sensors</i> , 2018, 18, 3533.	2.1	46
32	Precipitation Nowcasting with Orographic Enhanced Stacked Generalization: Improving Deep Learning Predictions on Extreme Events. <i>Atmosphere</i> , 2020, 11, 267.	1.0	45
33	Identification of GALNT14 as a novel neuroblastoma predisposition gene. <i>Oncotarget</i> , 2015, 6, 26335-26346.	0.8	43
34	Functional analysis of multiple genomic signatures demonstrates that classification algorithms choose phenotype-related genes. <i>Pharmacogenomics Journal</i> , 2010, 10, 310-323.	0.9	41
35	pyphysio: A physiological signal processing library for data science approaches in physiology. <i>SoftwareX</i> , 2019, 10, 100287.	1.2	41
36	Classification Tree Methods for Analysis of Mesoscale Distribution of <i>Ixodes ricinus</i> (Acari: Ixodidae) in Trentino, Italian Alps. <i>Journal of Medical Entomology</i> , 1996, 33, 888-893.	0.9	37

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37	Multi-omics integration for neuroblastoma clinical endpoint prediction. <i>Biology Direct</i> , 2018, 13, 5.	1.9	35
38	Parallelizing AdaBoost by weights dynamics. <i>Computational Statistics and Data Analysis</i> , 2007, 51, 2487-2498.	0.7	32
39	Modeling socio-demography to capture tuberculosis transmission dynamics in a low burden setting. <i>Journal of Theoretical Biology</i> , 2011, 289, 197-205.	0.8	32
40	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. <i>Nature Biotechnology</i> , 2017, 35, 1127-1128.	9.4	32
41	A Pan-Cancer Approach to Predict Responsiveness to Immune Checkpoint Inhibitors by Machine Learning. <i>Cancers</i> , 2019, 11, 1562.	1.7	31
42	Integrative Network Fusion: A Multi-Omics Approach in Molecular Profiling. <i>Frontiers in Oncology</i> , 2020, 10, 1065.	1.3	30
43	Predictability of drug-induced liver injury by machine learning. <i>Biology Direct</i> , 2020, 15, 3.	1.9	30
44	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , 2021, 22, 111.	3.8	29
45	A deep learning model to recognize food contaminating beetle species based on elytra fragments. <i>Computers and Electronics in Agriculture</i> , 2019, 166, 105002.	3.7	28
46	GBCNet: In-Field Grape Berries Counting for Yield Estimation by Dilated CNNs. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 4870.	1.3	28
47	Combining feature selection and DTW for time-varying functional genomics. <i>IEEE Transactions on Signal Processing</i> , 2006, 54, 2436-2443.	3.2	24
48	Effect of Size and Heterogeneity of Samples on Biomarker Discovery: Synthetic and Real Data Assessment. <i>PLoS ONE</i> , 2012, 7, e32200.	1.1	23
49	The HIM global metric and kernel for network comparison and classification. , 2015, , .		23
50	Semisupervised Learning for Molecular Profiling. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 110-118.	1.9	21
51	Assessing sources of inconsistencies in genotypes and their effects on genome-wide association studies with HapMap samples. <i>Pharmacogenomics Journal</i> , 2010, 10, 364-374.	0.9	21
52	Algebraic Comparison of Partial Lists in Bioinformatics. <i>PLoS ONE</i> , 2012, 7, e36540.	1.1	21
53	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	3.8	20
54	Stability Indicators in Network Reconstruction. <i>PLoS ONE</i> , 2014, 9, e89815.	1.1	20

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55	Variability in GWAS analysis: the impact of genotype calling algorithm inconsistencies. <i>Pharmacogenomics Journal</i> , 2010, 10, 324-335.	0.9	18
56	Batch effects in the BRLMM genotype calling algorithm influence GWAS results for the Affymetrix 500K array. <i>Pharmacogenomics Journal</i> , 2010, 10, 336-346.	0.9	18
57	Tumor-infiltrating T cells and PD-L1 expression in childhood malignant extracranial germ-cell tumors. <i>OncImmunity</i> , 2019, 8, e1542245.	2.1	18
58	A machine learning pipeline for quantitative phenotype prediction from genotype data. <i>BMC Bioinformatics</i> , 2010, 11, S3.	1.2	17
59	BIAS-VARIANCE CONTROL VIA HARD POINTS SHAVING. <i>International Journal of Pattern Recognition and Artificial Intelligence</i> , 2004, 18, 891-903.	0.7	16
60	Distillation of the clinical algorithm improves prognosis by multi-task deep learning in high-risk Neuroblastoma. <i>PLoS ONE</i> , 2018, 13, e0208924.	1.1	16
61	Comparison of Wearable and Clinical Devices for Acquisition of Peripheral Nervous System Signals. <i>Sensors</i> , 2020, 20, 6778.	2.1	16
62	Automatic model selection in cost-sensitive boosting. <i>Information Fusion</i> , 2003, 4, 3-10.	11.7	15
63	TAASRAD19, a high-resolution weather radar reflectivity dataset for precipitation nowcasting. <i>Scientific Data</i> , 2020, 7, 234.	2.4	15
64	Assessment of variability in GWAS with CRLMM genotyping algorithm on WTCCC coronary artery disease. <i>Pharmacogenomics Journal</i> , 2010, 10, 347-354.	0.9	14
65	A metaproteomic-based gut microbiota profiling in children affected by autism spectrum disorders. <i>Journal of Proteomics</i> , 2022, 251, 104407.	1.2	14
66	Machine learning models for predicting endocrine disruption potential of environmental chemicals. <i>Journal of Environmental Science and Health, Part C: Environmental Carcinogenesis and Ecotoxicology Reviews</i> , 2018, 36, 237-251.	2.9	12
67	AI Slipping on Tiles: Data Leakage in Digital Pathology. <i>Lecture Notes in Computer Science</i> , 2021, , 167-182.	1.0	12
68	An interactive effect of batch size and composition contributes to discordant results in GWAS with the CHIAMO genotyping algorithm. <i>Pharmacogenomics Journal</i> , 2010, 10, 355-363.	0.9	11
69	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	5.8	11
70	Tuning Cost-Sensitive Boosting and Its Application to Melanoma Diagnosis. <i>Lecture Notes in Computer Science</i> , 2001, , 32-42.	1.0	11
71	Quantifying the Child-€Therapist Interaction in ASD Intervention: An Observational Coding System. <i>Brain Sciences</i> , 2021, 11, 366.	1.1	10
72	Is Smiling the Key? Machine Learning Analytics Detect Subtle Patterns in Micro-Expressions of Infants with ASD. <i>Journal of Clinical Medicine</i> , 2021, 10, 1776.	1.0	10

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73	Orchestrating and sharing large multimodal data for transparent and reproducible research. Nature Communications, 2021, 12, 5797.	5.8	10
74	MASS-UMAP: Fast and Accurate Analog Ensemble Search in Weather Radar Archives. Remote Sensing, 2019, 11, 2922.	1.8	9
75	Application of Artificial Intelligence in Targeting Retinal Diseases. Current Drug Targets, 2020, 21, 1208-1215.	1.0	9
76	A Grid Environment for High-Throughput Proteomics. IEEE Transactions on Nanobioscience, 2007, 6, 117-123.	2.2	8
77	Integrating gene expression profiling and clinical data. International Journal of Approximate Reasoning, 2008, 47, 58-69.	1.9	8
78	Selection of Tree-Biased Classifiers with the Bootstrap 632+ Rule. Biometrical Journal, 1997, 39, 369-382.	0.6	7
79	DTW-MIC Coexpression Networks from Time-Course Data. PLoS ONE, 2016, 11, e0152648.	1.1	7
80	Diet and the Gut Microbiota – How the Gut. , 2015, , 225-245.		6
81	Physiological and self-report responses of parents of children with autism spectrum disorder to children crying. Research in Developmental Disabilities, 2018, 73, 31-39.	1.2	6
82	Efficient Feature Selection for PTR-MS Fingerprinting of Agroindustrial Products. Lecture Notes in Computer Science, 2008, , 42-51.	1.0	5
83	Highlighting Hard Patterns via AdaBoost Weights Evolution. Lecture Notes in Computer Science, 2002, , 72-80.	1.0	4
84	Speaker Normalization and Model Selection of Combined Neural Networks. Connection Science, 1997, 9, 31-50.	1.8	3
85	A Machine Learning Pipeline for Discriminant Pathways Identification. Lecture Notes in Computer Science, 2012, , 36-48.	1.0	3
86	Physiolyze: A Galaxy-based web service for Heart Rate Variability analysis with online processing. , 2014, , .		2
87	Differential Network Analysis and Graph Classification: A Glocal Approach. , 2016, , 17-30.		2
88	Strategies for containing an influenza pandemic: the case of Italy. , 2006, , .		1
89	TOFwave: reproducibility in biomarker discovery from time-of-flight mass spectrometry data. Molecular BioSystems, 2012, 8, 2845.	2.9	1
90	Stability in GRN Inference. Methods in Molecular Biology, 2019, 1883, 323-346.	0.4	1

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91	A Machine Learning Pipeline for Identification of Discriminant Pathways. , 2014, , 951-968.		1
92	Incremental learning of roughly represented concepts. Lecture Notes in Computer Science, 1993, , 192-198.	1.0	1
93	Semisupervised Profiling of Gene Expressions and Clinical Data. Lecture Notes in Computer Science, 2006, , 284-289.	1.0	0
94	Spectral Mapping: a Comparison of Connectionist Approaches. Perspectives in Neural Computing, 1997, , 270-277.	0.1	0