

# Willem Waegeman

## List of Publications by Year in descending order

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Version: 2024-02-01

89  
papers

3,077  
citations

236925

25  
h-index

182427

51  
g-index

98  
all docs

98  
docs citations

98  
times ranked

4237  
citing authors

#	ARTICLE	IF	CITATIONS
1	Valid prediction intervals for regression problems. <i>Artificial Intelligence Review</i> , 2023, 56, 577-613.	15.7	6
2	Novel Transformer Networks for Improved Sequence Labeling in genomics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 97-106.	3.0	15
3	Heterogeneity hampers the identification of general pressure injury risk factors in intensive care populations: A predictive modelling analysis. <i>Intensive and Critical Care Nursing</i> , 2022, 68, 103117.	2.9	17
4	CpG Transformer for imputation of single-cell methylomes. <i>Bioinformatics</i> , 2022, 38, 597-603.	4.1	17
5	Multi-target prediction for dummies using two-branch neural networks. <i>Machine Learning</i> , 2022, 111, 651-684.	5.4	5
6	High-Resolution Surveying With Small-Loop Frequency Domain Electromagnetic Systems: Efficient Survey Design and Adaptive Processing. <i>IEEE Geoscience and Remote Sensing Magazine</i> , 2021, 9, 167-183.	9.6	6
7	Cytometric fingerprints of gut microbiota predict Crohn's disease state. <i>ISME Journal</i> , 2021, 15, 354-358.	9.8	19
8	PhenoGMM: Gaussian Mixture Modeling of Cytometry Data Quantifies Changes in Microbial Community Structure. <i>MSphere</i> , 2021, 6, .	2.9	21
9	Aleatoric and epistemic uncertainty in machine learning: an introduction to concepts and methods. <i>Machine Learning</i> , 2021, 110, 457-506.	5.4	487
10	Ambient temperature and relative humidity-based drift correction in frequency domain electromagnetics using machine learning. <i>Near Surface Geophysics</i> , 2021, 19, 541-556.	1.2	5
11	Explainability in transformer models for functional genomics. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	19
12	Efficient set-valued prediction in multi-class classification. <i>Data Mining and Knowledge Discovery</i> , 2021, 35, 1435-1469.	3.7	12
13	Pressure injury prediction models for critically-ill patients should consider both the case-mix and local factors. <i>Intensive and Critical Care Nursing</i> , 2021, 65, 103033.	2.9	13
14	Predicting the Presence and Abundance of Bacterial Taxa in Environmental Communities through Flow Cytometric Fingerprinting. <i>MSystems</i> , 2021, 6, e0055121.	3.8	9
15	Improving the performance of machine learning models for biotechnology: The quest for deus ex machina. <i>Biotechnology Advances</i> , 2021, 53, 107858.	11.7	7
16	Bacterial species identification using MALDI-TOF mass spectrometry and machine learning techniques: A large-scale benchmarking study. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6157-6168.	4.1	20
17	Discriminating Bacterial Phenotypes at the Population and Single-Cell Level: A Comparison of Flow Cytometry and Raman Spectroscopy Fingerprinting. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 713-726.	1.5	16
18	Predictive design of sigma factor-specific promoters. <i>Nature Communications</i> , 2020, 11, 5822.	12.8	31

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19	Using structured pathology data to predict hospital-wide mortality at admission. <i>PLoS ONE</i> , 2020, 15, e0235117.	2.5	6
20	Fast Pathogen Identification Using Single-Cell Matrix-Assisted Laser Desorption/Ionization-Aerosol Time-of-Flight Mass Spectrometry Data and Deep Learning Methods. <i>Analytical Chemistry</i> , 2020, 92, 7523-7531.	6.5	30
21	Using structured pathology data to predict hospital-wide mortality at admission. , 2020, 15, e0235117.		0
22	Using structured pathology data to predict hospital-wide mortality at admission. , 2020, 15, e0235117.		0
23	Using structured pathology data to predict hospital-wide mortality at admission. , 2020, 15, e0235117.		0
24	Using structured pathology data to predict hospital-wide mortality at admission. , 2020, 15, e0235117.		0
25	A protocol for automated timber species identification using metabolome profiling. <i>Wood Science and Technology</i> , 2019, 53, 953-965.	3.2	27
26	Learning Single-Cell Distances from Cytometry Data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2019, 95, 782-791.	1.5	4
27	Coculturing Bacteria Leads to Reduced Phenotypic Heterogeneities. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	37
28	A hospital wide predictive model for unplanned readmission using hierarchical ICD data. <i>Computer Methods and Programs in Biomedicine</i> , 2019, 173, 177-183.	4.7	18
29	DeepRibo: a neural network for precise gene annotation of prokaryotes by combining ribosome profiling signal and binding site patterns. <i>Nucleic Acids Research</i> , 2019, 47, e36-e36.	14.5	58
30	Multi-target prediction: a unifying view on problems and methods. <i>Data Mining and Knowledge Discovery</i> , 2019, 33, 293-324.	3.7	55
31	Randomized Lasso Links Microbial Taxa with Aquatic Functional Groups Inferred from Flow Cytometry. <i>MSystems</i> , 2019, 4, .	3.8	14
32	Global hydro-climatic biomes identified via multitask learning. <i>Geoscientific Model Development</i> , 2018, 11, 4139-4153.	3.6	14
33	Terrestrial evaporation response to modes of climate variability. <i>Npj Climate and Atmospheric Science</i> , 2018, 1, .	6.8	49
34	Algebraic shortcuts for leave-one-out cross-validation in supervised network inference. <i>Briefings in Bioinformatics</i> , 2018, , .	6.5	8
35	Label-free Raman characterization of bacteria calls for standardized procedures. <i>Journal of Microbiological Methods</i> , 2018, 151, 69-75.	1.6	38
36	Detection of microbial disturbances in a drinking water microbial community through continuous acquisition and advanced analysis of flow cytometry data. <i>Water Research</i> , 2018, 145, 73-82.	11.3	29

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37	A Comparative Study of Pairwise Learning Methods Based on Kernel Ridge Regression. <i>Neural Computation</i> , 2018, 30, 2245-2283.	2.2	19
38	Effects of chlorhexidine gluconate oral care on hospital mortality: a hospital-wide, observational cohort study. <i>Intensive Care Medicine</i> , 2018, 44, 1017-1026.	8.2	102
39	Interpretation and visualisation of data from dairy herds. <i>In Practice</i> , 2018, 40, 195-203.	0.2	5
40	Novel approaches to assess the quality of fertility data stored in dairy herd management software. <i>Journal of Dairy Science</i> , 2017, 100, 4078-4089.	3.4	9
41	Linear filtering reveals false negatives in species interaction data. <i>Scientific Reports</i> , 2017, 7, 45908.	3.3	18
42	Stripping flow cytometry: How many detectors do we need for bacterial identification?. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2017, 91, 1184-1191.	1.5	17
43	Potentials and Limitations of Existing Forecasting Models for <i>Alternaria</i> on Potatoes: Challenges for Model Improvement. <i>Potato Research</i> , 2017, 60, 61-76.	2.7	6
44	Absolute quantification of microbial taxon abundances. <i>ISME Journal</i> , 2017, 11, 584-587.	9.8	273
45	A non-linear data-driven approach to reveal global vegetation sensitivity to climate. , 2017, , .		2
46	A non-linear Granger-causality framework to investigate climate-vegetation dynamics. <i>Geoscientific Model Development</i> , 2017, 10, 1945-1960.	3.6	110
47	Flow Cytometric Single-Cell Identification of Populations in Synthetic Bacterial Communities. <i>PLoS ONE</i> , 2017, 12, e0169754.	2.5	31
48	miSTAR: miRNA target prediction through modeling quantitative and qualitative miRNA binding site information in a stacked model structure. <i>Nucleic Acids Research</i> , 2016, 45, gkw1260.	14.5	18
49	Exact and efficient top-K inference for multi-target prediction by querying separable linear relational models. <i>Data Mining and Knowledge Discovery</i> , 2016, 30, 1370-1394.	3.7	1
50	Data-driven recipe completion using machine learning methods. <i>Trends in Food Science and Technology</i> , 2016, 49, 1-13.	15.1	18
51	Consistency of Probabilistic Classifier Trees. <i>Lecture Notes in Computer Science</i> , 2016, , 511-526.	1.3	7
52	Prediction of subacute ruminal acidosis based on milk fatty acids: A comparison of linear discriminant and support vector machine approaches for model development. <i>Computers and Electronics in Agriculture</i> , 2015, 111, 179-185.	7.7	19
53	Identification of Functionally Related Enzymes by Learning-to-Rank Methods. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 1157-1169.	3.0	4
54	Predicting spatio-temporal <i>Culicoides imicola</i> distributions in Spain based on environmental habitat characteristics and species dispersal. <i>Ecological Informatics</i> , 2014, 22, 69-80.	5.2	7

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55	A Two-Step Learning Approach for Solving Full and Almost Full Cold Start Problems in Dyadic Prediction. Lecture Notes in Computer Science, 2014, , 517-532.	1.3	12
56	Efficient regularized least-squares algorithms for conditional ranking on relational data. Machine Learning, 2013, 93, 321-356.	5.4	27
57	A field-specific web tool for the prediction of Fusarium head blight and deoxynivalenol content in Belgium. Computers and Electronics in Agriculture, 2013, 93, 140-148.	7.7	27
58	Erratum to "The logistic curve as a tool to describe the daily ruminal pH pattern and its link with milk fatty acids" (J. Dairy Sci. 95:5845-5865). Journal of Dairy Science, 2013, 96, 1323.	3.4	0
59	Combined exposure to cyanobacteria and carbaryl results in antagonistic effects on the reproduction of daphnia pulex. Environmental Toxicology and Chemistry, 2013, 32, 2153-2158.	4.3	14
60	Exploration and prediction of interactions between methanotrophs and heterotrophs. Research in Microbiology, 2013, 164, 1045-1054.	2.1	57
61	Habitat prediction and knowledge extraction for spawning European grayling ( <i>Thymallus thymallus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlacc 47, 1-6.	4.5	111
62	Influence of maize-wheat rotation systems on Fusarium head blight infection and deoxynivalenol content in wheat under low versus high disease pressure. Crop Protection, 2013, 52, 14-21.	2.1	36
63	Ordinal regression models for predicting deoxynivalenol in winter wheat. Plant Pathology, 2013, 62, 1319-1329.	2.4	22
64	A Kernel-Based Framework for Learning Graded Relations From Data. IEEE Transactions on Fuzzy Systems, 2012, 20, 1090-1101.	9.8	16
65	The logistic curve as a tool to describe the daily ruminal pH pattern and its link with milk fatty acids. Journal of Dairy Science, 2012, 95, 5845-5865.	3.4	19
66	Toward a Reliable Evaluation of Forecasting Systems for Plant Diseases: A Case Study Using Fusarium Head Blight of Wheat. Plant Disease, 2012, 96, 889-896.	1.4	23
67	On label dependence and loss minimization in multi-label classification. Machine Learning, 2012, 88, 5-45.	5.4	215
68	Learning partial ordinal class memberships with kernel-based proportional odds models. Computational Statistics and Data Analysis, 2012, 56, 928-942.	1.2	27
69	ERA ranking representability: The missing link between ordinal regression and multi-class classification. , 2011, , .		0
70	A discussion on the accuracy-complexity relationship in modelling fish habitat preference using genetic Takagi-Sugeno fuzzy systems. , 2011, , .		1
71	Connection between primary Fusarium inoculum on gramineous weeds, crop residues and soil samples and the final population on wheat ears in Flanders, Belgium. Crop Protection, 2011, 30, 1297-1305.	2.1	48
72	Bacterial species identification from MALDI-TOF mass spectra through data analysis and machine learning. Systematic and Applied Microbiology, 2011, 34, 20-29.	2.8	181

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73	Effect of model formulation on the optimization of a genetic Takagi-Sugeno fuzzy system for fish habitat suitability evaluation. <i>Ecological Modelling</i> , 2011, 222, 1401-1413.	2.5	52
74	Supervised learning algorithms for multi-class classification problems with partial class memberships. <i>Fuzzy Sets and Systems</i> , 2011, 184, 106-125.	2.7	15
75	On the ERA ranking representability of pairwise bipartite ranking functions. <i>Artificial Intelligence</i> , 2011, 175, 1223-1250.	5.8	10
76	An experimental comparison of cross-validation techniques for estimating the area under the ROC curve. <i>Computational Statistics and Data Analysis</i> , 2011, 55, 1828-1844.	1.2	116
77	From learning taxonomies to phylogenetic learning: Integration of 16S rRNA gene data into FAME-based bacterial classification. <i>BMC Bioinformatics</i> , 2010, 11, 69.	2.6	15
78	Learning intransitive reciprocal relations with kernel methods. <i>European Journal of Operational Research</i> , 2010, 206, 676-685.	5.7	28
79	A transitivity analysis of bipartite rankings in pairwise multi-class classification. <i>Information Sciences</i> , 2010, 180, 4099-4117.	6.9	10
80	On the role of cost-sensitive learning in multi-class brain-computer interfaces. <i>Biomedizinische Technik</i> , 2010, 55, 163-172.	0.8	2
81	Regret Analysis for Performance Metrics in Multi-Label Classification: The Case of Hamming and Subset Zero-One Loss. <i>Lecture Notes in Computer Science</i> , 2010, , 280-295.	1.3	24
82	Conditional Ranking on Relational Data. <i>Lecture Notes in Computer Science</i> , 2010, , 499-514.	1.3	10
83	A Survey on ROC-based Ordinal Regression. , 2010, , 127-154.		3
84	Kernel-based learning methods for preference aggregation. <i>4or</i> , 2009, 7, 169-189.	1.6	22
85	Learning to rank: a ROC-based graph-theoretic approach. <i>4or</i> , 2009, 7, 399-402.	1.6	1
86	ROC analysis in ordinal regression learning. <i>Pattern Recognition Letters</i> , 2008, 29, 1-9.	4.2	94
87	Learning layered ranking functions with structured support vector machines. <i>Neural Networks</i> , 2008, 21, 1511-1523.	5.9	12
88	On the scalability of ordered multi-class ROC analysis. <i>Computational Statistics and Data Analysis</i> , 2008, 52, 3371-3388.	1.2	26
89	Classifying carpets based on laser scanner data. <i>Engineering Applications of Artificial Intelligence</i> , 2008, 21, 907-918.	8.1	12