

# Willem Waegeman

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

88  
papers

1,832  
citations

22  
h-index

40  
g-index

98  
ext. papers

2,440  
ext. citations

5.6  
avg, IF

5.56  
L-index

#	Paper	IF	Citations
88	Multi-target prediction for dummies using two-branch neural networks. <i>Machine Learning</i> , <b>2022</b> , 111, 651	4	0
87	Bacterial species identification using MALDI-TOF mass spectrometry and machine learning techniques: A large-scale benchmarking study.. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 6157-6168	6.8	1
86	Improving the performance of machine learning models for biotechnology: The quest for deus ex machina. <i>Biotechnology Advances</i> , <b>2021</b> , 53, 107858	17.8	0
85	Aleatoric and epistemic uncertainty in machine learning: an introduction to concepts and methods. <i>Machine Learning</i> , <b>2021</b> , 110, 457-506	4	98
84	Ambient temperature and relative humidityBased drift correction in frequency domain electromagnetics using machine learning. <i>Near Surface Geophysics</i> , <b>2021</b> , 19, 541-556	1.6	2
83	Explainability in transformer models for functional genomics. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	6
82	Efficient set-valued prediction in multi-class classification. <i>Data Mining and Knowledge Discovery</i> , <b>2021</b> , 35, 1435	5.6	3
81	High-Resolution Surveying With Small-Loop Frequency Domain Electromagnetic Systems: Efficient Survey Design and Adaptive Processing. <i>IEEE Geoscience and Remote Sensing Magazine</i> , <b>2021</b> , 9, 167-183	8.9	2
80	Cytometric fingerprints of gut microbiota predict Crohn's disease state. <i>ISME Journal</i> , <b>2021</b> , 15, 354-358	11.9	6
79	PhenoGMM: Gaussian Mixture Modeling of Cytometry Data Quantifies Changes in Microbial Community Structure. <i>MSphere</i> , <b>2021</b> , 6,	5	6
78	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> , <b>2021</b> , 103117	3.1	2
77	Pressure injury prediction models for critically-ill patients should consider both the case-mix and local factors. <i>Intensive and Critical Care Nursing</i> , <b>2021</b> , 65, 103033	3.1	4
76	Predicting the Presence and Abundance of Bacterial Taxa in Environmental Communities through Flow Cytometric Fingerprinting. <i>MSystems</i> , <b>2021</b> , 6, e0055121	7.6	1
75	Using structured pathology data to predict hospital-wide mortality at admission. <i>PLoS ONE</i> , <b>2020</b> , 15, e0235117	3.7	4
74	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> , <b>2020</b> , 92, 7523-7531	7.8	16
73	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> , <b>2020</b> , 97, 713-726	4.6	9
72	Predictive design of sigma factor-specific promoters. <i>Nature Communications</i> , <b>2020</b> , 11, 5822	17.4	12

71	Novel transformer networks for improved sequence labeling in genomics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2020</b> , PP,	3	3
70	Using structured pathology data to predict hospital-wide mortality at admission <b>2020</b> , 15, e0235117		
69	Using structured pathology data to predict hospital-wide mortality at admission <b>2020</b> , 15, e0235117		
68	Using structured pathology data to predict hospital-wide mortality at admission <b>2020</b> , 15, e0235117		
67	Using structured pathology data to predict hospital-wide mortality at admission <b>2020</b> , 15, e0235117		
66	A protocol for automated timber species identification using metabolome profiling. <i>Wood Science and Technology</i> , <b>2019</b> , 53, 953-965	2.5	10
65	Learning Single-Cell Distances from Cytometry Data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , <b>2019</b> , 95, 782-791	4.6	3
64	Coculturing Bacteria Leads to Reduced Phenotypic Heterogeneities. <i>Applied and Environmental Microbiology</i> , <b>2019</b> , 85,	4.8	22
63	A hospital wide predictive model for unplanned readmission using hierarchical ICD data. <i>Computer Methods and Programs in Biomedicine</i> , <b>2019</b> , 173, 177-183	6.9	13
62	Randomized Lasso Links Microbial Taxa with Aquatic Functional Groups Inferred from Flow Cytometry. <i>MSystems</i> , <b>2019</b> , 4,	7.6	10
61	DeepRibo: a neural network for precise gene annotation of prokaryotes by combining ribosome profiling signal and binding site patterns. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, e36	20.1	30
60	Multi-target prediction: a unifying view on problems and methods. <i>Data Mining and Knowledge Discovery</i> , <b>2019</b> , 33, 293-324	5.6	33
59	Detection of microbial disturbances in a drinking water microbial community through continuous acquisition and advanced analysis of flow cytometry data. <i>Water Research</i> , <b>2018</b> , 145, 73-82	12.5	18
58	A Comparative Study of Pairwise Learning Methods Based on Kernel Ridge Regression. <i>Neural Computation</i> , <b>2018</b> , 30, 2245-2283	2.9	12
57	Effects of chlorhexidine gluconate oral care on hospital mortality: a hospital-wide, observational cohort study. <i>Intensive Care Medicine</i> , <b>2018</b> , 44, 1017-1026	14.5	57
56	Interpretation and visualisation of data from dairy herds. <i>In Practice</i> , <b>2018</b> , 40, 195-203	0.3	3
55	Global hydro-climatic biomes identified via multitask learning. <i>Geoscientific Model Development</i> , <b>2018</b> , 11, 4139-4153	6.3	10
54	Terrestrial evaporation response to modes of climate variability. <i>Npj Climate and Atmospheric Science</i> , <b>2018</b> , 1,	8	30

53	Algebraic shortcuts for leave-one-out cross-validation in supervised network inference. <i>Briefings in Bioinformatics</i> , <b>2018</b> ,	13.4	5
52	Label-free Raman characterization of bacteria calls for standardized procedures. <i>Journal of Microbiological Methods</i> , <b>2018</b> , 151, 69-75	2.8	24
51	Novel approaches to assess the quality of fertility data stored in dairy herd management software. <i>Journal of Dairy Science</i> , <b>2017</b> , 100, 4078-4089	4	7
50	Linear filtering reveals false negatives in species interaction data. <i>Scientific Reports</i> , <b>2017</b> , 7, 45908	4.9	13
49	A non-linear Granger-causality framework to investigate climate-vegetation dynamics. <i>Geoscientific Model Development</i> , <b>2017</b> , 10, 1945-1960	6.3	56
48	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> , <b>2017</b> , 91, 1184-1191	4.6	10
47	Potentials and Limitations of Existing Forecasting Models for Alternaria on Potatoes: Challenges for Model Improvement. <i>Potato Research</i> , <b>2017</b> , 60, 61-76	3.2	4
46	Absolute quantification of microbial taxon abundances. <i>ISME Journal</i> , <b>2017</b> , 11, 584-587	11.9	169
45	A non-linear data-driven approach to reveal global vegetation sensitivity to climate <b>2017</b> ,		2
44	Flow Cytometric Single-Cell Identification of Populations in Synthetic Bacterial Communities. <i>PLoS ONE</i> , <b>2017</b> , 12, e0169754	3.7	24
43	miSTAR: miRNA target prediction through modeling quantitative and qualitative miRNA binding site information in a stacked model structure. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e51	20.1	12
42	Data-driven recipe completion using machine learning methods. <i>Trends in Food Science and Technology</i> , <b>2016</b> , 49, 1-13	15.3	11
41	Consistency of Probabilistic Classifier Trees. <i>Lecture Notes in Computer Science</i> , <b>2016</b> , 511-526	0.9	7
40	Exact and efficient top-K inference for multi-target prediction by querying separable linear relational models. <i>Data Mining and Knowledge Discovery</i> , <b>2016</b> , 30, 1370-1394	5.6	1
39	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> , <b>2015</b> , 111, 179-185	6.5	12
38	Predicting spatio-temporal <i>Culicoides imicola</i> distributions in Spain based on environmental habitat characteristics and species dispersal. <i>Ecological Informatics</i> , <b>2014</b> , 22, 69-80	4.2	7
37	Identification of Functionally Related Enzymes by Learning-to-Rank Methods. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2014</b> , 11, 1157-69	3	4
36	A Two-Step Learning Approach for Solving Full and Almost Full Cold Start Problems in Dyadic Prediction. <i>Lecture Notes in Computer Science</i> , <b>2014</b> , 517-532	0.9	11

35	Efficient regularized least-squares algorithms for conditional ranking on relational data. <i>Machine Learning</i> , <b>2013</b> , 93, 321-356	4	24
34	A field-specific web tool for the prediction of Fusarium head blight and deoxynivalenol content in Belgium. <i>Computers and Electronics in Agriculture</i> , <b>2013</b> , 93, 140-148	6.5	20
33	Combined exposure to cyanobacteria and carbaryl results in antagonistic effects on the reproduction of <i>Daphnia pulex</i> . <i>Environmental Toxicology and Chemistry</i> , <b>2013</b> , 32, 2153-8	3.8	14
32	Exploration and prediction of interactions between methanotrophs and heterotrophs. <i>Research in Microbiology</i> , <b>2013</b> , 164, 1045-54	4	44
31	Habitat prediction and knowledge extraction for spawning European grayling ( <i>Thymallus thymallus</i> L.) using a broad range of species distribution models. <i>Environmental Modelling and Software</i> , <b>2013</b> , 47, 1-6	5.2	91
30	Influence of maize-wheat rotation systems on Fusarium head blight infection and deoxynivalenol content in wheat under low versus high disease pressure. <i>Crop Protection</i> , <b>2013</b> , 52, 14-21	2.7	27
29	Ordinal regression models for predicting deoxynivalenol in winter wheat. <i>Plant Pathology</i> , <b>2013</b> , 62, 1319-8	3.29	20
28	Learning partial ordinal class memberships with kernel-based proportional odds models. <i>Computational Statistics and Data Analysis</i> , <b>2012</b> , 56, 928-942	1.6	18
27	A Kernel-Based Framework for Learning Graded Relations From Data. <i>IEEE Transactions on Fuzzy Systems</i> , <b>2012</b> , 20, 1090-1101	8.3	15
26	The logistic curve as a tool to describe the daily ruminal pH pattern and its link with milk fatty acids. <i>Journal of Dairy Science</i> , <b>2012</b> , 95, 5845-65	4	15
25	Toward a Reliable Evaluation of Forecasting Systems for Plant Diseases: A Case Study Using Fusarium Head Blight of Wheat. <i>Plant Disease</i> , <b>2012</b> , 96, 889-896	1.5	22
24	On label dependence and loss minimization in multi-label classification. <i>Machine Learning</i> , <b>2012</b> , 88, 5-454		184
23	Connection between primary Fusarium inoculum on gramineous weeds, crop residues and soil samples and the final population on wheat ears in Flanders, Belgium. <i>Crop Protection</i> , <b>2011</b> , 30, 1297-1305	2.7	37
22	Bacterial species identification from MALDI-TOF mass spectra through data analysis and machine learning. <i>Systematic and Applied Microbiology</i> , <b>2011</b> , 34, 20-9	4.2	139
21	Effect of model formulation on the optimization of a genetic Takagi-Sugeno fuzzy system for fish habitat suitability evaluation. <i>Ecological Modelling</i> , <b>2011</b> , 222, 1401-1413	3	42
20	Supervised learning algorithms for multi-class classification problems with partial class memberships. <i>Fuzzy Sets and Systems</i> , <b>2011</b> , 184, 106-125	3.7	11
19	A discussion on the accuracy-complexity relationship in modelling fish habitat preference using genetic Takagi-Sugeno fuzzy systems <b>2011</b> ,		1
18	On the ERA ranking representability of pairwise bipartite ranking functions. <i>Artificial Intelligence</i> , <b>2011</b> , 175, 1223-1250	3.6	7

17	An experimental comparison of cross-validation techniques for estimating the area under the ROC curve. <i>Computational Statistics and Data Analysis</i> , <b>2011</b> , 55, 1828-1844	1.6	80
16	On the role of cost-sensitive learning in multi-class brain-computer interfaces. <i>Biomedizinische Technik</i> , <b>2010</b> , 55, 163-72	1.3	2
15	From learning taxonomies to phylogenetic learning: integration of 16S rRNA gene data into FAME-based bacterial classification. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 69	3.6	15
14	Learning intransitive reciprocal relations with kernel methods. <i>European Journal of Operational Research</i> , <b>2010</b> , 206, 676-685	5.6	26
13	A transitivity analysis of bipartite rankings in pairwise multi-class classification. <i>Information Sciences</i> , <b>2010</b> , 180, 4099-4117	7.7	10
12	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> , <b>2010</b> , 280-295	0.9	13
11	Conditional Ranking on Relational Data. <i>Lecture Notes in Computer Science</i> , <b>2010</b> , 499-514	0.9	10
10	A Survey on ROC-based Ordinal Regression <b>2010</b> , 127-154		1
9	Kernel-based learning methods for preference aggregation. <i>4or</i> , <b>2009</b> , 7, 169-189	1.4	19
8	Learning to rank: a ROC-based graph-theoretic approach. <i>4or</i> , <b>2009</b> , 7, 399-402	1.4	
7	ROC analysis in ordinal regression learning. <i>Pattern Recognition Letters</i> , <b>2008</b> , 29, 1-9	4.7	77
6	Learning layered ranking functions with structured support vector machines. <i>Neural Networks</i> , <b>2008</b> , 21, 1511-23	9.1	12
5	On the scalability of ordered multi-class ROC analysis. <i>Computational Statistics and Data Analysis</i> , <b>2008</b> , 52, 3371-3388	1.6	19
4	Classifying carpets based on laser scanner data. <i>Engineering Applications of Artificial Intelligence</i> , <b>2008</b> , 21, 907-918	7.2	9
3	PhenoGMM: Gaussian mixture modelling of microbial cytometry data enables efficient predictions of biodiversity		1
2	Novel transformer networks for improved sequence labeling in genomics		2
1	Valid prediction intervals for regression problems. <i>Artificial Intelligence Review</i> , 1	9.7	0