Anne-Laure Boulesteix

List of Publications by Year in descending order

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130 papers

12,005 citations

47006 47 h-index 29157 104 g-index

144 all docs

144 docs citations

times ranked

144

17391 citing authors

#	Article	IF	CITATIONS
1	Over-optimistic evaluation and reporting of novel cluster algorithms: an illustrative study. Advances in Data Analysis and Classification, 2023, 17, 211-238.	1.4	4
2	COMPANION: development of a patient-centred complexity and casemix classification for adult palliative care patients based on needs and resource use $\hat{a} \in \hat{a}$ a protocol for a cross-sectional multi-centre study. BMC Palliative Care, 2022, 21, 18.	1.8	3
3	Interaction forests: Identifying and exploiting interpretable quantitative and qualitative interaction effects. Computational Statistics and Data Analysis, 2022, 171, 107460.	1.2	7
4	Overâ€optimism in benchmark studies and the multiplicity of design and analysis options when interpreting their results. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2022, 12, .	6.8	9
5	Validation of cluster analysis results on validation data: A systematic framework. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2022, 12, .	6.8	29
6	Critical appraisal of artificial intelligence-based prediction models for cardiovascular disease. European Heart Journal, 2022, 43, 2921-2930.	2.2	50
7	Outcome of patients treated with extracorporeal life support in cardiogenic shock complicating acute myocardial infarction: 1-year result from the ECLS-Shock study. Clinical Research in Cardiology, 2021, 110, 1412-1420.	3.3	24
8	NetCoMi: network construction and comparison for microbiome data in R. Briefings in Bioinformatics, 2021, 22, .	6.5	222
9	Examining the robustness of observational associations to model, measurement and sampling uncertainty with the vibration of effects framework. International Journal of Epidemiology, 2021, 50, 266-278.	1.9	18
10	Improved Outcome Prediction Across Data Sources Through Robust Parameter Tuning. Journal of Classification, 2021, 38, 212-231.	2.2	5
11	Large-scale benchmark study of survival prediction methods using multi-omics data. Briefings in Bioinformatics, 2021, 22, .	6.5	53
12	The multiplicity of analysis strategies jeopardizes replicability: lessons learned across disciplines. Royal Society Open Science, 2021, 8, 201925.	2.4	29
13	On the optimistic performance evaluation of newly introduced bioinformatic methods. Genome Biology, 2021, 22, 152.	8.8	20
14	Sampling uncertainty versus method uncertainty: A general framework with applications to omics biomarker selection. Biometrical Journal, 2020, 62, 670-687.	1.0	12
15	Statistical learning approaches in the genetic epidemiology of complex diseases. Human Genetics, 2020, 139, 73-84.	3.8	14
16	Combining clinical and molecular data in regression prediction models: insights from a simulation study. Briefings in Bioinformatics, 2020, 21, 1904-1919.	6.5	11
17	A Replication Crisis in Methodological Research?. Significance, 2020, 17, 18-21.	0.4	21
18	Introduction to statistical simulations in health research. BMJ Open, 2020, 10, e039921.	1.9	24

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19	Single-center versus multi-center data sets for molecular prognostic modeling: a simulation study. Radiation Oncology, 2020, 15, 109.	2.7	3
20	On the asymptotic behaviour of the variance estimator of a <mml:math altimg="si7.svg" display="inline" id="d1e208" xmlns:mml="http://www.w3.org/1998/Math/MathML"><mml:mi>U</mml:mi></mml:math> -statistic. Journal of Statistical Planning and Inference, 2020, 209, 101-111.	0.6	3
21	Use of Resampling Procedures to Investigate Issues of Model Building and Its Stability. , 2020, , 1-24.		1
22	Modelling Individual Response to Treatment and Its Uncertainty:A Review of Statistical Methods and Challenges for Future Research. Boston Studies in the Philosophy and History of Science, 2020, , 319-344.	0.9	0
23	Making complex prediction rules applicable for readers: Current practice in random forest literature and recommendations. Biometrical Journal, 2019, 61, 1314-1328.	1.0	13
24	A plea for taking all available clinical information into account when assessing the predictive value of omics data. BMC Medical Research Methodology, 2019, 19, 162.	3.1	10
25	Essential guidelines for computational method benchmarking. Genome Biology, 2019, 20, 125.	8.8	114
26	Extracorporeal Life Support in Cardiogenic Shock Complicating Acute Myocardial Infarction. Journal of the American College of Cardiology, 2019, 73, 2355-2357.	2.8	79
27	Immune function testing in sepsis patients receiving sodium selenite. Journal of Critical Care, 2019, 52, 208-212.	2.2	5
28	Hyperparameters and tuning strategies for random forest. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2019, 9, e1301.	6.8	651
29	Independent validation of a new reirradiation risk score (RRRS) for glioma patients predicting post-recurrence survival: A multicenter DKTK/ROG analysis. Radiotherapy and Oncology, 2018, 127, 121-127.	0.6	37
30	On the choice and influence of the number of boosting steps for high-dimensional linear Cox-models. Computational Statistics, 2018, 33, 1195-1215.	1.5	20
31	Guest Editorialâ€"Special Collection Topic: Statistical Systems Theory in Cancer Modeling, Diagnosis, and Therapy. Cancer Informatics, 2018, 17, 117693511876094.	1.9	O
32	A computationally fast variable importance test for random forests for high-dimensional data. Advances in Data Analysis and Classification, 2018, 12, 885-915.	1.4	115
33	On the necessity and design of studies comparing statistical methods. Biometrical Journal, 2018, 60, 216-218.	1.0	66
34	Critical review of reporting of the data analysis step in metabolomics. Metabolomics, 2018, 14, 7.	3.0	52
35	Priority-Lasso: a simple hierarchical approach to the prediction of clinical outcome using multi-omics data. BMC Bioinformatics, 2018, 19, 322.	2.6	33
36	OC-0588: Validation of the reRT risk score (RRRS) in glioma patients: A multicenter DKTK/ROG analysis. Radiotherapy and Oncology, 2018, 127, S307-S308.	0.6	0

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37	Mediation analysis reveals common mechanisms of RUNX1 point mutations and RUNX1/RUNX1T1 fusions influencing survival of patients with acute myeloid leukemia. Scientific Reports, 2018, 8, 11293.	3.3	9
38	Random forest versus logistic regression: a large-scale benchmark experiment. BMC Bioinformatics, 2018, 19, 270.	2.6	446
39	Effects of the Cardio First AngelTM on chest compression performance. Technology and Health Care, 2018, 26, 69-80.	1.2	6
40	A computationally fast variable importance test for random forests for high-dimensional data. Advances in Data Analysis and Classification, 2018, 12, 885.	1.4	14
41	Improving cross-study prediction through addon batch effect adjustment or addon normalization. Bioinformatics, 2017, 33, 397-404.	4.1	18
42	Detection of influential points as a byproduct of resampling-based variable selection procedures. Computational Statistics and Data Analysis, 2017, 116, 19-31.	1.2	4
43	iPF-LASSO: integrative		

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55	Improved prediction of complex diseases by common genetic markers: state of the art and further perspectives. Human Genetics, 2016, 135, 259-272.	3.8	37
56	Random forest for ordinal responses: Prediction and variable selection. Computational Statistics and Data Analysis, 2016, 96, 57-73.	1.2	125
57	Which Resampling-Based Error Estimator for Benchmark Studies? A Power Analysis with Application to PLS-LDA. Springer Proceedings in Mathematics and Statistics, 2016, , 45-57.	0.2	1
58	Exhaled breath volatile organic and inorganic compound composition in end-stage renal disease. Clinical Nephrology, 2016, 86, 132-140.	0.7	9
59	Publication Bias in Methodological Computational Research. Cancer Informatics, 2015, 14s5, CIN.S30747.	1.9	15
60	Live music reduces stress levels in very lowâ€birthweight infants. Acta Paediatrica, International Journal of Paediatrics, 2015, 104, 360-367.	1.5	36
61	A measure of the impact of CV incompleteness on prediction error estimation with application to PCA and normalization. BMC Medical Research Methodology, 2015, 15, 95.	3.1	15
62	Gender mismatch in allograft aortic valve surgery. Interactive Cardiovascular and Thoracic Surgery, 2015, 21, 329-335.	1.1	2
63	Ten Simple Rules for Reducing Overoptimistic Reporting in Methodological Computational Research. PLoS Computational Biology, 2015, 11, e1004191.	3.2	43
64	Letter to the Editor: On the term 'interaction' and related phrases in the literature on Random Forests. Briefings in Bioinformatics, 2015, 16, 338-345.	6.5	48
65	Letter to the Editor: On Reviews and Papers on New Methods. Briefings in Bioinformatics, 2015, 16, 365-366.	6.5	O
66	A Statistical Framework for Hypothesis Testing in Real Data Comparison Studies. American Statistician, 2015, 69, 201-212.	1.6	29
67	On stability issues in deriving multivariable regression models. Biometrical Journal, 2015, 57, 531-555.	1.0	43
68	Investigating the prediction ability of survival models based on both clinical and omics data: two case studies. Statistics in Medicine, 2014, 33, 5310-5329.	1.6	36
69	Added predictive value of omics data: specific issues related to validation illustrated by two case studies. BMC Medical Research Methodology, 2014, 14, 117.	3.1	6
70	Cross-study validation for the assessment of prediction algorithms. Bioinformatics, 2014, 30, i105-i112.	4.1	75
71	Machine learning versus statistical modeling. Biometrical Journal, 2014, 56, 588-593.	1.0	65
72	An AUC-based permutation variable importance measure for random forests. BMC Bioinformatics, 2013, 14, 119.	2.6	179

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73	Correcting the Optimal Resamplingâ€Based Error Rate by Estimating the Error Rate of Wrapper Algorithms. Biometrics, 2013, 69, 693-702.	1.4	18
74	Molecular Differences between Chronic and Aggressive Periodontitis. Journal of Dental Research, 2013, 92, 1081-1088.	5.2	77
7 5	Homografts in aortic position: does blood group incompatibility have an impact on patient outcomes?â€. Interactive Cardiovascular and Thoracic Surgery, 2013, 16, 619-624.	1.1	4
76	On representative and illustrative comparisons with real data in bioinformatics: response to the letter to the editor by Smith $\langle i \rangle$ et al. $\langle i \rangle$. Bioinformatics, 2013, 29, 2664-2666.	4.1	22
77	What is the "normal―fetal heart rate?. PeerJ, 2013, 1, e82.	2.0	112
78	Application of Microarray Analysis on Computer Cluster and Cloud Platforms. Methods of Information in Medicine, 2013, 52, 65-71.	1.2	3
79	A Plea for Neutral Comparison Studies in Computational Sciences. PLoS ONE, 2013, 8, e61562.	2.5	86
80	Complexity Selection with Cross-validation for Lasso and Sparse Partial Least Squares Using High-Dimensional Data. Studies in Classification, Data Analysis, and Knowledge Organization, 2013, , 261-268.	0.2	7
81	Iterative Reconstruction of High-Dimensional Gaussian Graphical Models Based on a New Method to Estimate Partial Correlations under Constraints. PLoS ONE, 2013, 8, e60536.	2.5	1
82	Random forest Gini importance favours SNPs with large minor allele frequency: impact, sources and recommendations. Briefings in Bioinformatics, 2012, 13, 292-304.	6. 5	92
83	Breath isoprene concentrations in persons undergoing general anesthesia and in healthy volunteers. Journal of Breath Research, 2012, 6, 046004.	3.0	13
84	Overview of random forest methodology and practical guidance with emphasis on computational biology and bioinformatics. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2012, 2, 493-507.	6.8	516
85	An eight-gene expression signature for the prediction of survival and time to treatment in chronic lymphocytic leukemia. Leukemia, 2011, 25, 1639-1645.	7.2	59
86	AUC-RF: A New Strategy for Genomic Profiling with Random Forest. Human Heredity, 2011, 72, 121-132.	0.8	122
87	Inhibition of radiation induced migration of human head and neck squamous cell carcinoma cells by blocking of EGF receptor pathways. BMC Cancer, 2011, 11, 388.	2.6	50
88	Use of pretransformation to cope with extreme values in important candidate features. Biometrical Journal, 2011, 53, 673-688.	1.0	3
89	Stability Investigations of Multivariable Regression Models Derived from Low- and High-Dimensional Data. Journal of Biopharmaceutical Statistics, 2011, 21, 1206-1231.	0.8	104
90	Editorial. Briefings in Bioinformatics, 2011, 12, 187-188.	6.5	3

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91	Added predictive value of high-throughput molecular data to clinical data and its validation. Briefings in Bioinformatics, 2011, 12, 215-229.	6.5	46
92	Differential expression of the chemokines GRO-2, GRO-3, and interleukin-8 in colon cancer and their impact on metastatic disease and survival. International Journal of Colorectal Disease, 2010, 25, 573-581.	2.2	98
93	Testing the additional predictive value of high-dimensional molecular data. BMC Bioinformatics, 2010, 11, 78.	2.6	31
94	Mid-term outcomes of patients with PCI prior to CABG in comparison to patients with primary CABG. Vascular Health and Risk Management, 2010, 6, 495.	2.3	18
95	Over-optimism in bioinformatics: an illustration. Bioinformatics, 2010, 26, 1990-1998.	4.1	90
96	Over-optimism in bioinformatics research. Bioinformatics, 2010, 26, 437-439.	4.1	110
97	Centrosome abnormalities in head and neck squamous cell carcinoma (HNSCC). Acta Oto-Laryngologica, 2009, 129, 205-213.	0.9	12
98	Stability and aggregation of ranked gene lists. Briefings in Bioinformatics, 2009, 10, 556-568.	6.5	138
99	Regularized estimation of large-scale gene association networks using graphical Gaussian models. BMC Bioinformatics, 2009, 10, 384.	2.6	169
100	Optimal classifier selection and negative bias in error rate estimation: an empirical study on high-dimensional prediction. BMC Medical Research Methodology, 2009, 9, 85.	3.1	56
101	Survival prediction using gene expression data: A review and comparison. Computational Statistics and Data Analysis, 2009, 53, 1590-1603.	1.2	98
102	Comments on: Augmenting the bootstrap to analyze high dimensional genomic data. Test, 2008, 17, 31-35.	1.1	3
103	Time and rate of sinus formation in pilonidal sinus disease. International Journal of Colorectal Disease, 2008, 23, 359-364.	2.2	83
104	Methylene Blue halves the long-term recurrence rate in acute pilonidal sinus disease. International Journal of Colorectal Disease, 2008, 23, 181-187.	2.2	59
105	Penalized Partial Least Squares with applications to B-spline transformations and functional data. Chemometrics and Intelligent Laboratory Systems, 2008, 94, 60-69.	3.5	55
106	Conditional variable importance for random forests. BMC Bioinformatics, 2008, 9, 307.	2.6	2,129
107	CMA \hat{a} e" a comprehensive Bioconductor package for supervised classification with high dimensional data. BMC Bioinformatics, 2008, 9, 439.	2.6	84
108	Influence of diatoms on copepod reproduction. II. Uncorrelated effects of diatom-derived $\hat{l}\pm,\hat{l}^2,\hat{l}^3,\hat{l}$ -unsaturated aldehydes and polyunsaturated fatty acids on Calanus helgolandicus in the field. Progress in Oceanography, 2008, 77, 30-44.	3.2	48

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109	Microarray-Based Prediction of Tumor Response to Neoadjuvant Radiochemotherapy of Patients With Locally Advanced Rectal Cancer. Clinical Gastroenterology and Hepatology, 2008, 6, 53-61.	4.4	128
110	Microarray-based classification and clinical predictors: on combined classifiers and additional predictive value. Bioinformatics, 2008, 24, 1698-1706.	4.1	76
111	Evaluating Microarray-based Classifiers: An Overview. Cancer Informatics, 2008, 6, CIN.S408.	1.9	70
112	Effects of Aprotinin Dosage on Renal Function. Anesthesiology, 2008, 108, 189-198.	2.5	31
113	WilcoxCV: an R package for fast variable selection in cross-validation. Bioinformatics, 2007, 23, 1702-1704.	4.1	18
114	Methylation of Tumor-Related Genes in Neoadjuvant-Treated Gastric Cancer: Relation to Therapy Response and Clinicopathologic and Molecular Features. Clinical Cancer Research, 2007, 13, 5095-5102.	7.0	35
115	Aprotinin and Anaphylaxis: Analysis of 12,403 Exposures to Aprotinin in Cardiac Surgery. Annals of Thoracic Surgery, 2007, 84, 1144-1150.	1.3	65
116	Multiple Testing for SNP-SNP Interactions. Statistical Applications in Genetics and Molecular Biology, 2007, 6, Article37.	0.6	15
117	The Normal Fetal Heart Rate Study: Analysis Plan. Nature Precedings, 2007, , .	0.1	2
118	The Normal Fetal Heart Rate Study: Analysis Plan. Nature Precedings, 2007, , .	0.1	1
119	Unbiased split selection for classification trees based on the Gini Index. Computational Statistics and Data Analysis, 2007, 52, 483-501.	1.2	201
120	Maximally selected Chi-squared statistics and non-monotonic associations: An exact approach based on two cutpoints. Computational Statistics and Data Analysis, 2007, 51, 6295-6306.	1.2	12
121	Bias in random forest variable importance measures: Illustrations, sources and a solution. BMC Bioinformatics, 2007, 8, 25.	2.6	2,328
122	Identification of interaction patterns and classification with applications to microarray data. Computational Statistics and Data Analysis, 2006, 50, 783-802.	1.2	11
123	Maximally Selected Chi-square Statistics for Ordinal Variables. Biometrical Journal, 2006, 48, 451-462.	1.0	25
124	Maximally Selected Chi-Square Statistics and Binary Splits of Nominal Variables. Biometrical Journal, 2006, 48, 838-848.	1.0	20
125	Reader's Reaction to "Dimension Reduction for Classification with Gene Expression Microarray Data" by Dai et al (2006). Statistical Applications in Genetics and Molecular Biology, 2006, 5, Article16.	0.6	9
126	Partial least squares: a versatile tool for the analysis of high-dimensional genomic data. Briefings in Bioinformatics, 2006, 8, 32-44.	6.5	611

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127	Predicting transcription factor activities from combined analysis of microarray and ChIP data: a partial least squares approach. Theoretical Biology and Medical Modelling, 2005, 2, 23.	2.1	98
128	La gen \tilde{A}^3 mica funcional: herramientas para mejorar la sanidad y el bienestar del ganado. OIE Revue Scientifique Et Technique, 2005, 24, 355-377.	1.2	12
129	PLS Dimension Reduction for Classification with Microarray Data. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-30.	0.6	160
130	A CART-based approach to discover emerging patterns in microarray data. Bioinformatics, 2003, 19, 2465-2472.	4.1	74