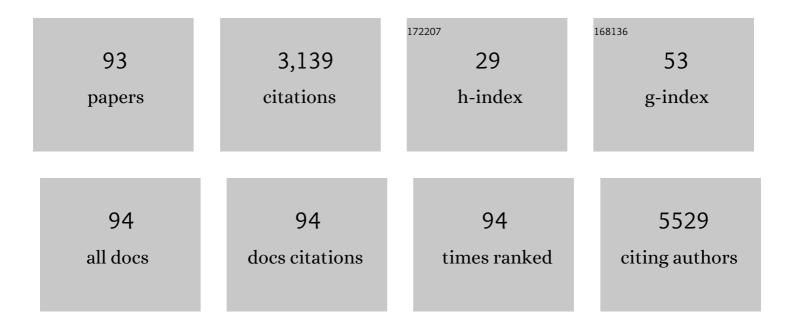
Wessel N Van Wieringen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4837746/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Sequential Learning of Regression Models by Penalized Estimation. Journal of Computational and Graphical Statistics, 2022, 31, 877-886.	0.9	3
2	Mechanical stress regulates bone regulatory gene expression independent of estrogen and vitamin D deficiency in rats. Journal of Orthopaedic Research, 2021, 39, 42-52.	1.2	9
3	C1 Inhibitor Administration Reduces Local Inflammation and Capillary Leakage, Without Affecting Long-term Wound Healing Parameters, in a Pig Burn Wound Model. Anti-Inflammatory and Anti-Allergy Agents in Medicinal Chemistry, 2021, 20, 150-160.	1.1	3
4	A parallel algorithm for ridge-penalized estimation of the multivariate exponential family from data of mixed types. Statistics and Computing, 2021, 31, 1.	0.8	0
5	Penalized estimation of the Gaussian graphical model from data with replicates. Statistics in Medicine, 2021, 40, 4279-4293.	0.8	5
6	NOX2 Expression Is Increased in Keratinocytes After Burn Injury. Journal of Burn Care and Research, 2020, 41, 427-432.	0.2	4
7	The spectral condition number plot for regularization parameter evaluation. Computational Statistics, 2020, 35, 629-646.	0.8	3
8	Analysis of Twitter data with the Bayesian fused graphical lasso. PLoS ONE, 2020, 15, e0235596.	1.1	1
9	A cancer drug atlas enables synergistic targeting of independent drug vulnerabilities. Nature Communications, 2020, 11, 2935.	5.8	57
10	ldentification of Deregulated Pathways, Key Regulators, and Novel miRNA-mRNA Interactions in HPV-Mediated Transformation. Cancers, 2020, 12, 700.	1.7	20
11	Updating of the Gaussian graphical model through targeted penalized estimation. Journal of Multivariate Analysis, 2020, 178, 104621.	0.5	4
12	Ridge estimation of network models from time ourse omics data. Biometrical Journal, 2019, 61, 391-405.	0.6	1
13	Plasma proteome in multiple sclerosis disease progression. Annals of Clinical and Translational Neurology, 2019, 6, 1582-1594.	1.7	21
14	Diagnostic Value of Cerebrospinal Fluid Neurofilament Light Protein in Neurology. JAMA Neurology, 2019, 76, 1035.	4.5	455
15	The Generalized Ridge Estimator of the Inverse Covariance Matrix. Journal of Computational and Graphical Statistics, 2019, 28, 932-942.	0.9	11
16	Shortâ€ŧerm LPS induces aortic valve thickening in ApoE*3Leiden mice. European Journal of Clinical Investigation, 2019, 49, e13121.	1.7	7
17	Reconstruction of molecular network evolution from crossâ€sectional omics data. Biometrical Journal, 2018, 60, 547-563.	0.6	3
18	Testing for Pathway (in)Activation by Using Gaussian Graphical Models. Journal of the Royal Statistical Society Series C: Applied Statistics, 2018, 67, 1419-1436.	0.5	5

#	Article	IF	CITATIONS
19	No Plasmatic Proteomic Signature at Clinical Disease Onset Associated With 11 Year Clinical, Cognitive and MRI Outcomes in Relapsing-Remitting Multiple Sclerosis Patients. Frontiers in Molecular Neuroscience, 2018, 11, 371.	1.4	3
20	A test for detecting differential indirect trans effects between two groups of samples. Statistical Applications in Genetics and Molecular Biology, 2018, 17, .	0.2	0
21	Rscreenorm: normalization of CRISPR and siRNA screen data for more reproducible hit selection. BMC Bioinformatics, 2018, 19, 301.	1.2	12
22	On the mean squared error of the ridge estimator of the covariance and precision matrix. Statistics and Probability Letters, 2017, 123, 88-92.	0.4	6
23	4H Leukodystrophy: A Brain Magnetic Resonance Imaging Scoring System. Neuropediatrics, 2017, 48, 152-160.	0.3	20
24	An empirical Bayes approach to network recovery using external knowledge. Biometrical Journal, 2017, 59, 932-947.	0.6	5
25	Gene network reconstruction using global-local shrinkage priors. Annals of Applied Statistics, 2017, 11, 41-68.	0.5	20
26	The Local and Systemic Inflammatory Response in a Pig Burn Wound Model With a Pivotal Role for Complement. Journal of Burn Care and Research, 2017, 38, e796-e806.	0.2	18
27	Cytotoxic Effects of the Therapeutic Radionuclide Rhenium-188 Combined with Taxanes in Human Prostate Carcinoma Cell Lines. Cancer Biotherapy and Radiopharmaceuticals, 2017, 32, 16-23.	0.7	6
28	Ridge estimation of the VAR(1) model and its time series chain graph from multivariate timeâ€course omics data. Biometrical Journal, 2017, 59, 172-191.	0.6	6
29	Prognostic modeling of oral cancer by gene profiles and clinicopathological co-variables. Oncotarget, 2017, 8, 59312-59323.	0.8	22
30	Distinguishing Three Unprofessional Behavior Profiles of Medical Students Using Latent Class Analysis. Academic Medicine, 2016, 91, 1276-1283.	0.8	26
31	Ridge estimation of inverse covariance matrices from high-dimensional data. Computational Statistics and Data Analysis, 2016, 103, 284-303.	0.7	58
32	Quantitative MRI in hypomyelinating disorders. Neurology, 2016, 87, 752-758.	1.5	16
33	Better prediction by use of coâ€data: adaptive groupâ€regularized ridge regression. Statistics in Medicine, 2016, 35, 368-381.	0.8	78
34	Aberrant methylation-mediated silencing of microRNAs contributes to HPV-induced anchorage independence. Oncotarget, 2016, 7, 43805-43819.	0.8	22
35	Transcriptomic Heterogeneity in Cancer as a Consequence of Dysregulation of the Gene–Gene Interaction Network. Bulletin of Mathematical Biology, 2015, 77, 1768-1786.	0.9	4
36	Application of a New Ridge Estimator of the Inverse Covariance Matrix to the Reconstruction of Gene-Gene Interaction Networks. Lecture Notes in Computer Science, 2015, , 170-179.	1.0	2

Wessel N Van Wieringen

#	Article	IF	CITATIONS
37	tigaR: integrative significance analysis of temporal differential gene expression induced by genomic abnormalities. BMC Bioinformatics, 2014, 15, 327.	1.2	2
38	A test for comparing two groups of samples when analyzing multiple omics profiles. BMC Bioinformatics, 2014, 15, 236.	1.2	19
39	Leukoencephalopathy with brainstem and spinal cord involvement and lactate elevation: clinical and genetic characterization and target for therapy. Brain, 2014, 137, 1019-1029.	3.7	82
40	Penalized differential pathway analysis of integrative oncogenomics studies. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 141-58.	0.2	2
41	Bayesian analysis of RNA sequencing data by estimating multiple shrinkage priors. Biostatistics, 2013, 14, 113-128.	0.9	116
42	CD98 marks a subpopulation of head and neck squamous cell carcinoma cells with stem cell properties. Stem Cell Research, 2013, 10, 477-488.	0.3	49
43	Expression signature in peripheral blood cells for molecular diagnosis of head and neck squamous cell carcinoma. Oral Diseases, 2013, 19, 452-455.	1.5	7
44	Identification of Lethal microRNAs Specific for Head and Neck Cancer. Clinical Cancer Research, 2013, 19, 5647-5657.	3.2	16
45	Modeling the DNA copy number aberration patterns in observational high-throughput cancer data. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 143-74.	0.2	0
46	Altered microRNA expression associated with chromosomal changes contributes to cervical carcinogenesis. Oncogene, 2013, 32, 106-116.	2.6	145
47	Modeling association between DNA copy number and gene expression with constrained piecewise linear regression splines. Annals of Applied Statistics, 2013, 7, .	0.5	8
48	Small bowel adenocarcinoma copy number profiles are more closely related to colorectal than to gastric cancers. Annals of Oncology, 2012, 23, 367-374.	0.6	38
49	Losses of Chromosome 5q and 14q Are Associated with Favorable Clinical Outcome of Patients with Gastric Cancer. Oncologist, 2012, 17, 653-662.	1.9	27
50	Restricted Diffusion in Vanishing White Matter. Archives of Neurology, 2012, 69, 723-7.	4.9	18
51	Matching of array CGH and gene expression microarray features for the purpose of integrative genomic analyses. BMC Bioinformatics, 2012, 13, 80.	1.2	14
52	Chromosomal profiles of highâ€grade cervical intraepithelial neoplasia relate to duration of preceding highâ€risk human papillomavirus infection. International Journal of Cancer, 2012, 131, E579-85.	2.3	37
53	Genomic aberrations relate early and advanced stage ovarian cancer. Cellular Oncology (Dordrecht), 2012, 35, 181-188.	2.1	7
54	HPV type-related chromosomal profiles in high-grade cervical intraepithelial neoplasia. BMC Cancer, 2012, 12, 36.	1.1	10

Wessel N Van Wieringen

#	Article	IF	CITATIONS
55	Leucoencephalopathy with brainstem and spinal cord involvement and high lactate: quantitative magnetic resonance imaging. Brain, 2011, 134, 3333-3341.	3.7	26
56	Measurement System Analysis for Binary Inspection: Continuous Versus Dichotomous Measurands. Journal of Quality Technology, 2011, 43, 99-112.	1.8	18
57	Statistical analysis of the cancer cell's molecular entropy using high-throughput data. Bioinformatics, 2011, 27, 556-563.	1.8	42
58	Preprocessing and downstream analysis of microarray DNA copy number profiles. Briefings in Bioinformatics, 2011, 12, 10-21.	3.2	48
59	To DNA or not to DNA? That Is the Question, When It Comes to Molecular Subtyping for the Clinic!. Clinical Cancer Research, 2011, 17, 4959-4964.	3.2	21
60	Exploratory Factor Analysis of Pathway Copy Number Data with an Application Towards the Integration with Gene Expression Data. Journal of Computational Biology, 2011, 18, 729-741.	0.8	3
61	Dithiocarbamates Induce Craniofacial Abnormalities and Downregulate sox9a during Zebrafish Development. Toxicological Sciences, 2010, 117, 209-217.	1.4	42
62	A Random Coefficients Model for Regional Co-Expression Associated with DNA Copy Number. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article25.	0.2	8
63	Genotype–phenotype correlation in vanishing white matter disease. Neurology, 2010, 75, 1555-1559.	1.5	56
64	Magnetic resonance imaging pattern recognition in hypomyelinating disorders. Brain, 2010, 133, 2971-2982.	3.7	247
65	Modeling and Evaluating Repeatability and Reproducibility of Ordinal Classifications. Technometrics, 2010, 52, 94-106.	1.3	26
66	Testing the prediction error difference between 2 predictors. Biostatistics, 2009, 10, 550-560.	0.9	52
67	Chromosomal Signatures of a Subset of High-Grade Premalignant Cervical Lesions Closely Resemble Invasive Carcinomas. Cancer Research, 2009, 69, 647-655.	0.4	53
68	Copy number gain at 8q12.1â€q22.1 is associated with a malignant tumor phenotype in salivary gland myoepitheliomas. Genes Chromosomes and Cancer, 2009, 48, 202-212.	1.5	15
69	Identification of genes putatively involved in the pathogenesis of diffuse large Bâ€cell lymphomas by integrative genomics. Genes Chromosomes and Cancer, 2009, 48, 250-260.	1.5	9
70	Risk modelling of outcome after general and trauma surgery (the IRIS score). British Journal of Surgery, 2009, 97, 128-133.	0.1	10
71	Genomic profiling identifies common HPV-associated chromosomal alterations in squamous cell carcinomas of cervix and head and neck. BMC Medical Genomics, 2009, 2, 32.	0.7	56
72	Nonparametric Testing for DNA Copy Number Induced Differential mRNA Gene Expression. Biometrics, 2009, 65, 19-29.	0.8	43

WESSEL N VAN WIERINGEN

#	Article	IF	CITATIONS
73	Survival prediction using gene expression data: A review and comparison. Computational Statistics and Data Analysis, 2009, 53, 1590-1603.	0.7	98
74	Genetic Classification of Oral and Oropharyngeal Carcinomas Identifies Subgroups with a Different Prognosis. Analytical Cellular Pathology, 2009, 31, 291-300.	0.7	5
75	Genetic classification of oral and oropharyngeal carcinomas identifies subgroups with a different prognosis. Cellular Oncology, 2009, 31, 291-300.	1.9	42
76	Flow cytometric lymphocyte subset enumeration: 10 years of external quality assessment in the Benelux countries. Cytometry Part B - Clinical Cytometry, 2008, 74B, 79-90.	0.7	31
77	Integrated genomic and transcriptional profiling identifies chromosomal loci with altered gene expression in cervical cancer. Genes Chromosomes and Cancer, 2008, 47, 890-905.	1.5	59
78	Measurement System Analysis for Binary Data. Technometrics, 2008, 50, 468-478.	1.3	31
79	A Test for Partial Differential Expression. Journal of the American Statistical Association, 2008, 103, 1039-1049.	1.8	19
80	Weighted clustering of called array CGH data. Biostatistics, 2008, 9, 484-500.	0.9	52
81	CGHcall: calling aberrations for array CGH tumor profiles. Bioinformatics, 2007, 23, 892-894.	1.8	208
82	Measurement System Analysis for Categorical Measurements: Agreement and Kappa-Type Indices. Journal of Quality Technology, 2007, 39, 191-202.	1.8	28
83	CGHregions: Dimension Reduction for Array CGH Data with Minimal Information Loss. Cancer Informatics, 2007, 3, 117693510700300.	0.9	42
84	Normalized, Segmented or Called aCGH Data?. Cancer Informatics, 2007, 3, 117693510700300.	0.9	12
85	Flow cytometric CD34+ stem cell enumeration: Lessons from nine years' external quality assessment within the Benelux countries. Cytometry Part B - Clinical Cytometry, 2007, 72B, 178-188.	0.7	32
86	Normalized, segmented or called aCGH data?. Cancer Informatics, 2007, 3, 321-7.	0.9	6
87	CGHregions: dimension reduction for array CGH data with minimal information loss. Cancer Informatics, 2007, 3, 55-63.	0.9	46
88	Temperature data analysis for 22 patients with advanced cervical carcinoma treated in Rotterdam using radiotherapy, hyperthermia and chemotherapy: A reference point is needed. International Journal of Hyperthermia, 2006, 22, 353-363.	1.1	30
89	Intra-luminal thermometry: Is tissue type assignment a necessity for thermal analysis?. International Journal of Hyperthermia, 2006, 22, 463-473.	1.1	4
90	ACE-it: a tool for genome-wide integration of gene dosage and RNA expression data. Bioinformatics, 2006, 22, 1919-1920.	1.8	29

#	Article	IF	CITATIONS
91	A Comparison of Methods for the Evaluation of Binary Measurement Systems. Quality Engineering, 2005, 17, 495-507.	0.7	30
92	On identifiability of certain latent class models. Statistics and Probability Letters, 2005, 75, 211-218.	0.4	8
93	Measurement System Analysis for Bounded Ordinal Data. Quality and Reliability Engineering International, 2004, 20, 383-395.	1.4	19