Wessel N Van Wieringen

List of Publications by Year in descending order

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93 papers 3,139 citations

172207 29 h-index 53 g-index

94 all docs 94 docs citations

94 times ranked 5529 citing authors

#	Article	IF	CITATIONS
1	Diagnostic Value of Cerebrospinal Fluid Neurofilament Light Protein in Neurology. JAMA Neurology, 2019, 76, 1035.	4.5	455
2	Magnetic resonance imaging pattern recognition in hypomyelinating disorders. Brain, 2010, 133, 2971-2982.	3.7	247
3	CGHcall: calling aberrations for array CGH tumor profiles. Bioinformatics, 2007, 23, 892-894.	1.8	208
4	Altered microRNA expression associated with chromosomal changes contributes to cervical carcinogenesis. Oncogene, 2013, 32, 106-116.	2.6	145
5	Bayesian analysis of RNA sequencing data by estimating multiple shrinkage priors. Biostatistics, 2013, 14, 113-128.	0.9	116
6	Survival prediction using gene expression data: A review and comparison. Computational Statistics and Data Analysis, 2009, 53, 1590-1603.	0.7	98
7	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
8	Better prediction by use of coâ€data: adaptive groupâ€regularized ridge regression. Statistics in Medicine, 2016, 35, 368-381.	0.8	78
9	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
10	Ridge estimation of inverse covariance matrices from high-dimensional data. Computational Statistics and Data Analysis, 2016, 103, 284-303.	0.7	58
11	A cancer drug atlas enables synergistic targeting of independent drug vulnerabilities. Nature Communications, 2020, 11 , 2935.	5.8	57
12	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
13	Genotype–phenotype correlation in vanishing white matter disease. Neurology, 2010, 75, 1555-1559.	1.5	56
14	Chromosomal Signatures of a Subset of High-Grade Premalignant Cervical Lesions Closely Resemble Invasive Carcinomas. Cancer Research, 2009, 69, 647-655.	0.4	53
15	Weighted clustering of called array CGH data. Biostatistics, 2008, 9, 484-500.	0.9	52
16	Testing the prediction error difference between 2 predictors. Biostatistics, 2009, 10, 550-560.	0.9	52
17	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
18	Preprocessing and downstream analysis of microarray DNA copy number profiles. Briefings in Bioinformatics, 2011, 12, 10-21.	3.2	48

#	Article	IF	Citations
19	CGHregions: dimension reduction for array CGH data with minimal information loss. Cancer Informatics, 2007, 3, 55-63.	0.9	46
20	Nonparametric Testing for DNA Copy Number Induced Differential mRNA Gene Expression. Biometrics, 2009, 65, 19-29.	0.8	43
21	CGHregions: Dimension Reduction for Array CGH Data with Minimal Information Loss. Cancer Informatics, 2007, 3, 117693510700300.	0.9	42
22	Dithiocarbamates Induce Craniofacial Abnormalities and Downregulate sox9a during Zebrafish Development. Toxicological Sciences, 2010, 117, 209-217.	1.4	42
23	Statistical analysis of the cancer cell's molecular entropy using high-throughput data. Bioinformatics, 2011, 27, 556-563.	1.8	42
24	Genetic classification of oral and oropharyngeal carcinomas identifies subgroups with a different prognosis. Cellular Oncology, 2009, 31, 291-300.	1.9	42
25	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
26	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
27	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
28	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
29	Measurement System Analysis for Binary Data. Technometrics, 2008, 50, 468-478.	1.3	31
30	A Comparison of Methods for the Evaluation of Binary Measurement Systems. Quality Engineering, 2005, 17, 495-507.	0.7	30
31	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
32	ACE-it: a tool for genome-wide integration of gene dosage and RNA expression data. Bioinformatics, 2006, 22, 1919-1920.	1.8	29
33	Measurement System Analysis for Categorical Measurements: Agreement and Kappa-Type Indices. Journal of Quality Technology, 2007, 39, 191-202.	1.8	28
34	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
35	Modeling and Evaluating Repeatability and Reproducibility of Ordinal Classifications. Technometrics, 2010, 52, 94-106.	1.3	26
36	Leucoencephalopathy with brainstem and spinal cord involvement and high lactate: quantitative magnetic resonance imaging. Brain, 2011, 134, 3333-3341.	3.7	26

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37	Distinguishing Three Unprofessional Behavior Profiles of Medical Students Using Latent Class Analysis. Academic Medicine, 2016, 91, 1276-1283.	0.8	26
38	Prognostic modeling of oral cancer by gene profiles and clinicopathological co-variables. Oncotarget, 2017, 8, 59312-59323.	0.8	22
39	Aberrant methylation-mediated silencing of microRNAs contributes to HPV-induced anchorage independence. Oncotarget, 2016, 7, 43805-43819.	0.8	22
40	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
41	Plasma proteome in multiple sclerosis disease progression. Annals of Clinical and Translational Neurology, 2019, 6, 1582-1594.	1.7	21
42	4H Leukodystrophy: A Brain Magnetic Resonance Imaging Scoring System. Neuropediatrics, 2017, 48, 152-160.	0.3	20
43	Gene network reconstruction using global-local shrinkage priors. Annals of Applied Statistics, 2017, 11, 41-68.	0.5	20
44	Identification of Deregulated Pathways, Key Regulators, and Novel miRNA-mRNA Interactions in HPV-Mediated Transformation. Cancers, 2020, 12, 700.	1.7	20
45	Measurement System Analysis for Bounded Ordinal Data. Quality and Reliability Engineering International, 2004, 20, 383-395.	1.4	19
46	A Test for Partial Differential Expression. Journal of the American Statistical Association, 2008, 103, 1039-1049.	1.8	19
47	A test for comparing two groups of samples when analyzing multiple omics profiles. BMC Bioinformatics, 2014, 15, 236.	1.2	19
48	Measurement System Analysis for Binary Inspection: Continuous Versus Dichotomous Measurands. Journal of Quality Technology, 2011, 43, 99-112.	1.8	18
49	Restricted Diffusion in Vanishing White Matter. Archives of Neurology, 2012, 69, 723-7.	4.9	18
50	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
51	Identification of Lethal microRNAs Specific for Head and Neck Cancer. Clinical Cancer Research, 2013, 19, 5647-5657.	3.2	16
52	Quantitative MRI in hypomyelinating disorders. Neurology, 2016, 87, 752-758.	1.5	16
53	Copy number gain at $8q12.1\hat{a} \in q22.1$ is associated with a malignant tumor phenotype in salivary gland myoepitheliomas. Genes Chromosomes and Cancer, 2009, 48, 202-212.	1.5	15
54	Matching of array CGH and gene expression microarray features for the purpose of integrative genomic analyses. BMC Bioinformatics, 2012, 13, 80.	1.2	14

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55	Normalized, Segmented or Called aCGH Data?. Cancer Informatics, 2007, 3, 117693510700300.	0.9	12
56	Rscreenorm: normalization of CRISPR and siRNA screen data for more reproducible hit selection. BMC Bioinformatics, 2018, 19, 301.	1.2	12
57	The Generalized Ridge Estimator of the Inverse Covariance Matrix. Journal of Computational and Graphical Statistics, 2019, 28, 932-942.	0.9	11
58	Risk modelling of outcome after general and trauma surgery (the IRIS score). British Journal of Surgery, 2009, 97, 128-133.	0.1	10
59	HPV type-related chromosomal profiles in high-grade cervical intraepithelial neoplasia. BMC Cancer, 2012, 12, 36.	1.1	10
60	Identification of genes putatively involved in the pathogenesis of diffuse large B ell lymphomas by integrative genomics. Genes Chromosomes and Cancer, 2009, 48, 250-260.	1.5	9
61	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
62	On identifiability of certain latent class models. Statistics and Probability Letters, 2005, 75, 211-218.	0.4	8
63	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
64	Modeling association between DNA copy number and gene expression with constrained piecewise linear regression splines. Annals of Applied Statistics, $2013, 7, \ldots$	0.5	8
65	Genomic aberrations relate early and advanced stage ovarian cancer. Cellular Oncology (Dordrecht), 2012, 35, 181-188.	2.1	7
66	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
67	Shortâ€term LPS induces aortic valve thickening in ApoE*3Leiden mice. European Journal of Clinical Investigation, 2019, 49, e13121.	1.7	7
68	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
69	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
70	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
71	Normalized, segmented or called aCGH data?. Cancer Informatics, 2007, 3, 321-7.	0.9	6
72	An empirical Bayes approach to network recovery using external knowledge. Biometrical Journal, 2017, 59, 932-947.	0.6	5

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73	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
74	Penalized estimation of the Gaussian graphical model from data with replicates. Statistics in Medicine, 2021, 40, 4279-4293.	0.8	5
7 5	Genetic Classification of Oral and Oropharyngeal Carcinomas Identifies Subgroups with a Different Prognosis. Analytical Cellular Pathology, 2009, 31, 291-300.	0.7	5
76	Intra-luminal thermometry: Is tissue type assignment a necessity for thermal analysis?. International Journal of Hyperthermia, 2006, 22, 463-473.	1.1	4
77	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
78	NOX2 Expression Is Increased in Keratinocytes After Burn Injury. Journal of Burn Care and Research, 2020, 41, 427-432.	0.2	4
79	Updating of the Gaussian graphical model through targeted penalized estimation. Journal of Multivariate Analysis, 2020, 178, 104621.	0.5	4
80	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
81	Reconstruction of molecular network evolution from crossâ€sectional omics data. Biometrical Journal, 2018, 60, 547-563.	0.6	3
82	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
83	The spectral condition number plot for regularization parameter evaluation. Computational Statistics, 2020, 35, 629-646.	0.8	3
84	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
85	Sequential Learning of Regression Models by Penalized Estimation. Journal of Computational and Graphical Statistics, 2022, 31, 877-886.	0.9	3
86	tigaR: integrative significance analysis of temporal differential gene expression induced by genomic abnormalities. BMC Bioinformatics, 2014, 15, 327.	1.2	2
87	Penalized differential pathway analysis of integrative oncogenomics studies. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 141-58.	0.2	2
88	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
89	Ridge estimation of network models from timeâ€course omics data. Biometrical Journal, 2019, 61, 391-405.	0.6	1
90	Analysis of Twitter data with the Bayesian fused graphical lasso. PLoS ONE, 2020, 15, e0235596.	1.1	1

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91	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	O
92	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
93	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	O