

Karsten M Borgwardt

List of Publications by Year in descending order

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Version: 2024-02-01

86
papers

8,758
citations

147566
31
h-index

91712
69
g-index

104
all docs

104
docs citations

104
times ranked

11483
citing authors

#	ARTICLE	IF	CITATIONS
1	Direct antimicrobial resistance prediction from clinical MALDI-TOF mass spectra using machine learning. <i>Nature Medicine</i> , 2022, 28, 164-174.	15.2	66
2	Determinants of SARS-CoV-2 transmission to guide vaccination strategy in an urban area. <i>Virus Evolution</i> , 2022, 8, veac002.	2.2	7
3	Prediction of recovery from multiple organ dysfunction syndrome in pediatric sepsis patients. <i>Bioinformatics</i> , 2022, 38, i101-i108.	1.8	5
4	Network-guided search for genetic heterogeneity between gene pairs. <i>Bioinformatics</i> , 2021, 37, 57-65.	1.8	9
5	Biological network analysis with deep learning. <i>Briefings in Bioinformatics</i> , 2021, 22, 1515-1530.	3.2	98
6	Using routine MRI data of depressed patients to predict individual responses to electroconvulsive therapy. <i>Experimental Neurology</i> , 2021, 335, 113505.	2.0	10
7	Accelerating Detection of Lung Pathologies with Explainable Ultrasound Image Analysis. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 672.	1.3	96
8	Ethnicity-based bias in clinical severity scores. <i>The Lancet Digital Health</i> , 2021, 3, e209-e210.	5.9	3
9	Early Prediction of Sepsis in the ICU Using Machine Learning: A Systematic Review. <i>Frontiers in Medicine</i> , 2021, 8, 607952.	1.2	62
10	RNA atlas of human bacterial pathogens uncovers stress dynamics linked to infection. <i>Nature Communications</i> , 2021, 12, 3282.	5.8	33
11	Machine Learning for Biomedical Time Series Classification: From Shapelets to Deep Learning. <i>Methods in Molecular Biology</i> , 2021, 2190, 33-71.	0.4	14
12	AraPheno and the AraGWAS Catalog 2020: a major database update including RNA-Seq and knockout mutation data for <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2020, 48, D1063-D1068.	6.5	44
13	Kernel conditional clustering and kernel conditional semi-supervised learning. <i>Knowledge and Information Systems</i> , 2020, 62, 899-925.	2.1	2
14	Large-scale DNA-based phenotypic recording and deep learning enable highly accurate sequence-function mapping. <i>Nature Communications</i> , 2020, 11, 3551.	5.8	36
15	Topological and kernel-based microbial phenotype prediction from MALDI-TOF mass spectra. <i>Bioinformatics</i> , 2020, 36, i30-i38.	1.8	15
16	Prediction of cancer driver genes through network-based moment propagation of mutation scores. <i>Bioinformatics</i> , 2020, 36, i508-i515.	1.8	19
17	Comorbidities, clinical signs and symptoms, laboratory findings, imaging features, treatment strategies, and outcomes in adult and pediatric patients with COVID-19: A systematic review and meta-analysis. <i>Travel Medicine and Infectious Disease</i> , 2020, 37, 101825.	1.5	118
18	Early prediction of circulatory failure in the intensive care unit using machine learning. <i>Nature Medicine</i> , 2020, 26, 364-373.	15.2	204

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19	Enhancing statistical power in temporal biomarker discovery through representative shapelet mining. <i>Bioinformatics</i> , 2020, 36, i840-i848.	1.8	2
20	Graph Kernels: State-of-the-Art and Future Challenges. <i>Foundations and Trends in Machine Learning</i> , 2020, 13, 531-712.	46.6	27
21	SPHN/PHRT: Forming a Swiss-Wide Infrastructure for Data-Driven Sepsis Research. <i>Studies in Health Technology and Informatics</i> , 2020, 270, 1163-1167.	0.2	3
22	Introduction to the special issue for the ECML PKDD 2019 journal track. <i>Machine Learning</i> , 2019, 108, 1191-1192.	3.4	0
23	Introduction to the special issue for the ECML PKDD 2019 journal track. <i>Data Mining and Knowledge Discovery</i> , 2019, 33, 1223-1224.	2.4	0
24	CASMAP: detection of statistically significant combinations of SNPs in association mapping. <i>Bioinformatics</i> , 2019, 35, 2680-2682.	1.8	8
25	Pretransplant Kinetics of Anti-HLA Antibodies in Patients on the Waiting List for Kidney Transplantation. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 2262-2274.	3.0	11
26	The AraGWAS Catalog: a curated and standardized <i>Arabidopsis thaliana</i> GWAS catalog. <i>Nucleic Acids Research</i> , 2018, 46, D1150-D1156.	6.5	83
27	Multi-target drug repositioning by bipartite block-wise sparse multi-task learning. <i>BMC Systems Biology</i> , 2018, 12, 55.	3.0	8
28	Kernelized rank learning for personalized drug recommendation. <i>Bioinformatics</i> , 2018, 34, 2808-2816.	1.8	44
29	graphkernels: R and Python packages for graph comparison. <i>Bioinformatics</i> , 2018, 34, 530-532.	1.8	26
30	Methods and Tools in Genome-wide Association Studies. <i>Methods in Molecular Biology</i> , 2018, 1819, 93-136.	0.4	11
31	Accurate and adaptive imputation of summary statistics in mixed-ethnicity cohorts. <i>Bioinformatics</i> , 2018, 34, i687-i696.	1.8	6
32	Aberrant working memory processing in major depression: evidence from multivoxel pattern classification. <i>Neuropsychopharmacology</i> , 2018, 43, 1972-1979.	2.8	29
33	Association mapping in biomedical time series via statistically significant shapelet mining. <i>Bioinformatics</i> , 2018, 34, i438-i446.	1.8	17
34	Genome-wide genetic heterogeneity discovery with categorical covariates. <i>Bioinformatics</i> , 2017, 33, 1820-1828.	1.8	15
35	AraPheno: a public database for <i>Arabidopsis thaliana</i> phenotypes. <i>Nucleic Acids Research</i> , 2017, 45, D1054-D1059.	6.5	91
36	easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies. <i>Plant Cell</i> , 2017, 29, 5-19.	3.1	98

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37	Multi-view Spectral Clustering on Conflicting Views. Lecture Notes in Computer Science, 2017, , 826-842.	1.0	5
38	Kernel Conditional Clustering. , 2017, , .		1
39	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. Cell, 2016, 166, 492-505.	13.5	594
40	Genetic architecture of nonadditive inheritance in Arabidopsis thaliana hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7317-E7326.	3.3	58
41	1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. Cell, 2016, 166, 481-491.	13.5	1,107
42	Genomic Profiles of Diversification and Genotype-Phenotype Association in Island Nematode Lineages. Molecular Biology and Evolution, 2016, 33, 2257-2272.	3.5	31
43	Significant Subgraph Mining with Multiple Testing Correction. , 2015, , .		22
44	Fast and Memory-Efficient Significant Pattern Mining via Permutation Testing. , 2015, , .		35
45	The Evaluation of Tools Used to Predict the Impact of Missense Variants Is Hindered by Two Types of Circularity. Human Mutation, 2015, 36, 513-523.	1.1	283
46	Genome-wide detection of intervals of genetic heterogeneity associated with complex traits. Bioinformatics, 2015, 31, i240-i249.	1.8	23
47	In silico phenotyping via co-training for improved phenotype prediction from genotype. Bioinformatics, 2015, 31, i303-i310.	1.8	9
48	Century-scale Methylome Stability in a Recently Diverged Arabidopsis thaliana Lineage. PLoS Genetics, 2015, 11, e1004920.	1.5	148
49	Multi-Task Feature Selection on Multiple Networks via Maximum Flows. , 2014, , .		7
50	Accurate indel prediction using paired-end short reads. BMC Genomics, 2013, 14, 132.	1.2	30
51	A Lasso multi-marker mixed model for association mapping with population structure correction. Bioinformatics, 2013, 29, 206-214.	1.8	99
52	Efficient network-guided multi-locus association mapping with graph cuts. Bioinformatics, 2013, 29, i171-i179.	1.8	52
53	Accurate detection of differential RNA processing. Nucleic Acids Research, 2013, 41, 5189-5198.	6.5	39
54	Detecting regulatory gene-environment interactions with unmeasured environmental factors. Bioinformatics, 2013, 29, 1382-1389.	1.8	12

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55	ShapePheno: unsupervised extraction of shape phenotypes from biological image collections. <i>Bioinformatics</i> , 2012, 28, 1001-1008.	1.8	4
56	GLIDE: GPU-Based Linear Regression for Detection of Epistasis. <i>Human Heredity</i> , 2012, 73, 220-236.	0.4	32
57	<i>Arabidopsis</i> Defense against <i>Botrytis cinerea</i> : Chronology and Regulation Deciphered by High-Resolution Temporal Transcriptomic Analysis. <i>Plant Cell</i> , 2012, 24, 3530-3557.	3.1	337
58	Spontaneous epigenetic variation in the <i>Arabidopsis thaliana</i> methylome. <i>Nature</i> , 2011, 480, 245-249.	13.7	681
59	Whole-genome sequencing of multiple <i>Arabidopsis thaliana</i> populations. <i>Nature Genetics</i> , 2011, 43, 956-963.	9.4	910
60	Kernel Methods in <i>Bioinformatics</i> . , 2011, , 317-334.		17
61	EPIBLASTER-fast exhaustive two-locus epistasis detection strategy using graphical processing units. <i>European Journal of Human Genetics</i> , 2011, 19, 465-471.	1.4	74
62	Guest editorial to the special issue on inductive logic programming, mining and learning in graphs and statistical relational learning. <i>Machine Learning</i> , 2011, 83, 133-135.	3.4	1
63	Two-locus association mapping in subquadratic time. , 2011, , .		8
64	Epistasis detection on quantitative phenotypes by exhaustive enumeration using GPUs. <i>Bioinformatics</i> , 2011, 27, i214-i221.	1.8	19
65	Statistical Tests for Detecting Differential RNA-Transcript Expression from Read Counts. <i>Nature Precedings</i> , 2010, , .	0.1	13
66	Spatio-Spectral Remote Sensing Image Classification With Graph Kernels. <i>IEEE Geoscience and Remote Sensing Letters</i> , 2010, 7, 741-745.	1.4	116
67	Discriminative frequent subgraph mining with optimality guarantees. <i>Statistical Analysis and Data Mining</i> , 2010, 3, 302-318.	1.4	32
68	Gene function prediction from synthetic lethality networks via ranking on demand. <i>Bioinformatics</i> , 2010, 26, 912-918.	1.8	23
69	A Robust Bayesian Two-Sample Test for Detecting Intervals of Differential Gene Expression in Microarray Time Series. <i>Journal of Computational Biology</i> , 2010, 17, 355-367.	0.8	84
70	Graph Mining on Brain Co-activation Networks. <i>Science, Engineering, and Biology Informatics</i> , 2010, , 279-293.	0.1	0
71	Near-optimal supervised feature selection among frequent subgraphs. , 2009, , .		76
72	The graphlet spectrum. , 2009, , .		34

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73	Predicting phenotypic effects of gene perturbations in <i>C. elegans</i> using an integrated network model. <i>BioEssays</i> , 2008, 30, 707-710.	1.2	2
74	Metropolis Algorithms for Representative Subgraph Sampling. , 2008, , .		84
75	The skew spectrum of graphs. , 2008, , .		23
76	Covariate Shift by Kernel Mean Matching. , 2008, , 131-160.		98
77	Supervised feature selection via dependence estimation. , 2007, , .		216
78	A dependence maximization view of clustering. , 2007, , .		68
79	Gene selection via the BAHSIC family of algorithms. <i>Bioinformatics</i> , 2007, 23, i490-i498.	1.8	44
80	Future trends in data mining. <i>Data Mining and Knowledge Discovery</i> , 2007, 15, 87-97.	2.4	128
81	Pattern Mining in Frequent Dynamic Subgraphs. <i>IEEE International Conference on Data Mining</i> , 2006, , .	0.0	91
82	Kernel extrapolation. <i>Neurocomputing</i> , 2006, 69, 721-729.	3.5	9
83	Integrating structured biological data by Kernel Maximum Mean Discrepancy. <i>Bioinformatics</i> , 2006, 22, e49-e57.	1.8	1,037
84	3DString. , 2006, , .		4
85	Class prediction from time series gene expression profiles using dynamical systems kernels. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006, , 547-58.	0.7	8
86	Protein function prediction via graph kernels. <i>Bioinformatics</i> , 2005, 21, i47-i56.	1.8	591