

Pekka E Marttinen

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

5,519
citations

236925

25
h-index

161849

54
g-index

64
all docs

64
docs citations

64
times ranked

7599
citing authors

#	ARTICLE	IF	CITATIONS
1	EEG Based Emotion Recognition: A Tutorial and Review. <i>ACM Computing Surveys</i> , 2023, 55, 1-57.	23.0	58
2	A Survey on Knowledge Graphs: Representation, Acquisition, and Applications. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2022, 33, 494-514.	11.3	769
3	Deep learning for depression recognition with audiovisual cues: A review. <i>Information Fusion</i> , 2022, 80, 56-86.	19.1	73
4	COVIDNet: An Automatic Architecture for COVID-19 Detection With Deep Learning From Chest X-Ray Images. <i>IEEE Internet of Things Journal</i> , 2022, 9, 11376-11384.	8.7	3
5	Modelling methicillin-resistant <i>Staphylococcus aureus</i> decolonization: interactions between body sites and the impact of site-specific clearance. <i>Journal of the Royal Society Interface</i> , 2022, 19, .	3.4	4
6	Errors-in-Variables Modeling of Personalized Treatment-Response Trajectories. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 201-208.	6.3	3
7	Multitask Recalibrated Aggregation Network for Medical Code Prediction. <i>Lecture Notes in Computer Science</i> , 2021, , 367-383.	1.3	6
8	Does the magic of BERT apply to medical code assignment? A quantitative study. <i>Computers in Biology and Medicine</i> , 2021, 139, 104998.	7.0	32
9	Computational modelling of self-reported dietary carbohydrate intake on glucose concentrations in patients undergoing Roux-en-Y gastric bypass versus one-anastomosis gastric bypass. <i>Annals of Medicine</i> , 2021, 53, 1885-1895.	3.8	5
10	Crop loss identification at field parcel scale using satellite remote sensing and machine learning. <i>PLoS ONE</i> , 2021, 16, e0251952.	2.5	1
11	Population analysis of <i>Legionella pneumophila</i> reveals a basis for resistance to complement-mediated killing. <i>Nature Communications</i> , 2021, 12, 7165.	12.8	11
12	Dilated Convolutional Attention Network for Medical Code Assignment from Clinical Text. , 2020, , .		10
13	Efficient Acquisition Rules for Model-Based Approximate Bayesian Computation. <i>Bayesian Analysis</i> , 2019, 14, .	3.0	24
14	A Bayesian model of acquisition and clearance of bacterial colonization incorporating within-host variation. <i>PLoS Computational Biology</i> , 2019, 15, e1006534.	3.2	7
15	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	6.1	168
16	Modelling GÅ–E with historical weather information improves genomic prediction in new environments. <i>Bioinformatics</i> , 2019, 35, 4045-4052.	4.1	40
17	Bacmeta: simulator for genomic evolution in bacterial metapopulations. <i>Bioinformatics</i> , 2018, 34, 2308-2310.	4.1	11
18	Gaussian process modelling in approximate Bayesian computation to estimate horizontal gene transfer in bacteria. <i>Annals of Applied Statistics</i> , 2018, 12, .	1.1	22

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19	Improving genomics-based predictions for precision medicine through active elicitation of expert knowledge. <i>Bioinformatics</i> , 2018, 34, i395-i403.	4.1	6
20	Interactive Elicitation of Knowledge on Feature Relevance Improves Predictions in Small Data Sets. , 2017, , .		12
21	Efficient Inference of Recent and Ancestral Recombination within Bacterial Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 1167-1182.	8.9	168
22	biMM: efficient estimation of genetic variances and covariances for cohorts with high-dimensional phenotype measurements. <i>Bioinformatics</i> , 2017, 33, 2405-2407.	4.1	11
23	Cluster analysis to estimate the risk of preeclampsia in the high-risk Prediction and Prevention of Preeclampsia and Intrauterine Growth Restriction (PREDO) study. <i>PLoS ONE</i> , 2017, 12, e0174399.	2.5	21
24	Speciation trajectories in recombining bacterial species. <i>PLoS Computational Biology</i> , 2017, 13, e1005640.	3.2	24
25	Dynamics and impact of homologous recombination on the evolution of <i>Legionella pneumophila</i> . <i>PLoS Genetics</i> , 2017, 13, e1006855.	3.5	41
26	Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes. <i>Nature Communications</i> , 2016, 7, 12797.	12.8	190
27	Substitutions of short heterologous DNA segments of intragenomic or extragenomic origins produce clustered genomic polymorphisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 15066-15071.	7.1	8
28	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , 2016, 7, 12460.	12.8	73
29	The impact of host metapopulation structure on the population genetics of colonizing bacteria. <i>Journal of Theoretical Biology</i> , 2016, 396, 53-62.	1.7	13
30	metaCCA: summary statistics-based multivariate meta-analysis of genome-wide association studies using canonical correlation analysis. <i>Bioinformatics</i> , 2016, 32, 1981-1989.	4.1	138
31	Recombination produces coherent bacterial species clusters in both core and accessory genomes. <i>Microbial Genomics</i> , 2015, 1, e000038.	2.0	37
32	Assessing multivariate gene-metabolome associations with rare variants using Bayesian reduced rank regression. <i>Bioinformatics</i> , 2014, 30, 2026-2034.	4.1	28
33	Plant Sterol Feeding Induces Tumor Formation and Alters Sterol Metabolism in the Intestine of <i>Apc^{Min}</i> Mice. <i>Nutrition and Cancer</i> , 2014, 66, 259-269.	2.0	8
34	Comprehensive Identification of Single Nucleotide Polymorphisms Associated with Beta-lactam Resistance within Pneumococcal Mosaic Genes. <i>PLoS Genetics</i> , 2014, 10, e1004547.	3.5	205
35	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. <i>Molecular Ecology</i> , 2014, 23, 2442-2451.	3.9	131
36	Single-Cell Genomics Reveals Hundreds of Coexisting Subpopulations in Wild <i>Prochlorococcus</i> . <i>Science</i> , 2014, 344, 416-420.	12.6	506

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37	Dense genomic sampling identifies highways of pneumococcal recombination. <i>Nature Genetics</i> , 2014, 46, 305-309.	21.4	371
38	Genome-wide association studies with high-dimensional phenotypes. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 413-31.	0.6	13
39	Detection of recombination events in bacterial genomes from large population samples. <i>Nucleic Acids Research</i> , 2012, 40, e6-e6.	14.5	179
40	Phylogeographic variation in recombination rates within a global clone of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Genome Biology</i> , 2012, 13, R126.	9.6	118
41	Finite Adaptation and Multistep Moves in the Metropolis-Hastings Algorithm for Variable Selection in Genome-Wide Association Analysis. <i>PLoS ONE</i> , 2012, 7, e49445.	2.5	12
42	Serum and CSF soluble CD26 and CD30 concentrations in healthy pediatric surgical outpatients. <i>Tissue Antigens</i> , 2012, 80, 368-375.	1.0	10
43	Bayesian Variable Selection in Searching for Additive and Dominant Effects in Genome-Wide Data. <i>PLoS ONE</i> , 2012, 7, e29115.	2.5	11
44	Reconstructing Population Histories from Single Nucleotide Polymorphism Data. <i>Molecular Biology and Evolution</i> , 2011, 28, 673-683.	8.9	37
45	Efficient Bayesian approach for multilocus association mapping including gene-gene interactions. <i>BMC Bioinformatics</i> , 2010, 11, 443.	2.6	6
46	Robust extraction of functional signals from gene set analysis using a generalized threshold free scoring function. <i>BMC Bioinformatics</i> , 2009, 10, 307.	2.6	35
47	Bayesian clustering and feature selection for cancer tissue samples. <i>BMC Bioinformatics</i> , 2009, 10, 90.	2.6	13
48	Bayesian learning of graphical vector autoregressions with unequal lag-lengths. <i>Machine Learning</i> , 2009, 75, 217-243.	5.4	5
49	Bayesian Clustering of Fuzzy Feature Vectors Using a Quasi-Likelihood Approach. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2009, 31, 74-85.	13.9	8
50	Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. <i>BMC Bioinformatics</i> , 2008, 9, 539.	2.6	760
51	Bayesian modeling of recombination events in bacterial populations. <i>BMC Bioinformatics</i> , 2008, 9, 421.	2.6	26
52	Bayesian identification of admixture events using multilocus molecular markers. <i>Molecular Ecology</i> , 2006, 15, 2833-2843.	3.9	569
53	Bayesian Model Learning Based on Predictive Entropy. <i>Journal of Logic, Language and Information</i> , 2006, 15, 5-20.	0.6	2
54	Bayesian search of functionally divergent protein subgroups and their function specific residues. <i>Bioinformatics</i> , 2006, 22, 2466-2474.	4.1	40

#	ARTICLE	IF	CITATIONS
55	BAPS 2: enhanced possibilities for the analysis of genetic population structure. <i>Bioinformatics</i> , 2004, 20, 2363-2369.	4.1	415