

# Jukka Corander

## List of Publications by Year in descending order

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Version: 2024-02-01

172  
papers

13,619  
citations

31976

53  
h-index

27406

106  
g-index

204  
all docs

204  
docs citations

204  
times ranked

14853  
citing authors

#	ARTICLE	IF	CITATIONS
1	Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. BMC Bioinformatics, 2008, 9, 539.	2.6	760
2	Bayesian Analysis of Genetic Differentiation Between Populations. Genetics, 2003, 163, 367-374.	2.9	730
3	Bayesian identification of admixture events using multilocus molecular markers. Molecular Ecology, 2006, 15, 2833-2843.	3.9	569
4	Hierarchical and Spatially Explicit Clustering of DNA Sequences with BAPS Software. Molecular Biology and Evolution, 2013, 30, 1224-1228.	8.9	568
5	Evolution and transmission of drug-resistant tuberculosis in a Russian population. Nature Genetics, 2014, 46, 279-286.	21.4	451
6	Producing polished prokaryotic pangenomes with the Panaroo pipeline. Genome Biology, 2020, 21, 180.	8.8	419
7	BAPS 2: enhanced possibilities for the analysis of genetic population structure. Bioinformatics, 2004, 20, 2363-2369.	4.1	415
8	Bayesian spatial modeling of genetic population structure. Computational Statistics, 2008, 23, 111-129.	1.5	377
9	Dense genomic sampling identifies highways of pneumococcal recombination. Nature Genetics, 2014, 46, 305-309.	21.4	371
10	Emergence of Epidemic Multidrug-Resistant Enterococcus faecium from Animal and Commensal Strains. MBio, 2013, 4, .	4.1	336
11	Fast and flexible bacterial genomic epidemiology with PopPUNK. Genome Research, 2019, 29, 304-316.	5.5	258
12	Global Emergence and Dissemination of Enterococci as Nosocomial Pathogens: Attack of the Clones?. Frontiers in Microbiology, 2016, 7, 788.	3.5	248
13	Core Genome Multilocus Sequence Typing Scheme for High-Resolution Typing of Enterococcus faecium. Journal of Clinical Microbiology, 2015, 53, 3788-3797.	3.9	240
14	Systematic longitudinal survey of invasive <i>Escherichia coli</i> in England demonstrates a stable population structure only transiently disturbed by the emergence of ST131. Genome Research, 2017, 27, 1437-1449.	5.5	231
15	Bayesian analysis of population structure based on linked molecular information. Mathematical Biosciences, 2007, 205, 19-31.	1.9	214
16	Patterns of genome evolution that have accompanied host adaptation in <i>Salmonella</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 863-868.	7.1	213
17	pyseer: a comprehensive tool for microbial pangenome-wide association studies. Bioinformatics, 2018, 34, 4310-4312.	4.1	208
18	Novel staphylococcal species that form part of a Staphylococcus aureus-related complex: the non-pigmented Staphylococcus argenteus sp. nov. and the non-human primate-associated Staphylococcus schweitzeri sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 15-22.	1.7	201

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19	RhierBAPS: An R implementation of the population clustering algorithm hierBAPS. Wellcome Open Research, 2018, 3, 93.	1.8	198
20	Identification of enterotoxigenic Escherichia coli (ETEC) clades with long-term global distribution. Nature Genetics, 2014, 46, 1321-1326.	21.4	192
21	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive Staphylococcus aureus in Europe. MBio, 2016, 7, .	4.1	192
22	Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes. Nature Communications, 2016, 7, 12797.	12.8	190
23	Detection of recombination events in bacterial genomes from large population samples. Nucleic Acids Research, 2012, 40, e6-e6.	14.5	179
24	Restricted Gene Flow among Hospital Subpopulations of Enterococcus faecium. MBio, 2012, 3, e00151-12.	4.1	177
25	Combined Analysis of Variation in Core, Accessory and Regulatory Genome Regions Provides a Super-Resolution View into the Evolution of Bacterial Populations. PLoS Genetics, 2016, 12, e1006280.	3.5	177
26	Fast hierarchical Bayesian analysis of population structure. Nucleic Acids Research, 2019, 47, 5539-5549.	14.5	173
27	Efficient Inference of Recent and Ancestral Recombination within Bacterial Populations. Molecular Biology and Evolution, 2017, 34, 1167-1182.	8.9	168
28	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. EBioMedicine, 2019, 43, 338-346.	6.1	168
29	Acinetobacter species in the skin microbiota protect against allergic sensitization and inflammation. Journal of Allergy and Clinical Immunology, 2014, 134, 1301-1309.e11.	2.9	163
30	Gene exchange drives the ecological success of a multi-host bacterial pathogen. Nature Ecology and Evolution, 2018, 2, 1468-1478.	7.8	156
31	Parallel independent evolution of pathogenicity within the genus <i>Yersinia</i> . Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6768-6773.	7.1	154
32	In defence of model-based inference in phylogeography. Molecular Ecology, 2010, 19, 436-446.	3.9	141
33	Recombination is a key driver of genomic and phenotypic diversity in a Pseudomonas aeruginosa population during cystic fibrosis infection. Scientific Reports, 2015, 5, 7649.	3.3	134
34	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. Molecular Ecology, 2014, 23, 2442-2451.	3.9	131
35	Ecological Overlap and Horizontal Gene Transfer in Staphylococcus aureus and Staphylococcus epidermidis. Genome Biology and Evolution, 2015, 7, 1313-1328.	2.5	130
36	Phylogeny, phylogeography and genetic diversity of the Pisum genus. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 4-18.	0.8	128

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37	Genomic signatures of human and animal disease in the zoonotic pathogen <i>Streptococcus suis</i> . <i>Nature Communications</i> , 2015, 6, 6740.	12.8	124
38	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	13.3	124
39	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960.	7.8	121
40	mlplasmids: a user-friendly tool to predict plasmid- and chromosome-derived sequences for single species. <i>Microbial Genomics</i> , 2018, 4, .	2.0	121
41	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
42	Fundamentals and Recent Developments in Approximate Bayesian Computation. <i>Systematic Biology</i> , 2017, 66, syw077.	5.6	115
43	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , 2018, 9, 5034.	12.8	115
44	The de novo genome assembly and annotation of a female domestic dromedary of North African origin. <i>Molecular Ecology Resources</i> , 2016, 16, 314-324.	4.8	106
45	Diversification of Colonization Factors in a Multidrug-Resistant <i>Escherichia coli</i> Lineage Evolving under Negative Frequency-Dependent Selection. <i>MBio</i> , 2019, 10, .	4.1	106
46	Plasmids Shaped the Recent Emergence of the Major Nosocomial Pathogen <i>Enterococcus faecium</i> . <i>MBio</i> , 2020, 11, .	4.1	91
47	Recent Recombination Events in the Core Genome Are Associated with Adaptive Evolution in <i>Enterococcus faecium</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1524-1535.	2.5	87
48	Bayesian inference of atomistic structure in functional materials. <i>Npj Computational Materials</i> , 2019, 5, .	8.7	81
49	Population Biology of Intestinal <i>Enterococcus</i> Isolates from Hospitalized and Nonhospitalized Individuals in Different Age Groups. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1820-1831.	3.1	75
50	Layered adaptive importance sampling. <i>Statistics and Computing</i> , 2017, 27, 599-623.	1.5	72
51	Genome evolution and the emergence of pathogenicity in avian <i>Escherichia coli</i> . <i>Nature Communications</i> , 2021, 12, 765.	12.8	69
52	Apparent nosocomial adaptation of <i>Enterococcus faecalis</i> predates the modern hospital era. <i>Nature Communications</i> , 2021, 12, 1523.	12.8	69
53	Improved Prediction of Bacterial Genotype-Phenotype Associations Using Interpretable Pangenome-Spanning Regressions. <i>MBio</i> , 2020, 11, .	4.1	66
54	Progression and mortality of interstitial lung disease in mixed connective tissue disease: a long-term observational nationwide cohort study. <i>Rheumatology</i> , 2018, 57, 255-262.	1.9	65

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55	Genomic Surveillance of <i>Enterococcus faecium</i> Reveals Limited Sharing of Strains and Resistance Genes between Livestock and Humans in the United Kingdom. <i>MBio</i> , 2018, 9, .	4.1	63
56	Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex. <i>Science Advances</i> , 2019, 5, eaaw3307.	10.3	61
57	An Adaptive Population Importance Sampler: Learning From Uncertainty. <i>IEEE Transactions on Signal Processing</i> , 2015, 63, 4422-4437.	5.3	60
58	Transfer of noncoding DNA drives regulatory rewiring in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16112-16117.	7.1	59
59	Integrated analysis of population genomics, transcriptomics and virulence provides novel insights into <i>Streptococcus pyogenes</i> pathogenesis. <i>Nature Genetics</i> , 2019, 51, 548-559.	21.4	58
60	Weak Epistasis May Drive Adaptation in Recombining Bacteria. <i>Genetics</i> , 2018, 208, 1247-1260.	2.9	51
61	Bayesian model learning based on a parallel MCMC strategy. <i>Statistics and Computing</i> , 2006, 16, 355-362.	1.5	47
62	Transcriptome Remodeling Contributes to Epidemic Disease Caused by the Human Pathogen <i>Streptococcus pyogenes</i> . <i>MBio</i> , 2016, 7, .	4.1	47
63	Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 830-842.	2.5	46
64	Dynamics of intestinal multidrug-resistant bacteria colonisation contracted by visitors to a high-endemic setting: a prospective, daily, real-time sampling study. <i>Lancet Microbe</i> , The, 2021, 2, e151-e158.	7.3	45
65	Genomic Epidemiology of Penicillin-Nonsusceptible Pneumococci with Nonvaccine Serotypes Causing Invasive Disease in the United States. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1104-1115.	3.9	44
66	Emergence and dissemination of antimicrobial resistance in <i>Escherichia coli</i> causing bloodstream infections in Norway in 2002-2017: a nationwide, longitudinal, microbial population genomic study. <i>Lancet Microbe</i> , The, 2021, 2, e331-e341.	7.3	43
67	Climate induces seasonality in pneumococcal transmission. <i>Scientific Reports</i> , 2015, 5, 11344.	3.3	41
68	Likelihood-free inference via classification. <i>Statistics and Computing</i> , 2018, 28, 411-425.	1.5	41
69	Designing ecologically optimized pneumococcal vaccines using population genomics. <i>Nature Microbiology</i> , 2020, 5, 473-485.	13.3	39
70	Recombination-mediated remodelling of host-pathogen interactions during <i>Staphylococcus aureus</i> niche adaptation. <i>Microbial Genomics</i> , 2015, 1, e000036.	2.0	39
71	A comprehensive and high-quality collection of <i>Escherichia coli</i> genomes and their genes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	38
72	Recombination produces coherent bacterial species clusters in both core and accessory genomes. <i>Microbial Genomics</i> , 2015, 1, e000038.	2.0	37

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73	Genome-wide epistasis and co-selection study using mutual information. <i>Nucleic Acids Research</i> , 2019, 47, e112-e112.	14.5	36
74	Parallell interacting MCMC for learning of topologies of graphical models. <i>Data Mining and Knowledge Discovery</i> , 2008, 17, 431-456.	3.7	35
75	Random Partition Models and Exchangeability for Bayesian Identification of Population Structure. <i>Bulletin of Mathematical Biology</i> , 2007, 69, 797-815.	1.9	34
76	The use of genome wide association methods to investigate pathogenicity, population structure and serovar in <i>Haemophilus parasuis</i> . <i>BMC Genomics</i> , 2014, 15, 1179.	2.8	34
77	Population structure in the <i>Neisseria</i> , and the biological significance of fuzzy species. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1208-1215.	3.4	33
78	Disease evolution in mixed connective tissue disease: results from a long-term nationwide prospective cohort study. <i>Arthritis Research and Therapy</i> , 2017, 19, 284.	3.5	31
79	Monomorphic genotypes within a generalist lineage of <i>Campylobacter jejuni</i> show signs of global dispersion. <i>Microbial Genomics</i> , 2016, 2, e000088.	2.0	31
80	Novel R Pipeline for Analyzing Biolog Phenotypic Microarray Data. <i>PLoS ONE</i> , 2015, 10, e0118392.	2.5	29
81	Whatâ€™s in a Name? Species-Wide Whole-Genome Sequencing Resolves Invasive and Noninvasive Lineages of <i>Salmonella enterica</i> Serotype Paratyphi B. <i>MBio</i> , 2016, 7, .	4.1	29
82	Gene Loss and Lineage-Specific Restriction-Modification Systems Associated with Niche Differentiation in the <i>Campylobacter jejuni</i> Sequence Type 403 Clonal Complex. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3641-3647.	3.1	27
83	Labeled directed acyclic graphs: a generalization of context-specific independence in directed graphical models. <i>Data Mining and Knowledge Discovery</i> , 2015, 29, 503-533.	3.7	27
84	Fine-Scale Haplotype Structure Reveals Strong Signatures of Positive Selection in a Recombining Bacterial Pathogen. <i>Molecular Biology and Evolution</i> , 2020, 37, 417-428.	8.9	27
85	PANINI: Pangenome Neighbour Identification for Bacterial Populations. <i>Microbial Genomics</i> , 2019, 5, .	2.0	27
86	Evidence for a primate origin of zoonotic <i>Helicobacter suis</i> colonizing domesticated pigs. <i>ISME Journal</i> , 2018, 12, 77-86.	9.8	26
87	Transcriptome Analysis Reveals Signature of Adaptation to Landscape Fragmentation. <i>PLoS ONE</i> , 2014, 9, e101467.	2.5	24
88	Population subdivision and the detection of recombination in non-typable <i>Haemophilus influenzae</i> . <i>Microbiology (United Kingdom)</i> , 2012, 158, 2958-2964.	1.8	24
89	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . <i>PLoS Biology</i> , 2020, 18, e3000878.	5.6	24
90	Two-phase importance sampling for inference about transmission trees. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141324.	2.6	22

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91	Understanding pneumococcal serotype 1 biology through population genomic analysis. BMC Infectious Diseases, 2016, 16, 649.	2.9	22
92	Mode and dynamics of vanA-type vancomycin resistance dissemination in Dutch hospitals. Genome Medicine, 2021, 13, 9.	8.2	22
93	The Contribution of Genetic Variation of Streptococcus pneumoniae to the Clinical Manifestation of Invasive Pneumococcal Disease. Clinical Infectious Diseases, 2019, 68, 61-69.	5.8	21
94	New Pathogenesis Mechanisms and Translational Leads Identified by Multidimensional Analysis of Necrotizing Myositis in Primates. MBio, 2020, 11, .	4.1	21
95	Using Bayesâ€™ theorem in behavioural crime linking of serial homicide. Legal and Criminological Psychology, 2013, 18, 356-370.	2.0	20
96	Sparse Markov Chains for Sequence Data. Scandinavian Journal of Statistics, 2014, 41, 639-655.	1.4	20
97	On the Outage Capacity of Orthogonal Space-Time Block Codes Over Multi-Cluster Scattering MIMO Channels. IEEE Transactions on Communications, 2015, 63, 1700-1711.	7.8	20
98	Bayesian identification of bacterial strains from sequencing data. Microbial Genomics, 2016, 2, e000075.	2.0	19
99	On the Identifiability of Transmission Dynamic Models for Infectious Diseases. Genetics, 2016, 202, 911-918.	2.9	17
100	Negative frequency-dependent selection and asymmetrical transformation stabilise multi-strain bacterial population structures. ISME Journal, 2021, 15, 1523-1538.	9.8	17
101	Different evolutionary trends form the twilight zone of the bacterial pan-genome. Microbial Genomics, 2021, 7, .	2.0	17
102	Bacterial genomic epidemiology with mixed samples. Microbial Genomics, 2021, 7, .	2.0	17
103	Identification of a Novel Genomic Island Associated with <i>vanD</i> -Type Vancomycin Resistance in Six Dutch Vancomycin-Resistant Enterococcus faecium Isolates. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	16
104	Directional gene flow and ecological separation in Yersinia enterocolitica. Microbial Genomics, 2015, 1, e000030.	2.0	16
105	Bayesian unsupervised classification framework based on stochastic partitions of data and a parallel search strategy. Advances in Data Analysis and Classification, 2009, 3, 3-24.	1.4	14
106	Genetic import and phenotype specific alleles associated with hyper-invasion in Campylobacter jejuni. BMC Genomics, 2015, 16, 852.	2.8	14
107	Context-specific independence in graphical log-linear models. Computational Statistics, 2016, 31, 1493-1512.	1.5	14
108	Phylogenomics of <i>Enterococcus faecalis</i> from wild birds: new insights into host-associated differences in core and accessory genomes of the species. Environmental Microbiology, 2019, 21, 3046-3062.	3.8	14

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109	High-resolution sweep metagenomics using fast probabilistic inference. Wellcome Open Research, 0, 5, 14.	1.8	14
110	Random projection based clustering for population genomics. , 2014, , .		13
111	A gradient adaptive population importance sampler. , 2015, , .		13
112	The impact of host metapopulation structure on the population genetics of colonizing bacteria. Journal of Theoretical Biology, 2016, 396, 53-62.	1.7	13
113	High-resolution sweep metagenomics using fast probabilistic inference. Wellcome Open Research, 2020, 5, 14.	1.8	13
114	A high-throughput multiplexing and selection strategy to complete bacterial genomes. GigaScience, 2021, 10, .	6.4	13
115	Convergent Amino Acid Signatures in Polyphyletic <i>Campylobacter jejuni</i> Subpopulations Suggest Human Niche Tropism. Genome Biology and Evolution, 2018, 10, 763-774.	2.5	12
116	K-Pax2: Bayesian identification of cluster-defining amino acid positions in large sequence datasets. Microbial Genomics, 2015, 1, e000025.	2.0	12
117	An adaptive population importance sampler. , 2014, , .		11
118	SEK: sparsity exploiting k-mer-based estimation of bacterial community composition. Bioinformatics, 2014, 30, 2423-2431.	4.1	11
119	Bacmeta: simulator for genomic evolution in bacterial metapopulations. Bioinformatics, 2018, 34, 2308-2310.	4.1	11
120	Quantifying bacterial evolution in the wild: A birthday problem for <i>Campylobacter</i> lineages. PLoS Genetics, 2021, 17, e1009829.	3.5	11
121	Population analysis of <i>Legionella pneumophila</i> reveals a basis for resistance to complement-mediated killing. Nature Communications, 2021, 12, 7165.	12.8	11
122	A high prevalence of bla OXA-48 in <i>Klebsiella (Raoultella) ornithinolytica</i> and related species in hospital wastewater in South West England. Microbial Genomics, 2021, 7, .	2.0	10
123	Co-evolutionary Signals Identify <i>Burkholderia pseudomallei</i> Survival Strategies in a Hostile Environment. Molecular Biology and Evolution, 2022, 39, .	8.9	10
124	Have I seen you before? Principles of Bayesian predictive classification revisited. Statistics and Computing, 2013, 23, 59-73.	1.5	9
125	Inverse finite-size scaling for high-dimensional significance analysis. Physical Review E, 2018, 97, 062112.	2.1	9
126	Genomic rearrangements uncovered by genome-wide co-evolution analysis of a major nosocomial pathogen, <i>Enterococcus faecium</i> . Microbial Genomics, 2020, 6, .	2.0	9



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127	A Naive Bayes Classifier for Protein Function Prediction. <i>In Silico Biology</i> , 2009, 9, 23-34.	0.9	8
128	Statistical Approach to Quality Control of Large Thermodynamic Databases. <i>Metallurgical and Materials Transactions B: Process Metallurgy and Materials Processing Science</i> , 2012, 43, 1113-1118.	2.1	8
129	Learning discrete decomposable graphical models via constraint optimization. <i>Statistics and Computing</i> , 2017, 27, 115-130.	1.5	7
130	Boosting heritability: estimating the genetic component of phenotypic variation with multiple sample splitting. <i>BMC Bioinformatics</i> , 2021, 22, 164.	2.6	7
131	Orthogonal MCMC algorithms. , 2014, , .		6
132	Smelly parallel MCMC chains. , 2015, , .		6
133	On the inconsistency of $\hat{\alpha}$ , “1-penalised sparse precision matrix estimation. <i>BMC Bioinformatics</i> , 2016, 17, 448.	2.6	6
134	Bayesian inference of physiologically meaningful parameters from body sway measurements. <i>Scientific Reports</i> , 2017, 7, 3771.	3.3	6
135	Kpax3: Bayesian bi-clustering of large sequence datasets. <i>Bioinformatics</i> , 2018, 34, 2132-2133.	4.1	6
136	Structure Learning of Contextual Markov Networks using Marginal Pseudo-likelihood. <i>Scandinavian Journal of Statistics</i> , 2017, 44, 455-479.	1.4	5
137	Genetic effects on life-history traits in the Glanville fritillary butterfly. <i>PeerJ</i> , 2017, 5, e3371.	2.0	5
138	Bayesian Unsupervised Learning of DNA Regulatory Binding Regions. <i>Advances in Artificial Intelligence</i> , 2009, 2009, 1-11.	0.9	5
139	The rocky road to personalized medicine: computational and statistical challenges. <i>Personalized Medicine</i> , 2012, 9, 109-114.	1.5	4
140	Bayesian predictive modeling and comparison of oil samples. <i>Journal of Chemometrics</i> , 2014, 28, 52-59.	1.3	4
141	The effect of recombination on the evolution of a population of <i>Neisseria meningitidis</i> . <i>Genome Research</i> , 2021, 31, 1258-1268.	5.5	4
142	ARK: Aggregation of Reads by K-Means for Estimation of Bacterial Community Composition. <i>PLoS ONE</i> , 2015, 10, e0140644.	2.5	4
143	International links between <i>Streptococcus pneumoniae</i> vaccine serotype 4 sequence type (ST) 801 in Northern European shipyard outbreaks of invasive pneumococcal disease. <i>Vaccine</i> , 2022, 40, 1054-1060.	3.8	4
144	On the finite-SNR Diversity-Multiplexing Tradeoff in large Rayleigh product channels. , 2015, , .		3

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145	Identifying Multiple Potential Metabolic Cycles in Time-Series from Biolog Experiments. PLoS ONE, 2016, 11, e0162276.	2.5	3
146	Marginal and simultaneous predictive classification using stratified graphical models. Advances in Data Analysis and Classification, 2016, 10, 305-326.	1.4	3
147	Bayesian Model Learning Based on Predictive Entropy. Journal of Logic, Language and Information, 2006, 15, 5-20.	0.6	2
148	Parallel interacting Markov adaptive importance sampling. , 2015, , .		2
149	Posterior Predictive Comparisons for the Two-sample Problem. Communications in Statistics - Theory and Methods, 2015, 44, 376-389.	1.0	2
150	Stratified Gaussian graphical models. Communications in Statistics - Theory and Methods, 2017, 46, 5556-5578.	1.0	2
151	PYLFIRE: Python implementation of likelihood-free inference by ratio estimation. Wellcome Open Research, 2019, 4, 197.	1.8	2
152	Baseline adjustment increases accurate interpretation of posturographic sway scores. Gait and Posture, 2015, 42, 285-288.	1.4	1
153	On the volume of a metric ball in unitary group. , 2015, , .		1
154	Computing exact clustering posteriors with subset convolution. Communications in Statistics - Theory and Methods, 2016, 45, 3048-3058.	1.0	1
155	Response to "Refined analyses suggest that recombination is a minor source of genomic diversity in Pseudomonas aeruginosa chronic cystic fibrosis infections" by Williams et al. (2016 ). Microbial Genomics, 2016, 2, e000054.	2.0	1
156	Resolving outbreak dynamics using approximate Bayesian computation for stochastic birth-death models. Wellcome Open Research, 0, 4, 14.	1.8	1
157	Likelihood-free inference with deep Gaussian processes. Computational Statistics and Data Analysis, 2022, 174, 107529.	1.2	1
158	Outage capacity of OSTBCs over pico-cellular MIMO channels. , 2014, , .		0
159	On the exact volume of metric balls in complex Grassmann manifolds. , 2015, , .		0
160	A tribute to Mats Gyllenberg, on the occasion of his 60th birthday. Journal of Mathematical Biology, 2016, 72, 793-795.	1.9	0
161	Identifying Bacterial Strains from Sequencing Data. Methods in Molecular Biology, 2018, 1807, 1-7.	0.9	0
162	High-dimensional structure learning of sparse vector autoregressive models using fractional marginal pseudo-likelihood. Statistics and Computing, 2021, 31, 1.	1.5	0

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163	Resolving outbreak dynamics using approximate Bayesian computation for stochastic birth–death models. <i>Wellcome Open Research</i> , 0, 4, 14.	1.8	0
164	Learning Cancer Drug Sensitivities in Large-Scale Screens from Multi-omics Data with Local Low-Rank Structure. <i>Lecture Notes in Computer Science</i> , 2020, , 67-79.	1.3	0
165	Sequentially Guided MCMC Proposals for Synthetic Likelihoods and Correlated Synthetic Likelihoods. <i>Bayesian Analysis</i> , 2022, -1, .	3.0	0
166	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
167	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
168	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
169	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
170	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
171	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
172	Evolution of Chlorhexidine Susceptibility and of the EfrEF Operon among <i>Enterococcus faecalis</i> from Diverse Environments, Clones, and Time Spans. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	0