

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	Co-evolutionary Signals Identify <i>Burkholderia pseudomallei</i> Survival Strategies in a Hostile Environment. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	10
2	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
3	Sequentially Guided MCMC Proposals for Synthetic Likelihoods and Correlated Synthetic Likelihoods. <i>Bayesian Analysis</i> , 2022, -1, .	3.0	0
4	Likelihood-free inference with deep Gaussian processes. <i>Computational Statistics and Data Analysis</i> , 2022, 174, 107529.	1.2	1
5	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
6	Negative frequency-dependent selection and asymmetrical transformation stabilise multi-strain bacterial population structures. <i>ISME Journal</i> , 2021, 15, 1523-1538.	9.8	17
7	Genome evolution and the emergence of pathogenicity in avian <i>Escherichia coli</i> . <i>Nature Communications</i> , 2021, 12, 765.	12.8	69
8	A comprehensive and high-quality collection of <i>Escherichia coli</i> genomes and their genes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	38
9	Boosting heritability: estimating the genetic component of phenotypic variation with multiple sample splitting. <i>BMC Bioinformatics</i> , 2021, 22, 164.	2.6	7
10	A high prevalence of bla OXA-48 in <i>Klebsiella (Raoultella) ornithinolytica</i> and related species in hospital wastewater in South West England. <i>Microbial Genomics</i> , 2021, 7, .	2.0	10
11	Apparent nosocomial adaptation of <i>Enterococcus faecalis</i> predates the modern hospital era. <i>Nature Communications</i> , 2021, 12, 1523.	12.8	69
12	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
13	Emergence and dissemination of antimicrobial resistance in <i>Escherichia coli</i> causing bloodstream infections in Norway in 2002â€“17: a nationwide, longitudinal, microbial population genomic study. <i>Lancet Microbe</i> , The, 2021, 2, e331-e341.	7.3	43
14	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
15	Different evolutionary trends form the twilight zone of the bacterial pan-genome. <i>Microbial Genomics</i> , 2021, 7, .	2.0	17
16	Quantifying bacterial evolution in the wild: A birthday problem for <i>Campylobacter</i> lineages. <i>PLoS Genetics</i> , 2021, 17, e1009829.	3.5	11
17	High-dimensional structure learning of sparse vector autoregressive models using fractional marginal pseudo-likelihood. <i>Statistics and Computing</i> , 2021, 31, 1.	1.5	0
18	Mode and dynamics of vanA-type vancomycin resistance dissemination in Dutch hospitals. <i>Genome Medicine</i> , 2021, 13, 9.	8.2	22

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19	Bacterial genomic epidemiology with mixed samples. <i>Microbial Genomics</i> , 2021, 7, .	2.0	17
20	A high-throughput multiplexing and selection strategy to complete bacterial genomes. <i>GigaScience</i> , 2021, 10, .	6.4	13
21	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
22	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
23	Producing polished prokaryotic pangenomes with the Panaroo pipeline. <i>Genome Biology</i> , 2020, 21, 180.	8.8	419
24	Plasmids Shaped the Recent Emergence of the Major Nosocomial Pathogen <i>Enterococcus faecium</i> . <i>MBio</i> , 2020, 11, .	4.1	91
25	New Pathogenesis Mechanisms and Translational Leads Identified by Multidimensional Analysis of Necrotizing Myositis in Primates. <i>MBio</i> , 2020, 11, .	4.1	21
26	Improved Prediction of Bacterial Genotype-Phenotype Associations Using Interpretable Pangenome-Spanning Regressions. <i>MBio</i> , 2020, 11, .	4.1	66
27	Designing ecologically optimized pneumococcal vaccines using population genomics. <i>Nature Microbiology</i> , 2020, 5, 473-485.	13.3	39
28	High-resolution sweep metagenomics using fast probabilistic inference. <i>Wellcome Open Research</i> , 2020, 5, 14.	1.8	13
29	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . <i>PLoS Biology</i> , 2020, 18, e3000878.	5.6	24
30	Genomic rearrangements uncovered by genome-wide co-evolution analysis of a major nosocomial pathogen, <i>Enterococcus faecium</i> . <i>Microbial Genomics</i> , 2020, 6, .	2.0	9
31	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
32	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
33	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
34	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
35	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
36	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0

#	ARTICLE	IF	CITATIONS
37	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
38	The Contribution of Genetic Variation of <i>Streptococcus pneumoniae</i> to the Clinical Manifestation of Invasive Pneumococcal Disease. <i>Clinical Infectious Diseases</i> , 2019, 68, 61-69.	5.8	21
39	Genome-wide epistasis and co-selection study using mutual information. <i>Nucleic Acids Research</i> , 2019, 47, e112-e112.	14.5	36
40	Fast and flexible bacterial genomic epidemiology with PopPUNK. <i>Genome Research</i> , 2019, 29, 304-316.	5.5	258
41	Fast hierarchical Bayesian analysis of population structure. <i>Nucleic Acids Research</i> , 2019, 47, 5539-5549.	14.5	173
42	Phylogenomics of <i>Enterococcus faecalis</i> from wild birds: new insights into host-associated differences in core and accessory genomes of the species. <i>Environmental Microbiology</i> , 2019, 21, 3046-3062.	3.8	14
43	Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex. <i>Science Advances</i> , 2019, 5, eaaw3307.	10.3	61
44	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	6.1	168
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	Bayesian inference of atomistic structure in functional materials. <i>Npj Computational Materials</i> , 2019, 5, .	8.7	81
47	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
48	PANINI: Pangenome Neighbour Identification for Bacterial Populations. <i>Microbial Genomics</i> , 2019, 5, .	2.0	27
49	PYLFIRE: Python implementation of likelihood-free inference by ratio estimation. <i>Wellcome Open Research</i> , 2019, 4, 197.	1.8	2
50	Bacmeta: simulator for genomic evolution in bacterial metapopulations. <i>Bioinformatics</i> , 2018, 34, 2308-2310.	4.1	11
51	Kpax3: Bayesian bi-clustering of large sequence datasets. <i>Bioinformatics</i> , 2018, 34, 2132-2133.	4.1	6
52	Convergent Amino Acid Signatures in Polyphyletic <i>Campylobacter jejuni</i> Subpopulations Suggest Human Niche Tropism. <i>Genome Biology and Evolution</i> , 2018, 10, 763-774.	2.5	12
53	Weak Epistasis May Drive Adaptation in Recombining Bacteria. <i>Genetics</i> , 2018, 208, 1247-1260.	2.9	51
54	Identification of a Novel Genomic Island Associated with <i>vanD</i> -Type Vancomycin Resistance in Six Dutch Vancomycin-Resistant <i>Enterococcus faecium</i> Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	16

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55	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
56	Likelihood-free inference via classification. <i>Statistics and Computing</i> , 2018, 28, 411-425.	1.5	41
57	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
58	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
59	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , 2018, 9, 5034.	12.8	115
60	pyseer: a comprehensive tool for microbial pangenome-wide association studies. <i>Bioinformatics</i> , 2018, 34, 4310-4312.	4.1	208
61	Inverse finite-size scaling for high-dimensional significance analysis. <i>Physical Review E</i> , 2018, 97, 062112.	2.1	9
62	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	7.8	156
63	Identifying Bacterial Strains from Sequencing Data. <i>Methods in Molecular Biology</i> , 2018, 1807, 1-7.	0.9	0
64	mlplasmids: a user-friendly tool to predict plasmid- and chromosome-derived sequences for single species. <i>Microbial Genomics</i> , 2018, 4, .	2.0	121
65	RhierBAPS: An R implementation of the population clustering algorithm hierBAPS. <i>Wellcome Open Research</i> , 2018, 3, 93.	1.8	198
66	Fundamentals and Recent Developments in Approximate Bayesian Computation. <i>Systematic Biology</i> , 2017, 66, syw077.	5.6	115
67	Layered adaptive importance sampling. <i>Statistics and Computing</i> , 2017, 27, 599-623.	1.5	72
68	Stratified Gaussian graphical models. <i>Communications in Statistics - Theory and Methods</i> , 2017, 46, 5556-5578.	1.0	2
69	Learning discrete decomposable graphical models via constraint optimization. <i>Statistics and Computing</i> , 2017, 27, 115-130.	1.5	7
70	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	13.3	124
71	Genomic Epidemiology of Penicillin-Nonsusceptible <i>Pneumococci</i> with Nonvaccine Serotypes Causing Invasive Disease in the United States. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1104-1115.	3.9	44
72	Structure Learning of Contextual Markov Networks using Marginal Pseudo-likelihood. <i>Scandinavian Journal of Statistics</i> , 2017, 44, 455-479.	1.4	5

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73	Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 830-842.	2.5	46
74	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960.	7.8	121
75	Systematic longitudinal survey of invasive <i>Escherichia coli</i> in England demonstrates a stable population structure only transiently disturbed by the emergence of ST131. <i>Genome Research</i> , 2017, 27, 1437-1449.	5.5	231
76	Bayesian inference of physiologically meaningful parameters from body sway measurements. <i>Scientific Reports</i> , 2017, 7, 3771.	3.3	6
77	Efficient Inference of Recent and Ancestral Recombination within Bacterial Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 1167-1182.	8.9	168
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	Genetic effects on life-history traits in the Glanville fritillary butterfly. <i>PeerJ</i> , 2017, 5, e3371.	2.0	5
80	Global Emergence and Dissemination of Enterococci as Nosocomial Pathogens: Attack of the Clones?. <i>Frontiers in Microbiology</i> , 2016, 7, 788.	3.5	248
81	Combined Analysis of Variation in Core, Accessory and Regulatory Genome Regions Provides a Super-Resolution View into the Evolution of Bacterial Populations. <i>PLoS Genetics</i> , 2016, 12, e1006280.	3.5	177
82	Identifying Multiple Potential Metabolic Cycles in Time-Series from Biolog Experiments. <i>PLoS ONE</i> , 2016, 11, e0162276.	2.5	3
83	Transcriptome Remodeling Contributes to Epidemic Disease Caused by the Human Pathogen <i>Streptococcus pyogenes</i> . <i>MBio</i> , 2016, 7, .	4.1	47
84	Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes. <i>Nature Communications</i> , 2016, 7, 12797.	12.8	190
85	Computing exact clustering posteriors with subset convolution. <i>Communications in Statistics - Theory and Methods</i> , 2016, 45, 3048-3058.	1.0	1
86	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive <i>Staphylococcus aureus</i> in Europe. <i>MBio</i> , 2016, 7, .	4.1	192
87	What'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
88	On the inconsistency of λ_1 -penalised sparse precision matrix estimation. <i>BMC Bioinformatics</i> , 2016, 17, 448.	2.6	6
89	Understanding pneumococcal serotype 1 biology through population genomic analysis. <i>BMC Infectious Diseases</i> , 2016, 16, 649.	2.9	22
90	A tribute to Mats Gyllenberg, on the occasion of his 60th birthday. <i>Journal of Mathematical Biology</i> , 2016, 72, 793-795.	1.9	0

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91	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
92	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
93	On the Identifiability of Transmission Dynamic Models for Infectious Diseases. <i>Genetics</i> , 2016, 202, 911-918.	2.9	17
94	Context-specific independence in graphical log-linear models. <i>Computational Statistics</i> , 2016, 31, 1493-1512.	1.5	14
95	Marginal and simultaneous predictive classification using stratified graphical models. <i>Advances in Data Analysis and Classification</i> , 2016, 10, 305-326.	1.4	3
96	Bayesian identification of bacterial strains from sequencing data. <i>Microbial Genomics</i> , 2016, 2, e000075.	2.0	19
97	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
98	Response to "Refined analyses suggest that recombination is a minor source of genomic diversity in <i>Pseudomonas aeruginosa</i> chronic cystic fibrosis infections" by Williams et al. (2016). <i>Microbial Genomics</i> , 2016, 2, e000054.	2.0	1
99	Baseline adjustment increases accurate interpretation of posturographic sway scores. <i>Gait and Posture</i> , 2015, 42, 285-288.	1.4	1
100	On the volume of a metric ball in unitary group. , 2015, , .		1
101	On the exact volume of metric balls in complex Grassmann manifolds. , 2015, , .		0
102	Genetic import and phenotype specific alleles associated with hyper-invasion in <i>Campylobacter jejuni</i> . <i>BMC Genomics</i> , 2015, 16, 852.	2.8	14
103	Novel R Pipeline for Analyzing Biolog Phenotypic Microarray Data. <i>PLoS ONE</i> , 2015, 10, e0118392.	2.5	29
104	On the finite-SNR Diversity-Multiplexing Tradeoff in large Rayleigh product channels. , 2015, , .		3
105	Parallel interacting Markov adaptive importance sampling. , 2015, , .		2
106	Smelly parallel MCMC chains. , 2015, , .		6
107	A gradient adaptive population importance sampler. , 2015, , .		13
108	An Adaptive Population Importance Sampler: Learning From Uncertainty. <i>IEEE Transactions on Signal Processing</i> , 2015, 63, 4422-4437.	5.3	60

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109	Population Biology of Intestinal Enterococcus Isolates from Hospitalized and Nonhospitalized Individuals in Different Age Groups. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1820-1831.	3.1	75
110	Recombination is a key driver of genomic and phenotypic diversity in a <i>Pseudomonas aeruginosa</i> population during cystic fibrosis infection. <i>Scientific Reports</i> , 2015, 5, 7649.	3.3	134
111	Patterns of genome evolution that have accompanied host adaptation in <i>Salmonella</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 863-868.	7.1	213
112	Climate induces seasonality in pneumococcal transmission. <i>Scientific Reports</i> , 2015, 5, 11344.	3.3	41
113	On the Outage Capacity of Orthogonal Space-Time Block Codes Over Multi-Cluster Scattering MIMO Channels. <i>IEEE Transactions on Communications</i> , 2015, 63, 1700-1711.	7.8	20
114	Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1313-1328.	2.5	130
115	Novel staphylococcal species that form part of a <i>Staphylococcus aureus</i> -related complex: the non-pigmented <i>Staphylococcus argenteus</i> sp. nov. and the non-human primate-associated <i>Staphylococcus schweitzeri</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 15-22.	1.7	201
116	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
117	Core Genome Multilocus Sequence Typing Scheme for High-Resolution Typing of <i>Enterococcus faecium</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 3788-3797.	3.9	240
118	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
119	Posterior Predictive Comparisons for the Two-sample Problem. <i>Communications in Statistics - Theory and Methods</i> , 2015, 44, 376-389.	1.0	2
120	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
121	K-Pax2: Bayesian identification of cluster-defining amino acid positions in large sequence datasets. <i>Microbial Genomics</i> , 2015, 1, e000025.	2.0	12
122	Directional gene flow and ecological separation in <i>Yersinia enterocolitica</i> . <i>Microbial Genomics</i> , 2015, 1, e000030.	2.0	16
123	Recombination-mediated remodelling of host-pathogen interactions during <i>Staphylococcus aureus</i> niche adaptation. <i>Microbial Genomics</i> , 2015, 1, e000036.	2.0	39
124	Recombination produces coherent bacterial species clusters in both core and accessory genomes. <i>Microbial Genomics</i> , 2015, 1, e000038.	2.0	37
125	ARK: Aggregation of Reads by K-Means for Estimation of Bacterial Community Composition. <i>PLoS ONE</i> , 2015, 10, e0140644.	2.5	4
126	Transcriptome Analysis Reveals Signature of Adaptation to Landscape Fragmentation. <i>PLoS ONE</i> , 2014, 9, e101467.	2.5	24

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127	Outage capacity of OSTBCs over pico-cellular MIMO channels. , 2014, , .		0
128	The use of genome wide association methods to investigate pathogenicity, population structure and serovar in <i>Haemophilus parasuis</i> . BMC Genomics, 2014, 15, 1179.	2.8	34
129	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. Molecular Ecology, 2014, 23, 2442-2451.	3.9	131
130	<i>Acinetobacter</i> 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
131	Bayesian predictive modeling and comparison of oil samples. Journal of Chemometrics, 2014, 28, 52-59.	1.3	4
132	An adaptive population importance sampler. , 2014, , .		11
133	Two-phase importance sampling for inference about transmission trees. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20141324.	2.6	22
134	Random projection based clustering for population genomics. , 2014, , .		13
135	Sparse Markov Chains for Sequence Data. Scandinavian Journal of Statistics, 2014, 41, 639-655.	1.4	20
136	Evolution and transmission of drug-resistant tuberculosis in a Russian population. Nature Genetics, 2014, 46, 279-286.	21.4	451
137	SEK: sparsity exploiting k-mer-based estimation of bacterial community composition. Bioinformatics, 2014, 30, 2423-2431.	4.1	11
138	Identification of enterotoxigenic <i>Escherichia coli</i> (ETEC) clades with long-term global distribution. Nature Genetics, 2014, 46, 1321-1326.	21.4	192
139	Orthogonal MCMC algorithms. , 2014, , .		6
140	Transfer of noncoding DNA drives regulatory rewiring in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16112-16117.	7.1	59
141	Dense genomic sampling identifies highways of pneumococcal recombination. Nature Genetics, 2014, 46, 305-309.	21.4	371
142	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
143	Using Bayesâ€™ theorem in behavioural crime linking of serial homicide. Legal and Criminological Psychology, 2013, 18, 356-370.	2.0	20
144	Have I seen you before? Principles of Bayesian predictive classification revisited. Statistics and Computing, 2013, 23, 59-73.	1.5	9

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145	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
146	Emergence of Epidemic Multidrug-Resistant <i>Enterococcus faecium</i> from Animal and Commensal Strains. <i>MBio</i> , 2013, 4, .	4.1	336
147	Hierarchical and Spatially Explicit Clustering of DNA Sequences with BAPS Software. <i>Molecular Biology and Evolution</i> , 2013, 30, 1224-1228.	8.9	568
148	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
149	Detection of recombination events in bacterial genomes from large population samples. <i>Nucleic Acids Research</i> , 2012, 40, e6-e6.	14.5	179
150	The rocky road to personalized medicine: computational and statistical challenges. <i>Personalized Medicine</i> , 2012, 9, 109-114.	1.5	4
151	Restricted Gene Flow among Hospital Subpopulations of <i>Enterococcus faecium</i> . <i>MBio</i> , 2012, 3, e00151-12.	4.1	177
152	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
153	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
154	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
155	Phylogeny, phylogeography and genetic diversity of the <i>Pisum</i> genus. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 4-18.	0.8	128
156	In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , 2010, 19, 436-446.	3.9	141
157	A Naive Bayes Classifier for Protein Function Prediction. <i>In Silico Biology</i> , 2009, 9, 23-34.	0.9	8
158	Bayesian unsupervised classification framework based on stochastic partitions of data and a parallel search strategy. <i>Advances in Data Analysis and Classification</i> , 2009, 3, 3-24.	1.4	14
159	Bayesian Unsupervised Learning of DNA Regulatory Binding Regions. <i>Advances in Artificial Intelligence</i> , 2009, 2009, 1-11.	0.9	5
160	Parallel interacting MCMC for learning of topologies of graphical models. <i>Data Mining and Knowledge Discovery</i> , 2008, 17, 431-456.	3.7	35
161	Bayesian spatial modeling of genetic population structure. <i>Computational Statistics</i> , 2008, 23, 111-129.	1.5	377
162	Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. <i>BMC Bioinformatics</i> , 2008, 9, 539.	2.6	760

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163	Bayesian analysis of population structure based on linked molecular information. <i>Mathematical Biosciences</i> , 2007, 205, 19-31.	1.9	214
164	Random Partition Models and Exchangeability for Bayesian Identification of Population Structure. <i>Bulletin of Mathematical Biology</i> , 2007, 69, 797-815.	1.9	34
165	Bayesian identification of admixture events using multilocus molecular markers. <i>Molecular Ecology</i> , 2006, 15, 2833-2843.	3.9	569
166	Bayesian model learning based on a parallel MCMC strategy. <i>Statistics and Computing</i> , 2006, 16, 355-362.	1.5	47
167	Bayesian Model Learning Based on Predictive Entropy. <i>Journal of Logic, Language and Information</i> , 2006, 15, 5-20.	0.6	2
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171	Resolving outbreak dynamics using approximate Bayesian computation for stochastic birth-death models. <i>Wellcome Open Research</i> , 0, 4, 14.	1.8	1
172	Resolving outbreak dynamics using approximate Bayesian computation for stochastic birth-death models. <i>Wellcome Open Research</i> , 0, 4, 14.	1.8	0