

# Paul Fearnhead

## List of Publications by Year in descending order

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Version: 2024-02-01

102  
papers

8,609  
citations

101496

36  
h-index

46771

89  
g-index

102  
all docs

102  
docs citations

102  
times ranked

9446  
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimal Detection of Changepoints With a Linear Computational Cost. <i>Journal of the American Statistical Association</i> , 2012, 107, 1590-1598.	1.8	1,367
2	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. <i>Nature Genetics</i> , 2007, 39, 645-649.	9.4	1,059
3	Improved particle filter for nonlinear problems. <i>IET Radar, Sonar &amp; Navigation</i> , 1999, 146, 2.	2.1	649
4	A Coalescent-Based Method for Detecting and Estimating Recombination From Gene Sequences. <i>Genetics</i> , 2002, 160, 1231-1241.	1.2	624
5	Constructing Summary Statistics for Approximate Bayesian Computation: Semi-Automatic Approximate Bayesian Computation. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2012, 74, 419-474.	1.1	378
6	Tracing the Source of Campylobacteriosis. <i>PLoS Genetics</i> , 2008, 4, e1000203.	1.5	365
7	Exact and efficient Bayesian inference for multiple changepoint problems. <i>Statistics and Computing</i> , 2006, 16, 203-213.	0.8	313
8	Estimating Recombination Rates From Population Genetic Data. <i>Genetics</i> , 2001, 159, 1299-1318.	1.2	272
9	Exact and computationally efficient likelihood-based estimation for discretely observed diffusion processes (with discussion). <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2006, 68, 333-382.	1.1	262
10	On-Line Inference for Multiple Changepoint Problems. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2007, 69, 589-605.	1.1	185
11	Rapid Evolution and the Importance of Recombination to the Gastroenteric Pathogen <i>Campylobacter jejuni</i> . <i>Molecular Biology and Evolution</i> , 2009, 26, 385-397.	3.5	160
12	On-line inference for hidden Markov models via particle filters. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2003, 65, 887-899.	1.1	145
13	Spatial epidemiology and natural population structure of <i>Campylobacter jejuni</i> colonizing a farmland ecosystem. <i>Environmental Microbiology</i> , 2005, 7, 1116-1126.	1.8	128
14	Markov chain Monte Carlo, Sufficient Statistics, and Particle Filters. <i>Journal of Computational and Graphical Statistics</i> , 2002, 11, 848-862.	0.9	107
15	The Zig-Zag process and super-efficient sampling for Bayesian analysis of big data. <i>Annals of Statistics</i> , 2019, 47, .	1.4	99
16	On optimal multiple changepoint algorithms for large data. <i>Statistics and Computing</i> , 2017, 27, 519-533.	0.8	94
17	Particle Filters for Partially Observed Diffusions. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2008, 70, 755-777.	1.1	91
18	A sequential smoothing algorithm with linear computational cost. <i>Biometrika</i> , 2010, 97, 447-464.	1.3	88

#	ARTICLE	IF	CITATIONS
19	A computationally efficient nonparametric approach for changepoint detection. <i>Statistics and Computing</i> , 2017, 27, 1293-1305.	0.8	86
20	Changepoint Detection in the Presence of Outliers. <i>Journal of the American Statistical Association</i> , 2019, 114, 169-183.	1.8	79
21	Approximate likelihood methods for estimating local recombination rates. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2002, 64, 657-680.	1.1	78
22	Exact Bayesian curve fitting and signal segmentation. <i>IEEE Transactions on Signal Processing</i> , 2005, 53, 2160-2166.	3.2	77
23	Computational methods for complex stochastic systems: a review of some alternatives to MCMC. <i>Statistics and Computing</i> , 2008, 18, 151-171.	0.8	74
24	Particle filters for mixture models with an unknown number of components. <i>Statistics and Computing</i> , 2004, 14, 11-21.	0.8	71
25	Analysis of changepoint models. , 2011, , 205-224.		68
26	SequenceLDhot: detecting recombination hotspots. <i>Bioinformatics</i> , 2006, 22, 3061-3066.	1.8	66
27	The Random Walk Metropolis: Linking Theory and Practice Through a Case Study. <i>Statistical Science</i> , 2010, 25, .	1.6	65
28	Inference for reaction networks using the linear noise approximation. <i>Biometrics</i> , 2014, 70, 457-466.	0.8	65
29	Sequential Monte Carlo Methods for State and Parameter Estimation in Abruptly Changing Environments. <i>IEEE Transactions on Signal Processing</i> , 2014, 62, 1245-1255.	3.2	64
30	Application of Coalescent Methods to Reveal Fine-Scale Rate Variation and Recombination Hotspots. <i>Genetics</i> , 2004, 167, 2067-2081.	1.2	62
31	Analysis of Recombination in <i>Campylobacter jejuni</i> from MLST Population Data. <i>Journal of Molecular Evolution</i> , 2005, 61, 333-340.	0.8	60
32	Computationally Efficient Changepoint Detection for a Range of Penalties. <i>Journal of Computational and Graphical Statistics</i> , 2017, 26, 134-143.	0.9	60
33	Particle Filters and Data Assimilation. <i>Annual Review of Statistics and Its Application</i> , 2018, 5, 421-449.	4.1	55
34	An exact Gibbs sampler for the Markov-modulated Poisson process. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2006, 68, 767-784.	1.1	54
35	Piecewise Deterministic Markov Processes for Continuous-Time Monte Carlo. <i>Statistical Science</i> , 2018, 33, .	1.6	47
36	A Novel Method with Improved Power To Detect Recombination Hotspots from Polymorphism Data Reveals Multiple Hotspots in Human Genes. <i>American Journal of Human Genetics</i> , 2005, 77, 781-794.	2.6	45

#	ARTICLE	IF	CITATIONS
37	Stochastic Gradient Markov Chain Monte Carlo. <i>Journal of the American Statistical Association</i> , 2021, 116, 433-450.	1.8	45
38	Exact filtering for partially observed continuous time models. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2004, 66, 771-789.	1.1	41
39	A Comparison of Three Estimators of the Population-Scaled Recombination Rate: Accuracy and Robustness. <i>Genetics</i> , 2005, 171, 2051-2062.	1.2	38
40	Fast nonconvex deconvolution of calcium imaging data. <i>Biostatistics</i> , 2020, 21, 709-726.	0.9	38
41	An Adaptive Sequential Monte Carlo Sampler. <i>Bayesian Analysis</i> , 2013, 8, .	1.6	37
42	Consistency of estimators of the population-scaled recombination rate. <i>Theoretical Population Biology</i> , 2003, 64, 67-79.	0.5	35
43	On the asymptotic efficiency of approximate Bayesian computation estimators. <i>Biometrika</i> , 2018, 105, 285-299.	1.3	34
44	Semi-automatic selection of summary statistics for ABC model choice. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 67-82.	0.2	32
45	Perfect Simulation from Population Genetic Models with Selection. <i>Theoretical Population Biology</i> , 2001, 59, 263-279.	0.5	30
46	Detecting Changes in Slope With an $L_0$ Penalty. <i>Journal of Computational and Graphical Statistics</i> , 2019, 28, 265-275.	0.9	30
47	On Estimating the Ability of NBA Players. <i>Journal of Quantitative Analysis in Sports</i> , 2011, 7, .	0.5	29
48	Piecewise deterministic Markov processes for scalable Monte Carlo on restricted domains. <i>Statistics and Probability Letters</i> , 2018, 136, 148-154.	0.4	29
49	The common ancestor at a nonneutral locus. <i>Journal of Applied Probability</i> , 2002, 39, 38-54.	0.4	28
50	Random-Weight Particle Filtering of Continuous Time Processes. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2010, 72, 497-512.	1.1	28
51	<i>Campylobacter jejuni</i> colonization and population structure in urban populations of ducks and starlings in New Zealand. <i>MicrobiologyOpen</i> , 2013, 2, 659-673.	1.2	28
52	Control variates for stochastic gradient MCMC. <i>Statistics and Computing</i> , 2019, 29, 599-615.	0.8	27
53	Using Random Quasi-Monte-Carlo Within Particle Filters, With Application to Financial Time Series. <i>Journal of Computational and Graphical Statistics</i> , 2005, 14, 751-769.	0.9	26
54	Bayesian Analysis of Isochores. <i>Journal of the American Statistical Association</i> , 2009, 104, 132-141.	1.8	25

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55	Efficient Bayesian analysis of multiple changepoint models with dependence across segments. <i>Statistics and Computing</i> , 2011, 21, 217-229.	0.8	25
56	Markov Chain Monte Carlo for Exact Inference for Diffusions. <i>Scandinavian Journal of Statistics</i> , 2013, 40, 294-321.	0.9	25
57	Whole-Genome Comparison of Two <i>Campylobacter jejuni</i> Isolates of the Same Sequence Type Reveals Multiple Loci of Different Ancestral Lineage. <i>PLoS ONE</i> , 2011, 6, e27121.	1.1	25
58	Bayesian Detection of Abnormal Segments in Multiple Time Series. <i>Bayesian Analysis</i> , 2017, 12, .	1.6	24
59	The common ancestor at a nonneutral locus. <i>Journal of Applied Probability</i> , 2002, 39, 38-54.	0.4	21
60	Markov Chain Monte Carlo, Sufficient Statistics, and Particle Filters. <i>Journal of Computational and Graphical Statistics</i> , 2002, 11, 848-862.	0.9	20
61	Most Recent Changepoint Detection in Panel Data. <i>Technometrics</i> , 2019, 61, 88-98.	1.3	19
62	Spatio-temporal epidemiology of <i>Campylobacter jejuni</i> enteritis, in an area of Northwest England, 2000-2002. <i>Epidemiology and Infection</i> , 2010, 138, 1384-1390.	1.0	18
63	Convergence of regression-adjusted approximate Bayesian computation. <i>Biometrika</i> , 2018, 105, 301-318.	1.3	18
64	Detecting Abrupt Changes in the Presence of Local Fluctuations and Autocorrelated Noise. <i>Journal of the American Statistical Association</i> , 2022, 117, 2147-2162.	1.8	18
65	Filtering recursions for calculating likelihoods for queues based on inter-departure time data. <i>Statistics and Computing</i> , 2004, 14, 261-266.	0.8	16
66	Ancestral processes for non-neutral models of complex diseases. <i>Theoretical Population Biology</i> , 2003, 63, 115-130.	0.5	14
67	Innovative and Additive Outlier Robust Kalman Filtering With a Robust Particle Filter. <i>IEEE Transactions on Signal Processing</i> , 2022, 70, 47-56.	3.2	14
68	Particle Metropolis-adjusted Langevin algorithms. <i>Biometrika</i> , 2016, 103, 701-717.	1.3	13
69	Relating and comparing methods for detecting changes in mean. <i>Stat</i> , 2020, 9, e291.	0.3	13
70	Particle Approximations of the Score and Observed Information Matrix for Parameter Estimation in State-Space Models With Linear Computational Cost. <i>Journal of Computational and Graphical Statistics</i> , 2016, 25, 1138-1157.	0.9	12
71	Direct simulation for discrete mixture distributions. <i>Statistics and Computing</i> , 2005, 15, 125-133.	0.8	11
72	The stationary distribution of allele frequencies when selection acts at unlinked loci. <i>Theoretical Population Biology</i> , 2006, 70, 376-386.	0.5	11

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73	Perfect Simulation From Nonneutral Population Genetic Models: Variable Population Size and Population Subdivision. <i>Genetics</i> , 2006, 174, 1397-1406.	1.2	10
74	Estimating the Relative Roles of Recombination and Point Mutation in the Generation of Single Locus Variants in <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> . <i>Journal of Molecular Evolution</i> , 2012, 74, 273-280.	0.8	9
75	Augmentation schemes for particle MCMC. <i>Statistics and Computing</i> , 2016, 26, 1293-1306.	0.8	9
76	Subset Multivariate Collective and Point Anomaly Detection. <i>Journal of Computational and Graphical Statistics</i> , 2022, 31, 574-585.	0.9	9
77	A linear time method for the detection of collective and point anomalies. <i>Statistical Analysis and Data Mining</i> , 2022, 15, 494-508.	1.4	9
78	Maximum-Likelihood Estimation of Coalescence Times in Genealogical Trees. <i>Genetics</i> , 2005, 171, 2073-2084.	1.2	8
79	Postprocessing of Genealogical Trees. <i>Genetics</i> , 2007, 177, 347-358.	1.2	8
80	Testing for a Change in Mean after Change-point Detection. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2022, 84, 1082-1104.	1.1	8
81	Filtering Methods for Mixture Models. <i>Journal of Computational and Graphical Statistics</i> , 2007, 16, 586-607.	0.9	7
82	Calculating Strength of Schedule, and Choosing Teams for March Madness. <i>American Statistician</i> , 2010, 64, 108-115.	0.9	7
83	MCMC for State-Space Models. <i>Chapman &amp; Hall/CRC Interdisciplinary Statistics Series</i> , 2011, , 513-530.	0.4	7
84	Classification of non-stationary time series. <i>Stat</i> , 2014, 3, 144-157.	0.3	6
85	Bayesian Sequential Experimental Design for Binary Response Data with Application to Electromyographic Experiments. <i>Bayesian Analysis</i> , 2014, 9, .	1.6	6
86	Scalable change-point and anomaly detection in cross-correlated data with an application to condition monitoring. <i>Annals of Applied Statistics</i> , 2022, 16, .	0.5	6
87	<b>sgmcmc</b> : An R Package for Stochastic Gradient Markov Chain Monte Carlo. <i>Journal of Statistical Software</i> , 2019, 91, .	1.8	5
88	Reversible Jump PDMP Samplers for Variable Selection. <i>Journal of the American Statistical Association</i> , 2023, 118, 2915-2927.	1.8	5
89	Estimating the relative rate of recombination to mutation in bacteria from single-locus variants using composite likelihood methods. <i>Annals of Applied Statistics</i> , 2015, 9, .	0.5	4
90	BayesProject: Fast computation of a projection direction for multivariate change-point detection. <i>Statistics and Computing</i> , 2020, 30, 1691-1705.	0.8	4

#	ARTICLE	IF	CITATIONS
91	Efficient Online Inference for Multiple Changepoint Problems. , 2006, , .		3
92	Tractable diffusion and coalescent processes for weakly correlated loci. Electronic Journal of Probability, 2015, 20, .	0.5	3
93	Quasi-Stationary Monte Carlo and the ScaLE algorithm. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2020, 82, 1167-1221.	1.1	3
94	Haplotypes: the joint distribution of alleles at linked loci. Journal of Applied Probability, 2003, 40, 505-512.	0.4	3
95	Haplotypes: the joint distribution of alleles at linked loci. Journal of Applied Probability, 2003, 40, 505-512.	0.4	2
96	On the Choice of Genetic Distance in Spatial-Genetic Studies. Genetics, 2007, 177, 427-434.	1.2	2
97	Editorial: Special issue on adaptive Monte Carlo methods. Statistics and Computing, 2008, 18, 341-342.	0.8	2
98	ON THE IDENTIFICATION AND MITIGATION OF WEAKNESSES IN THE KNOWLEDGE GRADIENT POLICY FOR MULTI-ARMED BANDITS. Probability in the Engineering and Informational Sciences, 2017, 31, 239-263.	0.6	2
99	Semi-automated simultaneous predictor selection for regression-SARIMA models. Statistics and Computing, 2020, 30, 1759-1778.	0.8	2
100	Motor unit number estimation via sequential Monte Carlo. Computational Statistics and Data Analysis, 2020, 144, 106845.	0.7	1
101	A Second-Order Approximation to the Log-Likelihood Surface for Mixture Models, With Application to the EM Algorithm. Journal of Computational and Graphical Statistics, 2004, 13, 739-750.	0.9	0
102	Comment on Article by Wyse et al.. Bayesian Analysis, 2011, 6, .	1.6	0