

Paul Fearnhead

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6886582/publications.pdf>

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 | Reversible Jump PDMP Samplers for Variable Selection. <i>Journal of the American Statistical Association</i> , 2023, 118, 2915-2927. | 1.8 | 5 |
| 2 | 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 |
| 3 | Subset Multivariate Collective and Point Anomaly Detection. <i>Journal of Computational and Graphical Statistics</i> , 2022, 31, 574-585. | 0.9 | 9 |
| 4 | 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 |
| 5 | Testing for a Change in Mean after Changepoint Detection. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2022, 84, 1082-1104. | 1.1 | 8 |
| 6 | 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 |
| 7 | 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 |
| 8 | Stochastic Gradient Markov Chain Monte Carlo. <i>Journal of the American Statistical Association</i> , 2021, 116, 433-450. | 1.8 | 45 |
| 9 | Fast nonconvex deconvolution of calcium imaging data. <i>Biostatistics</i> , 2020, 21, 709-726. | 0.9 | 38 |
| 10 | Motor unit number estimation via sequential Monte Carlo. <i>Computational Statistics and Data Analysis</i> , 2020, 144, 106845. | 0.7 | 1 |
| 11 | Quasi-stationary Monte Carlo and the ScaLE algorithm. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2020, 82, 1167-1221. | 1.1 | 3 |
| 12 | BayesProject: Fast computation of a projection direction for multivariate changepoint detection. <i>Statistics and Computing</i> , 2020, 30, 1691-1705. | 0.8 | 4 |
| 13 | Semi-automated simultaneous predictor selection for regression-SARIMA models. <i>Statistics and Computing</i> , 2020, 30, 1759-1778. | 0.8 | 2 |
| 14 | Relating and comparing methods for detecting changes in mean. <i>Stat</i> , 2020, 9, e291. | 0.3 | 13 |
| 15 | Control variates for stochastic gradient MCMC. <i>Statistics and Computing</i> , 2019, 29, 599-615. | 0.8 | 27 |
| 16 | The Zig-Zag process and super-efficient sampling for Bayesian analysis of big data. <i>Annals of Statistics</i> , 2019, 47, . | 1.4 | 99 |
| 17 | Detecting Changes in Slope With an L_0 Penalty. <i>Journal of Computational and Graphical Statistics</i> , 2019, 28, 265-275. | 0.9 | 30 |
| 18 | Changepoint Detection in the Presence of Outliers. <i>Journal of the American Statistical Association</i> , 2019, 114, 169-183. | 1.8 | 79 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Most Recent Changepoint Detection in Panel Data. <i>Technometrics</i> , 2019, 61, 88-98. | 1.3 | 19 |
| 20 | sgmcmc : An <i>R</i> Package for Stochastic Gradient Markov Chain Monte Carlo. <i>Journal of Statistical Software</i> , 2019, 91, . | 1.8 | 5 |
| 21 | Piecewise deterministic Markov processes for scalable Monte Carlo on restricted domains. <i>Statistics and Probability Letters</i> , 2018, 136, 148-154. | 0.4 | 29 |
| 22 | Particle Filters and Data Assimilation. <i>Annual Review of Statistics and Its Application</i> , 2018, 5, 421-449. | 4.1 | 55 |
| 23 | Piecewise Deterministic Markov Processes for Continuous-Time Monte Carlo. <i>Statistical Science</i> , 2018, 33, . | 1.6 | 47 |
| 24 | On the asymptotic efficiency of approximate Bayesian computation estimators. <i>Biometrika</i> , 2018, 105, 285-299. | 1.3 | 34 |
| 25 | Convergence of regression-adjusted approximate Bayesian computation. <i>Biometrika</i> , 2018, 105, 301-318. | 1.3 | 18 |
| 26 | Computationally Efficient Changepoint Detection for a Range of Penalties. <i>Journal of Computational and Graphical Statistics</i> , 2017, 26, 134-143. | 0.9 | 60 |
| 27 | On optimal multiple changepoint algorithms for large data. <i>Statistics and Computing</i> , 2017, 27, 519-533. | 0.8 | 94 |
| 28 | A computationally efficient nonparametric approach for changepoint detection. <i>Statistics and Computing</i> , 2017, 27, 1293-1305. | 0.8 | 86 |
| 29 | Bayesian Detection of Abnormal Segments in Multiple Time Series. <i>Bayesian Analysis</i> , 2017, 12, . | 1.6 | 24 |
| 30 | ON THE IDENTIFICATION AND MITIGATION OF WEAKNESSES IN THE KNOWLEDGE GRADIENT POLICY FOR MULTI-ARMED BANDITS. <i>Probability in the Engineering and Informational Sciences</i> , 2017, 31, 239-263. | 0.6 | 2 |
| 31 | Particle Metropolis-adjusted Langevin algorithms. <i>Biometrika</i> , 2016, 103, 701-717. | 1.3 | 13 |
| 32 | 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 |
| 33 | Augmentation schemes for particle MCMC. <i>Statistics and Computing</i> , 2016, 26, 1293-1306. | 0.8 | 9 |
| 34 | 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 |
| 35 | Tractable diffusion and coalescent processes for weakly correlated loci. <i>Electronic Journal of Probability</i> , 2015, 20, . | 0.5 | 3 |
| 36 | Classification of non-stationary time series. <i>Stat</i> , 2014, 3, 144-157. | 0.3 | 6 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | 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 |
| 38 | Inference for reaction networks using the linear noise approximation. <i>Biometrics</i> , 2014, 70, 457-466. | 0.8 | 65 |
| 39 | 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 |
| 40 | Bayesian Sequential Experimental Design for Binary Response Data with Application to Electromyographic Experiments. <i>Bayesian Analysis</i> , 2014, 9, . | 1.6 | 6 |
| 41 | Markov Chain Monte Carlo for Exact Inference for Diffusions. <i>Scandinavian Journal of Statistics</i> , 2013, 40, 294-321. | 0.9 | 25 |
| 42 | <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 |
| 43 | An Adaptive Sequential Monte Carlo Sampler. <i>Bayesian Analysis</i> , 2013, 8, . | 1.6 | 37 |
| 44 | 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 |
| 45 | 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 |
| 46 | 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 |
| 47 | Analysis of changepoint models. , 2011, , 205-224. | | 68 |
| 48 | Comment on Article by Wyse et al.. <i>Bayesian Analysis</i> , 2011, 6, . | 1.6 | 0 |
| 49 | Efficient Bayesian analysis of multiple changepoint models with dependence across segments. <i>Statistics and Computing</i> , 2011, 21, 217-229. | 0.8 | 25 |
| 50 | On Estimating the Ability of NBA Players. <i>Journal of Quantitative Analysis in Sports</i> , 2011, 7, . | 0.5 | 29 |
| 51 | MCMC for Stateâ€“Space Models. <i>Chapman & Hall/CRC Interdisciplinary Statistics Series</i> , 2011, , 513-530. | 0.4 | 7 |
| 52 | 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 |
| 53 | Spatio-temporal epidemiology of <i>Campylobacter jejuni</i> enteritis, in an area of Northwest England, 2000â€“2002. <i>Epidemiology and Infection</i> , 2010, 138, 1384-1390. | 1.0 | 18 |
| 54 | The Random Walk Metropolis: Linking Theory and Practice Through a Case Study. <i>Statistical Science</i> , 2010, 25, . | 1.6 | 65 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 55 | 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 |
| 56 | A sequential smoothing algorithm with linear computational cost. <i>Biometrika</i> , 2010, 97, 447-464. | 1.3 | 88 |
| 57 | Calculating Strength of Schedule, and Choosing Teams for March Madness. <i>American Statistician</i> , 2010, 64, 108-115. | 0.9 | 7 |
| 58 | Bayesian Analysis of Isochores. <i>Journal of the American Statistical Association</i> , 2009, 104, 132-141. | 1.8 | 25 |
| 59 | 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 |
| 60 | 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 |
| 61 | Editorial: Special issue on adaptive Monte Carlo methods. <i>Statistics and Computing</i> , 2008, 18, 341-342. | 0.8 | 2 |
| 62 | 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 |
| 63 | Tracing the Source of <i>Campylobacteriosis</i> . <i>PLoS Genetics</i> , 2008, 4, e1000203. | 1.5 | 365 |
| 64 | Postprocessing of Genealogical Trees. <i>Genetics</i> , 2007, 177, 347-358. | 1.2 | 8 |
| 65 | On the Choice of Genetic Distance in Spatial-Genetic Studies. <i>Genetics</i> , 2007, 177, 427-434. | 1.2 | 2 |
| 66 | Filtering Methods for Mixture Models. <i>Journal of Computational and Graphical Statistics</i> , 2007, 16, 586-607. | 0.9 | 7 |
| 67 | 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 |
| 68 | 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 |
| 69 | Efficient Online Inference for Multiple Changepoint Problems. , 2006, , . | | 3 |
| 70 | Perfect Simulation From Nonneutral Population Genetic Models: Variable Population Size and Population Subdivision. <i>Genetics</i> , 2006, 174, 1397-1406. | 1.2 | 10 |
| 71 | The stationary distribution of allele frequencies when selection acts at unlinked loci. <i>Theoretical Population Biology</i> , 2006, 70, 376-386. | 0.5 | 11 |
| 72 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 73 | 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 |
| 74 | Exact and efficient Bayesian inference for multiple changepoint problems. <i>Statistics and Computing</i> , 2006, 16, 203-213. | 0.8 | 313 |
| 75 | SequenceLDhot: detecting recombination hotspots. <i>Bioinformatics</i> , 2006, 22, 3061-3066. | 1.8 | 66 |
| 76 | 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 |
| 77 | 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 |
| 78 | Direct simulation for discrete mixture distributions. <i>Statistics and Computing</i> , 2005, 15, 125-133. | 0.8 | 11 |
| 79 | Maximum-Likelihood Estimation of Coalescence Times in Genealogical Trees. <i>Genetics</i> , 2005, 171, 2073-2084. | 1.2 | 8 |
| 80 | A Comparison of Three Estimators of the Population-Scaled Recombination Rate: Accuracy and Robustness. <i>Genetics</i> , 2005, 171, 2051-2062. | 1.2 | 38 |
| 81 | 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 |
| 82 | 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 |
| 83 | Exact Bayesian curve fitting and signal segmentation. <i>IEEE Transactions on Signal Processing</i> , 2005, 53, 2160-2166. | 3.2 | 77 |
| 84 | Application of Coalescent Methods to Reveal Fine-Scale Rate Variation and Recombination Hotspots. <i>Genetics</i> , 2004, 167, 2067-2081. | 1.2 | 62 |
| 85 | 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 |
| 86 | Particle filters for mixture models with an unknown number of components. <i>Statistics and Computing</i> , 2004, 14, 11-21. | 0.8 | 71 |
| 87 | 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 |
| 88 | A Second-Order Approximation to the Log-Likelihood Surface for Mixture Models, With Application to the EM Algorithm. <i>Journal of Computational and Graphical Statistics</i> , 2004, 13, 739-750. | 0.9 | 0 |
| 89 | 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 |
| 90 | Ancestral processes for non-neutral models of complex diseases. <i>Theoretical Population Biology</i> , 2003, 63, 115-130. | 0.5 | 14 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 91 | Consistency of estimators of the population-scaled recombination rate. <i>Theoretical Population Biology</i> , 2003, 64, 67-79. | 0.5 | 35 |
| 92 | Haplotypes: the joint distribution of alleles at linked loci. <i>Journal of Applied Probability</i> , 2003, 40, 505-512. | 0.4 | 2 |
| 93 | Haplotypes: the joint distribution of alleles at linked loci. <i>Journal of Applied Probability</i> , 2003, 40, 505-512. | 0.4 | 3 |
| 94 | The common ancestor at a nonneutral locus. <i>Journal of Applied Probability</i> , 2002, 39, 38-54. | 0.4 | 21 |
| 95 | The common ancestor at a nonneutral locus. <i>Journal of Applied Probability</i> , 2002, 39, 38-54. | 0.4 | 28 |
| 96 | Markov chain Monte Carlo, Sufficient Statistics, and Particle Filters. <i>Journal of Computational and Graphical Statistics</i> , 2002, 11, 848-862. | 0.9 | 107 |
| 97 | 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 |
| 98 | A Coalescent-Based Method for Detecting and Estimating Recombination From Gene Sequences. <i>Genetics</i> , 2002, 160, 1231-1241. | 1.2 | 624 |
| 99 | Markov Chain Monte Carlo, Sufficient Statistics, and Particle Filters. <i>Journal of Computational and Graphical Statistics</i> , 2002, 11, 848-862. | 0.9 | 20 |
| 100 | Perfect Simulation from Population Genetic Models with Selection. <i>Theoretical Population Biology</i> , 2001, 59, 263-279. | 0.5 | 30 |
| 101 | Estimating Recombination Rates From Population Genetic Data. <i>Genetics</i> , 2001, 159, 1299-1318. | 1.2 | 272 |
| 102 | Improved particle filter for nonlinear problems. <i>IET Radar, Sonar & Navigation</i> , 1999, 146, 2. | 2.1 | 649 |