

Jun S Liu

List of PR Articles by Year in descending order

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89

PR articles

4,985

PR citations

113398

31

PR h-index

72913

68

g-index

100

documents

12005

doc citations

114578

33

h-index

17146

citing authors

| # | ARTICLE | IF | PR CITATIONS |
|----|---|------|--------------|
| 1 | Monotone Cubic B-Splines with a Neural-Network Generator. Journal of Computational and Graphical Statistics, 2025, 34, 1102-1116. | 1.9 | 0 |
| 2 | A phylogenetic method linking nucleotide substitution rates to rates of continuous trait evolution. PLoS Computational Biology, 2024, 20, e1011995. | 3.2 | 10 |
| 3 | Partitioning and aggregating cross-tissue and tissue-specific genetic effects to identify gene-trait associations. Nature Communications, 2024, 15, . | 13.9 | 5 |
| 4 | Controlling False Discovery Rate Using Gaussian Mirrors. Journal of the American Statistical Association, 2023, 118, 222-241. | 3.5 | 27 |
| 5 | Partitioning Mallows Model and Its Inference for Rank Aggregation. Journal of the American Statistical Association, 2023, 118, 343-359. | 3.5 | 8 |
| 6 | Kernel-Based Partial Permutation Test for Detecting Heterogeneous Functional Relationship. Journal of the American Statistical Association, 2023, 118, 1429-1447. | 3.5 | 0 |
| 7 | False Discovery Rate Control via Data Splitting. Journal of the American Statistical Association, 2023, 118, 2503-2520. | 3.5 | 50 |
| 8 | Discovery of Targets for Immune-Metabolic Antitumor Drugs Identifies Estrogen-Related Receptor Alpha. Cancer Discovery, 2023, 13, 672-701. | 25.6 | 31 |
| 9 | Convergence rate of multiple-try Metropolis independent sampler. Statistics and Computing, 2023, 33, . | 1.1 | 2 |
| 10 | Monte Carlo Approximation of Bayes Factors via Mixing With Surrogate Distributions. Journal of the American Statistical Association, 2022, 117, 765-780. | 3.5 | 7 |
| 11 | On Posterior Consistency of Bayesian Factor Models in High Dimensions. Bayesian Analysis, 2022, 17, . | 1.5 | 2 |
| 12 | Neuronized Priors for Bayesian Sparse Linear Regression. Journal of the American Statistical Association, 2022, 117, 1695-1710. | 3.5 | 12 |
| 13 | A data-adaptive Bayesian regression approach for polygenic risk prediction. Bioinformatics, 2022, 38, 1938-1946. | 4.7 | 3 |
| 14 | Bayesian Analysis of Rank Data with Covariates and Heterogeneous Rankers. Statistical Science, 2022, 37, . | 1.9 | 7 |
| 15 | Multi-Cell-Type Openness-Weighted Association Studies for Trait-Associated Genomic Segments Prioritization. Genes, 2022, 13, 1220. | 2.6 | 0 |
| 16 | MIRACLE: an individual-specific approach to improve microRNA-target prediction based on a random contact model. Briefings in Bioinformatics, 2021, 22, . | 6.8 | 2 |
| 17 | A RIPK1-regulated inflammatory microglial state in amyotrophic lateral sclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 7.8 | 63 |
| 18 | Openness weighted association studies: leveraging personal genome information to prioritize non-coding variants. Bioinformatics, 2021, 37, 4737-4743. | 4.7 | 4 |

| # | ARTICLE | IF | PR CITATIONS |
|----|--|------|--------------|
| 19 | Limited memory optimizes cooperation in social dilemma experiments. Royal Society Open Science, 2021, 8, 210653. | 2.5 | 8 |
| 20 | Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 647-656. | 3.0 | 2 |
| 21 | An Extended Mallows Model for Ranked Data Aggregation. Journal of the American Statistical Association, 2020, 115, 730-746. | 3.5 | 9 |
| 22 | SIMPLEs: a single-cell RNA sequencing imputation strategy preserving gene modules and cell clusters variation. NAR Genomics and Bioinformatics, 2020, 2, . | 2.2 | 11 |
| 23 | IMMIGRATE: A Margin-Based Feature Selection Method with Interaction Terms. Entropy, 2020, 22, 291. | 1.8 | 0 |
| 24 | Determinants of transcription factor regulatory range. Nature Communications, 2020, 11, . | 13.9 | 67 |
| 25 | Wang-Landau algorithm as stochastic optimization and its acceleration. Physical Review E, 2020, 101, . | 2.2 | 4 |
| 26 | New Algorithms in RNA Structure Prediction Based on BHG. International Journal of Pattern Recognition and Artificial Intelligence, 2020, 34, 2050031. | 1.3 | 1 |
| 27 | Randomization Inference for Peer Effects. Journal of the American Statistical Association, 2019, 114, 1651-1664. | 3.5 | 15 |
| 28 | Landscape of B cell immunity and related immune evasion in human cancers. Nature Genetics, 2019, 51, 560-567. | 25.9 | 145 |
| 29 | Robust Variable and Interaction Selection for Logistic Regression and General Index Models. Journal of the American Statistical Association, 2019, 114, 271-286. | 3.5 | 27 |
| 30 | Bayesian Inference for Assessing Effects of Email Marketing Campaigns. Journal of Business and Economic Statistics, 2018, 36, 253-266. | 2.9 | 20 |
| 31 | Genome-Scale Signatures of Gene Interaction from Compound Screens Predict Clinical Efficacy of Targeted Cancer Therapies. Cell Systems, 2018, 6, 343-354.e5. | 6.0 | 48 |
| 32 | Systems biology analysis reveals new insights into invasive lung cancer. BMC Systems Biology, 2018, 12, . | 3.2 | 3 |
| 33 | A hotspots analysis-relation discovery representation model for revealing diabetes mellitus and obesity. BMC Systems Biology, 2018, 12, . | 3.2 | 6 |
| 34 | Interpretable selection and visualization of features and interactions using Bayesian forests. Statistics and Its Interface, 2018, 11, 503-513. | 0.4 | 2 |
| 35 | Personalized chemotherapy selection for breast cancer using gene expression profiles. Scientific Reports, 2017, 7, . | 3.5 | 15 |
| 36 | Fast <i>de novo</i> discovery of low-energy protein loop conformations. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1402-1412. | 2.7 | 11 |

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|----|--|------|--------------|
| 37 | Exploring genetic associations with ceRNA regulation in the human genome. <i>Nucleic Acids Research</i> , 2017, 45, 5653-5665. | 15.8 | 46 |
| 38 | MetaGen: reference-free learning with multiple metagenomic samples. <i>Genome Biology</i> , 2017, 18, . | 8.2 | 17 |
| 39 | On parallelizable Markov chain Monte Carlo algorithms with waste-recycling. <i>Statistics and Computing</i> , 2017, 28, 1073-1081. | 1.1 | 8 |
| 40 | CLIC, a tool for expanding biological pathways based on co-expression across thousands of datasets. <i>PLoS Computational Biology</i> , 2017, 13, e1005653. | 3.2 | 34 |
| 41 | Statistical inference for time course RNA-Seq data using a negative binomial mixed-effect model. <i>BMC Bioinformatics</i> , 2016, 17, . | 3.0 | 25 |
| 42 | High-dimensional genomic data bias correction and data integration using MANCIE. <i>Nature Communications</i> , 2016, 7, . | 13.9 | 54 |
| 43 | On the unsupervised analysis of domain-specific Chinese texts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6154-6159. | 7.8 | 27 |
| 44 | Predicting regulatory variants with composite statistic. <i>Bioinformatics</i> , 2016, 32, 2729-2736. | 4.7 | 45 |
| 45 | Signed support recovery for single index models in high-dimensions. <i>Annals of Mathematical Sciences and Applications</i> , 2016, 1, 379-426. | 0.2 | 10 |
| 46 | Long-term drug costs per life-month gained associated with first-line treatments for unresectable or metastatic melanoma. <i>Experimental Hematology and Oncology</i> , 2015, 5, . | 10.6 | 1 |
| 47 | Inference of transcriptional regulation in cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7731-7736. | 7.8 | 89 |
| 48 | Sequence determinants of improved CRISPR sgRNA design. <i>Genome Research</i> , 2015, 25, 1147-1157. | 4.6 | 618 |
| 49 | Bayesian Partition Models for Identifying Expression Quantitative Trait Loci. <i>Journal of the American Statistical Association</i> , 2015, 110, 1350-1361. | 3.5 | 2 |
| 50 | dslice: an R package for nonparametric testing of associations with application in QTL and gene set analysis. <i>Bioinformatics</i> , 2015, 31, 1842-1844. | 4.7 | 2 |
| 51 | Conformational sampling and structure prediction of multiple interacting loops in soluble and β -barrel membrane proteins using multi-loop distance-guided chain-growth Monte Carlo method. <i>Bioinformatics</i> , 2015, 31, 2646-2652. | 4.7 | 16 |
| 52 | Risk Classification With an Adaptive Naive Bayes Kernel Machine Model. <i>Journal of the American Statistical Association</i> , 2015, 110, 393-404. | 3.5 | 24 |
| 53 | Bayesian Aggregation of Order-Based Rank Data. <i>Journal of the American Statistical Association</i> , 2014, 109, 1023-1039. | 3.5 | 49 |
| 54 | Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. <i>Quantitative Biology</i> , 2013, 1, 156-174. | 1.0 | 31 |

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|----|---|-----|--------------|
| 55 | Bayesian Inference of Spatial Organizations of Chromosomes. PLoS Computational Biology, 2013, 9, e1002893. | 3.2 | 204 |
| 56 | On Delay Tomography: Fast Algorithms and Spatially Dependent Models. IEEE Transactions on Signal Processing, 2012, 60, 5685-5697. | 4.4 | 11 |
| 57 | A Multiresolution Method for Parameter Estimation of Diffusion Processes. Journal of the American Statistical Association, 2012, 107, 1558-1574. | 3.5 | 16 |
| 58 | Rasch Model and Its Extensions for Analysis of Aphasic Deficits in Syntactic Comprehension. Journal of the American Statistical Association, 2011, 106, 1304-1316. | 3.5 | 3 |
| 59 | Identifying Differentially Expressed Genes in Time Course Microarray Data. Statistics in Biosciences, 2009, 1, 144-159. | 0.3 | 19 |
| 60 | Bayesian Clustering of Transcription Factor Binding Motifs. Journal of the American Statistical Association, 2008, 103, 188-200. | 3.5 | 19 |
| 61 | Evolutionary Monte Carlo Methods for Clustering. Journal of Computational and Graphical Statistics, 2007, 16, 855-876. | 1.9 | 6 |
| 62 | Implementation of Estimating Function-Based Inference Procedures With Markov Chain Monte Carlo Samplers. Journal of the American Statistical Association, 2007, 102, 881-888. | 3.5 | 21 |
| 63 | Sequential Monte Carlo Methods for Statistical Analysis of Tables. Journal of the American Statistical Association, 2005, 100, 109-120. | 3.5 | 243 |
| 64 | Discussions on "A Bayesian Approach to DNA Sequence Segmentation". Biometrics, 2004, 60, 582-583. | 1.6 | 1 |
| 65 | Discovery of Conserved Sequence Patterns Using a Stochastic Dictionary Model. Journal of the American Statistical Association, 2003, 98, 55-66. | 3.5 | 51 |
| 66 | A new sequential importance sampling method and its application to the two-dimensional hydrophobic-hydrophilic model. Journal of Chemical Physics, 2002, 117, 3492-3498. | 2.9 | 59 |
| 67 | A Theory for Dynamic Weighting in Monte Carlo Computation. Journal of the American Statistical Association, 2001, 96, 561-573. | 3.5 | 26 |
| 68 | The Multiple-Try Method and Local Optimization in Metropolis Sampling. Journal of the American Statistical Association, 2000, 95, 121-134. | 3.5 | 261 |
| 69 | The Multiple-Try Method and Local Optimization in Metropolis Sampling. Journal of the American Statistical Association, 2000, 95, 121. | 3.5 | 47 |
| 70 | Parameter Expansion for Data Augmentation. Journal of the American Statistical Association, 1999, 94, 1264-1274. | 3.5 | 259 |
| 71 | Markovian Structures in Biological Sequence Alignments. Journal of the American Statistical Association, 1999, 94, 1. | 3.5 | 21 |
| 72 | Parameter Expansion for Data Augmentation. Journal of the American Statistical Association, 1999, 94, 1264. | 3.5 | 56 |

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|----|--|------|--------------|
| 73 | Rejection Control and Sequential Importance Sampling. Journal of the American Statistical Association, 1998, 93, 1022-1031. | 3.5 | 101 |
| 74 | Rejection Control and Sequential Importance Sampling. Journal of the American Statistical Association, 1998, 93, 1022. | 3.5 | 21 |
| 75 | Sequential Monte Carlo Methods for Dynamic Systems. Journal of the American Statistical Association, 1998, 93, 1032. | 3.5 | 931 |
| 76 | Extracting protein alignment models from the sequence database. Nucleic Acids Research, 1997, 25, 1665-1677. | 15.8 | 207 |
| 77 | Miscellanea. Peskun's theorem and a modified discrete-state Gibbs sampler. Biometrika, 1996, 83, 681-682. | 2.7 | 70 |
| 78 | Gibbs motif sampling: Detection of bacterial outer membrane protein repeats. Protein Science, 1995, 4, 1618-1632. | 6.0 | 374 |
| 79 | Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. Journal of the American Statistical Association, 1995, 90, 1156-1170. | 3.5 | 237 |
| 80 | Blind Deconvolution via Sequential Imputations. Journal of the American Statistical Association, 1995, 90, 567-576. | 3.5 | 260 |
| 81 | Blind Deconvolution via Sequential Imputations. Journal of the American Statistical Association, 1995, 90, 567. | 3.5 | 103 |
| 82 | Bayesian Models for Multiple Local Sequence Alignment and Gibbs Sampling Strategies. Journal of the American Statistical Association, 1995, 90, 1156. | 3.5 | 77 |
| 83 | Sequential Imputations and Bayesian Missing Data Problems. Journal of the American Statistical Association, 1994, 89, 278-288. | 3.5 | 696 |
| 84 | The Collapsed Gibbs Sampler in Bayesian Computations with Applications to a Gene Regulation Problem. Journal of the American Statistical Association, 1994, 89, 958-966. | 3.5 | 530 |
| 85 | The Collapsed Gibbs Sampler in Bayesian Computations with Applications to a Gene Regulation Problem. Journal of the American Statistical Association, 1994, 89, 958. | 3.5 | 67 |
| 86 | Sequential Imputations and Bayesian Missing Data Problems. Journal of the American Statistical Association, 1994, 89, 278. | 3.5 | 270 |
| 87 | Linear Combinations of Multiple Diagnostic Markers. Journal of the American Statistical Association, 1993, 88, 1350-1355. | 3.5 | 248 |
| 88 | Linear Combinations of Multiple Diagnostic Markers. Journal of the American Statistical Association, 1993, 88, 1350. | 3.5 | 38 |
| 89 | Quantitative and functional interrogation of parent-of-origin allelic expression biases in the brain. ELife, 0, 4, . | 1.6 | 86 |