

Gesine Reinert

List of Publications by Year in descending order

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Version: 2024-02-01

77
papers

2,316
citations

236925

25
h-index

233421

45
g-index

85
all docs

85
docs citations

85
times ranked

1557
citing authors

#	ARTICLE	IF	CITATIONS
1	Probabilistic and Statistical Properties of Words: An Overview. Journal of Computational Biology, 2000, 7, 1-46.	1.6	207
2	Alignment-Free Sequence Comparison (I): Statistics and Power. Journal of Computational Biology, 2009, 16, 1615-1634.	1.6	187
3	New developments of alignment-free sequence comparison: measures, statistics and next-generation sequencing. Briefings in Bioinformatics, 2014, 15, 343-353.	6.5	126
4	Stein's method and the zero bias transformation with application to simple random sampling. Annals of Applied Probability, 1997, 7, 935.	1.3	114
5	Alignment-Free Sequence Comparison (II): Theoretical Power of Comparison Statistics. Journal of Computational Biology, 2010, 17, 1467-1490.	1.6	105
6	Estimating the Number of Communities in a Network. Physical Review Letters, 2016, 117, 078301.	7.8	103
7	Multivariate normal approximation with Stein's method of exchangeable pairs under a general linearity condition. Annals of Probability, 2009, 37, .	1.8	84
8	Compound Poisson and Poisson Process Approximations for Occurrences of Multiple Words in Markov Chains. Journal of Computational Biology, 1998, 5, 223-253.	1.6	81
9	Alignment-Free Sequence Analysis and Applications. Annual Review of Biomedical Data Science, 2018, 1, 93-114.	6.5	78
10	Invariance principles for homogeneous sums: Universality of Gaussian Wiener chaos. Annals of Probability, 2010, 38, .	1.8	67
11	Deciphering chemotaxis pathways using cross species comparisons. BMC Systems Biology, 2010, 4, 3.	3.0	66
12	Stein's method for comparison of univariate distributions. Probability Surveys, 2017, 14, .	1.3	65
13	Poisson Process Approximation for Sequence Repeats, and Sequencing by Hybridization. Journal of Computational Biology, 1996, 3, 425-463.	1.6	59
14	Alignment-free protein interaction network comparison. Bioinformatics, 2014, 30, i430-i437.	4.1	48
15	Efficient method for estimating the number of communities in a network. Physical Review E, 2017, 96, 032310.	2.1	47
16	Use of exchangeable pairs in the analysis of simulations. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 2004, , 1-25.	1.0	46
17	New powerful statistics for alignment-free sequence comparison under a pattern transfer model. Journal of Theoretical Biology, 2011, 284, 106-116.	1.7	43
18	Chi-square approximation by Stein's method with application to Pearson's statistic. Annals of Applied Probability, 2017, 27, .	1.3	42

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19	Second order Poincaré inequalities and CLTs on Wiener space. Journal of Functional Analysis, 2009, 257, 593-609.	1.4	40
20	Three general approaches to Stein's method. Lecture Notes Series, Institute for Mathematical Sciences, 2005, , 183-221.	0.2	37
21	Approximating the epidemic curve. Electronic Journal of Probability, 2013, 18, .	1.0	37
22	Small worlds. Random Structures and Algorithms, 2001, 19, 54-74.	1.1	36
23	Distributional Transformations, Orthogonal Polynomials, and Stein Characterizations. Journal of Theoretical Probability, 2005, 18, 237-260.	0.8	36
24	Predicting and Validating Protein Interactions Using Network Structure. PLoS Computational Biology, 2008, 4, e1000118.	3.2	30
25	Measuring rank robustness in scored protein interaction networks. BMC Bioinformatics, 2019, 20, 446.	2.6	30
26	iPatch: Interprotein contact prediction using local network information. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2781-2797.	2.6	26
27	How threshold behaviour affects the use of subgraphs for network comparison. Bioinformatics, 2010, 26, i611-i617.	4.1	26
28	Bias in Epidemiological Studies of Conflict Mortality. Journal of Peace Research, 2008, 45, 653-663.	2.9	25
29	Inference of Markovian properties of molecular sequences from NGS data and applications to comparative genomics. Bioinformatics, 2016, 32, 993-1000.	4.1	25
30	Stein's Method for the Beta Distribution and the Pólya-Eggenberger Urn. Journal of Applied Probability, 2013, 50, 1187-1205.	0.7	24
31	Stein's Method for the Beta Distribution and the Pólya-Eggenberger Urn. Journal of Applied Probability, 2013, 50, 1187-1205.	0.7	23
32	Stein's Method and Stochastic Analysis of Rademacher Functionals. Electronic Journal of Probability, 2010, 15, .	1.0	21
33	Risk in a Large Claims Insurance Market with Bipartite Graph Structure. Operations Research, 2016, 64, 1159-1176.	1.9	20
34	Distances between nested densities and a measure of the impact of the prior in Bayesian statistics. Annals of Applied Probability, 2017, 27, .	1.3	20
35	Identifying networks with common organizational principles. Journal of Complex Networks, 2018, 6, 887-913.	1.8	20
36	Stein's method for discrete Gibbs measures. Annals of Applied Probability, 2008, 18, .	1.3	20

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37	Hypergraphs for predicting essential genes using multiprotein complex data. <i>Journal of Complex Networks</i> , 2021, 9, .	1.8	16
38	Functional module detection through integration of single-cell RNA sequencing data with protein-protein interaction networks. <i>BMC Genomics</i> , 2020, 21, 756.	2.8	13
39	A Weak Law of Large Numbers for Empirical Measures via Stein's Method. <i>Annals of Probability</i> , 1995, 23, 334.	1.8	12
40	The Power of Detecting Enriched Patterns: An HMM Approach. <i>Journal of Computational Biology</i> , 2010, 17, 581-592.	1.6	12
41	The Importance of Age and High Degree, in Protein-Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2012, 19, 785-795.	1.6	11
42	Multiple alignment-free sequence comparison. <i>Bioinformatics</i> , 2013, 29, 2690-2698.	4.1	11
43	Random subgraph counts and U -statistics: multivariate normal approximation via exchangeable pairs and embedding. <i>Journal of Applied Probability</i> , 2010, 47, 378-393.	0.7	11
44	Conditional risk measures in a bipartite market structure. <i>Scandinavian Actuarial Journal</i> , 2018, 2018, 328-355.	1.7	10
45	Robust gene coexpression networks using signed distance correlation. <i>Bioinformatics</i> , 2021, 37, 1982-1989.	4.1	10
46	Couplings for normal approximations with Stein's method. <i>DIMACS Series in Discrete Mathematics and Theoretical Computer Science</i> , 1998, , 193-207.	0.0	10
47	Approximating stationary distributions of fast mixing Glauber dynamics, with applications to exponential random graphs. <i>Annals of Applied Probability</i> , 2019, 29, .	1.3	10
48	Comparison of large networks with sub-sampling strategies. <i>Scientific Reports</i> , 2016, 6, 28955.	3.3	9
49	The Asymptotic Evolution of the General Stochastic Epidemic. <i>Annals of Applied Probability</i> , 1995, 5, .	1.3	7
50	First-order covariance inequalities via Stein's method. <i>Bernoulli</i> , 2020, 26, .	1.3	7
51	Large compound Poisson approximations for occurrences of multiple words. <i>Lecture Notes-monograph Series / Institute of Mathematical Statistics</i> , 1999, 33, 257-275.	1.0	6
52	A statistical approach using network structure in the prediction of protein characteristics. <i>Bioinformatics</i> , 2007, 23, 2314-2321.	4.1	6
53	Normal and Compound Poisson Approximations for Pattern Occurrences in NGS Reads. <i>Journal of Computational Biology</i> , 2012, 19, 839-854.	1.6	6
54	COGENT: evaluating the consistency of gene co-expression networks. <i>Bioinformatics</i> , 2021, 37, 1928-1929.	4.1	6

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55	Stein's method for the bootstrap. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 2004, , 93-132.	1.0	6
56	Random subgraph counts and U-statistics: multivariate normal approximation via exchangeable pairs and embedding. Journal of Applied Probability, 2010, 47, 378-393.	0.7	5
57	Mutual information and variants for protein domain-domain contact prediction. BMC Research Notes, 2012, 5, 472.	1.4	5
58	Local Network Patterns in Protein-Protein Interfaces. PLoS ONE, 2013, 8, e57031.	2.5	5
59	A nonparametric significance test for sampled networks. Bioinformatics, 2018, 34, 64-71.	4.1	5
60	Ruin probabilities for risk processes in a bipartite network. Stochastic Models, 2020, 36, 548-573.	0.5	5
61	Poisson approximation of subgraph counts in stochastic block models and a graphon model. ESAIM - Probability and Statistics, 2016, 20, 131-142.	0.5	4
62	On the Length of the Longest Exact Position Match in a Random Sequence. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 153-156.	3.0	3
63	Joint Vertex Degrees in the Inhomogeneous Random Graph Model $\hat{\mathcal{S}}(n, \{p_{ij}\})$. Advances in Applied Probability, 2012, 44, 139-165.	0.7	3
64	Assessment of model fit via network comparison methods based on subgraph counts. Journal of Complex Networks, 2019, 7, 226-253.	1.8	3
65	Correction: Small worlds. Random Structures and Algorithms, 2004, 25, 115-115.	1.1	2
66	The stationary distribution in the antivoter model: exact sampling and approximations. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 2004, , 75-92.	1.0	2
67	Poisson process approximation for repeats in one sequence and its application to sequencing by hybridization. Lecture Notes in Computer Science, 1996, , 209-219.	1.3	1
68	Total Variation Distance for Poisson Subset Numbers. Annals of Combinatorics, 2006, 10, 333-341.	0.6	1
69	Joint Vertex Degrees in the Inhomogeneous Random Graph Model $\hat{\mathcal{S}}(n, \{p_{ij}\})$. Advances in Applied Probability, 2012, 44, 139-165.	0.7	1
70	Stein's Method for Epidemic Processes. Monographs on Statistics and Applied Probability, 2000, , .	0.3	1
71	Extracting Information from Gene Coexpression Networks of <i>Rhizobium leguminosarum</i> . Journal of Computational Biology, 2022, , .	1.6	1
72	Generating weighted and thresholded gene coexpression networks using signed distance correlation. Network Science, 2022, 10, 131-145.	1.0	1

#	ARTICLE	IF	CITATIONS
73	Compound Poisson approximation of subgraph counts in stochastic block models with multiple edges. <i>Advances in Applied Probability</i> , 2018, 50, 759-782.	0.7	0
74	Estimating the correlation in network disturbance models. <i>Journal of Complex Networks</i> , 2021, 9, .	1.8	0
75	Probabilistic Aspects of Sequence Repeats and Sequencing by Hybridization. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 1997, , 631-641.	0.2	0
76	Triad-Based Comparison and Signatures of Directed Networks. <i>Studies in Computational Intelligence</i> , 2019, , 590-602.	0.9	0
77	Gaussian approximation of functionals: Malliavin calculus and Stein's method. , 2011, , 107-126.		0