Gesine Reinert

List of Publications by Year
in descending order

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	Extracting Information from Gene Coexpression Networks of <i>Rhizobium leguminosarum</i>. Journal of Computational Biology, 2022, , .	1.6	1
2	Generating weighted and thresholded gene coexpression networks using signed distance correlation. Network Science, 2022, 10, 131-145.	1.0	1
3	COGENT: evaluating the consistency of gene co-expression networks. Bioinformatics, 2021, 37, 1928-1929.	4.1	6
4	Robust gene coexpression networks using signed distance correlation. Bioinformatics, 2021, 37, 1982-1989.	4.1	10
5	Hypergraphs for predicting essential genes using multiprotein complex data. Journal of Complex Networks, 2021, 9, .	1.8	16
6	Estimating the correlation in network disturbance models. Journal of Complex Networks, 2021, 9, .	1.8	0
7	Functional module detection through integration of single-cell RNA sequencing data with protein–protein interaction networks. BMC Genomics, 2020, 21, 756.	2.8	13
8	Ruin probabilities for risk processes in a bipartite network. Stochastic Models, 2020, 36, 548-573.	0.5	5
9	First-order covariance inequalities via Stein's method. Bernoulli, 2020, 26, .	1.3	7
10	Assessment of model fit via network comparison methods based on subgraph counts. Journal of Complex Networks, 2019, 7, 226-253.	1.8	3
11	Measuring rank robustness in scored protein interaction networks. BMC Bioinformatics, 2019, 20, 446.	2.6	30
12	Triad-Based Comparison and Signatures of Directed Networks. Studies in Computational Intelligence, 2019, , 590-602.	0.9	0
13	Approximating stationary distributions of fast mixing Glauber dynamics, with applications to exponential random graphs. Annals of Applied Probability, 2019, 29, .	1.3	10
14	Identifying networks with common organizational principles. Journal of Complex Networks, 2018, 6, 887-913.	1.8	20
15	Alignment-Free Sequence Analysis and Applications. Annual Review of Biomedical Data Science, 2018, 1, 93-114.	6.5	78
16	A nonparametric significance test for sampled networks. Bioinformatics, 2018, 34, 64-71.	4.1	5
17	Conditional risk measures in a bipartite market structure. Scandinavian Actuarial Journal, 2018, 2018, 328-355.	1.7	10
18	Compound Poisson approximation of subgraph counts in stochastic block models with multiple edges. Advances in Applied Probability, 2018, 50, 759-782.	0.7	0

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19	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
20	Chi-square approximation by Stein's method with application to Pearson's statistic. Annals of Applied Probability, 2017, 27, .	1.3	42
21	Efficient method for estimating the number of communities in a network. Physical Review E, 2017, 96, 032310.	2.1	47
22	Stein's method for comparison of univariate distributions. Probability Surveys, 2017, 14, .	1.3	65
23	Estimating the Number of Communities in a Network. Physical Review Letters, 2016, 117, 078301.	7.8	103
24	Risk in a Large Claims Insurance Market with Bipartite Graph Structure. Operations Research, 2016, 64, 1159-1176.	1.9	20
25	Comparison of large networks with sub-sampling strategies. Scientific Reports, 2016, 6, 28955.	3.3	9
26	Inference of Markovian properties of molecular sequences from NGS data and applications to comparative genomics. Bioinformatics, 2016, 32, 993-1000.	4.1	25
27	Poisson approximation of subgraph counts in stochastic block models and a graphon model. ESAIM - Probability and Statistics, 2016, 20, 131-142.	0.5	4
28	Alignment-free protein interaction network comparison. Bioinformatics, 2014, 30, i430-i437.	4.1	48
29	New developments of alignment-free sequence comparison: measures, statistics and next-generation sequencing. Briefings in Bioinformatics, 2014, 15, 343-353.	6.5	126
30	Multiple alignment-free sequence comparison. Bioinformatics, 2013, 29, 2690-2698.	4.1	11
31	Approximating the epidemic curve. Electronic Journal of Probability, 2013, 18, .	1.0	37
32	Stein's Method for the Beta Distribution and the Pólya-Eggenberger Urn. Journal of Applied Probability, 2013, 50, 1187-1205.	0.7	23
33	Stein's Method for the Beta Distribution and the Pólya-Eggenberger Urn. Journal of Applied Probability, 2013, 50, 1187-1205.	0.7	24
34	Local Network Patterns in Protein-Protein Interfaces. PLoS ONE, 2013, 8, e57031.	2.5	5
35	Normal and Compound Poisson Approximations for Pattern Occurrences in NGS Reads. Journal of Computational Biology, 2012, 19, 839-854.	1.6	6
36	Joint Vertex Degrees in the Inhomogeneous Random Graph Model $\mathbb{G}(n, \{p_{ij}\})$. Advances in Applied Probability, 2012, 44, 139-165.	0.7	1

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37	The Importance of Age and High Degree, in Protein-Protein Interaction Networks. Journal of Computational Biology, 2012, 19, 785-795.	1.6	11
38	Mutual information and variants for protein domain-domain contact prediction. BMC Research Notes, 2012, 5, 472.	1.4	5
39	Joint Vertex Degrees in the Inhomogeneous Random Graph Model ₆„Š(n,{p_{ij}}). Advances in Applied Probability, 2012, 44, 139-165.	0.7	3
40	New powerful statistics for alignment-free sequence comparison under a pattern transfer model. Journal of Theoretical Biology, 2011, 284, 106-116.	1.7	43
41	Gaussian approximation of functionals: Malliavin calculus and Stein's method. , 2011, , 107-126.		0
42	Invariance principles for homogeneous sums: Universality of Gaussian Wiener chaos. Annals of Probability, 2010, 38, .	1.8	67
43	Deciphering chemotaxis pathways using cross species comparisons. BMC Systems Biology, 2010, 4, 3.	3.0	66
44	i₆€Patch: Interprotein contact prediction using local network information. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2781-2797.	2.6	26
45	Stein's Method and Stochastic Analysis of Rademacher Functionals. Electronic Journal of Probability, 2010, 15, .	1.0	21
46	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
47	How threshold behaviour affects the use of subgraphs for network comparison. Bioinformatics, 2010, 26, i611-i617.	4.1	26
48	The Power of Detecting Enriched Patterns: An HMM Approach. Journal of Computational Biology, 2010, 17, 581-592.	1.6	12
49	Alignment-Free Sequence Comparison (II): Theoretical Power of Comparison Statistics. Journal of Computational Biology, 2010, 17, 1467-1490.	1.6	105
50	Random subgraph counts and U-statistics: multivariate normal approximation via exchangeable pairs and embedding. Journal of Applied Probability, 2010, 47, 378-393.	0.7	11
51	Multivariate normal approximation with Stein's method of exchangeable pairs under a general linearity condition. Annals of Probability, 2009, 37, .	1.8	84
52	Second order Poincaré inequalities and CLTs on Wiener space. Journal of Functional Analysis, 2009, 257, 593-609.	1.4	40
53	Alignment-Free Sequence Comparison (I): Statistics and Power. Journal of Computational Biology, 2009, 16, 1615-1634.	1.6	187
54	Bias in Epidemiological Studies of Conflict Mortality. Journal of Peace Research, 2008, 45, 653-663.	2.9	25

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55	Predicting and Validating Protein Interactions Using Network Structure. PLoS Computational Biology, 2008, 4, e1000118.	3.2	30
56	Stein's method for discrete Gibbs measures. Annals of Applied Probability, 2008, 18, .	1.3	20
57	A statistical approach using network structure in the prediction of protein characteristics. Bioinformatics, 2007, 23, 2314-2321.	4.1	6
58	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
59	Total Variation Distance for Poisson Subset Numbers. Annals of Combinatorics, 2006, 10, 333-341.	0.6	1
60	Three general approaches to Stein's method. Lecture Notes Series, Institute for Mathematical Sciences, 2005, , 183-221.	0.2	37
61	Distributional Transformations, Orthogonal Polynomials, and Stein Characterizations. Journal of Theoretical Probability, 2005, 18, 237-260.	0.8	36
62	Correction: Small worlds. Random Structures and Algorithms, 2004, 25, 115-115.	1.1	2
63	Use of exchangeable pairs in the analysis of simulations. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 2004, , 1-25.	1.0	46
64	Stein's method for the bootstrap. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 2004, , 93-132.	1.0	6
65	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
66	Small worlds. Random Structures and Algorithms, 2001, 19, 54-74.	1.1	36
67	Probabilistic and Statistical Properties of Words: An Overview. Journal of Computational Biology, 2000, 7, 1-46.	1.6	207
68	Stein's Method for Epidemic Processes. Monographs on Statistics and Applied Probability, 2000, , .	0.3	1
69	Large compound Poisson approximations for occurrences of multiple words. Lecture Notes-monograph Series / Institute of Mathematical Statistics, 1999, 33, 257-275.	1.0	6
70	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
71	Couplings for normal approximations with Stein's method. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, 1998, , 193-207.	0.0	10
72	Stein's method and the zero bias transformation with application to simple random sampling. Annals of Applied Probability, 1997, 7, 935.	1.3	114

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73	Probabilistic Aspects of Sequence Repeats and Sequencing by Hybridization. Studies in Classification, Data Analysis, and Knowledge Organization, 1997, , 631-641.	0.2	0
74	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
75	Poisson Process Approximation for Sequence Repeats, and Sequencing by Hybridization. Journal of Computational Biology, 1996, 3, 425-463.	1.6	59
76	A Weak Law of Large Numbers for Empirical Measures via Stein's Method. Annals of Probability, 1995, 23, 334.	1.8	12
77	The Asymptotic Evolution of the General Stochastic Epidemic. Annals of Applied Probability, 1995, 5, .	1.3	7