

Carsten Wiuf

List of Publications by Year in descending order

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140
papers

8,708
citations

53794

45
h-index

48315

88
g-index

145
all docs

145
docs citations

145
times ranked

12649
citing authors

#	ARTICLE	IF	CITATIONS
1	Monitoring endangered freshwater biodiversity using environmental DNA. <i>Molecular Ecology</i> , 2012, 21, 2565-2573.	3.9	882
2	Estimating the size of the human interactome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6959-6964.	7.1	692
3	Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments. <i>Science</i> , 2003, 300, 791-795.	12.6	571
4	Diagnostic and Prognostic MicroRNAs in Stage II Colon Cancer. <i>Cancer Research</i> , 2008, 68, 6416-6424.	0.9	459
5	Subnets of scale-free networks are not scale-free: Sampling properties of networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4221-4224.	7.1	436
6	Development of a Hypoxia Gene Expression Classifier with Predictive Impact for Hypoxic Modification of Radiotherapy in Head and Neck Cancer. <i>Cancer Research</i> , 2011, 71, 5923-5931.	0.9	226
7	Gene expression classifier predicts for hypoxic modification of radiotherapy with nimorazole in squamous cell carcinomas of the head and neck. <i>Radiotherapy and Oncology</i> , 2012, 102, 122-129.	0.6	196
8	Common variants at VRK2 and TCF4 conferring risk of schizophrenia. <i>Human Molecular Genetics</i> , 2011, 20, 4076-4081.	2.9	193
9	Long-term persistence of bacterial DNA. <i>Current Biology</i> , 2004, 14, R9-R10.	3.9	189
10	Comprehensive Genome Methylation Analysis in Bladder Cancer: Identification and Validation of Novel Methylated Genes and Application of These as Urinary Tumor Markers. <i>Clinical Cancer Research</i> , 2011, 17, 5582-5592.	7.0	183
11	Recombination as a Point Process along Sequences. <i>Theoretical Population Biology</i> , 1999, 55, 248-259.	1.1	169
12	Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. <i>Nucleic Acids Research</i> , 2006, 35, 1-10.	14.5	166
13	Statistical Evidence for Miscoding Lesions in Ancient DNA Templates. <i>Molecular Biology and Evolution</i> , 2001, 18, 262-265.	8.9	151
14	Identification of endogenous retroviral reading frames in the human genome. <i>Retrovirology</i> , 2004, 1, 32.	2.0	148
15	SOX4 Expression in Bladder Carcinoma: Clinical Aspects and In vitro Functional Characterization. <i>Cancer Research</i> , 2006, 66, 3434-3442.	0.9	146
16	The Coalescent With Gene Conversion. <i>Genetics</i> , 2000, 155, 451-462.	2.9	124
17	A Simulation Study of the Reliability of Recombination Detection Methods. <i>Molecular Biology and Evolution</i> , 2001, 18, 1929-1939.	8.9	110
18	A bimodular mechanism of calcium control in eukaryotes. <i>Nature</i> , 2012, 491, 468-472.	27.8	110

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19	Model criticism based on likelihood-free inference, with an application to protein network evolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10576-10581.	7.1	106
20	Association between genetic variation in a region on chromosome 11 and schizophrenia in large samples from Europe. Molecular Psychiatry, 2012, 17, 906-917.	7.9	105
21	Statistical alignment: computational properties, homology testing and goodness-of-fit 1 Edited by J. Karn. Journal of Molecular Biology, 2000, 302, 265-279.	4.2	101
22	Crosslinks Rather Than Strand Breaks Determine Access to Ancient DNA Sequences From Frozen Sediments. Genetics, 2006, 173, 1175-1179.	2.9	100
23	Frequent occurrence of uniparental disomy in colorectal cancer. Carcinogenesis, 2007, 28, 38-48.	2.8	97
24	Assessing the Fidelity of Ancient DNA Sequences Amplified From Nuclear Genes. Genetics, 2006, 172, 733-741.	2.9	95
25	Role of Activating Fibroblast Growth Factor Receptor 3 Mutations in the Development of Bladder Tumors. Clinical Cancer Research, 2005, 11, 7709-7719.	7.0	87
26	The CATH database. Human Genomics, 2010, 4, 207.	2.9	84
27	Sampling properties of random graphs: The degree distribution. Physical Review E, 2005, 72, 036118.	2.1	80
28	Genome-wide scans using archived neonatal dried blood spot samples. BMC Genomics, 2009, 10, 297.	2.8	80
29	Conditional Genealogies and the Age of a Neutral Mutant. Theoretical Population Biology, 1999, 56, 183-201.	1.1	75
30	Powerful Inference with the D-Statistic on Low-Coverage Whole-Genome Data. G3: Genes, Genomes, Genetics, 2018, 8, 551-566.	1.8	71
31	Using Likelihood-Free Inference to Compare Evolutionary Dynamics of the Protein Networks of <i>H. pylori</i> and <i>P. falciparum</i> . PLoS Computational Biology, 2007, 3, e230.	3.2	69
32	The Probability and Chromosomal Extent of trans-specific Polymorphism. Genetics, 2004, 168, 2363-2372.	2.9	67
33	Quality assessment of DNA derived from up to 30 years old formalin fixed paraffin embedded (FFPE) tissue for PCR-based methylation analysis using SMART-MSP and MS-HRM. BMC Cancer, 2009, 9, 453.	2.6	61
34	Identifying parameter regions for multistationarity. PLoS Computational Biology, 2017, 13, e1005751.	3.2	61
35	Simplifying biochemical models with intermediate species. Journal of the Royal Society Interface, 2013, 10, 20130484.	3.4	59
36	The effects of incomplete protein interaction data on structural and evolutionary inferences. BMC Biology, 2006, 4, 39.	3.8	58

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37	Enzyme-sharing as a cause of multi-stationarity in signalling systems. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1224-1232.	3.4	58
38	Tumor-specific usage of alternative transcription start sites in colorectal cancer identified by genome-wide exon array analysis. <i>BMC Genomics</i> , 2011, 12, 505.	2.8	57
39	A likelihood approach to analysis of network data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 7566-7570.	7.1	56
40	Co-clustering and visualization of gene expression data and gene ontology terms for <i>Saccharomyces cerevisiae</i> using self-organizing maps. <i>Journal of Biomedical Informatics</i> , 2007, 40, 160-173.	4.3	55
41	High-density single nucleotide polymorphism array defines novel stage and location-dependent allelic imbalances in human bladder tumors. <i>Cancer Research</i> , 2005, 65, 34-45.	0.9	55
42	Germline Mutation in RNASEL Predicts Increased Risk of Head and Neck, Uterine Cervix and Breast Cancer. <i>PLoS ONE</i> , 2008, 3, e2492.	2.5	54
43	Ab initio identification of human microRNAs based on structure motifs. <i>BMC Bioinformatics</i> , 2007, 8, 478.	2.6	53
44	The Ancestry of a Sample of Sequences Subject to Recombination. <i>Genetics</i> , 1999, 151, 1217-1228.	2.9	53
45	Cellular Compartments Cause Multistability and Allow Cells to Process More Information. <i>Biophysical Journal</i> , 2013, 104, 1824-1831.	0.5	52
46	Genome-wide analysis of allelic imbalance in prostate cancer using the Affymetrix 50K SNP mapping array. <i>British Journal of Cancer</i> , 2007, 96, 499-506.	6.4	50
47	Evolution at the system level: the natural history of protein interaction networks. <i>Trends in Ecology and Evolution</i> , 2007, 22, 366-373.	8.7	46
48	Short Tandem Repeats in Human Exons: A Target for Disease Mutations. <i>BMC Genomics</i> , 2008, 9, 410.	2.8	45
49	Clonal Evolution in t(14;18)-Positive Follicular Lymphoma, Evidence for Multiple Common Pathways, and Frequent Parallel Clonal Evolution. <i>Clinical Cancer Research</i> , 2008, 14, 7180-7187.	7.0	45
50	Power-Law Kinetics and Determinant Criteria for the Preclusion of Multistationarity in Networks of Interacting Species. <i>SIAM Journal on Applied Dynamical Systems</i> , 2013, 12, 1685-1721.	1.6	45
51	Are microRNAs located in genomic regions associated with cancer?. <i>British Journal of Cancer</i> , 2006, 95, 1415-1418.	6.4	42
52	On the Number of Ancestors to a DNA Sequence. <i>Genetics</i> , 1997, 147, 1459-1468.	2.9	42
53	Do \hat{F}_{508} heterozygotes have a selective advantage?. <i>Genetical Research</i> , 2001, 78, 41-47.	0.9	40
54	Variable Elimination in Chemical Reaction Networks with Mass-Action Kinetics. <i>SIAM Journal on Applied Mathematics</i> , 2012, 72, 959-981.	1.8	40

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55	Lyapunov Functions, Stationary Distributions, and Non-equilibrium Potential for Reaction Networks. <i>Bulletin of Mathematical Biology</i> , 2015, 77, 1744-1767.	1.9	39
56	Consistency of estimators of population scaled parameters using composite likelihood. <i>Journal of Mathematical Biology</i> , 2006, 53, 821-841.	1.9	38
57	Product-Form Poisson-Like Distributions and Complex Balanced Reaction Systems. <i>SIAM Journal on Applied Mathematics</i> , 2016, 76, 411-432.	1.8	38
58	Fatgraph models of proteins. <i>Communications on Pure and Applied Mathematics</i> , 2010, 63, 1249-1297.	3.1	37
59	Recombination Analysis Using Directed Graphical Models. <i>Molecular Biology and Evolution</i> , 2001, 18, 97-99.	8.9	36
60	Modelling the contribution of family history and variation in single nucleotide polymorphisms to risk of schizophrenia: A Danish national birth cohort-based study. <i>Schizophrenia Research</i> , 2012, 134, 246-252.	2.0	33
61	From evidence to inference: Probing the evolution of protein interaction networks. <i>HFSP Journal</i> , 2009, 3, 290-306.	2.5	31
62	Preclusion of switch behavior in networks with mass-action kinetics. <i>Applied Mathematics and Computation</i> , 2012, 219, 1449-1467.	2.2	31
63	Estimation of tumor heterogeneity using CGH array data. <i>BMC Bioinformatics</i> , 2009, 10, 12.	2.6	30
64	An Algebraic Approach to Signaling Cascades with n Layers. <i>Bulletin of Mathematical Biology</i> , 2012, 74, 45-72.	1.9	30
65	Bounded coordinate-descent for biological sequence classification in high dimensional predictor space. , 2011, , .		28
66	Recombination in Human Mitochondrial DNA?. <i>Genetics</i> , 2001, 159, 749-756.	2.9	28
67	Increased cell motility and invasion upon knockdown of lipolysis stimulated lipoprotein receptor (LSR) in SW780 bladder cancer cells. <i>BMC Medical Genomics</i> , 2008, 1, 31.	1.5	27
68	Omics-based profiling of carcinoma of the breast and matched regional lymph node metastasis. <i>Proteomics</i> , 2008, 8, 5038-5052.	2.2	26
69	A Hidden Markov Model to estimate population mixture and allelic copy-numbers in cancers using Affymetrix SNP arrays. <i>BMC Bioinformatics</i> , 2007, 8, 434.	2.6	25
70	A computational method to preclude multistationarity in networks of interacting species. <i>Bioinformatics</i> , 2013, 29, 2327-2334.	4.1	25
71	Core signalling motif displaying multistability through multi-state enzymes. <i>Journal of the Royal Society Interface</i> , 2016, 13, 20160524.	3.4	25
72	A Coalescence Approach to Gene Conversion. <i>Theoretical Population Biology</i> , 2000, 57, 357-367.	1.1	24

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73	Importance Sampling for the Infinite Sites Model. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008, 7, Article32.	0.6	24
74	Variable elimination in post-translational modification reaction networks with mass-action kinetics. <i>Journal of Mathematical Biology</i> , 2013, 66, 281-310.	1.9	23
75	Graphical reduction of reaction networks by linear elimination of species. <i>Journal of Mathematical Biology</i> , 2017, 74, 195-237.	1.9	23
76	Simulating haplotype blocks in the human genome. <i>Bioinformatics</i> , 2003, 19, 289-290.	4.1	22
77	Tumor heterogeneity in neoplasms of breast, colon, and skin. <i>BMC Research Notes</i> , 2010, 3, 321.	1.4	20
78	A Coalescent Model of Recombination Hotspots. <i>Genetics</i> , 2003, 164, 407-417.	2.9	19
79	Evaluating Neanderthal Genetics and Phylogeny. <i>Journal of Molecular Evolution</i> , 2007, 64, 50-60.	1.8	18
80	Phosphorelays Provide Tunable Signal Processing Capabilities for the Cell. <i>PLoS Computational Biology</i> , 2013, 9, e1003322.	3.2	18
81	On the Genealogy of a Sample of Neutral Rare Alleles. <i>Theoretical Population Biology</i> , 2000, 58, 61-75.	1.1	17
82	Binomial subsampling. <i>Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences</i> , 2006, 462, 1181-1195.	2.1	17
83	Genotyping and annotation of Affymetrix SNP arrays. <i>Nucleic Acids Research</i> , 2006, 34, e100-e100.	14.5	17
84	Elimination of intermediate species in multiscale stochastic reaction networks. <i>Annals of Applied Probability</i> , 2016, 26, .	1.3	16
85	Chromosomal imbalance in the progression of high-risk non-muscle invasive bladder cancer. <i>BMC Cancer</i> , 2009, 9, 149.	2.6	15
86	A periodic pattern of SNPs in the human genome. <i>Genome Research</i> , 2007, 17, 1414-1419.	5.5	14
87	The association between genetic variants in hMLH1 and hMSH2 and the development of sporadic colorectal cancer in the Danish population. <i>BMC Medical Genetics</i> , 2008, 9, 52.	2.1	14
88	Exact analysis of intrinsic qualitative features of phosphorelays using mathematical models. <i>Journal of Theoretical Biology</i> , 2012, 300, 7-18.	1.7	13
89	Finding the positive feedback loops underlying multi-stationarity. <i>BMC Systems Biology</i> , 2015, 9, 22.	3.0	13
90	General theory for stochastic admixture graphs and F-statistics. <i>Theoretical Population Biology</i> , 2019, 125, 56-66.	1.1	13

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91	An Algebro-Topological Description of Protein Domain Structure. PLoS ONE, 2011, 6, e19670.	2.5	13
92	Convergence properties of the degree distribution of some growing network models. Bulletin of Mathematical Biology, 2006, 68, 1275-1291.	1.9	12
93	Incomplete and noisy network data as a percolation process. Journal of the Royal Society Interface, 2010, 7, 1411-1419.	3.4	12
94	A review of software for microarray genotyping. Human Genomics, 2011, 5, 304-9.	2.9	12
95	High-Resolution Melting Analysis for Mutation Screening of RGS11, RGS16, and RGS8 in Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 397-407.	2.5	12
96	Uniform Approximation of Solutions by Elimination of Intermediate Species in Deterministic Reaction Networks. SIAM Journal on Applied Dynamical Systems, 2017, 16, 2259-2286.	1.6	12
97	Large Scale Identification and Categorization of Protein Sequences Using Structured Logistic Regression. PLoS ONE, 2014, 9, e85139.	2.5	12
98	Inference on Recombination and Block Structure Using Unphased Data. Genetics, 2004, 166, 537-545.	2.9	11
99	DNA Copy Number Aberrations in Breast Cancer by Array Comparative Genomic Hybridization. Genomics, Proteomics and Bioinformatics, 2009, 7, 13-24.	6.9	11
100	The genealogy, site frequency spectrum and ages of two nested mutant alleles. Theoretical Population Biology, 2009, 75, 260-265.	1.1	10
101	A Beta-mixture model for dimensionality reduction, sample classification and analysis. BMC Bioinformatics, 2011, 12, 215.	2.6	10
102	Intermediates, catalysts, persistence, and boundary steady states. Journal of Mathematical Biology, 2017, 74, 887-932.	1.9	10
103	Graphical criteria for positive solutions to linear systems. Linear Algebra and Its Applications, 2018, 552, 166-193.	0.9	10
104	A proof of unlimited multistability for phosphorylation cycles. Nonlinearity, 2020, 33, 5629-5658.	1.4	10
105	Rare Alleles and Selection. Theoretical Population Biology, 2001, 59, 287-296.	1.1	9
106	On the minimum number of topologies explaining a sample of DNA sequences. Theoretical Population Biology, 2002, 62, 357-363.	1.1	9
107	Some notes on the combinatorial properties of haplotype tagging. Mathematical Biosciences, 2003, 185, 205-216.	1.9	9
108	Reply to Robert et al.: Model criticism informs model choice and model comparison. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, .	7.1	9

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109	Stationary distributions of systems with discreteness-induced transitions. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200243.	3.4	9
110	Discussion: Recent Common Ancestors of all Present-Day Individuals. <i>Advances in Applied Probability</i> , 1999, 31, 1027-1035.	0.7	9
111	Temporal development and collapse of an Arctic plant-pollinator network. <i>BMC Ecology</i> , 2009, 9, 24.	3.0	7
112	Node balanced steady states: Unifying and generalizing complex and detailed balanced steady states. <i>Mathematical Biosciences</i> , 2018, 301, 68-82.	1.9	7
113	Discussion: Recent Common Ancestors of all Present-Day Individuals. <i>Advances in Applied Probability</i> , 1999, 31, 1027-1035.	0.7	6
114	Bioinformatic identification of FGF, p38-MAPK, and calcium signalling pathways associated with carcinoma in situ in the urinary bladder. <i>BMC Cancer</i> , 2008, 8, 37.	2.6	6
115	Phosphorelay of non-orthodox two component systems functions through a bi-molecular mechanism in vivo: the case of ArcB. <i>Molecular BioSystems</i> , 2015, 11, 1348-1359.	2.9	6
116	epiC: statistical inference and profiling of DNA methylation from whole-genome bisulfite sequencing data. <i>Genome Biology</i> , 2017, 18, 38.	8.8	6
117	Conservation Laws in Biochemical Reaction Networks. <i>SIAM Journal on Applied Dynamical Systems</i> , 2017, 16, 2213-2232.	1.6	6
118	Signaling Cascades: Consequences of Varying Substrate and Phosphatase Levels. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 81-94.	1.6	6
119	Short Tandem Repeats and Genetic Variation. <i>Methods in Molecular Biology</i> , 2010, 628, 297-306.	0.9	6
120	Rseg – an R package to optimize segmentation of SNP array data. <i>Bioinformatics</i> , 2011, 27, 419-420.	4.1	5
121	Inferring population history from genealogical trees. <i>Journal of Mathematical Biology</i> , 2003, 46, 241-264.	1.9	4
122	Two Variance Results in Population Genetics Theory. <i>Mathematical Population Studies</i> , 2007, 14, 93-110.	2.2	4
123	Some properties of the conditioned reconstructed process with Bernoulli sampling. <i>Theoretical Population Biology</i> , 2018, 122, 36-45.	1.1	4
124	SNPTools: a software tool for visualization and analysis of microarray data. <i>Bioinformatics</i> , 2007, 23, 1550-1552.	4.1	3
125	A Markov Chain Approach to Randomly Grown Graphs. <i>Journal of Applied Mathematics</i> , 2008, 2008, 1-14.	0.9	3
126	Nonnegative Linear Elimination for Chemical Reaction Networks. <i>SIAM Journal on Applied Mathematics</i> , 2019, 79, 2434-2455.	1.8	3

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127	Coalescent models derived from birth–death processes. <i>Theoretical Population Biology</i> , 2021, 142, 1-11.	1.1	3
128	Linear Elimination in Chemical Reaction Networks. <i>SEMA SIMAI Springer Series</i> , 2019, , 177-193.	0.7	3
129	Conflicting results in SNP genotype assessment. <i>BioTechniques</i> , 2007, 43, 756-762.	1.8	2
130	Evolutionary Analysis of Protein Interaction Networks. , 2009, , 17-43.		2
131	LandScape: a simple method to aggregate p-values and other stochastic variables without a priori grouping. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2016, 15, 349-61.	0.6	2
132	Intermediates and Generic Convergence to Equilibria. <i>Bulletin of Mathematical Biology</i> , 2017, 79, 1662-1686.	1.9	2
133	Addition of flow reactions preserving multistationarity and bistability. <i>Mathematical Biosciences</i> , 2020, 320, 108295.	1.9	2
134	Quasi-Steady-State and Singular Perturbation Reduction for Reaction Networks with Noninteracting Species. <i>SIAM Journal on Applied Dynamical Systems</i> , 2022, 21, 782-816.	1.6	2
135	On the Liouville integrability of Edelstein's reaction system in \mathbb{R}^3 . <i>Chaos, Solitons and Fractals</i> , 2018, 108, 129-135.	5.1	1
136	The dynamics of stochastic mono-molecular reaction systems in stochastic environments. <i>Stochastic Processes and Their Applications</i> , 2021, 137, 106-148.	0.9	1
137	Fast reactions with non-interacting species in stochastic reaction networks. <i>Mathematical Biosciences and Engineering</i> , 2022, 19, 2720-2749.	1.9	1
138	Estimation of the covariance structure from SNP allele frequencies. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2022, 21, .	0.6	1
139	Using Likelihood-Free Inference to Compare Evolutionary Dynamics of the Protein Networks of <i>H.pylori</i> and <i>P.falciparum</i> . <i>PLoS Computational Biology</i> , 2005, preprint, e230.	3.2	0
140	On the sum of chemical reactions. <i>European Journal of Applied Mathematics</i> , 0, , 1-23.	2.9	0