Carsten Wiuf

List of Publications by Year
in descending order

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	Fast reactions with non-interacting species in stochastic reaction networks. Mathematical Biosciences and Engineering, 2022, 19, 2720-2749.	1.9	1
2	Quasi-Steady-State and Singular Perturbation Reduction for Reaction Networks with Noninteracting Species. SIAM Journal on Applied Dynamical Systems, 2022, 21, 782-816.	1.6	2
3	Estimation of the covariance structure from SNP allele frequencies. Statistical Applications in Genetics and Molecular Biology, 2022, 21, .	0.6	1
4	The dynamics of stochastic mono-molecular reaction systems in stochastic environments. Stochastic Processes and Their Applications, 2021, 137, 106-148.	0.9	1
5	Coalescent models derived from birth–death processes. Theoretical Population Biology, 2021, 142, 1-11.	1.1	3
6	Addition of flow reactions preserving multistationarity and bistability. Mathematical Biosciences, 2020, 320, 108295.	1.9	2
7	Stationary distributions of systems with discreteness-induced transitions. Journal of the Royal Society Interface, 2020, 17, 20200243.	3.4	9
8	A proof of unlimited multistability for phosphorylation cycles. Nonlinearity, 2020, 33, 5629-5658.	1.4	10
9	Nonnegative Linear Elimination for Chemical Reaction Networks. SIAM Journal on Applied Mathematics, 2019, 79, 2434-2455.	1.8	3
10	General theory for stochastic admixture graphs and F-statistics. Theoretical Population Biology, 2019, 125, 56-66.	1.1	13
11	Linear Elimination in Chemical Reaction Networks. SEMA SIMAI Springer Series, 2019, , 177-193.	0.7	3
12	Powerful Inference with the D-Statistic on Low-Coverage Whole-Genome Data. G3: Genes, Genomes, Genetics, 2018, 8, 551-566.	1.8	71
13	Some properties of the conditioned reconstructed process with Bernoulli sampling. Theoretical Population Biology, 2018, 122, 36-45.	1.1	4
14	On the Liouville integrability of Edelstein's reaction system in $\mathbb{R}^3$. Chaos, Solitons and Fractals, 2018, 108, 129-135.	5.1	1
15	Node balanced steady states: Unifying and generalizing complex and detailed balanced steady states. Mathematical Biosciences, 2018, 301, 68-82.	1.9	7
16	Graphical criteria for positive solutions to linear systems. Linear Algebra and Its Applications, 2018, 552, 166-193.	0.9	10
17	epiG: statistical inference and profiling of DNA methylation from whole-genome bisulfite sequencing data. Genome Biology, 2017, 18, 38.	8.8	6
18	Intermediates and Generic Convergence to Equilibria. Bulletin of Mathematical Biology, 2017, 79, 1662-1686.	1.9	2

#	Article	IF	Citations
19	Graphical reduction of reaction networks by linear elimination of species. Journal of Mathematical Biology, 2017, 74, 195-237.	1.9	23
20	Intermediates, catalysts, persistence, and boundary steady states. Journal of Mathematical Biology, 2017, 74, 887-932.	1.9	10
21	Conservation Laws in Biochemical Reaction Networks. SIAM Journal on Applied Dynamical Systems, 2017, 16, 2213-2232.	1.6	6
22	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
23	Identifying parameter regions for multistationarity. PLoS Computational Biology, 2017, 13, e1005751.	3.2	61
24	Elimination of intermediate species in multiscale stochastic reaction networks. Annals of Applied Probability, 2016, 26, .	1.3	16
25	Core signalling motif displaying multistability through multi-state enzymes. Journal of the Royal Society Interface, 2016, 13, 20160524.	3.4	25
26	Product-Form Poisson-Like Distributions and Complex Balanced Reaction Systems. SIAM Journal on Applied Mathematics, 2016, 76, 411-432.	1.8	38
27	LandScape: a simple method to aggregate p-values and other stochastic variables without a priori grouping. Statistical Applications in Genetics and Molecular Biology, 2016, 15, 349-61.	0.6	2
28	Phosphorelay of non-orthodox two component systems functions through a bi-molecular mechanism in vivo: the case of ArcB. Molecular BioSystems, 2015, 11, 1348-1359.	2.9	6
29	Lyapunov Functions, Stationary Distributions, and Non-equilibrium Potential for Reaction Networks. Bulletin of Mathematical Biology, 2015, 77, 1744-1767.	1.9	39
30	Finding the positive feedback loops underlying multi-stationarity. BMC Systems Biology, 2015, 9, 22.	3.0	13
31	Large Scale Identification and Categorization of Protein Sequences Using Structured Logistic Regression. PLoS ONE, 2014, 9, e85139.	2.5	12
32	Variable elimination in post-translational modification reaction networks with mass-action kinetics. Journal of Mathematical Biology, 2013, 66, 281-310.	1.9	23
33	Cellular Compartments Cause Multistability and Allow Cells to Process More Information. Biophysical Journal, 2013, 104, 1824-1831.	0.5	52
34	Power-Law Kinetics and Determinant Criteria for the Preclusion of Multistationarity in Networks of Interacting Species. SIAM Journal on Applied Dynamical Systems, 2013, 12, 1685-1721.	1.6	45
35	A computational method to preclude multistationarity in networks of interacting species. Bioinformatics, 2013, 29, 2327-2334.	4.1	25
36	Phosphorelays Provide Tunable Signal Processing Capabilities for the Cell. PLoS Computational Biology, 2013, 9, e1003322.	3.2	18

#	Article	IF	Citations
37	Simplifying biochemical models with intermediate species. Journal of the Royal Society Interface, 2013, 10, 20130484.	3.4	59
38	Variable Elimination in Chemical Reaction Networks with Mass-Action Kinetics. SIAM Journal on Applied Mathematics, 2012, 72, 959-981.	1.8	40
39	Gene expression classifier predicts for hypoxic modification of radiotherapy with nimorazole in squamous cell carcinomas of the head and neck. Radiotherapy and Oncology, 2012, 102, 122-129.	0.6	196
40	A bimodular mechanism of calcium control in eukaryotes. Nature, 2012, 491, 468-472.	27.8	110
41	Preclusion of switch behavior in networks with mass-action kinetics. Applied Mathematics and Computation, 2012, 219, 1449-1467.	2.2	31
42	Modelling the contribution of family history and variation in single nucleotide polymorphisms to risk of schizophrenia: A Danish national birth cohort-based study. Schizophrenia Research, 2012, 134, 246-252.	2.0	33
43	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
44	Enzyme-sharing as a cause of multi-stationarity in signalling systems. Journal of the Royal Society Interface, 2012, 9, 1224-1232.	3.4	58
45	Exact analysis of intrinsic qualitative features of phosphorelays using mathematical models. Journal of Theoretical Biology, 2012, 300, 7-18.	1.7	13
46	Monitoring endangered freshwater biodiversity using environmental DNA. Molecular Ecology, 2012, 21, 2565-2573.	3.9	882
47	An Algebraic Approach to Signaling Cascades with n Layers. Bulletin of Mathematical Biology, 2012, 74, 45-72.	1.9	30
48	Signaling Cascades: Consequences of Varying Substrate and Phosphatase Levels. Advances in Experimental Medicine and Biology, 2012, 736, 81-94.	1.6	6
49	Common variants at VRK2 and TCF4 conferring risk of schizophrenia. Human Molecular Genetics, 2011, 20, 4076-4081.	2.9	193
50	Comprehensive Genome Methylation Analysis in Bladder Cancer: Identification and Validation of Novel Methylated Genes and Application of These as Urinary Tumor Markers. Clinical Cancer Research, 2011, 17, 5582-5592.	7.0	183
51	A review of software for microarray genotyping. Human Genomics, 2011, 5, 304-9.	2.9	12
52	A Beta-mixture model for dimensionality reduction, sample classification and analysis. BMC Bioinformatics, 2011, 12, 215.	2.6	10
53	Tumor-specific usage of alternative transcription start sites in colorectal cancer identified by genome-wide exon array analysis. BMC Genomics, 2011, 12, 505.	2.8	57
54	Rseg—an R package to optimize segmentation of SNP array data. Bioinformatics, 2011, 27, 419-420.	4.1	5

#	Article	IF	Citations
55	Bounded coordinate-descent for biological sequence classification in high dimensional predictor space. , 2011, , .		28
56	High-Resolution Melting Analysis for Mutation Screening of RGSL1, RGS16, and RGS8 in Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 397-407.	2.5	12
57	Development of a Hypoxia Gene Expression Classifier with Predictive Impact for Hypoxic Modification of Radiotherapy in Head and Neck Cancer. Cancer Research, 2011, 71, 5923-5931.	0.9	226
58	An Algebro-Topological Description of Protein Domain Structure. PLoS ONE, 2011, 6, e19670.	2.5	13
59	The CATH database. Human Genomics, 2010, 4, 207.	2.9	84
60	Tumor heterogeneity in neoplasms of breast, colon, and skin. BMC Research Notes, 2010, 3, 321.	1.4	20
61	Fatgraph models of proteins. Communications on Pure and Applied Mathematics, 2010, 63, 1249-1297.	3.1	37
62	Incomplete and noisy network data as a percolation process. Journal of the Royal Society Interface, 2010, 7, 1411-1419.	3.4	12
63	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
64	Short Tandem Repeats and Genetic Variation. Methods in Molecular Biology, 2010, 628, 297-306.	0.9	6
65	From evidence to inference: Probing the evolution of protein interaction networks. HFSP Journal, 2009, 3, 290-306.	2.5	31
66	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
67	The genealogy, site frequency spectrum and ages of two nested mutant alleles. Theoretical Population Biology, 2009, 75, 260-265.	1.1	10
68	Estimation of tumor heterogeneity using CGH array data. BMC Bioinformatics, 2009, 10, 12.	2.6	30
69	Genome-wide scans using archived neonatal dried blood spot samples. BMC Genomics, 2009, 10, 297.	2.8	80
70	Chromosomal imbalance in the progression of high-risk non-muscle invasive bladder cancer. BMC Cancer, 2009, 9, 149.	2.6	15
71	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
72	Temporal development and collapse of an Arctic plant-pollinator network. BMC Ecology, 2009, 9, 24.	3.0	7

#	Article	IF	Citations
73	DNA Copy Number Aberrations in Breast Cancer by Array Comparative Genomic Hybridization. Genomics, Proteomics and Bioinformatics, 2009, 7, 13-24.	6.9	11
74	Evolutionary Analysis of Protein Interaction Networks. , 2009, , 17-43.		2
75	The association between genetic variants in hMLH1 and hMSH2 and the development of sporadic colorectal cancer in the Danish population. BMC Medical Genetics, 2008, 9, 52.	2.1	14
76	Increased cell motility and invasion upon knockdown of lipolysis stimulated lipoprotein receptor (LSR) in SW780 bladder cancer cells. BMC Medical Genomics, 2008, 1, 31.	1.5	27
77	Omicsâ€based profiling of carcinoma of the breast and matched regional lymph node metastasis. Proteomics, 2008, 8, 5038-5052.	2.2	26
78	Short Tandem Repeats in Human Exons: A Target for Disease Mutations. BMC Genomics, 2008, 9, 410.	2.8	45
79	Bioinformatic identification of FGF, p38-MAPK, and calcium signalling pathways associated with carcinoma in situin the urinary bladder. BMC Cancer, 2008, 8, 37.	2.6	6
80	Clonal Evolution in t(14;18)-Positive Follicular Lymphoma, Evidence for Multiple Common Pathways, and Frequent Parallel Clonal Evolution. Clinical Cancer Research, 2008, 14, 7180-7187.	7.0	45
81	Estimating the size of the human interactome. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6959-6964.	7.1	692
82	Importance Sampling for the Infinite Sites Model. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article32.	0.6	24
83	A Markov Chain Approach to Randomly Grown Graphs. Journal of Applied Mathematics, 2008, 2008, 1-14.	0.9	3
84	Diagnostic and Prognostic MicroRNAs in Stage II Colon Cancer. Cancer Research, 2008, 68, 6416-6424.	0.9	459
85	Germline Mutation in RNASEL Predicts Increased Risk of Head and Neck, Uterine Cervix and Breast Cancer. PLoS ONE, 2008, 3, e2492.	2.5	54
86	Genome-wide analysis of allelic imbalance in prostate cancer using the Affymetrix 50K SNP mapping array. British Journal of Cancer, 2007, 96, 499-506.	6.4	50
87	Using Likelihood-Free Inference to Compare Evolutionary Dynamics of the Protein Networks of H. pylori and P. falciparum. PLoS Computational Biology, 2007, 3, e230.	3.2	69
88	Frequent occurrence of uniparental disomy in colorectal cancer. Carcinogenesis, 2007, 28, 38-48.	2.8	97
89	SNPTools: a software tool for visualization and analysis of microarray data. Bioinformatics, 2007, 23, 1550-1552.	4.1	3
90	A periodic pattern of SNPs in the human genome. Genome Research, 2007, 17, 1414-1419.	5.5	14

#	Article	IF	Citations
91	Evolution at the system level: the natural history of protein interaction networks. Trends in Ecology and Evolution, 2007, 22, 366-373.	8.7	46
92	Two Variance Results in Population Genetics Theory. Mathematical Population Studies, 2007, 14, 93-110.	2.2	4
93	Conflicting results in SNP genotype assessment. BioTechniques, 2007, 43, 756-762.	1.8	2
94	A Hidden Markov Model to estimate population mixture and allelic copy-numbers in cancers using Affymetrix SNP arrays. BMC Bioinformatics, 2007, 8, 434.	2.6	25
95	Ab initio identification of human microRNAs based on structure motifs. BMC Bioinformatics, 2007, 8, 478.	2.6	53
96	Co-clustering and visualization of gene expression data and gene ontology terms for Saccharomyces cerevisiae using self-organizing maps. Journal of Biomedical Informatics, 2007, 40, 160-173.	4.3	55
97	Evaluating Neanderthal Genetics and Phylogeny. Journal of Molecular Evolution, 2007, 64, 50-60.	1.8	18
98	Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. Nucleic Acids Research, 2006, 35, 1-10.	14.5	166
99	Binomial subsampling. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2006, 462, 1181-1195.	2.1	17
100	The effects of incomplete protein interaction data on structural and evolutionary inferences. BMC Biology, 2006, 4, 39.	3.8	58
101	Consistency of estimators of population scaled parameters using composite likelihood. Journal of Mathematical Biology, 2006, 53, 821-841.	1.9	38
102	Convergence properties of the degree distribution of some growing network models. Bulletin of Mathematical Biology, 2006, 68, 1275-1291.	1.9	12
103	Genotyping and annotation of Affymetrix SNP arrays. Nucleic Acids Research, 2006, 34, e100-e100.	14.5	17
104	A likelihood approach to analysis of network data. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7566-7570.	7.1	56
105	Assessing the Fidelity of Ancient DNA Sequences Amplified From Nuclear Genes. Genetics, 2006, 172, 733-741.	2.9	95
106	SOX4 Expression in Bladder Carcinoma: Clinical Aspects and In vitro Functional Characterization. Cancer Research, 2006, 66, 3434-3442.	0.9	146
107	Crosslinks Rather Than Strand Breaks Determine Access to Ancient DNA Sequences From Frozen Sediments. Genetics, 2006, 173, 1175-1179.	2.9	100
108	Are microRNAs located in genomic regions associated with cancer?. British Journal of Cancer, 2006, 95, 1415-1418.	6.4	42

#	ARTICLE	IF	CITATIONS
109	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
110	Sampling properties of random graphs: The degree distribution. Physical Review E, 2005, 72, 036118.	2.1	80
111	Subnets of scale-free networks are not scale-free: Sampling properties of networks. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4221-4224.	7.1	436
112	Using Likelihood-Free Inference to Compare Evolutionary Dynamics of the Protein Networks of H.pylori and P.falciparum. PLoS Computational Biology, 2005, preprint, e230.	3.2	0
113	High-density single nucleotide polymorphism array defines novel stage and location-dependent allelic imbalances in human bladder tumors. Cancer Research, 2005, 65, 34-45.	0.9	55
114	The Probability and Chromosomal Extent of trans-specific Polymorphism. Genetics, 2004, 168, 2363-2372.	2.9	67
115	Inference on Recombination and Block Structure Using Unphased Data. Genetics, 2004, 166, 537-545.	2.9	11
116	Long-term persistence of bacterial DNA. Current Biology, 2004, 14, R9-R10.	3.9	189
117	Identification of endogenous retroviral reading frames in the human genome. Retrovirology, 2004, 1, 32.	2.0	148
118	Inferring population history from genealogical trees. Journal of Mathematical Biology, 2003, 46, 241-264.	1.9	4
119	Some notes on the combinatorial properties of haplotype tagging. Mathematical Biosciences, 2003, 185, 205-216.	1.9	9
120	Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments. Science, 2003, 300, 791-795.	12.6	571
121	Simulating haplotype blocks in the human genome. Bioinformatics, 2003, 19, 289-290.	4.1	22
122	A Coalescent Model of Recombination Hotspots. Genetics, 2003, 164, 407-417.	2.9	19
123	On the minimum number of topologies explaining a sample of DNA sequences. Theoretical Population Biology, 2002, 62, 357-363.	1.1	9
124	Rare Alleles and Selection. Theoretical Population Biology, 2001, 59, 287-296.	1.1	9
125	Recombination Analysis Using Directed Graphical Models. Molecular Biology and Evolution, 2001, 18, 97-99.	8.9	36
126	Statistical Evidence for Miscoding Lesions in Ancient DNA Templates. Molecular Biology and Evolution, 2001, 18, 262-265.	8.9	151

#	Article	IF	Citations
127	A Simulation Study of the Reliability of Recombination Detection Methods. Molecular Biology and Evolution, 2001, 18, 1929-1939.	8.9	110
128	Do ΔF508 heterozygotes have a selective advantage?. Genetical Research, 2001, 78, 41-47.	0.9	40
129	Recombination in Human Mitochondrial DNA?. Genetics, 2001, 159, 749-756.	2.9	28
130	Statistical alignment: computational properties, homology testing and goodness-of-fit 1 1Edited by J. Karn. Journal of Molecular Biology, 2000, 302, 265-279.	4.2	101
131	A Coalescence Approach to Gene Conversion. Theoretical Population Biology, 2000, 57, 357-367.	1.1	24
132	On the Genealogy of a Sample of Neutral Rare Alleles. Theoretical Population Biology, 2000, 58, 61-75.	1.1	17
133	The Coalescent With Gene Conversion. Genetics, 2000, 155, 451-462.	2.9	124
134	Recombination as a Point Process along Sequences. Theoretical Population Biology, 1999, 55, 248-259.	1.1	169
135	Conditional Genealogies and the Age of a Neutral Mutant. Theoretical Population Biology, 1999, 56, 183-201.	1.1	75
136	Discussion: Recent Common Ancestors of all Present-Day Individuals. Advances in Applied Probability, 1999, 31, 1027-1035.	0.7	6
137	The Ancestry of a Sample of Sequences Subject to Recombination. Genetics, 1999, 151, 1217-1228.	2.9	53
138	Discussion: Recent Common Ancestors of all Present-Day Individuals. Advances in Applied Probability, 1999, 31, 1027-1035.	0.7	9
139	On the Number of Ancestors to a DNA Sequence. Genetics, 1997, 147, 1459-1468.	2.9	42
140	On the sum of chemical reactions. European Journal of Applied Mathematics, 0, , 1-23.	2.9	0