

Thomas Mailund

List of Publications by Year in descending order

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Version: 2024-02-01

77
papers

6,710
citations

117625
34
h-index

74163
75
g-index

84
all docs

84
docs citations

84
times ranked

9866
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into bear evolution from a Pleistocene polar bear genome. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	11
2	Targeted conservation genetics of the endangered chimpanzee. Heredity, 2020, 125, 15-27.	2.6	11
3	Ancestral Population Genomics with Jox, a Coalescent Hidden Markov Model. Methods in Molecular Biology, 2020, 2090, 167-189.	0.9	1
4	Identifying loci under positive selection in complex population histories. Genome Research, 2019, 29, 1506-1520.	5.5	36
5	Direct estimation of mutations in great apes reconciles phylogenetic dating. Nature Ecology and Evolution, 2019, 3, 286-292.	7.8	122
6	The comparative genomics and complex population history of <i>Papio</i> baboons. Science Advances, 2019, 5, eaau6947.	10.3	115
7	Breaking Free: The Genomics of Allopolyploidy-Facilitated Niche Expansion in White Clover. Plant Cell, 2019, 31, 1466-1487.	6.6	89
8	A comprehensive genomic history of extinct and living elephants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2566-E2574.	7.1	142
9	Evidence that the rate of strong selective sweeps increases with population size in the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1613-1618.	7.1	40
10	Assembly and analysis of 100 full MHC haplotypes from the Danish population. Genome Research, 2017, 27, 1597-1607.	5.5	15
11	The ecological niche and distribution of Neanderthals during the Last Interglacial. Journal of Biogeography, 2017, 44, 51-61.	3.0	39
12	admixturegraph: an R package for admixture graph manipulation and fitting. Bioinformatics, 2017, 33, 1738-1740.	4.1	69
13	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. Nature, 2017, 548, 87-91.	27.8	130
14	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	8.8	131
15	Selective Sweeps across Twenty Millions Years of Primate Evolution. Molecular Biology and Evolution, 2016, 33, 3065-3074.	8.9	28
16	Nationwide Genomic Study in Denmark Reveals Remarkable Population Homogeneity. Genetics, 2016, 204, 711-722.	2.9	54
17	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	27.8	439
18	Spitting for Science: Danish High School Students Commit to a Large-Scale Self-Reported Genetic Study. PLoS ONE, 2016, 11, e0161822.	2.5	5

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19	Measurement Units in R. R Journal, 2016, 8, 486.	1.8	36
20	Extreme selective sweeps independently targeted the X chromosomes of the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6413-6418.	7.1	75
21	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. Nature Communications, 2015, 6, 5969.	12.8	164
22	Inference of Purifying and Positive Selection in Three Subspecies of Chimpanzees (Pan troglodytes) from Exome Sequencing. Genome Biology and Evolution, 2015, 7, 1122-1132.	2.5	33
23	Ancestral population genomics using coalescence hidden Markov models and heuristic optimisation algorithms. Computational Biology and Chemistry, 2015, 57, 80-92.	2.3	3
24	Strong Selective Sweeps on the X Chromosome in the Human-Chimpanzee Ancestor Explain Its Low Divergence. PLoS Genetics, 2015, 11, e1005451.	3.5	56
25	Unraveling recombination rate evolution using ancestral recombination maps. BioEssays, 2014, 36, 892-900.	2.5	5
26	Lineage Sorting in Apes. Annual Review of Genetics, 2014, 48, 519-535.	7.6	48
27	tqDist: a library for computing the quartet and triplet distances between binary or general trees. Bioinformatics, 2014, 30, 2079-2080.	4.1	75
28	A fine-scale recombination map of the human-chimpanzee ancestor reveals faster change in humans than in chimpanzees and a strong impact of GC-biased gene conversion. Genome Research, 2014, 24, 467-474.	5.5	37
29	Efficient computation in the IM model. Journal of Mathematical Biology, 2014, 68, 1423-1451.	1.9	38
30	A practical $O(n \log^2 n)$ time algorithm for computing the triplet distance on binary trees. BMC Bioinformatics, 2013, 14, S18.	2.6	5
31	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	27.8	768
32	zipHMMlib: a highly optimised HMM library exploiting repetitions in the input to speed up the forward algorithm. BMC Bioinformatics, 2013, 14, 339.	2.6	12
33	Algorithms for Computing the Triplet and Quartet Distances for Binary and General Trees. Biology, 2013, 2, 1189-1209.	2.8	14
34	Algorithms for Hidden Markov Models Restricted to Occurrences of Regular Expressions. Biology, 2013, 2, 1282-1295.	2.8	4
35	A New Isolation with Migration Model along Complete Genomes Infers Very Different Divergence Processes among Closely Related Great Ape Species. PLoS Genetics, 2012, 8, e1003125.	3.5	102
36	Extensive X-linked adaptive evolution in central chimpanzees. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2054-2059.	7.1	79

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37	Polar and brown bear genomes reveal ancient admixture and demographic footprints of past climate change. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2382-90.	7.1	310
38	Association Mapping and Disease: Evolutionary Perspectives. <i>Methods in Molecular Biology</i> , 2012, 856, 275-291.	0.9	2
39	Cultural Phylogenetics of the Tupi Language Family in Lowland South America. <i>PLoS ONE</i> , 2012, 7, e35025.	2.5	64
40	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , 2012, 486, 527-531.	27.8	445
41	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175.	27.8	663
42	Using Colored Petri Nets to Construct Coalescent Hidden Markov Models: Automatic Translation from Demographic Specifications to Efficient Inference Methods. <i>Lecture Notes in Computer Science</i> , 2012, , 32-50.	1.3	4
43	An Effort to Use Human-Based Exome Capture Methods to Analyze Chimpanzee and Macaque Exomes. <i>PLoS ONE</i> , 2012, 7, e40637.	2.5	28
44	Local Genealogies in a Linear Mixed Model for Genome-Wide Association Mapping in Complex Pedigreed Populations. <i>PLoS ONE</i> , 2011, 6, e27061.	2.5	6
45	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	27.8	541
46	A sub-cubic time algorithm for computing the quartet distance between two general trees. <i>Algorithms for Molecular Biology</i> , 2011, 6, 15.	1.2	13
47	Incomplete lineage sorting patterns among human, chimpanzee, and orangutan suggest recent orangutan speciation and widespread selection. <i>Genome Research</i> , 2011, 21, 349-356.	5.5	192
48	On Computing the Coalescence Time Density in an Isolation-With-Migration Model With Few Samples. <i>Genetics</i> , 2011, 187, 1241-1243.	2.9	53
49	Inference of Large Phylogenies Using Neighbour-Joining. <i>Communications in Computer and Information Science</i> , 2011, , 334-344.	0.5	19
50	Estimating Divergence Time and Ancestral Effective Population Size of Bornean and Sumatran Orangutan Subspecies Using a Coalescent Hidden Markov Model. <i>PLoS Genetics</i> , 2011, 7, e1001319.	3.5	79
51	HMMlib: A C++ Library for General Hidden Markov Models Exploiting Modern CPUs. , 2010, ,		10
52	Ancestral Population Genomics: The Coalescent Hidden Markov Model Approach. <i>Genetics</i> , 2009, 183, 259-274.	2.9	96
53	A Quadratic Time Algorithm for Computing the Quartet Distance between Two General Trees. , 2009, ,		0
54	Local Phylogeny Mapping of Quantitative Traits: Higher Accuracy and Better Ranking Than Single-Marker Association in Genomewide Scans. <i>Genetics</i> , 2009, 181, 747-753.	2.9	15

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55	A fast algorithm for genome-wide haplotype pattern mining. BMC Bioinformatics, 2009, 10, S74.	2.6	3
56	Haplotype frequencies in a sub-region of chromosome 19q13.3, related to risk and prognosis of cancer, differ dramatically between ethnic groups. BMC Medical Genetics, 2009, 10, 20.	2.1	16
57	Using biological networks to search for interacting loci in genome-wide association studies. European Journal of Human Genetics, 2009, 17, 1231-1240.	2.8	135
58	Investigating selection on viruses: a statistical alignment approach. BMC Bioinformatics, 2008, 9, 304.	2.6	8
59	SNPFile – A software library and file format for large scale association mapping and population genetics studies. BMC Bioinformatics, 2008, 9, 526.	2.6	5
60	Efficient whole-genome association mapping using local phylogenies for unphased genotype data. Bioinformatics, 2008, 24, 2215-2221.	4.1	11
61	Rapid Neighbour-Joining. Lecture Notes in Computer Science, 2008, , 113-122.	1.3	83
62	Genomic Relationships and Speciation Times of Human, Chimpanzee, and Gorilla Inferred from a Coalescent Hidden Markov Model. PLoS Genetics, 2007, 3, e7.	3.5	281
63	On Recombination-Induced Multiple and Simultaneous Coalescent Events. Genetics, 2007, 177, 2151-2160.	2.9	15
64	Comparative annotation of viral genomes with non-conserved gene structure. Bioinformatics, 2007, 23, 1080-1089.	4.1	9
65	Annotation of selection strengths in viral genomes. Bioinformatics, 2007, 23, 2978-2986.	4.1	13
66	Experiences with GeneRecon on MiG. Future Generation Computer Systems, 2007, 23, 580-586.	7.5	2
67	Fast calculation of the quartet distance between trees of arbitrary degrees. Algorithms for Molecular Biology, 2006, 1, 16.	1.2	21
68	The effective size of the Icelandic population and the prospects for LD mapping: inference from unphased microsatellite markers. European Journal of Human Genetics, 2006, 14, 1044-1053.	2.8	11
69	Recrafting the neighbor-joining method. BMC Bioinformatics, 2006, 7, 29.	2.6	41
70	Whole genome association mapping by incompatibilities and local perfect phylogenies. BMC Bioinformatics, 2006, 7, 454.	2.6	41
71	GeneRecon—a coalescent based tool for fine-scale association mapping. Bioinformatics, 2006, 22, 2317-2318.	4.1	8
72	CoaSim: A flexible environment for simulating genetic data under coalescent models. BMC Bioinformatics, 2005, 6, 252.	2.6	64

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73	Pigs in sequence space: A 0.66X coverage pig genome survey based on shotgun sequencing. BMC Genomics, 2005, 6, 70.	2.8	283
74	RBT—a tool for building refined Buneman trees. Bioinformatics, 2005, 21, 1711-1712.	4.1	4
75	Computing the Quartet Distance Between Trees of Arbitrary Degree. Lecture Notes in Computer Science, 2005, , 77-88.	1.3	5
76	QDist—quartet distance between evolutionary trees. Bioinformatics, 2004, 20, 1636-1637.	4.1	27
77	QuickJoin—fast neighbour-joining tree reconstruction. Bioinformatics, 2004, 20, 3261-3262.	4.1	34