

Mathias Currat

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

5,633
citations

136885

32
h-index

182361

51
g-index

55
all docs

55
docs citations

55
times ranked

7197
citing authors

#	ARTICLE	IF	CITATIONS
1	THE HIDDEN SIDE OF INVASIONS: MASSIVE INTROGRESSION BY LOCAL GENES. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, ???-???	1.1	658
2	The Fate of Mutations Surfing on the Wave of a Range Expansion. <i>Molecular Biology and Evolution</i> , 2006, 23, 482-490.	3.5	565
3	Intra-Deme Molecular Diversity in Spatially Expanding Populations. <i>Molecular Biology and Evolution</i> , 2003, 20, 76-86.	3.5	519
4	Early farmers from across Europe directly descended from Neolithic Aegeans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6886-6891.	3.3	376
5	Evolution of lactase persistence: an example of human niche construction. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011, 366, 863-877.	1.8	340
6	Upper Palaeolithic genomes reveal deep roots of modern Eurasians. <i>Nature Communications</i> , 2015, 6, 8912.	5.8	334
7	Modern Humans Did Not Admix with Neanderthals during Their Range Expansion into Europe. <i>PLoS Biology</i> , 2004, 2, e421.	2.6	242
8	Early Neolithic genomes from the eastern Fertile Crescent. <i>Science</i> , 2016, 353, 499-503.	6.0	230
9	Consequences of Range Contractions and Range Shifts on Molecular Diversity. <i>Molecular Biology and Evolution</i> , 2012, 29, 207-218.	3.5	204
10	The effect of the Neolithic expansion on European molecular diversity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005, 272, 679-688.	1.2	185
11	Strong reproductive isolation between humans and Neanderthals inferred from observed patterns of introgression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15129-15134.	3.3	146
12	Principal Component Analysis under Population Genetic Models of Range Expansion and Admixture. <i>Molecular Biology and Evolution</i> , 2010, 27, 1257-1268.	3.5	125
13	Molecular Analysis of the β -Globin Gene Cluster in the Niokholo Mandenka Population Reveals a Recent Origin of the β^S Senegal Mutation. <i>American Journal of Human Genetics</i> , 2002, 70, 207-223.	2.6	115
14	SPLATCHE2: a spatially explicit simulation framework for complex demography, genetic admixture and recombination. <i>Bioinformatics</i> , 2010, 26, 2993-2994.	1.8	113
15	Bayesian Estimation of Recent Migration Rates After a Spatial Expansion. <i>Genetics</i> , 2005, 170, 409-417.	1.2	112
16	Impact of Selection and Demography on the Diffusion of Lactase Persistence. <i>PLoS ONE</i> , 2009, 4, e6369.	1.1	107
17	The genetic history of Europeans. <i>Trends in Genetics</i> , 2012, 28, 496-505.	2.9	102
18	Recovering the geographic origin of early modern humans by realistic and spatially explicit simulations. <i>Genome Research</i> , 2005, 15, 1161-1167.	2.4	100

#	ARTICLE	IF	CITATIONS
19	Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe. <i>Nature Communications</i> , 2017, 8, 14615.	5.8	96
20	Molecular Diversity After a Range Expansion in Heterogeneous Environments. <i>Genetics</i> , 2006, 174, 2009-2020.	1.2	74
21	Colonization history of the Swiss Rhine basin by the bullhead (<i>Cottus gobio</i>): inference under a Bayesian spatially explicit framework. <i>Molecular Ecology</i> , 2008, 17, 757-772.	2.0	71
22	Distinct evolutionary strategies of human leucocyte antigen loci in pathogen-rich environments. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 830-839.	1.8	55
23	Combining genetic, historical and geographical data to reconstruct the dynamics of bioinvasions: application to the cane toad <i>Bufo marinus</i> . <i>Molecular Ecology Resources</i> , 2010, 10, 886-901.	2.2	54
24	Response to Comment on "Ongoing Adaptive Evolution of ASPM, a Brain Size Determinant in Homo sapiens" and "Microcephalin, a Gene Regulating Brain Size, Continues to Evolve Adaptively in Humans". <i>Science</i> , 2006, 313, 172b-172b.	6.0	51
25	Human Neutral Genetic Variation and Forensic STR Data. <i>PLoS ONE</i> , 2012, 7, e49666.	1.1	51
26	Influence of Admixture and Paleolithic Range Contractions on Current European Diversity Gradients. <i>Molecular Biology and Evolution</i> , 2013, 30, 57-61.	3.5	48
27	Human genetic differentiation across the Strait of Gibraltar. <i>BMC Evolutionary Biology</i> , 2010, 10, 237.	3.2	46
28	SPLATCHE3: simulation of serial genetic data under spatially explicit evolutionary scenarios including long-distance dispersal. <i>Bioinformatics</i> , 2019, 35, 4480-4483.	1.8	41
29	Local Population Structure in Arabian Peninsula Revealed by Y-STR Diversity. <i>Human Heredity</i> , 2009, 68, 45-54.	0.4	38
30	Signals of recent spatial expansions in the grey mouse lemur (<i>Microcebus murinus</i>). <i>BMC Evolutionary Biology</i> , 2010, 10, 105.	3.2	38
31	Harmonizing hybridization dissonance in conservation. <i>Communications Biology</i> , 2020, 3, 391.	2.0	38
32	Long-Distance Dispersal Shaped Patterns of Human Genetic Diversity in Eurasia. <i>Molecular Biology and Evolution</i> , 2016, 33, 946-958.	3.5	36
33	Modelling interspecific hybridization with genome exclusion to identify conservation actions: the case of native and invasive <i>Pelophylax</i> waterfrogs. <i>Evolutionary Applications</i> , 2015, 8, 199-210.	1.5	27
34	Hybridization and introgression during density-dependent range expansion: European wildcats as a case study. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 750-761.	1.1	22
35	The Spatial Signature of Introgression After a Biological Invasion With Hybridization. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	20
36	Computer simulation of human leucocyte antigen genes supports two main routes of colonization by human populations in East Asia. <i>BMC Evolutionary Biology</i> , 2015, 15, 240.	3.2	19

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37	Cryptic Biological Invasions: a General Model of Hybridization. <i>Scientific Reports</i> , 2018, 8, 2414.	1.6	16
38	Air temperature influences early Covid-19 outbreak as indicated by worldwide mortality. <i>Science of the Total Environment</i> , 2021, 792, 148312.	3.9	13
39	Forward-in-Time, Spatially Explicit Modeling Software to Simulate Genetic Lineages under Selection. <i>Evolutionary Bioinformatics</i> , 2015, 11s2, EBO.S33488.	0.6	12
40	Investigating population continuity with ancient DNA under a spatially explicit simulation framework. <i>BMC Genetics</i> , 2017, 18, 114.	2.7	12
41	Effect of hybridization with genome exclusion on extinction risk. <i>Conservation Biology</i> , 2018, 32, 1139-1149.	2.4	12
42	A General Model of Distant Hybridization Reveals the Conditions for Extinction in Atlantic Salmon and Brown Trout. <i>PLoS ONE</i> , 2014, 9, e101736.	1.1	11
43	Projecting introgression from domestic cats into European wildcats in the Swiss Jura. <i>Evolutionary Applications</i> , 2020, 13, 2101-2112.	1.5	11
44	Bayesian estimation of partial population continuity using ancient <sc>DNA</sc> and spatially explicit simulations. <i>Evolutionary Applications</i> , 2018, 11, 1642-1655.	1.5	10
45	Consequences of diverse evolutionary processes on american genetic gradients of modern humans. <i>Heredity</i> , 2018, 121, 548-556.	1.2	8
46	Investigating European Genetic History through Computer Simulations. <i>Human Heredity</i> , 2013, 76, 142-153.	0.4	7
47	Influence of Paleolithic range contraction, admixture and long-distance dispersal on genetic gradients of modern humans in Asia. <i>Molecular Ecology</i> , 2020, 29, 2150-2159.	2.0	4
48	Spatially explicit paleogenomic simulations support cohabitation with limited admixture between Bronze Age Central European populations. <i>Communications Biology</i> , 2021, 4, 1163.	2.0	3
49	Simulated patterns of mitochondrial diversity are consistent with partial population turnover in Bronze Age Central Europe. <i>American Journal of Biological Anthropology</i> , 2022, 177, 134-146.	0.6	1
50	Challenging ancient DNA results about putative HLA protection or susceptibility to <i>Yersina pestis</i> . <i>Molecular Biology and Evolution</i> , 2022, , .	3.5	1
51	Recipient of the 2013 <i>Molecular Ecology</i> Prize: Laurent Excoffier. <i>Molecular Ecology</i> , 2014, 23, 16-19.	2.0	0
52	Simulations of Human Dispersal and Genetic Diversity. <i>Evolutionary Studies</i> , 2021, , 231-256.	0.2	0