

Mathias Currat

List of Publications by Year in descending order

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52
papers

5,633
citations

136950
32
h-index

182427
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, ???-???.	2.3	658
2	The Fate of Mutations Surfing on the Wave of a Range Expansion. <i>Molecular Biology and Evolution</i> , 2006, 23, 482-490.	8.9	565
3	Intra-Deme Molecular Diversity in Spatially Expanding Populations. <i>Molecular Biology and Evolution</i> , 2003, 20, 76-86.	8.9	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.	7.1	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.	4.0	340
6	Upper Palaeolithic genomes reveal deep roots of modern Eurasians. <i>Nature Communications</i> , 2015, 6, 8912.	12.8	334
7	Modern Humans Did Not Admix with Neanderthals during Their Range Expansion into Europe. <i>PLoS Biology</i> , 2004, 2, e421.	5.6	242
8	Early Neolithic genomes from the eastern Fertile Crescent. <i>Science</i> , 2016, 353, 499-503.	12.6	230
9	Consequences of Range Contractions and Range Shifts on Molecular Diversity. <i>Molecular Biology and Evolution</i> , 2012, 29, 207-218.	8.9	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.	2.6	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.	7.1	146
12	Principal Component Analysis under Population Genetic Models of Range Expansion and Admixture. <i>Molecular Biology and Evolution</i> , 2010, 27, 1257-1268.	8.9	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.	6.2	115
14	SPLATCHE2: a spatially explicit simulation framework for complex demography, genetic admixture and recombination. <i>Bioinformatics</i> , 2010, 26, 2993-2994.	4.1	113
15	Bayesian Estimation of Recent Migration Rates After a Spatial Expansion. <i>Genetics</i> , 2005, 170, 409-417.	2.9	112
16	Impact of Selection and Demography on the Diffusion of Lactase Persistence. <i>PLoS ONE</i> , 2009, 4, e6369.	2.5	107
17	The genetic history of Europeans. <i>Trends in Genetics</i> , 2012, 28, 496-505.	6.7	102
18	Recovering the geographic origin of early modern humans by realistic and spatially explicit simulations. <i>Genome Research</i> , 2005, 15, 1161-1167.	5.5	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.	12.8	96
20	Molecular Diversity After a Range Expansion in Heterogeneous Environments. <i>Genetics</i> , 2006, 174, 2009-2020.	2.9	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.	3.9	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.	4.0	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.	4.8	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.	12.6	51
25	Human Neutral Genetic Variation and Forensic STR Data. <i>PLoS ONE</i> , 2012, 7, e49666.	2.5	51
26	Influence of Admixture and Paleolithic Range Contractions on Current European Diversity Gradients. <i>Molecular Biology and Evolution</i> , 2013, 30, 57-61.	8.9	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.	4.1	41
29	Local Population Structure in Arabian Peninsula Revealed by Y-STR Diversity. <i>Human Heredity</i> , 2009, 68, 45-54.	0.8	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.	4.4	38
32	Long-Distance Dispersal Shaped Patterns of Human Genetic Diversity in Eurasia. <i>Molecular Biology and Evolution</i> , 2016, 33, 946-958.	8.9	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.	3.1	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.	2.3	22
35	The Spatial Signature of Introgression After a Biological Invasion With Hybridization. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	2.2	20
36	Computer simulation of human leukocyte 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. Scientific Reports, 2018, 8, 2414.	3.3	16
38	Air temperature influences early Covid-19 outbreak as indicated by worldwide mortality. Science of the Total Environment, 2021, 792, 148312.	8.0	13
39	Forward-in-Time, Spatially Explicit Modeling Software to Simulate Genetic Lineages under Selection. Evolutionary Bioinformatics, 2015, 11s2, EBO.S33488.	1.2	12
40	Investigating population continuity with ancient DNA under a spatially explicit simulation framework. BMC Genetics, 2017, 18, 114.	2.7	12
41	Effect of hybridization with genome exclusion on extinction risk. Conservation Biology, 2018, 32, 1139-1149.	4.7	12
42	A General Model of Distant Hybridization Reveals the Conditions for Extinction in Atlantic Salmon and Brown Trout. PLoS ONE, 2014, 9, e101736.	2.5	11
43	Projecting introgression from domestic cats into European wildcats in the Swiss Jura. Evolutionary Applications, 2020, 13, 2101-2112.	3.1	11
44	Bayesian estimation of partial population continuity using ancient <scp>DNA</scp> and spatially explicit simulations. Evolutionary Applications, 2018, 11, 1642-1655.	3.1	10
45	Consequences of diverse evolutionary processes on american genetic gradients of modern humans. Heredity, 2018, 121, 548-556.	2.6	8
46	Investigating European Genetic History through Computer Simulations. Human Heredity, 2013, 76, 142-153.	0.8	7
47	Influence of Paleolithic range contraction, admixture and long-distance dispersal on genetic gradients of modern humans in Asia. Molecular Ecology, 2020, 29, 2150-2159.	3.9	4
48	Spatially explicit paleogenomic simulations support cohabitation with limited admixture between Bronze Age Central European populations. Communications Biology, 2021, 4, 1163.	4.4	3
49	Simulated patterns of mitochondrial diversity are consistent with partial population turnover in Bronze Age Central Europe. American Journal of Biological Anthropology, 2022, 177, 134-146.	1.1	1
50	Challenging ancient DNA results about putative HLA protection or susceptibility to <i>Yersina pestis</i>. Molecular Biology and Evolution, 2022, , .	8.9	1
51	Recipient of the 2013 <i>Molecular Ecology</i> Prize: Laurent Excoffier. Molecular Ecology, 2014, 23, 16-19.	3.9	0
52	Simulations of Human Dispersal and Genetic Diversity. Evolutionary Studies, 2021, , 231-256.	0.1	0