

# 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	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
2	Challenging ancient DNA results about putative HLA protection or susceptibility to <i>Yersinia pestis</i> . <i>Molecular Biology and Evolution</i> , 2022, , .	3.5	1
3	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
4	Simulations of Human Dispersal and Genetic Diversity. <i>Evolutionary Studies</i> , 2021, , 231-256.	0.2	0
5	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
6	Harmonizing hybridization dissonance in conservation. <i>Communications Biology</i> , 2020, 3, 391.	2.0	38
7	The Spatial Signature of Introgression After a Biological Invasion With Hybridization. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	20
8	Projecting introgression from domestic cats into European wildcats in the Swiss Jura. <i>Evolutionary Applications</i> , 2020, 13, 2101-2112.	1.5	11
9	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
10	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
11	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
12	Cryptic Biological Invasions: a General Model of Hybridization. <i>Scientific Reports</i> , 2018, 8, 2414.	1.6	16
13	Effect of hybridization with genome exclusion on extinction risk. <i>Conservation Biology</i> , 2018, 32, 1139-1149.	2.4	12
14	Consequences of diverse evolutionary processes on american genetic gradients of modern humans. <i>Heredity</i> , 2018, 121, 548-556.	1.2	8
15	Bayesian estimation of partial population continuity using ancient DNA and spatially explicit simulations. <i>Evolutionary Applications</i> , 2018, 11, 1642-1655.	1.5	10
16	Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe. <i>Nature Communications</i> , 2017, 8, 14615.	5.8	96
17	Investigating population continuity with ancient DNA under a spatially explicit simulation framework. <i>BMC Genetics</i> , 2017, 18, 114.	2.7	12
18	Early Neolithic genomes from the eastern Fertile Crescent. <i>Science</i> , 2016, 353, 499-503.	6.0	230

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19	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
20	Long-Distance Dispersal Shaped Patterns of Human Genetic Diversity in Eurasia. <i>Molecular Biology and Evolution</i> , 2016, 33, 946-958.	3.5	36
21	Forward-in-Time, Spatially Explicit Modeling Software to Simulate Genetic Lineages under Selection. <i>Evolutionary Bioinformatics</i> , 2015, 11s2, EBO.S33488.	0.6	12
22	Upper Palaeolithic genomes reveal deep roots of modern Eurasians. <i>Nature Communications</i> , 2015, 6, 8912.	5.8	334
23	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
24	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
25	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
26	Recipient of the 2013 <i>Molecular Ecology</i> Prize: Laurent Excoffier. <i>Molecular Ecology</i> , 2014, 23, 16-19.	2.0	0
27	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
28	Investigating European Genetic History through Computer Simulations. <i>Human Heredity</i> , 2013, 76, 142-153.	0.4	7
29	Distinct evolutionary strategies of human leukocyte antigen loci in pathogen-rich environments. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 830-839.	1.8	55
30	Consequences of Range Contractions and Range Shifts on Molecular Diversity. <i>Molecular Biology and Evolution</i> , 2012, 29, 207-218.	3.5	204
31	The genetic history of Europeans. <i>Trends in Genetics</i> , 2012, 28, 496-505.	2.9	102
32	Human Neutral Genetic Variation and Forensic STR Data. <i>PLoS ONE</i> , 2012, 7, e49666.	1.1	51
33	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
34	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
35	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
36	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

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37	Human genetic differentiation across the Strait of Gibraltar. <i>BMC Evolutionary Biology</i> , 2010, 10, 237.	3.2	46
38	SPLATCHE2: a spatially explicit simulation framework for complex demography, genetic admixture and recombination. <i>Bioinformatics</i> , 2010, 26, 2993-2994.	1.8	113
39	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
40	Impact of Selection and Demography on the Diffusion of Lactase Persistence. <i>PLoS ONE</i> , 2009, 4, e6369.	1.1	107
41	Local Population Structure in Arabian Peninsula Revealed by Y-STR Diversity. <i>Human Heredity</i> , 2009, 68, 45-54.	0.4	38
42	THE HIDDEN SIDE OF INVASIONS: MASSIVE INTROGRESSION BY LOCAL GENES. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, ???-???	1.1	658
43	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
44	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
45	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
46	Molecular Diversity After a Range Expansion in Heterogeneous Environments. <i>Genetics</i> , 2006, 174, 2009-2020.	1.2	74
47	Bayesian Estimation of Recent Migration Rates After a Spatial Expansion. <i>Genetics</i> , 2005, 170, 409-417.	1.2	112
48	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
49	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
50	Modern Humans Did Not Admix with Neanderthals during Their Range Expansion into Europe. <i>PLoS Biology</i> , 2004, 2, e421.	2.6	242
51	Intra-Deme Molecular Diversity in Spatially Expanding Populations. <i>Molecular Biology and Evolution</i> , 2003, 20, 76-86.	3.5	519
52	Molecular Analysis of the $\beta$ -Globin Gene Cluster in the Niokholo Mandenka Population Reveals a Recent Origin of the $\beta^S$ Senegal Mutation. <i>American Journal of Human Genetics</i> , 2002, 70, 207-223.	2.6	115