

# Gilles Guillot

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

3,990  
citations

304602

22  
h-index

265120

42  
g-index

48  
all docs

48  
docs citations

48  
times ranked

5418  
citing authors

#	ARTICLE	IF	CITATIONS
1	Editorial: Advances in Statistical Ecology: New Methods and Software. <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	1.1	0
2	Efforts needed for preventing breast and colorectal cancer through changes in dietary patterns. <i>European Journal of Public Health</i> , 2021, 31, 355-360.	0.1	2
3	Latitudinal variation in climate-associated genes imperils range edge populations. <i>Molecular Ecology</i> , 2020, 29, 4337-4349.	2.0	12
4	Dose-response analysis of toxicological and pharmacological mixtures with the model deviation ratio method: Problems and solutions. <i>Toxicology Letters</i> , 2020, 325, 62-66.	0.4	1
5	Investigating combined toxicity of binary mixtures in bees: Meta-analysis of laboratory tests, modelling, mechanistic basis and implications for risk assessment. <i>Environment International</i> , 2019, 133, 105256.	4.8	54
6	Global burden of diabetes: regional disparities in prevalence, incidence, and mortality. <i>Journal of Health Inequalities</i> , 2019, 5, 141-154.	0.1	1
7	Serological monitoring on milk and serum samples in a BVD eradication program: A field study in Belgium showing antibody ELISA performances and epidemiological aspects. <i>Preventive Veterinary Medicine</i> , 2018, 160, 136-144.	0.7	17
8	Guidance on dermal absorption. <i>EFSA Journal</i> , 2017, 15, e04873.	0.9	62
9	Spatial models for probabilistic prediction of wind power with application to annual-average and high temporal resolution data. <i>Stochastic Environmental Research and Risk Assessment</i> , 2017, 31, 1615-1631.	1.9	12
10	Outcome of the public consultation on the draft EFSA Guidance on dermal absorption. <i>EFSA Supporting Publications</i> , 2017, 14, 1250E.	0.3	0
11	A genomewide catalogue of single nucleotide polymorphisms in white-beaked and Atlantic white-sided dolphins. <i>Molecular Ecology Resources</i> , 2016, 16, 266-276.	2.2	16
12	Accurate continuous geographic assignment from low- to high-density SNP data. <i>Bioinformatics</i> , 2016, 32, 1106-1108.	1.8	16
13	Enhanced computational methods for quantifying the effect of geographic and environmental isolation on genetic differentiation. <i>Methods in Ecology and Evolution</i> , 2015, 6, 1270-1277.	2.2	13
14	A Spatial Model for the Instantaneous Estimation of Wind Power at a Large Number of Unobserved Sites. <i>Procedia Environmental Sciences</i> , 2015, 26, 131-134.	1.3	1
15	Validity of covariance models for the analysis of geographical variation. <i>Methods in Ecology and Evolution</i> , 2014, 5, 329-335.	2.2	9
16	Detecting correlation between allele frequencies and environmental variables as a signature of selection. A fast computational approach for genome-wide studies. <i>Spatial Statistics</i> , 2014, 8, 145-155.	0.9	52
17	Dismantling the Mantel tests. <i>Methods in Ecology and Evolution</i> , 2013, 4, 336-344.	2.2	397
18	Population dynamics of species-rich ecosystems: the mixture of matrix population models approach. <i>Methods in Ecology and Evolution</i> , 2013, 4, 316-326.	2.2	3

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19	A Unifying Model for the Analysis of Phenotypic, Genetic, and Geographic Data. <i>Systematic Biology</i> , 2012, 61, 897-911.	2.7	128
20	Identification of Adipocyte Genes Regulated by Caloric Intake. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2011, 96, E413-E418.	1.8	74
21	Estimating the location and shape of hybrid zones. <i>Molecular Ecology Resources</i> , 2011, 11, 1119-1123.	2.2	24
22	Splendor and misery of indirect measures of migration and gene flow. <i>Heredity</i> , 2011, 106, 11-12.	1.2	9
23	On the Informativeness of Dominant and Co-Dominant Genetic Markers for Bayesian Supervised Clustering. <i>The Open Statistics &amp; Probability Journal</i> , 2011, 3, 7-12.	0.4	7
24	Identification of Adipocyte Genes Regulated by Caloric Intake. <i>Endocrine Reviews</i> , 2010, 31, 945-945.	8.9	0
25	Using AFLP markers and the Geneland program for the inference of population genetic structure. <i>Molecular Ecology Resources</i> , 2010, 10, 1082-1084.	2.2	31
26	Identification of Adipocyte Genes Regulated by Caloric Intake. <i>Endocrinology</i> , 2010, 151, 5973-5973.	1.4	0
27	Response to comment on "On the inference of spatial structure from population genetics data". <i>Bioinformatics</i> , 2009, 25, 1805-1806.	1.8	5
28	On the inference of spatial structure from population genetics data. <i>Bioinformatics</i> , 2009, 25, 1796-1801.	1.8	36
29	Correcting for ascertainment bias in the inference of population structure. <i>Bioinformatics</i> , 2009, 25, 552-554.	1.8	31
30	Statistical methods in spatial genetics. <i>Molecular Ecology</i> , 2009, 18, 4734-4756.	2.0	319
31	Spatial Prediction of Weed Intensities From Exact Count Data and Image-Based Estimates. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2009, 58, 525-542.	0.5	10
32	A computer program to simulate multilocus genotype data with spatially autocorrelated allele frequencies. <i>Molecular Ecology Resources</i> , 2009, 9, 1112-1120.	2.2	54
33	Population substructure in Finland and Sweden revealed by the use of spatial coordinates and a small number of unlinked autosomal SNPs. <i>BMC Genetics</i> , 2008, 9, 54.	2.7	31
34	Inference of structure in subdivided populations at low levels of genetic differentiation—the correlated allele frequencies model revisited. <i>Bioinformatics</i> , 2008, 24, 2222-2228.	1.8	142
35	Analysing georeferenced population genetics data with Geneland: a new algorithm to deal with null alleles and a friendly graphical user interface. <i>Bioinformatics</i> , 2008, 24, 1406-1407.	1.8	258
36	Discrimination and scoring using small sets of genes for two-sample microarray data. <i>Mathematical Biosciences</i> , 2007, 205, 195-203.	0.9	4

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37	Bayesian Clustering Using Hidden Markov Random Fields in Spatial Population Genetics. <i>Genetics</i> , 2006, 174, 805-816.	1.2	284
38	Inference of a hidden spatial tessellation from multivariate data: application to the delineation of homogeneous regions in an agricultural field. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2006, 55, 407-430.	0.5	13
39	Genetic structure is influenced by landscape features: empirical evidence from a roe deer population. <i>Molecular Ecology</i> , 2006, 15, 1669-1679.	2.0	238
40	A network-based analysis of allergen-challenged CD4+ T cells from patients with allergic rhinitis. <i>Genes and Immunity</i> , 2006, 7, 514-521.	2.2	30
41	Geneland: a computer package for landscape genetics. <i>Molecular Ecology Notes</i> , 2005, 5, 712-715.	1.7	955
42	A Spatial Statistical Model for Landscape Genetics. <i>Genetics</i> , 2005, 170, 1261-1280.	1.2	538
43	Gibbs sampling for conditional spatial disaggregation of rain fields. <i>Water Resources Research</i> , 2004, 40, .	1.7	23
44	APPLICATION OF THE GIBBS SAMPLER TO THE CONDITIONAL SIMULATION OF RAIN FIELDS. , 2002, , .		0
45	Approximation of Sahelian rainfall fields with meta-Gaussian random functions. <i>Stochastic Environmental Research and Risk Assessment</i> , 1999, 13, 100-112.	1.9	28
46	Approximation of Sahelian rainfall fields with meta-Gaussian random functions. <i>Stochastic Environmental Research and Risk Assessment</i> , 1999, 13, 113-130.	1.9	22
47	Disaggregation of Sahelian mesoscale convective system rain fields: Further developments and validation. <i>Journal of Geophysical Research</i> , 1999, 104, 31533-31551.	3.3	28