

Olivier Francois

List of Publications by Year in descending order

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Version: 2024-02-01

102
papers

9,640
citations

101543

36
h-index

43889

91
g-index

116
all docs

116
docs citations

116
times ranked

11165
citing authors

#	ARTICLE	IF	CITATIONS
1	LEA: An R package for landscape and ecological association studies. <i>Methods in Ecology and Evolution</i> , 2015, 6, 925-929.	5.2	1,047
2	Approximate Bayesian Computation (ABC) in practice. <i>Trends in Ecology and Evolution</i> , 2010, 25, 410-418.	8.7	943
3	Bayesian clustering algorithms ascertaining spatial population structure: a new computer program and a comparison study. <i>Molecular Ecology Notes</i> , 2007, 7, 747-756.	1.7	640
4	Fast and Efficient Estimation of Individual Ancestry Coefficients. <i>Genetics</i> , 2014, 196, 973-983.	2.9	638
5	Testing for Associations between Loci and Environmental Gradients Using Latent Factor Mixed Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 1687-1699.	8.9	627
6	abc: an R package for approximate Bayesian computation (ABC). <i>Methods in Ecology and Evolution</i> , 2012, 3, 475-479.	5.2	617
7	Applications of landscape genetics in conservation biology: concepts and challenges. <i>Conservation Genetics</i> , 2010, 11, 375-385.	1.5	356
8	Non-linear regression models for Approximate Bayesian Computation. <i>Statistics and Computing</i> , 2010, 20, 63-73.	1.5	331
9	Bayesian Clustering Using Hidden Markov Random Fields in Spatial Population Genetics. <i>Genetics</i> , 2006, 174, 805-816.	2.9	284
10	Spatial Inference of Admixture Proportions and Secondary Contact Zones. <i>Molecular Biology and Evolution</i> , 2009, 26, 1963-1973.	8.9	282
11	Genome scan methods against more complex models: when and how much should we trust them?. <i>Molecular Ecology</i> , 2014, 23, 2006-2019.	3.9	265
12	Adaptive Genetic Variation on the Landscape: Methods and Cases. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2012, 43, 23-43.	8.3	250
13	Spatially explicit Bayesian clustering models in population genetics. <i>Molecular Ecology Resources</i> , 2010, 10, 773-784.	4.8	249
14	TESS3: fast inference of spatial population structure and genome scans for selection. <i>Molecular Ecology Resources</i> , 2016, 16, 540-548.	4.8	216
15	Controlling false discoveries in genome scans for selection. <i>Molecular Ecology</i> , 2016, 25, 454-469.	3.9	210
16	LFMM 2: Fast and Accurate Inference of Gene-Environment Associations in Genome-Wide Studies. <i>Molecular Biology and Evolution</i> , 2019, 36, 852-860.	8.9	183
17	Demographic History of European Populations of <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2008, 4, e1000075.	3.5	182
18	Which Random Processes Describe the Tree of Life? A Large-Scale Study of Phylogenetic Tree Imbalance. <i>Systematic Biology</i> , 2006, 55, 685-691.	5.6	154

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19	Forecasting changes in population genetic structure of alpine plants in response to global warming. <i>Molecular Ecology</i> , 2012, 21, 2354-2368.	3.9	127
20	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
21	apTreeshape: statistical analysis of phylogenetic tree shape. <i>Bioinformatics</i> , 2006, 22, 363-364.	4.1	109
22	The origins and diversification of C ₄ grasses and savanna-adapted ungulates. <i>Global Change Biology</i> , 2009, 15, 2397-2417.	9.5	103
23	On statistical tests of phylogenetic tree imbalance: The Sackin and other indices revisited. <i>Mathematical Biosciences</i> , 2005, 195, 141-153.	1.9	93
24	The Rise and Fall of African Rice Cultivation Revealed by Analysis of 246 New Genomes. <i>Current Biology</i> , 2018, 28, 2274-2282.e6.	3.9	84
25	A western Sahara centre of domestication inferred from pearl millet genomes. <i>Nature Ecology and Evolution</i> , 2018, 2, 1377-1380.	7.8	78
26	Detecting adaptive evolution based on association with ecological gradients: Orientation matters!. <i>Heredity</i> , 2015, 115, 22-28.	2.6	76
27	Yam genomics supports West Africa as a major cradle of crop domestication. <i>Science Advances</i> , 2019, 5, eaaw1947.	10.3	71
28	The mean, variance and limiting distribution of two statistics sensitive to phylogenetic tree balance. <i>Annals of Applied Probability</i> , 2006, 16, 2195.	1.3	69
29	Theory-Based Interventions Combining Mental Simulation and Planning Techniques to Improve Physical Activity: Null Results from Two Randomized Controlled Trials. <i>Frontiers in Psychology</i> , 2016, 7, 1789.	2.1	59
30	Guns, germs and dogs: On the origin of <i>Leishmania chagasi</i> . <i>Infection, Genetics and Evolution</i> , 2011, 11, 1091-1095.	2.3	56
31	Assumed and inferred spatial structure of populations: the Scandinavian brown bears revisited. <i>Molecular Ecology</i> , 2004, 13, 1327-1331.	3.9	52
32	Overdiagnosis from non-progressive cancer detected by screening mammography: stochastic simulation study with calibration to population based registry data. <i>BMJ: British Medical Journal</i> , 2011, 343, d7017-d7017.	2.3	49
33	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
34	Fast inference of individual admixture coefficients using geographic data. <i>Annals of Applied Statistics</i> , 2018, 12, .	1.1	48
35	An evolutionary strategy for global minimization and its Markov chain analysis. <i>IEEE Transactions on Evolutionary Computation</i> , 1998, 2, 77-90.	10.0	46
36	Design of evolutionary algorithms-A statistical perspective. <i>IEEE Transactions on Evolutionary Computation</i> , 2001, 5, 129-148.	10.0	42

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37	Global convergence for evolution strategies in spherical problems: some simple proofs and difficulties. <i>Theoretical Computer Science</i> , 2003, 306, 269-289.	0.9	38
38	Identifying outlier loci in admixed and in continuous populations using ancestral population differentiation statistics. <i>Molecular Ecology</i> , 2016, 25, 5029-5042.	3.9	38
39	LEA 3: Factor models in population genetics and ecological genomics with R. <i>Molecular Ecology Resources</i> , 2021, 21, 2738-2748.	4.8	36
40	Epigenetic Alterations of Maternal Tobacco Smoking during Pregnancy: A Narrative Review. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 5083.	2.6	36
41	Matrilineal Fertility Inheritance Detected in Hunter-Gatherer Populations Using the Imbalance of Gene Genealogies. <i>PLoS Genetics</i> , 2006, 2, e122.	3.5	30
42	Minimal clade size and external branch length under the neutral coalescent. <i>Advances in Applied Probability</i> , 2005, 37, 647-662.	0.7	29
43	Global Optimization with Exploration/Selection Algorithms and Simulated Annealing. <i>Annals of Applied Probability</i> , 2002, 12, .	1.3	29
44	Correcting Principal Component Maps for Effects of Spatial Autocorrelation in Population Genetic Data. <i>Frontiers in Genetics</i> , 2012, 3, 254.	2.3	28
45	Factor analysis of ancient population genomic samples. <i>Nature Communications</i> , 2020, 11, 4661.	12.8	28
46	Deviance Information Criteria for Model Selection in Approximate Bayesian Computation. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.6	26
47	At the Origin of a Worldwide Invasion: Unraveling the Genetic Makeup of the Caribbean Bridgehead Populations of the Dengue Vector <i>Aedes aegypti</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 56-71.	2.5	24
48	Microvascular MRI and Unsupervised Clustering Yields Histology-Resembling Images in Two Rat Models of Glioma. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2014, 34, 1354-1362.	4.3	23
49	Challenges Raised by Mediation Analysis in a High-Dimension Setting. <i>Environmental Health Perspectives</i> , 2020, 128, 55001.	6.0	22
50	Overdiagnosis and overtreatment associated with breast cancer mammography screening: A simulation study with calibration to population-based data. <i>Breast</i> , 2016, 28, 60-66.	2.2	21
51	First next-generation sequencing full-genome characterization of a hepatitis C virus genotype 7 divergent subtype. <i>Clinical Microbiology and Infection</i> , 2016, 22, 947.e1-947.e8.	6.0	21
52	The Genetical Bandwidth Mapping: A spatial and graphical representation of population genetic structure based on the Wombling method. <i>Theoretical Population Biology</i> , 2007, 71, 332-341.	1.1	20
53	Molecular basis of African yam domestication: analyses of selection point to root development, starch biosynthesis, and photosynthesis related genes. <i>BMC Genomics</i> , 2017, 18, 782.	2.8	20
54	Genome Wide Association Study Pinpoints Key Agronomic QTLs in African Rice <i>Oryza glaberrima</i> . <i>Rice</i> , 2020, 13, 66.	4.0	16

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55	Joint analysis of spatial genetic structure and inbreeding in a managed population of Scots pine. <i>Heredity</i> , 2009, 103, 90-96.	2.6	15
56	Genome-Scale Data Reveal Deep Lineage Divergence and a Complex Demographic History in the Texas Horned Lizard (<i>Phrynosoma cornutum</i>) throughout the Southwestern and Central United States. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	15
57	The Empirical Distribution of Singletons for Geographic Samples of DNA Sequences. <i>Frontiers in Genetics</i> , 2017, 8, 139.	2.3	13
58	Multiple introductions and population structure during the rapid expansion of the invasive Sahara mustard (<i>Brassica tournefortii</i>). <i>Ecology and Evolution</i> , 2019, 9, 7928-7941.	1.9	13
59	Minimal clade size and external branch length under the neutral coalescent. <i>Advances in Applied Probability</i> , 2005, 37, 647-662.	0.7	12
60	faststruct: model-based clustering made faster. <i>Molecular Ecology Notes</i> , 2006, 6, 980-983.	1.7	12
61	Invalid arguments against ABC: Reply to A.R. Templeton. <i>Trends in Ecology and Evolution</i> , 2010, 25, 490-491.	8.7	12
62	Convergence of a self-organizing stochastic neural network. <i>Neural Networks</i> , 1992, 5, 277-282.	5.9	11
63	Markovian perturbations of discrete iterations: Lyapunov functions, global minimization, and associative memory. <i>Mathematical and Computer Modelling</i> , 1999, 29, 81-95.	2.0	11
64	POPS: A Software for Prediction of Population Genetic Structure Using Latent Regression Models. <i>Journal of Statistical Software</i> , 2015, 68, .	3.7	11
65	Brownian models and coalescent structures. <i>Theoretical Population Biology</i> , 2004, 65, 249-261.	1.1	10
66	Prediction of group patterns in social mammals based on a coalescent model. <i>Journal of Theoretical Biology</i> , 2007, 249, 262-270.	1.7	10
67	Comment on "On the inference of spatial structure from population genetics data". <i>Bioinformatics</i> , 2009, 25, 1802-1804.	4.1	10
68	Wave-of-Advance Models of the Diffusion of the Y Chromosome Haplogroup R1b1b2 in Europe. <i>PLoS ONE</i> , 2011, 6, e21592.	2.5	10
69	Amplification and pyrosequencing of near-full-length hepatitis C virus for typing and monitoring antiviral resistant strains. <i>Clinical Microbiology and Infection</i> , 2016, 22, 460.e1-460.e10.	6.0	10
70	Gaussian approximations for phylogenetic branch length statistics under stochastic models of biodiversity. <i>Mathematical Biosciences</i> , 2007, 209, 108-123.	1.9	9
71	Naturalgwass: An R package for evaluating genomewide association methods with empirical data. <i>Molecular Ecology Resources</i> , 2018, 18, 789-797.	4.8	9
72	Predictions of Native American Population Structure Using Linguistic Covariates in a Hidden Regression Framework. <i>PLoS ONE</i> , 2011, 6, e16227.	2.5	9

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73	Managing Missing Data in the Hospital Survey on Patient Safety Culture: A Simulation Study. Journal of Patient Safety, 2021, 17, e98-e106.	1.7	7
74	A spectral theory for Wright's inbreeding coefficients and related quantities. PLoS Genetics, 2021, 17, e1009665.	3.5	7
75	Adaptive potential of <i>Coffea canephora</i> from Uganda in response to climate change. Molecular Ecology, 2022, 31, 1800-1819.	3.9	7
76	Ultradeep Pyrosequencing of NS3 To Predict Response to Triple Therapy with Protease Inhibitors in Previously Treated Chronic Hepatitis C Patients. Journal of Clinical Microbiology, 2015, 53, 389-397.	3.9	6
77	Niching in Monte Carlo Filtering Algorithms. Lecture Notes in Computer Science, 2002, , 19-30.	1.3	6
78	Stochastic comparison for Markov processes on a product of partially ordered sets. Statistics and Probability Letters, 1997, 33, 309-320.	0.7	5
79	Asymptotic Behavior of Neural Networks and Image Processing. NATO ASI Series Series B: Physics, 1991, , 219-229.	0.2	5
80	Statistical Procedures for Spatiotemporal Neuronal Data with Applications to Optical Recording of the Auditory Cortex. Neural Computation, 2000, 12, 1821-1838.	2.2	4
81	Probabilistic analysis of a genealogical model of animal group patterns. Journal of Mathematical Biology, 2010, 60, 451-468.	1.9	4
82	Ultradeep sequencing of B and non-B HIV-1 subtypes: Viral diversity and drug resistance mutations before and after one month of antiretroviral therapy in naive patients. Journal of Clinical Virology, 2017, 95, 13-19.	3.1	4
83	New insights into HCV replication in original cells from Aedes mosquitoes. Virology Journal, 2017, 14, 161.	3.4	4
84	Sparse latent factor regression models for genome-wide and epigenome-wide association studies. Statistical Applications in Genetics and Molecular Biology, 2022, 21, .	0.6	4
85	ON THE SPECTRAL GAP OF A TIME REVERSIBLE MARKOV CHAIN. Probability in the Engineering and Informational Sciences, 1999, 13, 95-101.	0.8	3
86	Spatial Correlation of Gene Expression Measures in Tissue Microarray Core Analysis. Journal of Theoretical Medicine, 2005, 6, 33-39.	0.5	3
87	A statistical approach to estimating the strength of cell-cell interactions under the differential adhesion hypothesis. Theoretical Biology and Medical Modelling, 2007, 4, 37.	2.1	3
88	Using high-throughput sequencing for investigating intra-host hepatitis C evolution over long retrospective periods. Infection, Genetics and Evolution, 2019, 67, 136-144.	2.3	3
89	Geometric inequalities for the eigenvalues of concentrated Markov chains. Journal of Applied Probability, 2000, 37, 15-28.	0.7	3
90	New rigorous results for the Hopfield's neural network model. Neural Networks, 1996, 9, 503-507.	5.9	2

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91	Geometric inequalities for the eigenvalues of concentrated Markov chains. Journal of Applied Probability, 2000, 37, 15-28.	0.7	2
92	Title is missing!. Journal of Statistical Physics, 2003, 110, 311-332.	1.2	2
93	Parameter estimation in a model for multidimensional recording of neuronal data: a Gibbsian approximation approach. Biological Cybernetics, 2003, 89, 170-178.	1.3	2
94	Conditional Coalescent Trees With Two Mutation Rates and Their Application to Genomic Instability. Genetics, 2006, 172, 1809-1820.	2.9	2
95	Risk Assessment for Hospitalâ€Acquired Diseases: A Riskâ€Theory Approach. Risk Analysis, 2009, 29, 565-575.	2.7	2
96	Diffusion and innovation rates for multidimensional neuronal data with large spatial covariances. Network: Computation in Neural Systems, 2000, 11, 211-220.	3.6	2
97	Improved bounds for the large-time behaviour of simulated annealing. Journal of Applied Probability, 2003, 40, 961-969.	0.7	2
98	Convergence Analysis of Evolution Strategies with Random Numbers of Offspring. Lecture Notes in Computer Science, 2008, , 21-30.	1.3	2
99	A multi-epoch model for the number of species within genera. Theoretical Population Biology, 2020, 133, 97-103.	1.1	1
100	Parallel simulations in ferromagnetic spin systems. Journal of Physics A, 1997, 30, 3393-3405.	1.6	0
101	Coalescent Models of Demographic History: Application to Plant Domestication. Population Genomics, 2020, , 1.	0.5	0
102	Increasing couplings for interacting particle systems. Comptes Rendus Mathematique, 1997, 324, 459-464.	0.5	0