

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	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
2	Adaptive potential of <i>Coffea canephora</i> from Uganda in response to climate change. <i>Molecular Ecology</i> , 2022, 31, 1800-1819.	3.9	7
3	Sparse latent factor regression models for genome-wide and epigenome-wide association studies. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2022, 21, .	0.6	4
4	Managing Missing Data in the Hospital Survey on Patient Safety Culture: A Simulation Study. <i>Journal of Patient Safety</i> , 2021, 17, e98-e106.	1.7	7
5	LEA 3: Factor models in population genetics and ecological genomics with R. <i>Molecular Ecology Resources</i> , 2021, 21, 2738-2748.	4.8	36
6	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
7	A spectral theory for Wright's inbreeding coefficients and related quantities. <i>PLoS Genetics</i> , 2021, 17, e1009665.	3.5	7
8	A multi-epoch model for the number of species within genera. <i>Theoretical Population Biology</i> , 2020, 133, 97-103.	1.1	1
9	Factor analysis of ancient population genomic samples. <i>Nature Communications</i> , 2020, 11, 4661.	12.8	28
10	Challenges Raised by Mediation Analysis in a High-Dimension Setting. <i>Environmental Health Perspectives</i> , 2020, 128, 55001.	6.0	22
11	Coalescent Models of Demographic History: Application to Plant Domestication. <i>Population Genomics</i> , 2020, , 1.	0.5	0
12	Genome Wide Association Study Pinpoints Key Agronomic QTLs in African Rice <i>Oryza glaberrima</i> . <i>Rice</i> , 2020, 13, 66.	4.0	16
13	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
14	Yam genomics supports West Africa as a major cradle of crop domestication. <i>Science Advances</i> , 2019, 5, eaaw1947.	10.3	71
15	Using high-throughput sequencing for investigating intra-host hepatitis C evolution over long retrospective periods. <i>Infection, Genetics and Evolution</i> , 2019, 67, 136-144.	2.3	3
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	Fast inference of individual admixture coefficients using geographic data. <i>Annals of Applied Statistics</i> , 2018, 12, .	1.1	48
18	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

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19	Naturalgwas: An R package for evaluating genomewide association methods with empirical data. <i>Molecular Ecology Resources</i> , 2018, 18, 789-797.	4.8	9
20	A western Sahara centre of domestication inferred from pearl millet genomes. <i>Nature Ecology and Evolution</i> , 2018, 2, 1377-1380.	7.8	78
21	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
22	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. <i>Journal of Clinical Virology</i> , 2017, 95, 13-19.	3.1	4
23	The Empirical Distribution of Singletons for Geographic Samples of DNA Sequences. <i>Frontiers in Genetics</i> , 2017, 8, 139.	2.3	13
24	New insights into HCV replication in original cells from Aedes mosquitoes. <i>Virology Journal</i> , 2017, 14, 161.	3.4	4
25	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
26	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
27	Controlling false discoveries in genome scans for selection. <i>Molecular Ecology</i> , 2016, 25, 454-469.	3.9	210
28	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
29	TESS3: fast inference of spatial population structure and genome scans for selection. <i>Molecular Ecology Resources</i> , 2016, 16, 540-548.	4.8	216
30	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
31	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
32	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
33	Detecting adaptive evolution based on association with ecological gradients: Orientation matters!. <i>Heredity</i> , 2015, 115, 22-28.	2.6	76
34	Ultradeep Pyrosequencing of NS3 To Predict Response to Triple Therapy with Protease Inhibitors in Previously Treated Chronic Hepatitis C Patients. <i>Journal of Clinical Microbiology</i> , 2015, 53, 389-397.	3.9	6
35	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
36	POPS: A Software for Prediction of Population Genetic Structure Using Latent Regression Models. <i>Journal of Statistical Software</i> , 2015, 68, .	3.7	11

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37	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
38	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
39	Fast and Efficient Estimation of Individual Ancestry Coefficients. <i>Genetics</i> , 2014, 196, 973-983.	2.9	638
40	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
41	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
42	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
43	Correcting Principal Component Maps for Effects of Spatial Autocorrelation in Population Genetic Data. <i>Frontiers in Genetics</i> , 2012, 3, 254.	2.3	28
44	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
45	abc: an R package for approximate Bayesian computation (ABC). <i>Methods in Ecology and Evolution</i> , 2012, 3, 475-479.	5.2	617
46	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
47	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
48	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
49	Deviance Information Criteria for Model Selection in Approximate Bayesian Computation. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.6	26
50	Predictions of Native American Population Structure Using Linguistic Covariates in a Hidden Regression Framework. <i>PLoS ONE</i> , 2011, 6, e16227.	2.5	9
51	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
52	Probabilistic analysis of a genealogical model of animal group patterns. <i>Journal of Mathematical Biology</i> , 2010, 60, 451-468.	1.9	4
53	Applications of landscape genetics in conservation biology: concepts and challenges. <i>Conservation Genetics</i> , 2010, 11, 375-385.	1.5	356
54	Non-linear regression models for Approximate Bayesian Computation. <i>Statistics and Computing</i> , 2010, 20, 63-73.	1.5	331

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55	Approximate Bayesian Computation (ABC) in practice. Trends in Ecology and Evolution, 2010, 25, 410-418.	8.7	943
56	Invalid arguments against ABC: Reply to A.R. Templeton. Trends in Ecology and Evolution, 2010, 25, 490-491.	8.7	12
57	Spatially explicit Bayesian clustering models in population genetics. Molecular Ecology Resources, 2010, 10, 773-784.	4.8	249
58	Comment on "On the inference of spatial structure from population genetics data". Bioinformatics, 2009, 25, 1802-1804.	4.1	10
59	The origins and diversification of <i>C₄</i> grasses and savanna-adapted ungulates. Global Change Biology, 2009, 15, 2397-2417.	9.5	103
60	Joint analysis of spatial genetic structure and inbreeding in a managed population of Scots pine. Heredity, 2009, 103, 90-96.	2.6	15
61	Risk Assessment for Hospital-Acquired Diseases: A Risk Theory Approach. Risk Analysis, 2009, 29, 565-575.	2.7	2
62	Spatial Inference of Admixture Proportions and Secondary Contact Zones. Molecular Biology and Evolution, 2009, 26, 1963-1973.	8.9	282
63	Demographic History of European Populations of <i>Arabidopsis thaliana</i> . PLoS Genetics, 2008, 4, e1000075.	3.5	182
64	Convergence Analysis of Evolution Strategies with Random Numbers of Offspring. Lecture Notes in Computer Science, 2008, , 21-30.	1.3	2
65	Gaussian approximations for phylogenetic branch length statistics under stochastic models of biodiversity. Mathematical Biosciences, 2007, 209, 108-123.	1.9	9
66	The Genetical Bandwidth Mapping: A spatial and graphical representation of population genetic structure based on the Wombling method. Theoretical Population Biology, 2007, 71, 332-341.	1.1	20
67	Prediction of group patterns in social mammals based on a coalescent model. Journal of Theoretical Biology, 2007, 249, 262-270.	1.7	10
68	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
69	Bayesian clustering algorithms ascertaining spatial population structure: a new computer program and a comparison study. Molecular Ecology Notes, 2007, 7, 747-756.	1.7	640
70	Bayesian Clustering Using Hidden Markov Random Fields in Spatial Population Genetics. Genetics, 2006, 174, 805-816.	2.9	284
71	The mean, variance and limiting distribution of two statistics sensitive to phylogenetic tree balance. Annals of Applied Probability, 2006, 16, 2195.	1.3	69
72	faststruct: model-based clustering made faster. Molecular Ecology Notes, 2006, 6, 980-983.	1.7	12

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73	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
74	apTreeshape: statistical analysis of phylogenetic tree shape. <i>Bioinformatics</i> , 2006, 22, 363-364.	4.1	109
75	Matrilineal Fertility Inheritance Detected in Hunter-Gatherer Populations Using the Imbalance of Gene Genealogies. <i>PLoS Genetics</i> , 2006, 2, e122.	3.5	30
76	Conditional Coalescent Trees With Two Mutation Rates and Their Application to Genomic Instability. <i>Genetics</i> , 2006, 172, 1809-1820.	2.9	2
77	Minimal clade size and external branch length under the neutral coalescent. <i>Advances in Applied Probability</i> , 2005, 37, 647-662.	0.7	12
78	Minimal clade size and external branch length under the neutral coalescent. <i>Advances in Applied Probability</i> , 2005, 37, 647-662.	0.7	29
79	Spatial Correlation of Gene Expression Measures in Tissue Microarray Core Analysis. <i>Journal of Theoretical Medicine</i> , 2005, 6, 33-39.	0.5	3
80	On statistical tests of phylogenetic tree imbalance: The Sackin and other indices revisited. <i>Mathematical Biosciences</i> , 2005, 195, 141-153.	1.9	93
81	Assumed and inferred spatial structure of populations: the Scandinavian brown bears revisited. <i>Molecular Ecology</i> , 2004, 13, 1327-1331.	3.9	52
82	Brownian models and coalescent structures. <i>Theoretical Population Biology</i> , 2004, 65, 249-261.	1.1	10
83	Title is missing!. <i>Journal of Statistical Physics</i> , 2003, 110, 311-332.	1.2	2
84	Parameter estimation in a model for multidimensional recording of neuronal data: a Gibbsian approximation approach. <i>Biological Cybernetics</i> , 2003, 89, 170-178.	1.3	2
85	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
86	Improved bounds for the large-time behaviour of simulated annealing. <i>Journal of Applied Probability</i> , 2003, 40, 961-969.	0.7	2
87	Niching in Monte Carlo Filtering Algorithms. <i>Lecture Notes in Computer Science</i> , 2002, , 19-30.	1.3	6
88	Global Optimization with Exploration/Selection Algorithms and Simulated Annealing. <i>Annals of Applied Probability</i> , 2002, 12, .	1.3	29
89	Design of evolutionary algorithms-A statistical perspective. <i>IEEE Transactions on Evolutionary Computation</i> , 2001, 5, 129-148.	10.0	42
90	Geometric inequalities for the eigenvalues of concentrated Markov chains. <i>Journal of Applied Probability</i> , 2000, 37, 15-28.	0.7	2

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91	Statistical Procedures for Spatiotemporal Neuronal Data with Applications to Optical Recording of the Auditory Cortex. <i>Neural Computation</i> , 2000, 12, 1821-1838.	2.2	4
92	Diffusion and innovation rates for multidimensional neuronal data with large spatial covariances. <i>Network: Computation in Neural Systems</i> , 2000, 11, 211-220.	3.6	2
93	Geometric inequalities for the eigenvalues of concentrated Markov chains. <i>Journal of Applied Probability</i> , 2000, 37, 15-28.	0.7	3
94	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
95	ON THE SPECTRAL GAP OF A TIME REVERSIBLE MARKOV CHAIN. <i>Probability in the Engineering and Informational Sciences</i> , 1999, 13, 95-101.	0.8	3
96	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
97	Parallel simulations in ferromagnetic spin systems. <i>Journal of Physics A</i> , 1997, 30, 3393-3405.	1.6	0
98	Stochastic comparison for Markov processes on a product of partially ordered sets. <i>Statistics and Probability Letters</i> , 1997, 33, 309-320.	0.7	5
99	Increasing couplings for interacting particle systems. <i>Comptes Rendus Mathematique</i> , 1997, 324, 459-464.	0.5	0
100	New rigorous results for the Hopfield's neural network model. <i>Neural Networks</i> , 1996, 9, 503-507.	5.9	2
101	Convergence of a self-organizing stochastic neural network. <i>Neural Networks</i> , 1992, 5, 277-282.	5.9	11
102	Asymptotic Behavior of Neural Networks and Image Processing. <i>NATO ASI Series Series B: Physics</i> , 1991, , 219-229.	0.2	5