

# Simon Tavarã©

## List of Publications by Year in descending order

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62  
papers

18,981  
citations

71102

41  
h-index

118850

62  
g-index

65  
all docs

65  
docs citations

65  
times ranked

34354  
citing authors

#	ARTICLE	IF	CITATIONS
1	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. <i>Nature</i> , 2021, 595, 585-590.	27.8	71
2	Statistical Inference for the Evolutionary History of Cancer Genomes. <i>Statistical Science</i> , 2020, 35, .	2.8	13
3	Ancestral inference from haplotypes and mutations. <i>Theoretical Population Biology</i> , 2018, 122, 12-21.	1.1	3
4	HDTD: analyzing multi-tissue gene expression data. <i>Bioinformatics</i> , 2016, 32, 2193-2195.	4.1	6
5	Metabolomic changes during cellular transformation monitored by metabolite correlation analysis and correlated with gene expression. <i>Metabolomics</i> , 2015, 11, 1848-1863.	3.0	14
6	Genetic Mapping of Natural Variation in Schooling Tendency in the Threespine Stickleback. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 761-769.	1.8	31
7	Contributions to Drug Resistance in Glioblastoma Derived from Malignant Cells in the Sub-Ependymal Zone. <i>Cancer Research</i> , 2015, 75, 194-202.	0.9	48
8	Testing the Mean Matrix in High-Dimensional Transposable Data. <i>Biometrics</i> , 2015, 71, 157-166.	1.4	8
9	Fkh1 and Fkh2 Bind Multiple Chromosomal Elements in the <i>S. cerevisiae</i> Genome with Distinct Specificities and Cell Cycle Dynamics. <i>PLoS ONE</i> , 2014, 9, e87647.	2.5	45
10	Intratumor heterogeneity in human glioblastoma reflects cancer evolutionary dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4009-4014.	7.1	1,471
11	Single-Molecule Genomic Data Delineate Patient-Specific Tumor Profiles and Cancer Stem Cell Organization. <i>Cancer Research</i> , 2013, 73, 41-49.	0.9	68
12	Assessing Senescence in <i>Drosophila</i> Using Video Tracking. <i>Methods in Molecular Biology</i> , 2013, 965, 501-516.	0.9	2
13	Transcriptional Dynamics Elicited by a Short Pulse of Notch Activation Involves Feed-Forward Regulation by E(spl)/Hes Genes. <i>PLoS Genetics</i> , 2013, 9, e1003162.	3.5	62
14	Independence of Repressive Histone Marks and Chromatin Compaction during Senescent Heterochromatic Layer Formation. <i>Molecular Cell</i> , 2012, 47, 203-214.	9.7	258
15	Calling Sample Mix-Ups in Cancer Population Studies. <i>PLoS ONE</i> , 2012, 7, e41815.	2.5	6
16	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. <i>Nature</i> , 2012, 486, 346-352.	27.8	4,708
17	Dating Primate Divergences through an Integrated Analysis of Palaeontological and Molecular Data. <i>Systematic Biology</i> , 2011, 60, 16-31.	5.6	195
18	Spatial Coupling of mTOR and Autophagy Augments Secretory Phenotypes. <i>Science</i> , 2011, 332, 966-970.	12.6	469

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19	Sparse Partitioning: Nonlinear regression with binary or tertiary predictors, with application to association studies. <i>Annals of Applied Statistics</i> , 2011, 5, .	1.1	3
20	Modeling Evolutionary Dynamics of Epigenetic Mutations in Hierarchically Organized Tumors. <i>PLoS Computational Biology</i> , 2011, 7, e1001132.	3.2	53
21	Data analysis issues for allele-specific expression using Illumina's GoldenGate assay. <i>BMC Bioinformatics</i> , 2010, 11, 280.	2.6	4
22	The cost of reducing starting RNA quantity for Illumina BeadArrays: A bead-level dilution experiment. <i>BMC Genomics</i> , 2010, 11, 540.	2.8	4
23	High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. <i>BMC Genetics</i> , 2010, 11, 25.	2.7	64
24	A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. <i>Nucleic Acids Research</i> , 2010, 38, e17-e17.	14.5	200
25	The microRNA miR-124 controls gene expression in the sensory nervous system of <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2010, 38, 3780-3793.	14.5	91
26	Inferring clonal expansion and cancer stem cell dynamics from DNA methylation patterns in colorectal cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4828-4833.	7.1	134
27	Estimating primate divergence times by using conditioned birth-and-death processes. <i>Theoretical Population Biology</i> , 2009, 75, 278-285.	1.1	30
28	Autophagy mediates the mitotic senescence transition. <i>Genes and Development</i> , 2009, 23, 798-803.	5.9	883
29	Hydrogen Peroxide Stimulates Activity and Alters Behavior in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2009, 4, e7580.	2.5	29
30	Simultaneous tracking of fly movement and gene expression using GFP. <i>BMC Biotechnology</i> , 2008, 8, 93.	3.3	22
31	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008, 26, 779-785.	17.5	619
32	Piwi and piRNAs Act Upstream of an Endogenous siRNA Pathway to Suppress Tc3 Transposon Mobility in the <i>Caenorhabditis elegans</i> Germline. <i>Molecular Cell</i> , 2008, 31, 79-90.	9.7	392
33	Modifier Effects between Regulatory and Protein-Coding Variation. <i>PLoS Genetics</i> , 2008, 4, e1000244.	3.5	33
34	An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). <i>Genome Research</i> , 2008, 18, 1518-1529.	5.5	350
35	beadarray: R classes and methods for Illumina bead-based data. <i>Bioinformatics</i> , 2007, 23, 2183-2184.	4.1	443
36	The Stem Cell Population of the Human Colon Crypt: Analysis via Methylation Patterns. <i>PLoS Computational Biology</i> , 2007, 3, e28.	3.2	85

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37	Transcriptional profiling of MnSOD-mediated lifespan extension in <i>Drosophila</i> reveals a species-general network of aging and metabolic genes. <i>Genome Biology</i> , 2007, 8, R262.	9.6	123
38	High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. <i>Genome Biology</i> , 2007, 8, R215.	9.6	275
39	Relative Impact of Nucleotide and Copy Number Variation on Gene Expression Phenotypes. <i>Science</i> , 2007, 315, 848-853.	12.6	1,546
40	Population genomics of human gene expression. <i>Nature Genetics</i> , 2007, 39, 1217-1224.	21.4	1,072
41	Modern computational approaches for analysing molecular genetic variation data. <i>Nature Reviews Genetics</i> , 2006, 7, 759-770.	16.3	172
42	A Unique Recent Origin of the Allotetraploid Species <i>Arabidopsis suecica</i> : Evidence from Nuclear DNA Markers. <i>Molecular Biology and Evolution</i> , 2006, 23, 1217-1231.	8.9	119
43	Genome-Wide Associations of Gene Expression Variation in Humans. <i>PLoS Genetics</i> , 2005, 1, e78.	3.5	467
44	Statistical Tests of the Coalescent Model Based on the Haplotype Frequency Distribution and the Number of Segregating Sites. <i>Genetics</i> , 2005, 169, 1763-1777.	2.9	46
45	Estimating a Nucleotide Substitution Rate for Maize from Polymorphism at a Major Domestication Locus. <i>Molecular Biology and Evolution</i> , 2005, 22, 2304-2312.	8.9	82
46	Similar gene expression patterns characterize aging and oxidative stress in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7663-7668.	7.1	353
47	Part I: Ancestral Inference in Population Genetics. <i>Lecture Notes in Mathematics</i> , 2004, , 1-188.	0.2	38
48	Approximate Bayesian Computation and MCMC. , 2004, , 99-113.		15
49	Markov chain Monte Carlo without likelihoods. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15324-15328.	7.1	853
50	Linkage disequilibrium: what history has to tell us. <i>Trends in Genetics</i> , 2002, 18, 83-90.	6.7	472
51	On a Test of Depaulis and Veuille. <i>Molecular Biology and Evolution</i> , 2001, 18, 1132-1133.	8.9	19
52	The Age of a Unique Event Polymorphism. <i>Genetics</i> , 2000, 156, 401-409.	2.9	29
53	The Effects of Rate Variation on Ancestral Inference in the Coalescent. <i>Genetics</i> , 2000, 156, 1427-1436.	2.9	27
54	The ages of mutations in gene trees. <i>Annals of Applied Probability</i> , 1999, 9, .	1.3	48

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55	The age of a mutation in a general coalescent tree. <i>Stochastic Models</i> , 1998, 14, 273-295.	0.3	215
56	Inferring Coalescence Times From DNA Sequence Data. <i>Genetics</i> , 1997, 145, 505-518.	2.9	678
57	Coalescents and Genealogical Structure Under Neutrality. <i>Annual Review of Genetics</i> , 1995, 29, 401-421.	7.6	378
58	Unrooted genealogical tree probabilities in the infinitely-many-sites model. <i>Mathematical Biosciences</i> , 1995, 127, 77-98.	1.9	92
59	The ages of alleles and a coalescent. <i>Advances in Applied Probability</i> , 1986, 18, 1-19.	0.7	183
60	The ages of alleles and a coalescent. <i>Advances in Applied Probability</i> , 1986, 18, 1-19.	0.7	91
61	Line-of-descent and genealogical processes, and their applications in population genetics models. <i>Theoretical Population Biology</i> , 1984, 26, 119-164.	1.1	547
62	On the genealogy of nested subsamples from a haploid population. <i>Advances in Applied Probability</i> , 1984, 16, 471-491.	0.7	108