

Yun S Song

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

88

papers

3,874

citations

30

h-index

61

g-index

102

ext. papers

5,452

ext. citations

8.2

avg, IF

5.84

L-index

#	Paper	IF	Citations
88	XYZeq: Spatially resolved single-cell RNA sequencing reveals expression heterogeneity in the tumor microenvironment. <i>Science Advances</i> , 2021 , 7,	14.3	8
87	EGGTART: A tool to visualize the dynamics of biophysical transport under the inhomogeneous l-TASEP. <i>Biophysical Journal</i> , 2021 , 120, 1309-1313	2.9	1
86	Likelihood-based deconvolution of bulk gene expression data using single-cell references. <i>Genome Research</i> , 2021 , 31, 1794-1806	9.7	1
85	Longitudinal single-cell epitope and RNA-sequencing reveals the immunological impact of type 1 interferon autoantibodies in critical COVID-19 2021 ,		9
84	SCITO-seq: single-cell combinatorial indexed cytometry sequencing. <i>Nature Methods</i> , 2021 , 18, 903-911	21.6	7
83	Type I interferon autoantibodies are associated with systemic immune alterations in patients with COVID-19. <i>Science Translational Medicine</i> , 2021 , 13, eabh2624	17.5	34
82	The distribution of waiting distances in ancestral recombination graphs. <i>Theoretical Population Biology</i> , 2021 , 141, 34-43	1.2	0
81	The Key Parameters that Govern Translation Efficiency. <i>Cell Systems</i> , 2020 , 10, 183-192.e6	10.6	20
80	Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity. <i>Genome Research</i> , 2020 ,	9.7	5
79	The yeast exoribonuclease Xrn1 and associated factors modulate RNA polymerase II processivity in 5Tand 3Tgene regions. <i>Journal of Biological Chemistry</i> , 2020 , 295, 11435-11454	5.4	9
78	Accurate assembly of the olive baboon (<i>Papio anubis</i>) genome using long-read and Hi-C data. <i>GigaScience</i> , 2020 , 9,	7.6	8
77	Efficiently inferring the demographic history of many populations with allele count data. <i>Journal of the American Statistical Association</i> , 2020 , 115, 1472-1487	2.8	33
76	Inference and analysis of population-specific fine-scale recombination maps across 26 diverse human populations. <i>Science Advances</i> , 2019 , 5, eaaw9206	14.3	29
75	Differences in the path to exit the ribosome across the three domains of life. <i>Nucleic Acids Research</i> , 2019 , 47, 4198-4210	20.1	38
74	Inference of complex population histories using whole-genome sequences from multiple populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 17115-17120	11.5	21
73	THREE-WAY CLUSTERING OF MULTI-TISSUE MULTI-INDIVIDUAL GENE EXPRESSION DATA USING SEMI-NONNEGATIVE TENSOR DECOMPOSITION. <i>Annals of Applied Statistics</i> , 2019 , 13, 1103-1127	2.1	10
72	Worldwide genetic variation of the IGHV and TRBV immune receptor gene families in humans. <i>Life Science Alliance</i> , 2019 , 2,	5.8	20

71	Necrotizing enterocolitis is preceded by increased gut bacterial replication, , and fimbriae-encoding bacteria. <i>Science Advances</i> , 2019 , 5, eaax5727	14.3	53
70	Model-based detection and analysis of introgressed Neanderthal ancestry in modern humans. <i>Molecular Ecology</i> , 2018 , 27, 3873-3888	5.7	41
69	Theoretical analysis of the distribution of isolated particles in totally asymmetric exclusion processes: Application to mRNA translation rate estimation. <i>Physical Review E</i> , 2018 , 97, 012106	2.4	15
68	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018 , 553, 203-207	50.4	178
67	Inference of population history using coalescent HMMs: review and outlook. <i>Current Opinion in Genetics and Development</i> , 2018 , 53, 70-76	4.9	24
66	High-throughput inference of pairwise coalescence times identifies signals of selection and enriched disease heritability. <i>Nature Genetics</i> , 2018 , 50, 1311-1317	36.3	32
65	Geometry of the Sample Frequency Spectrum and the Perils of Demographic Inference. <i>Genetics</i> , 2018 , 210, 665-682	4	15
64	The impact of ribosomal interference, codon usage, and exit tunnel interactions on translation elongation rate variation. <i>PLoS Genetics</i> , 2018 , 14, e1007166	6	43
63	A Likelihood-Free Inference Framework for Population Genetic Data using Exchangeable Neural Networks. <i>Advances in Neural Information Processing Systems</i> , 2018 , 31, 8594-8605	2.2	7
62	Early human dispersals within the Americas. <i>Science</i> , 2018 , 362,	33.3	118
61	Efficient computation of the joint sample frequency spectra for multiple populations. <i>Journal of Computational and Graphical Statistics</i> , 2017 , 26, 182-194	1.4	40
60	Time-Resolved Proteomics Extends Ribosome Profiling-Based Measurements of Protein Synthesis Dynamics. <i>Cell Systems</i> , 2017 , 4, 636-644.e9	10.6	39
59	OPERATOR NORM INEQUALITIES BETWEEN TENSOR UNFOLDINGS ON THE PARTITION LATTICE. <i>Linear Algebra and Its Applications</i> , 2017 , 520, 44-66	0.9	10
58	Robust and scalable inference of population history from hundreds of unphased whole genomes. <i>Nature Genetics</i> , 2017 , 49, 303-309	36.3	286
57	Loci associated with skin pigmentation identified in African populations. <i>Science</i> , 2017 , 358,	33.3	179
56	Na Li and Matthew Stephens on Modeling Linkage Disequilibrium. <i>Genetics</i> , 2016 , 203, 1005-6	4	2
55	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016 , 538, 201-206	50.4	759
54	Prediction of ribosome footprint profile shapes from transcript sequences. <i>Bioinformatics</i> , 2016 , 32, i183-i191	7.2	14

53	Two-Locus Likelihoods Under Variable Population Size and Fine-Scale Recombination Rate Estimation. <i>Genetics</i> , 2016 , 203, 1381-99	4	28
52	SpectralTDF: transition densities of diffusion processes with time-varying selection parameters, mutation rates and effective population sizes. <i>Bioinformatics</i> , 2016 , 32, 795-7	7.2	5
51	Deep Learning for Population Genetic Inference. <i>PLoS Computational Biology</i> , 2016 , 12, e1004845	5	137
50	Estimating Copy Number and Allelic Variation at the Immunoglobulin Heavy Chain Locus Using Short Reads. <i>PLoS Computational Biology</i> , 2016 , 12, e1005117	5	18
49	The Effects of Population Size Histories on Estimates of Selection Coefficients from Time-Series Genetic Data. <i>Molecular Biology and Evolution</i> , 2016 , 33, 3002-3027	8.3	12
48	The Site Frequency Spectrum for General Coalescents. <i>Genetics</i> , 2016 , 202, 1549-61	4	18
47	Riches of phenotype computationally extracted from microbial colonies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E2822-31	11.5	5
46	Transition Densities and Sample Frequency Spectra of Diffusion Processes with Selection and Variable Population Size. <i>Genetics</i> , 2015 , 200, 601-17	4	25
45	Multi-locus analysis of genomic time series data from experimental evolution. <i>PLoS Genetics</i> , 2015 , 11, e1005069	6	33
44	POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015 , 349, aab3884	33.3	317
43	Genetic and socioeconomic study of mate choice in Latinos reveals novel assortment patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 13621-6	11.5	26
42	TRACTABLE DIFFUSION AND COALESCENT PROCESSES FOR WEAKLY CORRELATED LOCI. <i>Electronic Journal of Probability</i> , 2015 , 20,	1.1	3
41	Fundamental limits on the accuracy of demographic inference based on the sample frequency spectrum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 7677-82	11.5	51
40	Efficient inference of population size histories and locus-specific mutation rates from large-sample genomic variation data. <i>Genome Research</i> , 2015 , 25, 268-79	9.7	50
39	SMAsh: a benchmarking toolkit for human genome variant calling. <i>Bioinformatics</i> , 2014 , 30, 2787-95	7.2	32
38	General triallelic frequency spectrum under demographic models with variable population size. <i>Genetics</i> , 2014 , 196, 295-311	4	21
37	A NOVEL SPECTRAL METHOD FOR INFERRING GENERAL DIPLOID SELECTION FROM TIME SERIES GENETIC DATA. <i>Annals of Applied Statistics</i> , 2014 , 8, 2203-2222	2.1	40
36	DESCARTESTRULE OF SIGNS AND THE IDENTIFIABILITY OF POPULATION DEMOGRAPHIC MODELS FROM GENOMIC VARIATION DATA. <i>Annals of Statistics</i> , 2014 , 42, 2469-2493	3.2	44

35	Distortion of genealogical properties when the sample is very large. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 2385-90	11.5	43
34	diCal-IBD: demography-aware inference of identity-by-descent tracts in unrelated individuals. <i>Bioinformatics</i> , 2014 , 30, 3430-1	7.2	17
33	Decoding coalescent hidden Markov models in linear time. <i>Lecture Notes in Computer Science</i> , 2014 , 8394, 100-114	0.9	6
32	A sequentially Markov conditional sampling distribution for structured populations with migration and recombination. <i>Theoretical Population Biology</i> , 2013 , 87, 51-61	1.2	33
31	Estimating variable effective population sizes from multiple genomes: a sequentially markov conditional sampling distribution approach. <i>Genetics</i> , 2013 , 194, 647-62	4	138
30	Genome-wide fine-scale recombination rate variation in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012 , 8, e1003090	6	155
29	Blockwise HMM computation for large-scale population genomic inference. <i>Bioinformatics</i> , 2012 , 28, 2008-15	7.2	15
28	A simple method for finding explicit analytic transition densities of diffusion processes with general diploid selection. <i>Genetics</i> , 2012 , 190, 1117-29	4	55
27	PAD APPROXIMANTS AND EXACT TWO-LOCUS SAMPLING DISTRIBUTIONS. <i>Annals of Applied Probability</i> , 2012 , 22, 576-607	2	12
26	CLOSED-FORM ASYMPTOTIC SAMPLING DISTRIBUTIONS UNDER THE COALESCENT WITH RECOMBINATION FOR AN ARBITRARY NUMBER OF LOCI. <i>Advances in Applied Probability</i> , 2012 , 44, 391-407	0.7	9
25	Closed-Form Asymptotic Sampling Distributions under the Coalescent with Recombination for an Arbitrary Number of Loci. <i>Advances in Applied Probability</i> , 2012 , 44, 391-407	0.7	5
24	An accurate sequentially Markov conditional sampling distribution for the coalescent with recombination. <i>Genetics</i> , 2011 , 187, 1115-28	4	42
23	General epistatic models of the risk of complex diseases. <i>Genetics</i> , 2010 , 186, 1467-73	4	12
22	A principled approach to deriving approximate conditional sampling distributions in population genetics models with recombination. <i>Genetics</i> , 2010 , 186, 321-38	4	24
21	AN ASYMPTOTIC SAMPLING FORMULA FOR THE COALESCENT WITH RECOMBINATION. <i>Annals of Applied Probability</i> , 2010 , 20, 1005-1028	2	16
20	Closed-form two-locus sampling distributions: accuracy and universality. <i>Genetics</i> , 2009 , 183, 1087-103	4	15
19	Joint estimation of gene conversion rates and mean conversion tract lengths from population SNP data. <i>Bioinformatics</i> , 2009 , 25, i231-9	7.2	15
18	Average probability that a "cold hit" in a DNA database search results in an erroneous attribution. <i>Journal of Forensic Sciences</i> , 2009 , 54, 22-7	1.8	13

17	Importance sampling and the two-locus model with subdivided population structure. <i>Advances in Applied Probability</i> , 2008 , 40, 473-500	0.7	12
16	IMPORTANCE SAMPLING AND THE TWO-LOCUS MODEL WITH SUBDIVIDED POPULATION STRUCTURE. <i>Advances in Applied Probability</i> , 2008 , 40, 473-500	0.7	25
15	Analytic computation of the expectation of the linkage disequilibrium coefficient r^2 . <i>Theoretical Population Biology</i> , 2007 , 71, 49-60	1.2	27
14	A graphical approach to multi-locus match probability computation: revisiting the product rule. <i>Theoretical Population Biology</i> , 2007 , 72, 96-110	1.2	6
13	Algorithms to distinguish the role of gene-conversion from single-crossover recombination in the derivation of SNP sequences in populations. <i>Journal of Computational Biology</i> , 2007 , 14, 1273-86	1.7	12
12	Properties of Subtree-Prune-and-Regraft Operations on Totally-Ordered Phylogenetic Trees. <i>Annals of Combinatorics</i> , 2006 , 10, 147-163	0.7	9
11	A concise necessary and sufficient condition for the existence of a galled-tree. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006 , 3, 186-91	3	7
10	Counting all possible ancestral configurations of sample sequences in population genetics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006 , 3, 239-51	3	12
9	Efficient computation of close lower and upper bounds on the minimum number of recombinations in biological sequence evolution. <i>Bioinformatics</i> , 2005 , 21 Suppl 1, i413-22	7.2	39
8	Minimum Recombination Histories by Branch and Bound. <i>Lecture Notes in Computer Science</i> , 2005 , 239-250	0	33
7	Parsimonious Reconstruction of Sequence Evolution and Haplotype Blocks. <i>Lecture Notes in Computer Science</i> , 2003 , 287-302	0.9	27
6	The key parameters that govern translation efficiency		1
5	Inference of complex population histories using whole-genome sequences from multiple populations		19
4	A Likelihood-Free Inference Framework for Population Genetic Data using Exchangeable Neural Networks		23
3	Efficiently inferring the demographic history of many populations with allele count data		14
2	Inference and analysis of population-specific fine-scale recombination maps across 26 diverse human populations		5
1	Robust and annotation-free analysis of alternative splicing across diverse cell types in mice		1