

# Yun S Song

## List of Publications by Year in descending order

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Version: 2024-02-01

82  
papers

6,541  
citations

136740

32  
h-index

95083

68  
g-index

102  
all docs

102  
docs citations

102  
times ranked

9308  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	13.7	1,216
2	Robust and scalable inference of population history from hundreds of unphased whole genomes. <i>Nature Genetics</i> , 2017, 49, 303-309.	9.4	550
3	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
4	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018, 553, 203-207.	13.7	304
5	Loci associated with skin pigmentation identified in African populations. <i>Science</i> , 2017, 358, .	6.0	260
6	Genome-Wide Fine-Scale Recombination Rate Variation in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012, 8, e1003090.	1.5	259
7	Early human dispersals within the Americas. <i>Science</i> , 2018, 362, .	6.0	230
8	Deep Learning for Population Genetic Inference. <i>PLoS Computational Biology</i> , 2016, 12, e1004845.	1.5	217
9	Estimating Variable Effective Population Sizes from Multiple Genomes: A Sequentially Markov Conditional Sampling Distribution Approach. <i>Genetics</i> , 2013, 194, 647-662.	1.2	187
10	Type I interferon autoantibodies are associated with systemic immune alterations in patients with COVID-19. <i>Science Translational Medicine</i> , 2021, 13, eabh2624.	5.8	155
11	Necrotizing enterocolitis is preceded by increased gut bacterial replication, <i>Klebsiella</i> , and fimbriae-encoding bacteria. <i>Science Advances</i> , 2019, 5, eaax5727.	4.7	120
12	Inference and analysis of population-specific fine-scale recombination maps across 26 diverse human populations. <i>Science Advances</i> , 2019, 5, eaaw9206.	4.7	111
13	Efficiently Inferring the Demographic History of Many Populations With Allele Count Data. <i>Journal of the American Statistical Association</i> , 2020, 115, 1472-1487.	1.8	90
14	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, 7677-7682.	3.3	82
15	Efficient inference of population size histories and locus-specific mutation rates from large-sample genomic variation data. <i>Genome Research</i> , 2015, 25, 268-279.	2.4	78
16	The impact of ribosomal interference, codon usage, and exit tunnel interactions on translation elongation rate variation. <i>PLoS Genetics</i> , 2018, 14, e1007166.	1.5	77
17	A Simple Method for Finding Explicit Analytic Transition Densities of Diffusion Processes with General Diploid Selection. <i>Genetics</i> , 2012, 190, 1117-1129.	1.2	69
18	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, 2385-2390.	3.3	68

#	ARTICLE	IF	CITATIONS
19	Descartes's rule of signs and the identifiability of population demographic models from genomic variation data. <i>Annals of Statistics</i> , 2014, 42, 2469-2493.	1.4	68
20	Differences in the path to exit the ribosome across the three domains of life. <i>Nucleic Acids Research</i> , 2019, 47, 4198-4210.	6.5	68
21	A novel spectral method for inferring general diploid selection from time series genetic data. <i>Annals of Applied Statistics</i> , 2014, 8, 2203-2222.	0.5	67
22	Model-based detection and analysis of introgressed Neanderthal ancestry in modern humans. <i>Molecular Ecology</i> , 2018, 27, 3873-3888.	2.0	67
23	Efficient Computation of the Joint Sample Frequency Spectra for Multiple Populations. <i>Journal of Computational and Graphical Statistics</i> , 2017, 26, 182-194.	0.9	64
24	XYSeq: Spatially resolved single-cell RNA sequencing reveals expression heterogeneity in the tumor microenvironment. <i>Science Advances</i> , 2021, 7, .	4.7	64
25	Multi-locus Analysis of Genomic Time Series Data from Experimental Evolution. <i>PLoS Genetics</i> , 2015, 11, e1005069.	1.5	63
26	Time-Resolved Proteomics Extends Ribosome Profiling-Based Measurements of Protein Synthesis Dynamics. <i>Cell Systems</i> , 2017, 4, 636-644.e9.	2.9	62
27	High-throughput inference of pairwise coalescence times identifies signals of selection and enriched disease heritability. <i>Nature Genetics</i> , 2018, 50, 1311-1317.	9.4	61
28	An Accurate Sequentially Markov Conditional Sampling Distribution for the Coalescent With Recombination. <i>Genetics</i> , 2011, 187, 1115-1128.	1.2	56
29	Two-Locus Likelihoods Under Variable Population Size and Fine-Scale Recombination Rate Estimation. <i>Genetics</i> , 2016, 203, 1381-1399.	1.2	54
30	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.	3.3	52
31	Inference of population history using coalescent HMMs: review and outlook. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 70-76.	1.5	51
32	Minimum Recombination Histories by Branch and Bound. <i>Lecture Notes in Computer Science</i> , 2005, , 239-250.	1.0	49
33	Efficient computation of close lower and upper bounds on the minimum number of recombinations in biological sequence evolution. <i>Bioinformatics</i> , 2005, 21, i413-i422.	1.8	45
34	A sequentially Markov conditional sampling distribution for structured populations with migration and recombination. <i>Theoretical Population Biology</i> , 2013, 87, 51-61.	0.5	43
35	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, 13621-13626.	3.3	41
36	Parsimonious Reconstruction of Sequence Evolution and Haplotype Blocks. <i>Lecture Notes in Computer Science</i> , 2003, , 287-302.	1.0	40

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37	SM a SH: a benchmarking toolkit for human genome variant calling. <i>Bioinformatics</i> , 2014, 30, 2787-2795.	1.8	40
38	The Key Parameters that Govern Translation Efficiency. <i>Cell Systems</i> , 2020, 10, 183-192.e6.	2.9	39
39	Transition Densities and Sample Frequency Spectra of Diffusion Processes with Selection and Variable Population Size. <i>Genetics</i> , 2015, 200, 601-617.	1.2	37
40	The Site Frequency Spectrum for General Coalescents. <i>Genetics</i> , 2016, 202, 1549-1561.	1.2	33
41	Worldwide genetic variation of the IGHV and TRBV immune receptor gene families in humans. <i>Life Science Alliance</i> , 2019, 2, e201800221.	1.3	33
42	Analytic computation of the expectation of the linkage disequilibrium coefficient. <i>Theoretical Population Biology</i> , 2007, 71, 49-60.	0.5	31
43	General Triallelic Frequency Spectrum Under Demographic Models with Variable Population Size. <i>Genetics</i> , 2014, 196, 295-311.	1.2	31
44	A Principled Approach to Deriving Approximate Conditional Sampling Distributions in Population Genetics Models with Recombination. <i>Genetics</i> , 2010, 186, 321-338.	1.2	30
45	Geometry of the Sample Frequency Spectrum and the Perils of Demographic Inference. <i>Genetics</i> , 2018, 210, 665-682.	1.2	29
46	Estimating Copy Number and Allelic Variation at the Immunoglobulin Heavy Chain Locus Using Short Reads. <i>PLoS Computational Biology</i> , 2016, 12, e1005117.	1.5	28
47	SCITO-seq: single-cell combinatorial indexed cytometry sequencing. <i>Nature Methods</i> , 2021, 18, 903-911.	9.0	28
48	Importance sampling and the two-locus model with subdivided population structure. <i>Advances in Applied Probability</i> , 2008, 40, 473-500.	0.4	28
49	The yeast exoribonuclease Xrn1 and associated factors modulate RNA polymerase II processivity in 5' and 3' gene regions. <i>Journal of Biological Chemistry</i> , 2020, 295, 11435-11454.	1.6	25
50	Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity. <i>Genome Research</i> , 2021, 31, 239-250.	2.4	24
51	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.	3.5	22
52	Closed-Form Two-Locus Sampling Distributions: Accuracy and Universality. <i>Genetics</i> , 2009, 183, 1087-1103.	1.2	20
53	Joint estimation of gene conversion rates and mean conversion tract lengths from population SNP data. <i>Bioinformatics</i> , 2009, 25, i231-i239.	1.8	20
54	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.	0.5	20

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55	Properties of Subtree-Prune-and-Regraft Operations on Totally-Ordered Phylogenetic Trees. <i>Annals of Combinatorics</i> , 2006, 10, 147-163.	0.3	19
56	An asymptotic sampling formula for the coalescent with Recombination. <i>Annals of Applied Probability</i> , 2010, 20, 1005-1028.	0.6	19
57	Blockwise HMM computation for large-scale population genomic inference. <i>Bioinformatics</i> , 2012, 28, 2008-2015.	1.8	19
58	diCal-IBD: demography-aware inference of identity-by-descent tracts in unrelated individuals. <i>Bioinformatics</i> , 2014, 30, 3430-3431.	1.8	19
59	Prediction of ribosome footprint profile shapes from transcript sequences. <i>Bioinformatics</i> , 2016, 32, i183-i191.	1.8	19
60	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.	0.8	18
61	Accurate assembly of the olive baboon ( <i>Papio anubis</i> ) genome using long-read and Hi-C data. <i>GigaScience</i> , 2020, 9, .	3.3	18
62	Likelihood-based deconvolution of bulk gene expression data using single-cell references. <i>Genome Research</i> , 2021, 31, 1794-1806.	2.4	16
63	Padé approximants and exact two-locus sampling distributions. <i>Annals of Applied Probability</i> , 2012, 22, 576-607.	0.6	15
64	Operator norm inequalities between tensor unfoldings on the partition lattice. <i>Linear Algebra and Its Applications</i> , 2017, 520, 44-66.	0.4	15
65	The distribution of waiting distances in ancestral recombination graphs. <i>Theoretical Population Biology</i> , 2021, 141, 34-43.	0.5	15
66	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, 1273-1286.	0.8	14
67	Average Probability that a "Cold Hit" in a DNA Database Search Results in an Erroneous Attribution. <i>Journal of Forensic Sciences</i> , 2009, 54, 22-27.	0.9	14
68	Counting All Possible Ancestral Configurations of Sample Sequences in Population Genetics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 239-251.	1.9	13
69	Importance sampling and the two-locus model with subdivided population structure. <i>Advances in Applied Probability</i> , 2008, 40, 473-500.	0.4	13
70	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, 186-191.	1.9	12
71	General Epistatic Models of the Risk of Complex Diseases. <i>Genetics</i> , 2010, 186, 1467-1473.	1.2	12
72	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.	0.4	12

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73	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.	2.8	12
74	Decoding Coalescent Hidden Markov Models in Linear Time. <i>Lecture Notes in Computer Science</i> , 2014, 8394, 100-114.	1.0	9
75	Na Li and Matthew Stephens on Modeling Linkage Disequilibrium. <i>Genetics</i> , 2016, 203, 1005-1006.	1.2	8
76	SpectralTDF: transition densities of diffusion processes with time-varying selection parameters, mutation rates and effective population sizes. <i>Bioinformatics</i> , 2016, 32, 795-797.	1.8	8
77	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.	0.4	7
78	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-E2831.	3.3	7
79	A graphical approach to multi-locus match probability computation: Revisiting the product rule. <i>Theoretical Population Biology</i> , 2007, 72, 96-110.	0.5	6
80	EGGTART: A tool to visualize the dynamics of Åbiophysical transport under the inhomogeneous I-TASEP. <i>Biophysical Journal</i> , 2021, 120, 1309-1313.	0.2	4
81	Tractable diffusion and coalescent processes for weakly correlated loci. <i>Electronic Journal of Probability</i> , 2015, 20, .	0.5	3
82	Transferability of Geometric Patterns from Protein Self-Interactions to Protein-Ligand Interactions. , 2021, , .		1