## John L Spouge

List of Publications by Year in descending order

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IOHN L SPOUCE

#	Article	IF	CITATIONS
1	Hemolysis Pathways during Storage of Erythrocytes and Inter-Donor Variability in Erythrocyte Morphology. Transfusion Medicine and Hemotherapy, 2021, 48, 39-47.	1.6	7
2	A comprehensive estimation of country-level basic reproduction numbers R0 for COVID-19: Regime regression can automatically estimate the end of the exponential phase in epidemic data. PLoS ONE, 2021, 16, e0254145.	2.5	12
3	Estimating the basic reproduction number of a pathogen in a single host when only a single founder successfully infects. PLoS ONE, 2020, 15, e0227127.	2.5	0
4	A linear-time algorithm that avoids inverses and computes Jackknife (leave-one-out) products like convolutions or other operators in commutative semigroups. Algorithms for Molecular Biology, 2020, 15, 17.	1.2	0
5	Figures of merit and statistics for detecting faulty species identification with DNA barcodes: A case study in Ramaria and related fungal genera. PLoS ONE, 2020, 15, e0237507.	2.5	7
6	Structural prediction of RNA switches using conditional base-pair probabilities. PLoS ONE, 2019, 14, e0217625.	2.5	1
7	An accurate approximation for the expected site frequency spectrum in a Galton–Watson process under an infinite sites mutation model. Theoretical Population Biology, 2019, 127, 7-15.	1.1	2
8	MultiDomainBenchmark: a multi-domain query and subject database suite. BMC Bioinformatics, 2019, 20, 77.	2.6	1
9	Empirical Null Estimation Using Zero-inflated Discrete Mixture Distributions and Its Application to Protein Domain Data. Biometrics, 2018, 74, 458-471.	1.4	9
10	Alignment-free genome comparison enables accurate geographic sourcing of white oak DNA. BMC Genomics, 2018, 19, 896.	2.8	6
11	Discovery of Kaposi's sarcoma herpesvirus-encoded circular RNAs and a human antiviral circular RNA. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12805-12810.	7.1	144
12	Conserved signatures indicate HIV-1 transmission is under strong selection and thus is not a "stochastic―process. Retrovirology, 2017, 14, 13.	2.0	6
13	Patterns of conserved gp120 epitope presentation on attached HIV-1 virions. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9893-E9902.	7.1	12
14	ALP & FALP: C++ libraries for pairwise local alignment <i>E</i> -values. Bioinformatics, 2016, 32, 304-305.	4.1	7
15	Measurement of a Barcode's Accuracy in Identifying Species. , 2016, , 29-41.		3
16	Most of the tight positional conservation of transcription factor binding sites near the transcription start site reflects their co-localization within regulatory modules. BMC Bioinformatics, 2016, 17, 479.	2.6	1
17	Changes in the Plasticity of HIV-1 Nef RNA during the Evolution of the North American Epidemic. PLoS ONE, 2016, 11, e0163688.	2.5	2
18	A New Method for Estimating Species Age Supports the Coexistence of Malaria Parasites and Their Mammalian Hosts. Molecular Biology and Evolution, 2015, 32, 1354-1364.	8.9	39

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19	Conserved Molecular Signatures in gp120 Are Associated with the Genetic Bottleneck during Simian Immunodeficiency Virus (SIV), SIV-Human Immunodeficiency Virus (SHIV), and HIV Type 1 (HIV-1) Transmission. Journal of Virology, 2015, 89, 3619-3629.	3.4	22
20	Frameshift alignment: statistics and post-genomic applications. Bioinformatics, 2014, 30, 3575-3582.	4.1	35
21	Within a sample from a population, the distribution of the number of descendants of a subsample's most recent common ancestor. Theoretical Population Biology, 2014, 92, 51-54.	1.1	5
22	Searching for repeats, as an example of using the generalised Ruzzo-Tompa algorithm to find optimal subsequences with gaps. International Journal of Bioinformatics Research and Applications, 2014, 10, 384.	0.2	2
23	Fungi in Thailand: A Case Study of the Efficacy of an ITS Barcode for Automatically Identifying Species within the Annulohypoxylon and Hypoxylon Genera. PLoS ONE, 2013, 8, e54529.	2.5	25
24	CBOL Protist Working Group: Barcoding Eukaryotic Richness beyond the Animal, Plant, and Fungal Kingdoms. PLoS Biology, 2012, 10, e1001419.	5.6	488
25	The Practical Evaluation of DNA Barcode Efficacy. Methods in Molecular Biology, 2012, 858, 365-377.	0.9	12
26	The ruzzo-tompa algorithm can find the maximal paths in weighted, directed graphs on a one-dimensional lattice. , 2012, , .		2
27	Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for <i>Fungi</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6241-6246.	7.1	4,012
28	New finite-size correction for local alignment score distributions. BMC Research Notes, 2012, 5, 286.	1.4	14
29	Objective method for estimating asymptotic parameters, with an application to sequence alignment. Physical Review E, 2011, 84, 031914.	2.1	4
30	Threshold Average Precision (TAP-k): a measure of retrieval designed for bioinformatics. Bioinformatics, 2010, 26, 1708-1713.	4.1	25
31	Estimating the Gumbel scale parameter for local alignment of random sequences by importance sampling with stopping times. Annals of Statistics, 2009, 37, 3697.	2.6	11
32	The whole alignment and nothing but the alignment: the problem of spurious alignment flanks. Nucleic Acids Research, 2008, 36, 5863-5871.	14.5	22
33	The biological function of some human transcription factor binding motifs varies with position relative to the transcription start site. Nucleic Acids Research, 2008, 36, 2777-2786.	14.5	19
34	The identification of complete domains within protein sequences using accurate E-values for semi-global alignment. Nucleic Acids Research, 2007, 35, 4678-4685.	14.5	15
35	Markov Additive Processes and Repeats in Sequences. Journal of Applied Probability, 2007, 44, 514-527.	0.7	3
36	Markov Additive Processes and Repeats in Sequences. Journal of Applied Probability, 2007, 44, 514-527.	0.7	3

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37	Inequalities on the overshoot beyond a boundary for independent summands with differing distributions. Statistics and Probability Letters, 2007, 77, 1486-1489.	0.7	2
38	Finite-size corrections to Poisson approximations in general renewal-success processes. Journal of Mathematical Analysis and Applications, 2005, 301, 401-418.	1.0	2
39	Accelerated convergence and robust asymptotic regression of the Gumbel scale parameter for gapped sequence alignment. Journal of Physics A, 2005, 38, 97-108.	1.6	5
40	The Gumbel pre-factor k for gapped local alignment can be estimated from simulations of global alignment. Nucleic Acids Research, 2005, 33, 4987-4994.	14.5	20
41	Path reversal, islands, and the gapped alignment of random sequences. Journal of Applied Probability, 2004, 41, 975-983.	0.7	1
42	Finding functional sequence elements by multiple local alignment. Nucleic Acids Research, 2004, 32, 189-200.	14.5	195
43	Statistical analysis of over-represented words in human promoter sequences. Nucleic Acids Research, 2004, 32, 949-958.	14.5	108
44	Searching for Multiple Words in a Markov Sequence. INFORMS Journal on Computing, 2004, 16, 341-347.	1.7	4
45	Path reversal, islands, and the gapped alignment of random sequences. Journal of Applied Probability, 2004, 41, 975-983.	0.7	4
46	The correlation error and finite-size correction in an ungapped sequence alignment. Bioinformatics, 2002, 18, 1236-1242.	4.1	10
47	Statistical significance of clusters of motifs represented by position specific scoring matrices in nucleotide sequences. Nucleic Acids Research, 2002, 30, 3214-3224.	14.5	106
48	Finite-size corrections to Poisson approximations of rare events in renewal processes. Journal of Applied Probability, 2001, 38, 554-569.	0.7	5
49	Lineage-Specific Gene Expansions in Bacterial and Archaeal Genomes. Genome Research, 2001, 11, 555-565.	5.5	110
50	Finite-size corrections to Poisson approximations of rare events in renewal processes. Journal of Applied Probability, 2001, 38, 554-569.	0.7	7
51	A practical method for simultaneously determining the effective burst sizes and cycle times of viruses. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 7017-7022.	7.1	3
52	The combinatorics and extreme value statistics of protein threading. Annals of Combinatorics, 1999, 3, 81-93.	0.6	1
53	Candidate Regulatory Sequence Elements for Cell Cycle-Dependent Transcription in <i>Saccharomyces cerevisiae</i> . Genome Research, 1999, 9, 775-792.	5.5	69
54	Increase of Primary HIV-1 Production in Human Peripheral Blood Mononuclear Cells by Intermittent Medium Replenishment. Biotechnology Progress, 1998, 14, 540-542.	2.6	2

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55	Single-particle survival in parallel gated trapping. Physical Review E, 1997, 55, 421-425.	2.1	8
56	Stochastically Gated Chemical Reactions. Journal of Physical Chemistry B, 1997, 101, 5026-5030.	2.6	5
57	HIV-1 infection kinetics in tissue cultures. Mathematical Biosciences, 1996, 138, 1-22.	1.9	46
58	A cytopathic infectivity assay of human immunodeficiency virus type 1 in human primary macrophages. Journal of Virological Methods, 1996, 59, 45-55.	2.1	8
59	Single-particle survival in gated trapping. Physical Review E, 1996, 54, 2248-2255.	2.1	37
60	Computation of the Gamma, Digamma, and Trigamma Functions. SIAM Journal on Numerical Analysis, 1994, 31, 931-944.	2.3	47
61	HIV requires multiple gp120 molecules for CD4-mediated infection. Nature, 1990, 346, 277-279.	27.8	209
62	Speeding up Dynamic Programming Algorithms for Finding Optimal Lattice Paths. SIAM Journal on Applied Mathematics, 1989, 49, 1552-1566.	1.8	27
63	Exact solutions for a diffusion-reaction process in one dimension. Physical Review Letters, 1988, 60, 871-874.	7.8	220
64	Hydrophobicity scales and computational techniques for detecting amphipathic structures in proteins. Journal of Molecular Biology, 1987, 195, 659-685.	4.2	627
65	Protein Antigenic Structures Recognized by T Cells; Potential Applications to Vaccine Design. Immunological Reviews, 1987, 98, 9-52.	6.0	144
66	Increasing stability with complexity in a system composed of unstable subsystems. Journal of Mathematical Analysis and Applications, 1986, 118, 502-518.	1.0	8
67	Equilibrium ring formation in polymer solutions. Journal of Statistical Physics, 1986, 43, 143-196.	1.2	25
68	Polymers and random graphs: Asymptotic equivalence to branching processes. Journal of Statistical Physics, 1985, 38, 573-587.	1.2	19
69	Monte Carlo results for random coagulation. Journal of Colloid and Interface Science, 1985, 107, 38-43.	9.4	42
70	An existence theorem for the discrete coagulation-fragmentation equations. Mathematical Proceedings of the Cambridge Philosophical Society, 1984, 96, 351-357.	0.4	56
71	Analytic results for finite systems of ringed flory polymers. Canadian Journal of Chemistry, 1984, 62, 1262-1264.	1.1	10
72	A branching-process solution of the polydisperse coagulation equation. Advances in Applied Probability, 1984, 16, 56-69.	0.7	7

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73	The size distribution for theA g RB f?g Model of polymerization. Journal of Statistical Physics, 1983, 31, 363-378.	1.2	27
74	Asymmetric bonding of identical units: a general AgRBf-g polymer model. Macromolecules, 1983, 16, 831-835.	4.8	26