

Joshua S Weitz

List of Publications by Year in descending order

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Version: 2024-02-01

139
papers

10,113
citations

36303

51
h-index

45317

90
g-index

194
all docs

194
docs citations

194
times ranked

12074
citing authors

#	ARTICLE	IF	CITATIONS
1	Re-examination of the $\frac{3}{4}$ -law of Metabolism. <i>Journal of Theoretical Biology</i> , 2001, 209, 9-27.	1.7	521
2	Repeatability and Contingency in the Evolution of a Key Innovation in Phage Lambda. <i>Science</i> , 2012, 335, 428-432.	12.6	401
3	Robust estimation of microbial diversity in theory and in practice. <i>ISME Journal</i> , 2013, 7, 1092-1101.	9.8	321
4	Synergy between the Host Immune System and Bacteriophage Is Essential for Successful Phage Therapy against an Acute Respiratory Pathogen. <i>Cell Host and Microbe</i> , 2017, 22, 38-47.e4.	11.0	315
5	Imaging and Analysis Platform for Automatic Phenotyping and Trait Ranking of Plant Root Systems. <i>Plant Physiology</i> , 2010, 152, 1148-1157.	4.8	306
6	GiA Roots: software for the high throughput analysis of plant root system architecture. <i>BMC Plant Biology</i> , 2012, 12, 116.	3.6	279
7	Statistical structure of host-phage interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E288-97.	7.1	275
8	Phage-bacteria infection networks. <i>Trends in Microbiology</i> , 2013, 21, 82-91.	7.7	273
9	The elemental composition of virus particles: implications for marine biogeochemical cycles. <i>Nature Reviews Microbiology</i> , 2014, 12, 519-528.	28.6	273
10	Re-examination of the relationship between marine virus and microbial cell abundances. <i>Nature Microbiology</i> , 2016, 1, 15024.	13.3	264
11	3D phenotyping and quantitative trait locus mapping identify core regions of the rice genome controlling root architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1695-704.	7.1	261
12	Coevolutionary arms races between bacteria and bacteriophage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 9535-9540.	7.1	245
13	Image-Based High-Throughput Field Phenotyping of Crop Roots. <i>Plant Physiology</i> , 2014, 166, 470-486.	4.8	239
14	A multitrophic model to quantify the effects of marine viruses on microbial food webs and ecosystem processes. <i>ISME Journal</i> , 2015, 9, 1352-1364.	9.8	223
15	Ocean viruses and their effects on microbial communities and biogeochemical cycles. <i>F1000 Biology Reports</i> , 2012, 4, 17.	4.0	213
16	Modeling shield immunity to reduce COVID-19 epidemic spread. <i>Nature Medicine</i> , 2020, 26, 849-854.	30.7	196
17	Viral tagging reveals discrete populations in <i>Synechococcus</i> viral genome sequence space. <i>Nature</i> , 2014, 513, 242-245.	27.8	183
18	Testing the metabolic theory of ecology. <i>Ecology Letters</i> , 2012, 15, 1465-1474.	6.4	155

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19	Multi-scale structure and geographic drivers of cross-infection within marine bacteria and phages. ISME Journal, 2013, 7, 520-532.	9.8	155
20	Digital imaging of root traits (DIRT): a high-throughput computing and collaboration platform for field-based root phenomics. Plant Methods, 2015, 11, 51.	4.3	146
21	The time scale of asymptomatic transmission affects estimates of epidemic potential in the COVID-19 outbreak. Epidemics, 2020, 31, 100392.	3.0	129
22	Genotypic recognition and spatial responses by rice roots. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2670-2675.	7.1	124
23	Awareness-driven behavior changes can shift the shape of epidemics away from peaks and toward plateaus, shoulders, and oscillations. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32764-32771.	7.1	120
24	Coevolution can reverse predator-prey cycles. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7486-7491.	7.1	111
25	Reconciling early-outbreak estimates of the basic reproductive number and its uncertainty: framework and applications to the novel coronavirus (SARS-CoV-2) outbreak. Journal of the Royal Society Interface, 2020, 17, 20200144.	3.4	103
26	The metabolic theory of ecology: prospects and challenges for plant biology. New Phytologist, 2010, 188, 696-710.	7.3	102
27	Leaf Extraction and Analysis Framework Graphical User Interface: Segmenting and Analyzing the Structure of Leaf Veins and Areoles. Plant Physiology, 2011, 155, 236-245.	4.8	100
28	Genomic differentiation among wild cyanophages despite widespread horizontal gene transfer. BMC Genomics, 2016, 17, 930.	2.8	96
29	A neutral metapopulation model of biodiversity in river networks. Journal of Theoretical Biology, 2007, 245, 351-363.	1.7	94
30	A virus or more in (nearly) every cell: ubiquitous networks of virus-host interactions in extreme environments. ISME Journal, 2018, 12, 1706-1714.	9.8	94
31	Modeling Post-death Transmission of Ebola: Challenges for Inference and Opportunities for Control. Scientific Reports, 2015, 5, 8751.	3.3	93
32	Alternative stable states in host-phage dynamics. Theoretical Ecology, 2008, 1, 13-19.	1.0	92
33	Dynamics of Indirectly Transmitted Infectious Diseases with Immunological Threshold. Bulletin of Mathematical Biology, 2009, 71, 845-862.	1.9	92
34	Genomic fluidity: an integrative view of gene diversity within microbial populations. BMC Genomics, 2011, 12, 32.	2.8	92
35	Mechanisms of multi-strain coexistence in host-phage systems with nested infection networks. Journal of Theoretical Biology, 2013, 332, 65-77.	1.7	91
36	Size and scaling of predator-prey dynamics. Ecology Letters, 2006, 9, 548-557.	6.4	90

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37	MULTISCALE MODEL OF CRISPR-INDUCED COEVOLUTIONARY DYNAMICS: DIVERSIFICATION AT THE INTERFACE OF LAMARCK AND DARWIN. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2015-2029.	2.3	89
38	Modeling the synergistic elimination of bacteria by phage and the innate immune system. <i>Journal of Theoretical Biology</i> , 2017, 429, 241-252.	1.7	88
39	The Evolution of Dispersal in Reserve Networks. <i>American Naturalist</i> , 2007, 170, 59-78.	2.1	86
40	Small-scale copy number variation and large-scale changes in gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16659-16664.	7.1	85
41	Unsupervised statistical clustering of environmental shotgun sequences. <i>BMC Bioinformatics</i> , 2009, 10, 316.	2.6	84
42	Viral ecology comes of age. <i>Environmental Microbiology Reports</i> , 2017, 9, 33-35.	2.4	81
43	An integrative approach to understanding microbial diversity: from intracellular mechanisms to community structure. <i>Ecology Letters</i> , 2010, 13, 1073-1084.	6.4	80
44	Revisiting the rules of life for viruses of microorganisms. <i>Nature Reviews Microbiology</i> , 2021, 19, 501-513.	28.6	77
45	Quantitative Models of Phage-Antibiotic Combination Therapy. <i>MSystems</i> , 2020, 5, .	3.8	73
46	Collective Decision Making in Bacterial Viruses. <i>Biophysical Journal</i> , 2008, 95, 2673-2680.	0.5	71
47	Lysis, lysogeny and virus-microbe ratios. <i>Nature</i> , 2017, 549, E1-E3.	27.8	69
48	Estimating the Cumulative Incidence of SARS-CoV-2 Infection and the Infection Fatality Ratio in Light of Waning Antibodies. <i>Epidemiology</i> , 2021, 32, 518-524.	2.7	69
49	A Null Model of Morphospace Occupation. <i>American Naturalist</i> , 2005, 166, E1-E13.	2.1	68
50	CRISPR-Induced Distributed Immunity in Microbial Populations. <i>PLoS ONE</i> , 2014, 9, e101710.	2.5	67
51	Systematic biases in disease forecasting - The role of behavior change. <i>Epidemics</i> , 2019, 27, 96-105.	3.0	65
52	Evaluating scaling models in biology using hierarchical Bayesian approaches. <i>Ecology Letters</i> , 2009, 12, 641-651.	6.4	60
53	Functional Biogeography of Ocean Microbes Revealed through Non-Negative Matrix Factorization. <i>PLoS ONE</i> , 2012, 7, e43866.	2.5	60
54	Real-time, interactive website for US-county-level COVID-19 event risk assessment. <i>Nature Human Behaviour</i> , 2020, 4, 1313-1319.	12.0	60

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55	BiMat: a MATLAB package to facilitate the analysis of bipartite networks. <i>Methods in Ecology and Evolution</i> , 2016, 7, 127-132.	5.2	58
56	Viral invasion fitness across a continuum from lysis to latency. <i>Virus Evolution</i> , 2019, 5, vez006.	4.9	57
57	A neutral theory of genome evolution and the frequency distribution of genes. <i>BMC Genomics</i> , 2012, 13, 196.	2.8	55
58	Forward-looking serial intervals correctly link epidemic growth to reproduction numbers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	54
59	Scaling and structure of dicotyledonous leaf venation networks. <i>Ecology Letters</i> , 2012, 15, 87-95.	6.4	51
60	A practical generation-interval-based approach to inferring the strength of epidemics from their speed. <i>Epidemics</i> , 2019, 27, 12-18.	3.0	51
61	Packing-limited growth. <i>Physical Review E</i> , 2002, 65, 056108.	2.1	47
62	A Primer for Microbiome Time-Series Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 310.	2.3	47
63	Allelic polymorphism shapes community function in evolving <i>Pseudomonas aeruginosa</i> populations. <i>ISME Journal</i> , 2020, 14, 1929-1942.	9.8	47
64	Hierarchical Ordering of Reticular Networks. <i>PLoS ONE</i> , 2012, 7, e36715.	2.5	44
65	Dangerous nutrients: Evolution of phytoplankton resource uptake subject to virus attack. <i>Journal of Theoretical Biology</i> , 2009, 257, 104-115.	1.7	42
66	A single-cell polony method reveals low levels of infected <i>Prochlorococcus</i> in oligotrophic waters despite high cyanophage abundances. <i>ISME Journal</i> , 2021, 15, 41-54.	9.8	40
67	Disease dynamics in a stochastic network game: a little empathy goes a long way in averting outbreaks. <i>Scientific Reports</i> , 2017, 7, 44122.	3.3	39
68	Networked SIS Epidemics With Awareness. <i>IEEE Transactions on Computational Social Systems</i> , 2017, 4, 93-103.	4.4	38
69	Limitations of Correlation-Based Inference in Complex Virus-Microbe Communities. <i>MSystems</i> , 2018, 3, .	3.8	37
70	To Lyse or Not to Lyse: Transient-Mediated Stochastic Fate Determination in Cells Infected by Bacteriophages. <i>PLoS Computational Biology</i> , 2011, 7, e1002006.	3.2	36
71	An empirical model of carbon flow through marine viruses and microzooplankton grazers. <i>Environmental Microbiology</i> , 2019, 21, 2171-2181.	3.8	35
72	Topological constraints in early multicellularity favor reproductive division of labor. <i>ELife</i> , 2020, 9, .	6.0	34

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73	Evolution, Interactions, and Biological Networks. <i>PLoS Biology</i> , 2007, 5, e11.	5.6	33
74	How microbes survive in the open ocean. <i>Science</i> , 2017, 357, 646-647.	12.6	33
75	Spatial Interactions and Oscillatory Tragedies of the Commons. <i>Physical Review Letters</i> , 2019, 122, 148102.	7.8	32
76	Distinguishing between Indirect and Direct Modes of Transmission Using Epidemiological Time Series. <i>American Naturalist</i> , 2013, 181, E43-E52.	2.1	31
77	An Algorithm-Independent Definition of Damage Spreading—Application to Directed Percolation. <i>Journal of Statistical Physics</i> , 1997, 88, 617-636.	1.2	30
78	The virus of my virus is my friend: Ecological effects of virophage with alternative modes of coinfection. <i>Journal of Theoretical Biology</i> , 2014, 354, 124-136.	1.7	30
79	A non-negative matrix factorization framework for identifying modular patterns in metagenomic profile data. <i>Journal of Mathematical Biology</i> , 2012, 64, 697-711.	1.9	28
80	Combined pigment and metatranscriptomic analysis reveals highly synchronized diel patterns of phenotypic light response across domains in the open oligotrophic ocean. <i>ISME Journal</i> , 2021, 15, 520-533.	9.8	28
81	When to be temperate: on the fitness benefits of lysis vs. lysogeny. <i>Virus Evolution</i> , 2020, 6, .	4.9	25
82	ClearedLeavesDB: an online database of cleared plant leaf images. <i>Plant Methods</i> , 2014, 10, 8.	4.3	24
83	Allometric covariation: a hallmark behavior of plants and leaves. <i>New Phytologist</i> , 2012, 193, 882-889.	7.3	21
84	Critical cell wall hole size for lysis in Gram-positive bacteria. <i>Journal of the Royal Society Interface</i> , 2013, 10, 20120892.	3.4	21
85	Contrasting Controls on Microzooplankton Grazing and Viral Infection of Microbial Prey. <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	21
86	Complex marine microbial communities partition metabolism of scarce resources over the diel cycle. <i>Nature Ecology and Evolution</i> , 2022, 6, 218-229.	7.8	21
87	Costs and benefits of reticulate leaf venation. <i>BMC Plant Biology</i> , 2014, 14, 234.	3.6	20
88	Dynamics of nutrient uptake strategies: lessons from the tortoise and the hare. <i>Theoretical Ecology</i> , 2011, 4, 163-177.	1.0	19
89	A framework for monitoring population immunity to SARS-CoV-2. <i>Annals of Epidemiology</i> , 2021, 63, 75-78.	1.9	19
90	Functional and Comparative Genomic Analysis of Integrated Prophage-Like Sequences in <i>Candidatus Liberibacter asiaticus</i> . <i>MSphere</i> , 2019, 4, .	2.9	18

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91	Estimates of Leaf Vein Density Are Scale Dependent. <i>Plant Physiology</i> , 2014, 164, 173-180.	4.8	16
92	Packing-limited growth of irregular objects. <i>Physical Review E</i> , 2003, 67, 016117.	2.1	15
93	Bacterivorous grazers facilitate organic matter decomposition: a stoichiometric modeling approach. <i>FEMS Microbiology Ecology</i> , 2009, 69, 170-179.	2.7	15
94	Stochasticity and the limits to confidence when estimating R of Ebola and other emerging infectious diseases. <i>Journal of Theoretical Biology</i> , 2016, 408, 145-154.	1.7	15
95	The importance of the generation interval in investigating dynamics and control of new SARS-CoV-2 variants. <i>Journal of the Royal Society Interface</i> , 2022, 19, .	3.4	15
96	Heterogeneity in susceptibility dictates the order of epidemic models. <i>Journal of Theoretical Biology</i> , 2021, 528, 110839.	1.7	14
97	Disentangling niche competition from grazing mortality in phytoplankton dilution experiments. <i>PLoS ONE</i> , 2017, 12, e0177517.	2.5	13
98	Caution in inferring viral strategies from abundance correlations in marine metagenomes. <i>Nature Communications</i> , 2019, 10, 501.	12.8	13
99	Heterogeneous viral strategies promote coexistence in virus-microbe systems. <i>Journal of Theoretical Biology</i> , 2019, 462, 65-84.	1.7	13
100	Optimizing the Timing and Composition of Therapeutic Phage Cocktails: A Control-Theoretic Approach. <i>Bulletin of Mathematical Biology</i> , 2020, 82, 75.	1.9	13
101	Surveillance-to-Diagnostic Testing Program for Asymptomatic SARS-CoV-2 Infections on a Large, Urban Campus in Fall 2020. <i>Epidemiology</i> , 2022, 33, 209-216.	2.7	13
102	Quantifying enzymatic lysis: estimating the combined effects of chemistry, physiology and physics. <i>Physical Biology</i> , 2010, 7, 046002.	1.8	12
103	Zero-sum allocational strategies determine the allometry of specific leaf area. <i>American Journal of Botany</i> , 2010, 97, 1808-1815.	1.7	12
104	Disease-dependent interaction policies to support health and economic outcomes during the COVID-19 epidemic. <i>IScience</i> , 2021, 24, 102710.	4.1	12
105	Multiple regimes of robust patterns between network structure and biodiversity. <i>Scientific Reports</i> , 2015, 5, 17856.	3.3	11
106	Not by (Good) Microbes Alone: Towards Immunocommensal Therapies. <i>Trends in Microbiology</i> , 2019, 27, 294-302.	7.7	11
107	Linking Light-Dependent Life History Traits with Population Dynamics for <i>Prochlorococcus</i> and Cyanophage. <i>MSystems</i> , 2020, 5, .	3.8	11
108	Modeling serological testing to inform relaxation of social distancing for COVID-19 control. <i>Nature Communications</i> , 2021, 12, 7063.	12.8	11

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109	Inferring phage-bacteria infection networks from time-series data. Royal Society Open Science, 2016, 3, 160654.	2.4	10
110	Overcoming the Law of the Hidden in Cyberinfrastructures. Trends in Plant Science, 2017, 22, 117-123.	8.8	10
111	The Effect of Strain Level Diversity on Robust Inference of Virus-Induced Mortality of Phytoplankton. Frontiers in Microbiology, 2018, 9, 1850.	3.5	10
112	A thermal trade-off between viral production and degradation drives virus-phytoplankton population dynamics. Ecology Letters, 2021, 24, 1133-1144.	6.4	10
113	Leapfrog dynamics in phage-bacteria coevolution revealed by joint analysis of cross-infection phenotypes and whole genome sequencing. Ecology Letters, 2022, 25, 876-888.	6.4	10
114	Scale-dependence of resource-biodiversity relationships. Journal of Theoretical Biology, 2003, 225, 205-214.	1.7	9
115	Conflicting attachment and the growth of bipartite networks. Physical Review E, 2016, 93, 032303.	2.1	9
116	A touch of sleep: biophysical model of contact-mediated dormancy of archaea by viruses. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20161037.	2.6	8
117	Timescales modulate optimal lysis-lysogeny decision switches and near-term phage reproduction. Virus Evolution, 2022, 8, .	4.9	8
118	A discrepancy between predictions of saturating nutrient uptake models and nitrogen-to-phosphorus stoichiometry in the surface ocean. Limnology and Oceanography, 2010, 55, 997-1008.	3.1	7
119	Infect while the iron is scarce: nutrient-explicit phage-bacteria games. Theoretical Ecology, 2021, 14, 467-487.	1.0	7
120	Quantitative Infection Dynamics of Cafeteria Roenbergensis Virus. Viruses, 2018, 10, 468.	3.3	6
121	CRISPR-Cas Systems to Probe Ecological Diversity and Host-Viral Interactions. , 2013, , 221-250.		6
122	Fluctuation domains in adaptive evolution. Theoretical Population Biology, 2010, 77, 6-13.	1.1	5
123	The Fiber Walk: A Model of Tip-Driven Growth with Lateral Expansion. PLoS ONE, 2014, 9, e85585.	2.5	5
124	Epidemic spread over networks with agent awareness and social distancing. , 2015, , .		5
125	Information sharing for a coordination game in fluctuating environments. Journal of Theoretical Biology, 2018, 454, 376-385.	1.7	5
126	Fighting microbial pathogens by integrating host ecosystem interactions and evolution. BioEssays, 2021, 43, 2000272.	2.5	5

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127	Cyanophages from a less virulent clade dominate over their sister clade in global oceans. ISME Journal, 2022, 16, 2169-2180.	9.8	5
128	Optimal control policies for evolutionary dynamics with environmental feedback. , 2018, , .		4
129	Quantifying Risk for SARS-CoV-2 Infection Among Nursing Home Workers for the 2020-2021 Winter Surge of the COVID-19 Pandemic in Georgia, USA. Journal of the American Medical Directors Association, 2022, 23, 942-946.e1.	2.5	4
130	CRISPR-Cas Systems to Probe Ecological Diversity and Host-Viral Interactions. , 2013, , 221-250.		3
131	Let My People Go (Home) to Spain: A Genealogical Model of Jewish Identities since 1492. PLoS ONE, 2014, 9, e85673.	2.5	3
132	The Future of Quantitative Viral Ecology. , 2016, , .		3
133	Phage in the time of cholera. Lancet Infectious Diseases, The, 2006, 6, 257-258.	9.1	2
134	Reacting to outbreaks at neighboring localities. Journal of Theoretical Biology, 2021, 520, 110632.	1.7	2
135	Disease-Dependent Interaction Policies to Support Health and Economic Outcomes During the COVID-19 Epidemic. SSRN Electronic Journal, 0, , .	0.4	2
136	Risk factors for severe acute respiratory coronavirus virus 2 (SARS-CoV-2) seropositivity among nursing home staff. Antimicrobial Stewardship & Healthcare Epidemiology, 2021, 1, .	0.5	2
137	Bifurcation Analysis of Gene Regulatory Circuits Subject to Copy Number Variation. SIAM Journal on Applied Dynamical Systems, 2010, 9, 799-826.	1.6	1
138	Dynamics of a contact process with ontogeny. Physical Review E, 2004, 70, 021915.	2.1	0
139	A guide to sensitivity analysis of quantitative models of gene expression dynamics. Methods, 2013, 62, 109-120.	3.8	0