

Joshua S Weitz

List of Publications by Year in descending order

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Version: 2024-02-01

139
papers

10,113
citations

36203

51
h-index

45213

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.	0.8	521
2	Repeatability and Contingency in the Evolution of a Key Innovation in Phage Lambda. <i>Science</i> , 2012, 335, 428-432.	6.0	401
3	Robust estimation of microbial diversity in theory and in practice. <i>ISME Journal</i> , 2013, 7, 1092-1101.	4.4	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.	5.1	315
5	Imaging and Analysis Platform for Automatic Phenotyping and Trait Ranking of Plant Root Systems. <i>Plant Physiology</i> , 2010, 152, 1148-1157.	2.3	306
6	GiA Roots: software for the high throughput analysis of plant root system architecture. <i>BMC Plant Biology</i> , 2012, 12, 116.	1.6	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.	3.3	275
8	Phage-bacteria infection networks. <i>Trends in Microbiology</i> , 2013, 21, 82-91.	3.5	273
9	The elemental composition of virus particles: implications for marine biogeochemical cycles. <i>Nature Reviews Microbiology</i> , 2014, 12, 519-528.	13.6	273
10	Re-examination of the relationship between marine virus and microbial cell abundances. <i>Nature Microbiology</i> , 2016, 1, 15024.	5.9	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.	3.3	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.	3.3	245
13	Image-Based High-Throughput Field Phenotyping of Crop Roots. <i>Plant Physiology</i> , 2014, 166, 470-486.	2.3	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.	4.4	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.	15.2	196
17	Viral tagging reveals discrete populations in <i>Synechococcus</i> viral genome sequence space. <i>Nature</i> , 2014, 513, 242-245.	13.7	183
18	Testing the metabolic theory of ecology. <i>Ecology Letters</i> , 2012, 15, 1465-1474.	3.0	155

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19	Multi-scale structure and geographic drivers of cross-infection within marine bacteria and phages. <i>ISME Journal</i> , 2013, 7, 520-532.	4.4	155
20	Digital imaging of root traits (DIRT): a high-throughput computing and collaboration platform for field-based root phenomics. <i>Plant Methods</i> , 2015, 11, 51.	1.9	146
21	The time scale of asymptomatic transmission affects estimates of epidemic potential in the COVID-19 outbreak. <i>Epidemics</i> , 2020, 31, 100392.	1.5	129
22	Genotypic recognition and spatial responses by rice roots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2670-2675.	3.3	124
23	Awareness-driven behavior changes can shift the shape of epidemics away from peaks and toward plateaus, shoulders, and oscillations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32764-32771.	3.3	120
24	Coevolution can reverse predator-prey cycles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7486-7491.	3.3	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. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200144.	1.5	103
26	The metabolic theory of ecology: prospects and challenges for plant biology. <i>New Phytologist</i> , 2010, 188, 696-710.	3.5	102
27	Leaf Extraction and Analysis Framework Graphical User Interface: Segmenting and Analyzing the Structure of Leaf Veins and Areoles. <i>Plant Physiology</i> , 2011, 155, 236-245.	2.3	100
28	Genomic differentiation among wild cyanophages despite widespread horizontal gene transfer. <i>BMC Genomics</i> , 2016, 17, 930.	1.2	96
29	A neutral metapopulation model of biodiversity in river networks. <i>Journal of Theoretical Biology</i> , 2007, 245, 351-363.	0.8	94
30	A virus or more in (nearly) every cell: ubiquitous networks of virus-host interactions in extreme environments. <i>ISME Journal</i> , 2018, 12, 1706-1714.	4.4	94
31	Modeling Post-death Transmission of Ebola: Challenges for Inference and Opportunities for Control. <i>Scientific Reports</i> , 2015, 5, 8751.	1.6	93
32	Alternative stable states in host-phage dynamics. <i>Theoretical Ecology</i> , 2008, 1, 13-19.	0.4	92
33	Dynamics of Indirectly Transmitted Infectious Diseases with Immunological Threshold. <i>Bulletin of Mathematical Biology</i> , 2009, 71, 845-862.	0.9	92
34	Genomic fluidity: an integrative view of gene diversity within microbial populations. <i>BMC Genomics</i> , 2011, 12, 32.	1.2	92
35	Mechanisms of multi-strain coexistence in host-phage systems with nested infection networks. <i>Journal of Theoretical Biology</i> , 2013, 332, 65-77.	0.8	91
36	Size and scaling of predator-prey dynamics. <i>Ecology Letters</i> , 2006, 9, 548-557.	3.0	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.	1.1	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.	0.8	88
39	The Evolution of Dispersal in Reserve Networks. <i>American Naturalist</i> , 2007, 170, 59-78.	1.0	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.	3.3	85
41	Unsupervised statistical clustering of environmental shotgun sequences. <i>BMC Bioinformatics</i> , 2009, 10, 316.	1.2	84
42	Viral ecology comes of age. <i>Environmental Microbiology Reports</i> , 2017, 9, 33-35.	1.0	81
43	An integrative approach to understanding microbial diversity: from intracellular mechanisms to community structure. <i>Ecology Letters</i> , 2010, 13, 1073-1084.	3.0	80
44	Revisiting the rules of life for viruses of microorganisms. <i>Nature Reviews Microbiology</i> , 2021, 19, 501-513.	13.6	77
45	Quantitative Models of Phage-Antibiotic Combination Therapy. <i>MSystems</i> , 2020, 5, .	1.7	73
46	Collective Decision Making in Bacterial Viruses. <i>Biophysical Journal</i> , 2008, 95, 2673-2680.	0.2	71
47	Lysis, lysogeny and virus-microbe ratios. <i>Nature</i> , 2017, 549, E1-E3.	13.7	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.	1.2	69
49	A Null Model of Morphospace Occupation. <i>American Naturalist</i> , 2005, 166, E1-E13.	1.0	68
50	CRISPR-Induced Distributed Immunity in Microbial Populations. <i>PLoS ONE</i> , 2014, 9, e101710.	1.1	67
51	Systematic biases in disease forecasting - The role of behavior change. <i>Epidemics</i> , 2019, 27, 96-105.	1.5	65
52	Evaluating scaling models in biology using hierarchical Bayesian approaches. <i>Ecology Letters</i> , 2009, 12, 641-651.	3.0	60
53	Functional Biogeography of Ocean Microbes Revealed through Non-Negative Matrix Factorization. <i>PLoS ONE</i> , 2012, 7, e43866.	1.1	60
54	Real-time, interactive website for US-county-level COVID-19 event risk assessment. <i>Nature Human Behaviour</i> , 2020, 4, 1313-1319.	6.2	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.	2.2	58
56	Viral invasion fitness across a continuum from lysis to latency. <i>Virus Evolution</i> , 2019, 5, vez006.	2.2	57
57	A neutral theory of genome evolution and the frequency distribution of genes. <i>BMC Genomics</i> , 2012, 13, 196.	1.2	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, .	3.3	54
59	Scaling and structure of dicotyledonous leaf venation networks. <i>Ecology Letters</i> , 2012, 15, 87-95.	3.0	51
60	A practical generation-interval-based approach to inferring the strength of epidemics from their speed. <i>Epidemics</i> , 2019, 27, 12-18.	1.5	51
61	Packing-limited growth. <i>Physical Review E</i> , 2002, 65, 056108.	0.8	47
62	A Primer for Microbiome Time-Series Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 310.	1.1	47
63	Allelic polymorphism shapes community function in evolving <i>Pseudomonas aeruginosa</i> populations. <i>ISME Journal</i> , 2020, 14, 1929-1942.	4.4	47
64	Hierarchical Ordering of Reticular Networks. <i>PLoS ONE</i> , 2012, 7, e36715.	1.1	44
65	Dangerous nutrients: Evolution of phytoplankton resource uptake subject to virus attack. <i>Journal of Theoretical Biology</i> , 2009, 257, 104-115.	0.8	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.	4.4	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.	1.6	39
68	Networked SIS Epidemics With Awareness. <i>IEEE Transactions on Computational Social Systems</i> , 2017, 4, 93-103.	3.2	38
69	Limitations of Correlation-Based Inference in Complex Virus-Microbe Communities. <i>MSystems</i> , 2018, 3, .	1.7	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.	1.5	36
71	An empirical model of carbon flow through marine viruses and microzooplankton grazers. <i>Environmental Microbiology</i> , 2019, 21, 2171-2181.	1.8	35
72	Topological constraints in early multicellularity favor reproductive division of labor. <i>ELife</i> , 2020, 9, .	2.8	34

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73	Evolution, Interactions, and Biological Networks. <i>PLoS Biology</i> , 2007, 5, e11.	2.6	33
74	How microbes survive in the open ocean. <i>Science</i> , 2017, 357, 646-647.	6.0	33
75	Spatial Interactions and Oscillatory Tragedies of the Commons. <i>Physical Review Letters</i> , 2019, 122, 148102.	2.9	32
76	Distinguishing between Indirect and Direct Modes of Transmission Using Epidemiological Time Series. <i>American Naturalist</i> , 2013, 181, E43-E52.	1.0	31
77	An Algorithm-Independent Definition of Damage Spreading—Application to Directed Percolation. <i>Journal of Statistical Physics</i> , 1997, 88, 617-636.	0.5	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.	0.8	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.	0.8	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.	4.4	28
81	When to be temperate: on the fitness benefits of lysis vs. lysogeny. <i>Virus Evolution</i> , 2020, 6, .	2.2	25
82	ClearedLeavesDB: an online database of cleared plant leaf images. <i>Plant Methods</i> , 2014, 10, 8.	1.9	24
83	Allometric covariation: a hallmark behavior of plants and leaves. <i>New Phytologist</i> , 2012, 193, 882-889.	3.5	21
84	Critical cell wall hole size for lysis in Gram-positive bacteria. <i>Journal of the Royal Society Interface</i> , 2013, 10, 20120892.	1.5	21
85	Contrasting Controls on Microzooplankton Grazing and Viral Infection of Microbial Prey. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	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.	3.4	21
87	Costs and benefits of reticulate leaf venation. <i>BMC Plant Biology</i> , 2014, 14, 234.	1.6	20
88	Dynamics of nutrient uptake strategies: lessons from the tortoise and the hare. <i>Theoretical Ecology</i> , 2011, 4, 163-177.	0.4	19
89	A framework for monitoring population immunity to SARS-CoV-2. <i>Annals of Epidemiology</i> , 2021, 63, 75-78.	0.9	19
90	Functional and Comparative Genomic Analysis of Integrated Prophage-Like Sequences in <i>Candidatus Liberibacter asiaticus</i> . <i>MSphere</i> , 2019, 4, .	1.3	18

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91	Estimates of Leaf Vein Density Are Scale Dependent. <i>Plant Physiology</i> , 2014, 164, 173-180.	2.3	16
92	Packing-limited growth of irregular objects. <i>Physical Review E</i> , 2003, 67, 016117.	0.8	15
93	Bacterivorous grazers facilitate organic matter decomposition: a stoichiometric modeling approach. <i>FEMS Microbiology Ecology</i> , 2009, 69, 170-179.	1.3	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.	0.8	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, .	1.5	15
96	Heterogeneity in susceptibility dictates the order of epidemic models. <i>Journal of Theoretical Biology</i> , 2021, 528, 110839.	0.8	14
97	Disentangling niche competition from grazing mortality in phytoplankton dilution experiments. <i>PLoS ONE</i> , 2017, 12, e0177517.	1.1	13
98	Caution in inferring viral strategies from abundance correlations in marine metagenomes. <i>Nature Communications</i> , 2019, 10, 501.	5.8	13
99	Heterogeneous viral strategies promote coexistence in virus-microbe systems. <i>Journal of Theoretical Biology</i> , 2019, 462, 65-84.	0.8	13
100	Optimizing the Timing and Composition of Therapeutic Phage Cocktails: A Control-Theoretic Approach. <i>Bulletin of Mathematical Biology</i> , 2020, 82, 75.	0.9	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.	1.2	13
102	Quantifying enzymatic lysis: estimating the combined effects of chemistry, physiology and physics. <i>Physical Biology</i> , 2010, 7, 046002.	0.8	12
103	Zero-sum allocational strategies determine the allometry of specific leaf area. <i>American Journal of Botany</i> , 2010, 97, 1808-1815.	0.8	12
104	Disease-dependent interaction policies to support health and economic outcomes during the COVID-19 epidemic. <i>IScience</i> , 2021, 24, 102710.	1.9	12
105	Multiple regimes of robust patterns between network structure and biodiversity. <i>Scientific Reports</i> , 2015, 5, 17856.	1.6	11
106	Not by (Good) Microbes Alone: Towards Immunocommensal Therapies. <i>Trends in Microbiology</i> , 2019, 27, 294-302.	3.5	11
107	Linking Light-Dependent Life History Traits with Population Dynamics for <i>Prochlorococcus</i> and Cyanophage. <i>MSystems</i> , 2020, 5, .	1.7	11
108	Modeling serological testing to inform relaxation of social distancing for COVID-19 control. <i>Nature Communications</i> , 2021, 12, 7063.	5.8	11

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109	Inferring phage-bacteria infection networks from time-series data. Royal Society Open Science, 2016, 3, 160654.	1.1	10
110	Overcoming the Law of the Hidden in Cyberinfrastructures. Trends in Plant Science, 2017, 22, 117-123.	4.3	10
111	The Effect of Strain Level Diversity on Robust Inference of Virus-Induced Mortality of Phytoplankton. Frontiers in Microbiology, 2018, 9, 1850.	1.5	10
112	A thermal trade-off between viral production and degradation drives virus-phytoplankton population dynamics. Ecology Letters, 2021, 24, 1133-1144.	3.0	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.	3.0	10
114	Scale-dependence of resource-biodiversity relationships. Journal of Theoretical Biology, 2003, 225, 205-214.	0.8	9
115	Conflicting attachment and the growth of bipartite networks. Physical Review E, 2016, 93, 032303.	0.8	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.	1.2	8
117	Timescales modulate optimal lysis-lysogeny decision switches and near-term phage reproduction. Virus Evolution, 2022, 8, .	2.2	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.	1.6	7
119	Infect while the iron is scarce: nutrient-explicit phage-bacteria games. Theoretical Ecology, 2021, 14, 467-487.	0.4	7
120	Quantitative Infection Dynamics of Cafeteria Roenbergensis Virus. Viruses, 2018, 10, 468.	1.5	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.	0.5	5
123	The Fiber Walk: A Model of Tip-Driven Growth with Lateral Expansion. PLoS ONE, 2014, 9, e85585.	1.1	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.	0.8	5
126	Fighting microbial pathogens by integrating host ecosystem interactions and evolution. BioEssays, 2021, 43, 2000272.	1.2	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.	4.4	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.	1.2	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.	1.1	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.	4.6	2
134	Reacting to outbreaks at neighboring localities. Journal of Theoretical Biology, 2021, 520, 110632.	0.8	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, .	0.2	2
137	Bifurcation Analysis of Gene Regulatory Circuits Subject to Copy Number Variation. SIAM Journal on Applied Dynamical Systems, 2010, 9, 799-826.	0.7	1
138	Dynamics of a contact process with ontogeny. Physical Review E, 2004, 70, 021915.	0.8	0
139	A guide to sensitivity analysis of quantitative models of gene expression dynamics. Methods, 2013, 62, 109-120.	1.9	0