

Joshua S Weitz

List of Publications by Year in descending order

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Version: 2024-02-01

139
papers

10,113
citations

36271

51
h-index

45285

90
g-index

194
all docs

194
docs citations

194
times ranked

12074
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Leapfrog dynamics in phage-bacteria coevolution revealed by joint analysis of cross-infection phenotypes and whole genome sequencing. <i>Ecology Letters</i> , 2022, 25, 876-888.	3.0	10
3	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
4	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. <i>Journal of the American Medical Directors Association</i> , 2022, 23, 942-946.e1.	1.2	4
5	Timescales modulate optimal lysis-lysogeny decision switches and near-term phage reproduction. <i>Virus Evolution</i> , 2022, 8, .	2.2	8
6	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
7	Cyanophages from a less virulent clade dominate over their sister clade in global oceans. <i>ISME Journal</i> , 2022, 16, 2169-2180.	4.4	5
8	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
9	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
10	Revisiting the rules of life for viruses of microorganisms. <i>Nature Reviews Microbiology</i> , 2021, 19, 501-513.	13.6	77
11	A thermal trade-off between viral production and degradation drives virus-phytoplankton population dynamics. <i>Ecology Letters</i> , 2021, 24, 1133-1144.	3.0	10
12	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
13	Infect while the iron is scarce: nutrient-explicit phage-bacteria games. <i>Theoretical Ecology</i> , 2021, 14, 467-487.	0.4	7
14	Reacting to outbreaks at neighboring localities. <i>Journal of Theoretical Biology</i> , 2021, 520, 110632.	0.8	2
15	Disease-dependent interaction policies to support health and economic outcomes during the COVID-19 epidemic. <i>IScience</i> , 2021, 24, 102710.	1.9	12
16	Heterogeneity in susceptibility dictates the order of epidemic models. <i>Journal of Theoretical Biology</i> , 2021, 528, 110839.	0.8	14
17	A framework for monitoring population immunity to SARS-CoV-2. <i>Annals of Epidemiology</i> , 2021, 63, 75-78.	0.9	19
18	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

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19	Fighting microbial pathogens by integrating host ecosystem interactions and evolution. <i>BioEssays</i> , 2021, 43, 2000272.	1.2	5
20	Risk factors for severe acute respiratory coronavirus virus 2 (SARS-CoV-2) seropositivity among nursing home staff. <i>Antimicrobial Stewardship & Healthcare Epidemiology</i> , 2021, 1, .	0.2	2
21	Modeling serological testing to inform relaxation of social distancing for COVID-19 control. <i>Nature Communications</i> , 2021, 12, 7063.	5.8	11
22	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
23	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
24	Modeling shield immunity to reduce COVID-19 epidemic spread. <i>Nature Medicine</i> , 2020, 26, 849-854.	15.2	196
25	When to be temperate: on the fitness benefits of lysis vs. lysogeny. <i>Virus Evolution</i> , 2020, 6, .	2.2	25
26	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
27	A Primer for Microbiome Time-Series Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 310.	1.1	47
28	Allelic polymorphism shapes community function in evolving <i>Pseudomonas aeruginosa</i> populations. <i>ISME Journal</i> , 2020, 14, 1929-1942.	4.4	47
29	Quantitative Models of Phage-Antibiotic Combination Therapy. <i>MSystems</i> , 2020, 5, .	1.7	73
30	Linking Light-Dependent Life History Traits with Population Dynamics for <i>Prochlorococcus</i> and Cyanophage. <i>MSystems</i> , 2020, 5, .	1.7	11
31	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
32	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
33	Topological constraints in early multicellularity favor reproductive division of labor. <i>ELife</i> , 2020, 9, .	2.8	34
34	Systematic biases in disease forecasting – The role of behavior change. <i>Epidemics</i> , 2019, 27, 96-105.	1.5	65
35	Viral invasion fitness across a continuum from lysis to latency. <i>Virus Evolution</i> , 2019, 5, vez006.	2.2	57
36	Contrasting Controls on Microzooplankton Grazing and Viral Infection of Microbial Prey. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	21

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37	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
38	An empirical model of carbon flow through marine viruses and microzooplankton grazers. <i>Environmental Microbiology</i> , 2019, 21, 2171-2181.	1.8	35
39	Spatial Interactions and Oscillatory Tragedies of the Commons. <i>Physical Review Letters</i> , 2019, 122, 148102.	2.9	32
40	Caution in inferring viral strategies from abundance correlations in marine metagenomes. <i>Nature Communications</i> , 2019, 10, 501.	5.8	13
41	Functional and Comparative Genomic Analysis of Integrated Prophage-Like Sequences in <i>Candidatus Liberibacter asiaticus</i> . <i>MSphere</i> , 2019, 4, .	1.3	18
42	Heterogeneous viral strategies promote coexistence in virus-microbe systems. <i>Journal of Theoretical Biology</i> , 2019, 462, 65-84.	0.8	13
43	Not by (Good) Microbes Alone: Towards Immunocommenseal Therapies. <i>Trends in Microbiology</i> , 2019, 27, 294-302.	3.5	11
44	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
45	Optimal control policies for evolutionary dynamics with environmental feedback. , 2018, , .		4
46	The Effect of Strain Level Diversity on Robust Inference of Virus-Induced Mortality of Phytoplankton. <i>Frontiers in Microbiology</i> , 2018, 9, 1850.	1.5	10
47	Quantitative Infection Dynamics of <i>Cafeteria roenbergensis</i> Virus. <i>Viruses</i> , 2018, 10, 468.	1.5	6
48	Information sharing for a coordination game in fluctuating environments. <i>Journal of Theoretical Biology</i> , 2018, 454, 376-385.	0.8	5
49	Limitations of Correlation-Based Inference in Complex Virus-Microbe Communities. <i>MSystems</i> , 2018, 3, .	1.7	37
50	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
51	Overcoming the Law of the Hidden in Cyberinfrastructures. <i>Trends in Plant Science</i> , 2017, 22, 117-123.	4.3	10
52	Lysis, lysogeny and virus-microbe ratios. <i>Nature</i> , 2017, 549, E1-E3.	13.7	69
53	How microbes survive in the open ocean. <i>Science</i> , 2017, 357, 646-647.	6.0	33
54	Networked SIS Epidemics With Awareness. <i>IEEE Transactions on Computational Social Systems</i> , 2017, 4, 93-103.	3.2	38

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55	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
56	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
57	Viral ecology comes of age. <i>Environmental Microbiology Reports</i> , 2017, 9, 33-35.	1.0	81
58	Disentangling niche competition from grazing mortality in phytoplankton dilution experiments. <i>PLoS ONE</i> , 2017, 12, e0177517.	1.1	13
59	Inferring phage-bacteria infection networks from time-series data. <i>Royal Society Open Science</i> , 2016, 3, 160654.	1.1	10
60	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
61	A touch of sleep: biophysical model of contact-mediated dormancy of archaea by viruses. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161037.	1.2	8
62	Genomic differentiation among wild cyanophages despite widespread horizontal gene transfer. <i>BMC Genomics</i> , 2016, 17, 930.	1.2	96
63	Stochasticity and the limits to confidence when estimating R_0 of Ebola and other emerging infectious diseases. <i>Journal of Theoretical Biology</i> , 2016, 408, 145-154.	0.8	15
64	Conflicting attachment and the growth of bipartite networks. <i>Physical Review E</i> , 2016, 93, 032303.	0.8	9
65	Re-examination of the relationship between marine virus and microbial cell abundances. <i>Nature Microbiology</i> , 2016, 1, 15024.	5.9	264
66	The Future of Quantitative Viral Ecology. , 2016, , .		3
67	Modeling Post-death Transmission of Ebola: Challenges for Inference and Opportunities for Control. <i>Scientific Reports</i> , 2015, 5, 8751.	1.6	93
68	Multiple regimes of robust patterns between network structure and biodiversity. <i>Scientific Reports</i> , 2015, 5, 17856.	1.6	11
69	Epidemic spread over networks with agent awareness and social distancing. , 2015, , .		5
70	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
71	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
72	The Fiber Walk: A Model of Tip-Driven Growth with Lateral Expansion. <i>PLoS ONE</i> , 2014, 9, e85585.	1.1	5

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73	Estimates of Leaf Vein Density Are Scale Dependent. <i>Plant Physiology</i> , 2014, 164, 173-180.	2.3	16
74	Image-Based High-Throughput Field Phenotyping of Crop Roots. <i>Plant Physiology</i> , 2014, 166, 470-486.	2.3	239
75	Costs and benefits of reticulate leaf venation. <i>BMC Plant Biology</i> , 2014, 14, 234.	1.6	20
76	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
77	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
78	Viral tagging reveals discrete populations in <i>Synechococcus</i> viral genome sequence space. <i>Nature</i> , 2014, 513, 242-245.	13.7	183
79	The elemental composition of virus particles: implications for marine biogeochemical cycles. <i>Nature Reviews Microbiology</i> , 2014, 12, 519-528.	13.6	273
80	ClearedLeavesDB: an online database of cleared plant leaf images. <i>Plant Methods</i> , 2014, 10, 8.	1.9	24
81	Let My People Go (Home) to Spain: A Genealogical Model of Jewish Identities since 1492. <i>PLoS ONE</i> , 2014, 9, e85673.	1.1	3
82	CRISPR-Induced Distributed Immunity in Microbial Populations. <i>PLoS ONE</i> , 2014, 9, e101710.	1.1	67
83	Phage-bacteria infection networks. <i>Trends in Microbiology</i> , 2013, 21, 82-91.	3.5	273
84	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
85	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
86	CRISPR-Cas Systems to Probe Ecological Diversity and Host-Viral Interactions. , 2013, , 221-250.		3
87	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
88	A guide to sensitivity analysis of quantitative models of gene expression dynamics. <i>Methods</i> , 2013, 62, 109-120.	1.9	0
89	Distinguishing between Indirect and Direct Modes of Transmission Using Epidemiological Time Series. <i>American Naturalist</i> , 2013, 181, E43-E52.	1.0	31
90	Robust estimation of microbial diversity in theory and in practice. <i>ISME Journal</i> , 2013, 7, 1092-1101.	4.4	321

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91	Multi-scale structure and geographic drivers of cross-infection within marine bacteria and phages. ISME Journal, 2013, 7, 520-532.	4.4	155
92	Critical cell wall hole size for lysis in Gram-positive bacteria. Journal of the Royal Society Interface, 2013, 10, 20120892.	1.5	21
93	CRISPR-Cas Systems to Probe Ecological Diversity and Host-Viral Interactions. , 2013, , 221-250.		6
94	Testing the metabolic theory of ecology. Ecology Letters, 2012, 15, 1465-1474.	3.0	155
95	Repeatability and Contingency in the Evolution of a Key Innovation in Phage Lambda. Science, 2012, 335, 428-432.	6.0	401
96	A neutral theory of genome evolution and the frequency distribution of genes. BMC Genomics, 2012, 13, 196.	1.2	55
97	GiA Roots: software for the high throughput analysis of plant root system architecture. BMC Plant Biology, 2012, 12, 116.	1.6	279
98	Functional Biogeography of Ocean Microbes Revealed through Non-Negative Matrix Factorization. PLoS ONE, 2012, 7, e43866.	1.1	60
99	Ocean viruses and their effects on microbial communities and biogeochemical cycles. F1000 Biology Reports, 2012, 4, 17.	4.0	213
100	Allometric covariation: a hallmark behavior of plants and leaves. New Phytologist, 2012, 193, 882-889.	3.5	21
101	Scaling and structure of dicotyledonous leaf venation networks. Ecology Letters, 2012, 15, 87-95.	3.0	51
102	MULTISCALE MODEL OF CRISPR-INDUCED COEVOLUTIONARY DYNAMICS: DIVERSIFICATION AT THE INTERFACE OF LAMARCK AND DARWIN. Evolution; International Journal of Organic Evolution, 2012, 66, 2015-2029.	1.1	89
103	A non-negative matrix factorization framework for identifying modular patterns in metagenomic profile data. Journal of Mathematical Biology, 2012, 64, 697-711.	0.8	28
104	Hierarchical Ordering of Reticular Networks. PLoS ONE, 2012, 7, e36715.	1.1	44
105	Statistical structure of host-phage interactions. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E288-97.	3.3	275
106	Leaf Extraction and Analysis Framework Graphical User Interface: Segmenting and Analyzing the Structure of Leaf Veins and Areoles. Plant Physiology, 2011, 155, 236-245.	2.3	100
107	Dynamics of nutrient uptake strategies: lessons from the tortoise and the hare. Theoretical Ecology, 2011, 4, 163-177.	0.4	19
108	Genomic fluidity: an integrative view of gene diversity within microbial populations. BMC Genomics, 2011, 12, 32.	1.2	92

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109	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
110	A discrepancy between predictions of saturating nutrient uptake models and nitrogen-to-phosphorus stoichiometry in the surface ocean. <i>Limnology and Oceanography</i> , 2010, 55, 997-1008.	1.6	7
111	Fluctuation domains in adaptive evolution. <i>Theoretical Population Biology</i> , 2010, 77, 6-13.	0.5	5
112	The metabolic theory of ecology: prospects and challenges for plant biology. <i>New Phytologist</i> , 2010, 188, 696-710.	3.5	102
113	An integrative approach to understanding microbial diversity: from intracellular mechanisms to community structure. <i>Ecology Letters</i> , 2010, 13, 1073-1084.	3.0	80
114	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
115	Quantifying enzymatic lysis: estimating the combined effects of chemistry, physiology and physics. <i>Physical Biology</i> , 2010, 7, 046002.	0.8	12
116	Zero-sum allocational strategies determine the allometry of specific leaf area. <i>American Journal of Botany</i> , 2010, 97, 1808-1815.	0.8	12
117	Bifurcation Analysis of Gene Regulatory Circuits Subject to Copy Number Variation. <i>SIAM Journal on Applied Dynamical Systems</i> , 2010, 9, 799-826.	0.7	1
118	Unsupervised statistical clustering of environmental shotgun sequences. <i>BMC Bioinformatics</i> , 2009, 10, 316.	1.2	84
119	Dangerous nutrients: Evolution of phytoplankton resource uptake subject to virus attack. <i>Journal of Theoretical Biology</i> , 2009, 257, 104-115.	0.8	42
120	Dynamics of Indirectly Transmitted Infectious Diseases with Immunological Threshold. <i>Bulletin of Mathematical Biology</i> , 2009, 71, 845-862.	0.9	92
121	Bacterivorous grazers facilitate organic matter decomposition: a stoichiometric modeling approach. <i>FEMS Microbiology Ecology</i> , 2009, 69, 170-179.	1.3	15
122	Evaluating scaling models in biology using hierarchical Bayesian approaches. <i>Ecology Letters</i> , 2009, 12, 641-651.	3.0	60
123	Alternative stable states in host-phage dynamics. <i>Theoretical Ecology</i> , 2008, 1, 13-19.	0.4	92
124	Collective Decision Making in Bacterial Viruses. <i>Biophysical Journal</i> , 2008, 95, 2673-2680.	0.2	71
125	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
126	The Evolution of Dispersal in Reserve Networks. <i>American Naturalist</i> , 2007, 170, 59-78.	1.0	86

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127	Evolution, Interactions, and Biological Networks. PLoS Biology, 2007, 5, e11.	2.6	33
128	A neutral metapopulation model of biodiversity in river networks. Journal of Theoretical Biology, 2007, 245, 351-363.	0.8	94
129	Phage in the time of cholera. Lancet Infectious Diseases, The, 2006, 6, 257-258.	4.6	2
130	Size and scaling of predator-prey dynamics. Ecology Letters, 2006, 9, 548-557.	3.0	90
131	A Null Model of Morphospace Occupation. American Naturalist, 2005, 166, E1-E13.	1.0	68
132	Coevolutionary arms races between bacteria and bacteriophage. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9535-9540.	3.3	245
133	Dynamics of a contact process with ontogeny. Physical Review E, 2004, 70, 021915.	0.8	0
134	Scale-dependence of resource-biodiversity relationships. Journal of Theoretical Biology, 2003, 225, 205-214.	0.8	9
135	Packing-limited growth of irregular objects. Physical Review E, 2003, 67, 016117.	0.8	15
136	Packing-limited growth. Physical Review E, 2002, 65, 056108.	0.8	47
137	Re-examination of the $\frac{3}{4}$ -law of Metabolism. Journal of Theoretical Biology, 2001, 209, 9-27.	0.8	521
138	An Algorithm-Independent Definition of Damage Spreading—Application to Directed Percolation. Journal of Statistical Physics, 1997, 88, 617-636.	0.5	30
139	Disease-Dependent Interaction Policies to Support Health and Economic Outcomes During the COVID-19 Epidemic. SSRN Electronic Journal, 0, , .	0.4	2