

Using network analysis to explore co-occurrence patterns

ISME Journal

6, 343-351

DOI: [10.1038/ismej.2011.119](https://doi.org/10.1038/ismej.2011.119)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Microbial control over carbon cycling in soil. <i>Frontiers in Microbiology</i> , 2012, 3, 348.	1.5	978
2	Fundamentals of Microbial Community Resistance and Resilience. <i>Frontiers in Microbiology</i> , 2012, 3, 417.	1.5	1,131
3	Computational systems biology and in silico modeling of the human microbiome. <i>Briefings in Bioinformatics</i> , 2012, 13, 769-780.	3.2	83
4	From Animalcules to an Ecosystem: Application of Ecological Concepts to the Human Microbiome. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2012, 43, 137-155.	3.8	68
5	Co-Occurrence Patterns of Plants and Soil Bacteria in the High-Alpine Subnival Zone Track Environmental Harshness. <i>Frontiers in Microbiology</i> , 2012, 3, 347.	1.5	54
7	Microbial interactions: from networks to models. <i>Nature Reviews Microbiology</i> , 2012, 10, 538-550.	13.6	2,693
8	Predicting bacterial community assemblages using an artificial neural network approach. <i>Nature Methods</i> , 2012, 9, 621-625.	9.0	159
9	Lineage-dependent ecological coherence in bacteria. <i>FEMS Microbiology Ecology</i> , 2012, 81, 574-582.	1.3	28
10	Effects of season and experimental warming on the bacterial community in a temperate mountain forest soil assessed by 16S rRNA gene pyrosequencing. <i>FEMS Microbiology Ecology</i> , 2012, 82, 551-562.	1.3	128
11	Modeling microbial community structure and functional diversity across time and space. <i>FEMS Microbiology Letters</i> , 2012, 332, 91-98.	0.7	38
12	Use of phytoplankton-derived dissolved organic carbon by different types of bacterioplankton. <i>Environmental Microbiology</i> , 2012, 14, 2348-2360.	1.8	214
13	Microbial community responses to anthropogenically induced environmental change: towards a systems approach. <i>Ecology Letters</i> , 2013, 16, 128-139.	3.0	258
14	Ecological Inferences from a deep screening of the complex bacterial consortia associated with the coral, <i>Porites astreoides</i> . <i>Molecular Ecology</i> , 2013, 22, 4349-4362.	2.0	59
15	Disturbance induced decoupling between host genetics and composition of the associated microbiome. <i>BMC Microbiology</i> , 2013, 13, 252.	1.3	119
16	Determining indicator taxa across spatial and seasonal gradients in the Columbia River coastal margin. <i>ISME Journal</i> , 2013, 7, 1899-1911.	4.4	149
17	Pathogen regulation of plant diversity via effective specialization. <i>Trends in Ecology and Evolution</i> , 2013, 28, 705-711.	4.2	80
18	Diversity patterns of uncultured Haptophytes unravelled by pyrosequencing in Naples Bay. <i>Molecular Ecology</i> , 2013, 22, 87-101.	2.0	70
19	Macroecological patterns of marine bacteria on a global scale. <i>Journal of Biogeography</i> , 2013, 40, 800-811.	1.4	53

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20	The soil resistome: The anthropogenic, the native, and the unknown. <i>Soil Biology and Biochemistry</i> , 2013, 63, 18-23.	4.2	153
21	Insights into functional bacterial diversity and its effects on Alpine bog ecosystem functioning. <i>Scientific Reports</i> , 2013, 3, 1955.	1.6	71
22	Fungal networks in yield-invigoring and -debilitating soils induced by prolonged potato monoculture. <i>Soil Biology and Biochemistry</i> , 2013, 65, 186-194.	4.2	197
23	From molecules to dynamic biological communities. <i>Biology and Philosophy</i> , 2013, 28, 241-259.	0.7	12
24	Metagenomics of Hydrocarbon Resource Environments Indicates Aerobic Taxa and Genes to be Unexpectedly Common. <i>Environmental Science & Technology</i> , 2013, 47, 10708-10717.	4.6	179
25	Exploring the interaction patterns in seasonal marine microbial communities with network analysis. , 2013, , .		2
26	123 of Metagenomics. , 2013, , 1-11.		1
27	High-throughput Sequencing: A Roadmap Toward Community Ecology. <i>Ecology and Evolution</i> , 2013, 3, 1125-1139.	0.8	36
28	Microbial modulators of soil carbon storage: integrating genomic and metabolic knowledge for global prediction. <i>Trends in Microbiology</i> , 2013, 21, 641-651.	3.5	429
29	Elucidating the microbial resuscitation cascade in biological soil crusts following a simulated rain event. <i>Environmental Microbiology</i> , 2013, 15, 2799-2815.	1.8	93
30	Upper Arctic Ocean water masses harbor distinct communities of heterotrophic flagellates. <i>Biogeosciences</i> , 2013, 10, 4273-4286.	1.3	33
31	Application of Natural Blends of Phytochemicals Derived from the Root Exudates of Arabidopsis to the Soil Reveal That Phenolic-related Compounds Predominantly Modulate the Soil Microbiome. <i>Journal of Biological Chemistry</i> , 2013, 288, 4502-4512.	1.6	452
32	A decade of seasonal dynamics and co-occurrences within freshwater bacterioplankton communities from eutrophic Lake Mendota, WI, USA. <i>ISME Journal</i> , 2013, 7, 680-684.	4.4	156
33	Detecting seasonal marine microbial communities with symmetrical non-negative matrix factorization. , 2013, , .		0
34	Parallel changes of taxonomic interaction networks in lacustrine bacterial communities induced by a poly-metallic perturbation. <i>Evolutionary Applications</i> , 2013, 6, 643-659.	1.5	30
35	Evidence of species recruitment and development of hot desert hypolithic communities. <i>Environmental Microbiology Reports</i> , 2013, 5, 219-224.	1.0	88
36	Diel gene expression profiles of a phosphorus limited mountain lake using metatranscriptomics. <i>Environmental Microbiology</i> , 2013, 15, 1190-1203.	1.8	41
37	Contrasts between the cryoconite and ice-marginal bacterial communities of Svalbard glaciers. <i>Polar Research</i> , 2013, 32, 19468.	1.6	46

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38	The Poultry-Associated Microbiome: Network Analysis and Farm-to-Fork Characterizations. PLoS ONE, 2013, 8, e57190.	1.1	104
40	Functional gene pyrosequencing and network analysis: an approach to examine the response of denitrifying bacteria to increased nitrogen supply in salt marsh sediments. Frontiers in Microbiology, 2013, 4, 342.	1.5	52
41	Microbial Competition in Polar Soils: A Review of an Understudied but Potentially Important Control on Productivity. Biology, 2013, 2, 533-554.	1.3	34
42	Bioinformatic Approaches Reveal Metagenomic Characterization of Soil Microbial Community. PLoS ONE, 2014, 9, e93445.	1.1	56
43	Pros and Cons of Ion-Torrent Next Generation Sequencing versus Terminal Restriction Fragment Length Polymorphism T-RFLP for Studying the Rumen Bacterial Community. PLoS ONE, 2014, 9, e101435.	1.1	63
44	Network topology reveals high connectance levels and few key microbial genera within soils. Frontiers in Environmental Science, 2014, 2, .	1.5	226
45	Bacteria dialog with Santa Rosalia: Are aggregations of cosmopolitan bacteria mainly explained by habitat filtering or by ecological interactions?. BMC Microbiology, 2014, 14, 284.	1.3	27
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47	Fluvial network organization imprints on microbial co-occurrence networks. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12799-12804.	3.3	193
48	Biogeography of anaerobic ammonia-oxidizing (anammox) bacteria. Frontiers in Microbiology, 2014, 5, 399.	1.5	160
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55	Endospores of thermophilic bacteria as tracers of microbial dispersal by ocean currents. ISME Journal, 2014, 8, 1153-1165.	4.4	139
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57	The microbiome of New World vultures. <i>Nature Communications</i> , 2014, 5, 5498.	5.8	264
58	Metagenomic analysis on seasonal microbial variations of activated sludge from a full-scale wastewater treatment plant over 4 years. <i>Environmental Microbiology Reports</i> , 2014, 6, 80-89.	1.0	159
59	The Potential of Metagenomic Approaches for Understanding Soil Microbial Processes. <i>Soil Science Society of America Journal</i> , 2014, 78, 3-10.	1.2	105
60	Linkage between bacterial and fungal rhizosphere communities in hydrocarbon-contaminated soils is related to plant phylogeny. <i>ISME Journal</i> , 2014, 8, 331-343.	4.4	190
61	Interactions in the microbiome: communities of organisms and communities of genes. <i>FEMS Microbiology Reviews</i> , 2014, 38, 90-118.	3.9	174
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63	Taxonomic relatedness shapes bacterial assembly in activated sludge of globally distributed wastewater treatment plants. <i>Environmental Microbiology</i> , 2014, 16, 2421-2432.	1.8	333
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68	Pyrosequencing analysis of bacterial community and assembly in activated sludge samples from different geographic regions in China. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 9119-9128.	1.7	55
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71	Meta-Analysis and Other Approaches for Synthesizing Structured and Unstructured Data in Plant Pathology. <i>Annual Review of Phytopathology</i> , 2014, 52, 453-476.	3.5	38
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76	Spatial heterogeneity and co-occurrence patterns of human mucosal-associated intestinal microbiota. <i>ISME Journal</i> , 2014, 8, 881-893.	4.4	206
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78	Network construction and structure detection with metagenomic count data. <i>BioData Mining</i> , 2015, 8, 40.	2.2	8
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80	Subgingival microbiome in patients with healthy and ailing dental implants. <i>Scientific Reports</i> , 2015, 5, 10948.	1.6	101
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83	Diversity of key players in the microbial ecosystems of the human body. <i>Scientific Reports</i> , 2015, 5, 15920.	1.6	30
84	Phylogeny-structured carbohydrate metabolism across microbiomes collected from different units in wastewater treatment process. <i>Biotechnology for Biofuels</i> , 2015, 8, 172.	6.2	17
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88	Synchronized dynamics of bacterial niche-specific functions during biofilm development in a cold seep brine pool. <i>Environmental Microbiology</i> , 2015, 17, 4089-4104.	1.8	24
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90	10 Years Later. <i>Advances in Ecological Research</i> , 2015, 53, 1-53.	1.4	43
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92	Microbial responses to changes in flow status in temporary headwater streams: a cross-system comparison. <i>Frontiers in Microbiology</i> , 2015, 6, 522.	1.5	41

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94	A network-based approach to disturbance transmission through microbial interactions. <i>Frontiers in Microbiology</i> , 2015, 6, 1182.	1.5	81
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103	Bipartite graphs for metagenomic data analysis and visualization. , 2015, , .		1
104	Environmental drivers of the distribution of nitrogen functional genes at a watershed scale. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	38
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117	Roles of Thermophiles and Fungi in Bitumen Degradation in Mostly Cold Oil Sands Outcrops. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6825-6838.	1.4	41
118	Is Planktonic Diversity Well Recorded in Sedimentary DNA? Toward the Reconstruction of Past Protistan Diversity. <i>Microbial Ecology</i> , 2015, 70, 865-875.	1.4	55
119	Aggregate-related changes in network patterns of nematodes and ammonia oxidizers in an acidic soil. <i>Soil Biology and Biochemistry</i> , 2015, 88, 101-109.	4.2	64
120	Multilayer network representation of membrane potential and cytosolic calcium concentration dynamics in beta cells. <i>Chaos, Solitons and Fractals</i> , 2015, 80, 76-82.	2.5	26
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124	Metagenomic and network analysis reveal wide distribution and co-occurrence of environmental antibiotic resistance genes. <i>ISME Journal</i> , 2015, 9, 2490-2502.	4.4	928
125	A framework for establishing predictive relationships between specific bacterial 16S rRNA sequence abundances and biotransformation rates. <i>Water Research</i> , 2015, 70, 471-484.	5.3	31
126	Metabolic dependencies drive species co-occurrence in diverse microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6449-6454.	3.3	588
127	Relationship between phylogenetic and nutritional diversity in Arctic (Kandalaksha Bay) seawater planktonic bacteria. <i>Annals of Microbiology</i> , 2015, 65, 2405-2414.	1.1	9
128	Ecology and exploration of the rare biosphere. <i>Nature Reviews Microbiology</i> , 2015, 13, 217-229.	13.6	926
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131	Athletic equipment microbiota are shaped by interactions with human skin. <i>Microbiome</i> , 2015, 3, 25.	4.9	36
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134	Microbial Invasions: The Process, Patterns, and Mechanisms. <i>Trends in Microbiology</i> , 2015, 23, 719-729.	3.5	330
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136	The dynamics of the bacterial diversity in the redox transition and anoxic zones of the Cariaco Basin assessed by parallel tag sequencing. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv088.	1.3	13
137	Diversity and complexity of microbial communities from a chlor-alkali tailings dump. <i>Soil Biology and Biochemistry</i> , 2015, 90, 101-110.	4.2	54
138	Soil particle size fractions harbour distinct microbial communities and differ in potential for microbial mineralisation of organic pollutants. <i>Soil Biology and Biochemistry</i> , 2015, 90, 255-265.	4.2	99
139	Bacterial networks and co-occurrence relationships in the lettuce root microbiota. <i>Environmental Microbiology</i> , 2015, 17, 239-252.	1.8	241
140	Dynamics in microbial communities: unraveling mechanisms to identify principles. <i>ISME Journal</i> , 2015, 9, 1488-1495.	4.4	257
141	A comparison of the wet and dry season DNA-based soil invertebrate community characteristics in large patches of the bromeliad <i>Bromelia pinguin</i> in a primary forest in Costa Rica. <i>Applied Soil Ecology</i> , 2015, 87, 99-107.	2.1	19
142	Crop monoculture rather than agriculture reduces the spatial turnover of soil bacterial communities at a regional scale. <i>Environmental Microbiology</i> , 2015, 17, 678-688.	1.8	71
143	Co-occurrence correlations of heavy metals in sediments revealed using network analysis. <i>Chemosphere</i> , 2015, 119, 1305-1313.	4.2	43
144	Protistan diversity in a permanently stratified meromictic lake (Lake <i>Atsee</i> , <i>SW</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	4.8	39
145	Bacterial assembly and temporal dynamics in activated sludge of a full-scale municipal wastewater treatment plant. <i>ISME Journal</i> , 2015, 9, 683-695.	4.4	393
146	Network analysis reveals that bacteria and fungi form modules that correlate independently with soil parameters. <i>Environmental Microbiology</i> , 2015, 17, 2677-2689.	1.8	166
147	5. Exploring Diversity of Soil Microorganisms: A Multidimensional Approach. , 2016, , 66-86.		0

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157	Anaerobic Biodegradation of Hydrocarbons: Metagenomics and Metabolomics. , 2016, , 1-42.		3
158	Bacterial Communities in the Rhizosphere of Amilaceous Maize (Zea mays L.) as Assessed by Pyrosequencing. Frontiers in Plant Science, 2016, 7, 1016.	1.7	58
159	Multiple Assembly Rules Drive the Co-occurrence of Orthopteran and Plant Species in Grasslands: Combining Network, Functional and Phylogenetic Approaches. Frontiers in Plant Science, 2016, 7, 1224.	1.7	6
160	Spatial scale drives patterns in soil bacterial diversity. Environmental Microbiology, 2016, 18, 2039-2051.	1.8	194
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163	Determinants of bacterial communities in Canadian agroforestry systems. Environmental Microbiology, 2016, 18, 1805-1816.	1.8	202
164	Microbial succession in response to pollutants in batch-enrichment culture. Scientific Reports, 2016, 6, 21791.	1.6	87
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168	Describe, understand and predict: why do we need networks in ecology?. <i>Functional Ecology</i> , 2016, 30, 1878-1882.	1.7	86
169	Hydrocarbon degraders establish at the costs of microbial richness, abundance and keystone taxa after crude oil contamination in permafrost environments. <i>Scientific Reports</i> , 2016, 6, 37473.	1.6	58
170	Inferior adaptation of bay sediments in a eutrophic shallow lake to winter season for organic matter decomposition. <i>Environmental Pollution</i> , 2016, 219, 794-803.	3.7	6
171	Bacterial and protist community changes during a phytoplankton bloom. <i>Limnology and Oceanography</i> , 2016, 61, 198-213.	1.6	22
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1609	Bacterial Microbiota and Soil Fertility of <i>Crocus sativus</i> L. Rhizosphere in the Presence and Absence of <i>Fusarium</i> spp.. <i>Land</i> , 2022, 11, 2048.	1.2	2
1610	Maize-soybean intercropping facilitates chemical and microbial transformations of phosphorus fractions in a calcareous soil. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1611	Depth-dependent patterns of soil microbial community in the E-waste dismantling area. <i>Journal of Hazardous Materials</i> , 2023, 444, 130379.	6.5	13
1612	Environmental factors and stochasticity affect the fungal community structures in the water and sediments of Hulun Lake, China. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	3
1613	Spatial and temporal change determined co-occurrence networks stability and community assembly processes of epipelagic seawater microbial community in the Nordic Sea. <i>Science of the Total Environment</i> , 2023, 859, 160321.	3.9	3
1614	Diversity and metabolic potentials of microbial communities associated with pollinator and cheater fig wasps in fig-fig wasp mutualism system. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
1615	Investigating the Assemblages of Two Groups of Collembola (Strong Furca and Weak Furca) under Different Agricultural Management Systems, Northeastern China. <i>Diversity</i> , 2022, 14, 994.	0.7	1
1616	Response of bacterial communities to shrub encroachment and forage planting in alpine grassland of the Qinghai-Tibetan Plateau. <i>Ecological Engineering</i> , 2023, 186, 106837.	1.6	1
1617	Long-term effects of biochar application on rhizobacteria community and winter wheat growth on the Loess Plateau in China. <i>Geoderma</i> , 2023, 429, 116250.	2.3	7
1618	Correlations among core species corresponding to the clinical staging of periodontitis. <i>Biocell</i> , 2023, 47, 431-439.	0.4	0
1619	Elevational distribution patterns and drivers of soil microbial diversity in the Sygera Mountains, southeastern Tibet, China. <i>Catena</i> , 2023, 221, 106738.	2.2	7
1620	Arsenic-triggered bacterial minorities correlate with arsenic accumulation in cabbage. <i>Geoderma</i> , 2023, 429, 116278.	2.3	0
1621	Presence and distribution of triazine herbicides and their effects on microbial communities in the Laizhou Bay, Northern China. <i>Marine Pollution Bulletin</i> , 2023, 186, 114460.	2.3	7
1622	Comparison of the microbial communities in pits with different sealing methods for Chinese strong-flavor liquor production. <i>LWT - Food Science and Technology</i> , 2023, 173, 114248.	2.5	0
1623	Metagenomic insights into the influence of thallium spill on sediment microbial community. <i>Environmental Pollution</i> , 2023, 317, 120660.	3.7	8
1624	Trophic interactions regulate microbial responses to environmental conditions and partially counteract nitrogen transformation potential in urban river bends. <i>Journal of Environmental Management</i> , 2023, 327, 116889.	3.8	1
1625	Spatio-temporal succession of microbial communities in plastisphere and their potentials for plastic degradation in freshwater ecosystems. <i>Water Research</i> , 2023, 229, 119406.	5.3	26

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1626	Changes in diversity patterns and assembly processes of soil nematode communities during forest secondary succession on the Loess Plateau. <i>Forest Ecology and Management</i> , 2023, 529, 120734.	1.4	3
1627	Taxonomic and functional dynamics of the soil microbiome from a tropical dry forest in kraft lignin-amended microcosms. <i>Applied Soil Ecology</i> , 2023, 183, 104766.	2.1	0
1628	Microbial community dynamics responding to nutrient allocation associated with soybean cultivar "Jake" ozone adaptation. <i>Science of the Total Environment</i> , 2023, 864, 161008.	3.9	3
1629	Predatory protists play predominant roles in suppressing soil-borne fungal pathogens under organic fertilization regimes. <i>Science of the Total Environment</i> , 2023, 863, 160986.	3.9	12
1630	Rhizosphere effect and water constraint jointly determined the roles of microorganism in soil phosphorus cycling in arid desert regions. <i>Catena</i> , 2023, 222, 106809.	2.2	6
1631	Nitrogen transformation promotes the anaerobic degradation of PAHs in water level fluctuation zone of the Three Gorges Reservoir in Yangtze River, China: Evidences derived from in-situ experiment. <i>Science of the Total Environment</i> , 2023, 864, 161034.	3.9	3
1632	Novel insights into aerobic denitrifying bacterial communities augmented denitrification capacity and mechanisms in lake waters. <i>Science of the Total Environment</i> , 2023, 864, 161011.	3.9	7
1633	Soil nutrients shape the composition and function of fungal communities in abandoned ancient rice terraces. <i>Journal of Environmental Management</i> , 2023, 329, 117064.	3.8	7
1634	Natural vegetation regeneration facilitated soil organic carbon sequestration and microbial community stability in the degraded karst ecosystem. <i>Catena</i> , 2023, 222, 106856.	2.2	4
1635	A longitudinal census of the bacterial community in raw milk correlated with <i>Staphylococcus aureus</i> clinical mastitis infections in dairy cattle. <i>Animal Microbiome</i> , 2022, 4, .	1.5	3
1636	Dietary Supplementation of Fruit from <i>Nitraria tangutorum</i> Improved Immunity and Abundance of Beneficial Ruminal Bacteria in Hu Sheep. <i>Animals</i> , 2022, 12, 3211.	1.0	3
1637	Abundant fungi dominate the complexity of microbial networks in soil of contaminated site: High-precision community analysis by full-length sequencing. <i>Science of the Total Environment</i> , 2023, 861, 160563.	3.9	8
1638	Interactions among heavy metals and methane-metabolizing microorganisms and their effects on methane emissions in Dajiuhe peatland. <i>Environmental Science and Pollution Research</i> , 0, , .	2.7	0
1639	Microbial community diversity and function analysis of <i>Aconitum carmichaelii</i> Debeaux in rhizosphere soil of farmlands in Southwest China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1640	Phagotrophic protist-mediated control of <i>Polymyxa graminis</i> in the wheat rhizosphere. <i>Plant and Soil</i> , 2023, 485, 333-347.	1.8	5
1641	The Endophytic Root Microbiome Is Different in Healthy and <i>Ralstonia solanacearum</i> -Infected Plants and Is Regulated by a Consortium Containing Beneficial Endophytic Bacteria. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5
1642	Inference of dynamic interaction networks: A comparison between Lotka-Volterra and multivariate autoregressive models. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	2
1643	Methane supply drives prokaryotic community assembly and networks at cold seeps of the South China Sea. <i>Molecular Ecology</i> , 2023, 32, 660-679.	2.0	9

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1646	Effects of Moss-Dominated Biocrusts on Soil Microbial Community Structure in an Ionic Rare Earth Tailings Area of Southern China. <i>Toxics</i> , 2022, 10, 782.	1.6	0
1647	A national-scale distribution of organochlorine pesticides (OCPs) in cropland soils and major types of food crops in China: Co-occurrence and associated risks. <i>Science of the Total Environment</i> , 2023, 861, 160637.	3.9	6
1648	Combined organic-inorganic fertilization builds higher stability of soil and root microbial networks than exclusive mineral or organic fertilization. <i>Soil Ecology Letters</i> , 2023, 5, .	2.4	7
1649	Prokaryotic and eukaryotic microbial communities associated with coral species have high host specificity in the South China Sea. <i>Science of the Total Environment</i> , 2023, 867, 161185.	3.9	7
1650	<i>Quercus ilex</i> Phyllosphere Microbiome Environmental-Driven Structure and Composition Shifts in a Mediterranean Contex. <i>Plants</i> , 2022, 11, 3528.	1.6	4
1651	Ecological co-occurrence and soil physicochemical factors drive the archaeal community in Amazonian soils. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	0
1652	ITS Metabarcoding Reveals the Effects of Oregano Essential Oil on <i>Fusarium oxysporum</i> and Other Fungal Species in Soil Samples. <i>Plants</i> , 2023, 12, 62.	1.6	1
1653	Microbial-Based Products to Control Soil-Borne Pathogens: Methods to Improve Efficacy and to Assess Impacts on Microbiome. <i>Microorganisms</i> , 2023, 11, 224.	1.6	6
1654	Diversity and Biogeography of Soil Bacterial Communities. <i>Climate Change Management</i> , 2023, , 1-13.	0.6	0
1655	Enhanced biodegradation of PAHs by biochar and a TiO ₂ @biochar composite under light irradiation: Photocatalytic mechanism, toxicity evaluation and ecological response. <i>Chemical Engineering Journal</i> , 2023, 458, 141495.	6.6	19
1656	Altered Organic Matter Chemical Functional Groups and Bacterial Community Composition Promote Crop Yield under Integrated Soil-Crop Management System. <i>Agriculture (Switzerland)</i> , 2023, 13, 134.	1.4	3
1657	Response of Microbial Communities on Cathode with Different Potentials in a Single-Chamber Reactor. <i>Current Microbiology</i> , 2023, 80, .	1.0	0
1658	A guide for comparing microbial co-occurrence networks. , 2023, 2, .		4
1659	Continuous-cropping-tolerant soybean cultivars alleviate continuous cropping obstacles by improving structure and function of rhizosphere microorganisms. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1660	Urbanization increases stochasticity and reduces the ecological stability of microbial communities in amphibian hosts. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
1661	Preliminary analysis of mucosal and salivary bacterial communities in oral lichen planus. <i>Oral Diseases</i> , 2023, 29, 2710-2722.	1.5	0
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1664	Response of soil microbial communities and rice yield to nitrogen reduction with green manure application in karst paddy areas. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1665	Effect of metal pollution on the distribution and co-occurrence pattern of bacterial, archaeal and fungal communities throughout the soil profiles. <i>Chemosphere</i> , 2023, 315, 137692.	4.2	8
1666	Enhancement of nitrogen fixation and diazotrophs by long-term polychlorinated biphenyl contamination in paddy soil. <i>Journal of Hazardous Materials</i> , 2023, 446, 130697.	6.5	5
1667	Changes in bacterial diversity, co-occurrence pattern, and potential pathogens following digestate fertilization: Extending pathogen management to field for anaerobic digestion of livestock manure. <i>Waste Management</i> , 2023, 158, 107-115.	3.7	4
1668	Conductive carrier promotes synchronous biofilm formation and granulation of anammox bacteria. <i>Journal of Hazardous Materials</i> , 2023, 447, 130754.	6.5	10
1669	Microbial population properties in the hierarchically structured aerobic granular sludge: Phenotype and genotype. <i>Science of the Total Environment</i> , 2023, 867, 161164.	3.9	4
1670	Soil bacterial community structure and functions but not assembly processes are affected by the conversion from monospecific <i>Cunninghamia lanceolata</i> plantations to mixed plantations. <i>Applied Soil Ecology</i> , 2023, 185, 104775.	2.1	4
1671	The putative maintaining mechanism of gut bacterial ecosystem in giant pandas and its potential application in conservation. <i>Evolutionary Applications</i> , 2023, 16, 36-47.	1.5	2
1672	Structure and Function Analysis of Cultivated <i>Meconopsis integrifolia</i> Soil Microbial Community Based on High-Throughput Sequencing and Culturability. <i>Biology</i> , 2023, 12, 160.	1.3	2
1674	Measuring Spatiotemporal Civil War Dimensions Using Community-Based Dynamic Network Representation (CoDNet). <i>IEEE Transactions on Computational Social Systems</i> , 2024, 11, 1506-1516.	3.2	0
1675	Grass-microbial inter-domain ecological networks associated with alpine grassland productivity. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
1676	Divergence of epibacterial community assemblage correlates with malformation disease severity in <i>Saccharina japonica</i> seedlings. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	2
1677	Changes in physiological profiles and co-occurrence patterns of soil microbial community following exposure to nanoceria and ionic cerium. <i>Environmental Science: Nano</i> , 2023, 10, 879-890.	2.2	1
1678	Response of Rhizosphere Bacterial Communities to Near-Natural Forest Management and Tree Species within Chinese Fir Plantations. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5
1679	Seasonal succession of microbial community co-occurrence patterns and community assembly mechanism in coal mining subsidence lakes. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	8
1680	A synthetic community of siderophore-producing bacteria increases soil selenium bioavailability and plant uptake through regulation of the soil microbiome. <i>Science of the Total Environment</i> , 2023, 871, 162076.	3.9	7
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1684	Relation analysis of bacterial community in soils of coal mines with potential ecological risk from heavy metals. <i>Environmental Technology and Innovation</i> , 2023, 30, 103125.	3.0	2
1685	Natural restoration enhances soil multitrophic network complexity and ecosystem functions in the Loess Plateau. <i>Catena</i> , 2023, 226, 107059.	2.2	3
1686	Biochar loaded with bacteria enhanced Cd/Zn phytoextraction by facilitating plant growth and shaping rhizospheric microbial community. <i>Environmental Pollution</i> , 2023, 327, 121559.	3.7	9
1687	Effects of tillage management on cbbL-carrying bacteria and soil organic carbon dynamics across aggregate size classes in the farmland of North China Plain. <i>Ecological Indicators</i> , 2023, 150, 110213.	2.6	7
1688	Pollution caused by mining reshaped the structure and function of bacterial communities in China's largest ion-adsorption rare earth mine watershed. <i>Journal of Hazardous Materials</i> , 2023, 451, 131221.	6.5	5
1689	Concurrent reductive decontamination of chromium (VI) and uranium (VI) in groundwater by Fe(0)-based autotrophic bioprocess. <i>Journal of Hazardous Materials</i> , 2023, 452, 131222.	6.5	2
1690	Distinct community assembly processes and habitat specialization driving the biogeographic patterns of abundant and rare bacterioplankton in a brackish coastal lagoon. <i>Science of the Total Environment</i> , 2023, 879, 163109.	3.9	8
1691	Specialist species of fungi and bacteria are more important than the intermediate and generalist species in near-urban agricultural soils. <i>Applied Soil Ecology</i> , 2023, 188, 104894.	2.1	1
1692	Weathering extents and anthropogenic influences shape the soil bacterial community along a subsurface zonation. <i>Science of the Total Environment</i> , 2023, 876, 162570.	3.9	1
1693	Rare microbial communities drive ecosystem multifunctionality in acidic soils of southern China. <i>Applied Soil Ecology</i> , 2023, 189, 104895.	2.1	8
1694	Soil bacterial communities of paddy are dependent on root compartment niches but independent of growth stages from Mollisols of Northeast China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
1695	Assembly processes of bacterial and fungal communities in metal(loid)s smelter soil. <i>Journal of Hazardous Materials</i> , 2023, 451, 131153.	6.5	9
1698	Microbial dynamics and bioreactor performance are interlinked with organic matter removal from wastewater treatment plant effluent. <i>Bioresource Technology</i> , 2023, 372, 128659.	4.8	2
1699	Disturbance and restoration of soil microbial communities after in-situ thermal desorption in a chlorinated hydrocarbon contaminated site. <i>Journal of Hazardous Materials</i> , 2023, 448, 130870.	6.5	8
1700	Interactions between dissolved organic matter and the microbial community are modified by microplastics and heat waves. <i>Journal of Hazardous Materials</i> , 2023, 448, 130868.	6.5	13
1701	Linking soil microbial community to the chemical composition of dissolved organic matter in a boreal forest during freeze-thaw cycles. <i>Geoderma</i> , 2023, 431, 116359.	2.3	5
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1704	Glacial Influence Affects Modularity in Bacterial Community Structure in Three Deep Andean North-Patagonian Lakes. <i>Microbial Ecology</i> , 2023, 86, 1869-1880.	1.4	1
1705	Non-additive effects of bamboo-derived biochar and dicyandiamide on soil greenhouse gas emissions, enzyme activity and bacterial community. <i>Industrial Crops and Products</i> , 2023, 194, 116385.	2.5	8
1706	Carbon amendment rather than nitrate fertilization dominated the reassembly of the total, denitrifying, and DNRA bacterial community in the anaerobic subsoil. <i>Journal of Soils and Sediments</i> , 2023, 23, 1913-1926.	1.5	0
1707	Dietary supplementation of solubles from shredded, steam-exploded pine particles modulates cecal microbiome composition in broiler chickens. <i>Journal of Animal Science and Technology</i> , 0, , .	0.8	1
1708	Co-cultivation of microalgae-activated sludge for municipal wastewater treatment: Exploring the performance, microbial co-occurrence patterns, microbiota dynamics and function during the startup stage. <i>Bioresource Technology</i> , 2023, 374, 128733.	4.8	14
1709	Inter-basin water diversion homogenizes microbial communities mainly through stochastic assembly processes. <i>Environmental Research</i> , 2023, 223, 115473.	3.7	10
1710	Environmental DNA metabarcoding reveals the influence of human activities on microeukaryotic plankton along the Chinese coastline. <i>Water Research</i> , 2023, 233, 119730.	5.3	12
1711	Temporal assessment of N-cycle microbial functions in a tropical agricultural soil using gene co-occurrence networks. <i>PLoS ONE</i> , 2023, 18, e0281442.	1.1	2
1712	Assembly and enrichment of rhizosphere and bulk soil microbiomes in <i>Robinia pseudoacacia</i> plantations during long-term vegetation restoration. <i>Applied Soil Ecology</i> , 2023, 187, 104835.	2.1	3
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1716	Geographical shifts in the successional dynamics of inland dune shrub communities. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	0
1717	Insights into the Methodological, Biotic and Abiotic Factors Influencing the Characterization of Xylem-Inhabiting Microbial Communities of Olive Trees. <i>Plants</i> , 2023, 12, 912.	1.6	5
1718	Cooperation of arbuscular mycorrhizal fungi and bacteria to facilitate the host plant growth dependent on soil pH. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
1719	Best practices for generating and analyzing 16S rRNA amplicon data to track coral microbiome dynamics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
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1722	Bacterial taxonomic and functional profiles from Bohai Sea to northern Yellow Sea. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
1723	Network analysis of 16S rRNA sequences suggests microbial keystone taxa contribute to marine N ₂ O cycling. <i>Communications Biology</i> , 2023, 6, .	2.0	0
1724	Dietary intake of table olives exerts antihypertensive effects in association with changes in gut microbiota in spontaneously hypertensive rats. <i>Food and Function</i> , 2023, 14, 2793-2806.	2.1	2
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1729	CNN_FunBar: Advanced Learning Technique for Fungi ITS Region Classification. <i>Genes</i> , 2023, 14, 634.	1.0	2
1730	Multivariate statistical and bioinformatic analyses for the seasonal variations of actinobacterial community structures in a drinking water reservoir. <i>Journal of Environmental Sciences</i> , 2024, 137, 1-17.	3.2	3
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1732	Bacterial diversity and co-occurrence patterns differ across a world-wide spatial distribution of habitats in glacier ecosystems. <i>Functional Ecology</i> , 2023, 37, 1520-1535.	1.7	2
1733	Assembly processes underlying bacterial community differentiation among geographically close mangrove forests. , 2023, 2, 73-88.		3
1734	Microbial community structure in rice rhizosheaths under drought stress. <i>Journal of Plant Ecology</i> , 2023, 16, .	1.2	3
1735	Seasonal variations of soil bacterial and fungal communities in a subtropical Eucalyptus plantation and their responses to throughfall reduction. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
1736	Diversity and assembly of root-associated microbiomes of rubber trees. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
1737	Bacterial co-occurrence patterns are more complex but less stable than archaea in enhanced oil recovery applied oil reservoirs. <i>Process Biochemistry</i> , 2023, 130, 40-49.	1.8	3
1738	Meadow transformations alter above- and below-ground ecological networks and ecosystem multifunctionality. <i>Functional Ecology</i> , 0, , .	1.7	0
1739	Facilitative interaction networks in experimental microbial community dynamics. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
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1742	Effects of biochar addition on aeolian soil microbial community assembly and structure. Applied Microbiology and Biotechnology, 0, , .	1.7	0
1743	An introduction to current and future aspect on growth promoting microbiome. , 2023, , 87-110.		0
1744	Soil microbial diversity, soil health and agricultural sustainability. , 2023, , 107-126.		1
1815	Rebound effects of energy efficiency improvement based on computable general equilibrium models: a systematic review. Energy Efficiency, 2023, 16, .	1.3	0
1961	An Overview of Biodiversity and Network Modeling Approaches: Applications to Sedimentary DNA Records. Developments in Paleoenvironmental Research, 2023, , 379-391.	7.5	0
1994	Physiological and biochemical methods for studying soil biota and their functions. , 2024, , 193-227.		0
2018	Microbial-Based Products and Soil Management Practices to Control Nematodes in Organic Horticultural Crops. Sustainability in Plant and Crop Protection, 2024, , 3-31.	0.2	0