

Quantifying spatiotemporal variability and noise in absolute replicate sampling

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Spatial metagenomic characterization of microbial biogeography in the gut. <i>Nature Biotechnology</i> , 2019, 37, 877-883.	17.5	103
2	Scalable and cost-effective ribonuclease-based rRNA depletion for transcriptomics. <i>Nucleic Acids Research</i> , 2020, 48, e20-e20.	14.5	42
3	Predictive interactome modeling for precision microbiome engineering. <i>Current Opinion in Chemical Engineering</i> , 2020, 30, 77-85.	7.8	16
4	How to Count Our Microbes? The Effect of Different Quantitative Microbiome Profiling Approaches. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 403.	3.9	65
5	Recording mobile DNA in the gut microbiota using an <i>Escherichia coli</i> CRISPR-Cas spacer acquisition platform. <i>Nature Communications</i> , 2020, 11, 95.	12.8	47
6	The quest for absolute abundance: The use of internal standards for DNA-based community ecology. <i>Molecular Ecology Resources</i> , 2021, 21, 30-43.	4.8	42
7	Reanalysis of the Mars500 experiment reveals common gut microbiome alterations in astronauts induced by long-duration confinement. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2223-2235.	4.1	12
8	Robust direct digital-to-biological data storage in living cells. <i>Nature Chemical Biology</i> , 2021, 17, 246-253.	8.0	51
9	Gradient Internal Standard Method for Absolute Quantification of Microbial Amplicon Sequencing Data. <i>MSystems</i> , 2021, 6, .	3.8	11
11	CODY enables quantitatively spatiotemporal predictions on in vivo gut microbial variability induced by diet intervention. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	17
13	Dynamic Bayesian Networks for Integrating Multi-omics Time Series Microbiome Data. <i>MSystems</i> , 2021, 6, .	3.8	19
14	Probiotics-induced changes in gut microbial composition and its effects on cognitive performance after stress: exploratory analyses. <i>Translational Psychiatry</i> , 2021, 11, 300.	4.8	50
15	Progress and Prospects of Mycorrhizal Fungal Diversity in Orchids. <i>Frontiers in Plant Science</i> , 2021, 12, 646325.	3.6	32
16	Mining microbes for mental health: Determining the role of microbial metabolic pathways in human brain health and disease. <i>Neuroscience and Biobehavioral Reviews</i> , 2021, 125, 698-761.	6.1	80
17	Measuring the absolute abundance of the microbiome by adding yeast containing 16S rRNA gene from a hyperthermophile. <i>MicrobiologyOpen</i> , 2021, 10, e1220.	3.0	3
19	Characterizing Microbiomes via Sequencing of Marker Loci: Techniques To Improve Throughput, Account for Cross-Contamination, and Reduce Cost. <i>MSystems</i> , 2021, 6, e0029421.	3.8	5
21	Next Generation Microbiome Research: Identification of Keystone Species in the Metabolic Regulation of Host-Gut Microbiota Interplay. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 719072.	3.7	21
22	A Simple, Cost-Effective, and Automation-Friendly Direct PCR Approach for Bacterial Community Analysis. <i>MSystems</i> , 2021, 6, e0022421.	3.8	6

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23	A quantitative sequencing framework for absolute abundance measurements of mucosal and luminal microbial communities. <i>Nature Communications</i> , 2020, 11, 2590.	12.8	74
26	Thermodynamic inference of data manifolds. <i>Physical Review Research</i> , 2020, 2, .	3.6	8
28	Links between Leafstalk Biomass of (<i>Cremastra appendiculata</i>) and Elevation by Big Data of Long-time Wild Investigation in Mei-County. <i>Journal of Drug Delivery and Therapeutics</i> , 2020, 10, 55-60.	0.5	0
29	Engineering living and regenerative fungal-bacterial biocomposite structures. <i>Nature Materials</i> , 2022, 21, 471-478.	27.5	47
30	High-throughput identification and quantification of single bacterial cells in the microbiota. <i>Nature Communications</i> , 2022, 13, 863.	12.8	8
31	Two <i>Blautia</i> Species Associated with Visceral Fat Accumulation: A One-Year Longitudinal Study. <i>Biology</i> , 2022, 11, 318.	2.8	16
32	Growth promotion and antibiotic induced metabolic shifts in the chicken gut microbiome. <i>Communications Biology</i> , 2022, 5, 293.	4.4	25
33	Standards for Collection, Preservation, and Transportation of Fecal Samples in TCM Clinical Trials. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 783682.	3.9	7
37	The systemic anti-microbiota IgG repertoire can identify gut bacteria that translocate across gut barrier surfaces. <i>Science Translational Medicine</i> , 2022, 14, .	12.4	21
38	Spatial, temporal and technical variability in the diversity of prokaryotes and fungi in agricultural soils. <i>Frontiers in Soil Science</i> , 0, 2, .	2.2	3
39	Absolute quantification and genome-centric analyses elucidate the dynamics of microbial populations in anaerobic digesters. <i>Water Research</i> , 2022, 224, 119049.	11.3	9
40	Decreased Gut Microbiome Tryptophan Metabolism and Serotonergic Signaling in Patients With Persistent Mental Health and Gastrointestinal Symptoms After COVID-19. <i>Clinical and Translational Gastroenterology</i> , 2022, 13, e00524.	2.5	12
41	Microbiota imbalance induced by dietary sugar disrupts immune-mediated protection from metabolic syndrome. <i>Cell</i> , 2022, 185, 3501-3519.e20.	28.9	102
43	SynMADE: synthetic microbiota across diverse ecosystems. <i>Trends in Biotechnology</i> , 2022, 40, 1405-1414.	9.3	20
44	Gut bacteria comparison between wild and captive neotropical otters. <i>Universitas Scientiarum</i> , 2020, 25, 359-384.	0.4	1
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48	High-throughput microbial culturomics using automation and machine learning. <i>Nature Biotechnology</i> , 2023, 41, 1424-1433.	17.5	39
49	Quantitative microbiome profiling reveals the developmental trajectory of the chicken gut microbiota and its connection to host metabolism. , 2023, 2, .		12

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50	EMBED: Essential MicroBiomE Dynamics, a dimensionality reduction approach for longitudinal microbiome studies. Npj Systems Biology and Applications, 2023, 9, .	3.0	0
51	Field and laboratory guidelines for reliable bioinformatic and statistical analysis of bacterial shotgun metagenomic data. Critical Reviews in Biotechnology, 0, , 1-19.	9.0	1
53	Qu-omics elucidates the formation and spatio-temporal differentiation mechanism underlying the microecology of high temperature Daqu. Food Chemistry, 2024, 438, 137988.	8.2	3