

Simple statistical identification and removal of contaminated metagenomics data

Microbiome

6, 226

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Citation Report

#	ARTICLE	IF	CITATIONS
1	PERFect: PERmutation Filtering test for microbiome data. <i>Biostatistics</i> , 2019, 20, 615-631.	0.9	34
2	Benchmarking Metagenomics Tools for Taxonomic Classification. <i>Cell</i> , 2019, 178, 779-794.	13.5	364
3	Cobble community DNA as a tool to monitor patterns of biodiversity within kelp forest ecosystems. <i>Molecular Ecology Resources</i> , 2019, 19, 1470-1485.	2.2	23
4	Characterization of fungal biodiversity and communities associated with the reef macroalga <i>Sargassum ilicifolium</i> reveals fungal community differentiation according to geographic locality and algal structure. <i>Marine Biodiversity</i> , 2019, 49, 2601-2608.	0.3	19
5	Unfolding the Human Milk Microbiome Landscape in the Omics Era. <i>Frontiers in Microbiology</i> , 2019, 10, 1378.	1.5	61
6	Detection of low-density <i>Plasmodium falciparum</i> infections using amplicon deep sequencing. <i>Malaria Journal</i> , 2019, 18, 219.	0.8	40
7	The Predominant Oral Microbiota Is Acquired Early in an Organized Pattern. <i>Scientific Reports</i> , 2019, 9, 10550.	1.6	65
8	Drivers and patterns of microbial community assembly in a Lyme disease vector. <i>Ecology and Evolution</i> , 2019, 9, 7768-7779.	0.8	30
9	Visualization of microbes by 16S in situ hybridization in term and preterm placentas without intraamniotic infection. <i>American Journal of Obstetrics and Gynecology</i> , 2019, 221, 146.e1-146.e23.	0.7	96
10	Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. <i>GigaScience</i> , 2019, 8, .	3.3	132
11	Captivity and Infection by the Fungal Pathogen <i>Batrachochytrium salamandrivorans</i> Perturb the Amphibian Skin Microbiome. <i>Frontiers in Microbiology</i> , 2019, 10, 1834.	1.5	39
12	Longitudinal microbiome profiling reveals impermanence of probiotic bacteria in domestic pigeons. <i>PLoS ONE</i> , 2019, 14, e0217804.	1.1	12
13	Role for the mammalian female reproductive tract microbiome in pregnancy outcomes. <i>Physiological Genomics</i> , 2019, 51, 390-399.	1.0	50
14	A single faecal microbiota transplantation modulates the microbiome and improves clinical manifestations in a rat model of colitis. <i>EBioMedicine</i> , 2019, 48, 630-641.	2.7	53
15	Optimisation and Benchmarking of Targeted Amplicon Sequencing for Mycobiome Analysis of Respiratory Specimens. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4991.	1.8	28
16	Viral respiratory infections and the oropharyngeal bacterial microbiota in acutely wheezing children. <i>PLoS ONE</i> , 2019, 14, e0223990.	1.1	14
17	A Bioinformatics Guide to Plant Microbiome Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 1313.	1.7	54
18	Seagrass-associated fungal communities show distance decay of similarity that has implications for seagrass management and restoration. <i>Ecology and Evolution</i> , 2019, 9, 11288-11297.	0.8	32

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19	Microbiota analysis optimization for human bronchoalveolar lavage fluid. <i>Microbiome</i> , 2019, 7, 141.	4.9	27
20	Microbial communities of the house fly <i>Musca domestica</i> vary with geographical location and habitat. <i>Microbiome</i> , 2019, 7, 147.	4.9	70
21	Rectal swabs are a reliable proxy for faecal samples in infant gut microbiota research based on 16S-rRNA sequencing. <i>Scientific Reports</i> , 2019, 9, 16072.	1.6	29
22	Molecular analysis of the endobronchial stent microbial biofilm reveals bacterial communities that associate with stent material and frequent fungal constituents. <i>PLoS ONE</i> , 2019, 14, e0217306.	1.1	16
23	Laboratory contamination in airway microbiome studies. <i>BMC Microbiology</i> , 2019, 19, 187.	1.3	31
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25	Complex interactions between the microbiome and cancer immune therapy. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 2019, 56, 567-585.	2.7	28
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27	Successful strategies for human microbiome data generation, storage and analyses. <i>Journal of Biosciences</i> , 2019, 44, 1.	0.5	1
28	Sputum microbiota and inflammation at stable state and during exacerbations in a cohort of chronic obstructive pulmonary disease (COPD) patients. <i>PLoS ONE</i> , 2019, 14, e0222449.	1.1	21
29	Controlling for Contaminants in Low-Biomass 16S rRNA Gene Sequencing Experiments. <i>MSystems</i> , 2019, 4, .	1.7	166
30	microDecon: A highly accurate readâ€ubtraction tool for the postâ€sequencing removal of contamination in metabarcoding studies. <i>Environmental DNA</i> , 2019, 1, 14-25.	3.1	115
31	Microbiota data from low biomass milk samples is markedly affected by laboratory and reagent contamination. <i>PLoS ONE</i> , 2019, 14, e0218257.	1.1	36
32	Characterisation of coral-associated bacterial communities in an urbanised marine environment shows strong divergence over small geographic scales. <i>Coral Reefs</i> , 2019, 38, 1097-1106.	0.9	38
33	Quantifying and Understanding Well-to-Well Contamination in Microbiome Research. <i>MSystems</i> , 2019, 4, .	1.7	132
34	Rigorous Statistical Methods for Rigorous Microbiome Science. <i>MSystems</i> , 2019, 4, .	1.7	7
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36	Habitat fragmentation is associated with dietary shifts and microbiota variability in common vampire bats. <i>Ecology and Evolution</i> , 2019, 9, 6508-6523.	0.8	61

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38	Microbiota of the Gut-Lymph Node Axis: Depletion of Mucosa-Associated Segmented Filamentous Bacteria and Enrichment of <i>Methanobrevibacter</i> by Colistin Sulfate and Linco-Spectin in Pigs. <i>Frontiers in Microbiology</i> , 2019, 10, 599.	1.5	11
39	Integrated Analysis of Human Milk Microbiota With Oligosaccharides and Fatty Acids in the CHILD Cohort. <i>Frontiers in Nutrition</i> , 2019, 6, 58.	1.6	74
40	Towards precision quantification of contamination in metagenomic sequencing experiments. <i>Microbiome</i> , 2019, 7, 62.	4.9	63
41	A different suite: The assemblage of distinct fungal communities in water-damaged units of a poorly-maintained public housing building. <i>PLoS ONE</i> , 2019, 14, e0213355.	1.1	20
42	Plant selection initiates alternative successional trajectories in the soil microbial community after disturbance. <i>Ecological Monographs</i> , 2019, 89, e01367.	2.4	31
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50	Characterization of the Mycobiome of the Seagrass, <i>Zostera marina</i> , Reveals Putative Associations With Marine Chytrids. <i>Frontiers in Microbiology</i> , 2019, 10, 2476.	1.5	34
51	Host phylogeny, diet, and habitat differentiate the gut microbiomes of Darwin's finches on Santa Cruz Island. <i>Scientific Reports</i> , 2019, 9, 18781.	1.6	35
52	An inter-island comparison of Darwin's finches reveals the impact of habitat, host phylogeny, and island on the gut microbiome. <i>PLoS ONE</i> , 2019, 14, e0226432.	1.1	14
53	Discordant transmission of bacteria and viruses from mothers to babies at birth. <i>Microbiome</i> , 2019, 7, 156.	4.9	71
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63	Microbiome Diagnostics. Clinical Chemistry, 2020, 66, 68-76.	1.5	27
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89	Niche- and Gender-Dependent Immune Reactions in Relation to the Microbiota Profile in Pediatric Patients with Otitis Media with Effusion. <i>Infection and Immunity</i> , 2020, 88, .	1.0	12
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92	Co-infection of Chicken Layers With <i>Histomonas meleagridis</i> and Avian Pathogenic <i>Escherichia coli</i> Is Associated With Dysbiosis, Cecal Colonization and Translocation of the Bacteria From the Gut Lumen. <i>Frontiers in Microbiology</i> , 2020, 11, 586437.	1.5	16
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131	An Assessment of Environmental Metabarcoding Protocols Aiming at Favoring Contemporary Biodiversity in Inventories of Deep-Sea Communities. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	36
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133	Lack of Evidence for Microbiota in the Placental and Fetal Tissues of Rhesus Macaques. <i>MSphere</i> , 2020, 5, .	1.3	29
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149	Crop Management Impacts the Soybean (<i>Glycine max</i>) Microbiome. <i>Frontiers in Microbiology</i> , 2020, 11, 1116.	1.5	48
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157	Microbial composition of enigmatic bird parasites: <i>Wolbachia</i> and <i>Spiroplasma</i> are the most important bacterial associates of quill mites (Acariformes: <i>Syringophilidae</i>). <i>MicrobiologyOpen</i> , 2020, 9, e964.	1.2	12
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