

Resource Summary Report

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[metagenomeseq](#)

RRID:SCR_024246

Type: Tool

Proper Citation

metagenomeseq (RRID:SCR_024246)

Resource Information

URL: <https://bioconductor.org/packages/metagenomeSeq/>

Proper Citation: metagenomeseq (RRID:SCR_024246)

Description: Software R package to determine features that are differentially abundant between two or more groups of multiple samples. Used to address the effects of both normalization and under-sampling of microbial communities on disease association detection and testing of feature correlations.

Resource Type: software toolkit, software resource

Keywords: determine features that are differentially abundant, two or more groups of multiple samples, disease association detection, testing of feature correlations,

Resource Name: metagenomeseq

Resource ID: SCR_024246

Alternate IDs: OMICS_07813

Alternate URLs: <https://sources.debian.org/src/r-bioc-metagenomeseq/>

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260729T044602+0000

Ratings and Alerts

No rating or validation information has been found for metagenomeseq.

No alerts have been found for metagenomeseq.

Data and Source Information

Usage and Citation Metrics

We found 227 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Castonguay-Paradis S, et al. (2025) The Human Fecal Endocannabinoidome Mediator Profile Is Mainly Defined by the Fecal Microbiota and Diet. *The Journal of clinical endocrinology and metabolism*, 110(3), 739.

Tian P, et al. (2025) Acidity, sugar, and alcohol contents during the fermentation of Osmanthus-flavored sweet rice wine and microbial community dynamics. *PeerJ*, 13, e18826.

Gao CY, et al. (2025) Abdominal ultrasound stimulation alleviates DSS-induced colitis and behavioral disorders in mice by mediating the microbiota-gut-brain axis balance. *Neurotherapeutics : the journal of the American Society for Experimental NeuroTherapeutics*, 22(2), e00494.

Ahn JS, et al. (2025) Comparison of metagenomic analysis of fecal and gastrointestinal tract samples for identifying beneficial gut microorganisms. *Frontiers in microbiology*, 16, 1533580.

Spiegelhauer MR, et al. (2025) Protection against experimental necrotizing enterocolitis by fecal filtrate transfer requires an active donor virome. *Gut microbes*, 17(1), 2486517.

Liu X, et al. (2025) Comprehensive metabolomic and microbial analysis of tobacco rhizosphere soil responses to crop rotation and fertilization. *Frontiers in plant science*, 16, 1595870.

Hao W, et al. (2025) Intestinal epithelial Dicer1 regulates gut microbiome and Alzheimer's pathology in App-knock-in mice. *Alzheimer's research & therapy*, 17(1), 202.

Li YL, et al. (2025) Roles of oral and gut microbiota in acute myocardial infarction. *Journal of advanced research*, 74, 319.

Escobar Marcillo DI, et al. (2025) Microbiome analysis in individuals with human papillomavirus oral infection. *Scientific reports*, 15(1), 2953.

Yan Z, et al. (2025) Dietary microbiota-mediated shifts in gut microbial ecology and pathogen interactions in giant pandas (*Ailuropoda melanoleuca*). *Communications biology*, 8(1), 864.

Feng Y, et al. (2025) The fecal resistome of beef cattle from conventional grain-fed and grass-fed systems in the Western United States. *BMC microbiology*, 26(1), 3.

Zieschank V, et al. (2025) Tolerance to land-use changes through natural modulations of the plant microbiome. *The ISME journal*, 19(1).

Xu Y, et al. (2025) A computational framework for inferring species dynamics and interactions with applications in microbiota ecology. *NPJ systems biology and applications*, 11(1), 87.

Rehner J, et al. (2025) Examining spatial microbiome variations across gastrointestinal tract regions in obesity. *Scientific reports*, 15(1), 25423.

Clark-Boucher D, et al. (2025) Group-wise normalization in differential abundance analysis of microbiome samples. *BMC bioinformatics*, 26(1), 196.

Bak GR, et al. (2025) Changes in the potato rhizosphere microbiota richness and diversity occur in a growth stage-dependent manner. *Scientific reports*, 15(1), 2284.

Petitclerc I, et al. (2025) Association between gestational diabetes mellitus, maternal health and diet, and gut microbiota in mother-infant dyads. *BMC pregnancy and childbirth*, 25(1), 486.

Deng D, et al. (2025) Microbiome analysis of gut microbiota in patients with colorectal polyps and healthy individuals. *Scientific reports*, 15(1), 7126.

Castonguay-Paradis S, et al. (2025) Seasonal variations in circulating endocannabinoidome mediators and gut microbiota composition in humans. *Gut microbes*, 17(1), 2476563.

Chiu YT, et al. (2025) The Post-Cholecystectomy Gut Microbiota Follows a Time-Varying Change-A Pilot Study. *JGH open : an open access journal of gastroenterology and hepatology*, 9(12), e70329.