

Resource Summary Report

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Metastats

RRID:SCR_014610

Type: Tool

Proper Citation

Metastats (RRID:SCR_014610)

Resource Information

URL: <http://metastats.cbcb.umd.edu/detection.html>

Proper Citation: Metastats (RRID:SCR_014610)

Description: A statistical software package for comparing metagenomic datasets and clinical data sets comprised of two treatment populations, with each treatment population being made up of multiple samples. It relies on a non-parametric t-test.

Resource Type: data analysis software, data processing software, software application, software resource, web application

Keywords: microbiome, statistics, software, metagenomics, clinical data, data analysis software, machine learning, web application, bio.tools

Availability: Open source, Acknowledgement requested

Resource Name: Metastats

Resource ID: SCR_014610

Alternate IDs: biotools:metastats

Alternate URLs: <https://bio.tools/metastats>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260821T194024+0000

Ratings and Alerts

No rating or validation information has been found for Metastats.

No alerts have been found for Metastats.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 390 mentions in open access literature.

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

Liu YY, et al. (2026) Assessing whether rectal swabs reflect appendiceal microbiota profiles in acute appendicitis: a 16S rRNA-based comparative study. Gut pathogens, 18(1), 10.

Su WH, et al. (2026) Gut microbiota and metabolomic alterations in newborns of mothers with gestational diabetes mellitus. Clinical and experimental pediatrics, 69(1), 26.

Han P, et al. (2026) Salivary Microvesicle Methylome and Microbiome Profiles in Periodontitis: An Exploratory Study. Journal of clinical periodontology, 53(6), 911.

Van Hoeck V, et al. (2026) N-acetylated chito-oligosaccharides and xylanase improve intestinal health and production performance in laying hens. Poultry science, 105(6), 106698.

Ma S, et al. (2026) Synergistic regulation of selenium yeast and vitamin E on the rumen microbiota-VFA-liver axis in lambs. BMC microbiology, 26(1).

Cao L, et al. (2026) Alterations in Oral Cecal Transit Time and Small Intestinal Microbiota in Minimal Hepatic Encephalopathy With Small Intestinal Bacterial Overgrowth. Clinical and translational gastroenterology, 17(5), e01012.

Lin X, et al. (2025) Oral exposure to LaNiO₃ regulates the immune system, modulates gut flora, and induces intestinal autophagy in mice. Nanoscale advances, 7(16), 5007.

Yu X, et al. (2025) Lower respiratory tract co-infection of Streptococcus pneumoniae and respiratory syncytial virus shapes microbial landscape and clinical outcomes in children. Frontiers in cellular and infection microbiology, 15, 1593053.

Fang S, et al. (2025) The comparison of gut microbiota between different types of epilepsy in children. Microbial cell factories, 24(1), 64.

Chen X, et al. (2025) Influence of Bacillus subtilis supplementation on growth performance and gut microbial composition in broiler chickens based on low-protein diets. Poultry science, 104(12), 106002.

Liu F, et al. (2025) Isolation of Bacillus cereus and its probiotic effect on growth performance, antioxidant capacity, and intestinal barrier protection of broilers. Poultry science, 104(4), 104944.

Zhang WJ, et al. (2025) Role of gut microbiota in bempedoic acid against hyperlipidemia: a new candidate target for bempedoic acid on the therapeutic regulation. Frontiers in

pharmacology, 16, 1584273.

An L, et al. (2025) Gut microbiota modulation via fecal microbiota transplantation mitigates hyperoxaluria and calcium oxalate crystal depositions induced by high oxalate diet. Gut microbes, 17(1), 2457490.

He M, et al. (2025) Mining the Impact of Mechanical-Stamping Heterogeneity on the Macro- and Micro-Levels of Nongxiangxing daqu. Foods (Basel, Switzerland), 14(21).

Khan I, et al. (2025) Integrated analysis of blood microbiome and metabolites reveals key biomarkers and functional pathways in myocardial infarction. Journal of translational medicine, 23(1), 797.

Jia X, et al. (2025) Metagenomic analysis reveals the abundance changes of bacterial communities and antibiotic resistance genes in the influent and effluent of hospital wastewater. PloS one, 20(10), e0335723.

Sun H, et al. (2025) Investigating the correlation between phenotype, cecal microbiome, and serum metabolome in laying ducks with different shell strength. Poultry science, 104(10), 105558.

Shi ZH, et al. (2025) Changes in fecal microbiota of dairy cows with and without endometritis. BMC veterinary research, 21(1), 201.

Wei C, et al. (2025) Aerobic exercise regulates gut microbiota profiles and metabolite in the early stage of Alzheimer's disease. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(2), e70327.

Meng F, et al. (2025) Postoperative wound microbiota in diabetic patients with perianal abscess: a 16s rRNA gene sequencing study. BMC microbiology, 25(1), 756.