

Resource Summary Report

Generated by SPARC SAWG on Jul 28, 2026

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, software resource, software application, data processing software, 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: 20260728T043441+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 382 mentions in open access literature.

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

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

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.

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.

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.

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.

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.

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.

Jin S, et al. (2025) Akkermansia muciniphila ameliorates chronic stress-induced colorectal tumor growth by releasing outer membrane vesicles. Gut microbes, 17(1), 2555618.

Li P, et al. (2025) Dietary Enterococcus faecium NCIMB 11181 supplementation mitigates intestinal and systemic inflammation induced by avian pathogenic Escherichia coli O78 infection in broiler chickens. Poultry science, 104(11), 105656.

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.

Ji W, et al. (2025) Characteristics of methanotrophic communities and their physicochemical driving mechanisms in estuarine and nearshore wetlands of Qinghai Lake. iScience, 28(8), 113040.

Lan Y, et al. (2025) Microbiome analysis reveals dynamic changes of gut microbiota in Guizhou horse and Dutch Warmblood horses. Frontiers in microbiology, 16, 1562482.

Vinzelj J, et al. (2025) The anaerobic gut fungal community in ostriches (Struthio camelus). bioRxiv : the preprint server for biology.

Liao X, et al. (2025) Alterations in the gastric and small intestinal microbiota of mice exposed to short-term and long-term hypoxia. Scientific reports, 15(1), 42615.

Ma J, et al. (2024) Oral microbiome dysbiosis may be associated with intra cranial aneurysms. BMC oral health, 24(1), 1235.

Zhen L, et al. (2024) Melatonin feeding changed the microbial diversity and metabolism of the broiler cecum. Frontiers in microbiology, 15, 1422272.