

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 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 processing software, web application, data analysis software, software resource, software 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: 20260731T042913+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 [kravitz2](#) .

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

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.

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.

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.

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.

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.

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.

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.

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

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.

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.

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.

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

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.

Zhong L, et al. (2024) Nanopore-based metagenomics analysis reveals microbial presence in amniotic fluid: A prospective study. *Heliyon*, 10(6), e28163.

Fakhraldeen SA, et al. (2024) Shotgun metagenomics reveals the interplay between microbiome diversity and environmental gradients in the first marine protected area in the northern Arabian Gulf. *Frontiers in microbiology*, 15, 1479542.