Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 12, 2025

Pavian

RRID:SCR_016679
Type: Tool

Proper Citation

Pavian (RRID:SCR_016679)

Resource Information

URL: https://github.com/fbreitwieser/pavian

Proper Citation: Pavian (RRID:SCR_016679)

Description: Software R package for interactive analysis of metagenomics classification results with a special focus on infectious disease diagnosis. Used for analyzing and visualization of metagenomics classification results from classifiers such as Kraken, Centrifuge and MetaPhlAn. Provides an alignment viewer for validation of matches to a particular genome.

Resource Type: analysis service resource, service resource, production service resource, data analysis service, web application, software resource

Defining Citation: DOI:10.1101/084715

Keywords: interactive, analysis, metagenomics, classification, result, infectious, disease, diagnosis, data, visualization, bio.tools

Funding: NHGRI R01 HG006677;
NIGMS R01 GM083873;
U. S. Army Research Office W911NF1410490

Availability: Free, Freely available

Resource Name: Pavian

Resource ID: SCR_016679

Alternate IDs: biotools:pavian

Alternate URLs: https://fbreitwieser.shinyapps.io/pavian/, https://bio.tools/pavian

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250509T060212+0000

Ratings and Alerts

No rating or validation information has been found for Pavian.

No alerts have been found for Pavian.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Soni J, et al. (2025) Protocol for investigating intracellular microbial diversity using single-cell RNA-seq in immune cells of SARS-CoV-2-positive and recovered patients. STAR protocols, 6(1), 103546.

Lim FS, et al. (2024) Advancing pathogen surveillance by nanopore sequencing and genotype characterization of Acheta domesticus densovirus in mass-reared house crickets. Scientific reports, 14(1), 8525.

Siallagan ZL, et al. (2024) Metagenomic analysis of deep-sea bacterial communities in the Makassar and Lombok Straits. Scientific reports, 14(1), 25472.

Dzofou Ngoumelah D, et al. (2024) Effect of model methanogens on the electrochemical activity, stability, and microbial community structure of Geobacter spp. dominated biofilm anodes. NPJ biofilms and microbiomes, 10(1), 17.

Lu Z, et al. (2024) Diagnosing and reintegrating traceability of infectious diseases via metagenomic next-generation sequencing: Study of a severe case of Rickettsia japonica infection. Infectious medicine, 3(1), 100094.

Yu J, et al. (2024) Comparison of metagenomic next-generation sequencing and blood culture for diagnosis of bloodstream infections. Frontiers in cellular and infection microbiology, 14, 1338861.

Juteršek M, et al. (2024) Transcriptome-informed identification and characterization of

Planococcus citri cis- and trans-isoprenyl diphosphate synthase genes. iScience, 27(4), 109441.

Barrio-Hernandez I, et al. (2023) Clustering predicted structures at the scale of the known protein universe. Nature, 622(7983), 637.

Lim Y, et al. (2023) Metagenomic data from surface seawater of the east coast of South Korea. Scientific data, 10(1), 647.

Yang XT, et al. (2023) Insight into the mechanism of gallstone disease by proteomic and metaproteomic characterization of human bile. Frontiers in microbiology, 14, 1276951.

Gómez M, et al. (2023) Characterizing viral species in mosquitoes (Culicidae) in the Colombian Orinoco: insights from a preliminary metagenomic study. Scientific reports, 13(1), 22081.

Piro VC, et al. (2022) Contamination detection and microbiome exploration with GRIMER. GigaScience, 12.

Al-Ahmad A, et al. (2021) How Do Polymer Coatings Affect the Growth and Bacterial Population of a Biofilm Formed by Total Human Salivary Bacteria?-A Study by 16S-RNA Sequencing. Microorganisms, 9(7).

Santos A, et al. (2020) Computational methods for 16S metabarcoding studies using Nanopore sequencing data. Computational and structural biotechnology journal, 18, 296.

Hatfield RG, et al. (2020) The Application of Nanopore Sequencing Technology to the Study of Dinoflagellates: A Proof of Concept Study for Rapid Sequence-Based Discrimination of Potentially Harmful Algae. Frontiers in microbiology, 11, 844.

Abouelkhair MA, et al. (2020) Non-SARS-CoV-2 genome sequences identified in clinical samples from COVID-19 infected patients: Evidence for co-infections. PeerJ, 8, e10246.

Che Y, et al. (2019) Mobile antibiotic resistome in wastewater treatment plants revealed by Nanopore metagenomic sequencing. Microbiome, 7(1), 44.

Turner AD, et al. (2018) New Invasive Nemertean Species (Cephalothrix Simula) in England with High Levels of Tetrodotoxin and a Microbiome Linked to Toxin Metabolism. Marine drugs, 16(11).