

# Resource Summary Report

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## Pavian

RRID:SCR\_016679

Type: Tool

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### Proper Citation

Pavian (RRID:SCR\_016679)

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### 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, data analysis service, production service resource, service resource, software resource, web application

**Defining Citation:** [DOI:10.1101/084715](https://doi.org/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:** 20260905T132812+0000

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## Ratings and Alerts

No rating or validation information has been found for Pavian.

No alerts have been found for Pavian.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Lim FS, et al. (2026) No longer uncertain: the validation of tenebrionid insects as hosts of Blattambidensovirus incertum1 isolates by phylogeny and infection studies. The Journal of general virology, 107(2).

Morsli M, et al. (2026) Enhancing diabetic foot osteomyelitis diagnosis with metagenomics next-generation sequencing, proof of concept. Diabetic medicine : a journal of the British Diabetic Association, 43(4), e70235.

Han Y, et al. (2026) Co-occurrence of diverse defense systems shapes complex microbe-virus relationships in deep-sea cold seeps. Nature communications, 17(1), 1427.

Rachmatika R, et al. (2026) Comparative characterization of oral and cloacal microbiomes in captive adult and juvenile coconut lorikeets (Trichoglossus haematodus) using full-length 16S rRNA sequencing. Veterinary world, 19(5), 2117.

Khodadad CLM, et al. (2026) Microbial community characterization of multi-crop growouts in the XROOTS aeroponic-hydroponic system on the International Space Station. Frontiers in microbiomes, 5, 1779816.

Nakamoto JA, et al. (2026) Structural and functional diversity of toxin-antitoxin-chaperone systems. Cell reports, 45(3), 117024.

Cunningham-Oakes E, et al. (2026) Implementing portable, real-time 16S rRNA sequencing in the healthcare sector enhances antimicrobial stewardship. EBioMedicine, 129, 106317.

Sun N, et al. (2025) Comparative analysis of metagenomic next-generation sequencing for pathogenic identification in clinical body fluid samples. BMC microbiology, 25(1), 165.

Gutiérrez-Sarmiento W, et al. (2025) The Body Wall Microbiome of the Terrestrial Slug Deroceras laeve Reveals Potential Endosymbionts and Shares Core Organisms with Other Mollusks. Microbial ecology, 88(1), 136.

Peng J, et al. (2025) Diverse quorum sensing systems regulate microbial communication and biogeochemical processes in deep-sea cold seeps. *Microbiome*, 14(1), 16.

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.

Cholewińska P, et al. (2025) Presence of microplastic particles increased abundance of pathogens and antimicrobial resistance genes in microbial communities from the Oder river water and sediment. *Scientific reports*, 15(1), 16338.

Nunes Neto JP, et al. (2025) Molecular Detection of Yellow Fever Virus in *Haemagogus janthinomys* Mosquitoes (Diptera: Culicidae) in a Rural Settlement in the State of Pará, Brazilian Amazon, 2024. *Viruses*, 17(9).

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.

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.

Lee CS, et al. (2024) Gut *Bifidobacterium longum* is associated with better native liver survival in patients with biliary atresia. *JHEP reports : innovation in hepatology*, 6(7), 101090.

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.