Resource Summary Report

Generated by NIF on Apr 17, 2025

LMAT

RRID:SCR_004646
Type: Tool

Proper Citation

LMAT (RRID:SCR_004646)

Resource Information

URL: https://computation-rnd.llnl.gov/lmat/

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Description: Open-source software tool to assign taxonomic labels to as many reads as possible in very large metagenomic datasets and report the taxonomic profile of the input sample. The quick "single pass" analysis of every read allows read binning to support additional more computationally expensive analysis such as metagenomic assembly or sensitive database searches on targeted subsets of reads.

Abbreviations: LMAT

Synonyms: Livermore Metagenomics Analysis Toolkit

Resource Type: software resource

Defining Citation: PMID:23828782

Keywords: c++, metagenomic, metagenomic classification, genome, virus, taxonomy, database, reference genome

Funding:

Availability: Open unspecified license

Resource Name: LMAT

Resource ID: SCR_004646

Alternate IDs: OMICS_02285

Record Creation Time: 20220129T080225+0000

Record Last Update: 20250410T065202+0000

Ratings and Alerts

No rating or validation information has been found for LMAT.

No alerts have been found for LMAT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Saettele AL, et al. (2022) Prolonged Dexamethasone Exposure Enhances Zebrafish Lateral-Line Regeneration But Disrupts Mitochondrial Homeostasis and Hair Cell Function. Journal of the Association for Research in Otolaryngology : JARO, 23(6), 683.

Morrison MD, et al. (2021) Investigation of Spaceflight Induced Changes to Astronaut Microbiomes. Frontiers in microbiology, 12, 659179.

Avila-Herrera A, et al. (2020) Crewmember microbiome may influence microbial composition of ISS habitable surfaces. PloS one, 15(4), e0231838.

Mejia R, et al. (2020) Impact of intestinal parasites on microbiota and cobalamin gene sequences: a pilot study. Parasites & vectors, 13(1), 200.

Sichtig H, et al. (2019) FDA-ARGOS is a database with public quality-controlled reference genomes for diagnostic use and regulatory science. Nature communications, 10(1), 3313.

Vijayvargiya P, et al. (2019) Application of metagenomic shotgun sequencing to detect vector-borne pathogens in clinical blood samples. PloS one, 14(10), e0222915.

Namroodi S, et al. (2018) Frequency of exposure of endangered Caspian seals to Canine distemper virus, Leptospira interrogans, and Toxoplasma gondii. PloS one, 13(4), e0196070.

Thissen JB, et al. (2018) A novel variant of torque teno virus 7 identified in patients with Kawasaki disease. PloS one, 13(12), e0209683.

Devault AM, et al. (2017) A molecular portrait of maternal sepsis from Byzantine Troy. eLife, 6.

Martí JM, et al. (2017) Health and Disease Imprinted in the Time Variability of the Human Microbiome. mSystems, 2(2).

Treangen TJ, et al. (2016) Identification and Genomic Analysis of a Novel Group C Orthobunyavirus Isolated from a Mosquito Captured near Iquitos, Peru. PLoS neglected tropical diseases, 10(4), e0004440.

Ounit R, et al. (2015) CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative k-mers. BMC genomics, 16(1), 236.

Ames SK, et al. (2015) Using populations of human and microbial genomes for organism detection in metagenomes. Genome research, 25(7), 1056.

Gardner SN, et al. (2015) Targeted amplification for enhanced detection of biothreat agents by next-generation sequencing. BMC research notes, 8, 682.

Filippidou S, et al. (2015) Under-detection of endospore-forming Firmicutes in metagenomic data. Computational and structural biotechnology journal, 13, 299.