Resource Summary Report

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DiScRIBinATE

RRID:SCR_004862
Type: Tool

Proper Citation

DiScRIBinATE (RRID:SCR_004862)

Resource Information

URL: http://metagenomics.atc.tcs.com/binning/DiScRIBinATE/

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Description: Software for accurate taxonomic classification of metagenomic sequences using a similarity based binning method. User needs to perform a similarity search of the input metagenomic sequences (reads) against the nr protein database using BLASTx search. The generated blastx output is then taken as the input by the DiScRIBinATE program.

Abbreviations: DiScRIBinATE

Synonyms: DiScRIBinATE: Distance Score Ratio for Improved Binning and Taxonomic Estimation, Distance Score Ratio for Improved Binning and Taxonomic Estimation

Resource Type: software resource

Defining Citation: PMID:21106121

Keywords: metagenome, classification, sequence

Funding:

Availability: Free for academic use, Non-commercial, Commercial use with permission, Acknowledgement requested, Copyright - Tata Consultancy Services

Resource Name: DiScRIBinATE

Resource ID: SCR_004862

Alternate IDs: OMICS_01453

Record Creation Time: 20220129T080227+0000

Record Last Update: 20250410T065213+0000

Ratings and Alerts

No rating or validation information has been found for DiScRIBinATE.

No alerts have been found for DiScRIBinATE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Das A, et al. (2016) Xenobiotic Metabolism and Gut Microbiomes. PloS one, 11(10), e0163099.

Escobar-Zepeda A, et al. (2015) The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. Frontiers in genetics, 6, 348.

Peabody MA, et al. (2015) Evaluation of shotgun metagenomics sequence classification methods using in silico and in vitro simulated communities. BMC bioinformatics, 16, 363.

Dutta A, et al. (2014) Binpairs: utilization of Illumina paired-end information for improving efficiency of taxonomic binning of metagenomic sequences. PloS one, 9(12), e114814.