Package ‘microbiomeMQC’

September 16, 2024

Type Package

Title Calculate 4 Key Reporting Measures

Version 1.0.2

Maintainer Jacob Dehinsilu <jacobdehinsilu@outlook.com>

Description Perform calculations for the WHO International Reference Reagents for the microbiome. Using strain, species or genera abundance tables generated through analysis of 16S ribosomal RNA sequencing or shotgun sequencing which included a reference reagent. This package will calculate measures of sensitivity, False positive relative abundance, diversity, and similarity based on mean average abundances with respect to the reference reagent.

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Imports readxl, vegan

Suggests testthat, knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Author Jacob Dehinsilu [aut, cre] (<https://orcid.org/0000-0001-9041-970X>),
Ravneet Bhuller [aut]

Depends R (>= 3.5.0)

Repository CRAN

Date/Publication 2024-09-16 07:20:02 UTC

Contents

`microbiomeMQC` *Calculate 4 key reporting measures*

Description

Calculate the 4 key reporting measures for the WHO International Reference Reagents for the microbiome

Usage

```
microbiomeMQC(input, taxonomic_level, output)
```

Arguments

`input`	Path to the .xlsx or .csv file.e.g. "C:\Users\joeblogs\Desktop\data.xlsx"
`taxonomic_level`	The taxonomic level ("strain", "species", or "genus") that you are using.
`output`	Path to save the output CSV file (file path must end with the file name e.g. "C:\Users\joeblogs\Desktop\MQC.csv"

Details

The 4 key reporting measures (using the example of species) are:

Sensitivity: How many species from the reagent are correctly identified.

Diversity: The total number of species detected.

FPRA: The relative abundance of false positives.

Similarity: The Bray-Curtis dissimilarity in composition between the species profile reported and the 'ground truth' profile of the reagent.

To see how the data should be formatted do: data(MQC_testdata) FP = false positive i.e. those bacteria that do not appear in the reagent

Value

No return value. The function writes the results to the specified CSV file.

Examples

```
input <- system.file("extdata", "MQC_testdata.csv", package = "microbiomeMQC")
output <- tempfile(fileext = ".csv")
microbiomeMQC(input, "species", output)
```

`MQC_testdata` *MQC_testdata*

Description

Data used for demonstrating the functionality of the microbiomeMQC package.

Usage

```
data(MQC_testdata)
```

Format

An object of class `data.frame` with 26 rows and 6 columns:

Column1	species
Column2	DNA_hilo_RR
Column3	perfect result
Column4	high FPRA example
Column5	high diversity example
Column6	low sensitivity example

Source

Generated by the package authors for demonstration purposes.

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