Package: microbiomeMQC (via r-universe)

Type Package

Title Calculate 4 Key Reporting Measures

Version 1.0.2

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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

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Depends R (>= 3.5.0)

Repository CRAN

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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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