Package 'molBV'

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Type Package

Title The Immune Landscape of Molecular Bacterial Vaginosis and HPV Natural History

Version 1.0

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Description We demonstrate that 16S rRNA amplicon sequencing and a novel pipeline can be used to generate a molecular Nugent BV score (molBV) corresponding to the Nugent score 0 - 10. This algorithm is independent of the region of 16S rRNA amplified, the sequencing platform and source population.

License GPL (>=2)

Encoding UTF-8

LazyData true

NeedsCompilation no

Imports phyloseq, ggplot2, ggpubr

RoxygenNote 7.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

Depends R (>= 3.5.0)

R topics documented:

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exampleMicrobiomeData   *Example microbiome data*

Description

A data frame contains the count table of the 183 genus in the 80 samples.

Usage

```
exampleMicrobiomeData
```

Format

A data frame with 183 rows (genus) and 80 columns (samples). All values are non-negative integers.

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molBV   *Perform the calculation of the molBV scores*

Description

Perform the calculation of the molBV scores

Usage

```
molBV(inputData, outputTable = NULL)
```

Arguments

inputData   Either a biom file or a matrix-like R object with sample IDs as columns and
               genera as rows.

outputTable   The path and name of the output table to be generated. Default is NULL.

Details

- If `inputData` is biom file, package 'phyloseq' is needed to process it. Some warnings related to the greengenes database can be ignored.
- If `inputData` is a matrix/data frame, please make sure that the genera labels (row names) match the green-genes convention, which is necessary when calculating the score for each reference frame.
- If `outputTable` is specified, a table contains the sample map with the molBV socres will be generated.

Value

A data frame contains the sample map with the molBV socres.

- SID - Sample IDs.
- Column 2 to 12 - Counts of the genus that used to calculated the scores.
- molBV - Calculated molBV scores.

References

Usyk et al. The Immune Landscape of Molecular Bacterial Vaginosis and HPV Natural History. https://doi.org/10.21203/rs.3.rs-613095/v1

Examples

```
map_with_molBVScores <- molBV(exampleMicrobiomeData, outputTable = NULL)
print(map_with_molBVScores)
range(map_with_molBVScores$molBV)

exampleBiomFile <- system.file("extdata", "converted_otu.biom", package = "molBV")
map_with_molBVScores <- molBV(exampleBiomFile, outputTable = "map_with_molBV.txt")
#A txt file "map_with_molBV.txt" will be generated in current working directory.
```

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molecuL | *The coefficients in the formula*

Description

A data frame contains the coefficients for each BV association ratio (column beta and intercept).

Usage

```
molecuL
```

Format

A data frame with 10 rows and 6 variables:

bug1 Lactobacillus

bug2 10 genus used in the formula

R2 R square values

beta beta coefficients

intercept intercept coefficients

weight from 10 to 1

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