

Package ‘QuanT’

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Title QuanT

Version 0.0.0.9000

Description Identifying unmeasured heterogeneity in microbiome data via quantile thresholding.

License GPL (>= 3)

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

Depends R (>= 2.10)

LazyData true

Imports dplyr,
Matrix,
nortest,
quantreg,
RSpectra

Suggests BiocManager,
ggplot2,
knitr,
mgcv,
rmarkdown,
RUVSeq,
sva

VignetteBuilder knitr

URL <https://github.com/jiuyaolu/QuanT>

BugReports <https://github.com/jiuyaolu/QuanT/issues>

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crc	<i>CRC dataset</i>
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Description

Data from curatedMetagenomicData data package

Usage

```
crc
```

Format

crc is a list containing the following components:

otu the absolute abundance(count) matrix

rela the relative abundance matrix

batchid the batch(study) indicator

condition a factor with three levels: adenoma, CRC, control

age a factor with two levels: adult, senior

subtype a factor with five levels: adenoma, carcinoma, adenocarcinoma, advancedadenoma, control

gender a factor with two levels: male, female

QuanT	<i>QuanT</i>
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Description

QuanT runs the QuanT algorithm. It takes as input the abundance matrix and covariates, and outputs the QSVs.

Usage

```
QuanT(dat, covariates, q = NULL)
```

Arguments

dat	The abundance matrix with rows as samples and columns as taxa. This is supposed to be relative abundances after preprocessing.
covariates	All the known variables including the primary variable of interest and other covariates.
q	The quantile levels to be used. If NULL, QuanT will choose the quantile levels based on the proportion of zeroes in the data.

Value

QuanT outputs the QSVs, which are surrogates for the unmeasured heterogeneity in the data. They are stored in a matrix with the same number of rows as dat.

Examples

```
covariates = model.matrix(~ subtype + age + gender, data=crc)[-1]
qsv = QuanT(crc$rela, covariates)
plot(qsv[,1:2], col=crc$batchid)
```

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