

Package ‘PathoStat’

May 7, 2024

Type Package

Title PathoStat Statistical Microbiome Analysis Package

Version 1.30.0

Date 2020-03-27

Author Solaiappan Manimaran <manimaran_1975@hotmail.com>, Matthew Bendall <bendall@gwmail.gwu.edu>, Sandro Valenzuela Diaz <sandrolvalenzuelad@gmail.com>, Eduardo Castro <castronallar@gmail.com>, Tyler Faits <tfaits@gmail.com>, Yue Zhao <jasonzhao0307@gmail.com>, Anthony Nicholas Federico <anfed@bu.edu>, W. Evan Johnson <wej@bu.edu>

Maintainer Solaiappan Manimaran <manimaran_1975@hotmail.com>, Yue Zhao <jasonzhao0307@gmail.com>

Description The purpose of this package is to perform Statistical Microbiome Analysis on metagenomics results from sequencing data samples. In particular, it supports analyses on the PathoScope generated report files. PathoStat provides various functionalities including Relative Abundance charts, Diversity estimates and plots, tests of Differential Abundance, Time Series visualization, and Core OTU analysis.

URL <https://github.com/mani2012/PathoStat>

BugReports <https://github.com/mani2012/PathoStat/issues>

License GPL (>= 2)

Depends R (>= 3.5)

Imports limma, corpcor, matrixStats, reshape2, scales, ggplot2, rentrez, DT, tidyr, plyr, dplyr, phyloseq, shiny, stats, methods, XML, graphics, utils, BiocStyle, edgeR, DESeq2, ComplexHeatmap, plotly, webshot, vegan, shinyjs, glmnet, gmodels, ROCR, RColorBrewer, knitr, devtools, ape

Collate 'pathoStat.R' 'utils.R' 'taxonomy.R' 'biomarker.R' 'allClasses.R' 'visualization.R' 'differentialAnalysis.R'

biocViews Microbiome, Metagenomics, GraphAndNetwork, Microarray,
PatternLogic, PrincipalComponent, Sequencing, Software,
Visualization, RNASeq, ImmunoOncology

RoxygenNote 6.1.1

Encoding UTF-8

Suggests rmarkdown, testthat

VignetteBuilder knitr

git_url <https://git.bioconductor.org/packages/PathoStat>

git_branch RELEASE_3_19

git_last_commit f3f9b98

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-06

Contents

| | |
|--|----|
| Bootstrap_LOOCV_LR_AUC | 3 |
| Chisq_Test_Pam | 4 |
| findRAfromCount | 4 |
| findTaxonMat | 5 |
| findTaxonomy | 6 |
| findTaxonomy300 | 6 |
| Fisher_Test_Pam | 7 |
| formatTaxTable | 8 |
| getShinyInput | 8 |
| getShinyInputCombat | 9 |
| getShinyInputOrig | 9 |
| getSignatureFromMultipleGlmnet | 10 |
| GET_PAM | 10 |
| grepTid | 11 |
| loadPathoscopeReports | 12 |
| loadPstat | 13 |
| log2CPM | 13 |
| LOOAUC_simple_multiple_noplot_one_df | 14 |
| LOOAUC_simple_multiple_one_df | 14 |
| PathoStat-class | 15 |
| percent | 16 |
| phyloseq_to_edgeR | 16 |
| plotPCAPlotly | 17 |
| plotPCoAPlotly | 18 |
| pstat_data | 19 |
| readPathoscopeData | 19 |
| runPathoStat | 20 |
| savePstat | 21 |

| | |
|---------------------------------|-----------|
| <i>Bootstrap_LOOCV_LR_AUC</i> | 3 |
| setShinyInput | 21 |
| setShinyInputCombat | 22 |
| setShinyInputOrig | 22 |
| summarizeTable | 23 |
| TranslateIdToTaxLevel | 23 |
| Wilcox_Test_df | 24 |
| Index | 25 |

Bootstrap_LOOCV_LR_AUC
Do bootstrap and LOOCV

Description

Do bootstrap and LOOCV

Usage

Bootstrap_LOOCV_LR_AUC(df, targetVec, nboot = 50)

Arguments

| | |
|-----------|--|
| df | Row is sample, column is feature. Required |
| targetVec | y vector. Required |
| nboot | number of BOOTSTRAP |

Value

bootstrap loocv result dataframe

Examples

```
data('iris')
Bootstrap_LOOCV_LR_AUC(iris[,1:4],
c(rep(1,100), rep(0,50)), nboot = 3)
```

| | |
|----------------|---|
| Chisq_Test_Pam | <i>Given PAM and disease/control annotation, do Chi-square test for each row of PAM</i> |
|----------------|---|

Description

Given PAM and disease/control annotation, do Chi-square test for each row of PAM

Usage

```
Chisq_Test_Pam(pam, label.vec.num, pvalue.cutoff = 0.05)
```

Arguments

| | |
|---------------|---|
| pam | Input data object that contains the data to be tested. Required |
| label.vec.num | The target binary condition. Required |
| pvalue.cutoff | choose p-value cut-off |

Value

df.output object

Examples

```
tmp <- matrix(rbinom(12,1,0.5), nrow = 3)
rownames(tmp) <- c("a", "b", "c")
Chisq_Test_Pam(tmp, c(1,1,0,0))
```

| | |
|-----------------|--|
| findRAfromCount | <i>Return the Relative Abundance (RA) data for the given count OTU table</i> |
|-----------------|--|

Description

Return the Relative Abundance (RA) data for the given count OTU table

Usage

```
findRAfromCount(count_otu)
```

Arguments

| | |
|-----------|-----------------|
| count_otu | Count OTU table |
|-----------|-----------------|

Value

ra_otu Relative Abundance (RA) OTU table

Examples

```
data_dir <- system.file("data", package = "PathoStat")
infileName <- "pstat_data.rda"
pstat_test <- loadPstat(data_dir, infileName)
ra_otu <- findRAfromCount(phyloseq::otu_table(pstat_test))
```

| | |
|--------------|---|
| findTaxonMat | <i>Find the Taxonomy Information Matrix</i> |
|--------------|---|

Description

Find the Taxonomy Information Matrix

Usage

```
findTaxonMat(names, taxonLevels)
```

Arguments

| | |
|-------------|----------------------------------|
| names | Row names of the taxonomy matrix |
| taxonLevels | Taxon Levels of all tids |

Value

taxmat Taxonomy Information Matrix

Examples

```
example_data_dir <- system.file("example/data", package = "PathoStat")
pathoreport_file_suffix <- "-sam-report.tsv"
datlist <- readPathoscopeData(example_data_dir, pathoreport_file_suffix,
input.files.name.vec = as.character(1:6))
dat <- datlist$data
ids <- rownames(dat)
tids <- unlist(lapply(ids, FUN = grepTid))
# taxonLevels <- findTaxonomy(tids[1:5])
# taxmat <- findTaxonMat(ids[1:5], taxonLevels)
```

findTaxonomy

Find the taxonomy for unlimited tids

Description

Find the taxonomy for unlimited tids

Usage

```
findTaxonomy(tids)
```

Arguments

tids Given taxonomy ids

Value

taxondata Data with the taxonomy information

Examples

```
example_data_dir <- system.file("example/data", package = "PathoStat")
pathoreport_file_suffix <- "-sam-report.tsv"
datlist <- readPathoscopeData(example_data_dir, pathoreport_file_suffix,
input.files.name.vec = as.character(1:6))
dat <- datlist$data
ids <- rownames(dat)
tids <- unlist(lapply(ids, FUN = grepTid))
# taxonLevels <- findTaxonomy(tids[1:5])
```

findTaxonomy300*Find the taxonomy for maximum 300 tids*

Description

Find the taxonomy for maximum 300 tids

Usage

```
findTaxonomy300(tids)
```

Arguments

tids Given taxonomy ids

Value

taxondata Data with the taxonomy information

Examples

```
example_data_dir <- system.file("example/data", package = "PathoStat")
pathoreport_file_suffix <- "-sam-report.tsv"
datlist <- readPathoscopeData(example_data_dir,
  pathoreport_file_suffix, input.files.name.vec = as.character(1:6))
dat <- datlist$data
ids <- rownames(dat)
tids <- unlist(lapply(ids, FUN = grepTid))
# taxonLevels <- findTaxonomy300(tids[1:5])
```

| | |
|-----------------|---|
| Fisher_Test_Pam | <i>Given PAM and disease/control annotation, do Chi-square test for each row of PAM</i> |
|-----------------|---|

Description

Given PAM and disease/control annotation, do Chi-square test for each row of PAM

Usage

```
Fisher_Test_Pam(pam, label.vec.num, pvalue.cutoff = 0.05)
```

Arguments

| | |
|---------------|---|
| pam | Input data object that contains the data to be tested. Required |
| label.vec.num | The target binary condition. Required |
| pvalue.cutoff | choose p-value cut-off |

Value

df.output object

Examples

```
tmp <- matrix(rbinom(12,1,0.5), nrow = 3)
rownames(tmp) <- c("a", "b", "c")
Fisher_Test_Pam(tmp, c(1,1,0,0))
```

| | |
|----------------|--|
| formatTaxTable | <i>Format taxonomy table for rendering</i> |
|----------------|--|

Description

Format taxonomy table for rendering

Usage

```
formatTaxTable(ttable)
```

Arguments

| | |
|--------|----------------|
| ttable | Taxonomy table |
|--------|----------------|

Value

Formatted table suitable for rendering with. DT::renderDataTable

| | |
|---------------|---|
| getShinyInput | <i>Getter function to get the shinyInput option</i> |
|---------------|---|

Description

Getter function to get the shinyInput option

Usage

```
getShinyInput()
```

Value

shinyInput option

Examples

```
getShinyInput()
```

`getShinyInputCombat` *Getter function to get the shinyInputCombat option*

Description

Getter function to get the shinyInputCombat option

Usage

```
getShinyInputCombat()
```

Value

shinyInputCombat option

Examples

```
getShinyInputCombat()
```

`getShinyInputOrig` *Getter function to get the shinyInputOrig option*

Description

Getter function to get the shinyInputOrig option

Usage

```
getShinyInputOrig()
```

Value

shinyInputOrig option

Examples

```
getShinyInputOrig()
```

```
getSignatureFromMultipleGlmnet
```

Use Lasso to do feature selection

Description

Use Lasso to do feature selection

Usage

```
getSignatureFromMultipleGlmnet(df.input, target.vec, nfolds = 10,  
  logisticRegression = TRUE, nRun = 100, alpha = 1)
```

Arguments

| | |
|--------------------|---|
| df.input | Row is sample, column is feature. Required |
| target.vec | y vector. Required |
| nfolds | glmnet CV nfolds |
| logisticRegression | doing logistic regression or linear regression. |
| nRun | number of glmnet runs |
| alpha | same as in glmnet |

Value

signature

Examples

```
data('iris')  
getSignatureFromMultipleGlmnet(iris[,1:4],  
  c(rep(1,100), rep(0,50)), nfolds = 3, nRun = 10)
```

```
GET_PAM
```

transform cpm counts to presence-absence matrix

Description

transform cpm counts to presence-absence matrix

Usage

```
GET_PAM(df)
```

Arguments

df Input data object that contains the data to be tested. Required

Value

df.output object

Examples

```
GET_PAM(data.frame(a = c(1,3,0), b = c(0,0.1,2)))
```

grepTid *Greps the tid from the given identifier string*

Description

Greps the tid from the given identifier string

Usage

```
grepTid(id)
```

Arguments

id Given identifier string

Value

tid string

Examples

```
grepTid("ti|700015|org|Coriobacterium_glomerans_PW2")
```

`loadPathoscopeReports` *Loads all data from a set of PathoID reports. For each column in the PathoID report, construct a matrix where the rows are genomes and the columns are samples. Returns a list where each element is named according to the PathoID column. For example, `ret[["Final.Best.Hit.Read.Numbers"]]` on the result of this function will get you the final count matrix. Also includes elements "total_reads" and "total_genomes" from the first line of the PathoID report.*

Description

Loads all data from a set of PathoID reports. For each column in the PathoID report, construct a matrix where the rows are genomes and the columns are samples. Returns a list where each element is named according to the PathoID column. For example, `ret[["Final.Best.Hit.Read.Numbers"]]` on the result of this function will get you the final count matrix. Also includes elements "total_reads" and "total_genomes" from the first line of the PathoID report.

Usage

```
loadPathoscopeReports(reportfiles, nrows = NULL)
```

Arguments

| | |
|--------------------------|---|
| <code>reportfiles</code> | Paths to report files |
| <code>nrows</code> | Option to read first N rows of PathoScope reports |

Value

Returns a list where each element is named according to the PathoID column. For example, `ret[["Final.Best.Hit.Read.Numbers"]]` on the result of this function will get you the final count matrix. Also includes elements "total_reads" and "total_genomes" from the first line of the PathoID report.

Examples

```
input_dir <- system.file("example/data", package = "PathoStat")
reportfiles <- list.files(input_dir, pattern = "*-sam-report.tsv",
full.names = TRUE)
```

| | |
|-----------|---|
| loadPstat | <i>Load the R data(.rda) file with pathostat object</i> |
|-----------|---|

Description

Load the R data(.rda) file with pathostat object

Usage

```
loadPstat(indir = ".", infileName = "pstat_data.rda")
```

Arguments

| | |
|------------|----------------------------------|
| indir | Input Directory of the .rda file |
| infileName | File name of the .rda file |

Value

pstat pathostat object (NULL if it does not exist)

Examples

```
data_dir <- system.file("data", package = "PathoStat")
infileName <- "pstat_data.rda"
pstat <- loadPstat(data_dir, infileName)
```

| | |
|---------|--|
| log2CPM | <i>Compute log2(counts per mil reads) and library size for each sample</i> |
|---------|--|

Description

Compute log2(counts per mil reads) and library size for each sample

Usage

```
log2CPM(qcounts, lib.size = NULL)
```

Arguments

| | |
|----------|-----------------------------|
| qcounts | quantile normalized counts |
| lib.size | default is colsums(qcounts) |

Value

list containing log2(quantile counts per mil reads) and library sizes

Examples

```
log2CPM(matrix(1:12, nrow = 3))
```

```
LOOAUC_simple_multiple_noplot_one_df
      LOOCV
```

Description

LOOCV

Usage

```
LOOAUC_simple_multiple_noplot_one_df(df, targetVec)
```

Arguments

| | |
|-----------|--|
| df | Row is sample, column is feature. Required |
| targetVec | y vector. Required |

Value

mean auc

Examples

```
data('iris')
LOOAUC_simple_multiple_noplot_one_df(iris[,1:4],
c(rep(1,100), rep(0,50)))
```

```
LOOAUC_simple_multiple_one_df
      LOOCV with ROC curve
```

Description

LOOCV with ROC curve

Usage

```
LOOAUC_simple_multiple_one_df(df, targetVec)
```

Arguments

| | |
|-----------|--|
| df | Row is sample, column is feature. Required |
| targetVec | y vector. Required |

Value

the ROC

Examples

```
data('iris')
LOOAUC_simple_multiple_one_df(iris[,1:4],
c(rep(1,100), rep(0,50)))
```

| | |
|-----------------|--|
| PathoStat-class | <i>PathoStat class to store PathoStat input data including phyloseq object</i> |
|-----------------|--|

Description

Contains all currently-supported BatchQC output data classes:

Details

slots:

average_count a single object of class `otu_tableOrNULL`

besthit_count a single object of class `otu_tableOrNULL`

highconf_count a single object of class `otu_tableOrNULL`

lowconf_count a single object of class `otu_tableOrNULL`

Examples

```
otumat = matrix(sample(1:100, 100, replace = TRUE), nrow = 10, ncol = 10)
rownames(otumat) <- paste0("OTU", 1:nrow(otumat))
colnames(otumat) <- paste0("Sample", 1:ncol(otumat))
taxmat = matrix(sample(letters, 70, replace = TRUE),
nrow = nrow(otumat), ncol = 7)
rownames(taxmat) <- rownames(otumat)
colnames(taxmat) <- c("Domain", "Phylum", "Class",
"Order", "Family", "Genus", "Species")
OTU = phyloseq::otu_table(otumat, taxa_are_rows = TRUE)
TAX = phyloseq::tax_table(taxmat)
physeq = phyloseq::phyloseq(OTU, TAX)
pathostat1(physeq)
```

| | |
|---------|---------------------------|
| percent | <i>Compute percentage</i> |
|---------|---------------------------|

Description

Compute percentage

Usage

```
percent(x, digits = 2, format = "f")
```

Arguments

| | |
|--------|-------------------------------|
| x | a number or a vector |
| digits | how many digit of percentage |
| format | numeric format, "f" for float |

Value

the percentage

Examples

```
percent.vec <- percent(c(0.9, 0.98))
```

| | |
|-------------------|---|
| phyloseq_to_edgeR | <i>Convert phyloseq OTU count data into DGEList for edgeR package</i> |
|-------------------|---|

Description

Further details.

Usage

```
phyloseq_to_edgeR(physeq, group, method = "RLE", ...)
```

Arguments

| | |
|--------|---|
| physeq | (Required). |
| group | (Required). A character vector or factor giving the experimental group/condition for each sample/library. |
| method | (Optional). |
| ... | Additional arguments passed on to |

Value

dispersion

Examples

```
data_dir_test <- system.file("data", package = "PathoStat")
pstat_test <- loadPstat(indir=data_dir_test,
  infileName="pstat_data_2_L1.rda")
phyloseq_to_edgeR(pstat_test, group="Sex")
```

plotPCAPlotly

Plot PCA

Description

Plot PCA

Usage

```
plotPCAPlotly(df.input, condition.color.vec,
  condition.color.name = "condition", condition.shape.vec = NULL,
  condition.shape.name = "condition", columnTitle = "Title",
  pc.a = "PC1", pc.b = "PC2")
```

Arguments

| | |
|----------------------|--|
| df.input | Input data object that contains the data to be plotted. Required |
| condition.color.vec | color vector. Required |
| condition.color.name | color variable name. Required |
| condition.shape.vec | shape vector. Required |
| condition.shape.name | shape variable name. Required |
| columnTitle | Title to be displayed at top of heatmap. |
| pc.a | pc.1 |
| pc.b | pc.2 |

Value

the plot

Examples

```
data('iris')
plotPCoAPlotly(t(iris[,1:4]),
condition.color.vec = c(rep(1,100), rep(0,50)),
condition.shape.vec = c(rep(0,100), rep(1,50)))
```

plotPCoAPlotly

Plot PCoA

Description

Plot PCoA

Usage

```
plotPCoAPlotly(physeq.input, condition.color.vec,
condition.color.name = "condition", condition.shape.vec = NULL,
condition.shape.name = "condition", method = "bray",
columnTitle = "Title", pc.a = "Axis.1", pc.b = "Axis.2")
```

Arguments

| | |
|----------------------|--|
| physeq.input | Input data object that contains the data to be plotted. Required |
| condition.color.vec | color vector. Required |
| condition.color.name | color variable name. Required |
| condition.shape.vec | shape vector. Required |
| condition.shape.name | shape variable name. Required |
| method | which distance metric |
| columnTitle | Title to be displayed at top of heatmap. |
| pc.a | pc.1 |
| pc.b | pc.2 |

Value

the plot

Examples

```
data_dir_test <- system.file("data", package = "PathoStat")
pstat_test <- loadPstat(indir=data_dir_test,
infileName="pstat_data_2_L1.rda")
plotPCoAPlotly(pstat_test, condition.color.vec = rbinom(33,1,0.5),
condition.shape.vec = rbinom(33,1,0.5))
```

| | |
|------------|--|
| pstat_data | <i>pathostat object generated from example pathoscope report files</i> |
|------------|--|

Description

This example data consists of 33 samples from a diet study with 11 subjects taking 3 different diets in random order

Usage

```
pstat
```

Format

pathostat object extension of phyloseq-class experiment-level object:

otu_table OTU table with 41 taxa and 33 samples

sample_data Sample Data with 33 samples by 18 sample variables

tax_table Taxonomy Table with 41 taxa by 9 taxonomic ranks

sample_data Phylogenetic Tree with 41 tips and 40 internal nodes

Value

pathostat object

| | |
|--------------------|---|
| readPathoscopeData | <i>Reads the data from PathoScope reports and returns a list of final guess relative abundance and count data</i> |
|--------------------|---|

Description

Reads the data from PathoScope reports and returns a list of final guess relative abundance and count data

Usage

```
readPathoscopeData(input_dir = ".",
  pathoreport_file_suffix = "-sam-report.tsv", use.input.files = FALSE,
  input.files.path.vec = NULL, input.files.name.vec = NULL)
```

Arguments

`input_dir` Directory where the tsv files from PathoScope are located
`pathoreport_file_suffix` PathoScope report files suffix
`use.input.files` whether input dir to pathoscope files or directly pathoscope files
`input.files.path.vec` vector of pathoscope file paths
`input.files.name.vec` vector of pathoscope file names

Value

List of final guess relative abundance and count data

Examples

```

example_data_dir <- system.file("example/data", package = "PathoStat")
pathoreport_file_suffix <- "-sam-report.tsv"
datlist <- readPathoscopeData(example_data_dir, pathoreport_file_suffix,
input.files.name.vec = as.character(1:6))
  
```

| | |
|--------------|--|
| runPathoStat | <i>Statistical Microbiome Analysis on the pathostat input and generates a html report and produces interactive shiny app plots</i> |
|--------------|--|

Description

Statistical Microbiome Analysis on the pathostat input and generates a html report and produces interactive shiny app plots

Usage

```

runPathoStat(pstat = NULL, report_dir = ".",
report_option_binary = "111111111", interactive = TRUE)
  
```

Arguments

`pstat` phyloseq extension pathostat object
`report_dir` Output report directory path
`report_option_binary` 9 bits Binary String representing the plots to display and hide in the report
`interactive` when TRUE, opens the interactive shinyApp

Value

outputfile The output file with all the statistical plots

Examples

```
runPathoStat(interactive = FALSE)
```

| | |
|-----------|---|
| savePstat | <i>Save the pathostat object to R data(.rda) file</i> |
|-----------|---|

Description

Save the pathostat object to R data(.rda) file

Usage

```
savePstat(pstat, outdir = ".", outfileName = "pstat_data.rda")
```

Arguments

| | |
|-------------|-----------------------------------|
| pstat | pathostat object |
| outdir | Output Directory of the .rda file |
| outfileName | File name of the .rda file |

Value

outfile .rda file

Examples

```
data_dir_test <- system.file("data", package = "PathoStat")
pstat_test <- loadPstat(indir=data_dir_test,
  infileName="pstat_data_2_L1.rda")
outfile <- savePstat(pstat_test)
```

| | |
|---------------|---|
| setShinyInput | <i>Setter function to set the shinyInput option</i> |
|---------------|---|

Description

Setter function to set the shinyInput option

Usage

```
setShinyInput(x)
```

Arguments

| | |
|---|-------------------|
| x | shinyInput option |
|---|-------------------|

Value

shinyInput option

Examples

```
setShinyInput(NULL)
```

setShinyInputCombat *Setter function to set the shinyInputCombat option*

Description

Setter function to set the shinyInputCombat option

Usage

```
setShinyInputCombat(x)
```

Arguments

x shinyInputCombat option

Value

shinyInputCombat option

Examples

```
setShinyInputCombat(NULL)
```

setShinyInputOrig *Setter function to set the shinyInputOrig option*

Description

Setter function to set the shinyInputOrig option

Usage

```
setShinyInputOrig(x)
```

Arguments

x shinyInputOrig option

Value

shinyInputOrig option

Examples

```
setShinyInputOrig(NULL)
```

| | |
|----------------|-------------------------|
| summarizeTable | <i>Summarize sample</i> |
|----------------|-------------------------|

Description

Creates a table of summary metrics

Usage

```
summarizeTable(pstat)
```

Arguments

pstat Input pstat

Value

A data.frame object of summary metrics.

Examples

```
data_dir_test <- system.file("data", package = "PathoStat")
pstat_test <- loadPstat(indir=data_dir_test,
  infileName="pstat_data_2_L1.rda")
st.tmp <- summarizeTable(pstat_test)
```

| | |
|-----------------------|--|
| TranslateIdToTaxLevel | <i>Find the taxonomy for the given taxon id name</i> |
|-----------------------|--|

Description

Find the taxonomy for the given taxon id name

Usage

```
TranslateIdToTaxLevel(pstat, input.id.vec, tax.level)
```

Arguments

| | |
|--------------|---------------------|
| pstat | pathostat object |
| input.id.vec | names containing id |
| tax.level | target taxon level |

Value

target taxon level names

Examples

```
data_dir_test <- system.file("data", package = "PathoStat")
pstat_test <- loadPstat(indir=data_dir_test,
  infileName="pstat_data_2_L1.rda")
names.new <- TranslateIdToTaxLevel(pstat_test,
  c("ti|862962|org|Bacteroides_fragilis_638R",
    "ti|697329|org|Ruminococcus_albus_7" ),
  "genus")
```

Wilcox_Test_df

Mann-whitney test for a dataframe

Description

Mann-whitney test for a dataframe

Usage

```
Wilcox_Test_df(df, label.vec.num, pvalue.cutoff = 0.05)
```

Arguments

| | |
|---------------|---|
| df | Input data object that contains the data to be tested. Required |
| label.vec.num | The target binary condition. Required |
| pvalue.cutoff | choose p-value cut-off |

Value

df.output object

Examples

```
data('iris')
Wilcox_Test_df(t(iris[,1:4]),
  c(rep(1,100), rep(0,50)))
```


Index

* datasets

- [pstat_data](#), 19
- [Bootstrap_LOOCV_LR_AUC](#), 3
- [Chisq_Test_Pam](#), 4
- [findRAfromCount](#), 4
- [findTaxonMat](#), 5
- [findTaxonomy](#), 6
- [findTaxonomy300](#), 6
- [Fisher_Test_Pam](#), 7
- [formatTaxTable](#), 8
- [GET_PAM](#), 10
- [getShinyInput](#), 8
- [getShinyInputCombat](#), 9
- [getShinyInputOrig](#), 9
- [getSignatureFromMultipleGlmnet](#), 10
- [grepTid](#), 11
- [loadPathoscopeReports](#), 12
- [loadPstat](#), 13
- [log2CPM](#), 13
- [LOOAUC_simple_multiple_noplot_one_df](#), 14
- [LOOAUC_simple_multiple_one_df](#), 14
- [PathoStat-class](#), 15
- [pathostat1 \(PathoStat-class\)](#), 15
- [percent](#), 16
- [phyloseq_to_edgeR](#), 16
- [plotPCAPlotly](#), 17
- [plotPCoAPlotly](#), 18
- [pstat \(pstat_data\)](#), 19
- [pstat_data](#), 19
- [readPathoscopeData](#), 19
- [runPathoStat](#), 20
- [savePstat](#), 21
- [setShinyInput](#), 21
- [setShinyInputCombat](#), 22
- [setShinyInputOrig](#), 22
- [summarizeTable](#), 23
- [TranslateIdToTaxLevel](#), 23
- [Wilcox_Test_df](#), 24