Package 'microbiomeExplorer'

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Type Package

Title Microbiome Exploration App

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Description The MicrobiomeExplorer R package is designed to facilitate the analysis and visualization of marker-gene survey feature data.
It allows a user to perform and visualize typical microbiome analytical workflows either through the command line or an interactive
Shiny application included with the package. In addition to applying common analytical workflows the application enables automated
analysis report generation.

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Imports shinyjs (>= 2.0.0), shinydashboard, shinycssloaders, shinyWidgets, rmarkdown (>= 1.9.0), DESeq2, RColorBrewer, dplyr, tidyr, purrr, rlang, knitr, readr, DT (>= 0.12.0), biomformat, tools, stringr, vegan, matrixStats, heatmaply, car, broom, limma, reshape2, tibble, forcats, lubridate, methods, plotly (>= 4.9.1)

Depends shiny, magrittr, metagenomeSeq, Biobase

Suggests V8, testthat (>= 2.1.0)

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`abundanceHeatmap` *Abundance Heatmap module - server*

Description

Abundance Heatmap module - server

Usage

```
abundanceHeatmap(
  input,
  output,
  session,
  aggDat,
  featLevel,
  colorOptions,
  levelOpts,
  hmSort,
  hmFeatList,
  reset
)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
aggDat	aggregated MRExperiment
featLevel	chosen feature level (aggregation level)
colorOptions	reactive storing filters selected via data input
levelOpts	all available level choices for this dataset
hmSort	reactive storing sorting method for heatmap
hmFeatList	reactive storing list of features to include in heatmap
reset	boolean reactive which resets the module if TRUE

Value

R code needed to generate the heatmap

Author(s)

Janina Reeder

---

abundanceHeatmapUI *Abundance Heatmap module - UI*

Description

Abundance Heatmap module - UI

Usage

```
abundanceHeatmapUI(id)
```

Arguments

id	namespace identifier

Value

box holding the UI code

Author(s)

Janina Reeder

addFeatData *Add feature data to MRobj.*

Description

This function adds feature data to the featureData slot in an MRexperiment object.

Usage

```
addFeatData(MRobj, featdata = NULL)
```

Arguments

MRobj	An MRexperiment object.
featdata	Feature data frame or file path.

Value

An updated MRexperiment object.

addPhenoData *Add phenotype data to object.*

Description

This function adds phenotype data to the phenoData slot in an MRexperiment object.

Usage

```
addPhenoData(MRobj, phenodata = NULL)
```

Arguments

MRobj	An MRexperiment object.
phenodata	Phenotype data frame or file path.

Value

An updated MRexperiment object.

add_plotly_config *Adds a config call based on plotly::config*

Description

Adds a config call based on plotly::config

Usage

```
add_plotly_config(.data)
```

Arguments

.data	plotly data object to apply the config call to

Value

plotly::config call

add_plotly_layout *Adds a layout call based on plotly::layout*

Description

Adds a layout call based on plotly::layout

Usage

```
add_plotly_layout(.data, plotTitle, xaxis_text, ylab)
```

Arguments

.data	plotly data object to apply the layout call to
plotTitle	plot title to use
xaxis_text	x axis label to use
ylab	y axis label to use

Value

plotly::layout call

aggFeatures *Aggregates counts by level*

Description

This function aggregates counts by a level specified in the featureData slot of the MRexperiment object.

Usage

```
aggFeatures(MRobj, level = NULL, sort = TRUE)
```

Arguments

MRobj	An MRexperiment object.
level	Level to aggregate over. If NULL, no aggregation occurs.
sort	boolean determining if resulting aggregated MRexperiment should be sorted based on rowSums; default is TRUE

Value

Aggregated MRexperiment object or matrix depending on out.

Examples

```
data("mouseData", package = "metagenomeSeq")
aggFeatures(mouseData, level = "genus")
```

aggregationTab *Aggregation module server function*

Description

Aggregation module server function

Usage

```
aggregationTab(
  input,
  output,
  session,
  resetInput,
  levelOpts,
  chosenLevel,
  meData
)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
resetInput	boolean updated to TRUE if new data is available
levelOpts	available levels to aggregate on (depends on input data)
chosenLevel	previously selected level (passed from different instance)
meData	the main MRexperiment object

Value

reactive list holding aggregated object, aggregation code and boolean on normalization

Author(s)

Janina Reeder

---

aggregationTabUI *Aggregation module ui function*

Description

Aggregation module ui function

Usage

```
aggregationTabUI(id)
```

Arguments

id	namespace identifier

Value

box holding aggregation input elements

Author(s)

Janina Reeder

Examples

```
aggregationTabUI("atu_id")
```

`alphaDiversity` *Alpha Diversity module - server*

Description

Alpha Diversity module - server

Usage

```
alphaDiversity(
  input,
  output,
  session,
  aggDat,
  featLevel,
  intraSettings,
  colorOptions,
  reset
)
```

Arguments

`input`	shiny input
`output`	shiny output
`session`	shiny session
`aggDat`	aggregated MRExperiment
`featLevel`	chosen feature level (aggregation level)
`intraSettings`	analysis settings as passed over from analysis input module
`colorOptions`	phenotype selections: used for color choices
`reset`	boolean reactive which resets the module if TRUE

Value

R code used to make the alpha diversity plot

Author(s)

Janina Reeder

alphaDiversityUI *Alpha Diversity module - UI*

Description

Alpha Diversity module - UI

Usage

```
alphaDiversityUI(id)
```

Arguments

id	namespace identifier

Value

box holding the UI code

Author(s)

Janina Reeder

avgAbundance *Relative abundance plot module - server*

Description

Relative abundance plot module - server

Usage

```
avgAbundance(
  input,
  output,
  session,
  aggDat,
  featLevel,
  featureSettings,
  normalizedData,
  reset
)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
aggDat	aggregated MRExperiment
featLevel	chosen feature level (aggregation level)
featureSettings	analysis input settings passed over to this module
normalizedData	boolean indicating whether data has been normalized
reset	boolean reactive which resets the module if TRUE

Value

list storing plot clicks and number of features displayed (passed to feature plot module) as well as the R code to make plot

---

avgAbundanceUI *Relative abundance plot module - UI*

Description

Relative abundance plot module - UI

Usage

```
avgAbundanceUI(id)
```

Arguments

id	namespace identifier

Value

box containing the ui code

Author(s)

Janina Reeder

`betaDiversity` *Beta Diversity module - server*

Description

Beta Diversity module - server

Usage

```
betaDiversity(
  input,
  output,
  session,
  aggDat,
  aggLevel,
  colorOptions,
  shapeOptions,
  betadistance,
  betaSettings,
  reset
)
```

Arguments

`input`	shiny input
`output`	shiny output
`session`	shiny session
`aggDat`	MRExperiment storing data
`aggLevel`	aggregation level
`colorOptions`	phenotype selection options for color
`shapeOptions`	phenotype selection options for shape
`betadistance`	distance measured used for beta diversity analysis
`betaSettings`	input choices for beta diversity
`reset`	boolean reactive which resets the module if TRUE

Value

R code needed to generate the beta diversity plot

Author(s)

Janina Reeder

betaDiversityUI *Beta Diversity module - UI*

Description

Beta Diversity module - UI

Usage

```
betaDiversityUI(id)
```

Arguments

id	namespace identifier

Value

box holding the ui code

Author(s)

Janina Reeder

betaInput *Server side for the analysis input module handling analysis control*

Description

Server side for the analysis input module handling analysis control

Usage

```
betaInput(input, output, session, meData, adonisOptions, reset)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
meData	MRExperiment object storing all data
adonisOptions	phenodata colums ready for adonis analysis
reset	reactive boolean determining if all inputs should be reset

Value

list holding all chosen values and the selected feature

Author(s)

Janina Reeder

`betaInputUI` *Main beta analysis input module. Set up to handle all analysis tabs in the app depending on given parameters*

Description

Main beta analysis input module. Set up to handle all analysis tabs in the app depending on given parameters

Usage

```
betaInputUI(id)
```

Arguments

`id`	element identifier - namespace

Value

box containing ui element

Author(s)

Janina Reeder

`buildEmptyPlotlyPlot` *Creates an empty plotly plot using the given labels on the x and y axis*

Description

Creates an empty plotly plot using the given labels on the x and y axis

Usage

```
buildEmptyPlotlyPlot(xaxis_text, ylab)
```

Arguments

`xaxis_text`	x axis label
`ylab`	y axis label

Value

call to plotly_empty

`buildPlottingDF` *Sets up a dataframe used by several plotting functions by joining the required data with relevant phenotype data*

Description

Sets up a dataframe used by several plotting functions by joining the required data with relevant phenotype data

Usage

```
buildPlottingDF(
  df,
  phenoTable,
  x_var = NULL,
  facet1 = NULL,
  facet2 = NULL,
  col_by = NULL,
  col_name = col_by,
  id_var = NULL
)
```

Arguments

`df`	dataframe storing plotting data values
`phenoTable`	pData of the MRexperiment; all following parameters must be a column of the phenoTable
`x_var`	main plotting variable
`facet1`	column-based faceting (can be NULL)
`facet2`	row-based faceting (can be NULL)
`col_by`	coloring factor (can be NULL)
`col_name`	character to be used as name for col_by
`id_var`	variable used to connect samples longitudinally (can be NULL)

Value

dataframe obtained by joining df and relevant columns of phenoTable

calculatePCAs *Function to compute the PCAs for a given distance matrix*

Description

Function to compute the PCAs for a given distance matrix

Usage

```
calculatePCAs(distmat, pcas)
```

Arguments

distmat	the distance matrix
pcas	2-element vector of PCAs to include in results

Value

the x slot limited to pcas after calling stats::prcomp on distmat

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
distmat <- computeDistMat(aggdat, dist_method = "bray")
calculatePCAs(distmat, c(1,2))
```

computeCI_Interval *Helper function to calculate the confidence interval for a cor.test*

Description

Helper function to calculate the confidence interval for a cor.test

Usage

```
computeCI_Interval(num, mS, method)
```

Arguments

num	number of samples
mS	results of cor.test
method	statistical method used for cor.test

Value

named vector holding lower and upper thresholds

computeDistMat *Function to compute the distance matrix using vegdist from the vegan package*

Description

Function to compute the distance matrix using vegdist from the vegan package

Usage

```
computeDistMat(aggdat, dist_method, log = TRUE, nfeatures = nrow(aggmat))
```

Arguments

aggdat	aggregated MRExperiment
dist_method	distance method from vegan package (See ?vegan::vegdist for details)
log	transform count matrix to log2; default is TRUE
nfeatures	number of features to use; default is all

Value

distance as dist

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
computeDistMat(aggdat, dist_method = "bray")
```

corrAnalysis *corr Analysis Module - server*

Description

corr Analysis Module - server

Usage

```
corrAnalysis(
  input,
  output,
  session,
  data,
  levelOpts,
  chosenLevel,
  resetInput,
  aggData
)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
data	the main data object returned from data_input_module
levelOpts	available levels to aggregate on (depends on input data)
chosenLevel	previously selected level (passed from different instance)
resetInput	reactive boolean determining if reset is required
aggData	the aggregated MRExperiment object

Value

reactive holding code to be used in reports

---

corrAnalysisUI *corr Analysis Module - UI*

Description

corr Analysis Module - UI

Usage

```
corrAnalysisUI(id)
```

Arguments

id	namespace identifier

Value

fluidRow containing the ui code

Author(s)

Janina Reeder

Examples

```
corrAnalysisUI("coranalysis_id")
```

`corrFeature` *Scatterplot of two features*

Description

This function plots a scatterplot of two features along with sample correlation statistics.

Usage

```
corrFeature(
  aggdat,
  feat1,
  feat2,
  log = TRUE,
  method = c("spearman", "pearson", "kendall"),
  addRegression = TRUE,
  col_by = NULL,
  facet1 = NULL,
  facet2 = NULL,
  plotTitle = "",
  xlab = NULL,
  ylab = NULL,
  allowWebGL = TRUE,
  pwidth = 550,
  pheight = 200
)
```

Arguments

`aggdat`	aggregated MRExperiment
`feat1`	Feature 1.
`feat2`	Feature 2.
`log`	Log2 transform data. Default is TRUE.
`method`	Correlation coefficient. One of "spearman" (default), "pearson", or "kendall".
`addRegression`	boolean parameter indicating whether linear regression line should be drawn; default: TRUE
`col_by`	Phenotype for coloring.

facet1	Phenotype for facet 1.
facet2	Phenotype for facet 2.
plotTitle	Plot title. Default is no title.
xlab	X-axis label. Default is feat1.
ylab	Y-axis label. Default is feat2.
allowWebGL	boolean indicating if WebGL should be used for large data
pwidth	overall plot width; default is 550
pheight	overall plot height; default is 200

Value

list holding plotly plot and lm fit

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
corrFeature(aggdat, feat1 = "Bacteroides", feat2 = "Prevotella")
```

---

corrInput *Server side for the analysis input module handling analysis control*

Description

Server side for the analysis input module handling analysis control

Usage

```
corrInput(
  input,
  output,
  session,
  type,
  meData,
  facetOptions = NULL,
  reset,
  aggDat = reactive(NULL)
)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
type	of the correlation (feature vs phenotype)
meData	MRExperiment object storing all data
facetOptions	named vector of available facet choices
reset	reactive boolean determining if all inputs should be reset
aggDat	aggregated MRExperiment object (default is NULL)

Value

list holding all chosen values and the selected feature

Author(s)

Janina Reeder

---

corrInputUI *Main correlation analysis input module. Handles correlation analysis tab in the app*

Description

Main correlation analysis input module. Handles correlation analysis tab in the app

Usage

```
corrInputUI(id, type)
```

Arguments

id	element identifier - namespace
type	determines if 'feature' or 'pheno' correlation

Value

box containing ui element

Author(s)

Janina Reeder

corrPhenotype *Scatterplot of a feature and a phenotype*

Description

This function plots a scatterplot of a feature and a phenotype along with sample correlation statistics.

Usage

```
corrPhenotype(
  aggdat,
  feature,
  phenotype,
  log = TRUE,
  method = c("spearman", "pearson", "kendall"),
  addRegression = TRUE,
  col_by = NULL,
  facet1 = NULL,
  facet2 = NULL,
  plotTitle = "",
  xlab = NULL,
  ylab = NULL,
  allowWebGL = TRUE,
  pwidth = 550,
  pheight = 200
)
```

Arguments

aggdat	aggregated MRExperiment
feature	Feature input.
phenotype	Phenotype input (must be numeric)
log	Log2 transform data. Default is TRUE.
method	Correlation coefficient. One of "spearman" (default), "pearson", or "kendall".
addRegression	boolean parameter indicating whether linear regression line should be drawn; default: TRUE
col_by	Phenotype for coloring.
facet1	Phenotype for facet 1.
facet2	Phenotype for facet 2. (WIP/TODO)
plotTitle	Plot title. Default is no title.
xlab	X-axis label. Default is feat1.
ylab	Y-axis label. Default is feat2.
allowWebGL	boolean indicating if WebGL should be used for large data
pwidth	overall plot width; default is 550
pheight	overall plot height; default is 200

Value

list holding plotly plot and lm fit

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
corrPhenotype(aggdat, feature = "Bacteroides", phenotype = "relativeTime")
```

---

createHeader *Makes header for R script*

Description

This function makes the header for the report R script to be rendered by knitr into Rmarkdown and rendered into HTML, PDF, or Word.

Usage

```
createHeader(
  title = "MicrobiomeExplorer Report",
  author = "",
  date = "",
  data.source = "",
  output = getOption("me.reportformat"),
  toc = TRUE
)
```

Arguments

title	Title of the report.
author	Author of the report.
date	Date of the report.
data.source	R code used to obtain the dataset
output	Output of Rmarkdown file.
toc	Table of contents. Default is TRUE.

Details

This was adapted from https://yihui.name/knitr/demo/stitch/

Value

A character vector where each element is a line in the R script.

`dataInput` *Main Data input server where the user selects files to upload to the app or connects to database*

Description

Main Data input server where the user selects files to upload to the app or connects to database

Usage

```
dataInput(
  input,
  output,
  session,
  dataSource,
  dataFilterRep,
  qcRep,
  addPheno,
  resetReports
)
```

Arguments

`input`	module input
`output`	module output
`session`	app session
`dataSource`	reactive Value storing commands for loading data
`dataFilterRep`	reactive Value storing commands for filtering data
`qcRep`	reactive Value storing commands for producing qc plots
`addPheno`	reactive boolean keeping track of phenodata changes
`resetReports`	reactive boolean indicating whether reports need to be reset

Value

list of reactives containing the uploaded and filtered data as well as the filterChoices on phenotypes

Author(s)

Janina Reeder

dataInputUI *Main Data input UI where the user selects files to upload to the app or connects to database*

Description

Main Data input UI where the user selects files to upload to the app or connects to database

Usage

```
dataInputUI(id)
```

Arguments

id	module identifier

Value

fluidRow holding UI interface

Author(s)

Janina Reeder

Examples

```
dataInputUI("datainput_id")
```

designPairs *Produce design matrix of pairwise comparisons*

Description

This function takes in the levels of a factor phenotype and outputs a design matrix of all pairwise comparisons.

Usage

```
designPairs(levels)
```

Arguments

levels	Character vector of the levels of a factor phenotype

Value

A model matrix

`diffAnalysis` *diff Analysis Module - server*

Description

diff Analysis Module - server

Usage

```
diffAnalysis(
  input,
  output,
  session,
  data,
  levelOpts,
  chosenLevel,
  resetInput,
  aggData,
  normalizedData
)
```

Arguments

`input`	shiny input
`output`	shiny output
`session`	shiny session
`data`	the main data object returned from data_input_module
`levelOpts`	available levels to aggregate on (depends on input data)
`chosenLevel`	previously selected level (passed from different instance)
`resetInput`	reactive boolean determining if reset is required
`aggData`	the aggregated MRExperiment object
`normalizedData`	boolean indicating if normalization was done

Value

reactive holding code to be used in reports

Author(s)

Janina Reeder

diffAnalysisUI *Diff Analysis Module - UI*

Description

Diff Analysis Module - UI

Usage

```
diffAnalysisUI(id)
```

Arguments

id	namespace identifier

Value

fluidRow containing the ui code

Author(s)

Janina Reeder

Examples

```
diffAnalysisUI("diffanalysis_id")
```

diffInput *Server side for the analysis input module handling analysis control*

Description

Server side for the analysis input module handling analysis control

Usage

```
diffInput(input, output, session, meData, facetOptions = NULL, reset)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
meData	MRExperiment object storing all data
facetOptions	named vector of available facet choices
reset	reactive boolean determining if all inputs should be reset

Value

list holding all chosen values and the selected feature

Author(s)

Janina Reeder

`diffInputUI` *Main diffanalysis input module. Set up to handle diff analysis tabs in the app depending on given parameters*

Description

Main diffanalysis input module. Set up to handle diff analysis tabs in the app depending on given parameters

Usage

```
diffInputUI(id)
```

Arguments

`id`	element identifier - namespace

Value

box containing ui element

Author(s)

Janina Reeder

`diffTable` *Differential analysis module server code*

Description

Differential analysis module server code

Usage

```
diffTable(
  input,
  output,
  session,
  aggDat,
  featLevel,
  diffSettings,
  reset,
  normalized
)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
aggDat	aggregated MRExperiment
featLevel	chosen feature level (aggregation level)
diffSettings	reactive storing values selected in analysis input interface
reset	boolean reactive which resets the module if TRUE
normalized	boolean reactive indicating if data has been normalized

Value

list containing R code for analysis and for feature plots

Author(s)

Janina Reeder

---

diffTableUI *Differential Analysis module UI*

Description

Differential Analysis module UI

Usage

```
diffTableUI(id)
```

Arguments

id	namespace identifier

Value

row containing the UI elements

Author(s)

Janina Reeder

`extendPhenoData` *Extends existing phenodata for an object*

Description

This function adds phenotype data to the phenoData slot in an MRexperiment object.

Usage

```
extendPhenoData(MRobj, phenodata = NULL)
```

Arguments

`MRobj`	An MRexperiment object.
`phenodata`	Phenotype data frame or file path.

Value

An updated MRexperiment object.

`featAbundance` *Feature plot module - server*

Description

Feature plot module - server

Usage

```
featAbundance(
  input,
  output,
  session,
  aggDat,
  featLevel,
  intraSettings,
  selectedFeat,
  featName,
```

```
  numOfFeats,
  ylabMode,
  normalizedData,
  reset
)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
aggDat	aggregated MRExperiment
featLevel	chosen feature level (aggregation level)
intraSettings	analysis settings passed over from analysis input module
selectedFeat	feature selected via drop down element of analysis input
featName	plotly click event passed via relative abundance
numOfFeats	number of features shown in relative abundance plot (affects plotly click data)
ylabMode	character indication if raw \"Reads\" or \"Percentage\" should be shown
normalizedData	boolean indicating whether data has been normalized
reset	boolean reactive which resets the module if TRUE

Value

R code needed to build the feature plot

Author(s)

Janina Reeder

---

featAbundanceUI *Feature plot module - UI*

Description

Feature plot module - UI

Usage

```
featAbundanceUI(id)
```

Arguments

id	namespace identifier

Value

box holding the UI code

`featureAnalysis` *feature Analysis Module - server*

Description

feature Analysis Module - server

Usage

```
featureAnalysis(
  input,
  output,
  session,
  data,
  resetInput,
  aggData,
  normalizedData
)
```

Arguments

`input`	shiny input
`output`	shiny output
`session`	shiny session
`data`	the main data object returned from data_input_module
`resetInput`	reactive boolean determining if reset is required
`aggData`	the aggregated MRExperiment object
`normalizedData`	boolean indicating if normalization was done

Value

reactive holding code to be used in reports

Author(s)

Janina Reeder

featureAnalysisUI *feature Analysis Module - UI*

Description

feature Analysis Module - UI

Usage

```
featureAnalysisUI(id)
```

Arguments

id	namespace identifier

Value

fluidRow containing the ui code

Author(s)

Janina Reeder

Examples

```
featureAnalysisUI("featureanalysis_id")
```

featureCorr *Feature correlation analysis server module*

Description

Feature correlation analysis server module

Usage

```
featureCorr(
  input,
  output,
  session,
  aggDat,
  colorOptions,
  corFeatBase,
  corFeat2,
  corFacet1,
```

```
  corFacet2,
  corMethod,
  reset
)
```

Arguments

input	module input
output	module output
session	app session
aggDat	aggregated MRExperiment
colorOptions	reactive storing filters available via data input
corFeatBase	first correlation feature
corFeat2	second correlation feature
corFacet1	first correlation facet
corFacet2	second correlation facet
corMethod	correlation method to use
reset	boolean reactive which resets the module if TRUE

Value

R code used to do the correlation analysis (character)

Author(s)

Janina Reeder

---

featureCorrUI *Feature correlation analysis module UI*

Description

Feature correlation analysis module UI

Usage

```
featureCorrUI(id)
```

Arguments

id	namespace identifier

Value

box containing the UI elements

Author(s)

Janina Reeder

`featureInput` *Server side for the feature analysis input module*

Description

Server side for the feature analysis input module

Usage

```
featureInput(
  input,
  output,
  session,
  meData,
  facetOptions = NULL,
  reset,
  aggDat = reactive(NULL)
)
```

Arguments

`input`	shiny input
`output`	shiny output
`session`	shiny session
`meData`	MRExperiment object storing all data
`facetOptions`	named vector of available facet choices
`reset`	reactive boolean determining if all inputs should be reset
`aggDat`	aggregated MRExperiment object (default is NULL)

Value

list holding all chosen values and the selected feature

Author(s)

Janina Reeder

featureInputUI *Main feature analysis input module. Set up to handle all analysis tabs in the app depending on given parameters*

Description

Main feature analysis input module. Set up to handle all analysis tabs in the app depending on given parameters

Usage

```
featureInputUI(id)
```

Arguments

id	element identifier - namespace

Value

box containing ui element

Author(s)

Janina Reeder

featureTable *Feature table module server code*

Description

Feature table module server code

Usage

```
featureTable(input, output, session, meData, featureModRep)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
meData	MRExperiment storing the data
featureModRep	reactiveValue storing modifications performed on fData

Value

feature table server fragment - no return value

Author(s)

Janina Reeder

`featureTableUI` *Feature table UI module*

Description

Feature table UI module

Usage

```
featureTableUI(id)
```

Arguments

`id`	namespace identifier

Value

fluidRow containing the UI code for feature tables

Author(s)

Janina Reeder

Examples

```
featureTableUI("feature_id")
```

`fileUpload` *Module handling file upload for the application: server*

Description

Module handling file upload for the application: server

Usage

```
fileUpload(
  input,
  output,
  session,
  meData,
  meName,
  initializeData,
  addPheno,
  dataSource,
  resetFile = reactive(NULL)
)
```

Arguments

`input`	module input
`output`	module output
`session`	app session
`meData`	main reactive storing the MRexperiment data
`meName`	main reactive storing the filename uploaded
`initializeData`	reactiveVal keeping track of new uploads to reset data
`addPheno`	reactiveVal keeping track of phenodata changes
`dataSource`	reactive Value storing commands for loading data
`resetFile`	indicating if module should be reset

Value

boolean denoting successful upload of a file

Author(s)

Janina Reeder

`fileUploadUI` *Module handling file upload for the application: UI In a deployed version this module should be replaced with database access*

Description

Module handling file upload for the application: UI In a deployed version this module should be replaced with database access

Usage

```
fileUploadUI(id)
```

Arguments

`id`	module identifier

Value

div holding ui elements

Author(s)

Janina Reeder

`filterByPheno` *Function to filter the MRexperiment by certain phenotype values*

Description

Function to filter the MRexperiment by certain phenotype values

Usage

```
filterByPheno(MRobj, rm_phenovalues)
```

Arguments

`MRobj`	the MRexperiment to subset
`rm_phenovalues`	list of named vectors with names corresponding to column names in pData and values representing phenotypes within the column

Value

the filtered MRobj

Author(s)

Janina Reeder

Examples

```
data("mouseData", package = "metagenomeSeq")
filterByPheno(MRobj = mouseData,
  rm_phenovalues = list("diet" = c("BK"),"mouseID" = c("PM1","PM10")))
```

---

filterMEData *Function to filter the MRexperiment data by numerical parameters*

Description

Function to filter the MRexperiment data by numerical parameters

Usage

```
filterMEData(MRobj, minpresence = 1, minfeats = 2, minreads = 2)
```

Arguments

MRobj	MRExperiment object to filter
minpresence	minimum sample presence per feature
minfeats	minimum number of features per sample
minreads	minimum number of reads per sample

Value

the filtered MRobj

Author(s)

Janina Reeder

Examples

```
data("mouseData", package = "metagenomeSeq")
filterMEData(MRobj = mouseData, minpresence = 4, minfeats = 300)
```

`generateReport` *Generates report*

Description

This function generates the pieces of the report, which includes the R script, Rmarkdown file, and any Rmarkdown outputs.

Usage

```
generateReport(
  rcode,
  filename = "report",
  dir = "out",
  title = "MicrobiomeExplorer Report",
  author = "",
  date = "`r format(Sys.time(), '%d %B, %Y')`",
  data.source = "",
  output = c("html_document"),
  toc = TRUE,
  intro_text = NULL
)
```

Arguments

`rcode`	A named list where each element corresponds to a different analysis (Alpha diversity, Beta diversity). The name of the list is used to denote the first part of the code chunks in each analysis section (alpha, beta). Each element is itself a list of R commands corresponding to a code chunk.
`filename`	Name of output files. Default is "report".
`dir`	Directory of output. Default is "out".
`title`	Title of the report.
`author`	Author of the report.
`date`	Date of the report.
`data.source`	R code used to obtain the dataset
`output`	Output of Rmarkdown file. Options defined in global.R
`toc`	Table of contents. Default is TRUE.
`intro_text`	Introductory text to include with the report (optional)

Details

Adapted from https://yihui.name/knitr/demo/stitch/

Value

A character vector where each element is a line in the R script.

`getFeatModCode` *Helper function returning the fData modifications as strings for report generation*

Description

Helper function returning the fData modifications as strings for report generation

Usage

```
getFeatModCode(featureanno)
```

Arguments

`featureanno`	type of feature annotation; values are "Mark unknown" or "Roll down"

Value

String containing R code performing the modification

`getFeatSplitCode` *Helper function returning the fData modifications as strings for report generation*

Description

Helper function returning the fData modifications as strings for report generation

Usage

```
getFeatSplitCode(splittaxonomy)
```

Arguments

`splittaxonomy`	name of column to split on

Value

String containing R code performing the modification

`getFileType` *Helper function assigning different file extensions to specific short texts identifying the types*

Description

Helper function assigning different file extensions to specific short texts identifying the types

Usage

```
getFileType(fileext)
```

Arguments

`fileext`	the file extension found after '.'

Value

character string for the filetype

Author(s)

Janina Reeder

`getFilterChoices` *Helper function to filter phenodata for interesting phenotypes to be used for filtering or subsetting*

Description

Helper function to filter phenodata for interesting phenotypes to be used for filtering or subsetting

Usage

```
getFilterChoices(MRobj)
```

Arguments

`MRobj`	the MRexperiment storing the data

Value

list of named vectors with names being pData column headers and values being unique entries; columns with only one entry or those with different values for each samples are omitted

Author(s)

Janina Reeder

`getLegendLevel` *Function to find a non-empty facet in the last row. This will be the one to be connected to the plot legend to avoid duplicates within*

Description

Function to find a non-empty facet in the last row. This will be the one to be connected to the plot legend to avoid duplicates within

Usage

```
getLegendLevel(df2, facets, facet2s)
```

Arguments

`df2`	plotting data frame
`facets`	column facets
`facet2s`	row facets

Value

the name of the column-based facet which can be used as legend

`getPhenoChanges` *Helper function returning the code used to modify the data types of the pheno table*

Description

Helper function returning the code used to modify the data types of the pheno table

Usage

```
getPhenoChanges(phenotype, datatype)
```

Arguments

`phenotype`	name of the phenotype column header
`datatype`	variable type to assign to column

Value

String storing code to perform modification

Author(s)

Janina Reeder

`getPhenoModCode` *Helper function returning the code used to modify the phenotable as a string*

Description

Helper function returning the code used to modify the phenotable as a string

Usage

```
getPhenoModCode(name, pheno1, pheno2)
```

Arguments

`name`	interaction name
`pheno1`	first interaction phenotype
`pheno2`	second interaction phenotype

Value

String storing code to perform modification

Author(s)

Janina Reeder

`getWidths` *Helper function to account for issues plotly has with very small widths (these end up being 1 and cover the entire plotting area)*

Description

Helper function to account for issues plotly has with very small widths (these end up being 1 and cover the entire plotting area)

Usage

```
getWidths(df2, facets, x_var, drop = TRUE)
```

Arguments

`df2`	dataframe storing plotting data
`facets`	column facets
`x_var`	x variable
`drop`	passed on as .drop to dplyr::group_by

Value

widths for each facet

`heatmapInput` *Server side for the analysis input module handling analysis control*

Description

Server side for the analysis input module handling analysis control

Usage

```
heatmapInput(input, output, session, meData, reset, aggDat = reactive(NULL))
```

Arguments

`input`	shiny input
`output`	shiny output
`session`	shiny session
`meData`	MRExperiment object storing all data
`reset`	reactive boolean determining if all inputs should be reset
`aggDat`	aggregated MRExperiment object (default is NULL)

Value

list holding all chosen values and the selected feature

Author(s)

Janina Reeder

`heatmapInputUI` *Heatmap analysis input module. Set up to handle all analysis tabs in the app depending on given parameters*

Description

Heatmap analysis input module. Set up to handle all analysis tabs in the app depending on given parameters

Usage

```
heatmapInputUI(id)
```

Arguments

id	element identifier - namespace

Value

box containing ui element

Author(s)

Janina Reeder

---

interAnalysis *inter Analysis Module - server*

Description

inter Analysis Module - server

Usage

```
interAnalysis(
  input,
  output,
  session,
  data,
  levelOpts,
  chosenLevel,
  resetInput,
  aggData
)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
data	the main data object returned from data_input_module
levelOpts	available levels to aggregate on (depends on input data)
chosenLevel	previously selected level (passed from different instance)
resetInput	reactive boolean determining if reset is required
aggData	the aggregated MRExperiment object

Value

reactive holding code to be used in reports

interAnalysisUI *inter Analysis Module - UI*

Description

inter Analysis Module - UI

Usage

```
interAnalysisUI(id)
```

Arguments

id	namespace identifier

Value

fluidRow containing the ui code

Author(s)

Janina Reeder

Examples

```
interAnalysisUI("interanalysis_id")
```

intraAnalysis *Intra Analysis Module - server*

Description

Intra Analysis Module - server

Usage

```
intraAnalysis(
  input,
  output,
  session,
  data,
  levelOpts,
  chosenLevel,
  resetInput,
  aggData,
  normalizedData
)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
data	the main data object returned from data_input_module
levelOpts	available levels to aggregate on (depends on input data)
chosenLevel	previously selected level (passed from different instance)
resetInput	reactive boolean determining if reset is required
aggData	the aggregated MRExperiment object
normalizedData	boolean indicating if normalization was done

Value

reactive holding code to be used in reports

Author(s)

Janina Reeder

---

intraAnalysisUI *Intra Analysis Module - UI*

Description

Intra Analysis Module - UI

Usage

```
intraAnalysisUI(id)
```

Arguments

id	namespace identifier

Value

fluidRow containing the ui code

Author(s)

Janina Reeder

Examples

```
intraAnalysisUI("intraanalysis_id")
```

`intraInput` *Server side for the intra analysis input module*

Description

Server side for the intra analysis input module

Usage

```
intraInput(
  input,
  output,
  session,
  meData,
  facetOptions = NULL,
  reset,
  aggDat = reactive(NULL)
)
```

Arguments

`input`	shiny input
`output`	shiny output
`session`	shiny session
`meData`	MRExperiment object storing all data
`facetOptions`	named vector of available facet choices
`reset`	reactive boolean determining if all inputs should be reset
`aggDat`	aggregated MRExperiment object (default is NULL)

Value

list holding all chosen values and the selected feature

Author(s)

Janina Reeder

intraInputUI *Main intra analysis input module. Set up to handle all analysis tabs in the app depending on given parameters*

Description

Main intra analysis input module. Set up to handle all analysis tabs in the app depending on given parameters

Usage

```
intraInputUI(id)
```

Arguments

id	element identifier - namespace

Value

box containing ui element

Author(s)

Janina Reeder

longAnalysis *long Analysis Module - server*

Description

long Analysis Module - server

Usage

```
longAnalysis(
  input,
  output,
  session,
  data,
  levelOpts,
  chosenLevel,
  resetInput,
  aggData,
  normalizedData
)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
data	the main data object returned from data_input_module
levelOpts	available levels to aggregate on (depends on input data)
chosenLevel	previously selected level (passed from longerent instance)
resetInput	reactive boolean determining if reset is required
aggData	the aggregated MRExperiment object
normalizedData	boolean indicating if normalization was done

Value

reactive holding code to be used in reports

Author(s)

Janina Reeder

---

longAnalysisUI *Long Analysis Module - UI*

Description

Long Analysis Module - UI

Usage

```
longAnalysisUI(id)
```

Arguments

id	namespace identifier

Value

fluidRow containing the ui code

Author(s)

Janina Reeder

Examples

```
longAnalysisUI("longanalysis_id")
```

`longInput` *Server side for the analysis input module handling analysis control*

Description

Server side for the analysis input module handling analysis control

Usage

```
longInput(
  input,
  output,
  session,
  meData,
  facetOptions = NULL,
  reset,
  aggDat = reactive(NULL)
)
```

Arguments

`input`	shiny input
`output`	shiny output
`session`	shiny session
`meData`	MRexperiment object storing all data
`facetOptions`	named vector of available facet choices
`reset`	reactive boolean determining if all inputs should be reset
`aggDat`	aggregated MRexperiment

Value

list holding all chosen values and the selected feature

Author(s)

Janina Reeder

`longInputUI` *Main diffanalysis input module. Set up to handle diff analysis tabs in the app depending on given parameters*

Description

Main diffanalysis input module. Set up to handle diff analysis tabs in the app depending on given parameters

Usage

```
longInputUI(id)
```

Arguments

`id`	element identifier - namespace

Value

box containing ui element

Author(s)

Janina Reeder

`longResults` *Longitudinal analysis module server code*

Description

Longitudinal analysis module server code

Usage

```
longResults(
  input,
  output,
  session,
  aggDat,
  featLevel,
  longSettings,
  normalizedData,
  reset
)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
aggDat	aggregated MRExperiment
featLevel	chosen feature level (aggregation level)
longSettings	reactive storing values selected in analysis input interface
normalizedData	reactive boolean indicating if data has been normalized
reset	boolean reactive which resets the module if TRUE

Value

list containing R code for analysis and for feature plots

Author(s)

Janina Reeder

---

longResultsUI *Longitudinal Analysis module UI*

Description

Longitudinal Analysis module UI

Usage

```
longResultsUI(id)
```

Arguments

id	namespace identifier

Value

row containing the UI elements

Author(s)

Janina Reeder

makeQCPlot *Plots sequencing statistics scatterplot*

Description

This function makes a scatterplot of read and feature counts for each sample. It was adjusted based on original work by Mo Huang

Usage

```
makeQCPlot(
  MRobj,
  col_by = NULL,
  log = "none",
  filter_feat = 0,
  filter_read = 0,
  allowWebGL = TRUE,
  pwidth = 550,
  pheight = 550
)
```

Arguments

MRobj	metagenomeSeq object to be plotted
col_by	factor by which to color the points
log	character indicating which (if any) axes should be shown as log
filter_feat	Numeric Y-coordinate to draw horizontal dashed line to indicate feature filtering. If 0 (default), no line is drawn.
filter_read	Numeric X-coordinate to draw vertical dashed line to indicate read count filtering. If 0 (default), no line is drawn.
allowWebGL	boolean indicating if webGL should be added
pwidth	overall plot width; default is 550 (125 are added for legend)
pheight	overall plot height; default is 550

Value

the plotly QC plot

Author(s)

Janina Reeder

Examples

```
data("mouseData", package = "metagenomeSeq")
makeQCPlot(mouseData)
```

`normalizeData` *Calls appropriate normalization functions depending on input parameter The two available methods included in the package are based on either calculating proportions or by using cumulative sum scaling (CSS), Paulson, et al. Nat Meth 2013.*

Description

Calls appropriate normalization functions depending on input parameter The two available methods included in the package are based on either calculating proportions or by using cumulative sum scaling (CSS), Paulson, et al. Nat Meth 2013.

Usage

```
normalizeData(MRobj, norm_method)
```

Arguments

`MRobj`	the MRexperiment
`norm_method`	method to use for normalization; CSS or Proportional

Value

the normalized MRobj

Examples

```
data("mouseData", package = "metagenomeSeq")
normalizeData(mouseData, norm_method = "CSS")
```

`parseInteractionName` *Helper function used to build a correct interactionName based on the chosen columns*

Description

Helper function used to build a correct interactionName based on the chosen columns

Usage

```
parseInteractionName(interactionName)
```

Arguments

`interactionName`	as chosen by user. This may not be good to store internally

Value

updated interactionName or warning/error string

`phenotypeCorr` *Phenotype correlation analysis server module*

Description

Phenotype correlation analysis server module

Usage

```
phenotypeCorr(
  input,
  output,
  session,
  aggDat,
  colorOptions,
  corFeatBase,
  corPheno,
  corFacet1,
  corFacet2,
  corMethod,
  reset
)
```

Arguments

`input`	shiny input
`output`	shiny output
`session`	shiny session
`aggDat`	aggregated MRExperiment
`colorOptions`	reactive storing filters available via data input
`corFeatBase`	first correlation feature
`corPheno`	correlation phenotype
`corFacet1`	first correlation facet
`corFacet2`	second correlation facet
`corMethod`	correlation method to use
`reset`	boolean reactive which resets the module if TRUE

Value

R code used to do the correlation analysis (character)

Author(s)

Janina Reeder

---

phenotypeCorrUI *Phenotype correlation analysis module*

Description

Phenotype correlation analysis module

Usage

```
phenotypeCorrUI(id)
```

Arguments

id	namespace identifier

Value

box containing the UI element

Author(s)

Janina Reeder

---

phenotypeTable *Phenotype table server module*

Description

Phenotype table server module

Usage

```
phenotypeTable(input, output, session, meData, phenoModRep, addPheno)
```

Arguments

input	shiny input
output	shiny output
session	shiny session
meData	MRExperiment storing the data
phenoModRep	reactive Value storing any phenotable modifications made
addPheno	reactive boolean keeping track of pheno data modifications

Value

phenotype table server fragment - no return value

Author(s)

Janina Reeder

`phenotypeTableUI` *Phenotype table UI module*

Description

Phenotype table UI module

Usage

```
phenotypeTableUI(id)
```

Arguments

`id`	namespace identifier

Value

fluidRow holding the ui code

Author(s)

Janina Reeder

Examples

```
phenotypeTableUI("phenotype_id")
```

`plotAbundance` *Plot relative abundance*

Description

This function plots the relative abundance of the top abundant features.

Usage

```
plotAbundance(
  aggdat,
  level,
  x_var = "SAMPLE_ID",
  ind = seq_len(10),
  plotTitle = "",
  ylab = "Reads",
  facet1 = NULL,
  facet2 = NULL,
  source = "A",
  pwidth = 650,
  pheight = 150
)
```

Arguments

`aggdat`	aggregated MRExperiment object
`level`	Feature level.
`x_var`	Phenotype to aggregate over on X-axis. Default by "SAMPLE_ID".
`ind`	Indices of top abundant features to plot. Rest of features are aggregated and displayed as "other".
`plotTitle`	Plot title. Default shows no title.
`ylab`	Y-axis label. Default is "Reads"
`facet1`	Phenotype for facet 1.
`facet2`	Phenotype for facet 2.
`source`	name of the plot (needed for event handling); default is "A"
`pwidth`	overall plot width; default is 650
`pheight`	overall plot height; default is 150

Value

plotly plot

Author(s)

Janina Reeder

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
plotAbundance(aggdat, level = "genus", x_var = "diet")
```

---

plotAlpha *Plot alpha diversity*

Description

This function plots the alpha diversity. See ?vegan::diversity for details on the available index

Usage

```
plotAlpha(
  aggdat,
  level,
  index = c("shannon", "simpson", "invsimpson", "richness"),
  x_var = "SAMPLE_ID",
  ylab = index,
  col_by = NULL,
  facet1 = NULL,
  facet2 = NULL,
  plotTitle = "",
  pwidth = 500,
  pheight = 150
)
```

Arguments

aggdat	aggregated MRExperiment
level	Feature level
index	Diversity index, one of "shannon", "simpson", "invsimpson" or "richness" (=number of features). Default is "shannon".
x_var	Phenotype to aggregate over on X-axis. Default by "SAMPLE_ID".
ylab	Y-axis label. Default is "Reads".
col_by	Phenotype for coloring.
facet1	Phenotype for facet 1.
facet2	Phenotype for facet 2.
plotTitle	Plot title. By default, no title is used.
pwidth	overall plot width; default is 650
pheight	overall plot height; default is 150

Value

plotly plot object

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
plotAlpha(aggdat, level = "genus", index = "shannon", x_var = "diet")
```

---

plotAvgAbundance *Plot average relative abundance*

Description

This function plots the average relative abundance of the top abundant features.

Usage

```
plotAvgAbundance(
  aggdat,
  level,
  ind = seq_len(10),
  plotTitle = "",
  ylab = "Reads",
  facet1 = NULL,
  facet2 = NULL,
  source = "A",
  pwidth = 500,
  pheight = 150
)
```

Arguments

aggdat	aggregated MRExperiment object
level	Feature level.
ind	Indices of top abundant features to plot. Rest of features are aggregated and displayed as "other".
plotTitle	Plot title. Default shows no title.
ylab	Y-axis label. Default is "Reads"
facet1	Phenotype for facet 1.
facet2	Phenotype for facet 2.
source	name of the plot (needed for event handling); default is "A"
pwidth	overall plot width; default is 500
pheight	overall plot height; default is 150

Value

plotly plot

Author(s)

Janina Reeder

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
plotAvgAbundance(aggdat, level = "genus")
```

---

plotBeta *Plot beta diversity*

Description

This functions plots the beta diversity as a PCoA plot.

Usage

```
plotBeta(
  aggdat,
  dim = c(1, 2),
  log = TRUE,
  dist_method = "bray",
  pcas = NULL,
  nfeatures = nrow(aggdat),
  col_by = NULL,
  shape_by = NULL,
  plotTitle = "",
  xlab = NULL,
  ylab = NULL,
  pt_size = 8,
  plotText = NULL,
  confInterval = NULL,
  allowWebGL = TRUE,
  pwidth = 550,
  pheight = 550
)
```

Arguments

aggdat	aggregated MRExperiment
dim	Vector of length 2 specifying which dimensions to plot.
log	Log2 transform data. Default is TRUE.
dist_method	Which distance method to use. See ?vegan::vegdist for more vegdist() for options. Default is "bray".
pcas	precalculated pcas to avoid recalculation via CalcPCs
nfeatures	Number of top features in terms of standard deviation. Default is all.
col_by	Phenotype for coloring.
shape_by	Phenotype for shape.
plotTitle	Plot title. By default, becomes PCoA (codedist.method).
xlab	X-axis label. By default, shows dimension and percent variance explained.
ylab	Y-axis label. By default, shows dimension and percent variance explained.
pt_size	the size of the markers
plotText	adonis text to be added to plot
confInterval	numeric value indicating confidence level for ellipses
allowWebGL	boolean indicating if WebGL should be used
pwidth	overall plot width; default is 550 (125 are added for legend)
pheight	overall plot height; default is 550

Value

plotly plot object

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
plotBeta(aggdat)
```

---

plotHeatmap *Plot heatmap*

Description

This function plots a heatmap of feature abundance.

Usage

```
plotHeatmap(
  aggdat,
  features = NULL,
  log = TRUE,
  sort_by = c("Fano", "MAD", "Variance"),
  nfeat = 50,
  col_by = NULL,
  row_by = NULL,
  plotTitle = ""
)
```

Arguments

aggdat	aggregated MRExperiment
features	Vector of features to plot. If NULL, the top ‘nfeat‘ features in terms of ‘sort_by‘ will be plotted.
log	Log2 transform data. Default is TRUE.
sort_by	Dispersion measure to sort features, one of "Fano", "MAD", and "Variance"
nfeat	Number of features to display. Default is 50.
col_by	Vector of phenotypes for coloring.
row_by	Name of feature level for coloring.
plotTitle	Plot title. By default, no title.

Value

plotly heatmap

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
plotHeatmap(aggdat, sort_by = "Fano")
```

---

plotLongFeature *Plot longitudinal features*

Description

This function plots the reads of a particular feature over different time points.

Usage

```
plotLongFeature(
  aggdat,
  feature,
  x_var,
  id_var = "SAMPLE_ID",
  plotTitle = NULL,
  ylab = "Reads",
  log = FALSE,
  showLines = TRUE,
  fixedHeight = NULL,
  x_levels = NULL,
  pwidth = 650
)
```

Arguments

aggdat	aggregated MRExperiment
feature	Feature to plot.
x_var	Phenotype to show along on X-axis.
id_var	phenotype used to connect data points. Default is "SAMPLE_ID"
plotTitle	Plot title. Default shows no title.
ylab	Y-axis label. Default is "Reads"
log	Log2 transform data. Default is FALSE.
showLines	add lines between the points
fixedHeight	sets a specific plot height (differential analysis)
x_levels	restrict to specific levels of x_var (differential analysis)
pwidth	overall plot width; default is 650

Value

plotly object holding long feature plot

Author(s)

Janina Reeder, Mo Huang

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
plotLongFeature(aggdat, feature = "Prevotella", x_var = "diet",
                id_var = "mouseID")
```

plotlyHistogram *Function plotting a plotly histogram on the given histvalue*

Description

Function plotting a plotly histogram on the given histvalue

Usage

```
plotlyHistogram(
  histvalue,
  plotTitle,
  xaxisTitle = "",
  yaxisTitle = "",
  pwidth = 200,
  pheight = 200
)
```

Arguments

histvalue	the value to plot as a histogram
plotTitle	title of the plot
xaxisTitle	name of xaxis; default is ""
yaxisTitle	name of yaxis; default is ""
pwidth	overall plot width; default is 200
pheight	overall plot height; default is 200

Value

plotly plot object

Examples

```
data("mouseData", package = "metagenomeSeq")
plotlyHistogram(histvalue = colSums(MRcounts(mouseData) > 0),
  plotTitle = "Feature distribution",
  xaxisTitle = "features", yaxisTitle = "frequency")
```

`plotlySampleBarplot` *Function plotting a barplot showing number of OTUs per samples*

Description

Function plotting a barplot showing number of OTUs per samples

Usage

```
plotlySampleBarplot(
  MRobj,
  col_by = NULL,
  xaxisTitle = "",
  yaxisTitle = "",
  pwidth = 600,
  pheight = 450,
  sortbyfreq = FALSE,
  pheno_sort = NULL,
  x_levels = NULL
)
```

Arguments

`MRobj`	containing data to plot
`col_by`	phenotype to color bars by; default is NULL
`xaxisTitle`	name of xaxis; default is ""
`yaxisTitle`	name of yaxis; default is ""
`pwidth`	overall plot width; default is 600
`pheight`	overall plot height; default is 450
`sortbyfreq`	boolean determining if bars should be sorted by frequency; default is FALSE
`pheno_sort`	order of pheno levels to sort by; ignored if sortbyfreq is TRUE
`x_levels`	character vector holding x values in order to be shown

Value

plotly plot object

Examples

```
data("mouseData", package = "metagenomeSeq")
plotlySampleBarplot(mouseData)
```

plotSingleFeature *Plot features*

Description

This function plots the reads of a particular feature or set of features.

Usage

```
plotSingleFeature(
  aggdat,
  feature = "other",
  x_var = "SAMPLE_ID",
  ind = seq_len(10),
  plotTitle = NULL,
  ylab = "Reads",
  xlab = NULL,
  facet1 = NULL,
  facet2 = NULL,
  log = FALSE,
  showPoints = FALSE,
  fixedHeight = NULL,
  x_levels = NULL,
  pwidth = 500
)
```

Arguments

aggdat	aggregated MRExperiment
feature	Feature to plot.
x_var	Phenotype to aggregate over on X-axis. Default by "SAMPLE_ID".
ind	Indices of top abundant features to plot. Needed to determine appropriate color
plotTitle	Plot title. Default shows no title.
ylab	Y-axis label. Default is "Reads"
xlab	X-axis label. If NULL, x_var will be used as label.
facet1	Phenotype for facet 1.
facet2	Phenotype for facet 2.
log	Log2 transform data. Default is FALSE.
showPoints	add points for each sample on plot
fixedHeight	sets a specific plot height (differential analysis)
x_levels	restrict to specific levels of x_var (differential analysis)
pwidth	overall plot width; default is 650

Value

plotly plot object

Author(s)

Janina Reeder

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
plotSingleFeature(aggdat, feature = "Prevotella", x_var = "diet")
```

---

readData *Reads in data*

Description

This function reads in an MRexperiment object saved as an RDS file, a Biom file, or a tab - delimited count matrix with features as rows and samples as columns.

Usage

```
readData(filepath, type = "RDS")
```

Arguments

filepath	Relative or absolute file path of data object.
type	The type of file to be read; default is "RDS", other options are "RDATA", "BIOM", "TAB", "CSV"

Value

An MRexperiment object.

`relAbundance` *Relative abundance plot module - server*

Description

Relative abundance plot module - server

Usage

```
relAbundance(
  input,
  output,
  session,
  aggDat,
  featLevel,
  intraSettings,
  normalizedData,
  reset
)
```

Arguments

`input`	shiny input
`output`	shiny output
`session`	shiny session
`aggDat`	aggregated MRExperiment
`featLevel`	chosen feature level (aggregation level)
`intraSettings`	analysis input settings passed over to this module
`normalizedData`	boolean indicating whether data has been normalized
`reset`	boolean reactive which resets the module if TRUE

Value

list storing plot clicks and number of features displayed (passed to feature plot module) as well as the R code to make plot

`relAbundanceUI` *Relative abundance plot module - UI*

Description

Relative abundance plot module - UI

Usage

```
relAbundanceUI(id)
```

Arguments

`id`	namespace identifier

Value

box containing the ui code

Author(s)

Janina Reeder

`replaceWithUnknown` *Helper function to replace any un-annotated features with the term unknown*

Description

Helper function to replace any un-annotated features with the term unknown

Usage

```
replaceWithUnknown(featcol)
```

Arguments

`featcol`	vector of entried to be replaced where needed (fData column)

Value

modified featcol

Author(s)

Janina Reeder

Examples

```
data("mouseData", package = "metagenomeSeq")
featcol <- fData(mouseData)[["genus"]]
featcol[featcol == "NA"] <- NA
replaceWithUnknown(featcol)
```

`reportList` *Report tab module server*

Description

Report tab module server

Usage

```
reportList(
  input,
  output,
  session,
  dataSource,
  preprocessRep,
  qcRep,
  analysisRep,
  aggIndex,
  reset
)
```

Arguments

`input`	module input
`output`	module output
`session`	app session
`dataSource`	R code to obtain data for rendering
`preprocessRep`	R code containing preprocessing steps of data
`qcRep`	R Code to generate QC plots
`analysisRep`	R Code to generate all analyses saved to reports
`aggIndex`	boolean value representing aggregation steps in analysisRep
`reset`	boolean reactive which resets the module if TRUE

Value

report list server fragment - no return value

Author(s)

Janina Reeder

reportListUI *report tab ui*

Description

report tab ui

Usage

```
reportListUI(id)
```

Arguments

id	namespace identifier

Value

fluidRow holding ui elements

Author(s)

Janina Reeder

Examples

```
reportListUI("reportlist_id")
```

reportRow *Report Row*

Description

Report Row

Usage

```
reportRow(input, output, session, type, content)
```

Arguments

input	module input
output	module output
session	app session
type	boolean indicating whether checkbox should be included
content	R code to show

Value

reactive boolean indicating whether row is selected

Author(s)

Janina Reeder

`reportRowUI` *Report row module consisting of a checkbox, image and description/R code area*

Description

Report row module consisting of a checkbox, image and description/R code area

Usage

```
reportRowUI(id, type)
```

Arguments

`id`	namespace identifier
`type`	boolean indicating if a selector checkbox should be added

Value

div holding the UI code

Author(s)

Janina Reeder

`rollDownFeatures` *Helper function which rolls down annotated from closest higher order with annotation*

Description

Helper function which rolls down annotated from closest higher order with annotation

Usage

```
rollDownFeatures(featrow)
```

Arguments

`featrow`	vector of entries to be replaced where needed (fData row)

Value

modified featurerow

Author(s)

Janina Reeder

Examples

```
data("mouseData", package = "metagenomeSeq")
featrow <- fData(mouseData)[5,]
rollDownFeatures(featrow)
```

`runDiffTest` *Performs differential abundance testing*

Description

This function performs differential abundance testing between groups of a specified phenotype. Four methods are available: limma, Kruskal-Wallis, ZILN and DESeq2 (see details).

Usage

```
runDiffTest(
  aggdat,
  level,
  phenotype,
  phenolevels = NULL,
  log = TRUE,
  coef = NULL,
  method = c("limma", "Kruskal-Wallis", "DESeq2")
)
```

Arguments

`aggdat`	aggregated MRExperiment
`level`	Feature level.
`phenotype`	Phenotype to test.
`phenolevels`	levels of the phenotype to restrict the comparison to
`log`	Log2 transform data. Default is TRUE.
`coef`	Numeric which indicates which pairwise comparison to analyze when there are more than two groups. Corresponds to the column number of the model matrix produced by `designPairs()`. If NULL, a test of any difference between all groups is performed.
`method`	Differential testing method. One of "limma" (default), "Kruskal-Wallis", or "DESeq2".

Details

limma is a differential expression tool for microarray data using linear models. It can also be applied to microbiome data.

The Kruskal-Wallis test is a non-parametric rank test which examines if groups come from the same distribution. A significant result indicates at least one group is distributionally different than another group.

ZILN is a zero-inflated log-normal model implemented in `fitFeatureModel()` of the `metagenomeSeq` package.

DeSeq2 performs differential gene expression analysis based on the negative binomial distribution

Value

data.frame holding results of the differential analysis

Examples

```
data("mouseData", package = "metagenomeSeq")
aggdat <- aggFeatures(mouseData, level = "genus")
runDiffTest(aggdat = aggdat,level = "genus",
            phenotype = "diet", method = "Kruskal-Wallis")
```

---

runMicrobiomeExplorer *Main function to start the Microbiome Explorer Shiny app via a command line call*

Description

Main function to start the Microbiome Explorer Shiny app via a command line call

Usage

```
runMicrobiomeExplorer()
```

Value

the shiny application

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