Package ‘microbiomeDASim’

May 30, 2024

Type Package
Title Microbiome Differential Abundance Simulation
Version 1.18.0
Author Justin Williams, Hector Corrada Bravo, Jennifer Tom, Joseph Nathaniel Paulson
Maintainer Justin Williams <williazo@ucla.edu>
Description A toolkit for simulating differential microbiome data designed for longitudinal analyses. Several functional forms may be specified for the mean trend. Observations are drawn from a multivariate normal model. The objective of this package is to be able to simulate data in order to accurately compare different longitudinal methods for differential abundance.
License MIT + file LICENSE
Imports graphics, ggplot2, MASS, tmvtnorm, Matrix, mvtnorm, pbapply, stats, phyloseq, metagenomeSeq, Biobase
Depends R (>= 3.6.0)
Encoding UTF-8
LazyData false
Roxygen list(markdown = TRUE)
RoxygenNote 7.0.2
Suggests testthat (>= 2.1.0), knitr, devtools
VignetteBuilder knitr
biocViews Microbiome, Visualization, Software
BugReports https://github.com/williazo/microbiomeDASim/issues
URL https://github.com/williazo/microbiomeDASim
git_url https://git.bioconductor.org/packages/microbiomeDASim
git_branch RELEASE_3_19
git_last_commit cd16e6c
git_last_commit_date 2024-04-30
Repository Bioconductor 3.19
Date/Publication 2024-05-29
final_output_gen

Generating the final combined bug output

Description

Generating the final combined bug output

Usage

final_output_gen(
  no_diff_feat,
  diff_abun_features,
  diff_Y,
  null_Y,
  diff_bugs,
  nodiff_bugs,
  final_output = NULL
)

Arguments

no_diff_feat number of non differentially abundant features
diff_abun_features number of differentially abundant features
diff_Y simulated outcome for differentially abundant features
null_Y  simulated outcome for non differentially abundant features
diff_bugs  sample information for differentially abundant features
nodiff_bugs  sample information for non differentially abundant features
final_output  final object that will store the simulated data

Value

final output list with the OTU table and corresponding bug feature data.frame

---

**form_beta_check**  
**Beta Specification Check**

---

**Description**

Function for checking that the appropriate beta parameters are specified for each of the mean trend specifications

**Usage**

form_beta_check(form, beta, IP, timepoints)

**Arguments**

form  character value specifying the type of time trend. Options include 'linear', 'quadratic', 'cubic', 'M', 'W', 'L_up', and 'L_down'.

beta  vector specifying the appropriate parameters for functional trend. See details of mean_trend for explanation for each form

IP  vector specifying the inflection points. See details of mean_trend for explanation for each form

timepoints  numeric vector specifying the points to fit the functional trend. @keywords internal

**Value**

Nothing returned unless an error is returned.
gen_norm_microbiome_norm_feature_check

Checking that features are specified appropriately

Description
Checking that features are specified appropriately

Usage
gen_microbiome_norm_feature_check(features, diff_abun_features)

Arguments

features Numeric value specifying the total number of features to simulate in the microbiome. Must be greater than zero

diff_abun_features Number of features to simulate with differentially abundant pattern. Must be between zero and number of features specified

Value
Potential warning message if no differentially abundant features or all differentially abundant features are specified

gen_norm_microbiome Generate Longitudinal Differential Abundance from Multivariate Normal

Description
Generate Longitudinal Differential Abundance from Multivariate Normal

Usage
gen_normal_microbiome(
features = 10,
diff_abun_features = 5,
n_control,
n_treat,
control_mean,
sigma,
um_timepoints,
t_interval,
rho,
Arguments

features numeric value specifying the number of features/microbes to simulate. Default is 10.
diff_abun_features numeric value specifying the number of differentially abundant features. Default is 5.
n_control integer value specifying the number of control individuals
n_treat integer value specifying the number of treated individuals
control_mean numeric value specifying the mean value for control subjects. All control subjects are assumed to have the same population mean value.
sigma numeric value specifying the global population standard deviation for both control and treated individuals.
num_timepoints integer value specifying the number of timepoints per subject.
t_interval numeric vector of length two specifying the interval of time from which to draw observations \([t_1, t_q]\). Assumed to be equally spaced over the interval unless asynch_time is set to TRUE.
rho value for the correlation parameter. Must be between \([0, 1]\). See \texttt{mvrnorm_corr_gen} for details.
corr_str correlation structure selected. See \texttt{mvrnorm_corr_gen} for details.
func_form character value specifying the functional form for the longitudinal mean trend. See \texttt{mean_trend} for details.
beta vector value specifying the parameters for the differential abundance function. See \texttt{mean_trend} for details.
IP vector specifying any inflection points. Depends on the type of functional form specified. See \texttt{mean_trend} for details. By default this is set to NULL.
missing_pct numeric value that must be between \([0, 1]\) that specifies what percentage of the individuals will have missing values.
missing_per_subject integer value specifying how many observations per subject should be dropped. Note that we assume that all individuals must have baseline value, meaning that the maximum number of missing_per_subject is equal to num_timepoints - 1.
**gen_norm_microbiome_obs**

Value

This function returns a list with the following objects:

- **Y** The full simulated feature sample matrix where each row represents a feature and each column a sample. Note that the differential and non-differential bugs are marked by row.names.

Examples

```r
gen_norm_microbiome_obs(features = 5, diff_abun_features = 2,
                          n_control = 10, n_treat = 10, control_mean = 8, sigma = 1,
                          num_timepoints = 5, t_interval = c(0, 4), rho = 0.8,
                          corr_str = "compound", func_form = "linear", beta = c(0, 1),
                          missing_pct = 0.3, missing_per_subject = 2)
```

---

**Description**

Generate Longitudinal Differential Abundance from Multivariate Normal with Observed Data

Usage

```r
gen_norm_microbiome_obs(
    features = 10,
    diff_abun_features = 5,
    id,
    time,
    group,
    ref,
    control_mean,
    sigma,
    rho,
```
cor_str = c("ar1", "compound", "ind"),
func_form = c("linear", "quadratic", "cubic", "M", "W", "L_up", "L_down"),
beta,
IP = NULL,
dis_plot = FALSE,
plot_trend = FALSE,
zero_trunc = TRUE
)

Arguments

features numeric value specifying the number of features/microbes to simulate. Default is 10.
diff_abun_features numeric value specifying the number of differentially abundant features. Default is 5.
id vector of length N that identifies repeated measurements for each unit
time vector of length N that determines when values will be sampled for each unit
group factor vector with two levels indicating the group assignment for each respective id
ref character value identifying which group value to treat as control and which value to treat as treatment
control_mean numeric value specifying the mean value for control subjects. all control subjects are assumed to have the same population mean value.
sigma numeric value specifying the global population standard deviation for both control and treated individuals.
rho value for the correlation parameter. must be between [0, 1]. see mvrnorm_corr_gen for details.
corr_str correlation structure selected. see mvrnorm_corr_gen for details.
func_form character value specifying the functional form for the longitudinal mean trend. see mean_trend for details.
beta vector value specifying the parameters for the differential abundance function. see mean_trend for details.
IP vector specifying any inflection points. depends on the type of functional form specified. see mean_trend for details. by default this is set to NULL.
dis_plot logical argument on whether to plot the simulated data or not. by default plotting is turned off.
plot_trend specifies whether to plot the true mean trend. see mean_trend for details.
zero_trunc logical indicator designating whether simulated outcomes should be zero truncated. default is set to TRUE

Value

This function returns a list with the following objects

Y The full simulated feature sample matrix where each row represent a feature and each column a sample. Note that the differential and non-differential bugs are marked by row.names
Examples

```r
set.seed(011520)
id_list <- lapply(seq_len(60), function(i){
  obs <- sample(5:10, size=1)
id_rep <- rep(i, obs)
})
time_interval <- c(0, 10)
time_list <- lapply(id_list, function(x){
time_len <- length(x)
times <- runif(time_len, min=time_interval[1], max=time_interval[2])
times <- times[order(times)]
})
group_list <- lapply(id_list, function(x){
group_len <- length(x)
  tx_ind <- sample(seq_len(2), 1)
  tx_group <- ifelse(tx_ind==1, "Control", "Treatment")
groups <- rep(tx_group, group_len)
})
id <- unlist(id_list)
group <- factor(unlist(group_list), levels = c(“Control”, “Treatment”))
time <- unlist(time_list)

# control times
ct <- unlist(lapply(unique(id[group=="Control"]), function(x){
  length(id[id==x])
}))
tt <- unlist(lapply(unique(id[group=="Treatment"]), function(x){
  length(id[id==x])
}))
mean(ct)
mean(tt)
gen_norm_microbiome_obs(features=4, diff_abun_features=2,
id=id, time=time, group=group, ref="Control", control_mean=2,
sigma=1, rho=0.7, corr_str="compound", func_form="L_up",
beta=1, IP=5, zero_trunc=TRUE)
```

**ggplot_spaghetti**

*Spaghetti Plots using ggplot2*

**Description**

This function allows the user to create spaghetti plots for individuals with time varying covariates. You can also break this down into subgroups to analyze different trends.
Usage

ggplot_spaghetti(
    y,
    id,
    time,
    alpha = 0.2,
    method = "loess",
    jit = 0,
    group = NULL
)

Arguments

y
  This is the y-axis parameter to specify. Generally it is a continuous variable.

id
  This is the id parameter that identifies the unique individuals or units.

time
  This is the time vector and must be numeric.

alpha
  Scalar value between [0,1] that specifies the transparency of the lineplots.

method
  Character value that specifies which type of method to use for fitting. Optional
  methods come from `geom_smooth` function.

jit
  Scalar value that specifies how much you want to jitter each individual observa-
  tion. Useful if many of the values share the same y values at a time point.

group
  Specifies a grouping variable to be used, and will plot it by color on one single
  plot.

Details

  Note that the data must be in long format.

Value

  Plots a time series data by each individual/unit with group trends overlayed.

Examples

library(ggplot2)
num_subjects_per_group <- 15
sim_obj <- mvrnorm_sim(n_control=num_subjects_per_group,
    n_treat=num_subjects_per_group,
    control_mean=5, sigma=1, num_timepoints=5,
    t_interval = c(0, 4),
    rho=0.95, corr_str='ar1', func_form='linear',
    beta=c(0, 0.25),
    missing_pct=0.6, missing_per_subject=2)

with(sim_obj$df, suppressWarnings(ggplot_spaghetti(y=Y_obs, id=ID, time=time,
    jit=0.1, group=group)))+
  labs(title="Simulated Microbiome Data from Multivariate Normal",
    y="Normalized Reads", x="Time") +
mean_trend

scale_linetype_manual(values=c("solid","dashed"), name="Group") +
scale_color_manual(values=c("#F8766D", "#00BFC4"), name="Group")

IP_form_check
Inflection point check for mean_trend

Description
Inflection point check for mean_trend

Usage
IP_form_check(form, beta, IP, timepoints)

Arguments
form character value specifying the type of time trend. Options include 'linear', 'quadratic', 'cubic', 'M', 'W', 'L_up', and 'L_down'.
beta vector specifying the appropriate parameters for functional trend. See details of mean_trend for explanation for each form
IP vector specifying the inflection points. See details of mean_trend for explanation for each form
timepoints numeric vector specifying the points to fit the functional trend.

Value
Updated inflection point vector

mean_trend
Function for Generating Various Longitudinal Mean Trends

Description
In order to investigate different functional forms of longitudinal differential abundance we allow the mean time trend to take a variety of forms. These functional forms include linear, quadratic, cubic, M, W, L_up, or L_down. For each form the direction/concavity/fold change can be specified using the beta parameter.

Usage
mean_trend(
  timepoints,
  form = c("linear", "quadratic", "cubic", "M", "W", "L_up", "L_down"),
  beta,
  IP = NULL,
  plot_trend = FALSE
)
Arguments

- **timepoints**: numeric vector specifying the points to fit the functional trend.
- **form**: character value specifying the type of time trend. Options include 'linear', 'quadratic', 'cubic', 'M', 'W', 'L_up', and 'L_down'.
- **beta**: vector specifying the appropriate parameters for the equation. In the case of 'linear', beta should be a two-dimensional vector specifying the intercept and slope. See details for the further explanation of the beta value for each form.
- **IP**: vector specifying the inflection points where changes occur for functional forms M, W, and L trends.
- **plot_trend**: logical value indicating whether a plot should be produced for the time trend. By default this is set to TRUE.

Details

**Linear Form Notes:**

\[ f(x) = \beta_0 + \beta_1 x + \beta_2 x^2 \]

- Sign of \( \beta_1 \) determines whether the trend is increasing (+) or decreasing (-)

**Quadratic Form Notes:**

\[ f(x) = \beta_0 + \beta_1 x + \beta_2 x^2 \]

- Critical point for quadratic function occurs at the point \( -\frac{\beta_1}{2\beta_2} \)
- \( \beta_2 \) determines whether the quadratic is concave up (+) or concave down (-)

**Cubic Form Notes:**

\[ f(x) = \beta_0 + \beta_1 x + \beta_2 x^2 + \beta_3 x^3 \]

- Point of Inflection for cubic function occurs \( -\frac{\beta_2}{3\beta_3} \)
- Critical points for cubic function occur at \( -\frac{\beta_2 \pm \sqrt{\beta_2^2 - 3\beta_1 \beta_3}}{3\beta_3} \)
- Can generate piecewise linear trends, i.e. 'V' form, by placing either one of the IP points outside of the timepoints specified

**M/W Form Notes:**

- Must specify beta as (\( \beta_0, \beta_1 \)) and IP as (\( IP_1, IP_2, IP_3 \))
- This form should be specified with an initial intercept, \( \beta_0 \), and slope, \( \beta_1 \), that will connect to the first point of change (IP) specified.
- Subsequent slopes are constructed such that the mean value at the second IP value and final timepoint are 0
- The mean value at the third IP is set to be equal to the calculated mean value at the first IP based on the specified intercept and slope.
- \( \beta_0 \)=intercept, i.e. timepoint when y=0
- \( \beta_1 \)=slope between \( \beta_0 \) and \( IP_1 \)
L_up Form Notes:
The structure of this form assumes that there is no trend from $t_1$ to $IP_1$. Then at the point of change specified, $IP_1$, there occurs a linearly increasing trend with slope equal to $\beta_{\text{slope}}$ up to the last specified timepoint $t_q$.

- Must specify beta as $(\beta_{\text{slope}})$, and must be positive
- Specify a single point of change (IP) variable where positive trend will start
- IP must be between $[t_1, t_q]$

L_down Form Notes:
Similarly, the L_down form assumes that there are two region within the range of timepoints. The first region is a decreasing trend and the second region has no trend. The decreasing trend must start with a Y intercept greater than zero, and the slope must be specified as negative. There is one point of change (IP), but this is calculated automatically based on the values of the Y intercept and slope provided, $IP=-\beta_{\text{yintercept}}/\beta_{\text{slope}}$.

- Must specify beta as $(\beta_{\text{yintercept}}, \beta_{\text{slope}})$ where $\beta_{\text{yintercept}}>0$ and $\beta_{\text{slope}}<0$
- IP variable should be specified as NULL, if value is provided it will be ignored.

Value
This function returns a list of the following
- form - character value repeating the form selected
- trend - data.frame with the variables $\mu$ representing the estimated mean value at timepoints used for fitting the trend
- beta - returning the numeric vector used to fit the functional form

Examples

#Quadratic Form
mean_trend(timepoints=seq(0, 6, length.out=20),
          form='quadratic', beta=1/4 * c(-1, 3, -0.5), plot_trend=TRUE)

#M Form
mean_trend(timepoints=seq(0, 10, length.out=100), form='M',
          beta=c(0, 5), IP=10 * c(1/4, 2/4, 3/4), plot_trend=TRUE)

#in this case the IP points are selected so that peaks are evenly
distributed but this does not have to be true in general

#L_up Form
mean_trend(timepoints=seq(0, 10, length.out=100), form='L_up',
          beta=1, IP=5, plot_trend=TRUE)

#L_down Form
mean_trend(timepoints=seq(0, 10, length.out=100), form='L_down',
          beta=c(4, -0.5), IP=NULL, plot_trend=TRUE)
mean_trend_beta_vec

Create beta vector for mean_trend for all functional forms

Description
Create beta vector for mean_trend for all functional forms

Usage
mean_trend_beta_vec(form, beta, IP, timepoints)

Arguments
- **form**: character value specifying the type of time trend. Options include 'linear', 'quadratic', 'cubic', 'M', 'W', 'L_up', and 'L_down'.
- **beta**: vector specifying the appropriate parameters for functional trend. See details of mean_trend for explanation for each form
- **IP**: vector specifying the inflection points. See details of mean_trend for explanation for each form
- **timepoints**: numeric vector specifying the points to fit the functional trend.

Value
Vector with beta values used to create mean_trend

mean_trend_design_mat
Create Design Matrix for mean_trend function

Description
By taking in the user specified parameters, we can return a design matrix to use when creating the differential longitudinal abundance.

Usage
mean_trend_design_mat(form, beta, IP, timepoints)

Arguments
- **form**: character value specifying the type of time trend. Options include 'linear', 'quadratic', 'cubic', 'M', 'W', 'L_up', and 'L_down'.
- **beta**: vector specifying the appropriate parameters for functional trend. See details of mean_trend for explanation for each form
- **IP**: vector specifying the inflection points. See details of mean_trend for explanation for each form
- **timepoints**: numeric vector specifying the points to fit the functional trend.
Value

Numeric matrix with values that will be used to generate functional trends

---

**mvrnorm_corr_gen**

*Generate Multivariate Random Normal Longitudinal Data*

---

**Description**

For this methodology we assume that we draw a set of \( n \) independent each with \( q_i \) observations.

**Usage**

```r
mvrnorm_corr_gen(
  n,
  obs,
  t,
  mu,
  sigma,
  rho,
  corr_str = c("ar1", "compound", "ind"),
  zero_trunc = TRUE
)
```

**Arguments**

- **n**: integer scalar representing the total number of individuals
- **obs**: vector of length \( n \) specifying the number of observations per individual.
- **t**: vector corresponding to the timepoints for each individual.
- **mu**: vector specifying the mean value for individuals.
- **sigma**: scalar specifying the standard deviation for all observations.
- **rho**: numeric scalar value between \([0, 1]\) specifying the amount of correlation between. assumes that the correlation is consistent for all subjects.
- **corr_str**: character value specifying the correlation structure. Currently available methods are \'ar1\', \'compound\', and \'ind\' which correspond to first-order autoregressive, compound or equicorrelation, and independence respectively.
- **zero_trunc**: logical value to specifying whether the generating distribution should come from a multivariate zero truncated normal or an untruncated multivariate normal. by default we assume that zero truncation occurs since this is assumed in our microbiome setting.
Value

This function returns a list with the following objects:

df - data.frame object with complete outcome Y, subject ID, time, group, and outcome with missing data

Y - vector of complete outcome

Mu - vector of complete mean specifications used during simulation

Sigma - block diagonal symmetric matrix of complete data used during simulation

N - total number of observations

Examples

size <- 15
reps <- 4
N <- size*reps

mvrnorm_corr_gen(n=size, obs=rep(reps, size), t=rep(seq_len(4), size),
mu=rep(1, N), sigma=2, rho=0.9, corr_str="ar1")

Description

This function is used in the gen_norm_microbiome call when the user specified the method as mvrnorm.

Usage

mvrnorm_sim(
    n_control, 
    n_treat, 
    control_mean, 
    sigma, 
    num_timepoints, 
    t_interval, 
    rho, 
    corr_str = c("ar1", "compound", "ind"), 
    func_form = c("linear", "quadratic", "cubic", "M", "W", "L_up", "L_down"), 
    beta, 
    IP = NULL, 
    missing_pct, 
    missing_per_subject, 
    miss_val = NA, 
    dis_plot = FALSE, 
    plot_trend = FALSE,
zero_trunc = TRUE,
  asynch_time = FALSE
)

Arguments

n_control  integer value specifying the number of control individuals
n_treat    integer value specifying the number of treated individuals
control_mean numeric value specifying the mean value for control subjects. all control sub-
            jects are assummed to have the same population mean value.
sigma      numeric value specifying the global population standard deviation for both con-
            trol and treated individuals.
num_timepoints either an integer value specifying the number of timepoints per subject or a
            vector of timepoints for each subject. If supplying a vector the lenght of the
            vector must equal the total number of subjects.
t_interval numeric vector of length two specifying the interval of time from which to draw
            observatoins [t_1, t_q]. Assumed to be equally spaced over the interval unless
            asynch_time is set to TRUE.
rho        value for the correlation parameter. must be between [0, 1]. see mvrnorm_corr_gen
            for details.
corr_str   correlation structure selected. see mvrnorm_corr_gen for details.
func_form  character value specifying the functional form for the longitudinal mean trend.
            see mean_trend for details.
beta       vector value specifying the parameters for the differential abundance function.
            see mean_trend for details.
IP         vector specifying any inflection points. depends on the type of functional form
            specified. see mean_trend for details. by default this is set to NULL.
missing_pct numeric value that must be between [0, \1] that specifies what percentage of the
            individuals will have missing values.
missing_per_subject integer value specifying how many observations per subject should be dropped.
            note that we assume that all individuals must have baseline value, meaning that
            the maximum number of missing_per_subject is equal to num_timepoints - 1.
miss_val   value used to induce missingness from the simulated data. by default missing
            values are assummed to be NA but other common choices include 0.
dis_plot   logical argument on whether to plot the simulated data or not. by default plotting
            is turned off.
plot_trend specifies whether to plot the true mean trend. see mean_trend for details.
zero_trunc logical indicator designating whether simulated outcomes should be zero truncated.
            default is set to TRUE
asynch_time logical indicator designed to randomly sample timepoints over a specified interval if set to TRUE. default is FALSE.
**Value**

This function returns a list with the following objects:

- `df` - data.frame object with complete outcome `Y`, subject ID, time, group, and outcome with missing data
- `Y` - vector of complete outcome
- `Mu` - vector of complete mean specifications used during simulation
- `Sigma` - block diagonal symmetric matrix of complete data used during simulation
- `N` - total number of observations
- `miss_data` - data.frame object that lists which ID's and timepoints were randomly selected to induce missingness
- `Y_obs` - vector of outcome with induced missingness

**Examples**

```r
num_subjects_per_group <- 20
sim_obj <- mvrnorm_sim(n_control=num_subjects_per_group,
                       n_treat=num_subjects_per_group,
                       control_mean=5, sigma=1, num_timepoints=5,
                       t_interval=c(0, 4), rho=0.95, corr_str='ar1',
                       func_form='linear', beta=c(0, 0.25),
                       missing_pct=0.6, missing_per_subject=2)

# checking the output
head(sim_obj$df)

# total number of observations is 2(num_subjects_per_group)(num_timepoints)
sim_obj$N

# there should be approximately 60% of the IDs with missing observations
length(unique(sim_obj$miss_data$miss_id))/length(unique(sim_obj$df$ID))

# checking the subject covariance structure
sim_obj$Sigma[seq_len(5), seq_len(5)]
```

---

**Description**

This function is used in the `gen_norm_microbiome_obs` call.
mvrnorm_sim_obs

Usage

mvrnorm_sim_obs(
  id,
  time,
  group,
  ref,
  control_mean,
  sigma,
  rho,
  corr_str = c("ar1", "compound", "ind"),
  func_form = c("linear", "quadratic", "cubic", "M", "W", "L_up", "L_down"),
  beta,
  IP = NULL,
  dis_plot = FALSE,
  plot_trend = FALSE,
  zero_trunc = TRUE
)

Arguments

id vector of length N that identifies repeated measurements for each unit

time vector of length N that determines when values will be sampled for each unit

group factor vector with two levels indicating the group assignment for each respective id

ref character value identifying which group value to treat as control and which value to treat as treatment

control_mean numeric value specifying the mean value for control subjects. all control subjects are assumed to have the same population mean value.

sigma numeric value specifying the global population standard deviation for both control and treated individuals.

rho value for the correlation parameter. must be between [0, 1]. see mvrnorm_corr_gen for details.

corr_str correlation structure selected. see mvrnorm_corr_gen for details.

func_form character value specifying the functional form for the longitudinal mean trend. see mean_trend for details.

beta vector value specifying the parameters for the differential abundance function. see mean_trend for details.

IP vector specifying any inflection points. depends on the type of functional form specified. see mean_trend for details. by default this is set to NULL.

dis_plot logical argument on whether to plot the simulated data or not. by default plotting is turned off.

plot_trend specifies whether to plot the true mean trend. see mean_trend for details.

zero_trunc logical indicator designating whether simulated outcomes should be zero truncated. default is set to TRUE
Value

This function returns a list with the following objects:

df - data.frame object with complete outcome \( Y \), subject ID, time, group, and outcome with missing data

\( Y \) - vector of complete outcome

\( \text{Mu} \) - vector of complete mean specifications used during simulation

\( \text{Sigma} \) - block diagonal symmetric matrix of complete data used during simulation

\( N \) - total number of observations

Examples

```r
set.seed(011520)
id_list <- lapply(seq_len(30), function(i){
  obs <- sample(seq_len(10), size=1)
  id_rep <- rep(i, obs)
})

time_interval <- c(0, 10)
time_list <- lapply(id_list, function(x){
  time_len <- length(x)
  times <- runif(time_len, min=time_interval[1], max=time_interval[2])
  times <- times[order(times)]
})

group_list <- lapply(id_list, function(x){
  group_len <- length(x)
  tx_ind <- sample(seq_len(2), 1)
  tx_group <- ifelse(tx_ind==1, "Control", "Treatment")
  groups <- rep(tx_group, group_len)
})
 id <- unlist(id_list)
group <- factor(unlist(group_list), levels = c("Control", "Treatment"))
time <- unlist(time_list)

# N=173 total repeated measurements
length(id)

# 15 control and 15 treated subjects
table(group[unique(id)])

# control times
c <- unlist(lapply(unique(id[group=="Control"]), function(x){
  length(id[id==x])
})))

# treatment times
tt <- unlist(lapply(unique(id[group=="Treatment"]), function(x){
  length(id[id==x])
})))
```
On average the treatment group has one more observation than control

```r
mean(ct)
mean(tt)
```

```r
mvrnorm_sim_obs(id=id, time=time, group=group, ref="Control", control_mean=2, 
sigma=1, rho=0.7, corr_str="compound", func_form="L_up", 
beta=1, IP=5, plot_trend=TRUE, dis_plot=TRUE, zero_trunc=TRUE)
```

---

**sigma_corr_function**

*Generating the longitudinal correlation matrix for repeated observations*

**Description**

Generating the longitudinal correlation matrix for repeated observations

**Usage**

```r
sigma_corr_function(t, sigma, corr_str, rho)
```

**Arguments**

- `t` : timepoints for repeated observations
- `sigma` : the standard deviation parameter for the covariance matrix
- `corr_str` : the type of correlation structure chosen. Options currently available include "ar1", "compound", and "ind"
- `rho` : the correlation coefficient for non-independent structures

**Value**

Return the covariance matrix V as a list

---

**simulate2MRexperiment**

*Convert simulated output to MRexperiment object*

**Description**

In order to allow investigators to more easily incorporate simulated data, this package converts the raw output into an MRexperiment object used in the `metagenomeSeq` package.

**Usage**

```r
simulate2MRexperiment(obj, missing = FALSE)
```
**Arguments**

- obj: output from either `gen_norm_microbiome` or `mvrnorm_sim`
- missing: logical indicator for objects from `mvrnorm_sim`. If missing = TRUE then create MRexperiment object with Y_obs else use Y.

**Value**

An MRexperiment object

**Examples**

```r
bug_gen <- gen_norm_microbiome(features=6, diff_abun_features=3,
                                n_control=30, n_treat=20, control_mean=2,
                                sigma=2, num_timepoints=4, t_interval=c(0, 3),
                                rho=0.9, corr_str="compound", func_form="M",
                                beta=c(4, 3), IP=c(2, 3.3, 6),
                                missing_pct=0.2, missing_per_subject=2,
                                miss_val=0, asynch_time=TRUE)

bug_gen_MR <- simulate2MRexperiment(bug_gen)
class(bug_gen_MR)
```

**simulate2phyloseq**  

*Convert simulated output to phyloseq object*

**Description**

This function will convert simulated data into a phyloseq object.

**Usage**

```r
simulate2phyloseq(obj, missing = FALSE)
```

**Arguments**

- obj: output from either `gen_norm_microbiome` or `mvrnorm_sim`
- missing: logical indicator for objects from `mvrnorm_sim`. If missing = TRUE then create MRexperiment object with Y_obs else use Y.

**Value**

A phyloseq object
Examples

```r
bug_gen <- gen_norm_microbiome(features=6, diff_abun_features=3,
    n_control=30, n_treat=20, control_mean=2,
    sigma=2, num_timepoints=4, t_interval=c(0, 3),
    rho=0.9, corr_str="compound", func_form="M",
    beta=c(4, 3), IP=c(2, 3.3, 6),
    missing_pct=0.2, missing_per_subject=2,
    miss_val=0, asynch_time=TRUE)

bug_gen_phyloseq <- simulate2MRexperiment(bug_gen)
class(bug_gen_phyloseq)
```

---

timepoint_process  *Function for processing and checking the inputed timepoints*

**Description**

To allow for increased flexibility the user may specify the number of timepoints as either a single value or separately for each individual. There is also an added option about whether to draw the timepoints evenly spaced across the interval of interest or whether to randomly draw them.

**Usage**

```r
timepoint_process(
    num_timepoints,  
    t_interval,      
    n,               
    asynch_time,     
    missing_per_subject
)
```

**Arguments**

- **num_timepoints**: either an integer value specifying the number of timepoints per subject or a vector of timepoints for each subject. If supplying a vector the length of the vector must equal the total number of subjects.
- **t_interval**: numeric vector of length two specifying the interval of time from which to draw observations \([t_1, t_q]\). Assumed to be equally spaced over the interval unless `asynch_time` is set to TRUE.
- **n**: numeric value representing the total number of observations
- **asynch_time**: logical indicator designed to randomly sample timepoints over a specified interval if set to TRUE.
Details

It is assumed that there is a known time interval of interest over which samples will be collected longitudinally on subjects. This interval is specified as \([t_1, t_q]\). All subjects are assumed to have baseline observations, i.e., \(t_1\).

Over this study interval each subject can have a potentially different number of measurements taken. In the most simple case we assume that all subjects will have the same number of measurements and can specify \(\text{num\_timepoints}\) as a single scalar value. Otherwise, we must specify how many timepoints will be collected for each individual. In this latter case \(\text{num\_timepoints}\) must have the same length as the number of subjects.

Finally, we can select whether we want the timepoints to be drawn at equal spaces over our study interval, or whether we want to randomly sample asynchronous timepoints. In the asynchronous case we randomly draw from a uniform distribution over the study interval with the restriction that the first observation must occur at \(t_1\).

Value

Returns a list of the number of timepoints and the times for each unit

---

**trunc_bugs**

*Function for inducing truncation of outcome*

**Description**

Function for inducing truncation of outcome

**Usage**

```r
trunc_bugs(Y, N, Mu, Sigma, zero_trunc)
```

**Arguments**

- **Y**
  - The original \(N \times 1\) vector of simulated multivariate outcomes
- **N**
  - Total number of observations equal to sum of repeated measurements for all individuals
- **Mu**
  - \(N \times 1\) vector representing the mean values
- **Sigma**
  - \(N \times N\) numeric matrix representing the covariance matrix for the feature
- **zero_trunc**
  - Logical indicator whether to perform zero-truncation

**Value**

Potentially truncated outcome vector \(Y\)
Index

* internal
  final_output_gen, 2
  gen_microbiome_norm_feature_check, 4
  IP_form_check, 10
  mean_trend_beta_vec, 13
  mean_trend_design_mat, 13
  sigma_corr_function, 20
  timepoint_process, 22
  trunc_bugs, 23

final_output_gen, 2
form_beta_check, 3

  gen_microbiome_norm_feature_check, 4
  gen_norm_microbiome, 4, 15, 21
  gen_norm_microbiome_obs, 6, 17
  geom_smooth, 9
  ggplot_spaghetti, 8

  IP_form_check, 10

  mean_trend, 3, 5–7, 10, 10, 13, 16, 18
  mean_trend_beta_vec, 13
  mean_trend_design_mat, 13
  metagenomeSeq, 20
  mvrnorm_corr_gen, 5, 7, 14, 16, 18
  mvrnorm_sim, 15, 21
  mvrnorm_sim_obs, 17

  phyloseq, 21

  sigma_corr_function, 20
  simulate2MRexperiment, 20
  simulate2phyloseq, 21

  timepoint_process, 22
  trunc_bugs, 23

24