Package 'circacompare'

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Title Analyses of Circadian Data

Version 0.1.1

Description Uses non-linear regression to statistically compare two circadian rhythms.
Groups are only compared if both are rhythmic (amplitude is non-zero).
Performs analyses regarding mesor, phase, and amplitude, reporting on estimates and statistical differences, for each, between groups.
Details can be found in Parsons et al (2020) <doi:10.1093/bioinformatics/btz730>.

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R topics documented:

circacompare	*circacompare*

Description

`circacompare` performs a comparison between two rhythmic groups of data. It tests for rhythmicity and then fits a nonlinear model with parametrization to estimate and statistically support differences in mesor, amplitude, and phase between groups.

Usage

```
circacompare(
  x,
  col_time,
  col_group,
  col_outcome,
  period = 24,
  alpha_threshold = 0.05,
  timeout_n = 10000,
  control = list()
)
```

Arguments

x	data.frame. This is the data.frame which contains the rhythmic data for two groups in a tidy format.
col_time	The name of the column within the data.frame, x, which contains time in hours at which the data were collected.
col_group	The name of the column within the data.frame, x, which contains the grouping variable. This should only have two levels.
col_outcome	The name of the column within the data.frame, x, which contains outcome measure of interest.
period	The period of the rhythm. For circadian rhythms, leave this as the default value, 24.
alpha_threshold	
	The level of alpha for which the presence of rhythmicity is considered. Default is 0.05.
timeout_n	The upper limit for the model fitting attempts. Default is 10,000.
control	list. Used to control the parameterization of the model.

Value

list

Examples

```
df <- make_data(phi1 = 6)
out <- circacompare(x = df, col_time = "time", col_group = "group",
                    col_outcome = "measure")
out
```

---

circacompare_mixed   *circacompare_mixed*

Description

circacompare_mixed is similar to circacompare but allows for some simple, user-specified random-effects on the rhythmic parameters of choice.

Usage

```
circacompare_mixed(
  x,
  col_time,
  col_group,
  col_outcome,
  col_id,
  randomeffects = c(),
  period = 24,
  alpha_threshold = 0.05,
  nlme_control = list(),
  nlme_method = "REML",
  verbose = FALSE,
  timeout_n = 10000,
  control = list()
)
```

Arguments

x	data.frame. This is the data.frame which contains the rhythmic data for two groups in a tidy format.
col_time	The name of the column within the data.frame, x, which contains time in hours at which the data were collected.
col_group	The name of the column within the data.frame, x, which contains the grouping variable. This should only have two levels.
col_outcome	The name of the column within the data.frame, x, which contains outcome measure of interest.
col_id	The name of the column within the data.frame, x, which contains the identifying values for the random effect, such as subject_id.
randomeffects	which rhythmic parameters to allow random effects. The default is to include no rhythmic parameters.

period	The period of the rhythm. For circadian rhythms, leave this as the default value, 24.
alpha_threshold	
	The level of alpha for which the presence of rhythmicity is considered. Default is to 0.05.
nlme_control	A list of control values for the estimation algorithm to replace the default values returned by the function nlme::nlmeControl. Defaults to an empty list.
nlme_method	A character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "REML".
verbose	An optional logical value. If TRUE information on the evolution of the iterative algorithm is printed. Default is FALSE.
timeout_n	The upper limit for the model fitting attempts. Default is 10000.
control	list. Used to control the parameterization of the model.

Value

list

Examples

```
# Generate some data with within-id correlation for phase-shift (phi1)
set.seed(99)
phi1_in <- 3.15

mixed_data <- function(n){
  counter <- 1
  for(i in 1:n){
    x <- make_data(k1=0, alpha1=0, phi1=rnorm(1, phi1_in, 0.5), hours=72, noise_sd = 1)
    x$id <- counter
    counter <- counter + 1
    if(i==1){res <- x}else{res <- rbind(res, x)}
  }
  return(res)
}
df <- mixed_data(20)
out <- circacompare_mixed(
  x = df,
  col_time = "time",
  col_group = "group",
  col_outcome = "measure",
  col_id = "id",
  control=list(grouped_params=c("phi"), random_params=c("phi1"))
)
out
```

---

circa_single	*circa_single*

Description

`circa_single` performs an analysis on a single rhythmic dataset. It estimates the mesor, amplitude and phase of the data provided.

Usage

```
circa_single(
  x,
  col_time,
  col_outcome,
  period = 24,
  alpha_threshold = 0.05,
  timeout_n = 10000,
  return_figure = TRUE,
  control = list()
)
```

Arguments

x	data.frame. This is the data.frame which contains the rhythmic data in a tidy format.
col_time	The name of the column within the data.frame, x, which contains time in hours at which the data were collected.
col_outcome	The name of the column within the data.frame, x, which contains outcome measure of interest.
period	The period of the rhythm. For circadian rhythms, leave this as the default value, 24.
alpha_threshold	
	The level of alpha for which the presence of rhythmicity is considered. Default is 0.05.
timeout_n	The upper limit for the model fitting attempts. Default is 10,000.
return_figure	Whether or not to return a ggplot graph of the rhythm and cosine model.
control	`list`. Used to control the parameterization of the model.

Value

list

Examples

```
df <- make_data()
df <- df[df$group=="g1",]
circa_single(x = df, col_time = "time", col_outcome="measure")
```

circa_single_mixed *circa_single_mixed*

Description

`circa_single_mixed` is similar to `circa_single` but allows for some simple, user-specified random-effects on the rhythmic parameters of choice.

Usage

```
circa_single_mixed(
  x,
  col_time,
  col_outcome,
  col_id,
  randomeffects = c("k", "alpha", "phi"),
  period = 24,
  alpha_threshold = 0.05,
  nlme_control = list(),
  nlme_method = "ML",
  verbose = FALSE,
  timeout_n = 10000,
  return_figure = TRUE,
  control = list()
)
```

Arguments

x	data.frame. This is the data.frame which contains the rhythmic data in a tidy format.
col_time	The name of the column within the data.frame, x, which contains time in hours at which the data were collected.
col_outcome	The name of the column within the data.frame, x, which contains outcome measure of interest.
col_id	The name of the column within the data.frame, x, which contains the identifying values for the random effect, such as `subject_id`.
randomeffects	which rhythmic parameters to allow random effects. The default is to include all rhythmic parameters.
period	The period of the rhythm. For circadian rhythms, leave this as the default value, 24.
alpha_threshold	The level of alpha for which the presence of rhythmicity is considered. Default is to `0.05`.
nlme_control	A list of control values for the estimation algorithm to replace the default values returned by the function nlme::nlmeControl. Defaults to an empty list.

nlme_method	A character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "ML".
verbose	An optional logical value. If `TRUE` information on the evolution of the iterative algorithm is printed. Default is `FALSE`.
timeout_n	The upper limit for the model fitting attempts. Default is `10000`.
return_figure	Whether or not to return a ggplot graph of the rhythm and cosine model.
control	`list`. Used to control the parameterization of the model.

Value

list

Examples

```
set.seed(42)
mixed_data <- function(n){
  counter <- 1
  for(i in 1:n){
      x <- make_data(k1=rnorm(1, 10, 2), alpha1=0, phi1=0)
      x$id <- counter
      counter <- counter + 1
      if(i==1){res <- x}else{res <- rbind(res, x)}
  }
  return(res)
}
df <- mixed_data(n=50)
out <- circa_single_mixed(x = df, col_time = "time", col_outcome = "measure",
                          col_id = "id", randomeffects = c("k"))
```

---

make_data   *make_data*

Description

Generate example circadian data with specified phase shift between groups

Usage

```
make_data(
  k = 0,
  k1 = 3,
  alpha = 10,
  alpha1 = 4,
  phi = 0,
  phi1 = 3.15,
  tau = 24,
  hours = 48,
```

```
  noise_sd = 0.1,
  seed = NULL
)
```

Arguments

k	mesor of group 1.
k1	change in mesor in group 2 from group 1.
alpha	amplitude rhythm for group 1.
alpha1	change in amplitude in group 2 from group 1
phi	phase of rhythm, in radian-hours, in group 1.
phi1	change in phase, in radian-hours, in group 2 from group 1
tau	period of the rhythm, shared between both groups.
hours	the number of hours/datapoints to sample.
noise_sd	the standard deviation of the noise term.
seed	random seed for generating data.

Value

data.frame

Examples

```
data <- make_data(k1=3, alpha1=4, phi1 = 6)
```

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