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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