Package ‘GLMMcosinor’

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Type  Package
Title  Fit a Cosinor Model Using a Generalised Mixed Modelling Framework
Version  0.2.0
Description  Allows users to fit a cosinor model using the 'glmmTMB' framework. This extends on existing cosinor modelling packages, including 'cosinor' and 'circacompare', by including a wide range of available link functions and the capability to fit mixed models. The cosinor model is described by Cornelissen (2014) <doi:10.1186/1742-4682-11-16>.
License  GPL (>= 3)
URL  https://github.com/ropensci/GLMMcosinor,
     https://ropensci.github.io/GLMMcosinor/
BugReports  https://github.com/ropensci/GLMMcosinor/issues
Imports  assertthat, cowplot, ggforce, ggplot2, glmmTMB, lme4, rlang, scales, stats
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Author  Rex Parsons [aut, cre] (<https://orcid.org/0000-0002-6053-8174>),
        Oliver Jayasinghe [aut],
        Nicole White [aut] (<https://orcid.org/0000-0002-9292-0773>),
        Oliver Rawashdeh [aut, fnd] (<https://orcid.org/0000-0002-7147-4778>),
        Prasad Chunduri [ctb, fnd] (<https://orcid.org/0000-0001-7297-7580>),

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amp_acro

Used to specify a cosinor component in the model formula.

Description

Checks the validity of user inputs before creating an updated formula and associated modifications to the data.frame.

Usage

amp_acro(time_col, n_components = 1, group, period, ...)

amp_acro
amp_acro

Arguments

- **time_col**: A numeric column within the `data.frame()` passed by via the `data` argument containing the time values.
- **n_components**: The Number of cosinor components in the model.
- **group**: A vector of the names for the group factors (column names within the `data.frame()` passed by via the `data` argument).
- **period**: A numeric value or vector containing the period. The number of values should be equal to `n_components`.
- **...**: Extra arguments for use within `GLMMcosinor`.

Value

A `data.frame` and formula appropriate for use by `data_processor()`.

Examples

```r
# Single component cosinor model
cglmm(
  vit_d ~ amp_acro(time_col = time, group = "X", period = 12),
  data = vitamind
)

# 2-component cosinor model with simulated data
sim_data <- simulate_cosinor(
  n = 500,
  mesor = 5,
  amp = c(2, 1),
  acro = c(1, 1.5),
  beta.mesor = 2,
  beta.amp = c(2, 1),
  beta.acro = c(1, 1.5),
  family = "gaussian",
  period = c(12, 6),
  n_components = 2,
  beta.group = TRUE,
)

cglmm(
  Y ~ group + amp_acro(times,
    n_components = 2,
    group = "group",
    period = c(12, 6)
  ),
  data = sim_data,
  family = gaussian
)
```
autoplot.cglmm  

Plot a cosinor model

Description

Given a cglmm model fit, generate a plot of the data with the fitted values. Optionally allows for plotting by covariates.

Usage

```r
## S3 method for class 'cglmm'
autoplot(
  object,
  ci_level = 0.95,
  x_str,
  type = "response",
  xlims,
  pred.length.out,
  points_per_min_cycle_length = 20,
  superimpose.data = FALSE,
  data_opacity = 0.3,
  predict.ribbon = TRUE,
  ranef_plot = NULL,
  cov_list = NULL,
  quietly = TRUE,
  ...
)
```

Arguments

- `object` An cglmm object.
- `ci_level` The level for calculated confidence intervals. Defaults to 0.95.
- `x_str` A character vector naming variable(s) to be plotted. Default has no value and plots all groups.
- `type` A character that will be passed as an argument to predict.cglmm(), specifying the type of prediction (e.g., "response", or "link"). See ?glmmTMB::predict.glmmTMB for full list of possible inputs.
- `xlims` A vector of length two containing the limits for the x-axis.
- `pred.length.out` An integer value that specifies the number of predicted data points. The larger the value, the more smooth the fitted line will appear. If missing, uses points_per_min_cycle_length to generate a sensible default value.
- `points_per_min_cycle_length` Used to determine the number of samples to create plot if pred.length.out is missing.
autoplot.cglmm

superimpose.data
A logical. If TRUE, data from the original data used to fit the model (object) will be superimposed over the predicted fit.

data_opacity
A number between 0 and 1 inclusive that controls the opacity of the superimposed data. (Used as the alpha when calling ggplot2::geom_point()).
predict.ribbon
A logical. If TRUE, a prediction interval is plotted.
ranef_plot
Specify the random effects variables that you wish to plot. If not specified, only the fixed effects will be visualised.
cov_list
Specify the levels of the covariates that you wish to plot as a list. For example, if you have two covariates: var1, and var 2, you could fix the level to be plotted as such cov_list = list(var1 = 'a', var2 = 1), where 'a' is a level in 'var1', and 1 is a level in 'var2'. See the examples for a demonstration. If not specified, the reference level of the covariate(s) will be used.
points_per_min_cycle_length
is the number of points plotted per the minimum cycle length (period) of all cosinor components in the model.
quietly
A logical. If TRUE, shows warning messages when wrangling data and fitting model. Defaults to TRUE.
...
Additional, ignored arguments.

Value

Returns a ggplot object.

Examples

# A simple model
model <- cglmm(
  vit_d ~ X + amp_acro(time, group = "X", period = 12),
  data = vitamind
)
autoplot(model, x_str = "X")

# Plotting a model with various covariates
test_data <- vitamind[vitamind$X == 1, ]
test_data$var1 <- sample(c("a", "b", "c"), size = nrow(test_data), replace = TRUE)
test_data$var2 <- rnorm(n = nrow(test_data))

object <- cglmm(
  vit_d ~ amp_acro(time, period = 12) + var1 + var2,
  data = test_data
)
autoplot(object,
  cov_list = list(  
    var1 = "a",
    var2 = 1
  ),
  superimpose.data = TRUE
)
cglmm

Fit cosinor model with \{glmmTMB\}

Description

Given an outcome and time variable, fit the cosinor model with optional covariate effects.

Usage

cglmm(
  formula,
  data,
  family = stats::gaussian(),
  quietly = TRUE,
  dispformula = ~1,
  ziformula = ~0,
  ...
)

Arguments

- **formula**: A formula specifying the cosinor model to be fit. The cosinor portion of the formula is controlled by including amp_acro() on the right hand side of the formula. See amp_acro for more details.
- **data**: A data.frame containing the variables used in the model.
- **family**: A family function or a character string naming a family function. See ?family and ?glmmTMB::family_glmmTMB for options.
- **quietly**: A logical. If TRUE, shows warning messages when wrangling data and fitting model. Defaults to TRUE.
- **dispformula**: A one-sided (i.e., no response variable) formula for dispersion combining fixed and random effects, including cosinor components using amp_acro(). Defaults to ~1.
- **ziformula**: A one-sided (i.e., no response variable) formula for zero-inflation combining fixed and random effects, including cosinor components using amp_acro(). Defaults to ~0.
- **...**: Optional additional arguments passed to glmmTMB::glmmTMB().

Value

Returns a fitted cosinor model as a cglmm object.

References

Examples

```r
# Single component cosinor model
cglmm(
  vit.d ~ amp_acro(time_col = time, group = "X", period = 12),
  data = vitamind
)

# 2-component cosinor model with simulated data
sim_data <- simulate_cosinor(
  n = 500,
  mesor = 5,
  amp = c(2, 1),
  acro = c(1, 1.5),
  beta.mesor = 2,
  beta.amp = c(2, 1),
  beta.acro = c(1, 1.5),
  family = "gaussian",
  period = c(12, 6),
  n_components = 2,
  beta.group = TRUE,
)

cglmm(
  Y ~ group + amp_acro(times,
    n_components = 2,
    group = "group",
    period = c(12, 6)
  ),
  data = sim_data,
  family = gaussian
)
```

cosinor_mixed

```
cosinor_mixed dataset for cosinor modelling examples.
```

Description

Simulated data set to illustrate a mixed cosinor model. The Y column contains a simulated outcome variable that varies over the time variable (times). The subject column is a grouping variable that can be used as a random effect. The rhythm has a period of 24 hours. Data was simulated using `simulate_cosinor`.

Usage

```
cosinor_mixed
```

Format

A data.frame with 3 variables: Y, times, and subject.
fit_model_and_process  Fit the cosinor GLMM model using the output from update_formula_and_data() and a new formula

Description
Fit the cosinor GLMM model using the output from update_formula_and_data() and a new formula

Usage
fit_model_and_process(obj, formula, ...)

Arguments
- obj: Output from update_formula_and_data().
- formula: A (optionally) new formula to use when fitting the cosinor model (maybe with random effects) or other covariates found in the data.
- ...: Optional additional arguments passed to glmmTMB::glmmTMB().

Value
Returns a fitted cosinor model as a cglmm object.

Examples
# Use vitamind data but add a "patient" identifier used as a random effect
vitamind2 <- vitamind
vitamind2$patient <- sample(LETTERS[1:5], size = nrow(vitamind2), replace = TRUE)

# Use update_formula_and_data() to perform wrangling steps of cglmm()
# without yet fitting the model
data_and_formula <- update_formula_and_data(
data = vitamind2,
formula = vit_d ~ X + amp_acro(time,
group = "X",
period = 12
)
)

data_and_formula$newformula

# fit model while adding random effect to cosinor model formula.
mod <- fit_model_and_process(
obj = data_and_formula,
Generates a polar plot with elliptical confidence intervals

Usage

polar_plot(
  x,
  ci_level = 0.95,
  n_breaks = 5,
  component_index = NULL,
  grid_angle_segments = 8,
  radial_units = c("radians", "degrees", "period"),
  clockwise = FALSE,
  text_size = 3,
  text_opacity = 0.5,
  fill_colours,
  ellipse_opacity = 0.3,
  circle_linetype = "dotted",
  start = c("right", "left", "top", "bottom"),
  view = c("full", "zoom", "zoom_origin"),
  overlay_parameter_info = FALSE,
  quietly = TRUE,
  show_component_labels = TRUE,
  xlims,
  ylims,
  ...
)

Arguments

x An object of class cgllmm

ci_level The level for calculated confidence ellipses. Defaults to 0.95.

n_breaks The number of concentric circles that will be plotted using the scales::breaks_pretty() function. By default, 5 breaks will be used. The number of breaks may be adjusted to result in an even interval. For example, if n_breaks is 3, but the
maximum plot radius is 8, instead of plotting circles in intervals in 1.6, this
interval will be rounded to 2 to result in the sequence: 0, 2, 4, 6, 8. See
scales::breaks_pretty for more details.

**component_index**

A number that corresponds to a particular component from the cglm() ob-
ject that will be used to create polar plot. If missing (default), then plots for
all components will be arranged in the returned plot. If a single or multiple
values are provided, then these components will be returned. (for example
component_index = 1, component_index = c(1, 3)).

**grid_angle_segments**

An integer. Determines the total number of segments in the background of the
polar plot. For example, a value of 4 will create quadrants around the origin.
Defaults to 8.

**radial_units**

A character specifying the angular units of the plot. Possible values are one of
c('radians', 'degrees', 'period'). These units relate to the period of the
component being visualised.
'radians': [0, 2π]
'degrees': [0, 360]
'period': [0, period]

**clockwise**

A logical. If TRUE, the angles increase in a clockwise fashion. If FALSE, anti-
clockwise. Defaults to FALSE.

**text_size**

A number controlling the font size of the text labels. Defaults to 3.

**text_opacity**

A numeric between 0 and 1 inclusive that controls the opacity of the text labels.

**fill_colours**

A character vector containing colours that will be mapped to levels within a
group. If the model has components with different number of levels per factor,
the length of this input should match the greatest number of levels. If not, or if
the number of levels exceeds the length of the default argument (8), colours are
generated using rainbow().

**ellipse_opacity**

A numeric between 0 and 1 inclusive that controls the opacity of the confidence
ellipses. Defaults to 0.3.

**circle_linetype**

A character or numeric that determines the linetype of the radial circles in
background of the polar plot. See ?linetype for more details.

**start**

A character, within c("right", "left", "top", "bottom") that determines
where angle 0 is located. If start = "top", and clockwise = TRUE, the angle
will rotate clockwise, starting at the '12 o-clock' position on a clock.

**view**

A character, within c("full", "zoom", "zoom_origin") that controls the view
of the plots.
'full': maintains a full view of the polar plot, including the background radial circles.

'zoom': finds the minimum view window which contains all confidence ellipses.

'zoom_origin': zooms into the confidence ellipses (like "zoom"), but also keeps the origin within f
overlay_parameter_info
A logical argument. If TRUE, more information about the acrophase and amplitude are displayed on the polar plots.

quietly
Analogous to verbose, this logical argument controls whether messages are displayed in the console.

show_component_labels
Logical argument, TRUE by default. When TRUE, the polar plots have labels corresponding to their components.

xlims
A vector of length two containing the limits for the x-axis.

ylims
A vector of length two containing the limits for the y-axis.

... Additional, ignored arguments.

Value
Returns a ggplot object.

Examples

data(vitamind)
model <- cglmm(
  vit_d ~ X + amp_acro(time, group = "X", period = 12),
  data = vitamind
)
polar_plot(model, radial_units = "period")

---

polar_plot.cglmm  Generates a polar plot with elliptical confidence intervals

Description
Generates a polar plot with elliptical confidence intervals

Usage

## S3 method for class 'cglmm'
polar_plot(
  x,
  ci_level = 0.95,
  n_breaks = 5,
  component_index = NULL,
  grid_angle_segments = 8,
  radial_units = c("radians", "degrees", "period"),
  clockwise = FALSE,
  text_size = 3.5,
  text_opacity = 1,
  fill_colours,
  ellipse_opacity = 0.3,
  ...)
circle_linetype = "dotted",
start = c("right", "left", "top", "bottom"),
view = c("full", "zoom", "zoom_origin"),
overlay_parameter_info = FALSE,
quietly = TRUE,
show_component_labels = TRUE,
xlims,
ylims,
...)

Arguments

x An object of class cglmm

ci_level The level for calculated confidence ellipses. Defaults to 0.95.

n_breaks The number of concentric circles that will be plotted using the scales::breaks_pretty() function. By default, 5 breaks will be used. The number of breaks may be adjusted to result in an even interval. For example, if n_breaks is 3, but the maximum plot radius is 8, instead of plotting circles in intervals in 1.6, this interval will be rounded to 2 to result in the sequence: 0, 2, 4, 6, 8. See ?scales::breaks_pretty for more details.

component_index A number that corresponds to a particular component from the cglmm() object that will be used to create polar plot. If missing (default), then plots for all components will be arranged in the returned plot. If a single or multiple values are provided, then these components will be returned. (for example component_index = 1, component_index = c(1, 3)).

grid_angle_segments An integer. Determines the total number of segments in the background of the polar plot. For example, a value of 4 will create quadrants around the origin. Defaults to 8.

radial_units A character specifying the angular units of the plot. Possible values are one of c(‘radians’, ‘degrees’, ‘period’). These units relate to the period of the component being visualised.

‘radians’: [0, 2π]
‘degrees’: [0, 360]
‘period’: [0, period]

clockwise A logical. If TRUE, the angles increase in a clockwise fashion. If FALSE, anticlockwise. Defaults to FALSE.

text_size A number controlling the font size of the text labels. Defaults to 3.

text_opacity A numeric between 0 and 1 inclusive that controls the opacity of the text labels.

fill_colours A character vector containing colours that will be mapped to levels within a group. If the model has components with different number of levels per factor, the length of this input should match the greatest number of levels. If not, or if the number of levels exceeds the length of the default argument (8), colours are generated using rainbow().
ellipse_opacity
A numeric between 0 and 1 inclusive that controls the opacity of the confidence ellipses. Defaults to 0.3.

circle_linetype
A character or numeric that determines the linetype of the radial circles in background of the polar plot. See ?linetype for more details.

start
A character, within c("right", "left", "top", "bottom") that determines where angle 0 is located. If start = "top", and clockwise = TRUE, the angle will rotate clockwise, starting at the '12 o-clock' position on a clock.

view
A character, within c("full", "zoom", "zoom_origin") that controls the view of the plots.
'full': maintains a full view of the polar plot, including the background radial circles.
'zoom': finds the minimum view window which contains all confidence ellipses.
'zoom_origin': zooms into the confidence ellipses (like "zoom"), but also keeps the origin within frame.

overlay_parameter_info
A logical argument. If TRUE, more information about the acrophase and amplitude are displayed on the polar plots.

quietly
Analogous to verbose, this logical argument controls whether messages are displayed in the console.

show_component_labels
Logical argument, TRUE by default. When TRUE, the polar plots have labels corresponding to their components.

xlims
A vector of length two containing the limits for the x-axis.

ylims
A vector of length two containing the limits for the y-axis.

... Additional, ignored arguments.

Value
Returns a ggplot object.

Examples
model <- cgllm(
  vit_d ~ X + amp_acro(time, group = "X", period = 12),
  data = vitamind
)
polar_plot(model, radial_units = "period")
**predict.cglmm**  
*Predict from a cosinor model*

---

**Description**

Given a time variable and optional covariates, generate predicted values from a cosinor fit. Default prediction is the mean value, optionally can predict at a given month.

**Usage**

```r
## S3 method for class 'cglmm'
predict(object, newdata, ...)
```

**Arguments**

- `object`: An object of class `cglmm`.
- `newdata`: Optional new data.
- `...`: Other arguments passed to `glmmTMB:::predict.glmmTMB`.

**Value**

Returns predicted values from the cosinor model.

**Examples**

```r
fit <- cglmm(vit_d ~ X + amp_acro(time, 
            group = "X", 
            n_components = 1, 
            period = 12 
        ), data = vitamind)
predict(fit)
```

---

**print.cglmm**  
*Print a brief summary of the cglmm model.*

---

**Description**

Print a brief summary of the cglmm model.

**Usage**

```r
## S3 method for class 'cglmm'
print(x, digits = getOption("digits"), ...)
```
Arguments

- `x` A `cglmm` object.
- `digits` Controls the number of digits displayed in the summary output.
- `...` Additional, ignored arguments.

Value

`print(x)` returns `x` invisibly.

Examples

```r
# Single component cosinor model
cglmm(
  vit_d ~ amp.acro(time_col = time, group = "X", period = 12),
  data = vitamind
)
```

Description

Print test of model

Usage

```r
## S3 method for class 'cglmmSubTest'
print(x, ...)
```

Arguments

- `x` A `sub_test_cosinor` object.
- `...` Additional, ignored arguments.

Value

`print(x)` returns `x` invisibly.

Examples

```r
data_2_component <- simulate_cosinor(
  n = 10000,
  mesor = 5,
  amp = c(2, 5),
  acro = c(0, pi),
  beta.mesor = 4,
  beta.amp = c(3, 4),
  beta.acro = c(0, pi / 2),
```
family = "gaussian",
    n_components = 2,
    period = c(10, 12),
    beta.group = TRUE
}
mod_2_component <- cglmm(
    Y ~ group + amp_acro(times,
        n_components = 2, group = "group",
        period = c(10, 12)
    ),
    data = data_2_component
)
test_output <- test_cosinor_levels(
    mod_2_component,
    param = "amp",
    x_str = "group"
)
print(test_output$global.test)

---

**print.cglmmSummary**

*Print the summary of a cosinor model*

**Description**

Print the summary of a cosinor model

**Usage**

```r
## S3 method for class 'cglmmSummary'
print(x, digits = getOption("digits"), ...)
```

**Arguments**

- `x`  
  An object of class `cglmmSummary`
- `digits`  
  Controls the number of digits displayed in the summary output
- `...`  
  Currently unused

**Value**

print returns `x` invisibly.

**Examples**

```r
fit <- cglmm(vit_d ~ X + amp_acro(time,
    group = "X",
    n_components = 1,
    period = 12
), data = vitamind)
```
print.cglmmTest

summary(fit)

---

**print.cglmmTest**  
*Print results of test of cosinor model*

**Description**

Print results of test of cosinor model

**Usage**

```r
## S3 method for class 'cglmmTest'
print(x, ...)  
```

**Arguments**

- `x`: A `test_cosinor` object.
- `...`: Arguments passed to `print`

**Value**

`print(x)` returns `x` invisibly.

**Examples**

```r
data_2_component <- simulate_cosinor(
  n = 10000,
  mesor = 5,
  amp = c(2, 5),
  acro = c(0, pi),
  beta.mesor = 4,
  beta.amp = c(3, 4),
  beta.acro = c(0, pi / 2),
  family = "gaussian",
  n_components = 2,
  period = c(10, 12),
  beta.group = TRUE
)
mod_2_component <- cglmm(
  Y ~ group + amp_acro(times,
    n_components = 2, group = "group",
    period = c(10, 12)
  ),
  data = data_2_component
)
test_cosinor_levels(
  mod_2_component,
  param = "amp",
  x_str = "group"
)
```
**Description**

see `?glmmTMB::sigma` for more details.

**Usage**

```r
## S3 method for class 'cglmm'
sigma(object, ...)
```

**Arguments**

- `object`: An object of class `cglmm`.
- `...`: (ignored; for method compatibility)

**Value**

a numeric.

**Examples**

```r
testdata_poisson <- simulate_cosinor(100,
    n_period = 2,
    mesor = 7,
    amp = c(0.1, 0.5),
    acro = c(1, 1),
    beta.mesor = 4.4,
    beta.amp = c(0.1, 0.46),
    beta.acro = c(0.5, -1.5),
    family = "poisson",
    period = c(12, 6),
    n_components = 2,
    beta.group = TRUE
)

mod <- cglmm(
    Y ~ group + amp_acro(times,
        period = c(12, 6),
        n_components = 2,
        group = "group"
    ),
    data = testdata_poisson,
    family = glmmTMB::nbinom1()
)

sigma(mod)
```
**simulate_cosinor**

Simulate data from a cosinor model

**Description**

This function simulates data from a cosinor model with a single covariate, where the time scale is month, and optionally allows for single covariate effects on the mean, amplitude, and acrophase.

**Usage**

```r
simulate_cosinor(
  n,
  mesor,
  amp,
  acro,
  period = 24,
  n_components,
  beta.group = FALSE,
  beta.mesor,
  beta.amp,
  beta.acro,
  n_period = 1,
  family = c("gaussian", "poisson", "binomial", "gamma"),
  ...
)
```

**Arguments**

- **n**
  - The sample size. An integer greater than 0.
- **mesor**
  - A numeric. The MESOR (midline estimating statistic of rhythm) for group = 0. The MESOR is independent of the cosinor components, so only one value is allowed even if there are multiple components in the data being simulated.
- **amp**
  - A numeric. The amplitude value (for group = 0 if grouped data are being simulated (beta.group = TRUE)). If simulating data with multiple components, specify a vector with values for each component. E.g: `amp = c(5, 10)`.
- **acro**
  - A numeric. The acrophase value in radians (for group = 0 if grouped data are being simulated (beta.group = TRUE)). If simulating data with multiple components, specify a vector with values for each component. E.g: `acro = c(0, pi)` for two components.
- **period**
  - The period of the rhythm data (for group = 0 if grouped data are being simulated (beta.group = TRUE)). If simulating data with multiple components, specify a vector with values for each component. E.g: `period = c(12, 6)` for two components.
- **n_components**
  - The number of components in the model. This must match the length of the inputs for amp and acro.
summary.cglmm

Summary a cosinor model Given a time variable and optional covariates, generate inference a cosinor fit. Gives estimates, confidence intervals, and tests for the raw parameters, and for the mean, amplitude, and acrophase parameters. If the model includes covariates, the function returns the estimates of the mean, amplitude, and acrophase for the group with covariates equal to 1 and equal to 0. This may not be the desired result for continuous covariates.

**beta.group**
A logical. If TRUE a second group of data will be simulated and included in the returned data set. If FALSE, beta.acro, beta.mesor, and beta.amp arguments will be ignored.

**beta.mesor**
A numeric. The MESOR value term for group = 1

**beta.amp**
A numeric. The amplitude value for group = 1. If simulating data with multiple components, specify a vector with values for each component. E.g: amp = c(2, 8).

**beta.acro**
A numeric. The acrophase value in radians (for group = 1. If simulating data with multiple components, specify a vector with values for each component. E.g: acr = c(2, 5) for two components.

**n_period**
A numeric. The number of cycles of the rhythm to be simulated.

**family**
A character. The family (see ?family) of the simulated dataset. Can handle values in c("poisson", "binomial","gamma", "gaussian").

**...**
Extra arguments, including alpha that controls the shape argument when sampling from a gamma distribution (when family = "gamma"; default is 1), and sd (standard deviation) which is used when sampling from a normal distribution (when family = "gaussian"; default is 1). To specify these parameters for the beta (treatment) group, use beta.alpha and beta.sd.

**Value**

Returns simulated data in a data.frame.

**Examples**

```r
simulate_cosinor(
  n = 100,
  mesor = 1,
  amp = 1,
  acro = 1,
  period = 24,
  family = "gaussian"
)
```

---

**summary.cglmm**

Summarize a cosinor model Given a time variable and optional covariates, generate inference a cosinor fit. Gives estimates, confidence intervals, and tests for the raw parameters, and for the mean, amplitude, and acrophase parameters. If the model includes covariates, the function returns the estimates of the mean, amplitude, and acrophase for the group with covariates equal to 1 and equal to 0. This may not be the desired result for continuous covariates.
Description

Summarize a cosinor model. Given a time variable and optional covariates, generate inference a cosinor fit. Gives estimates, confidence intervals, and tests for the raw parameters, and for the mean, amplitude, and acrophase parameters. If the model includes covariates, the function returns the estimates of the mean, amplitude, and acrophase for the group with covariates equal to 1 and equal to 0. This may not be the desired result for continuous covariates.

Usage

```r
## S3 method for class 'cglm'
summary(object, ci_level = 0.95, ...)
```

Arguments

- `object`: An object of class `cglm`.
- `ci_level`: The level for calculated confidence intervals. Defaults to 0.95.
- `...`: Currently unused.

Value

Returns a summary of the `cglm` model as a `cglmSummary` object.

Examples

```r
fit <- cglm(vit_d ~ X + amp_acro(time,
  group = "X",
  n_components = 1,
  period = 12
), data = vitamind)
summary(fit)
```

---

test_cosinor_components

Test for differences in a cosinor model between components.

Description

Given a time variable and optional covariates, generate inference a cosinor fit. For the covariate named (or vector of covariates), this function performs a Wald test comparing the group with covariates equal to 1 to the group with covariates equal to 0. This may not be the desired result for continuous covariates.
Usage

```r
test_cosinor_components(
  x,
  x_str = NULL,
  param = "amp",
  comparison_A = 1,
  comparison_B = 2,
  level_index = 0,
  ci_level = 0.95
)
```

Arguments

- `x`: An `cglm` object.
- `x_str`: A character. The name of the grouping variable within which differences in the selected cosinor characteristic (amplitude or acrophase) will be tested. If there is no grouping variable in the model, then this can be left as NULL (default).
- `param`: A character. Either "amp" or "acr" for testing differences in amplitude or acrophase, respectively.
- `comparison_A`: An integer. Refers to the component number that is to act as the reference group for the comparison.
- `comparison_B`: An integer. Refers to the component number that is to act as the comparator group.
- `level_index`: An integer. If `comparison_type = "components"`, `level_index` indicates which level of the grouping variable is being used for the comparison between components.
- `ci_level`: The level for calculated confidence intervals. Defaults to 0.95.

Value

Returns a `test_cosinor` object.

Examples

```r
data_2_component <- simulate_cosinor(
  n = 10000,
  mesor = 5,
  amp = c(2, 5),
  acro = c(0, pi),
  beta.mesor = 4,
  beta.amp = c(3, 4),
  beta.acro = c(0, pi / 2),
  family = "gaussian",
  n_components = 2,
  period = c(10, 12),
  beta.group = TRUE
)
mod_2_component <- cglmm(
  Y ~ group + amp_acro(times,
    n_components = 2, group = "group",
    period = c(10, 12)
  ),
  data = data_2_component
)

test_cosinor_components(mod_2_component, param = "amp", x_str = "group")

test_cosinor_levels  Test for differences in a cosinor model between levels of the grouping variable.

Description

Given a time variable and optional covariates, generate inference a cosinor fit. For the covariate named (or vector of covariates), this function performs a Wald test comparing the group with covariates equal to 1 to the group with covariates equal to 0. This may not be the desired result for continuous covariates.

Usage

test_cosinor_levels(
  x,
  x_str,
  param = "amp",
  comparison_A,
  comparison_B,
  component_index = 1,
  ci_level = 0.95
)

Arguments

x  An cglmm object.

x_str  A character. The name of the grouping variable within which differences in the selected cosinor characteristic (amplitude or acrophase) will be tested.

param  A character. Either "amp" or "acr" for testing differences in amplitude or acrophase, respectively.

comparison_A  An integer, or string. Refers to the first level within the grouping variable x_str that is to act as the reference group in the comparison. Ensure that it corresponds to the name of the level in the original dataset.

comparison_B  An integer, or string. Refers to the second level within the grouping variable x_str that is to act as the comparator group in the comparison. Ensure that it corresponds to the name of the level in the original dataset.
component_index
An integer. If comparison_type = "levels", component_index indicates which component is being compared between the levels of the grouping variable.

ci_level
The level for calculated confidence intervals. Defaults to 0.95.

Value
Returns a test_cosinor object.

Examples

data_2_component <- simulate_cosinor(
  n = 10000,
  mesor = 5,
  amp = c(2, 5),
  acro = c(0, pi),
  beta.mesor = 4,
  beta.amp = c(3, 4),
  beta.acro = c(0, pi / 2),
  family = "gaussian",
  n_components = 2,
  period = c(10, 12),
  beta.group = TRUE
)
mod_2_component <- cglmm(
  Y ~ group + amp_acro(times,
    n_components = 2, group = "group",
    period = c(10, 12)
  ),
  data = data_2_component
)
test_cosinor_levels(mod_2_component, param = "amp", x_str = "group")

update_formula_and_data
Update data and formula for fitting cglmm model

Description
Update data and formula for fitting cglmm model

Usage
update_formula_and_data(
  data,
  formula,
  family = "gaussian",
  quietly = TRUE,
  dispformula = ~1,
Arguments

- **data**: input data for fitting cglmm model.
- **formula**: model formula, specified by user including `amp_acro()`.
- **family**: the model family.
- **quietly**: controls whether messages from `amp_acro` are displayed. TRUE by default
- **dispformula**: The formula specifying the dispersion model
- **ziformula**: The formula specifying the zero-inflation model

Value

Returns a list.

Examples

```r
# Use vitamind data but add a "patient" identifier used as a random effect
vitamind2 <- vitamind
vitamind2$patient <- sample(LETTERS[1:5], size = nrow(vitamind2), replace = TRUE)

# Use update_formula_and_data() to perform wrangling steps of cglmm()
# without yet fitting the model
data_and_formula <- update_formula_and_data(
  data = vitamind2,
  formula = vit_d ~ X + amp_acro(time,
    group = "X",
    period = 12
  )
)

# print formula from above
data_and_formula$newformula

# fit model while adding random effect to cosinor model formula.
mod <- fit_model_and_process(
  obj = data_and_formula,
  formula = update.formula(
    data_and_formula$newformula, . ~ . + (1 | patient)
  )
)

mod
mod$fit # printing the `glmmTMB` model within shows Std.Dev. of random effect
```
vitamind

Vitamin D dataset for cosinor modelling examples.

Description

Simulated data set to illustrate the cosinor model. The `vit_d` column contains the blood vitamin D levels which vary over time (`time`). The rhythm of the vitamin D fluctuations follows a cosine function and can be modelled with a cosinor model. The `X` column is a binary covariate representing two groups of patients and is associated with the characteristics of the rhythm. The rhythm has a period of about 12 hours.

Usage

`vitamind`

Format

A `data.frame` with 3 variables: `vit_d`, `time`, and `X`. 
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