Package ‘limorhyde’

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Title Differential Analysis of Rhythmic Transcriptome Data

Version 1.0.1

Description A flexible approach, inspired by cosinor regression, for
differential analysis of rhythmic transcriptome data. See Singer and Hughey

Depends R (>= 3.4)

License GPL-2

https://github.com/hugheylab/limorhyde

Encoding UTF-8

RoxygenNote 7.1.2

Imports pbs (>= 1.1)

Suggests annotate (>= 1.58.0), data.table (>= 1.12.2), foreach (>=
1.4.4), ggplot2 (>= 2.2.1), knitr (>= 1.20), limma (>= 3.36.1),
matrixStats (>= 0.56.0), org.Mm.eg.db (>= 3.6.0), qs (>=
0.25.2), rmarkdown (>= 1.9), testthat (>= 3.0.4)

VignetteBuilder knitr

BugReports https://github.com/hugheylab/limorhyde/issues

NeedsCompilation no

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getCosinorBasis  Basis matrix for cosinor

Description
Generate basis matrix for cosinor regression.

Usage
getCosinorBasis(x, period, intercept)

Arguments
- x: Values of the predictor variable.
- period: Period for the predictor variable.
- intercept: If TRUE, a column of ones will be included in the basis.

Value
A matrix with a row for each value of x and a column for each component of the decomposition.

Examples
b = getCosinorBasis(seq(0, 20, 4), period = 24, intercept = FALSE)

getSplineBasis  Basis matrix for periodic splines

Description
Generate basis matrix for a periodic B-spline using pbs::pbs().

Usage
getSplineBasis(x, period, nKnots, intercept)

Arguments
- x: Values of the predictor variable.
- period: Period for the predictor variable.
- nKnots: Number of internal knots.
- intercept: If TRUE, a column of ones will be included in the basis.
limorhyde

Value

A matrix with a row for each value of x and a column for each component of the decomposition.

Examples

b = getSplineBasis(seq(0, 20, 4), period = 24, nKnots = 3, intercept = FALSE)

limorhyde  Convert a periodic time variable into components usable in linear models

Description

Decompose a periodic time variable into multiple components based on either the first harmonic of a Fourier series or on a periodic smoothing spline.

Usage

limorhyde(
  time,
  colnamePrefix = NULL,
  period = 24,
  sinusoid = TRUE,
  nKnots = 3,
  intercept = FALSE
)

Arguments

time  Numeric vector of times, e.g., at which samples were acquired.
colnamePrefix  Character string with which to prefix the column names of the basis.
period  Number corresponding to the period to use for the decomposition (in the same units as time).
sinusoid  If TRUE, the decomposition is based on cosinor, i.e., cosine and sine. If FALSE, the decomposition is based on a periodic smoothing spline from the pbs package.
nKnots  Number of internal knots for the periodic spline. Only used if sinusoid is FALSE.
intercept  If TRUE, a column of ones will be included in the basis.

Value

A matrix with a row for each sample and a column for each component of the time decomposition.
Examples

# create an example data frame
nSamples = 12
d = data.frame(
    sample = paste0('sample_', 1:nSamples),
    genotype = factor(rep(c('WT', 'KO'), each = nSamples / 2),
                      levels = c('WT', 'KO'),
    zt = rep(seq(0, 24 - 24 / nSamples * 2, 24 / nSamples * 2), times = 2),
    stringsAsFactors = FALSE)

# call limorhyde
limo = limorhyde(d$zt, 'zt_')
d = cbind(d, limo)

# create a design matrix that could be used with methods such as limma
design = model.matrix(~ genotype * (zt_cos + zt_sin), data = d)
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