

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 (2018) <[doi:10.1177/0748730418813785](https://doi.org/10.1177/0748730418813785)>.

Depends R (>= 3.4)

License GPL-2

URL <https://limorhyde.hugheylab.org>,
<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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Repository CRAN

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getCosinorBasis	<i>Basis matrix for cosinor</i>
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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	<i>Basis matrix for periodic splines</i>
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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.

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	<i>Convert a periodic time variable into components usable in linear models</i>
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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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