Package ‘limorhyde’

October 13, 2022

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
Author Jake Hughey [aut, cre],
Jordan Singer [ctb]
Maintainer Jake Hughey <jakejhughey@gmail.com>
Repository CRAN
Date/Publication 2022-02-18 08:20:05 UTC

R topics documented:

getCosinorBasis .................................................. 2
getSplineBasis .................................................. 2
limorhyde ...................................................... 3
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**
```r
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.
Value

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

Examples

\[ b = \text{getSplineBasis}(\text{seq}(0, 20, 4), \text{period} = 24, \text{nKnots} = 3, \text{intercept} = \text{FALSE}) \]

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

\[
\text{limorhyde(} \\
\quad \text{time,} \\
\quad \text{colnamePrefix = NULL,} \\
\quad \text{period = 24,} \\
\quad \text{sinusoid = TRUE,} \\
\quad \text{nKnots = 3,} \\
\quad \text{intercept = FALSE} \\
\text{)}
\]

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)
Index

g getCosinorBasis, 2
getSplineBasis, 2
limorhyde, 3
pbs::pbs(), 2