Package 'echo.find'

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Type Package

Title Finding Rhythms Using Extended Circadian Harmonic Oscillators (ECHO)

Version 4.0.1

Description Provides a function (echo_find()) designed to find rhythms from data using extended harmonic oscillators. For more information, see H. De los Santos et al. (2020) <doi:10.1093/bioinformatics/btz617> .

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Encoding UTF-8

LazyData true

Imports minpack.lm (>= 1.2.1), boot (>= 1.3-22)

URL https://github.com/delosh653/ECHO

RoxygenNote 6.1.1

Suggests knitr, rmarkdown, ggplot2

VignetteBuilder knitr

NeedsCompilation no

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`echo.find` *echo.find: Provides a function (echo_find) designed to find rhythms from data using extended harmonic oscillators.*

Description

To read more about our inital work on this project and cite us, see Circadian Rhythms in Neurospora Exhibit Biologically Relevant Driven and Damped Harmonic Oscillations by H. De los Santos et al. (2017)

`echo_find` *Function to calculate the results for all genes using the extended circadian harmonic oscillator (ECHO) method.*

Description

Function to calculate the results for all genes using the extended circadian harmonic oscillator (ECHO) method.

Usage

```
echo_find(genes, begin, end, resol, num_reps, low = 1, high = 2,
  run_all_per, paired, rem_unexpr, rem_unexpr_amt = 70,
  rem_unexpr_amt_below = 0, is_normal, is_de_linear_trend, is_smooth,
  run_conf = F, which_conf = "Bootstrap", harm_cut = 0.03,
  over_cut = 0.15, seed = 30)
```

Arguments

`genes`	data frame of genes with the following specifications: first row is column labels, first column has gene labels/names, and all other columns have expression data. This expression data must be ordered by time point then by replicate, and must have evenly spaced time points. Any missing data must have cells left blank.
`begin`	first time point for dataset
`end`	last time point for dataset
`resol`	resolution of time points
`num_reps`	number of replicates
`low`	lower limit when looking for rhythms, in hours. May be unused if finding rhythms of any length within timecouse (run_all_per is TRUE).
`high`	upper limit when looking for rhythms, in hours. May be unused if finding rhythms of any length within timecouse (run_all_per is TRUE).
`run_all_per`	boolean which indicates whether or not rhythms of any length within timecourse should be searched for.

paired	if replicate data, whether the replicates are related (paired) or not (unpaired)
rem_unexpr	boolean indicating whether genes with less than rem_unexpr_amt percent expression should not be considered
rem_unexpr_amt	percentage of expression for which genes should not be considered if rem_unexpr is TRUE
rem_unexpr_amt_below	cutoff for expression
is_normal	boolean that indicates whether data should be normalized or not
is_de_linear_trend	boolean that indicates whether linear trends should be removed from data or not
is_smooth	boolean that indicates whether data should be smoothed or not
run_conf	boolean of whether or not to run confidence intervals
which_conf	string of which type of confidence interval to compute ("Bootstrap" or "Jackknife")
harm_cut	postive number indicating the cutoff for a gene to be considered harmonic
over_cut	postive number indicating the cutoff for a gene to be considered repressed/overexpressed
seed	number for random seed to fix for bootstrapping for confidence intervals

Value

results, a data frame which contains:

Gene Name	gene name
Convergence	depreciated result, always 0, will be removed in future versions
Iterations	depreciated result, always 0, will be removed in future versions
Amplitude.Change.Coefficient	Amplitude change coefficient value for fit
Oscillation Type	Type of oscillation (damped, driven, etc.)
Initial.Amplitude	Initial amplitude value for fit
Radian.Frequency	Radian frequency for fit
Period	Period for fit (in time units)
Phase Shift	Phase shift for fit (radians)
Hours Shifted	Phase shift for fit (hours)
Equilibrium Value	Equilibrium shift for fit
Slope	Slope value of original data, if linear baseline is removed
Tau	Kendall's tau between original and fitted values
P-value	P-value calculated based on Kendall's tau
BH Adj P-Value	Benjamini-Hochberg adjusted p-values

BY Adj P-Value	Benjamini-Yekutieli adjusted p-values
CI.PARAM.Low	Lower confidence interval bound for all parameters, if calculated
CI.PARAM.High	Higher confidence interval bound for all parameters, if calculated
Original TPX.Y	Processed values for gene expression at time point X, replicate Y
Fitted TPX	Fitted values for gene expression at time point X

Examples

```
# for more elaboration, please see the vignette
# "expressions" is the example echo.find data frame
 # long example - commented out
echo_find(genes = expressions, begin = 2, end = 48, resol = 2,
  num_reps = 3, low = 20, high = 26, run_all_per = FALSE,
  paired = FALSE, rem_unexpr = FALSE, rem_unexpr_amt = 70, rem_unexpr_amt_below=0,
  is_normal = FALSE, is_de_linear_trend = FALSE, is_smooth = FALSE)
```

---

expressions *Synthetic expression data for 12 genes.*

Description

A dataset containing the names and expression values for 12 synthetically generated samples. This example data has time points from 2 to 48 hours with 2 hour resolution and 3 replicates. Random missing data is also included. Synthetic data was created by randomly selecting parameters for the extended harmonic oscillator equation (see journal paper link in vignette for the equation), then adding random uniform noise to each expression.

Usage

```
expressions
```

Format

A data frame with 12 rows and 73 variables (column 1: sample labels, columns to 2 to 73: numerical values for gene expression in the forsmat CTX.Y (time point X, replicate Y)).

Details

Note the data format: its first column first column has gene labels/names, and all other columns have expression data. This expression data is ordered by time point then by replicate, and has evenly spaced time points. Any missing data has cells left blank.

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