

Package ‘deltaccd’

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Type Package

Title Quantify Rhythmic Gene Co-Expression Relative to a Reference

Version 1.0.2

Description Infer progression of circadian rhythms in transcriptome data in which samples are not labeled with time of day and coverage of the circadian cycle may be incomplete. See Shilts et al. (2018) <[doi:10.7717/peerj.4327](https://doi.org/10.7717/peerj.4327)>.

URL <https://deltaccd.hugheylab.org>,
<https://github.com/hugheylab/deltaccd>

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LazyData true

LazyDataCompression gzip

RoxygenNote 7.1.2

Depends R (>= 3.4)

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rlang (>= 0.4.11), scales (>= 0.5.0), statmod (>= 1.4.30),
data.table (>= 1.14.0)

Suggests doParallel (>= 1.0.11), knitr, rmarkdown, testthat (>= 3.0.0), vdiff

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calcCCD	<i>Calculate clock correlation distance (CCD).</i>
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Description

Quantify the similarity of gene co-expression between a reference and a test dataset. Statistical significance is calculated using permutation of the genes.

Usage

```
calcCCD(
  refCor,
  emat,
  groupVec = NULL,
  refEmat = NULL,
  nPerm = 1000,
  geneNames = NULL,
  dopar = FALSE,
  scale = FALSE
)
```

Arguments

refCor	Correlation matrix to be used as the reference, such as comes from getRefCor() . Should contain Spearman correlation values.
emat	Matrix of expression values, where each row corresponds to a gene and each column corresponds to a sample. The rownames and colnames of refCor should be present in the rownames of emat. For the p-value calculation, it is important that emat include all measured genes, not just those in refCor.
groupVec	Optional vector indicating the group to which group each sample belongs. If not provided, the function assumes all samples belong to the same group.
refEmat	Optional expression matrix for calculating co-expression for the reference, with the same organization as emat. Only used if refCor is not provided.
nPerm	Number of permutations for assessing statistical significance.
geneNames	Optional vector indicating a subset of genes in refCor, emat, and/or refEmat to use for calculating the CCD.

dopar	Logical indicating whether to process features in parallel. Make sure to register a parallel backend first.
scale	Logical indicating whether to scale CCD by the number of gene pairs.

Value

A data.table with columns for group name, CCD, and p-value.

See Also

[getRefCor\(\)](#), [calcDeltaCCD\(\)](#), [plotHeatmap\(\)](#)

Examples

```
set.seed(35813)

refCor = getRefCor()
ccdResult = calcCCD(refCor, GSE19188$emat, GSE19188$groupVec, nPerm = 100)
```

calcDeltaCCD	<i>Calculate delta clock correlation distance.</i>
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Description

Calculate the difference between the clock correlation distances (CCDs), relative to a reference, for two groups of samples. Statistical significance is calculated using permutation of the samples that belong to either of those two groups.

Usage

```
calcDeltaCCD(  
  refCor,  
  emat,  
  groupVec,  
  groupNormal,  
  refEmat = NULL,  
  nPerm = 1000,  
  geneNames = NULL,  
  dopar = FALSE,  
  scale = FALSE  
)
```

Arguments

refCor	Correlation matrix to be used as the reference, such as comes from <code>getRefCor()</code> . Should contain Spearman correlation values.
emat	Matrix of expression values, where each row corresponds to a gene and each column corresponds to a sample. The rownames and colnames of refCor should be present in the rownames of emat. For the p-value calculation, it is important that emat include all measured genes, not just those in refCor.
groupVec	Vector indicating the group to which group each sample belongs. It's ok for groupVec to have more than two groups.
groupNormal	Value indicating the group in groupVec that corresponds to normal or healthy. Other groups will be compared to this group.
refEmat	Optional expression matrix for calculating co-expression for the reference, with the same organization as emat. Only used if refCor is not provided.
nPerm	Number of permutations for assessing statistical significance.
geneNames	Optional vector indicating a subset of genes in refCor, emat, and/or refEmat to use for calculating the CCD.
dopar	Logical indicating whether to process features in parallel. Make sure to register a parallel backend first.
scale	Logical indicating whether to use scaled CCDs to calculate difference.

Value

A data.table with columns for group 1, group 2, deltaCCD, and p-value. In each row, the deltaCCD is the CCD of group 2 minus the CCD of group 1, so group 1 corresponds to groupNormal.

See Also

[getRefCor\(\)](#), [calcCCD\(\)](#), [plotHeatmap\(\)](#)

Examples

```
set.seed(35813)

refCor = getRefCor()
deltaCcdResult = calcDeltaCCD(
  refCor, GSE19188$emat, GSE19188$groupVec, 'healthy', nPerm = 100)
```

getRefCor	<i>Retrieve the reference correlation matrix for circadian gene co-expression.</i>
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Description

The pan-tissue reference matrix is based on a fixed-effects meta-analysis of eight circadian transcriptome datasets from mice, as described in Shilts et al. 2018([doi: 10.7717/peerj.4327](https://doi.org/10.7717/peerj.4327)). The human blood reference matrix is based an analysis of three microarray datasets (manuscript in preparation).

Usage

```
getRefCor(
  species = c("human", "mouse"),
  tissue = c("pan", "blood"),
  useEntrezGeneId = TRUE
)
```

Arguments

species	Currently either 'human' or 'mouse'. Only affects the row and column names of the correlation matrix, not the actual values.
tissue	One of either 'pan' or 'blood'.
useEntrezGeneId	If FALSE, row and column names of correlation matrix will correspond to gene symbols (e.g., PER2).

Value

A matrix of Spearman correlation values.

See Also

[GSE19188](#), [plotRefHeatmap\(\)](#), [calcCCD\(\)](#), [calcDeltaCCD\(\)](#)

GSE19188	<i>Gene expression data for GSE19188.</i>
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Description

Data of gene expression measured by microarray for samples from human non-small cell lung cancer.

Usage

```
GSE19188
```

Format

A list with two objects:

emat Matrix of normalized expression values, where each row corresponds to a gene (rownames are Entrez Gene IDs) and each column corresponds to a sample. To save space, genes have been downsampled.

groupVec Vector of condition (tumor or healthy) for each sample.

Source

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19188>

See Also

[getRefCor\(\)](#), [calcCCD\(\)](#), [calcDeltaCCD\(\)](#)

plotHeatmap

Visualize gene co-expression.

Description

Make heatmaps of the co-expression (Spearman correlation) between pairs of selected genes in a dataset.

Usage

```
plotHeatmap(geneNames, emat, groupVec = NULL)
```

Arguments

geneNames	Vector indicating the subset of genes in the rownames of emat for which to calculate the correlations in expression.
emat	Matrix of expression values, where each row corresponds to a gene and each column corresponds to a sample. The elements of geneNames should be present in the rownames of emat.
groupVec	Optional vector indicating the group to which group each sample belongs. If not provided, the function assumes all samples belong to the same group.

Value

A ggplot object, which can be saved using `ggplot2::ggsave()`. Heatmap colors will be directly comparable to any heatmaps created by this function or by `plotRefHeatmap()`.

See Also

[calcCCD\(\)](#), [calcDeltaCCD\(\)](#), [plotRefHeatmap\(\)](#)

Examples

```
refCor = getRefCor()
pRef = plotRefHeatmap(refCor)
pTest = plotHeatmap(rownames(refCor), GSE19188$emat, GSE19188$groupVec)
```

plotRefHeatmap	<i>Visualize the reference pattern of gene co-expression.</i>
----------------	---

Description

Make a heatmap of the reference correlation matrix for gene co-expression.

Usage

```
plotRefHeatmap(refCor)
```

Arguments

refCor Correlation matrix, such as comes from [getRefCor\(\)](#).

Value

A ggplot object, which can be saved using [ggplot2::ggsave\(\)](#). Heatmap colors will be directly comparable to any heatmaps created by this function or by [plotHeatmap\(\)](#).

See Also

[getRefCor\(\)](#), [plotHeatmap\(\)](#)

Examples

```
refCor = getRefCor()
pRef = plotRefHeatmap(refCor)
pTest = plotHeatmap(rownames(refCor), GSE19188$emat, GSE19188$groupVec)
```

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