Package 'TEKRABber'

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Type Package

Title An R package estimates the correlations of orthologs and transposable elements between two species

Version 1.17.0

Description TEKRABber is made to provide a user-friendly pipeline for comparing orthologs and transposable elements (TEs) between two species. It considers the orthology confidence between two species from BioMart to normalize expression counts and detect differentially expressed orthologs/TEs. Then it provides one to one correlation analysis for desired orthologs and TEs. There is also an app function to have a first insight on the result. Users can prepare orthologs/TEs RNA-seq expression data by their own preference to run TEKRABber following the data structure mentioned in the vignettes.

URL https://github.com/ferygood/TEKRABber

BugReports https://github.com/ferygood/TEKRABber/issues

Encoding UTF-8

License LGPL (>=3)

Imports AnnotationHub, apeglm, biomaRt, dplyr, doParallel, DESeq2, foreach, magrittr, Rcpp (>= 1.0.7), rtracklayer, SCBN, stats, utils

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`appTEKRABber` *appTEKRABber*

Description

Provide a shiny UI for presenting the results from DE analysis and correlation analysis.

Usage

```
appTEKRABber(corrRef, corrCompare, DEobject)
```

Arguments

`corrRef`	correlation results for reference using corrOrtholgScale()
`corrCompare`	correlation results for comparison using corrOrthologScale()
`DEobject`	DE object using DEgeneTE()

Value

provide an interactive shinyapp

Examples

```
data(speciesCounts)
hmGene <- speciesCounts$hmGene
hmTE <- speciesCounts$hmTE
chimpGene <- speciesCounts$chimpGene
chimpTE <- speciesCounts$chimpTE

data(fetchDataHmChimp)
fetchData <- fetchDataHmChimp
inputBundle <- DECorrInputs(fetchData)

meta <- data.frame(
species = c(rep("human", ncol(hmGene) - 1),
            rep("chimpanzee", ncol(chimpGene) - 1)))

meta$species <- factor(meta$species, levels = c("human", "chimpanzee"))
rownames(meta) <- colnames(inputBundle$geneInputDESeq2)
hmchimpDE <- DEgeneTE(
    geneTable = inputBundle$geneInputDESeq2,
    teTable = inputBundle$teInputDESeq2,
    metadata = meta,
    expDesign = TRUE)

# use only 10 rows of Genes and TEs
hmCorrResult <- corrOrthologTE(
    geneInput = hmchimpDE$geneCorrInputRef[c(1:10),],
    teInput = hmchimpDE$teCorrInputRef[c(1:10),],
    corrMethod = "pearson",
    padjMethod = "fdr")

chimpCorrResult <- corrOrthologTE(
    geneInput = hmchimpDE$geneCorrInputCompare[c(1:10), ],
    teInput = hmchimpDE$teCorrInputCompare[c(1:10), ],
    corrMethod = "pearson",
    padjMethod = "fdr")


#library(plotly)
#appTEKRABber(
    #corrRef = hmCorrResult,
    #corrCompare = chimpCorrResult,
    #DEobject = hmchimpDE)
```

`corrOrthologTE` *Estimate correlation comparing orthologs and TEs*

Description

To estimate correlation comparing orthologs and TEs one-by-one from inputs. You can specify the correlation and adjusted p-value methods (see details in parameters). If you want to save your outputs instead of just returning them, please specify the fileDir and fileName with the extension .csv. The default fileName is TEKRABber_geneTECorrReusult.csv.

Usage

```
corrOrthologTE(geneInput, teInput, corrMethod = "pearson",
padjMethod = "fdr", numCore=1, fileDir=NULL,
fileName="TEKRABber_geneTECorrResult.csv")
```

Arguments

geneInput	gene count input for correlation from using DECorrInputs()
teInput	te count input for correlation from using DECorrInputs()
corrMethod	correlation method, including pearson, kendall, spearman. Default is pearson.
padjMethod	method to return adjusted p-value, and default is fdr. See ?p.adjust
numCore	number of cores to run parallel. Default is 1. You can use detectCores() to get how many cores you can use.
fileDir	the name of directory for saving output files. Default is NULL.
fileName	the name for saving output files. Default is "TEKRABber_geneTECorrResult.csv"

Value

a dataframe includes correlation coefficient, pvalue, padj

Examples

```
data(ctInputDE)
geneInputDE <- ctInputDE$gene
teInputDE <- ctInputDE$te

metaExp <- data.frame(experiment = c(rep("control", 5), rep("treatment", 5)))
rownames(metaExp) <- colnames(geneInputDE)
metaExp$experiment <- factor(
    metaExp$experiment,
    levels = c("control", "treatment")
)

resultDE <- DEgeneTE(
    geneTable = geneInputDE,
    teTable = teInputDE,
    metadata = metaExp,
    expDesign = FALSE
)

controlCorr <- corrOrthologTE(
    geneInput = resultDE$geneCorrInputRef[c(1:10),],
    teInput = resultDE$teCorrInputRef[c(1:10),],
    numCore = 1,
    corrMethod = "pearson",
    padjMethod = "fdr"
)
```

ctInputDE — *Input expression data of gene/TE for differentially expressed analysis within same species*

Description

TEKRABber can also be used comparing orthologs and transposable elements within same species, i.e., control and treatment. Here we provide an example data for demonstration. This data was based on syn8466812 RNA-seq (Allen M et al., 2016). However, the expression data was modified due to confidential agreement. Therefore, it cannot represent the original data.

Usage

```
data(ctInputDE)
```

Format

An object contains 2 expression data:

gene input gene data for DE analysis comparing control and treatment

te input TE data for DE analysis comparing control and treatment

Examples

```
data(ctInputDE)
geneInputDE <- ctInputDE$gene
teInputDE <- ctInputDE$te
```

DECorrInputs — *Generate all the input files for TEKRABber downstream analysis*

Description

Generate all the inputs files for differentially expressed orthologous genes/TEs analysis, and for correlation analysis. The output is a list containing 6 dataframes.

Usage

```
DECorrInputs(fetchData)
```

Arguments

fetchData	output list from TEKRABber::orthologScale()

Value

create inputs for DE analysis and correlations: (1) geneInputDESeq2 (2) teInputDESeq2 (3) geneCorrInputRef (4) geneCorrInputCompare (5) TECorrInputRef (6) TECorrInputCompare

Examples

```
data(speciesCounts)
data(hg38_panTro6_rmsk)
hmGene <- speciesCounts$hmGene
chimpGene <- speciesCounts$chimpGene
hmTE <- speciesCounts$hmTE
chimpTE <- speciesCounts$chimpTE

## For demonstration, here we only select 1000 rows to save time
set.seed(1234)
hmGeneSample <- hmGene[sample(nrow(hmGene), 1000), ]
chimpGeneSample <- chimpGene[sample(nrow(chimpGene), 1000), ]

fetchData <- orthologScale(
    speciesRef = "hsapiens",
    speciesCompare = "ptroglodytes",
    geneCountRef = hmGeneSample,
    geneCountCompare = chimpGeneSample,
    teCountRef = hmTE,
    teCountCompare = chimpTE,
    rmsk = hg38_panTro6_rmsk,
    version = 105
)

inputBundle <- DECorrInputs(fetchData)
```

DEgeneTE *Estimate differentially expressed genes and TEs*

Description

To estimate differentially expressed genes and TEs, DEgeneTE() takes gene inputs and TE inputs from the results using the DECorrInputs function. You need to specify your metadata and expDesign based on your design. If you also want to save the output, please specify the fileDir parameter.

Usage

```
DEgeneTE(geneTable, teTable, metadata, expDesign=TRUE, fileDir=NULL)
```

Arguments

geneTable	gene input table from using DECorrInputs()
teTable	TE input table from using DECorrInputs()
metadata	an one column dataframe with rownames same as the column name of gene/te count table. Column name must be **species** or **experiment**.
expDesign	Logic value for comparing between or within species. **TRUE** for comparing between two species, and **FALSE** for comparing between control and treatment.
fileDir	the name and path of directory for saving output files. Default is NULL.

Value

return DESeq2 res and normalized gene counts.

Examples

```
## comparing between species:
## (1) set expDesign = TRUE
## (2) column name of metadata needs to be "species".

data(fetchDataHmChimp)
fetchData <- fetchDataHmChimp

inputBundle <- DECorrInputs(fetchData)

meta <- data.frame(species=c(rep("human", ncol(fetchData$geneRef) - 1),
    rep("chimpanzee", ncol(fetchData$geneCompare) - 1))
)
rownames(meta) <- colnames(inputBundle$geneInputDESeq2)
meta$species <- factor(meta$species, levels = c("human", "chimpanzee"))

hmchimpDE <- DEgeneTE(
    geneTable = inputBundle$geneInputDESeq2,
    teTable = inputBundle$teInputDESeq2,
    metadata = meta,
    expDesign = TRUE
)
```

`fetchDataHmChimp` *Example output comparing human and chimpanzee data using orhtologScale()*

Description

An output list of data contains 7 elements after using orthologScale(), including (1) orthology table comparing human and chimpanzee. (2) scaling factor for orthologous genes (3) gene count table from reference species (4) gnee count table from species you want to compare (5) scaling factor for TEs (6) TE count table from reference species (7) TE count table from the species you want to compare. The aim to provide this dataset is to save time for user running the vignettes and give a template for demonstration.

Usage

```
data(fetchDataHmChimp)
```

Format

An object contains 2 elements:

orthologTable orthology information from Ensembl

scaleFactor scaling factor to normalize data

Examples

```
data(fetchDataHmChimp)
fetchData <- fetchDataHmChimp
fetchData$orthologTable
fetchData$scaleFactor
```

hg38_panTro6_rmsk *Repeatmasker track annotations with human and chimpanzee*

Description

This Repeatmasker track annotations table was first downloaded from UCSC Genome Table Browser and it included the name, class, and average gene length in repeats(transposable elements). This data is used for demonstrate an example for user how to provide a annotation table to normalize their data which in this case comparing human(hg38) to chimpanzee(panTro6).

Usage

```
data(hg38_panTro6_rmsk)
```

Format

An object of class `grouped_df` (inherits from `tbl_df`, `tbl`, `data.frame`) with 12550 rows and 4 columns.

Examples

```
data(hg38_panTro6_rmsk)
```

orthologScale *Normalized orthologous genes and TEs between two species*

Description

Normalize orthologous genes and TEs between two species with a scaling factor using their expression level and gene lengths.

Usage

```
orthologScale(speciesRef, speciesCompare, geneCountRef,
geneCountCompare, teCountRef, teCountCompare, rmsk, version)
```

Arguments

`speciesRef`	The scientific name for your reference species. i.e., hsapiens
`speciesCompare`	The scientific name for your species to compare. i.e., ptroglodytes
`geneCountRef`	Gene count from your reference species. First column should be Ensmebl gene ID.
`geneCountCompare`	Gene count from the species you want to compare. First column should be Ensembl gene ID.
`teCountRef`	TE count from your reference species. First column should be teName.
`teCountCompare`	TE count from the species you want to compare. First column should be teName.
`rmsk`	a repeatmasker table including 4 columns: (1) the name of TE (2) the class of TE (3) The average length of that TE from your reference species (4) The average length of that TE from the species you want to compare.
`version`	for specify Ensembl version. Default is NULL for getting the latest version

Value

a list of outputs: (1) orthologTable, orthology information (2) c_ortholog, scaling factor for orthologous genes (3) geneRef, gene count table for reference species (4) geneCompare, normalized gene count table for species compared (5) c_te, scaling factor for TEs (6) teRef, TE count table for reference species (7) teCompare, normalized TE count table for species compared.

Examples

```
data(speciesCounts)
data(hg38_panTro6_rmsk)
hmGene <- speciesCounts$hmGene
chimpGene <- speciesCounts$chimpGene
hmTE <- speciesCounts$hmTE
chimpTE <- speciesCounts$chimpTE

## For demonstration, here we only select 1000 rows to save time
set.seed(1234)
hmGeneSample <- hmGene[sample(nrow(hmGene), 1000), ]
chimpGeneSample <- chimpGene[sample(nrow(chimpGene), 1000), ]

fetchData <- orthologScale(
    speciesRef = "hsapiens",
    speciesCompare = "ptroglodytes",
    geneCountRef = hmGeneSample,
    geneCountCompare = chimpGeneSample,
    teCountRef = hmTE,
    teCountCompare = chimpTE,
    rmsk = hg38_panTro6_rmsk,
    version = 105
)
```

---

prepareRMSK *Prepare a table from two species RepeatMakser track from UCSC genome Table*

Description

create a table to the rmsk argument in orthologScale(). Before version 1.8, TEKRABber requires user to prepare this table by themselves and this function can help user automatically get the RepeatMasker table from UCSC. The arguments required are the abbreviation of the version of reference (case-sensitive). For example, "hg38" for human. Note: currently only 91 genomes provided. Check if the reference exists with GenomeInfoDb::registered_UCSC_genomes().

Usage

```
prepareRMSK(refSpecies, compareSpecies)
```

Arguments

refSpecies	the version of reference species, i.e. hg38
compareSpecies	the version of compared species, i.e. panTro6

Value

Dataframe with four columns: repName, repClass, rLen and cLen

Examples

```
df_rmsk <- prepareRMSK(refSpecies = "hg38", compareSpecies = "panTro6")
```

`rcpp_corr` *Estimate the correlation between genes and transposable elements*

Description

Estimate the correlation between genes and transposable elements

Usage

```
rcpp_corr(df1, df2, Method)
```

Arguments

`df1`	First dataframe
`df2`	Second dataframe
`Method`	correlation method

Value

a dataframe containing correlation results

`speciesCounts` *Gene/TE expression data from human/chimpanzee brain RNA-seq*

Description

Dataset contains 4 expression data from human and chimpanzee brain RNA-seq. We select raw fastq data from 10 humans and 10 chimpanzees from (Khrameeva E et al., 2020). Gene expression is generated using HISAT2 and featureCounts (Kim D et al., 2019; Liao Y et al., 2014). Transposable elements (TEs) expression is generated with multi-mapping option using STAR and TEtranscripts (Dobin A et al., 2013; Jin Y et al., 2015).

Usage

```
data(speciesCounts)
```

Format

An object contains 4 expression counts:

hmGene human gene expression data

hmTE human TE expression

chimpGene chimpanzee gene expression data

chimpTE chimpanzee TE expression data

Examples

```
data(speciesCounts)
hmGene <- speciesCounts$hmGene
hmTE <- speciesCounts$hmTE
chimpGene <- speciesCounts$chimpGene
chimpTE <- speciesCounts$chimpTE
```

TEKRABber *An R package estimates the correlations of orthologs and transposable elements between two species*

Description

TEKRABber is made to provide an user-friendly pipeline for comparing orthologs and transposable elements (TEs) between two species. It considers the orthology confidence between two species from BioMart to normalize expression counts and detect differentially expressed ortholog/TEs. Then it provides one to one correlation analysis for desired orthologs and TEs. There is also an app function to have a first insight on the result. Users can prepare orthologs/TEs RNA-seq expression data by their own preference to run TEKRABber following the data structure mentioned in the vignettes.

Details

TEKRABber analysis pipeline includes 5 main functions:

1. **orthologScale**(): obtain orthology information and calculate scaling factor. 2. **DECorrInputs**(): create the input files for running DE/correlation analysis. 3. **DEgeneTE**(): run DE analysis on orthologs and transposable elements. 4. **corrOrthologTE**(): estimate correlation between selected orthologs and transposable elements. 5. **appTEKRABber**(): (optional) find first insight from data using an local webapp. Find more details in vignette or on the helping page, i.e. ?orthologScale

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TEKRABber GitHub Repo

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