

# Package ‘TEKRABber’

April 11, 2023

**Type** Package

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

**Version** 1.2.0

**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** GPL (>= 2)

**Imports** apeglm, biomaRt, DESeq2, Rcpp (>= 1.0.7), SCBN, SummarizedExperiment, stats, utils

**LinkingTo** Rcpp

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**VignetteEngine** knitr

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appTEKRABber

*Visualize TEKRABber results with shiny app*

---

### Description

To help user explore their results using TEKRABber, this function visualizes the results using a self-written shiny app with two tabs, including the expression and correlation of genes and TEs. To run it, you need to create four variables and assign them with your DE result, correlation results and metadata to appDE, appRef, appCompare and appMeta. Please see the example below for more details.

### Usage

```
appTEKRABber()
```

### Value

An app to display differentially expressed genes/TEs and the correlation results

**Examples**

```

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

data(fetchDataHmChimp)
fetchData <- fetchDataHmChimp

inputBundle <- DECorrInputs(
  orthologTable = fetchData$orthologTable,
  scaleFactor = fetchData$scaleFactor,
  geneCountRef = hmGene,
  geneCountCompare = chimpGene,
  teCountRef = hmTE,
  teCountCompare = chimpTE
)

# create metadata for DE analysis
meta <- data.frame(species=c(rep("human", ncol(hmGene) - 1),
  rep("chimpanzee", ncol(chimpGene) - 1))
)
rownames(meta) <- colnames(inputBundle$geneInputDESeq2)
meta$species <- factor(meta$species, levels = c("human", "chimpanzee"))

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

data(speciesCorr)
hmGeneCorrInput <- assay_tekcorrset(speciesCorr, "gene", "human")
hmTECorrInput <- assay_tekcorrset(speciesCorr, "te", "human")
chimpGeneCorrInput <- assay_tekcorrset(speciesCorr, "gene", "chimpanzee")
chimpTECorrInput <- assay_tekcorrset(speciesCorr, "te", "chimpanzee")

# Correlation analysis
hmCorrResult <- corrOrthologTE(
  geneInput = hmGeneCorrInput,
  teInput = hmTECorrInput,
  corrMethod = "pearson",
  padjMethod = "fdr"
)
chimpCorrResult <- corrOrthologTE(
  geneInput = chimpGeneCorrInput,
  teInput = chimpTECorrInput,
  corrMethod = "pearson",
  padjMethod = "fdr"
)

```

```

)

# assign results and metadata to appDE, appRef, appCompare, and appMeta
appDE <- hmchimpDE
appRef <- hmCorrResult
appCompare <- chimpCorrResult
appMeta <- meta

if (interactive()){
  appTEKRABber()
}

```

---

assay\_tekcorrset      *Access genes and transposable elements expression data*

---

### Description

a function only used for accessing the expression data from a TekCorrSet class object to demonstrate examples in vignettes. demonstration.

### Usage

```
assay_tekcorrset(tecorrset, expType, sample)
```

### Arguments

tecorrset	TekCorrSet object
expType	Indicate which data you want to access. It should be "gene" or "te".
sample	The species name or experimental design. It should be "human" and "chimpanzee" when you are running comparing species design. "control" and "treatment" are for running same species design.

### Value

a dataframe contains expression genes or transposable elements.

### Examples

```

data(speciesCorr)
hmGeneCorrInput <- assay_tekcorrset(speciesCorr, "gene", "human")
hmTECorrInput <- assay_tekcorrset(speciesCorr, "te", "human")
chimpGeneCorrInput <- assay_tekcorrset(speciesCorr, "gene", "chimpanzee")
chimpTECorrInput <- assay_tekcorrset(speciesCorr, "te", "chimpanzee")

```

---

`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_geneTECorrResult.csv`.

## Usage

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

## Arguments

<code>geneInput</code>	gene count input for correlation from using <code>DECorrInputs()</code>
<code>teInput</code>	te count input for correlation from using <code>DECorrInputs()</code>
<code>corrMethod</code>	correlation method, including pearson, kendall, spearman. Default is pearson.
<code>padjMethod</code>	method to return adjusted p-value, and default is fdr. See <code>?p.adjust</code>
<code>fileDir</code>	the name of directory for saving output files. Default is <code>NULL</code> .
<code>fileName</code>	the name for saving output files. Default is <code>"TEKRABber_geneTECorrResult.csv"</code>

## Value

a dataframe includes correlation coefficient, pvalue, padj

## Examples

```
library(SummarizedExperiment)  
data(speciesCorr)  
hmGeneCorrInput <- assay_tekcorrset(speciesCorr, "gene", "human")  
hmTECorrInput <- assay_tekcorrset(speciesCorr, "te", "human")  
  
corrOrthologTE(  
  geneInput=hmGeneCorrInput,  
  teInput=hmTECorrInput,  
  corrMethod="pearson",  
  padjMethod="fdr",  
  fileDir=NULL  
)
```

---

ctCorr	<i>Normalized Gene/TE expression toy data in control and treatment in same species for correlation analysis</i>
--------	---

---

### Description

Dataset contains gene/TE expression data from control and treatment based on syn8466812 RNA-seq (Allen M et al., 2016) for correlation analysis. These data were also modified due to confidential agreement. Therefore, it cannot represent the original data. For a quick demonstration, we only use 10 genes and 10 transposable elements.

### Usage

```
data(ctCorr)
```

### Format

An object of class "TekCorrSet" which contains 4 expression counts and you can access it specifying the parameters using `assay_tekcorrset()`:

**assay\_tekcorrset(ctCorr, "gene", "control")** control gene expression data

**assay\_tekcorrset(ctCorr, "te", "control")** control TE expression data

**assay\_tekcorrset(ctCorr, "gene", "treatment")** treatment gene expression data

**assay\_tekcorrset(ctCorr, "te", "treatment")** treatment TE expression data

### Examples

```
data(ctCorr)
geneConCorrInput <- assay_tekcorrset(ctCorr, "gene", "control")
teConCorrInput <- assay_tekcorrset(ctCorr, "te", "control")
geneTreatCorrInput <- assay_tekcorrset(ctCorr, "gene", "treatment")
teTreatCorrInput <- assay_tekcorrset(ctCorr, "te", "treatment")
```

---

ctInputDE	<i>Input expression data of gene/TE for differentially expressed analysis within same species</i>
-----------	---

---

### 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 genes/TEs analysis, and for correlation analysis. The output is a list containing 6 dataframes.

**Usage**

```
DECORRINPUTS(orthologTable, scaleFactor, geneCountRef,
geneCountCompare, teCountRef, teCountCompare)
```

**Arguments**

orthologTable	orthologTable output from using orthologScale()
scaleFactor	scaleFactor output from using orthologScale()
geneCountRef	Gene counts from your reference species. First column should be Ensembl gene ID.
geneCountCompare	Gene counts from the species you want to compare. First column should also be Ensembl gene ID.
teCountRef	TE counts from your reference species. First column should be TE's name.
teCountCompare	TE counts from the species you want to compare. First column should also be TE's name.

**Value**

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

## Examples

```

data(speciesCounts)
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
)

inputBundle <- DECorrInputs(
  orthologTable=fetchData$orthologTable,
  scaleFactor=fetchData$scaleFactor,
  geneCountRef=hmGene,
  geneCountCompare=chimpGene,
  teCountRef=hmTE,
  teCountCompare=chimpTE
)

```

---

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 <b>species</b> or <b>experiment</b> .



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

data(fetchDataHmChimp)
fetchData <- fetchDataHmChimp

inputBundle <- DECorrInputs(
  orthologTable = fetchData$orthologTable,
  scaleFactor = fetchData$scaleFactor,
  geneCountRef = hmGene,
  geneCountCompare = chimpGene,
  teCountRef = hmTE,
  teCountCompare = chimpTE
)

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

**Description**

An output list of data contains 2 elements after using `orthologScale()`. The first one is the orthology table comparing human and chimpanzee. The second one is the scaling factor. The purpose of providing 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
```

---

<code>orthologScale</code>	<i>Get orthology information from Ensembl</i>
----------------------------	---

---

**Description**

Get orthology information from Ensembl using biomaRt and calculate scaling factor between two species using the confidence of orthology score and expression counts.

**Usage**

```
orthologScale(speciesRef, speciesCompare, geneCountRef,
geneCountCompare)
```

**Arguments**

<code>speciesRef</code>	The scientific name for your reference species. i.e., <code>hsapiens</code>
<code>speciesCompare</code>	The scientific name for your species to compare. i.e., <code>ptroglodytes</code>
<code>geneCountRef</code>	Gene count from your reference species. First column should be Ensembl gene ID
<code>geneCountCompare</code>	Gene count from the species you want to compare. First column should also be Ensembl gene ID

**Value**

There are two outputs:(1) orthologTable: orthology information from BioMart (2) scale\_factor: for normalizing expression counts

**Examples**

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

## 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
)
```

---

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

---

speciesCorr	<i>A subsets of normalized Gene/TE expression data from human/chimpanzee brain RNA-seq for correlation analysis demonstration</i>
-------------	---

---

### Description

An object of class "TekCorrSet" which contains 4 expression counts. These data are generated from speciesCounts using TEKCRABber pipeline. For a quick demo, we only select 50 orthologs and 50 transposable elements.

### Usage

```
data(speciesCorr)
```

### Format

An object of class "TekCorrSet" which contains 4 expression counts and you can access it specifying the parameters using assay\_tekcorrset():

**assay\_tekcorrset(speciesCorr, "gene", "human")** human gene expression data

**assay\_tekcorrset(speciesCorr, "te", "human")** human TE expression data

**assay\_tekcorrset(speciesCorr, "gene", "chimpanzee")** chimpanzee gene expression data

**assay\_tekcorrset(speciesCorr, "te", "chimpanzee")** chimpanzee TE expression data

### Examples

```
data(speciesCorr)
hmGeneCorrInput <- assay_tekcorrset(speciesCorr, "gene", "human")
hmTECorrInput <- assay_tekcorrset(speciesCorr, "te", "human")
chimpGeneCorrInput <- assay_tekcorrset(speciesCorr, "gene", "chimpanzee")
chimpTECorrInput <- assay_tekcorrset(speciesCorr, "te", "chimpanzee")
```

---

speciesCounts	<i>Gene/TE expression data from human/chimpanzee brain RNA-seq</i>
---------------	--

---

### 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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