

Package ‘ceRNAR’

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Type Package

Title ceRNAR: An R Package for Identification and Analysis of ceRNAs-miRNA Triplets

Version 1.1.0

Author Yi-Wen Hsiao[†], Lin Wang[†] and Tzu-Pin Lu

Maintainer Yi-Wen Hsiao <d08849010@ntu.edu.tw>

Description

This R package is designed for identification and analysis of ceRNA-miRNA triplets via integration of miRNA and RNA expression data at specific miRNA expression level. CeRNAR integrates three main steps: identification of ceRNA pairs, segment clustering, and peak merging. In addition, it also provides some downstream analyses of identified ceRNA-miRNA triplets, including network analysis, functional annotation, and survival analysis.

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Encoding UTF-8

Depends R(>= 4.2.0),

Biobase,
cvms,
dplyr,
ggplot2,
magrittr,
rlang,
foreach,
SPONGE

Imports cowplot,

data.table,
DNAcopy,
doParallel,
GGally,
HelpersMG,
psych,
purrr,
quantmod,
R.utils,
stringr,
tidyr,
zoo,
parallel,
utils,
grDevices

RoxygenNote 7.2.1

Suggests rmarkdown,
knitr,
ggpubr,
survival,
survminer,
GOSemSim,
network,
egg,
enrichplot,
AnnotationDbi,
clusterProfiler,
RJAMI

SystemRequirements ceRNAR supports Linux, macOS and Window

BugReports <https://github.com/ywhsiao/ceRNAR/issues>

URL <https://github.com/ywhsiao/ceRNAR>

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ceRNACustomize	<i>A function for uploading customized data</i>
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Description

A function to allow users to upload their own data

Usage

```
ceRNACustomize(
  path_prefix,
  project_name = "demo",
  disease_name = "DLBC",
  gene_exp = gene_exp,
  mirna_exp = mirna_exp,
  surv_data = surv_data
)
```

Arguments

path_prefix	user's working directory
project_name	the project name that users can assign (default: demo)
disease_name	the abbreviation of disease that users are interested in (default: DLBC)
gene_exp	location of gene expression data (default: gene_exp)
mirna_exp	location of miRNA expression data (default: mirna_exp)
surv_data	location of survival data (default: surv_data)

Examples

```
data(gene_exp)
data(mirna_exp)
data(surv_data)
ceRNACustomize(
  path_prefix = '~/',
  project_name = 'demo',
  disease_name = 'DLBC',
  gene_exp = gene_exp,
  mirna_exp = mirna_exp,
  surv_data = surv_data
)
```

ceRNAFunction

Functional enrichment analysis

Description

A function to conduct Functional enrichment analysis for biological interpretation. The databases supported in this function include Gene Ontology (GO; <http://geneontology.org/>) and Kyoto Encyclopedia of Genes and Genomes (KEGG; <https://www.genome.jp/kegg/>).

Usage

```
ceRNAFunction(path_prefix, project_name, disease_name, pairs_cutoff)
```

Arguments

path_prefix	user's working directory
project_name	the project name that users can assign (default: demo)
disease_name	the abbreviation of disease that users are interested in (default: DLBC)
pairs_cutoff	at least the number of ceRNA pairs that a mirna must have (default: 1)

Examples

```
ceRNAFunction(
  path_prefix = '~/',
  project_name = 'demo',
  disease_name = 'DLBC',
  pairs_cutoff = 1
)
```

ceRNAIntergate

*Integration of the possible ceRNA pairs among published tools***Description**

A function to integrate the possible ceRNA pairs that are found by ceRNAR algorithm with those from other tools, such as SPONGE (List et al., 2019) and RJAMI (Hornakova et al., 2018.)

Usage

```
ceRNAIntergate(path_prefix, project_name, disease_name)
```

Arguments

path_prefix	user's working directory
project_name	the project name that users can assign
disease_name	the abbreviation of disease that users are interested in

Examples

```
ceRNAIntergate(
  path_prefix = '~/',
  project_name = 'demo',
  disease_name = 'DLBC'
)
```

ceRNALocation	<i>Visualization for peak location</i>
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Description

A function to visualize the peak location at certain miRNA level

Usage

```
ceRNALocation(path_prefix, project_name, disease_name, mirna, window_size)
```

Arguments

path_prefix	user's working directory
project_name	the project name that users can assign
disease_name	the abbreviation of disease that users are interested in
mirna	a specific mirna name (such as hsa-miR-101-3p) assigned by user
window_size	the number of samples for each window and usually about one third of total samples

Examples

```
ceRNALocation(  
  path_prefix = '~/',  
  project_name = 'demo',  
  disease_name = 'DLBC',  
  mirna='hsa-miR-101-3p',  
  window_size = 45/5  
)
```

ceRNAMethod	<i>Main ceRNAR algorithm</i>
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Description

A function to conduct three steps in algorithm, including pairs filtering, segment clustering and peak merging

Usage

```
ceRNAMethod(  
  path_prefix,  
  project_name = "demo",  
  disease_name = "DLBC",  
  window_size = 10,  
  cor_method = "pearson",  
  cor_threshold_peak = 0.85  
)
```

Arguments

path_prefix	user's working directory
project_name	the project name that users can assign (default: demo)
disease_name	the abbreviation of disease that users are interested in (default: DLBC)
window_size	the number of samples for each window (default: 10)
cor_method	selection of correlation methods, including pearson and spearman (default: pearson)
cor_threshold_peak	peak threshold of correlation value between 0 and 1 (default: 0.85)

Examples

```
ceRNAMethod(
  path_prefix = '~/',
  project_name = 'demo',
  disease_name = 'DLBC',
  window_size = 10,
  cor_method = 'pearson',
  cor_threshold_peak = 0.85
)
```

ceRNAModule

*Network analysis and visualization***Description**

A function to analyze and visualize potential network of identified ceRNAs

Usage

```
ceRNAModule(
  path_prefix,
  project_name,
  disease_name,
  pairs_cutoff = 5,
  column_sum = 1
)
```

Arguments

path_prefix	user's working directory
project_name	the project name that users can assign
disease_name	the abbreviation of disease that users are interested in
pairs_cutoff	at least the number of ceRNA pairs that a mirna must have
column_sum	the number of ceRNAs

Examples

```
ceRNAModule(
  path_prefix = '~/ ',
  project_name = 'demo',
  disease_name = 'DLBC',
  pairs_cutoff = 5,
  column_sum = 1
)
```

ceRNApairFiltering	<i>one of three steps in main ceRNAR algorithm</i>
--------------------	--

Description

A function to conduct one of three steps in algorithm, that is, pairs filtering

Usage

```
ceRNApairFiling(
  path_prefix,
  project_name = "demo",
  disease_name = "DLBC",
  window_size = 10,
  cor_method = "pearson"
)
```

Arguments

path_prefix	user's working directory
project_name	the project name that users can assign (default: demo)
disease_name	the abbreviation of disease that users are interested in (default: DLBC)
window_size	the number of samples for each window (default:10)
cor_method	selection of correlation methods, including pearson and spearman (default: pearson)

Examples

```
ceRNApairFiling(
  path_prefix = '~/ ',
  project_name = 'demo',
  disease_name = 'DLBC',
  window_size = 10,
  cor_method = 'pearson'
)
```

ceRNAputativePairs	<i>Extraction of putative mRNA-miRNA pairs</i>
--------------------	--

Description

A function to obtain putative mRNA-miRNA pairs from several databases

Usage

```
ceRNAputativePairs(
  path_prefix,
  project_name = "demo",
  disease_name = "DLBC",
  filtering = "less"
)
```

Arguments

path_prefix	user's working directory
project_name	the project name that users can assign
disease_name	the abbreviation of disease that users are interested in
filtering	three different filtering criteria, including strict, moderate and less. (Default: less)

Examples

```
ceRNAputativePairs(
  path_prefix = '~/ ',
  project_name = 'demo',
  disease_name = 'DLBC',
  filtering = 'less'
)
```

ceRNASurvival	<i>Survival analysis and visualization</i>
---------------	--

Description

A function to analyze the survival outcome when people carry the identified ceRNAs and visualize the results using Kaplan-Meier plot

Usage

```
ceRNASurvival(path_prefix, project_name, disease_name, mirnas)
```


Arguments

path_prefix	user's working directory
project_name	the project name that users can assign
disease_name	the abbreviation of disease that users are interested in
mirnas	a list of mirna name

Examples

```
ceRNASurvival(
  path_prefix = '~/',
  project_name = 'demo',
  disease_name = 'DLBC',
  mirnas = 'hsa-miR-101-3p'
)
```

ceRNATCGA

*Retrieval of public TCGA data from GDC Xena Hub***Description**

A function to retrieve TCGA data from GDC Xena Hub (<https://xenabrowser.net/datapages/>)

Usage

```
ceRNATCGA(
  path_prefix,
  project_name = "TCGA",
  disease_name = "DLBC",
  timeout = 5e+05
)
```

Arguments

path_prefix	user's working directory
project_name	the project name that users can assign (default = 'TCGA')
disease_name	the abbreviation of disease that users are interested in (default = 'DLBC')
timeout	the allowance time for downloading TCGA data (default = 1000)

Examples

```
ceRNATCGA(
  path_prefix = '~/',
  project_name = 'TCGA',
  disease_name = 'DLBC'
)
```

ceRNAValidate	<i>Externally experimental validation for the potential ceRNA pairs</i>
---------------	---

Description

A function to validate the potential ceRNA pairs based on the miRSponge database (<http://www.bio-bigdata.net/miRSponge>)

Usage

```
ceRNAValidate(path_prefix, project_name = "TCGA", disease_name)
```

Arguments

path_prefix	user's working directory
project_name	the project name that users can assign
disease_name	the abbreviation of disease that users are interested in

Examples

```
ceRNAValidate(
  path_prefix = '~/ ',
  project_name = 'demo',
  disease_name = 'DLBC'
)
```

gene_exp	<i>Example gene expression dataset for ceRNAR</i>
----------	---

Description

A data set with the gene expression for 45 subjects

Usage

```
data(gene_exp)
```

Format

A R data frame with 185 rows and 45 variables

expression data Numeric gene expression matrix with each columns as a different individual and each row as a separate gene.

Source

<<https://www.github.com/ywhsiao/ceRNAR>>

Examples

```
data(gene_exp)
```

mirna_exp

*Example mirna expression dataset for ceRNAR***Description**

A data set with the mirna expression for 45 subjects

Usage

```
data(mirna_exp)
```

Format

A R data frame with 78 rows and 45 variables

expression data Numeric mirna expression matrix with each columns as a different individual and each row as a separate miRNA.

Source

<<https://www.github.com/ywhsiao/ceRNAR>>

Examples

```
data(mirna_exp)
```

SegmentClusteringPlusPeakMerging

*two of three steps in main ceRNAR algorithm***Description**

A function to conduct two of three steps in algorithm, that is, segment clustering and peak merging

Usage

```
SegmentClusteringPlusPeakMerging(
  path_prefix,
  project_name = "demo",
  disease_name = "DLBC",
  cor_threshold_peak = 0.85,
  window_size = 10
)
```

Arguments

path_prefix	user's working directory
project_name	the project name that users can assign (default: demo)
disease_name	the abbreviation of disease that users are interested in (default: DLBC)
cor_threshold_peak	peak threshold of correlation value between 0 and 1 (default: 0.85)
window_size	the number of samples for each window (default:10)

Examples

```
SegmentClusteringPlusPeakMerging(  
  path_prefix = '~/ ',  
  project_name = 'demo',  
  disease_name = "DLBC",  
  cor_threshold_peak = 0.85,  
  window_size = 9  
)
```

surv_data

Example survival dataset for ceRNAR

Description

A data set with the survival outcome for 45 subjects

Usage

```
data(surv_data)
```

Format

A R data frame with 78 rows and 45 variables

survival data Numeric survival matrix with two columns, including status and time, and each row as a different individual.

Source

<<https://www.github.com/ywhsiao/ceRNAR>>

Examples

```
data(surv_data)
```

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