

# Package ‘PTC’

July 13, 2020

**Type** Package

**Title** Pseudo-temporal Causality Approach

**Version** 1.0.0

**Description** PTC package provides tools find miRNA-mRNA causal regulatory relationships during biological processes. Causal inference is made by assuming a linear dependence model between the predictors (miRNAs) and a target mRNA (response variable). This model is assumed invariant throughout the whole process.

The model is created from gene expression sequential data. PTC transforms static gene expression datasets to sequential data (via a Pseudotime analysis). PTC identifies causal regulatory relationships by testing violations to the invariance property (Peters et al., 2015; Pfister et al., 2018) for those sets that contains only miRNAs that biologically can interact with each target gene.

**License** GPL-3.0

**Encoding** UTF-8

**LazyData** true

**Imports** miRBaseConverter,  
CancerSubtypes,  
seqICP,  
miRBaseConverter

**RoxygenNote** 7.1.1

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Confirmed.fromList	<i>Confirmed.fromList</i>
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**Description**

Returns a list with all experimentally confirmed interactions inferred by PTC.

**Usage**

Confirmed.fromList(InterList, GroundT)

**Arguments**

- |           |  |
|-----------|--|
| InterList | A list where each element has the following structure: <ul style="list-style-type: none"><li>• name: mRNA name.</li><li>• data: Names of the miRNAs inferred as parents by PTC.</li></ul>  |
| GroundT   | A list where each element has the following structure: <ul style="list-style-type: none"><li>• name: mRNA name.</li><li>• data: Names of the miRNAs whose interactions with the mRNA have been experimentally confirmed.</li></ul> |

**Value**

- A list where each element has the following structure:
- |      |   |
|------|---|
| name | Name of a mRNA inferred by PTC with at least one confirmed interaction. |
| data | Names of the miRNAs whose miRNA-mRNA interactions are in the GroundT.   |

**See Also**

[PTC](#), [GroundT](#)

**Examples**

```
## Not run:
data(TCGA_BRCAdata)
data(GroundT)
test1<-PTC(miRNAs=TCGA_BRCAdata$miRs,mRNAs=TCGA_BRCAdata$mRNAs, VIM=TCGA_BRCAdata$mRNAs[,"VIM"])
t1.Confirmed<-Confirmed.fromList(test1$Plist$Names,GroundT)

## End(Not run)
```

---

Confirmed.fromMatrix	<i>Confirmed.fromMatrix</i>
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**Description**

Given a matrix with miRNA-mRNA interactions, returns a matrix with all of those interactions that are present in the GroundT.

**Usage**

Confirmed.fromMatrix(InterMatrix, GroundT)

**Arguments**

- |             |  |
|-------------|--|
| InterMatrix | A matrix containing miRNA-mRNA interactions. The first columns corresponds to miRNAs. The second column corresponds to mRNA.   |
| GroundT     | A list where each element has the following structure: <ul style="list-style-type: none"><li>• name: mRNA name.</li><li>• data: Names of the miRNAs whose interactions with the mRNA have been experimentally confirmed.</li></ul> |

**Value**

A matrix containing all interactions in InterMatrix that are in the GroundT

**See Also**

[PTC](#), [GroundT](#) [Confirmed.fromList](#) [InterList.toMatrix](#)

**Examples**

```
## Not run:
data(TCGA_BRCAdata)
data(GroundT)
test1<-PTC(miRNAs=TCGA_BRCAdata$miRs,mRNAs=TCGA_BRCAdata$mRNAs, VIM=TCGA_BRCAdata$mRNAs[,"VIM"])
aux<-InterList.toMatrix(test1$Plist$Names)
t1.Confirmed<-Confirmed.fromMatrix(aux,GroundT)

## End(Not run)
```

---

Extract.Parents	<i>Extract.Parents</i>
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**Description**

Uses the outcomes of [PTC.GeneSel](#) and [PTC.TestInvariance](#) to create a list of all mRNAs with at least one causal parent.

**Usage**

Extract.Parents(PTC.outcome, Predictors)

**Arguments**

PTC.outcome	A list containing the results of the function <a href="#">PTC.TestInvariance</a> . Each element of the list must have the following form: <ul style="list-style-type: none"> <li>• name: mRNA name</li> <li>• data: indexes indicating the position of the inferred miRNAs in the vector of plausible parents.</li> </ul>
Predictors	A list containing the set of miRNAs to be used as predictors (plausible parents) of each mRNA, obtained from <a href="#">PTC.GeneSel</a> .

**Value**

A list of 3 elements.

Index	Indexes of miRNAs inferred as causal parents of each mRNA. The indexes correspond to miRNAs position in the set of plausible parents of each mRNA.
Names	A list where each element corresponds to a mRNA and contains the names of the miRNAs that are inferred as causal parents of that mRNA.
genes	Names of all mRNAs with at least one parent inferred by PTC.

**Examples**

```
## Not run:
data(TCGA_BRCAdata)
data(TScan)
seqData<-PTC.ptime(TCGA_BRCAdata,TCGA_BRCAdata$mRNAs[, "VIM"])
SelData<-PTC.GeneSel(seqData, nmiR = 30, nmR = 1500)
PParents<-PTC.findPP(TScan, miRs=SelData$miRs, mRs="SORCS1")
temp <-SelData$PParents[["SORCS1"]]
SORCS1.X.TScan=SelData$d[,temp]
SORCS1.Parents<-PTC.TestInvariance(Y=SelData$d[, "SORCS1", drop = F], X=SORCS1.X.TScan)
names(SORCS1.Parents)<-"SORCS1"
SORCS1.Parents<-Extract.Parents(SORCS1.Parents,SelData$PParents["SORCS1"])

## End(Not run)
```

---

getDatabyMAD

getDatabyMAD

---

**Description**

Given a gene expression matched data including miRNAs-mRNAs, finds the nmiR miRNAs and the nmR mRNAs with the largest Median Absolute Deviation (MAD).

**Usage**

```
getDatabyMAD(seqData, nmiR, nmR)
```

**Arguments**

seqData	<p>A list with two elements:</p> <ul style="list-style-type: none"> <li>• A matrix with miRNAs gene expression.</li> <li>• A matrix with mRNAs gene expression.</li> </ul> <p>Columns represent miRNAs/mRNAs and rows represent time samples. Columns names must correspond to miRNAs/mRNAs names.</p>
nmiR	Number of miRNAs to be selected as predictor candidates.
nmR	Number of mRNAs to be selected as target variables.

**Value**

A list containing samples of miRs and mRs. The elements of the list are:

d	The data with rows being samples and columns being miRs and mRs.
miRs	The names of the selected miRs.
mRs	The names of the selected mRs.

**Author(s)**

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**References**

Taosheng Xu, Thuc Duy Le, Lin Liu, Ning Su, Rujing Wang, Bingyu Sun, Antonio Colaprico, Gianluca Bontempi, Jiuyong Li. CancerSubtypes: an R/Bioconductor package for molecular cancer subtype identification, validation, and visualization. *Bioinformatics* 33(19): 3131–3133 (2017). <https://doi.org/10.1093/bioinformatics/btx378>

**See Also**

[FSbyMAD](#)

**Examples**

```
TCGA_BRCAdata
nmiR <- 30
nmR <- 1500
l <- getDatabyMAD(TCGA_BRCAdata, nmiR, nmR)
```

---

GroundT	<i>Confirmed interactions in miR-Tarbase 6.1, Tarbase 7.0 and miRWalk 2.0</i>
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**Description**

File containing a list containing the experimentally confirmed miRNA-mRNA interactions from the databases described above.

**Usage**

```
GroundT
```

## Format

A list where each element has the following structure:

- name mRNA name.
- data names of miRNAs whose interactions with the mRNA can be founded in at least one of the databases described above.

## References

Chou, C.-H.; Chang, N.-W.; Shrestha, S.; Hsu, S.-D.; Lin, Y.-L.; Lee, W.-H.; Yang, C.-D.; Hong, H.-C.; Wei, T.-Y.; Tu, S.-J. & others miRTarBase 2016: updates to the experimentally validated miRNA-target interactions database Nucleic acids research, Oxford University Press , 2015, 44, D239-D247

Vlachos, I. S.; Paraskevopoulou, M. D.; Karagkouni, D.; Georgakilas, G.; Vergoulis, T.; Kanellos, I.; Anastasopoulos, I.-L.; Maniou, S.; Karathanou, K.; Kalfakakou, D. & others DIANA-TarBase v7. 0: indexing more than half a million experimentally supported miRNA: mRNA interactions Nucleic acids research, Oxford University Press, 2014, 43, D153-D159

Dweep, H. and Gretz, N. miRWalk2. 0: a comprehensive atlas of microRNA-target interactions Nature methods, Nature Publishing Group, 2015, 12, 697

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InterList.toMatrix	<i>InterList.toMatrix</i>
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## Description

Given a list of mRNAs containing the set of their inferred parents (e.g. the output of [Extract.Parents](#)), it returns a matrix with the miRNA-mRNA interactions. Each row represents an interaction. The first column contains miRNAs. The second column contains mRNAs

## Usage

```
InterList.toMatrix(InterList)
```

## Arguments

InterList	A list where each element has the following structure: <ul style="list-style-type: none"> <li>• name: mRNA name.</li> <li>• data: Names of the miRNAs inferred as parents by PTC.</li> </ul>
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## Value

A matrix with 2 columns containing the miRNA-mRNA interactions.

**Examples**

```
## Not run:
data(TCGA_BRCAdata)
data(TScan)
seqData<-PTC.ptime(TCGA_BRCAdata,TCGA_BRCAdata$mRNAs[, "VIM"])
SelData<-PTC.GeneSel(seqData, topk_miR = 30, topk_mR = 1500)
PParents<-PTC.findPP(TScan, miRs=SelData$miRs, mRs="SORCS1")
temp <-SelData$PParents[["SORCS1"]]
SORCS1.X.TScan=SelData$d[,temp]
SORCS1.Parents<-PTC.TestInvariance(Y=SelData$d[, "SORCS1"], X=SORCS1.X.TScan)
SORCS1.Parents<-Extract.Parents(SORCS1.Parents,SelData$PParents[["SORCS1"]])
SORCS1.relMatrix<-na.omit(InterList.toMatrix(SORCS1.Parents$Plist$Names))

## End(Not run)
```

---

InterMatrix.toList	<i>InterMatrix.toList</i>
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---

**Description**

Given a matrix containing miRNA-mRNA pairs, creates a /codelist where each element corresponds to a mRNA and contains all miRNA linked to that mRNA.

**Usage**

```
InterMatrix.toList(InterMatrix)
```

**Arguments**

**InterMatrix**      a two column matrix. The first column corresponds to miRNA. the second column corresponds to mRNA.

**Value**

A list where each element has the following structure:

name:                mRNA name.  
data:                Names of the miRNAs linked to the current mRNA

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PTC	<i>PTC</i>
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**Description**

PTC estimates the causal parents of a set of nmR mRNAs, given a set of nmiR predictors (miRNAs). This estimation assumes a linear model

$$Y_t = \beta X_t + \epsilon$$

With  $Y_t$ ,  $X_t$  the sequential data of a target and predictors respectively, and  $\epsilon$  independent and identically distributed errors for the n time points in the time series.  $Y_t$ ,  $X_t$  are the sequential data obtained after a pseudotime analysis.

## Usage

```
PTC(miRNAs, mRNAs, VIM, nmiR=30, nmR=1500, ngrid=2, alpha=0.02, complements = TRUE,
    explore.all=TRUE, silent=TRUE)
```

## Arguments

miRNAs	A matrix containing gene expression data of miRNAs. A total of nmiR miRNAs from this matrix are selected to be used as predictors candidates. Columns represent miRNAs, rows represent samples.
mRNAs	A matrix containing gene expression data from mRNAs. A total of nmR mRNAs from this matrix are selected to be used as response variables. Columns represent mRNAs, rows represent samples.
VIM	VIM expression to be used for calculating VIM_Time.
nmiR	Number of miRNAs to be selected as predictor candidates.
nmR	Number of mRNAs to be selected as target variables.
ngrid	Number of segments of the time series data used for creating the different environments required for the statistical test. ngrid=2 by default.
alpha	Significance level for the statistical test. alpha=0.2 by default.
complements	If TRUE (default), each environment is compared against its complement. If FALSE all environments are compared pairwise.
explore.all	If TRUE(default), PTC explores all combinations of predictors and returns the union set of all combinations that does not violate the invariance property. If FALSE PTC returns the first set that does not violate the invariance property. Exploration is made starting from the set of all predictors and reducing the size of the set by one predictor at a time.
silent	If TRUE (default), PTC displays the currently evaluated set. If FALSE, PTC only displays the number of sets to be explored in the current iteration.

## Value

A list consisting of the following elements:

**PList** A list of three elements:

- **Index:** A list. For each target gene with at least one parent. The index of the parents.
- **names:** For each target gene with at least one parent. The names of the parents.
- **genes:** The names of all target genes with at least one parent.

**Summary** A matrix representing miRNA-mRNA regulatory interactions inferred by PTC. The columns of the matrix are:

1. **rank:** Rank of the inferred interaction
2. **miR:** Names of miRNA (Parent)
3. **mR:** Names of mRNA (Child)
4. **Score:** Score as calculated by [PTC.RankByContext](#)

## Author(s)

Andres Mauricio Cifuentes\_Bernal, Vu VH Pham, Xiaomei Li, Lin Liu, JiuyongLi and Thuc Duy Le



**See Also**

[PTC.ptime](#), [PTC.GeneSel](#), [PTC.TestInvariance](#).

**Examples**

```
## Not run:
data(TCGA_BRCAdata)
test1<-PTC(miRNAs=TCGA_BRCAdata$miRs, mRNAs=TCGA_BRCAdata$mRNAs
, VIM=TCGA_BRCAdata$mRNAs[, "VIM"])

## End(Not run)
```

---

PTC.ConfirmedInTopK	<i>This fuction finds the number of confirmed interactions, given a matrix of interacions miR-mR, and a Ground Truth</i>
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---

**Description**

This fuction finds the number of confirmed interactions, given a matrix of interacions miR-mR, and a Ground Truth

**Usage**

```
PTC.ConfirmedInTopK(
  GT,
  relationshipsM,
  topK,
  GT_miR_EMT = NULL,
  GT_mR_EMT = NULL
)
```

**Arguments**

GT:	a list where each element has name=gene, data= confirmed miRs able to bind that gene
relationshipsM:	A matrix [n,2]
topK:	a vector including all topK

**Value**

A matrix [n,3], where the additional column has a score calculated as the mean of all context score of each miR-mR pair

PTC.findPP

*PTC.findPP***Description**

For each mRNA, creates a set of miRNAs (plausible parents) that can biologically target that mRNA. A total of `nmiR` miRNAs and `nmR` mRNAs with the largest gene expression Median Absolute Deviation (MAD) are selected as predictor candidates and target mRNAs respectively.

The set of plausible parents of each gene is a subset of the predictor candidates and contains those miRNA that can bind the gene as predicted by TargetScan 7.0. miRNAs names are converted to miRBase v. 21 during selection process.

**Usage**

```
PTC.findPP(TScan, miRs, mRs)
```

**Arguments**

TScan	A matrix containing miRNA-mRNA interactions predicted by TargetScan 7.0. The first and second columns contain miRNAs names from miRBase versions 18 and 17 respectively. The third column contains the names of the target mRNAs.
miRs	A vector containing the names of miRNAs to be verified. These names corresponds to the names of predictor candidates.
mRs	A vector containing the names of mRNAs to be verified. These names corresponds to the names of target genes (response variables).

**Value**

A list containing the set of miRNAs that can bind each target mRNA:

**See Also**

[PTC](#), [PTC.GeneSel](#), [TScan](#)

**Examples**

```
## Not run:
data(TCGA_BRCAdata)
data(TScan)
seqData<-PTC.ptime(TCGA_BRCAdata,TCGA_BRCAdata$mRNAs[, "VIM"])
SelData<-PTC.GeneSel(seqData, topk_miR = 30, topk_mR = 1500)
PParents<-PTC.findPP(TScan, miRs=SelData$miRs, mRs=SelData$mRs)

## End(Not run)
```

PTC.GeneSel

*PTC.GeneSel***Description**

Creates a set of miRNAs (plausible parents) for each mRNA among nmR mRNAs that can biologically target that mRNA. A total of nmiR miRNAs and nmR mRNAs with the largest gene expression Median Absolute Deviation (MAD) are selected as predictor candidates and target mRNAs respectively.

The set of plausible parents of each gene is a subset of the predictor candidates and contains those miRNA that can bind the gene as predicted by TargetScan 7.0. miRNAs names are converted to miRBase v. 21 during selection process

**Usage**

```
PTC.GeneSel(seqData, nmiR = 30, nmR = 1500)
```

**Arguments**

seqData	<p>A list with two elements:</p> <ul style="list-style-type: none"> <li>• A matrix with miRNAs gene expression.</li> <li>• A matrix with mRNAs gene expression.</li> </ul> <p>Columns represent miRNAs/mRNAs and rows represent time samples. Columns names must correspond to miRNAs/mRNAs names.</p>
nmiR	Number of miRNAs to be selected as predictor candidates.
nmR	Number of mRNAs to be selected as target variables.

**Value**

A list containing four elements:

miRs	nmiR miRNAs names (version miRBase v. 21) selected by MAD
mRs	nmR mRNAs names selected by MAD
d	<p>A matrix with nmiR + nmR columns, containing miRNAs:mRNAs gene expression. Columns [1 : nmiR] correspond to miRNAs data. Columns [nmiR+1 : nmiR+nmR]</p> <p>correspond to mRNAs data. Rows correspond to samples.</p>
PParents	A list containing the set of miRNAs to be used as predictors (plausible parents) of each mRNA. This set contains the miRNAs among the predictor candidates that can bind the target gene as predicted by TargetScan 7.0

**See Also**

[PTC](#), [getDatabyMAD](#), [miRNAVersionConvert](#), [PTC.findPP](#)

**Examples**

```
## Not run:
seqData<-PTC.ptime(TCGA_BRCAdata,TCGA_BRCAdata$miRNAs[, "VIM"])
SelData<-PTC.GeneSel(seqData, nmiR = 30, nmR = 1500)

## End(Not run)
```

PTC.miRv21

*PTC.miRv21***Description**

Takes a vector containing miRNAs names and returns the miRBase v.21 version of them.

**Usage**

```
PTC.miRv21(miRs)
```

**Arguments**

miRs                      miRNAs names to be changed to version miRBase v.21

**Value**

nmiR A vector with the miRNAs names (version miRBase v.21)

**See Also**

[PTC](#), [miRNAVersionConvert](#), [PTC.GeneSel](#)

**Examples**

```
## Not run:
data(TCGA_BRCAdata)
miRnamesv21<-PTC.miRv21(colnames(TCGA_BRCAdata$miRs))

## End(Not run)
```

PTC.ptime

*PTC.ptime***Description**

Orders the gene expression by VIM\_Time order. miRNAs names are changed to miRBase v.21

**Usage**

```
PTC.ptime(matchedData, VIM)
```

**Arguments**

matchedData	A List with two elements. A miRNA gene expressions matrix (1st element) and A mRNA gene expressions matrix (2nd element). Columns represent miRNAs and rows represent samples.
VIM	VIM expression to be used for calculating VIM_Time.

**Value**

Pseudotime ordered matched data.

**See Also**

[PTC](#)

**Examples**

```
## Not run:
data(TCGA_BRCAdata)
Time_series<-PTC.ptime(TCGA_BRCAdata, TCGA_BRCAdata$mRNAs[, "VIM"])

## End(Not run)
```

---

PTC.RankByContext	<i>PTC.RankByTScontext</i>
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---

**Description**

This fuction uses TS70 Conserved\_Site\_Context\_Scores (from [http://www.targetscan.org/cgi-bin/targetscan/data\\_download.cgi?db=vert\\_70](http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=vert_70) to rank a matrix of inferred miRNA-mRNA relationships.

**Usage**

```
PTC.RankByContext(TS70context, relationshipsM)
```

**Arguments**

TS70context:	A matrix containing conserved site context++ scores. The headers of the matrix from TargetScan must be conserved when the file is imported into R.
relationshipsM:	A matrix with two columns containing miRNAs and mRNAs names. First column represents miRNAs and second column mRNAs (e.g the output of <a href="#">InterList.toMatrix</a> ).

**Value**

A relationship matrix with four columns [Rank, miRNA, mRNA, Score]. The more negative the score, the best the rank of the corresponding miRNA-mRNA pair.

**See Also**

[PTC](#)

## Examples

```
## Not run:
data(TCGA_BRCAdata)
data(TScan)
data(TS7.0_Conserved_Site_Context_Scores)
seqData<-PTC.ptime(TCGA_BRCAdata,TCGA_BRCAdata$mRNAs[, "VIM"])
SelData<-PTC.GeneSel(seqData, topk_miR = 30, topk_mR = 1500)
PParents<-PTC.findPP(TScan, miRs=SelData$miRs, mRs="SORCS1")
temp <-SelData$PParents[["SORCS1"]]
SORCS1.X.TScan=SelData$d[,temp]
SORCS1.Parents<-PTC.TestInvariance(Y=SelData$d[, "SORCS1"], X=SORCS1.X.TScan)
SORCS1.Parents<-Extract.Parents(SORCS1.Parents,SelData$PParents[["SORCS1"]])
SORCS1.relMatrix<-na.omit(InterList.toMatrix(SORCS1.Parents$Plist$Names))
SORCS1.Summary<-PTC.RankByContext(TS7.0_Conserved_Site_Context_Scores
                                ,SORCS1.relMatrix)

## End(Not run)
```

---

PTC.TestInvariance	<i>PTC.TestInvariance</i>
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---

## Description

Finds a set of miRNAs (predictors) that are causal parents of a target gene. This set is defined as the union of sets that are invariant. Invariance is determined by using the decoupled test from [seqICP]seqICP.s.

## Usage

```
PTC.TestInvariance(
  Y,
  X,
  ngrid = 2,
  alpha = 0.02,
  explore.all = TRUE,
  silent = TRUE,
  complements = TRUE
)
```

## Arguments

Y	[nx1] A vector containing the sequential gene expression of a target gene Y.
X	[nxp] A matrix containing the sequential gene expression of p plausible parents (miRNAs that can bind the target mRNA).
ngrid	Number of segments of the time series data used for creating the different environments required for the statistical test. ngrid=2 by default.
alpha	Significance level for the statistical test. alpha=0.2 by default.
explore.all	If TRUE(default), PTC explores all combinations of predictors and returns the union set of all combinations that does not violate the invariance property. If FALSE PTC returns the first set that does not violate the invariance property. Exploration is made starting from the set of all predictors and reducing the size of the set by one predictor at a time.

silent	If TRUE (default), PTC displays the currently evaluated set. If FALSE, PTC only displays the number of sets to be explored in the current iteration.
complements	If TRUE (default), each environment is compared against its complement. If FALSE all environments are compared pairwise.

**Value**

Parents	A set containing the indexes of the parents inferred by PTC. These indexes correspond to the indexes of the miRNAs in the set of Plausible Parents. The Plausible Parents are the miRNAs obtained from <a href="#">PTC.GeneSel</a>
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**See Also**

[PTC](#), [seqICP.s](#)

**Examples**

```
## Not run:
data(TCGA_BRCAdata)
data(TScan)
seqData<-PTC.ptime(TCGA_BRCAdata,TCGA_BRCAdata$mRNAs[, "VIM"])
SelData<-PTC.GeneSel(seqData, topk_miR = 30, topk_mR = 1500)
PParents<-PTC.findPP(TScan, miRs=SelData$miRs, mRs="SORCS1")
temp <-SelData$PParents[["SORCS1"]]
SORCS1.X.TScan=SelData$d[,temp]
SORCS1.Parents<-PTC.TestInvariance(Y=SelData$d[, "SORCS1"], X=SORCS1.X.TScan)

## End(Not run)
```

---

SC\_miRNAsdata

---

*Original miRNAs dataset from GSE114071*


---

**Description**

File containing miRNA normalized and log2 transformed gene expression of 2822 miRNAs from 21 samples.

**Usage**

```
SC_miRNAsdata
```

**Format**

A matrix with 2822 rows and 23 columns. samples are represented in rows. Columns contains miRNAs names, description and samples

**References**

Wang, N., Zheng, J., Chen, Z. et al. "Single-cell microRNA-mRNA co-sequencing reveals non-genetic heterogeneity and mechanisms of microRNA regulation." Nat Commun 10, 95 (2019). <https://doi.org/10.1038/s41467-018-07981-6>

---

SC\_mRNAsdata

*Original mRNAs dataset from GSE114071*


---

### Description

File containing mRNA gene expression of 23284 mRNAs from 22 samples.

### Usage

SC\_mRNAsdata

### Format

A matrix with 23285 rows and 24 columns. samples are represented in rows (from row 2). Columns contains miRNAs names, description and samples

### References

Wang, N., Zheng, J., Chen, Z. et al. "Single-cell microRNA-mRNA co-sequencing reveals non-genetic heterogeneity and mechanisms of microRNA regulation." Nat Commun 10, 95 (2019). <https://doi.org/10.1038/s41467-018-07981-6>

---

TCGA\_BRCAdata

*miRNA-mRNA matched bulk data from TCGA BRCA project*


---

### Description

File containing BRCA gene expression matched data of 518 miRNAs and 17403 mRNAs from 503 samples.

### Usage

TCGA\_BRCAdata

### Format

A list object with 2 elements: miRs and mRNAs

### References

Pham, V., Zhang, J., Liu, L. et al. "Identifying miRNA-mRNA regulatory relationships in breast cancer with invariant causal prediction." BMC Bioinformatics 20, 143 (2019). <https://doi.org/10.1186/s12859-019-2668-x>



---

TS7.0\_Conserved\_Site\_Context\_Scores

*TargetScan 7.0 Conserved Site Context Scores.*

---

**Description**

File containing a matrix with the TargetScan 7.0 Context++ scores and contributions for all conserved miRNA sites, downloaded from [http://www.targetscan.org/cgi-bin/targetscan/data\\_download.cgi?db=vert\\_70](http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=vert_70)

**Usage**

TS7.0\_Conserved\_Site\_Context\_Scores

**Format**

A matrix with TargetScan 7.0 Conserved Site Context Scores data.

**References**

Agarwal, V.; Bell, G. W.; Nam, J.-W. & Bartel, D. P. Predicting effective microRNA target sites in mammalian mRNAs eLife, eLife Sciences Publications, Ltd, 2015, 4

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TScan

*TargetScan 7.0*

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**Description**

File containing a matrix with miRNAs and predicted targets from TargetScan Release 7.0

**Usage**

TScan

**Format**

A matrix with 3 columns

- miRNAs names v18
- miRNAs names v17
- predicted target (mRNA)

**References**

Agarwal, V.; Bell, G. W.; Nam, J.-W. & Bartel, D. P. Predicting effective microRNA target sites in mammalian mRNAs eLife, eLife Sciences Publications, Ltd, 2015, 4

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