# Package ‘aracne.networks’

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**Type** Package  
**Title** ARACNe-inferred gene networks from TCGA tumor datasets  
**Version** 1.0.0  
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**Description** This package contains ARACNe-inferred networks from TCGA tumor datasets. It also contains a function to export them into plain-text format.  
**License** file LICENSE  
**LazyData** TRUE  
**biocViews** ExperimentData, Genome, Homo_sapiens_Data, CancerData  
**NeedsCompilation** no  
**Depends** R (&gt;= 3.3), viper

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Description

This package contains ARACNe-inferred networks from TCGA tumor datasets and functions to import new ones and export them into text form.

Details

- Package: aracne.networks
- Type: Package
- License: LGPL-3
- LazyLoad: yes

Author(s)

Federico M. Giorgi
Maintainer: Federico M. Giorgi <federico.giorgi@gmail.com>

References


Examples

```r
### Create a random regulon with two hubs
# The first hub will have 100 targets
# The second hub will have 67 targets
regulon<-list()
regulon[["hub1"]]<-list(
tfmode=setNames(runif(100,-1,1),paste0("target",sample(1:1000,100))),
likelihood=runif(100,0,1)
)
regulon[["hub2"]]<-list(
```

```r
```
regulonblca

```
tfmode=setNames(runif(67,-1,1),paste0("target",sample(1:1000,67))),
likelihood=runif(67,0,1)
)
class(regulon)<-"regulon"
write.regulon(regulon,file="network.txt")
```

### Print a the Prostate Adenocarcinoma (prad) network to standard output
# The gene ids are in Entrez format
data(regulonprad)
write.regulon(regulonblca,file="",n=10)

---

**regulonblca**  
*Human Bladder Carcinoma context-specific ARACNe interactome*

**Description**

The interactome is a human Bladder Carcinoma context-specific regulatory network reverse engineered by the ARACNe-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```
data(regulonblca)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

**References**


**Examples**

```
data(regulonblca)
write.regulon(regulonblca,n=10)
```
regulonbrca  
*Human Breast Carcinoma context-specific ARACNe interactome*

**Description**

The interactome is a human Breast Carcinoma context-specific regulatory network reverse engineered by the ARACNe-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulonbrca)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

**References**


**Examples**

```r
data(regulonbrca)
write.regulon(regulonbrca,n=10)
```

reguloncesc  
*Human Cervical Squamous Carcinoma context-specific ARACNe interactome*

**Description**

The interactome is a human Cervical Squamous Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(reguloncesc)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.
reguloncoad

References


Examples

```r
data(reguloncoad)
write.regulon(reguloncoad,n=10)
```

reguloncoad  
**Human Colon Adenocarcinoma context-specific ARACNe interactome**

Description

The interactome is a human Colon Adenocarcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

Usage

```r
data(reguloncoad)
```

Value

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

References


Examples

```r
data(reguloncoad)
write.regulon(reguloncoad,n=10)
```
regulonesca  

**Human Esophageal Carcinoma context-specific ARACNe interactome**

**Description**

The interactome is a human Esophageal Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulonesca)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

**References**


**Examples**

```r
data(regulonesca)
write.regulon(regulonesca,n=10)
```

regulongbm  

**Human Glioblastoma context-specific ARACNe interactome**

**Description**

The interactome is a human Glioblastoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulongbm)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.
regulonhnsc

References


Examples

data(regulongbm)
write.regulon(regulongbm,n=10)

| regulonhnsc | Human Head and Neck Squamous Carcinoma context-specific ARACNe interactome |

Description

The interactome is a human Head and Neck Squamous Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

Usage

data(regulonhnsc)

Value

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

References


Examples

data(regulonhnsc)
write.regulon(regulonhnsc,n=10)
Description

The interactome is a human Kidney Renal Clear Cell Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

Usage

data(regulonkirc)

Value

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

References


Examples

data(regulonkirc)
write.regulon(regulonkirc,n=10)

Description

The interactome is a human Kidney Papillary Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

Usage

data(regulonkirp)
Value

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

References


Examples

data(regulonkirp)
write.regulon(regulonkirp,n=10)

regulonlaml                Human Acute Myeloid Leukemia context-specific ARACNe interactome

Description

The interactome is a human Acute Myeloid Leukemia context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class `regulon` where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

Usage

data(regulonlaml)

Value

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

References


Examples

data(regulonlaml)
write.regulon(regulonlaml,n=10)
**regulonlihc**

*Human Liver Hepatocellular Carcinoma context-specific ARACNe interactome*

**Description**

The interactome is a human Liver Hepatocellular Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulonlihc)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

**References**


**Examples**

```r
data(regulonlihc)
write.regulon(regulonlihc,n=10)
```

---

**regulonluad**

*Human Lung Adenocarcinoma context-specific ARACNe interactome*

**Description**

The interactome is a human Lung Adenocarcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulonluad)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.
regulonlusc

References


Examples

data(regulonluscd)
write.regulon(regulonluscd, n=10)

---

regulonluscd        Human Lung Squamous Carcinoma context-specific ARACNe interactome

Description

The interactome is a human Lung Squamous Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

Usage

data(regulonluscd)

Value

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

References


Examples

data(regulonluscd)
write.regulon(regulonluscd, n=10)
**regulonov**  
*Human Ovarian Carcinoma context-specific ARACNe interactome*

**Description**

The interactome is a human Ovarian Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulonov)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

**References**


**Examples**

```r
data(regulonov)
write.regulon(regulonov,n=10)
```

---

**regulonpaad**  
*Human Pancreas Carcinoma context-specific ARACNe interactome*

**Description**

The interactome is a human Pancreas Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulonpaad)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.
**References**


**Examples**

```r
data(regulonpaad)
write.regulon(regulonpaad, n=10)
```

---

**regulonpcpg Human Pheochromocytoma and Paraganglioma context-specific ARACNe interactome**

**Description**

The interactome is a human Pheochromocytoma and Paraganglioma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulonpcpg)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

**References**


**Examples**

```r
data(regulonpcpg)
write.regulon(regulonpcpg, n=10)
```
**Description**

The interactome is a human Prostate Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class 'regulon' where each element represents a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

data(regulonprad)

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

**References**


**Examples**

data(regulonprad)
write.regulon(regulonprad,n=10)

---

**Description**

The interactome is a human Rectal Adenocarcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class 'regulon' where each element represents a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

data(regulonread)

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.
regulonsarc

References


Examples

    data(regulonread)
    write.regulon(regulonread, n=10)

---

regulonsarc  

Human Sarcoma context-specific ARACNe interactome

Description

The interactome is a human Sarcoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represents a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

Usage

    data(regulonsarc)

Value

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

References


Examples

    data(regulonsarc)
    write.regulon(regulonsarc, n=10)
**Description**

The interactome is a human Stomach Adenocarcinoma context-specific regulatory network reverse engineered by the ARACNe-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulonstad)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

**References**


**Examples**

```r
data(regulonstad)
write.regulon(regulonstad,n=10)
```

---

**Description**

The interactome is a human Testicular Cancer context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulontgct)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.
Regulonthca

References


Examples

data(regulontgct)
write.regulon(regulontgct,n=10)

Description

The interactome is a human Thyroid Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class ‘regulon’ where each element represent a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

Usage

data(regulonthca)

Value

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

References


Examples

data(regulonthca)
write.regulon(regulonthca,n=10)
**regulonthym**

Human Thymoma context-specific ARACNe interactome

**Description**

The interactome is a human Thymoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class 'regulon' where each element represents a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulonthym)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.

**References**


**Examples**

```r
data(regulonthym)
write.regulon(regulonthym,n=10)
```

---

**regulonucec**

Human Utherine Corpus Endometroid Carcinoma context-specific ARACNe interactome

**Description**

The interactome is a human Utherine Corpus Endometroid Carcinoma context-specific regulatory network reverse engineered by the ARACNE-AP algorithm. The interactome is contained in a list object of S3 class 'regulon' where each element represents a transcriptional regulator (transcription factor) and contains two vectors: (1) a named numeric vector indicating the mode of regulation (MoR) for each target gene, whose ID is indicated by the names attribute of the vector. (2) a numeric vector indicating the confidence score for the TF-target interaction.

**Usage**

```r
data(regulonucec)
```

**Value**

Object of class regulon (regulon-class) containing network data generated by ARACNe-AP.
References


Examples

data(regulonucec)
write.regulon(regulonucec,n=10)

write.regulon An object of class regulon
Print a regulon object into a text file

Description

This function will print the network into an output stream. Four columns will be printed: the Regulator id, the Target id, the Mode of Action (MoA, based on Spearman correlation that indicates the sign of the connection and ranges between -1 and +1), the Likelihood (essentially an edge weight that indicates how strong the mutual information for an edge is when compared to the maximum observed MI in the network, it ranges between 0 and 1).

Usage

write.regulon(
  regulon,
  file="",
  sep="\t",
  header=TRUE,
  n=Inf,
  regulator=NULL
)

Arguments

regulon An object of class regulon
file File name where the network will be printed
sep String, a separator for the fields (default = "\t")
header Logical. If a header should be printed. Default is TRUE
n Numeric. How many interactions to print. Default is Inf
regulator String. A particular regulator. Default is NULL

Value

Text output containing the network in tabular format.
Examples

```r
### Create a random regulon with two hubs
# The first hub will have 100 targets
# The second hub will have 67 targets
regulon<-list()
regulon[["hub1"]]<-list(
    tfmode=setNames(runif(100,-1,1),paste0("target",sample(1:1000,100))),
    likelihood=runif(100,0,1)
)
regulon[["hub2"]]<-list(
    tfmode=setNames(runif(67,-1,1),paste0("target",sample(1:1000,67))),
    likelihood=runif(67,0,1)
)
class(regulon)<-"regulon"
write.regulon(regulon,file="network.txt")

### Print a the Prostate Adenocarcinoma (prad) network to standard output
# The gene ids are in Entrez format
data(regulonprad)
write.regulon(regulonprad,file="",n=10)
```
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