

# Package ‘aracne.networks’

April 11, 2023

**Type** Package

**Title** ARACNe-inferred gene networks from TCGA tumor datasets

**Version** 1.24.0

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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 (>= 3.3), viper

**git\_url** <https://git.bioconductor.org/packages/aracne.networks>

**git\_branch** RELEASE\_3\_16

**git\_last\_commit** 28d1fd2

**git\_last\_commit\_date** 2022-11-01

**Date/Publication** 2023-04-11

## R topics documented:

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aracne.networks-package

*ARACNe-inferred gene networks from TCGA tumor datasets*

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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

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## References

Giorgi, F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* 2016  
 Alvarez, M.J. et al. (2016) Functional characterization of somatic mutations in cancer using network-based inference of protein activity. *Nature Genetics* 2016

## Examples

```
### 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(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

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. Bioinformatics doi: 10.1093/bioinformatics/btw216.

## 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

```
data(regulonbrca)
```

## Value

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

## References

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. Bioinformatics doi: 10.1093/bioinformatics/btw216.

## Examples

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

---

|             |  |
|-------------|--|
| reguloncesc | <i>Human Cervical Squamous Carcinoma context-specific ARACNe interactome</i> |
|-------------|--|

---

**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**

```
data(reguloncesc)
```

**Value**

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

**References**

Giorgi, F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**Examples**

```
data(reguloncesc)
write.regulon(reguloncesc, n=10)
```

---

|             |   |
|-------------|---|
| reguloncoad | <i>Human Colon Adenocarcinoma context-specific ARACNe interactome</i> |
|-------------|---|

---

**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**

```
data(reguloncoad)
```

**Value**

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

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. Bioinformatics doi: 10.1093/bioinformatics/btw216.

**Examples**

```
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**

```
data(regulonesca)
```

**Value**

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

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. Bioinformatics doi: 10.1093/bioinformatics/btw216.

**Examples**

```
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**

```
data(regulongbm)
```

**Value**

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**Examples**

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

---

`regulonhnc`*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(regulonhnc)
```

**Value**

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**Examples**

```
data(regulohnsc)
write.regulon(regulohnsc,n=10)
```

---

regulonkirc

*Human Kidney Renal Clear Cell Carcinoma context-specific ARACNe interactome*

---

**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**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**Examples**

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



---

|             |   |
|-------------|---|
| regulonkirp | <i>Human Kidney Papillary Carcinoma context-specific ARACNe interactome</i> |
|-------------|---|

---

### 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

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

### Examples

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

---

|             |   |
|-------------|---|
| regulonlaml | <i>Human Acute Myeloid Leukemia context-specific ARACNe interactome</i> |
|-------------|---|

---

### 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**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**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**

```
data(regulonlihc)
```

**Value**

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**Examples**

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

---

|             |  |
|-------------|--|
| regulonluad | <i>Human Lung Adenocarcinoma context-specific ARACNe interactome</i> |
|-------------|--|

---

**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**

```
data(regulonluad)
```

**Value**

Object of class regulon ([regulon-class](#)) containing network data generated by ARACNE-AP.

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. Bioinformatics doi: 10.1093/bioinformatics/btw216.

**Examples**

```
data(regulonluad)
write.regulon(regulonluad,n=10)
```

---

|             |  |
|-------------|--|
| regulonlusc | <i>Human Lung Squamous Carcinoma context-specific ARACNe interactome</i> |
|-------------|--|

---

**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(regulonlusc)
```

**Value**

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

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. Bioinformatics doi: 10.1093/bioinformatics/btw216.

**Examples**

```
data(regulonlusc)
write.regulon(regulonlusc,n=10)
```

---

regulonnet

*Human Neuroendocrine tumor context-specific ARACNe interactome*

---

**Description**

The interactome is a human Neuroendocrine tumor 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(regulonnet)
```

**Value**

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

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. Bioinformatics doi: 10.1093/bioinformatics/btw216.

**Examples**

```
data(regulonnet)
write.regulon(regulonnet, 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**

```
data(regulonov)
```

**Value**

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

**References**

Giorgi, F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**Examples**

```
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**

```
data(regulonpaad)
```

**Value**

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**Examples**

```
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**

```
data(regulonpcpg)
```

**Value**

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**Examples**

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

---

regulonprad

*Human Prostate Carcinoma context-specific ARACNe interactome*

---

### 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 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(regulonprad)
```

### Value

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

### References

Giorgi, F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

### Examples

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

---

regulonread

*Human Rectal Adenocarcinoma context-specific ARACNe interactome*

---

### 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 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(regulonread)
```

**Value**

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**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 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(regulonsarc)
```

**Value**

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**Examples**

```
data(regulonsarc)
write.regulon(regulonsarc,n=10)
```



---

|             |   |
|-------------|---|
| regulonstad | <i>Human Stomach Adenocarcinoma context-specific ARACNe interactome</i> |
|-------------|---|

---

### 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

```
data(regulonstad)
```

### Value

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

### References

Giorgi, F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

### Examples

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

---

|             |  |
|-------------|--|
| regulontgct | <i>Human Testicular Cancer context-specific ARACNe interactome</i> |
|-------------|--|

---

### 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

```
data(regulontgct)
```

**Value**

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

**References**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. Bioinformatics doi: 10.1093/bioinformatics/btw216.

**Examples**

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

---

regulonthca

*Human Thyroid Carcinoma context-specific ARACNe interactome*

---

**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**

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. Bioinformatics doi: 10.1093/bioinformatics/btw216.

**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 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(regulonthym)
```

### Value

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNE-AP.

### References

Giorgi,F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

### Examples

```
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 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(regulonucec)
```

**Value**

Object of class `regulon` ([regulon-class](#)) containing network data generated by ARACNe-AP.

**References**

Giorgi, F.M. et al. (2016) ARACNe-AP: Gene Network Reverse Engineering through Adaptive Partitioning inference of Mutual Information. *Bioinformatics* doi: 10.1093/bioinformatics/btw216.

**Examples**

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

---

|                            |  |
|----------------------------|--|
| <code>write.regulon</code> | <i>Print a regulon object into a text file</i> |
|----------------------------|--|

---

**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**

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

**Value**

Text output containing the network in tabular format.

**Examples**

```
### 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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