Package 'aracne.networks'

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Type Package

Title ARACNe-inferred gene networks from TCGA tumor datasets

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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

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Contents

aracne.networks-package 2
regulonblca 3
regulonbrca 4
reguloncesc 4
regulonesca 6
regulongbm 6
regulonhnsc 7
regulonkirc 8
regulonkirp 8
regulonlaml 9

regulonlihc 10
regulonluad 10
regulonlusc 11
regulonnet 12
regulonov 12
regulonpaad 13
regulonpcpg 14
regulonprad 14
regulonread 15
regulonsarc 16
regulonstad 16
regulontgct 17
regulonthca 18
regulonthym 18
regulonucec 19
write.regulon 20

Index **22**

`aracne.networks-package`
ARACNe-inferred gene networks from TCGA tumor datasets

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)

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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 *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

```
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` *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

```
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)
```

`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

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(regulonhnsc)
write.regulon(regulonhnsc,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 — *Human Kidney Papillary Carcinoma context-specific ARACNe interactome*

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` *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

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 — *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

```
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` *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(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 *Human Stomach Adenocarcinoma context-specific ARACNe interactome*

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` *Human Testicular Cancer context-specific ARACNe interactome*

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)
```

`write.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

```
### 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)
```

Index

∗ **datasets**
regulonblca, 3
regulonbrca, 4
regulonc esc, 4
regulonc oad, 5
regulonesca, 6
regulongbm, 6
regulonhnsc, 7
regulonkirc, 8
regulonkirp, 8
regulonlaml, 9
regulonlihc, 10
regulonluad, 10
regulonlusc, 11
regulonnet, 12
regulonov, 12
regulonpaad, 13
regulonpcpg, 14
regulonprad, 14
regulonread, 15
regulonsarc, 16
regulonstad, 16
regulontgct, 17
regulonthca, 18
regulonthym, 18
regulonucec, 19

aracne.networks
*(*aracne.networks-package*)*, 2
aracne.networks-package, 2

regulon-class, *3–19*
regulonblca, 3
regulonbrca, 4
regulonc esc, 4
regulonc oad, 5
regulonesca, 6
regulongbm, 6
regulonhnsc, 7
regulonkirc, 8
regulonkirp, 8
regulonlaml, 9
regulonlihc, 10
regulonluad, 10
regulonlusc, 11
regulonnet, 12
regulonov, 12
regulonpaad, 13
regulonpcpg, 14
regulonprad, 14
regulonread, 15
regulonsarc, 16
regulonstad, 16
regulontgct, 17
regulonthca, 18
regulonthym, 18
regulonucec, 19

write.regulon, 20