Package: SignatuR (via r-universe)

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Title Signatures for single-cell data analysis

Version 0.3.0

Description A database of useful signatures for single-cell data analysis. Query the existing signatures or use it to organize your own gene sets in a hierarchical structure.

Depends R(>= 4.1.0)

Imports data.tree, tools

Suggests DiagrammeR

License GPL-3

Encoding UTF-8

LazyData FALSE

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AddNode *Add node to DB*

Description

Add a new internal node to the DB. This generates a local, updated copy of the database.

Usage

```
AddNode(db, parent_node, name = "New_signature", reference = NA)
```

Arguments

`db`	The database object to be updated
`parent_node`	The parent node where the new node should be added
`name`	Name for the new node
`reference`	Optional text to describe the node

Value

An update database containing the new node

Examples

```
data(SignatuR)
SignatuR <- AddNode(SignatuR, parent_node=SignatuR$Hs, name="New_category")
```

AddSignature *Add signature to DB*

Description

Add a new signature to the DB. This generates a local, updated copy of the database.

Usage

```
AddSignature(
  db,
  node,
  name = "New_signature",
  signature = NULL,
  reference = NA,
  overwrite = FALSE
)
```

Arguments

`db`	The database object to be updated
`node`	A database node where the new signature should be added
`name`	Signature name
`signature`	Gene signature, as a vector of genes
`reference`	A text describing source of the signature or other comments
`overwrite`	Whether to replace an already existing signature with the same name

Value

An update database containing the new signature

Examples

```
data(SignatuR)
SignatuR <- AddSignature(SignatuR, node=SignatuR$Mm$Cell_types,
   name="T_cell", reference="A simple T cell signature", signature=c("Cd2","Cd3d","Cd3e"))
```

`GetSignature` *Get signatures from DB*

Description

Return one or more signatures from a specified database node. If an intermediate node is specified, all signatures below that node are returned as a list of signatures.

Usage

```
GetSignature(node)
```

Arguments

`node`	A database node, either internal or leaf

Value

A single signature or list of signatures

Examples

```
data(SignatuR)
# Single signature
GetSignature(SignatuR$Mm$Programs$HeatShock)
# Multiple signature from intermediate node
s <- GetSignature(SignatuR$Mm$Programs)
lapply(s, head)
```

`LoadSignatuR` *Load SignatuR from local file*

Description

Load a file storing a SignatuR object. See also the function SaveSignatuR for saving existing DB.

Usage

```
LoadSignatuR(file = "mySignatuR.csv")
```

Arguments

`file`	Source file (.csv, .rds or .rda)

Value

A SignatuR object

See Also

SaveSignatuR

Examples

```
data(SignatuR)
# Save DB
SaveSignatuR(SignatuR, file="mySignatuR.csv")
# Load it back
mySignatuR <- LoadSignatuR("mySignatuR.csv")
```

`RemoveSignature` *Remove signature from DB*

Description

Remove a given signature or node from the database

Usage

```
RemoveSignature(node)
```

Arguments

`node`	A database node to be removed

Value

Nothing. The DB is modified in place.

Examples

```
data(SignatuR)
RemoveSignature(SignatuR$Hs$Compartments$TCR)
```

`SaveSignatuR` *Save a local copy of SignatuR*

Description

Store a modified copy of your SignatuR DB, in different formats. Saving to .csv allows editing of signatures in a text or spreadsheet program

Usage

```
SaveSignatuR(db, file = "mySignatuR.csv")
```

Arguments

`db`	The database object to be saved
`file`	Destination file (.csv, .rds or .rda)

See Also

LoadSignatuR

Examples

```
data(SignatuR)
# Save DB
SaveSignatuR(SignatuR, file="mySignatuR.csv")
# Load it back
mySignatuR <- LoadSignatuR("mySignatuR.csv")
```

`SignatuR` *A database of gene signatures for single-cell data analysis*

Description

The DB is structured in a tree format, using the `data.tree` data type. See the examples below to browse and access this data type. print(SignatuR)

Usage

```
SignatuR
```

Format

A `data.tree` object with signatures organized by species and category. Gene lists are stored in the "Signature" attribute, comments and references for the signature are stored in the "Reference" attribute.

See database structure `SignatuR`

See database with annotations `print(SignatuR, "Reference","Signature")`

Plot database structure `library(DiagrammeR)`
`plot(SignatuR)`

Extract a specific signature `GetSignature(SignatuR$Mm$Programs$HeatShock)`

Extract all signatures below a given node `GetSignature(SignatuR$Mm$Programs)`

Add a new signature to the DB `SignatuR <- AddSignature(SignatuR, node=SignatuR$Mm$Cell_types,name="T_ce`

Add a new node to the DB `SignatuR <- AddNode(SignatuR, parent_node=SignatuR$Hs, name="New_category")`

Save a local copy of your modified SignatuR DB `SaveSignatuR(SignatuR, file="mySignatuR.csv")`

Load a local copy of SignatuR from disk `mySignatuR <- LoadSignatuR("mySignatuR.csv")`

Save updated database (for developers) `usethis::use_data(SignatuR, overwrite = TRUE)`

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