Package ‘miRNAmeConverter’

November 21, 2016

Type Package

Title Convert miRNA Names to Different miRBase Versions

Version 1.2.0

Description Package containing an S4 class for translating mature
miRNA names to different miRBase versions, sequence retrieval,
checking names for validity and detecting miRBase version of
a given set of names (data from http://www.mirbase.org/).

License Artistic-2.0

Imports DBI, AnnotationDbi

Depends miRBaseVersions.db

biocViews Preprocessing, miRNA

LazyData TRUE

Suggests methods, testthat, knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 5.0.1

NeedsCompilation no

Author Stefan Haunsberger [aut, cre]

Maintainer Stefan J. Haunsberger <stefan.haunsberger@gmail.com>

R topics documented:

assessMiRNASwappingMIMAT ........................................... 2
assessVersion ............................................................. 3
checkMiRNAName ......................................................... 4
currentVersion ........................................................... 5
currentVersion<- ......................................................... 5
example.miRNAs .......................................................... 6
miRNAmeConverter ....................................................... 6
MiRNANameConverter .................................................... 7
MiRNANameConverter,ANY-method .................................... 8
nOrganisms ................................................................. 9
nOrganisms<- .............................................................. 9
nTotalEntries ............................................................. 10
nTotalEntries<- .......................................................... 11
saveResults ............................................................... 11
assessMiRNASwappingMIMAT

Check if given miRNA names can be assigned to unique MIMAT accessions among all versions

Description

This function checks if the names from a given set of mature miRNAs have a unique MIMAT ID. Check if given miRNA names can be assigned to unique MIMAT accessions among all versions

This function checks if the names from a given set of mature miRNAs have a unique MIMAT ID.

Usage

assessMiRNASwappingMIMAT(this, miRNAs, verbose = FALSE)

Arguments

this Object of class 'MiRNANameConverter'
miRNAs A character vector of miRNA names
verbose A boolean to either show more (TRUE) or less information (FALSE)

Details

Although the majority of miRNA names can be assigned to a unique MIMAT ID (accession) some miRNAs changed MIMAT ID in different versions. This function takes the input miRNA names and checks each one of them if they have a unique MIMAT ID over all versions. If a miRNA changes MIMAT ID in a version it will be comprised in the return vector.

Value

A character vector containing miRNA names that do not have a unique MIMAT ID

Author(s)

Stefan Haunsberger
assessVersion

Assess miRBase version

Description

This function detects the most likely miRBase version of a given miRNA set. Assess miRBase version

This function detects the most likely miRBase version of a given miRNA set.

Usage

assessVersion(this, miRNAs, verbose = FALSE)

## S4 method for signature 'MiRNANameConverter'
assessVersion(this, miRNAs, verbose = FALSE)

Arguments

this Object of class 'MiRNANameConverter'
miRNAs A character vector of miRNA names
verbose A boolean to either show more (TRUE) or less information (FALSE)

Details

This function takes a set of miRNA names and detects the most likely miRBase version of this given set of 'miRNAs'. First all miRNAs will be checked for validity (if they are actual miRNA names checkMiRNAName and the set that passes the check will be further processed.

Value

A data frame with two columns: version and frequency (decreasing order by frequency, version) + version: miRBase version + frequency: the number of valid miRNAs that could be assigned to the version respectively

Methods (by class)

- MiRNANameConverter: Method for assessing the most likely miRBase version that a given set of miRNA names is from.

Author(s)

Stefan Haunsberger

Examples

nc = MiRNANameConverter(); # Instance of class 'MiRNANameConverter'
assessVersion(nc, miRNAs = c("hsa-miR-140", "hsa-miR-125a"))
checkMiRNAName

Check miRNA names for validity

Description

This function checks for a given set of mature 'miRNAs' (names) if the names are listed in any miRBase version respectively.

Usage

checkMiRNAName(this, miRNAs, verbose = FALSE)

## S4 method for signature 'MiRNANameConverter'
checkMiRNAName(this, miRNAs, verbose = FALSE)

Arguments

this Object of class 'MiRNANameConverter'
miRNAs A character vector of miRNA names
verbose A boolean to either show more (TRUE) or less information (FALSE)

Details

This function takes the input miRNA names and checks each one of them for validity. The check is done by taking each miRNA and searches for an existing entry in the miRBase database among all versions. miRNAs that are listed in any version will be comprised in the return vector respectively. If no valid miRNA was detected, a character(0) will be returned.

Value

A character vector containing a set of valid miRNA names

Methods (by class)

• MiRNANameConverter: Method for checking for valid miRNA names

Author(s)

Stefan Haunsberger

Examples

nc = MiRNANameConverter() # Instance of class 'MiRNANameConverter'
# Test with correct inputs
checkMiRNAName(nc, miRNAs = c("hsa-miR-29a", "hsa-miR-642"))
**currentVersion**

**Description**

This function returns the highest miRBase version that is provided by the package.

**Usage**

`currentVersion(this)`

```r
## S4 method for signature 'MiRNANameConverter'
currentVersion(this)
```

**Arguments**

- `this` Object of class `MiRNANameConverter`

**Details**

The maximum miRBase version of the package is evaluated and set in the object initialization.

**Value**

A numeric value

**Methods (by class)**

- `MiRNANameConverter`: Retrieve highest supported miRBase version

**Author(s)**

Stefan Haunsberger

**Examples**

```r
nc = MiRNANameConverter(); # Instance of class 'MiRNANameConverter'
currentVersion(nc);
```

---

**currentVersion<-**

**Description**

Set the highest version that is supported by the package.

**Usage**

`currentVersion(this) <- value`
miRNAmeConverter

Arguments

this Object of class ”
value A numeric value

Details

The value for the highest version is a static variable. It is initialized in the initialization method when an instance of a MiRNANameConverter class is created.

Value

Object of class ”

Author(s)

Stefan Haunsberger

description

description

Sample names including miRNA names, non-miRNA names and other. It also includes duplicates.

Usage

description

Format

A character vector containing names.

description

Description

This function returns an instance of a MiRNAmeConverter class. Handling mature miRNA names from different miRBase versions This package contains algorithms for dealing with mature miRNA names from different miRBase release versions. The functions are provided in form of methods as part of the MiRNANameConverter-class. The data of all the miRBase release versions is stored in the miRBaseVersions.db annotation package. The MiRNAmeConverter package contains one class that has two categories of functions: getters-functions and algorithms.

Classes

The MiRNANameConverter
MiRNANameConverter

**Getter functions**

The getter functions provide access to the slots of the class.

**Algorithms**

There are three algorithms for dealing with miRNA names from different miRBase releases, the `assessVersion`, `checkMiRNAName` and `translateMiRNAName`.

- **translateMiRNAName**  The algorithm coded in this function can translate given miRNA names to different miRBase release versions.
- **checkMiRNAName**  This function is used to check if a given miRNA name is listed in the current miRBase release.
- **assessVersion**  The `assessVersion`-function is useful when one wants to assess the miRBase version of a given set of mature miRNA names.

**Author(s)**

Stefan Haunsberger <stefanhaunsberger@rcsi.ie>

**See Also**

`
miRBaseVersions.db`

for more information about the database holding all major miRBase release versions)

**Examples**

```r
# Translate a mature miRNA name to miRBase version 21.0
nc = MiRNANameConverter(); # Object instantiation
translateMiRNAName(nc, "hsa-miR-29a", version = 21.0)
```

**Description**

This function returns back an instance of a `MiRNANameConverter` object.

**Usage**

`MiRNANameConverter(...)`

**Arguments**

... any optional arguments
Slots

- .dbconn  Database connection
- .currentVersion  Current miRBase version
- .validVersions  Valid/Supported miRBase versions
- .nOrganisms  Number of different organisms supported
- .nTotalEntries  Total number of mature miRNA names among all provided miRBase release versions in the miRBaseVersions.db package.
- .validOrganisms  Valid organisms

Author(s)

Stefan Haunsberger

Description

This function returns an instance of a MiRNANameConverter class.

Usage

```r
## S4 method for signature 'ANY'
MiRNANameConverter()
```

Details

This function initializes an object of the class MiRNANameConverter. It is a wrapper for `new()`.

Value

an object of class 'MiRNANameConverter'

Author(s)

Stefan Haunsberger

See Also

`new`

Examples

```r
nc = MiRNANameConverter() # Instance of class 'MiRNANameConverter'
```
**nOrganisms**

---

**nOrganisms**

Get number of organisms

---

**Description**

This function returns the number of different organisms that are provided by the package.

**Usage**

```
roOrganisms(this)
```

```
## S4 method for signature 'MiRNANameConverter'
roOrganisms(this)
```

**Arguments**

- `this`: Object of class `MiRNANameConverter`

**Details**

The number of different organisms is evaluated and set in the object initialization.

**Value**

A numeric value

**Methods (by class)**

- `MiRNANameConverter`: Retrieve number of organisms

**Author(s)**

Stefan Haunsberger

**Examples**

```r
nc = MiRNANameConverter(); # Instance of class 'MiRNANameConverter'
roOrganisms(nc);
```

---

**nOrganisms<--**

Set number of organisms

---

**Description**

This function sets the number of different organisms that are provided by the package.

**Usage**

```
roOrganisms(this) <- value
```
nTotalEntries

Arguments

this Object of class MiRNANameConverter
value An integer value

Details

The number of different organisms is evaluated and set in the object initialization.

Value

A MiRNANameConverter object

Author(s)

Stefan Haunsberger

Description

This function returns the total number of entries contained in the mimat table. The number is the sum of the entries of all miRBase versions provided by the package.

Usage

nTotalEntries(this)

## S4 method for signature 'MiRNANameConverter'
nTotalEntries(this)

Arguments

this Object of class MiRNANameConverter

Details

The total number is evaluated and set in the object initialization.

Value

A numeric value

Methods (by class)

- MiRNANameConverter: Retrieve total number of miRNA entries

Author(s)

Stefan Haunsberger
Examples

nc = MiRNANameConverter(); # Instance of class 'MiRNANameConverter'
nTotalEntries(nc);

---

Set total number database entries

Description

This function sets the total number of entries contained in the miMat table. The number is the sum of the entries of all miRBase versions provided by the package.

Usage

nTotalEntries(this) <- value

Arguments

this Object of class MiRNANameConverter
value An integer value

Details

The total number is evaluated and set in the object initialization.

Value

A MiRNANameConverter object

Author(s)

Stefan Haunsberger

---

Save miRNA translation results

Description

This function saves the data frame returned from translateMiRNAName inclusive the attribute 'description'. Save miRNA translation results

Usage

saveResults(this, df, outputFilename, outputPath, sep = "\t", quote = FALSE, verbose = FALSE, ...)

## S4 method for signature 'MiRNANameConverter,data.frame'
saveResults(this, df, outputFilename, outputPath, sep = "\t", quote = FALSE, verbose = FALSE, ...)
Arguments

this       Object of class 'MiRNANameConverter'
df         A data.frame with translated results
outputFilename A filename for the output file, such as 'filename.txt'
outputPath  A file path (character string) to the target directory
sep         Separator
quote       If all data values shall be surrounded by ('"')
verbose     Boolean to either show more (TRUE) or less information (FALSE)
...         Arguments that can be passed on to write.table

Details

This function saves a data frame that has been returned by translateMiRNAName. The attribute 'description' of the data frame will be stored as well.

Methods (by class)

• this = MiRNANameConverter, df = data.frame: Method for saving translation results

Author(s)

Stefan Haunsberger

See Also

write.table for additional parameter values for the `...` argument, attr for how to retrieve attributes

Examples

nc = MiRNANameConverter(); # Instance of class 'MiRNANameConverter'
res = translateMiRNAName(nc, miRNAs = c("hsa-miR-140", "hsa-miR-125a"),
                          versions = c(15, 16, 20, 21))
# Save translation results
saveResults(nc, res)
translateMiRNAName

Arguments

  object Object of class MiRNANameConverter

Details

  This function prints some information to the console.

Author(s)

  Stefan Haunsberger

See Also

  show

Description

  This function translates input miRNA names to different miRBase versions. Translate miRNA name
  This function translates input miRNA names to different miRBase versions.

Usage

  translateMiRNAName(this, miRNAs, versions, sequenceFormat = 1,
                     verbose = FALSE)

  ## S4 method for signature 'MiRNANameConverter,character'
  translateMiRNAName(this, miRNAs,
                     versions, sequenceFormat = 1, verbose = FALSE)

Arguments

  this Object of class 'MiRNANameConverter'
  miRNAs A character vector of miRNA names
  versions An integer or numerical vector containing the target versions
  sequenceFormat Integer value indicating the return format for the data frame containing sequence
                    information 1=only sequences, 2=miRNA name and sequence
  verbose A boolean to either show more (TRUE) or less information (FALSE)

Details

  The translation and sequence retrieval are done in 5 main steps: 1) Only take miRNA names that
do not swap MIMAT IDs among versions (assessMiRNASwappingMIMAT) 2) Check, if the miRNA
  names are valid names (checkMiRNAName) 3) Receive unique MIMAT IDs for each valid miRNA -
  If there are miRNAs that have basically the same name, only use miRNA names from the highest
  version 4) Check if the found MIMAT IDs are still listed in the current miRBase version - If not,
eglect it because then it is not considered to be a miRNA anymore 5) Receive names from desired
  versions
validOrganisms

Value

A (n x m) data frame where n is the number of valid miRNAs and m the number of columns
(minimum 3 columns, MIMAT-ID (accession), input miRNA name, current version) In addition
an attribute 'description' is added to the data frame where to each miRNA some notes are added
(for example why a certain miRNA is not in the output). Sequence information is attached as the
attribute 'sequence'.

Methods (by class)

- this = MiRNANameConverter, miRNAs = character: Method for translating miRNA
  name(s) to different miRBase versions

Author(s)

Stefan Haunsberger

See Also

attr for attributes

Examples

nc = MiRNANameConverter(); # Instance of class 'MiRNANameConverter'
res = translateMiRNAName(nc, miRNAs = c("hsa-miR-140", "hsa-miR-125a"),
  versions = c(15, 16, 20, 21))
res
attributes(res)

validOrganisms

Get valid organisms

Description

This function returns all organisms where mature miRNA names are available in any of the provided
miRBase versions.

Usage

validOrganisms(this)

## S4 method for signature 'MiRNANameConverter'
validOrganisms(this)

Arguments

this Object of class MiRNAmeConverter

Details

The valid organisms are evaluated and set in the object initialization.
validOrganisms <-

Value
A numeric value

Methods (by class)
• MiRNANameConverter: Retrieve all supported organisms

Author(s)
Stefan Haunsberger

Examples
nc = MiRNANameConverter(); # Instance of class 'MiRNANameConverter'
validOrganisms(nc);

validOrganisms<-' Set valid organisms

Description
This function sets all organisms where mature miRNA names are available in any of the provided miRBase versions.

Usage
validOrganisms(this) <- value

Arguments
this Object of class MiRNANameConverter
value A character vector

Details
The valid organisms are evaluated and set in the object initialization.

Value
A MiRNANameConverter object

Author(s)
Stefan Haunsberger
validVersions <- Get valid versions

Description
This function returns all valid miRBase versions provided by the package.

Usage
validVersions(this)

## S4 method for signature 'MiRNANameConverter'
validVersions(this)

Arguments
this Object of class MiRNANameConverter

Value
A numeric vector

Methods (by class)
• MiRNANameConverter: Retrieve supported miRBase versions

Author(s)
Stefan Haunsberger

Examples
validVersions
nc = MiRNANameConverter(); # Instance of class 'MiRNANameConverter'
validVersions(nc);

validVersions<- Set valid versions

Description
Set version values that are supported by the package.

Usage
validVersions(this) <- value

Arguments
this Object of class MiRNANameConverter
value A vector of numeric values
Details

The value for the highest versions is a static variable. It is initialized in the initialization method when an instance of a MiRNANameConverter class is created.

Value

A MiRNANameConverter object

Author(s)

Stefan Haunsberger
Index

*Topic datasets
  example.miRNAs, 6

assessMiRNASwappingMIMAT, 2, 13
assessVersion, 3, 7
assessVersion,MiRNANameConverter-method
  (assessVersion), 3
attr, 12, 14

checkMiRNAName, 4, 7, 13
checkMiRNAName,MiRNANameConverter-method
  (checkMiRNAName), 4
currentVersion, 5
currentVersion,MiRNANameConverter-method
  (currentVersion), 5
currentVersion<-, 5

eexample.miRNAs, 6

miRNAmeConverter, 6
miRNAmeConverter-package
  (miRNAmeConverter), 6
MiRNANameConverter, 7
MiRNANameConverter,ANY-method, 8

new, 8
nOrganisms, 9
nOrganisms,MiRNANameConverter-method
  (nOrganisms), 9
nOrganisms<-, 9
nTotalEntries, 10
nTotalEntries,MiRNANameConverter-method
  (nTotalEntries), 10
nTotalEntries<-, 11

saveResults, 11
saveResults,MiRNANameConverter,data.frame-method
  (saveResults), 11
show, 13
show,MiRNANameConverter-method, 12

translateMiRNAName, 7, 13
translateMiRNAName,MiRNANameConverter,character-method
  (translateMiRNAName), 13

validOrganisms, 14
validOrganisms,MiRNANameConverter-method
  (validOrganisms), 14
validOrganisms<-, 15
validVersions, 16
validVersions,MiRNANameConverter-method
  (validVersions), 16
validVersions<-, 16

write.table, 12