Package ‘miRNAmeConverter’

March 28, 2017

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/).

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Imports DBI, AnnotationDbi

Depends miRBaseVersions.db

biocViews Preprocessing, miRNA

LazyData TRUE

Suggests methods, testthat, knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 5.0.1

NeedsCompilation no

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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.

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

**Usage**

```r
assessVersion(this, miRNAs, verbose = FALSE)
```

## S4 method for signature 'MiRNANameConverter'

```r
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**

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

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

currentVersion Get current version

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

Usage
currentVersion(this)

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


currentVersion<- Set current version

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

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

Usage

example.miRNAs

Format

A character vector containing names.

Description

This function returns an instance of a MiRNANameConverter 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)
```

---

**MiRNANameConverter**

*Instantiate from MiRNANameConverter class*

**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**

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>This function returns the number of different organisms that are provided by the package.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Usage</th>
</tr>
</thead>
<tbody>
<tr>
<td>nOrganisms(this)</td>
</tr>
</tbody>
</table>

**Arguments**

- **this**: Object of class `MiRNANameConverter`

**Details**

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

<table>
<thead>
<tr>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>A numeric value</td>
</tr>
</tbody>
</table>

**Methods (by class)**

- `MiRNANameConverter`: Retrieve number of organisms

**Author(s)**

Stefan Haunsberger

**Examples**

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

---

**nOrganisms<-**

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>This function sets the number of different organisms that are provided by the package.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Usage</th>
</tr>
</thead>
<tbody>
<tr>
<td>nOrganisms(this) &lt;- value</td>
</tr>
</tbody>
</table>
**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**

```r
nTotalEntries(this)
```

```r
## 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);

nTotalEntries<- 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
	his 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

saveResults Save miRNA translation results

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

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, ...)
show.MiRNANameConverter-method

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

```r
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)
```

show,MiRNANameConverter-method

Show-method

Description

This function prints object specific information Show-method

This function prints object specific information

Usage

```r
## S4 method for signature 'MiRNANameConverter'
show(object)
```
translateMiRNAName

Arguments

object Object of class MiRNANameConverter

Details

This function prints some information to the console.

Author(s)

Stefan Haunsberger

See Also

show

translateMiRNAName  Translate miRNA name

Description

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

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,
neglect it because then it is not considered to be a miRNA anymore 5) Receive names from desired
versions
Value

A \((n \times m)\) 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 MiRNANameConverter

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**
```r
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 <-

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
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