Package ‘miRBaseConverter’

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Type Package

Title A comprehensive and high-efficiency tool for converting and
retrieving the information of miRNAs in different miRBase
versions

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Author Taosheng Xu<taosheng.x@gmail.com>, Thuc Le<Thuc.Le@unisa.edu.au>

Maintainer Taosheng Xu<taosheng.x@gmail.com>

Imports stats

Depends R (>= 3.4)

Description A comprehensive tool for converting and retrieving the miRNA Name, Accession, Se-
quence, Version, History and Family information in different miRBase versions. It can pro-
cess a huge number of miRNAs in a short time without other depends.

License GPL (>= 2)

LazyData TRUE

Suggests BiocGenerics, RUnit, knitr, rtracklayer, utils

VignetteBuilder knitr

biocViews Software, miRNA

URL https://github.com/taoshengxu/miRBaseConverter

BugReports https://github.com/taoshengxu/miRBaseConverter/issues

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R topics documented:

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checkMiRNAAlive

Description
This function checks the miRNA status (Alive or Dead) in the latest miRBase version.

Usage

checkMiRNAAlive(Accessions, verbose = TRUE)

Arguments

Accessions A character vector representing the miRNA Accessions in miRBase.
verbose Logical value. If true, the dead miRNAs will be printed the console.

Value
A character vector of Accessions for all alive miRNAs. The names of the return vector are the position indexes in the input Accessions.

Author(s)
Xu, Taosheng <taosheng.x@gmail.com>

Examples

data(miRNATest)
## The input is miRNA Accessions
Accessions=miRNATest$Accession
alive_Accession=checkMiRNAAlive(Accessions)

## The input is miRNA names
miRNANames=miRNATest$miRNA_Name
version=checkMiRNAVersion(miRNANames,verbose = TRUE)
result=miRNA_NameToAccession(miRNANames,version = version)
**checkMiRNAFamily**

Accessions=result$Accession
alive_Accession2=checkMiRNAAlive(Accessions)

---

**Description**

This function checks the miRNA family for a list of miRNA Names.

**Usage**

checkMiRNAFamily(Accessions)

**Arguments**

Accessions A character vector representing the miRNA Accessions in miRBase.

**Value**

A data frame with four columns. The number of rows equal to the input Accessions. The four columns are defined as below:

- **Accession** : The input miRNA accessions.
- **miRNAName_v21** : The miRNA names (version 21) corresponding to the Accession.
- **FamilyAccession** : The accession of the family.
- **Family** : The family name.

**Author(s)**

Xu, Taosheng <taosheng.x@gmail.com>

**Examples**

data(miRNATest)
## The input is miRNA Accessions
Accessions=miRNATest$Accession
Family_Info1=checkMiRNAFamily(Accessions)

## The input is miRNA names
miRNANames=miRNATest$miRNA_Name
version=checkMiRNAVersion(miRNANames,verbose = TRUE)
result=miRNA_NameToAccession(miRNANames,version=version)
Accessions=result$Accession
Family_Info2=checkMiRNAFamily(Accessions)
**checkMiRNAVersion**  
*check the miRNA Version in miRBase*

**Description**  
This function checks the most possible miRBase version for a list of miRNA names.

**Usage**  
```
checkMiRNAVersion(miRNANames, verbose = TRUE)
```

**Arguments**
- `miRNANames`: A character vector representing the miRNA names.
- `verbose`: Logical value. If true, the detail version information is printed in the console for user reference.

**Value**  
A single character value or a character vector represent the most possible miRBase version for the list of miRNA names.

**Author(s)**  
Xu, Taosheng <taosheng.x@gmail.com>

**Examples**
```
data(miRNATest)
miRNANames=miRNATest$miRNA_Name
version=checkMiRNAVersion(miRNANames,verbose=TRUE)
```

**getAllMiRNAs**  
*Get all miRNAs in the specified miRBase version*

**Description**  
This function gets all miRNAs in the specified miRBase version.

**Usage**  
```
getAllMiRNAs(version = "v22", type = "all", species = "all")
```
getAllSpecies

Arguments

version A character value representing the specified miRBase version for retrieval. Users can apply the function getAllVersionInfo() to get the available miRNA version names. The optional values are in below:
"v6","v7_1","v8","v8_1","v8_2","v9","v9_1",
"v9_2","v10","v10_1","v11","v12","v13","v14",
"v15","v16","v17","v18","v19","v20","v21","v22"

type A character value representing the miRNA type for retrieval.
• "precursor"
• "mature"
• "all" : precursor and mature

species A character value representing the abbreviation of species. Users can apply the getAllSpecies() function to get the available abbreviation of species. If species is set to "all", the miRNAs of all species will return.

Value

A data frame with three columns. The three columns are defined as below:
• Accession
• Name
• Sequence

Author(s)

Xu, Taosheng <taosheng.x@gmail.com>

Examples

miRNAs=getAllMiRNAs(version="v22", type="all", species="hsa")

getAllSpecies Get all species of miRNAs embodied in miRBase repository

Description

This function return a reference for all species of miRNAs including the abbreviation and full name.

Usage

getAllSpecies()
getAllVersionInfo

Value

A dataframe A data frame with two columns. The two columns are defined as below:

- **Species**
- **FullName**

Author(s)

Xu, Taosheng <taosheng.x@gmail.com>

Examples

```R
getAllSpecies()
```

---

**getAllVersionInfo**   
*Get all miRBase version information*

Description

This function return a reference for all miRBase versions’ information including Version name, Release date, miRNA number and Status.

Usage

```R
getAllVersionInfo()
```

Value

The detailed version information is printed in the console for user reference.

Author(s)

Xu, Taosheng <taosheng.x@gmail.com>

Examples

```R
getAllVersionInfo()
```
getMiRNAHistory

*Get the detailed information of a single specified miRNA in all miRBase versions.*

**Description**

This function returns all available miRBase versions’ information of a single specified miRNA.

**Usage**

```
getMiRNAHistory(Accession)
```

**Arguments**

- **Accession**
  A character representing the single Accession.

**Value**

A data frame including all the history information (Precursor, Mature, Sequence) of the specified miRNA. Each row represents a miRBase version.

**Author(s)**

Xu, Taosheng <taosheng.x@gmail.com>

**Examples**

```r
#####1, The input is a miRNA Name
miRNAName="hsa-miR-26b-5p"
result1=miRNA_NameToAccession(miRNAName, version="v22")
Accession=result1$Accession
result2=getMiRNAHistory(Accession)

#####2, The input is miRNA Accession
Accession="MIMAT0000765"
result3=getMiRNAHistory(Accession)
```

---

getMiRNASequence

*Get the miRNA sequences*

**Description**

This function returns the miRNA sequences for a list of miRNAs.

**Usage**

```
getMiRNASequence(Accessions, targetVersion = "v22")
```
**Arguments**

Accessions: A character vector representing the miRNA Accessions in miRBase.

targetVersion: A character value representing the target miRBase version corresponding the Accessions. Users can apply the function `getAllVersionInfo()` to get the available miRNA version names. The optional values are in below: "v6","v7_1","v8","v8_1","v8_2","v9","v9_1","v9_2","v10","v10_1","v11","v12","v13","v14","v15","v16","v17","v18","v19","v20","v21","v22"

**Value**

A nx2 data frame. The number of row equals to input miRNAs. The two columns are defined as below:

- **Accession**: The original miRNA (Column 1).

- **miRNASequence_{targetVersion}**: The return miRNA sequence (in specified version) corresponding to the input miRNAs (Column 2).

**Author(s)**

Xu, Taosheng <taosheng.x@gmail.com>

**Examples**

```r
#1, The input are miRNA Accessions
data(miRNATest)
Accessions=miRNATest$Accession
result1=getMiRNASequence(Accessions,targetVersion="v13")
result2=getMiRNASequence(Accessions,targetVersion="v22")

#2, The input are miRNA Names
data(miRNATest)
miRNANames=miRNATest$miRNA_Name
result3=mRNAVersionConvert(miRNANames,targetVersion="v22",exact=TRUE)
Accessions=result3$Accession
result4=getMiRNASequence(Accessions,targetVersion="v22")
```

---

**getMiRNATable**

*Get the full miRNAs information table of the specified miRBase version*

**Description**

This function returns the full miRNAs information table of the specified miRBase version.

**Usage**

```r
getMiRNATable(version = "v22", species = "all")
```
**Arguments**

**version**
A character value representing the specified miRBase version for retrieval. Users can apply the function `getAllVersionInfo()` to get the available miRNA version names. The optional values are in below:
- "v6","v7_1","v8","v8_1","v8_2","v9","v9_1","v9_2","v10","v10_1","v11","v12","v13","v14","v15","v16","v17","v18","v19","v20","v21","v22"

**species**
A character value representing the abbreviation of species. Users can apply the function `getAllSpecies()` to get the available abbreviation of species. If species is set to "all", the miRNAs of all species will return.

**Value**

A data frame

**Author(s)**

Xu, Taosheng <taosheng.x@gmail.com>

**Examples**

```r
miRNA_Tab=getMiRNAData(version="v22",species="hsa")
```

---

**goTo_miRBase**

Open the miRBase webpages of the specified miRNAs

**Description**

This function redirects the miRBase webpage of the specified miRNAs

**Usage**

`goTo_miRBase(Accessions)`

**Arguments**

**Accessions**
A character vector representing the miRNA Accessions in miRBase. We restrict the number of queried miRNAs each time. The maximum number of the input miRNAs is 15.

**Value**

No values

**Author(s)**

Xu, Taosheng <taosheng.x@gmail.com>
Examples

```r
### 1. A step-loop
Accession1="MI0000447"
goTo_miRBase(Accession1)

### 2. A mature miRNA
Accession2="MIMAT0026477"
goTo_miRBase(Accession2)

### 3. A list of miRNAs
Accession3=miRNATest$Accession[1:10]
goTo_miRBase(Accession3)
```

---

**goTo_miRNAFamily**

*Open the miRNA family webpages of the specified miRNAs*

---

**Description**

This function redirects the miRBase miRNA family webpages of the specified miRNA families.

**Usage**

```r
goTo_miRNAFamily(FamilyAccessions, verbose = TRUE)
```

**Arguments**

- **FamilyAccessions**
  A character vector representing the miRNA family Accessions in miRBase. We restrict the queried number of miRNA family each time. The maximum number of the input miRNA families is 15.

- **verbose**
  Logical value. If true, the invalid miRNA Family will be printed the console.

**Value**

No values

**Author(s)**

Xu, Taosheng <taosheng.x@gmail.com>

**Examples**

```r
data(miRNATest)
Accessions=miRNATest$Accession
Family_Info=checkMiRNAFamily(Accessions)
FamilyAccessions=Family_Info$FamilyAccession[1:15]
goTo_miRNAFamily(FamilyAccessions)
```
miRNATest

Description

- **Accession**: miRNA Accessions in miRBase
- **miRNA_Name**: miRNA names

Format

A data frame

Note

This is a mixed miRNA name collection of some species for the examples’ test in the package.

Examples

data(miRNATest)

miRNAVersionConvert

miRBase version convert for miRNA Names

Description

This function converts a group of any species’ miRNA names (including precursor and mature miRNA) to the specified miRBase version if the miRNAs have been defined in miRBase.

Usage

miRNAVersionConvert(miRNANames, targetVersion = "v22", exact = TRUE, verbose = TRUE)

Arguments

- **miRNANames**: A character vector representing the source miRNA names needed to be convert.
- **targetVersion**: A character value representing the target miRBase version corresponding the source miRNA names. Users can apply the function `getAllVersionInfo()` to get the available miRNA version names. The optional values are in below: "v6","v7_1","v8","v8_1","v8_2","v9","v9_1","v9_2","v10","v10_1","v11","v12","v13","v14","v15","v16","v17","v18","v19","v20","v21","v22"
- **exact**: Logical value. If true, the result will be the most exactly matched result. If FALSE, the result will include all the possible matched miRNA name. If one miRNA can match multiple names. All the matched names are concatenated with ";".
- **verbose**: Logical value. If true, it will print the multiple matched miRNA Names and Accessions to the console.
miRNA_AccessionToName

Value

A data frame with three columns. The number of rows equal to the input miRNA names. The three columns are defined as below:

- **OriginalName**: The original miRNA names (Column 1).

- **TargetName**: The converted miRBase names (in specified version) corresponding to the original miRNA names (Column 2).

- **Accession**: The corresponding miRBase Accessions (Column 3).

Note

Please note: Due to some miRNA names changing many times in history. Even if choose the third parameter “exact”=TRUE, it may still have some miRNAs that can’t match the unique name in the target version. In order to return the accurate result as possible, we also concatenate the multiple matched miRNA names with "&". This is the rare case but it happens sometimes.

Author(s)

Xu, Taosheng <taosheng.x@gmail.com>

Examples

data(miRNATest)
miRNANames=miRNATest$miRNA_Name
result1=miRNAVersionConvert(miRNANames,targetVersion="v13",exact=TRUE,verbose=TRUE)
result2=miRNAVersionConvert(miRNANames,targetVersion="v22",exact=TRUE,verbose=TRUE)
result3=miRNAVersionConvert(miRNANames,targetVersion="v22",exact=FALSE,verbose=TRUE)

miRNANames=c("hsa-let-7c","hsa-miR-3190-3p","hsa-miR-3190-3p","hsa-miR-34b","hsa-miR-378","hsa-miR-499a-3p","hsa-miR-499a-5p","hsa-miR-500","hsa-miR-516a-5p","hsa-miR-550","hsa-miR-589")
result4=miRNAVersionConvert(miRNANames, targetVersion="v22", exact=TRUE, verbose=TRUE)

miRNA_AccessionToName  miRBase Accession to miRNA Name in specified version

Description

This function converts a group of any species’ miRNA Accessions (including precursor and mature miRNA) to a specified miRBase version if the Accessions have been defined in miRBase.

Usage

miRNA_AccessionToName(Accessions, targetVersion = "v22")
**miRNA_MatureToPrecursor**

Convert the mature miRNAs to the corresponding precursors

**Description**

This function converts the mature miRNAs to the corresponding precursors in the specified miRBase version.

**Usage**

```
miRNA_MatureToPrecursor(miRNANames, version = NULL)
```
**miRNA_NameToAccession**

Arguments

- **miRNANames**: A character vector representing the miRNA names.
- **version**: The default is **NULL** representing the most possible latest version of the input miRNA Names will be checked automatically. Otherwise, a character value representing the version corresponding the input miRNA Names. Users can apply the function `getAllVersionInfo()` to get the available miRNA version names. The optional values are in below: "v6","v7_1","v8","v8_2","v9","v9_1","v9_2","v10","v10_1","v11","v12","v13","v14","v15","v16","v17","v18","v19","v20","v21","v22"

Value

A data frame(nx2). The number of rows equal to the input miRNA Names. The two columns are defined as below:

- **OriginalName**: The input miRNA Names.
- **Precursor**: The corresponding precursors of the mature miRNAs.

Author(s)

Xu, Taosheng <taosheng.x@gmail.com>

Examples

data(miRNATest)
miRNANames=miRNATest$miRNA_Name
result=miRNA_MatureToPrecursor(miRNANames)

---

**miRNA_NameToAccession  The miRBase miRNA names with specified version to Accessions**

**Description**

This function converts a group of any species’ miRNA name to the Accessions defined in miRBase.

**Usage**

```r
miRNA_NameToAccession(miRNANames, version = "v22")
```

**Arguments**

- **miRNANames**: A character vector representing the source miRNA names needed to be convert.
- **version**: A character value representing the version corresponding the miRNANames. Users can apply the function `getAllVersionInfo()` to get the available miRNA version names. The optional values are in below: "v6","v7_1","v8","v8_2","v9","v9_1","v9_2","v10","v10_1","v11","v12","v13","v14","v15","v16","v17","v18","v19","v20","v21","v22"
Value

A nx2 data frame. The number of rows equal to the input miRNA names. The two columns are defined as below:

- miRNAName_{Version} : The input miRNA names (Column 1).
- Accession : The convert Accession(Column 2).

Author(s)

Xu, Taosheng <taosheng.x@gmail.com>

Examples

data(miRNATest)
miRNANames=miRNATest$miRNA_Name
version=checkMiRNAVersion(miRNANames,verbose=TRUE)
result1=miRNA_NameToAccession(miRNANames,version=version)
result2=miRNA_AccessionToName(result1[,2],targetVersion="v22")
result3=miRNAVersionConvert(miRNANames,targetVersion="v22",exact=TRUE)

miRNA_PrecursorToMature

Convert the precursors to the corresponding mature miRNAs

Description

This function converts the precursors to the corresponding mature miRNAs in the specified miR-Base version.

Usage

miRNA_PrecursorToMature(miRNANames, version = NULL)

Arguments

- miRNANames : A character vector representing the miRNA names.
- version : The default is NULL representing the most possible latest version of the input miRNA Names will be checked automatically. Otherwise, a character value representing the version corresponding the input miRNA Names. Users can apply the function getAllVersionInfo() to get the available miRNA version names. The optional values are in below: "v6","v7_1","v8","v8_2","v9","v9_1","v9_2","v10","v10_1","v11","v12","v13","v14", "v15","v16","v17","v18","v19","v20","v21","v22"
**miRNA_PrecursorToMature**

### Value

A data frame(nx3). The number of rows equal to the input miRNA names. The three columns are defined as below:

- **OriginalName**: The input miRNA Names.
- **Mature1**: The corresponding mature miRNAs (always midnight p).  
- **Mature2**: The corresponding mature miRNAs (always morning p).

### Note

If the input miRNA Names mingle mature miRNA names, the mature miRNA names will match to themselves in the output.

### Author(s)

Xu, Taosheng <taosheng.x@gmail.com>

### Examples

```r
result=miRNA_PrecursorToMature(miRNANames)
```
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