The miRBase database (Griffiths-Jones, 2004; Griffiths-Jones, Grocock, Dongen, Bateman, & Enright, 2006; Griffiths-Jones, Saini, Dongen, & Enright, 2008; Kozomara & Griffiths-Jones, 2011, 2014) is the official repository for miRNAs and includes a miRNA naming convention (AMBROS et al., 2003; Meyers et al., 2008). Over the years of development miRNAs have been added to, or deleted from the database, while some miRNA names have been changed. As a result, each version of the miRBase database can differ substantially from previous versions.

The miRBaseVersions.db R package has been developed to provide an easy accessible repository for several different miRBase release versions.

1. Introduction

The miRBaseVersions.db package is an annotation package which includes mature miRNA names from 21 miRBase release versions. Due to ongoing growth and changes with each release miRNA names can have different names in different versions or even are not listed as valid miRNAs anymore. This annotation package serves as a repository and can be used for quick lookup for mature miRNA names. The miRBaseVersions.db package has implemented the AnnotationDbi-select interface. By implementing this select interface the user is able to use the same methods as for any other annotation package.

The main four implemented methods are

- `columns`, presents the values one can retrieve in the final result,
- `keytypes`, which presents the tables that can be used in this package,
- `keys`, is used to get viable keys of a particular `keytype` and
- `select`, which is used to extract data from the annotation package by using values provided by the other three methods.

To load the package and gain access to the functions just run the following command:

```r
library(miRBaseVersions.db)
```

## Loading required package: DBI

Vignette Info

This vignette has been generated using an R Markdown file with knitr:rmarkdown as vignette engine (Boettiger, 2015; Francois, 2014; Xie, 2014, 2015b, 2015a).
Database information

The data is the miRNAmeConverter package is stored in an SQLite database. All entries contained in the database were downloaded from the miRBase ftp-site. The following versions are available:

<table>
<thead>
<tr>
<th>miRBase Version</th>
<th># Mature Entries</th>
<th>Release Date</th>
</tr>
</thead>
<tbody>
<tr>
<td>6.0</td>
<td>1591</td>
<td>04/05</td>
</tr>
<tr>
<td>7.1</td>
<td>3101</td>
<td>10/05</td>
</tr>
<tr>
<td>8.0</td>
<td>3228</td>
<td>02/06</td>
</tr>
<tr>
<td>8.1</td>
<td>3684</td>
<td>05/06</td>
</tr>
<tr>
<td>8.2</td>
<td>3834</td>
<td>07/06</td>
</tr>
<tr>
<td>9.0</td>
<td>4167</td>
<td>10/06</td>
</tr>
<tr>
<td>9.1</td>
<td>4274</td>
<td>02/07</td>
</tr>
<tr>
<td>9.2</td>
<td>4430</td>
<td>05/07</td>
</tr>
<tr>
<td>10.0</td>
<td>5395</td>
<td>08/07</td>
</tr>
<tr>
<td>10.1</td>
<td>5718</td>
<td>12/07</td>
</tr>
<tr>
<td>11.0</td>
<td>6703</td>
<td>04/08</td>
</tr>
<tr>
<td>12.0</td>
<td>9110</td>
<td>09/08</td>
</tr>
<tr>
<td>13.0</td>
<td>10097</td>
<td>03/09</td>
</tr>
<tr>
<td>14.0</td>
<td>11663</td>
<td>09/09</td>
</tr>
<tr>
<td>15.0</td>
<td>15632</td>
<td>04/10</td>
</tr>
<tr>
<td>16.0</td>
<td>17341</td>
<td>08/10</td>
</tr>
<tr>
<td>17.0</td>
<td>19724</td>
<td>04/11</td>
</tr>
<tr>
<td>18.0</td>
<td>21643</td>
<td>11/11</td>
</tr>
<tr>
<td>19.0</td>
<td>25141</td>
<td>08/12</td>
</tr>
<tr>
<td>20.0</td>
<td>30424</td>
<td>06/13</td>
</tr>
<tr>
<td>21.0</td>
<td>35828</td>
<td>06/14</td>
</tr>
</tbody>
</table>

from 228 organisms.

2. Use Cases

2.1 Function keytypes

Use this function to receive table names from where data can be retrieved:

```r
keytypes(miRBaseVersions.db);
```

```r
## [1] "MIMAT"  "VW-MIMAT-10.0"  "VW-MIMAT-10.1"  "VW-MIMAT-11.0"
## [5] "VW-MIMAT-12.0"  "VW-MIMAT-13.0"  "VW-MIMAT-14.0"  "VW-MIMAT-15.0"
## [9] "VW-MIMAT-16.0"  "VW-MIMAT-17.0"  "VW-MIMAT-18.0"  "VW-MIMAT-19.0"
## [13] "VW-MIMAT-20.0"  "VW-MIMAT-21.0"  "VW-MIMAT-6.0"  "VW-MIMAT-7.1"
## [17] "VW-MIMAT-8.0"  "VW-MIMAT-8.1"  "VW-MIMAT-8.2"  "VW-MIMAT-9.0"
## [21] "VW-MIMAT-9.1"  "VW-MIMAT-9.2"
```

The output lists 22 tables where each one of them can be queried. The keytype “MIMAT” is the main table containing all records from all supported miRBase release versions. Keytypes starting with the prefix “VW-MIMAT” are so called SQL views. For example the keytype “VW-MIMAT-21.0” is an SQL view from the “MIMAT” table which only holds records from miRBase version 21.0.
2.2 Function columns

Use the `columns` function to retrieve information about the kind of variables you can retrieve in the final output:

```
columns(miRBaseVersions.db);
```

```
## [1] "ACCESSION" "NAME" "ORGANISM" "SEQUENCE" "VERSION"
```

All 5 columns are available for all 22 keytypes.

2.3 Function keys

The `keys` function returns all viable keys of a particular `keytype`. The following example retrieves all possible keys for miRBase release version 6.0.

```
k = head(keys(miRBaseVersions.db, keytype = "VW-MIMAT-6.0"));
k;
```

```
## [1] "MIMAT0000001" "MIMAT0000002" "MIMAT0000003" "MIMAT0000004"
## [5] "MIMAT0000005" "MIMAT0000006"
```

2.4 Function select

The `select` function is used to extract data. As input values the function takes outputs received from the other three functions `keys`, `columns` and `keytypes`.

For example to extract all information about the mature accession ‘MIMAT0000092’ we can run the following command:

```
result = select(miRBaseVersions.db, 
               keys = "MIMAT0000092", 
               keytype = "MIMAT", 
               columns = "*")
result;
```

```
##    ACCESSION NAME          SEQUENCE VERSION ORGANISM
## 1 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 21.0  hsa
## 2 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 20.0  hsa
## 3 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 19.0  hsa
## 4 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 18.0  hsa
## 5 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 17.0  hsa
## 6 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 16.0  hsa
## 7 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 15.0  hsa
## 8 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 14.0  hsa
## 9 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 13.0  hsa
##10 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 12.0  hsa
##11 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 11.0  hsa
##12 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 10.1  hsa
##13 MIMAT0000092 hsa-miR-92a-3p UAUUGCACUUGCCGCCGU 10.0  hsa
##14 MIMAT0000092 hsa-miR-92a UAUUGCACUUGCCGCCGU  9.2  hsa
##15 MIMAT0000092 hsa-miR-92a UAUUGCACUUGCCGCCGU  9.1  hsa
```
As we can see the result returns all miRNA names the accession had among the different miRBase releases. If we for example only want to extract the fields for ‘accession’, ‘name’ and ‘version’ we simply run the following command:

```r
result = select(miRBaseVersions.db,
                keys = "MIMAT0000092",
                keytype = "MIMAT",
                columns = c("ACCESSION", "NAME", "VERSION"))
```

In comparison to the previous output with parameter `columns = "*"` this time only the selected columns were returned.

**Additional information**

**Packages loaded via namespace**

The following packages are used in the `miRBaseVersions.db` package:
• AnnotationDbi_1.32.3 (Pages, Carlson, Falcon, & Li, n.d.)
• DBI_0.3.1 (Databases, 2014)
• RSQLite_1.0.0 (Wickham, James, & Falcon, 2014)
• gtools_3.5.0 (Warnes, Bolker, & Lumley, 2015)

Future Aspects

This database can only be of good use if it will be kept up to date. Therefore we plan to include new miRBase releases as soon as possible.

References


