

Introduction to LRBaseDbi and LRBase.XXX.eg.db-type packages

Koki Tsuyuzaki¹, Manabu Ishii¹, and Itoshi Nikaido¹.

July 10, 2018

¹Laboratory for Bioinformatics Research, RIKEN Center for Biosystems Dynamics Research,
Japan
k.t.the-answer@hotmail.co.jp

1 Introduction

This document provides the way to use LRBaseDbi and LRBase.XXX.eg.db-type packages. LRBase.XXX.eg.db-type packages provide the pair list of ligand - receptor genes. The packages are generated by the LRBaseDbi package. LRBaseDbi has two role; class-definition and the construction of LRBase.XXX.eg.db-type packages. LRBaseDbi defines the class "LRBaseDb" and unify the objects's behavior such as column function described later. The makeLRBasePackage function of LRBaseDbi generates the user's original LRBase.XXX.eg.db-type packages.

2 makeLRBasePackage

Here we use makeLRBasePackage function to create a LRBase.XXX.eg.db-type package. Only user have to specify are 1. a LR-list containing the columns "GENEID_L" (ligand NCBI Gene IDs) and "GENEID_R" (receptor NCBI Gene IDs) and 2. a meta information table describing the LR-list. Here we use the demo data of LR-list of FANTOM5 project.

```
> library('LRBaseDbi')

[1] "LRBaseDbi" "stats"      "graphics"  "grDevices" "utils"      "datasets"
[7] "methods"   "base"

> example('makeLRBasePackage')

mkLRBP> ## makeLRBasePackage enable users to construct
mkLRBP> ## user's own custom LRBase package
mkLRBP> data(FANTOM5)

mkLRBP> head(FANTOM5)
  GENEID_L GENEID_R SOURCEID SOURCEDB
```

Introduction to LRBaseDbi and LRBase.XXX.eg.db-type packages

```
1      805      19      - FANTOM5
2      808      19      - FANTOM5
3      801      19      - FANTOM5
4     5360      19      - FANTOM5
5     9699      19      - FANTOM5
6    50944      19      - FANTOM5
```

```
mkLRBP> # We are also needed to prepare meta data as follows.
mkLRBP> data(metaFANTOM5)
```

```
mkLRBP> metaFANTOM5
```

	NAME	VALUE
1	SOURCEDATE	22-July-2015
2	SOURCENAME	FANTOM5
3	SOURCEURL	http://fantom.gsc.riken.jp/5/suppl/Ramilowski_et_al_2015/data/PairsLigRec.txt
4	DBSCHEMA	FANTOM5.Hsa.eg.db
5	DBSCHEMAVERSION	1.0
6	ORGANISM	Homo sapiens
7	SPECIES	Human
8	package	AnnotationDbi
9	Db type	LRBaseDb
10	VERSION	2018

```
mkLRBP> ## sets up a temporary directory for this example
```

```
mkLRBP> ## (users won't need to do this step)
```

```
mkLRBP> destination <- tempfile()
```

```
mkLRBP> dir.create(destination)
```

```
mkLRBP> ## makes an Organism package for human called Homo.sapiens
```

```
mkLRBP> makeLRBasePackage(pkgname = "FANTOM5.Hsa.eg.db",
```

```
mkLRBP+   data = FANTOM5,
```

```
mkLRBP+   metadata = metaFANTOM5,
```

Introduction to LRBaseDbi and LRBase.XXX.eg.db-type packages

```
mkLRBP+    organism = "Homo sapiens",
mkLRBP+    version = "0.99.0",
mkLRBP+    maintainer = "Koki Tsuyuzaki <k.t.the-answer@hotmail.co.jp>",
mkLRBP+    author = "Koki Tsuyuzaki",
mkLRBP+    destDir = destination,
mkLRBP+    license="Artistic-2.0")
Creating package in /var/folders/k0/tk8gl4bj2_v2mbjx80ydszwn0000gn/T//RtmpkPGJzQ/file185093a91714
$value
[1] TRUE

$visible
[1] FALSE
```

After makeLRBasePackage, FANTOM5.Hsa.eg.db is generated. Here, we will install the package.

```
> filepath <- list.files(destination, full.names=TRUE)
> install.packages(filepath, repos=NULL, type='source')
> library('FANTOM5.Hsa.eg.db')
```

3 columns, keytypes, keys, and select

All LRBase.XXX.eg.db-type package has same name object and it is instantiated by LRBaseDb-class. Many data access function for this object are implemented. For example, columns returns the rows which we can retrieve in LRBase.XXX.eg.db-type packages. keytypes returns the rows which can be used as the optional parameter in keys and select functions against LRBase.XXX.eg.db-type packages. keys function returns the value of keytype. select function returns the rows in particular columns, which are having user-specified keys. This function returns the result as a dataframe.

```
> columns(FANTOM5.Hsa.eg.db)
[1] "GENEID_L" "GENEID_R" "SOURCEDB" "SOURCEID"
> keytypes(FANTOM5.Hsa.eg.db)
[1] "GENEID_L" "GENEID_R" "SOURCEDB" "SOURCEID"
> key_FN5 <- keys(FANTOM5.Hsa.eg.db, keytype='GENEID_R')
> head(select(FANTOM5.Hsa.eg.db, keys=key_FN5[1:2],
+           columns=c('GENEID_L', 'GENEID_R'), keytype='GENEID_R'))
  GENEID_L GENEID_R
1      805      19
```

2	808	19
3	801	19
4	5360	19
5	9699	19
6	50944	19

4 Other functions

Other additional functions like `species`, `nomenclature`, and `listDatabases` are available. In each LRBase.XXX.eg.db-type package, `species` function returns the common name and `nomenclature` returns the scientific name. `listDatabases` function returns the source of data. `dbInfo` returns the information of the package. `dbfile` returns the directory where sqlite file is stored. `dbschema` returns the schema of database. `dbconn` returns the connection to the sqlite database.

```
> species(FANTOM5.Hsa.eg.db)
[1] "Human"
> nomenclature(FANTOM5.Hsa.eg.db)
[1] "Homo sapiens"
> listDatabases(FANTOM5.Hsa.eg.db)
SOURCEDB
1 FANTOM5
> dbInfo(FANTOM5.Hsa.eg.db)
      NAME
1 SOURCEDATE
2 SOURCENAME
3 SOURCEURL
4 DBSCHEMA
5 DBSCHEMAVERSION
6 ORGANISM
7 SPECIES
8 package
9 Db type
10 VERSION
                                     VALUE
1                                     22-July-2015
2                                     FANTOM5
3 http://fantom.gsc.riken.jp/5/suppl/Ramilowski_et_al_2015/data/PairsLigRec.txt
4                                     FANTOM5.Hsa.eg.db
```

Introduction to LRBaseDbi and LRBase.XXX.eg.db-type packages

```
5                                     1.0
6                                 Homo sapiens
7                                 Human
8                                 AnnotationDbi
9                                 LRBaseDb
10                                2018

> dbfile(FANTOM5.Hsa.eg.db)

[1] "/Library/Frameworks/R.framework/Versions/3.5/Resources/library/FANTOM5.Hsa.eg.db/extdata/FANTOM5.Hsa.eg.db"

> dbschema(FANTOM5.Hsa.eg.db)

[1] "CREATE TABLE `METADATA` (\n  `NAME` TEXT,\n  `VALUE` TEXT\n)"
[2] "CREATE TABLE `DATA` (\n  `GENEID_L` INTEGER,\n  `GENEID_R` INTEGER,\n  `SOURCEID` TEXT,\n  `VALUE` TEXT\n)"

> dbconn(FANTOM5.Hsa.eg.db)

<SQLiteConnection>
  Path: /Library/Frameworks/R.framework/Versions/3.5/Resources/library/FANTOM5.Hsa.eg.db/extdata/FANTOM5.Hsa.eg.db
  Extensions: TRUE
```

5 Redirecting to the scTensor package

Description for any LRBase-related packages is written in the vignette of *scTensor* package.

Please follow the link below

<http://www.bioconductor.org/packages/release/bioc/html/scTensor.html>

or just type

```
> source('http://bioconductor.org/biocLite.R')
> biocLite('scTensor')
> library('scTensor')
> vignette('scTensor')
```

in R console window.