

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

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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
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,
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_v2mbjx80ydsznw0000gn/T//RtmpKdI15E/file5ef772
$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 implmented. 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" "SOURCEID" "SOURCEID"

> keytypes(FANTOM5.Hsa.eg.db)

[1] "GENEID_L" "GENEID_R" "SOURCEID" "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	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	
7	SPECIES	
8	package	
9	Db type	
10	VERSION	

```

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"
```

```
> 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)"
```

```
> dbconn(FANTOM5.Hsa.eg.db)
```

```
<SQLiteConnection>
```

```
Path: /Library/Frameworks/R.framework/Versions/3.5/Resources/library/FANTOM5.Hsa.eg.db/extdata
```

```
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.