

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

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## 1 Introduction

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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 (L-R) genes. The packages are generated by the LRBaseDbi package. LRBaseDbi has two roles; class-definition and construction of LRBase.XXX.eg.db-type packages. LRBaseDbi defines a class "LRBaseDb" and unifies the object'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

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Here we use makeLRBasePackage function to create a LRBase.XXX.eg.db-type package. Only users have to specify are 1. a L-R corresponding table containing the columns "GENEID\_L" (NCBI Gene IDs of the ligand) and "GENEID\_R" (NCBI Gene IDs of the receptor) and 2. a meta-information table describing the L-R list. Here we use the demo data of L-R list of the FANTOM5 project.

```
> library('LRBaseDbi')  
  
[1] "LRBaseDbi" "stats"      "graphics"  "grDevices" "utils"      "datasets"  
[7] "methods"   "base"  
  
> if(interactive()){  
+   example('makeLRBasePackage')  
+ }  
  
NULL
```

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

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

### 3 columns, keytypes, keys, and select

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All LRBase.XXX.eg.db-type package has the same name object and it is instantiated by the LRBaseDb-class. Many data access functions 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 key-type. `select` function returns the rows in particular columns, which are having user-specified keys. This function returns the result as a data frame.

```
> if(interactive()){
+   columns(FANTOM5.Hsa.eg.db)
+   keytypes(FANTOM5.Hsa.eg.db)
+   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'))
+ }
```

### 4 Other functions

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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.

```
> if(interactive()){
+   species(FANTOM5.Hsa.eg.db)
+   nomenclature(FANTOM5.Hsa.eg.db)
+   listDatabases(FANTOM5.Hsa.eg.db)
+   dbInfo(FANTOM5.Hsa.eg.db)
+   dbfile(FANTOM5.Hsa.eg.db)
+   dbschema(FANTOM5.Hsa.eg.db)
+ }
```

```
+ dbconn(FANTOM5.Hsa.eg.db)
+ }
```

## 5 Redirecting to the scTensor package

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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

```
> if(interactive()){
+   if (!requireNamespace('BiocManager', quietly = TRUE)){
+     install.packages('BiocManager')
+   }
+   BiocManager::install('scTensor')
+   library('scTensor')
+   vignette('scTensor')
+ }
```

in R console window.