

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"  
  
> if(interactive()){  
+   example('makeLRBasePackage')  
+ }  
  
NULL
```

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

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```
> if(interactive()){
+   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.

```
> 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

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)
+ }
```

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

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

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

in R console window.