

How to use MeSH-related Packages

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1 Introduction

This document provides the way to use MeSH-related packages; *MeSH.db*, *MeSH.AOR.db*, *MeSH.PCR.db*, *MeSH.XXX.eg.db*-type packages, *MeSHdbi*, and *meshr* packages. MeSH (Medical Subject Headings) is the NLM (U. S. National Library of Medicine) controlled vocabulary used to manually index articles for MEDLINE/PubMed [1] and is a collection of a comprehensive life science vocabulary. MeSH contains more than 25,000 clinical and

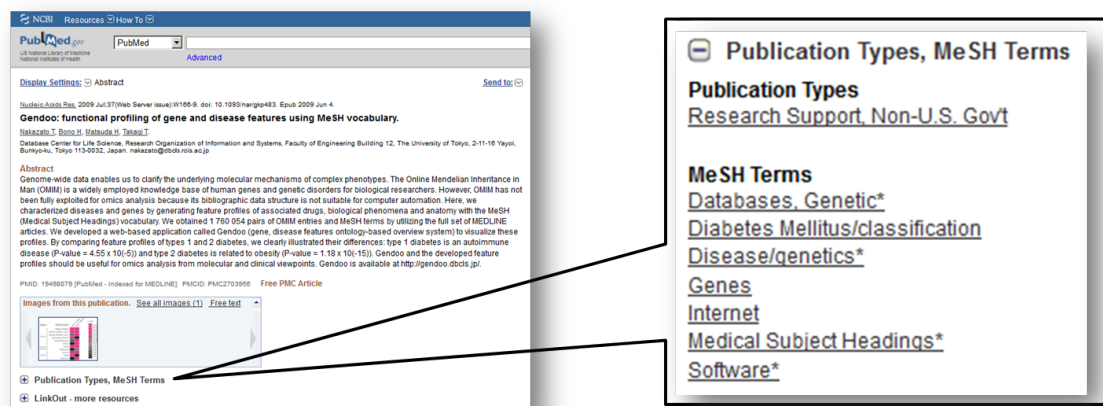


Figure 1: MeSH Term

biological terms. The amount of MeSH term is about twice as large as that of GO (Gene Ontology)[2] and its categories are also wider. MeSH in 2014 proposed its 19 categories and *MeSH.db* provides 16 of them, which are actually assigned to some MeSH terms. Each category is expressed as single capital alphabet as abbreviation defined by NLM. Therefore MeSH is an expected to be much detailed and exhaustive gene annotation tool. Some software or databases using MeSH are now proposed [3, 4, 5, 6].

This vignette introduces R/Bioconductor packages for handling MeSH in R. Original MeSH data is accessible by NLM FTP site (<http://www.nlm.nih.gov/mesh/filelist.html>). The data are downloadable as plain-text format (ASCII MeSH; d2014.bin / q2014.bin). These files were pre-processed by our data-processing pipeline (figure 2) and corresponding information is summarized as a table in SQLite3 file and packed into *MeSH.db*, *MeSH.AOR.db*, and *MeSH.PCR.db*.

Abbreviation	Category
A	Anatomy
B	Organisms
C	Diseases
D	Chemicals and Drugs
E	Analytical, Diagnostic and Therapeutic Techniques and Equipment
F	Psychiatry and Psychology
G	Phenomena and Processes
H	Disciplines and Occupations
I	Anthropology, Education, Sociology and Social Phenomena
J	Technology and Food and Beverages
K	Humanities
L	Information Science
M	Persons
N	Health Care
V	Publication Type
Z	Geographical Locations

MeSH.db provides the corresponding table which contains MeSH ID, MeSH term, MeSH category, synonym, qualifier ID, and qualifier term. Qualifier term means more rough annotation (subheadings) than MeSH. MeSH has hierarchical structure like GO. Such structure is provided as *MeSH.AOR.db* (AOR: ancestor-offspring Relationships) and *MeSH.PCR.db* (PCR: parent-child Relationships as corresponding table).

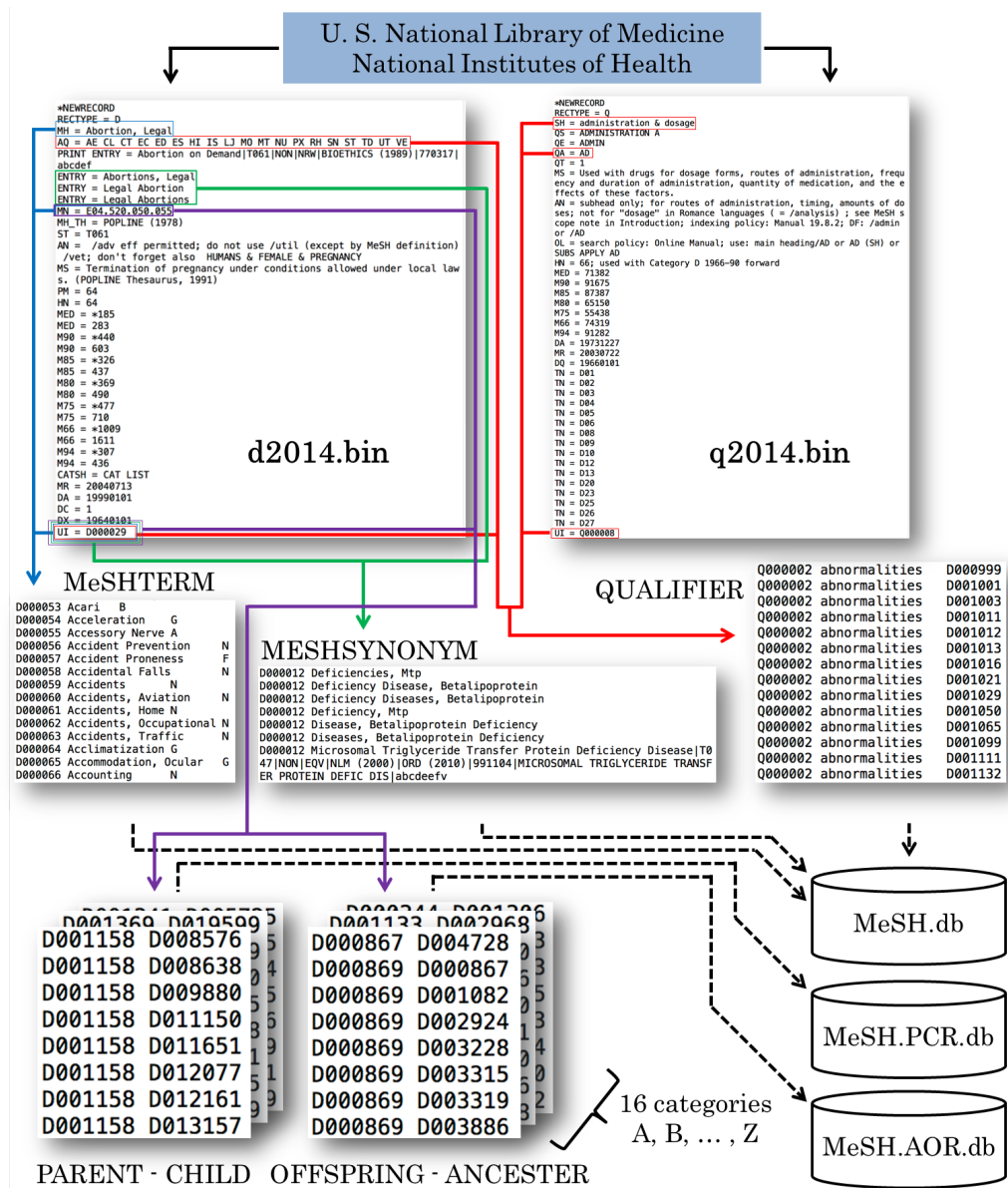


Figure 2: Data pre-process for MeSH.db

1.2 The correspondence between MeSH ID and NCBI Entrez Gene ID

MeSH.XXX.eg.db (XXX is an abbreviation of species name such as Hsa: Homo sapiens) packages provide the correspondence between Entrez Gene IDs and NLM MeSH IDs. Such correspondence in wide variety of organisms are summarized as each MeSH.XXX.eg.db by three way of methods, Gendoo[4], gene2pubmed, and RBBH (reciprocal BLAST best Hit).

Gendoo is the web-application based on text-mining of PubMed. Co-occurrence relations in PubMed document are exhaustively retrieved and much relevant correspondence are filtered by some information science techniques.

gene2pubmed is the correspondence between Entrez Gene IDs and NLM PubMed IDs. These relationship is manually assigned by NCBI curator teams. We also summarized the relationship between MeSH Terms and PubMed IDs from licensed-PubMed, then merged as Gene IDs - MeSH IDs correspondence.

For some minor species including non-model organisms, which have no sufficient databases for annotation, we defined 15 well-annotated organisms and 100 minor-organisms, then conducted RBBH between all possible combinations using BLASTP search.

Method	Way of corresponding Entrez Gene IDs and MeSH IDs
Gendoo	Text-mining
gene2pubmed	Manual curation by NCBI teams
RBBH	sequence homology with BLASTP search (E-value $< 10^{-50}$)

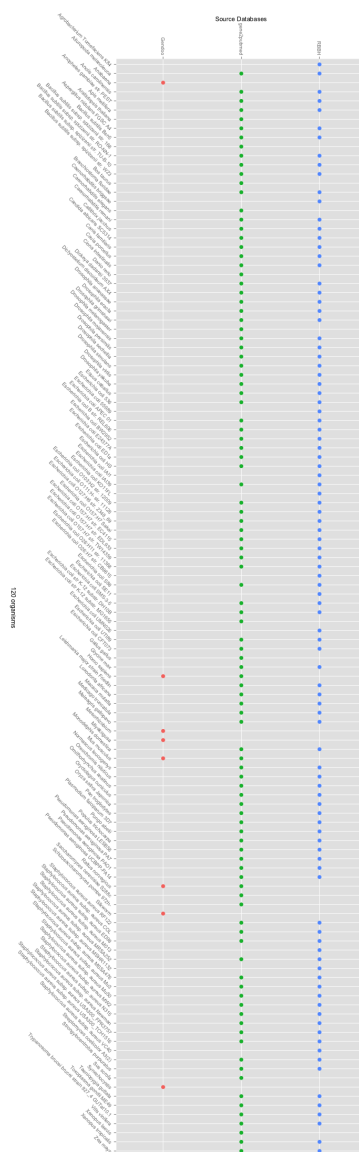


Figure 3: 120 organisms for MeSH.XXX.eg.db and those source databases

1.3 Database interface package for MeSH-related packages

We also implemented a database interface (DBI) package named *MeSHDbi*. This package is important because of two reasons. First reason is a unification of DBI functions for MeSH-related packages. *MeSH.db*, *MeSH.AOR.db*, *MeSH.PCR.db*, and *MeSH.XXX.db* packages inherit the *MeSHDbi*-class defined by *MeSHDbi* and behavior of these packages is uniformly designed. Second reason is supporting construction of user's original *MeSH.XXX.db* package. Due to the rapid development of DNA sequence technology, wide variety of genome sequences are more and more determined and the correspondence of Gene IDs and MeSH IDs may be designed by many databases [3, 4, 5, 6]. Therefore, we prepared the function to create *MeSH.XXX.db* package for a situation in which users can retrieved the relationship between Gene IDs and MeSH IDs by some means.

1.4 MeSH term enrichment analysis

To analyze MeSH-related packages with omics data, we implement *meshr* package, which is for conducting enrichment analysis using MeSH data. This package internally imports *MeSH.db*, *MeSH.AOR.db*, *MeSH.PCR.db* and *MeSH.XXX.db*, then conducts enrichment analysis to detect highly enriched MeSH terms in gene sets of interesting species.

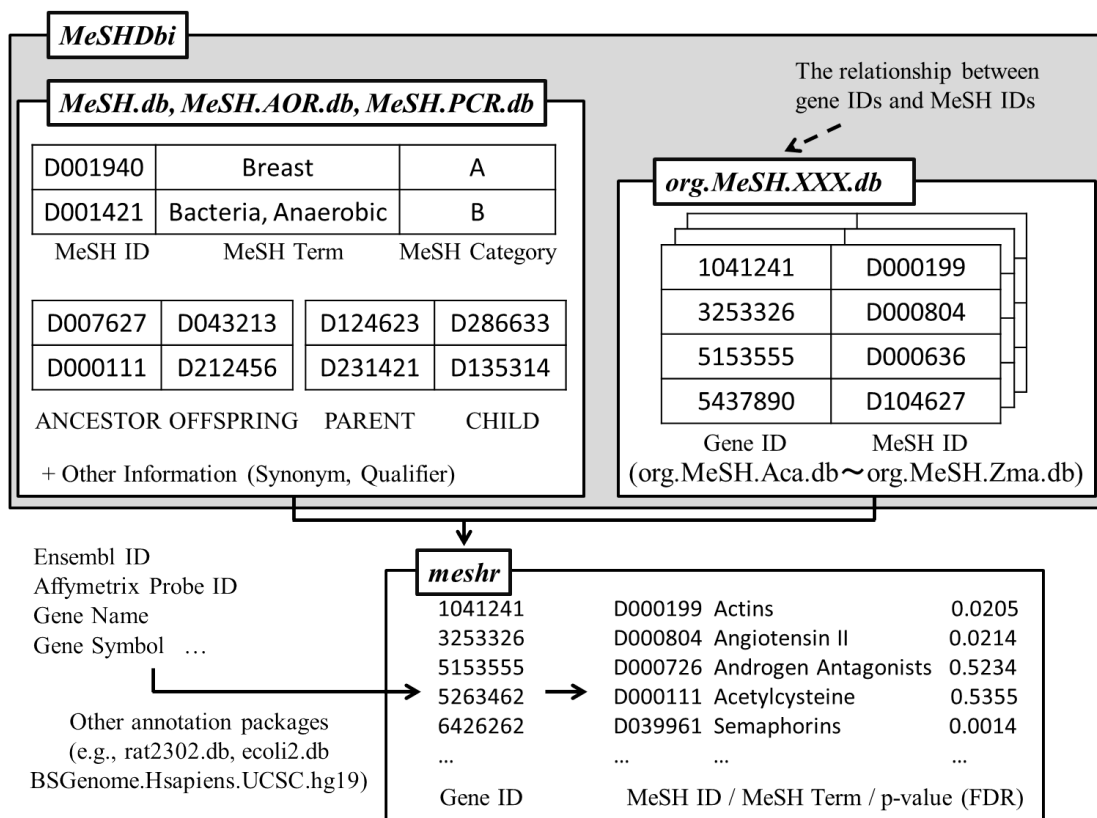


Figure 4: The relationship of meshr and other MeSH-related packages

2 Exercise

2.1 Access MeSH Term

2.1.1 columns, keytypes, keys, and select

In our packages, all data are extracted by only 4 functions defined by *AnnotationDbi*; **keytypes**, **columns**, **keys** and **select**. In this section, we demonstrate how to use these functions by using *MeSH.db*.

At first, install and load the *MeSH.db*.

```
> library(MeSH.db)
```

`ls` function shows all objects in this package. *MeSH.db* object is generated. This is also package's name and all MeSH-related packages provide the object named as package name (e.g., *MeSH.db*, *MeSH.Mmu.eg.db*).

```
> ls("package:MeSH.db")
```

```
[1] "MeSH.db"
```

```
> MeSH.db
```

```
[1] "##### class ####"
```

```
[1] "MeSHDb"
```

```
attr(,"package")
```

```
[1] "MeSHDbi"
```

```
[1] "##### connection ####"
```

```
<SQLiteConnection>
```

```
[1] "##### package name ####"
```

```
[1] "MeSH.db"
```

Here, we use **columns**, **keytypes**, **keys** and **select** against *MeSH.db*.

columns returns the rows which we can retrieve in *MeSH.db*.

```
> columns(MeSH.db)
```

```
[1] "MESHID"      "MESHTERM"    "CATEGORY"    "SYNONYM"     "QUALIFIERID"
```

```
[6] "QUALIFIER"
```

keytypes returns the rows which can be used as the optional parameter in **keys** and **select** functions against *MeSH.db*.

```
> keytypes(MeSH.db)
```

```
[1] "MESHID"      "MESHTERM"    "CATEGORY"    "SYNONYM"     "QUALIFIERID"
```

```
[6] "QUALIFIER"
```


keys function returns the value of keytype.

```
> k <- keys(MeSH.db, keytype = "MESHID")
> length(k)
```

```
[1] 27149
```

```
> head(k)
```

```
[1] "D000001" "D000002" "D000003" "D000004" "D000005" "D000006"
```

select function returns rows in particular columns, which are having user-specified keys. This function provides the data as a dataframe. Now, we will retrieve the rows in which MESHID is equivalent to MESHTERM.

```
> select(MeSH.db, keys = k[1:10], columns = c("MESHID", "MESHTERM"),
+       keytype = "MESHID")
```

	MESHID	MESHTERM
1	D000001	Calcimycin
141	D000002	Temefos
219	D000003	Abattoirs
246	D000004	Abbreviations as Topic
255	D000005	Abdomen
271	D000006	Abdomen, Acute
382	D000007	Abdominal Injuries
493	D000008	Abdominal Neoplasms
619	D000009	Abdominal Muscles
700	D000010	Abducens Nerve

2.1.2 Annotation of *Leukemia*

Next, we will retrieve some information about *Leukemia* by our packages.

select function retrieves rows in which MESHTERM is "*Leukemia*" in the MeSH.db table.

```
> LEU <- select(MeSH.db, keys = "Leukemia", columns = c("MESHID",  
+ "MESHTERM", "CATEGORY", "SYNONYM"), keytype = "MESHTERM")  
> LEU
```

	MESHID	MESHTERM	CATEGORY
1	D007938	Leukemia	C
38	D007938	Leukemia	C
75	D007938	Leukemia	C
112	D007938	Leukemia	C
149	D007938	Leukemia	C

	SYNONYM
1	Leucocythaemias
38	Leucocythaemia T191 NON EQV NLM (2012) 110224 abcdef
75	Leucocythemias
112	Leucocythemia T191 NON EQV NLM (2012) 110224 abcdef
149	Leukemias

select function shows that MESHID of *Leukemia* is D007938 and *Leukemia* is categorized as C (Diseases). *Leukemia* has some synonyms like *Leucocythaemias*, *Leucocythaemia*, *Leucocythemias* and *Leukemias*.

As mentioned above, MeSH has hierarchical structures. *MeSH.AOR.db* and *MeSH.PCR.db* packages provide such hierarchical information of MeSH. For example, *MeSH.AOR.db* enable us to examine the top terms of *Leukemia*.

```
> library("MeSH.AOR.db")  
> ANC <- select(MeSH.AOR.db, keys = "D007938", columns = c("ANCESTOR",  
+ "OFFSPRING"), keytype = "OFFSPRING")  
> ANC
```

	ANCESTOR	OFFSPRING
1	D009370	D007938

D009370 has found above *Leukemia*.

These MeSH IDs can be translated to MeSH Term.

```
> select(MeSH.db, keys = ANC[1, 1], columns = c("MESHTERM"), keytype = "MESHID")  
  
MESHTERM  
1 Neoplasms by Histologic Type
```

In this way, we can specify that *Leukemia* is categorized as one of *NeoplasmsbyHistologicType*.

Once keytype-parameter set to opposite direction (OFFSPRING to ANCESTOR), other MeSH IDs in lower hierarchies also can be retrieved.

```
> OFF <- select(MeSH.AOR.db, keys = "D007938", columns = c("ANCESTOR",
+ "OFFSPRING"), keytype = "ANCESTOR")
> OFF
```

	ANCESTOR	OFFSPRING
1	D007938	D007942
2	D007938	D007943
3	D007938	D007945
4	D007938	D007946
5	D007938	D007951
6	D007938	D007952
7	D007938	D007953
8	D007938	D016582
9	D007938	D016583

```
> select(MeSH.db, keys = OFF[, 2], columns = c("MESHTERM"), keytype = "MESHID")
```

	MESHTERM
1	Leukemia, Experimental
505	Leukemia, Hairy Cell
764	Leukemia, Lymphoid
1023	Leukemia, Mast-Cell
1208	Leukemia, Myeloid
2022	Leukemia, Plasma Cell
2281	Leukemia, Radiation-Induced
2466	Leukemia, Feline
2571	Enzootic Bovine Leukosis

There are a lot of MeSH terms, which means *Leukemia* has many lower hierarchies.

MeSH.PCR.db provides the directly lower (or upper) terms.

```
> library("MeSH.PCR.db")
> CHI <- select(MeSH.PCR.db, keys = LEU[1, 1], columns = c("PARENT",
+ "CHILD"), keytype = "PARENT")
> head(CHI)
```

	PARENT	CHILD
1	D007938	D001353
2	D007938	D001752
3	D007938	D004915
4	D007938	D007939
5	D007938	D007940
6	D007938	D007941

```
> head(select(MeSH.db, keys = CHI[, 2], columns = c("MESHTERM"),
+           keytype = "MESHID"))
```

	MESHTERM
1	Avian Leukosis
106	Blast Crisis
365	Leukemia, Erythroblastic, Acute
1068	Leukemia L1210
1176	Leukemia L5178
1284	Leukemia P388

Leukemia has a lot of subtypes like *AvianLeukosis*, *BlastCrisis*, *Leukemia*, *Erythroblastic*, *Acute* and so on.

2.1.3 Other functions

Some optional functions for much complex data acquisition are also provided. In this section, users may need some basic *SQL* knowledge (see also *RSQLite*).

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 constructed by *RSQLite*.

```
> dbInfo(MeSH.db)
```

	NAME	VALUE
1	SOURCEDATE	19-Nov-2013
2	SOURCENAME	Medical Subject Headings
3	SOURCEURL	http://www.nlm.nih.gov/mesh/filelist.html
4	DBSCHEMA	MeSH.db
5	DBSCHEMAVERSION	1.0
6	MESHVERSION	2014
7	package	MeSH.db
8	Db type	MeSH.Db

```
> dbfile(MeSH.db)
```

```
[1] "/Library/Frameworks/R.framework/Versions/3.1/Resources/library/MeSH.db/extdata/MeSH.db"
```

```
> dbschema(MeSH.db)
```

```
[1] "CREATE TABLE DATA (\n  MESHID CHAR(7) NOT NULL,\n  MESHTERM VARCHAR(100) NOT NULL,\n  CATEGORY VARCHAR(100) NOT NULL,\n  SYNONYM VARCHAR(100) NOT NULL,\n  QUALIFIERID VARCHAR(100) NOT NULL,\n  QUALIFIER VARCHAR(100) NOT NULL)\n[2] "CREATE TABLE METADATA (\n  NAME VARCHAR(80),\n  VALUE VARCHAR(255)\n)"
```

```
> dbconn(MeSH.db)
```

```
<SQLiteConnection>
```

dbschema shows the data is stored as a table named "DATA" in the sqlite database and the table has six columns; MESHID, MESHTERM, CATEGORY, SYNONYM, QUALIFIERID, and QUALIFIER. Therefore, we can retrieve data by much complex SQL query like below;

```
> library("RSQLite")
```

```
> SQL1 <- paste("SELECT MESHTERM, QUALIFIERID, QUALIFIER FROM DATA",  
+ "WHERE MESHID = 'D000001'", "AND QUALIFIERID = 'Q000494'")
```

```
> dbGetQuery(dbconn(MeSH.db), SQL1)
```

	MESHTERM	QUALIFIERID	QUALIFIER
1	Calcimycin	Q000494	pharmacology
2	Calcimycin	Q000494	pharmacology
3	Calcimycin	Q000494	pharmacology
4	Calcimycin	Q000494	pharmacology
5	Calcimycin	Q000494	pharmacology

```
> SQL2 <- paste("SELECT ANCESTOR, OFFSPRING FROM DATA", "WHERE OFFSPRING = 'D000002'",
+ "OR OFFSPRING = 'D000003'", "OR OFFSPRING = 'D000004'", "OR ANCESTOR = 'D009275'")
> dbGetQuery(dbconn(MeSH.AOR.db), SQL2)
```

	ANCESTOR	OFFSPRING
1	D063086	D000002
2	D008462	D000003
3	D009275	D000004
4	D009275	D000851
5	D009275	D004850

```
> SQL3 <- paste("SELECT PARENT, CHILD FROM DATA", "WHERE PARENT = 'D000005'",
+ "AND NOT CHILD = 'D004312'")
> dbGetQuery(dbconn(MeSH.PCR.db), SQL3)
```

	PARENT	CHILD
1	D000005	D006119
2	D000005	D007264
3	D000005	D008643
4	D000005	D008646
5	D000005	D009852
6	D000005	D010529
7	D000005	D010537
8	D000005	D012187
9	D000005	D014472
10	D000005	D034841
11	D000005	D034861
12	D000005	D054048

2.2 MeSH.XXX.eg.db-type packages

2.2.1 Annotation of 120 organisms

As well as *MeSH.db*, *MeSH.AOR.db*, and *MeSH.PCR.db*, *MeSH.XXX.eg.db*-type packages also use 4 functions (**keytypes**, **columns**, **keys** and **select**) to extract data.

```
> library("MeSH.Hsa.eg.db")
> columns(MeSH.Hsa.eg.db)

[1] "GENEID"          "MESHID"          "MESHCATEGORY" "SOURCEID"        "SOURCEDB"

> keytypes(MeSH.Hsa.eg.db)

[1] "GENEID"          "MESHID"          "MESHCATEGORY" "SOURCEID"        "SOURCEDB"

> key_HSA <- keys(MeSH.Hsa.eg.db, keytype = "MESHID")
> select(MeSH.db, keys = key_HSA[1:10], columns = c("MESHID", "MESHTERM"),
+        keytype = "MESHID")

      MESHID          MESHTERM
1    D000001      Calcimycin
141  D000002        Temefos
219  D000005        Abdomen
235  D000006      Abdomen, Acute
346  D000007      Abdominal Injuries
457  D000008      Abdominal Neoplasms
583  D000009      Abdominal Muscles
664  D000010      Abducens Nerve
1139 D000011 Abelson murine leukemia virus
1178 D000012      Abetalipoproteinemia
```

Moreover, these packages have other additional functions like **species**, **nomenclature**, **listDatabases**. In each *MeSH.XXX.eg.db*, **species** function returns the common name and **nomenclature** returns the scientific name.

```
> library("MeSH.Aca.eg.db")
> library("MeSH.Atu.K84.eg.db")
> library("MeSH.Bsu.168.eg.db")
> library("MeSH.Syn.eg.db")
> species(MeSH.Hsa.eg.db)

[1] "Human"

> species(MeSH.Aca.eg.db)

[1] "Lizard"

> species(MeSH.Atu.K84.eg.db)
```

```

[1] NA

> species(MeSH.Bsu.168.eg.db)

[1] NA

> species(MeSH.Syn.eg.db)

[1] "Cyanobacteria"

> nomenclature(MeSH.Hsa.eg.db)

[1] "Homo sapiens"

> nomenclature(MeSH.Aca.eg.db)

[1] "Anolis carolinensis"

> nomenclature(MeSH.Atu.K84.eg.db)

[1] "Agrobacterium Tumefaciens K84"

> nomenclature(MeSH.Bsu.168.eg.db)

[1] "Bacillus subtilis subsp. spizizenii str. 168"

> nomenclature(MeSH.Syn.eg.db)

[1] "Synechocystis"

```

listDatabases function returns the source of data (figure 3). In regard to RBBH, name of organisms is returned. These values are important when users specify the database for MeSH Term enrichment analysis (see the section 2.4).

```

> listDatabases(MeSH.Hsa.eg.db)

      SOURCEDB
1      gendoo
2 gene2pubmed

> listDatabases(MeSH.Aca.eg.db)

      SOURCEDB
1      Arabidopsis thaliana
2 Bacillus subtilis subsp. spizizenii str. 168
3      Bos taurus
4      Danio rerio
5      Drosophila melanogaster
6      Escherichia coli str K-12 substr. MG1655

```



```

7          Gallus gallus
8          Homo sapiens
9          Mus musculus
10         Rattus norvegicus
11         Saccharomyces cerevisiae S288c
12         Schizosaccharomyces pombe 972h-
13         Sus scrofa
14         Xenopus laevis
15         gene2pubmed

```

```
> listDatabases(MeSH.Atu.K84.eg.db)
```

```

          SOURCEDB
1          Arabidopsis thaliana
2 Bacillus subtilis subsp. spizizenii str. 168
3          Bos taurus
4          Caenorhabditis elegans
5          Danio rerio
6          Drosophila melanogaster
7 Escherichia coli str K-12 substr. MG1655
8          Gallus gallus
9          Homo sapiens
10         Mus musculus
11         Rattus norvegicus
12         Saccharomyces cerevisiae S288c
13         Schizosaccharomyces pombe 972h-
14         Sus scrofa
15         Xenopus laevis

```

```
> listDatabases(MeSH.Bsu.168.eg.db)
```

```

          SOURCEDB
1 gene2pubmed

```

```
> listDatabases(MeSH.Syn.eg.db)
```

```

          SOURCEDB
1 gendoo

```

2.3 MeSHDbi

2.3.1 User's custom MeSH.XXX.eg.db package

Although most of users may not be conscious of this package, *MeSHDbi* is important for our MeSH packages. This package regulates class definition of MeSH object (MeSHDb-class). Besides, this package constructs user's original *MeSH.XXX.eg.db* package. **makeGeneMeSHPackage** easily constructs such package.

```
> library("MeSHDbi")
> example("makeGeneMeSHPackage")
```

```
mGMSHP> ## makeGeneMeSHPackage enable users to construct
mGMSHP> ## user's own custom MeSH package
mGMSHP>
mGMSHP> ## this is test data which means the relationship between
mGMSHP> ## Entrez gene IDs of Pseudomonas aeruginosa PA01
mGMSHP> ## and its MeSH IDs.
mGMSHP> data(PA01)
```

```
mGMSHP> head(PA01)
  GENEID MESHID MESHCATEGORY SOURCEID
1 877657 D000265           D    937805
2 877657 D000265           D    937805
3 877657 D001412           B    937805
4 877657 D001412           B    937805
5 877657 D001426           D    937805
6 877657 D001483           G    937805

                                SOURCEDB
1 Bacillus subtilis subsp. spizizenii str. 168
2 Bacillus subtilis subsp. spizizenii str. 168
3 Bacillus subtilis subsp. spizizenii str. 168
4 Bacillus subtilis subsp. spizizenii str. 168
5 Bacillus subtilis subsp. spizizenii str. 168
6 Bacillus subtilis subsp. spizizenii str. 168
```

```
mGMSHP> # We are also needed to prepare meta data as follows.
mGMSHP> data(metaPA01)
```

```
mGMSHP> metaPA01
      NAME                                     VALUE
1  SOURCEDATE                               31-July-2013
2  SOURCENAME                               BLASTP
3  SOURCEURL ftp://ftp.ncbi.nlm.nih.gov/gene/DATA/
4  DBSCHEMA                                org.Pae.PA01.MeSH.db
5  DBSCHEMAVERSION                          1.0
6  ORGANISM                                Pseudomonas aeruginosa PA01
```

```

7      SPECIES
8      package           AnnotationDbi
9      Db type           BLASTDb

mGMSHP> ## sets up a temporary directory for this example
mGMSHP> ## (users won't need to do this step)
mGMSHP> destination <- tempfile()

mGMSHP> dir.create(destination)

mGMSHP> ## makes an Organism package for human called Homo.sapiens
mGMSHP> makeGeneMeSHPackage(pkgname = "org.MeSH.Pae.db",
mGMSHP+                               data = PA01,
mGMSHP+       metadata = metaPA01,
mGMSHP+                               organism = "Pseudomonas aeruginosa PA01",
mGMSHP+                               version = "1.0.0",
mGMSHP+                               maintainer = "Koki Tsuyuzaki <k.t.the-answer",
mGMSHP+                               author = "Koki Tsuyuzaki",
mGMSHP+                               destDir = destination,
mGMSHP+                               license="Artistic-2.0")
Creating package in /var/folders/k0/tk8gl4bj2_v2mbjx80ydszwn0000gn/T//RtmpdX6i1k/file5ece361
[1] TRUE

```

2.4 meshr

2.4.1 MeSH enrichment analysis

The *meshr* package is designed to conduct an enrichment analysis for MeSH. The idea behind this package is analogous to GO enrichment analysis, where sets of genes is analyzed to extract common annotated biological properties. The usage of *meshr* closely follows that of the Bioconductor *GStats* package. Thus, users who are familiar with *GStats* may easily handle *meshr*.

The *meshr* package accepts selected and universal genes as input, and returns significantly overrepresented MeSH terms. It is used in conjunction with *MeSH.db* package and one of the annotation packages, (e.g., *MeSH.Hsa.eg.db*). This section serves as a quick guide to the *meshr*, while illustrating entire process to perform a MeSH enrichment analysis.

Here, we use the example data set taken from the Bioconductor package *cummeRbund*. The example data are located in `library/cummeRbund/extdata/`. This RNA-Seq data were taken from three samples, "iPS", "hESC", and "Fibroblasts". We first created two objects of gene sets, i.e., selected and universal genes, by comparing significantly regulated genes between iPS and hESC under the significance level of 0.05, then mapped the Gene Symbols to Entrez Gene IDs through the *org.Hs.eg.db* package. Pre-processed Gene IDs are easily accessible by **data** function.

```
> library("meshr")
> data(geneid.cummeRbund)
> data(sig.geneid.cummeRbund)
```

Finally 303 universal genes and 104 selected genes are detected and subsequently used for the MeSH enrichment analysis.

```
> dim(geneid.cummeRbund)[1]
[1] 303
> dim(sig.geneid.cummeRbund)[1]
[1] 104
```

We proceed to uncover a characteristic of MeSH terms that the set of identified genes share each other via the *meshr* package. We first load the required packages.

```
> library("fdrtool")
> library("MeSH.Hsa.eg.db")
```

We create a parameter instance by specifying the objects of selected and universal genes, the name of the annotation package, the category of MeSH, the database of correspondence between Gene IDs and MeSH IDs (see also **listDatabases** in the section 2.2.1), *p*-value cutoff, and the choice of a multiple-testing correction method. In this first example, we use *MeSH.Hsa.eg.db* because the above RNA-seq data is extracted from human cells. We choose C (Diseases) category, gendoo database, *p*-value cutoff 0.05, and no multiple-testing adjustment. For more details on description of all the arguments, readers are referred to the **MeSHHyperGParams-class** help page.

```
> meshParams <- new("MeSHHyperGParams", geneIds = sig.geneid.cummeRbund[,
+   2], universeGeneIds = geneid.cummeRbund[, 2], annotation = "MeSH.Hsa.eg.db",
+   category = "C", database = "gendoo", pvalueCutoff = 0.05,
+   pAdjust = "none")
```

The **meshHyperGTest** function carries out a hypergeometric test and returns an instance of class **MeSHHyperGResult**.

```
> meshR <- meshHyperGTest(meshParams)
```

Simply typing the **MeSHHyperGResult** class gives a brief description of the analysis, including the choice of a MeSH category, the annotation data used, and a total number of identified overrepresented MeSH terms.

```
> meshR
```

Full details of the result is obtained by calling the **summary** function on the **MeSH-HyperGResult** instance. This presents significantly enriched MeSH ID, MeSH term, and their associated *p*-values.

```
> head(summary(meshR))
```

Switching to test another MeSH category and another database can be easily done. For example, to choose the category as G (Phenomena and Processes) and the database as gene2pubmed, we can do the following.

```
> category(meshParams) <- "G"
> database(meshParams) <- "gene2pubmed"
> meshR <- meshHyperGTest(meshParams)
> meshR
```

3 Setup

This vignette was built on:

```
> sessionInfo()
```

R version 3.1.1 (2014-07-10)

Platform: x86_64-apple-darwin13.4.0 (64-bit)

locale:

```
[1] ja_JP.UTF-8/ja_JP.UTF-8/ja_JP.UTF-8/C/ja_JP.UTF-8/ja_JP.UTF-8
```

attached base packages:

```
[1] grid      parallel stats      graphics grDevices utils      datasets
[8] methods   base
```

other attached packages:

```
[1] meshr_1.2.3          org.Hs.eg.db_2.14.0      cummeRbund_2.6.1
[4] Gviz_1.8.4           rtracklayer_1.24.2      GenomicRanges_1.16.4
[7] IRanges_1.22.10     fastcluster_1.1.15      reshape2_1.4.1
[10] ggplot2_1.0.0        Category_2.30.0         GO.db_2.14.0
[13] Matrix_1.1-4         AnnotationDbi_1.26.1     GenomeInfoDb_1.0.2
[16] Biobase_2.24.0       BiocGenerics_0.10.0     fdrtool_1.2.13
[19] MeSH.Syn.eg.db_1.2.1 MeSH.Bsu.168.eg.db_1.2.1 MeSH.Atu.K84.eg.db_1.2.1
[22] MeSH.Aca.eg.db_1.2.1 MeSH.Hsa.eg.db_1.2.1    RSQLite_1.0.0
[25] DBI_0.3.1            MeSH.PCR.db_1.0.0       MeSH.AOR.db_1.0.0
[28] MeSH.db_1.2.0        MeSHDbi_1.0.2
```

loaded via a namespace (and not attached):

```
[1] acepack_1.3-3.3      annotate_1.42.1          base64enc_0.1-2
[4] BatchJobs_1.5        BBmisc_1.8             BiocParallel_0.6.1
[7] biomaRt_2.20.0       Biostrings_2.32.1      biovizBase_1.12.3
[10] bitops_1.0-6         brew_1.0-6             BSgenome_1.32.0
[13] checkmate_1.5.1     cluster_1.15.2         codetools_0.2-9
[16] colorspace_1.2-4     dichromat_2.0-0        digest_0.6.8
[19] fail_1.2             foreach_1.4.2          foreign_0.8-62
[22] Formula_1.1-2       genefilter_1.46.1      GenomicAlignments_1.0.6
[25] GenomicFeatures_1.16.3 graph_1.42.0           GSEABase_1.26.0
[28] gtable_0.1.2        Hmisc_3.14-5           iterators_1.0.7
[31] lattice_0.20-29     latticeExtra_0.6-26    MASS_7.3-37
[34] matrixStats_0.12.2  munsell_0.4.2          nnet_7.3-8
[37] plyr_1.8.1          proto_0.3-10           R.methodsS3_1.6.1
[40] RBGL_1.40.1         RColorBrewer_1.1-2     Rcpp_0.11.3
[43] RCurl_1.95-4.5      rpart_4.1-8            Rsamtools_1.16.1
[46] scales_0.2.4        sendmailR_1.2-1        splines_3.1.1
[49] stats4_3.1.1        stringr_0.6.2          survival_2.37-7
```

[52]	tools_3.1.1	VariantAnnotation_1.10.5	XML_3.98-1.1
[55]	xtable_1.7-4	XVector_0.4.0	zlibbioc_1.10.0

References

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