

How to use the MeSH.db Package

Koki Tsuyuzaki¹, Itoshi Nikaido², and Gota Morota³.

September 24, 2013

¹Department of Medical and Life Science, Tokyo University of Science.

²Bioinformatics Research Unit, RIKEN Advanced Center for Computing and Communication.

³Department of Animal Sciences, University of Wisconsin-Madison.

`k.t.the-answer@hotmail.co.jp`

Contents

1	Introduction	2
2	Getting started	4
3	Methods	4
4	Data	4
5	Examples	8
5.1	Exercises in columns, keytypes, keys and select	8
5.2	Annotation of <i>Leukemia</i>	10
6	Setup	14

1 Introduction

This document provides the way to use *MeSH.db* package. MeSH (Medical Subject Headings) is the NLM controlled vocabulary used to manually index articles for MEDLINE/Pubmed [1].

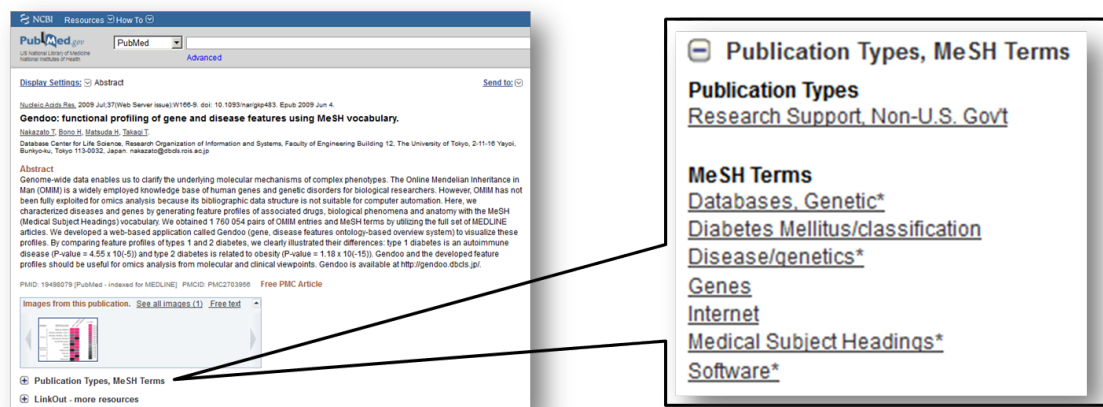


Figure 1: MeSH Term

The amount of vocabulary in MeSH is about twice as large as that of GO (Gene Ontology)[2] and its category is also wider. Therefore MeSH is expected to be much detailed and exhaustive gene annotation tool. Some softwares or databases using MeSH are now proposed [3, 4, 5, 6].

MeSH.db is a free R package for handling MeSH in R. Its data are retrieved from NLM ftp site (<http://www.nlm.nih.gov/mesh/filelist.html>). MeSH in 2013 has 19 hierarchies and *MeSH.db* provides 16 of them, which are actually assigned to some MeSH Terms. Each category is expressed as single capital alphabet defined by NLM as abbreviations.

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 has hierarchical structures like GO. *MeSH.db* provides its Ancestor-Offspring Relationships (AOR) and Parent-Child Relationships (PCR) as corresponding table (dataframe). Data of PCR and AOR are also used for calculating the conditional probability in enrichment analysis (*meshr* package).

2 Getting started

To load the *MeSH.db* package, just type `library(MeSH.db)`. 5 methods and 36 data are provided by *MeSH.db*.

3 Methods

Following 5 methods are provided by *MeSH.db*.

MeSH	Function for retrieval of the summary of all object in MeSH.db
MeSH_dbconn	Function for retrieval of the connection of .sqlite database
MeSH_dbfile	Function for retrieval of the directory of .sqlite file
MeSH_dbschema	Function for retrieval of the schema of .sqlite database
MeSH_dbInfo	Function for retrieval of the information of .sqlite database

4 Data

Following 36 data are provided by *MeSH.db*.

MeSHMAPCOUNTS	The number of row of all data
MeSHTERM	MeSH Term
MeSHSYNONYM	The synonym of MeSH Term
MeSHQUALIFIER	Substantial Information of MeSH Term
MeSHAAOR	Ancestor-Offspring Relationships in A category
MeSHBAOR	Ancestor-Offspring Relationships in B category
MeSHCAOR	Ancestor-Offspring Relationships in C category
MeSHDAOR	Ancestor-Offspring Relationships in D category
MeSHEAOR	Ancestor-Offspring Relationships in E category
MeSHFAOR	Ancestor-Offspring Relationships in F category
MeSHGAOR	Ancestor-Offspring Relationships in G category
MeSHHAOR	Ancestor-Offspring Relationships in H category
MeSHIAOR	Ancestor-Offspring Relationships in I category
MeSHJAOR	Ancestor-Offspring Relationships in J category
MeSHKAOR	Ancestor-Offspring Relationships in K category
MeSHLAOR	Ancestor-Offspring Relationships in L category
MeSHMAOR	Ancestor-Offspring Relationships in M category
MeSHNAOR	Ancestor-Offspring Relationships in N category
MeSHVAOR	Ancestor-Offspring Relationships in V category
MeSHZAOR	Ancestor-Offspring Relationships in Z category
MeSHAPCR	Parent-Child Relationships in A category
MeSHBPCR	Parent-Child Relationships in B category
MeSHCPCR	Parent-Child Relationships in C category
MeSHDPCR	Parent-Child Relationships in D category
MeSHEPCR	Parent-Child Relationships in E category
MeSHFPCR	Parent-Child Relationships in F category
MeSHGPCR	Parent-Child Relationships in G category
MeSHHPCR	Parent-Child Relationships in H category
MeSHIPCR	Parent-Child Relationships in I category
MeSHJPCR	Parent-Child Relationships in J category
MeSHKPCR	Parent-Child Relationships in K category
MeSHLPCR	Parent-Child Relationships in L category
MeSHMPCR	Parent-Child Relationships in M category
MeSHNPCR	Parent-Child Relationships in N category
MeSHVPCR	Parent-Child Relationships in V category
MeSHZPCR	Parent-Child Relationships in Z category

In *MeSH.db*, all data are extracted by 4 functions defined by *AnnotationForge*; **keytypes**, **columns**, **keys** and **select**. **keys** function has 1 parameter (keytype) and **select** function also has 3 parameters (keys, columns and keytype). **columns** is the columns which you can retrieved by **select** and **keytype** is the columns which you can specify as the parameter in **keys** and **select** functions.

Object Name	columns	keytype
MeSHMAPCOUNTS	MAPNAME, COUNT	MAPNAME
MeSHTERM	MESHID, MESHTERM, CATEGORY	MESHID, MESHTERM, CATEGORY
MeSHSYNONYM	MESHID, MESHSYNONYM	MESHID
MeSHQUALIFIER	QUALIFIERID, SUBHEADING, MESHID	QUALIFIERID, MESHID
MeSHAAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHBAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHCAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHDAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHEAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHFAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHGAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHHAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHIAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHJAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHKAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHLAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID

MeSHMAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHNAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHVAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHZAOR	ANCESTERMESHID, OFFSPRINGMESHID	ANCESTERMESHID, OFFSPRINGMESHID
MeSHAPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHBPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHCPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHDPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHEPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHFPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHGPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHHPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHIPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHJPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHKPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHLPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHMPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHNPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHVPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID
MeSHZPCR	PARENTMESHID, CHILDMESHID	PARENTMESHID, CHILDMESHID

5 Examples

5.1 Exercises in columns, keytypes, keys and select

MeSH.db uses columns, keytypes, keys and select functions defined by *AnnotationForge*. In this section we will show you how to use these functions in *MeSH.db*.

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

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

ls shows all object in *MeSH.db*.

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

```
[1] "MeSH"           "MeSH_dbconn"   "MeSH_dbfile"   "MeSH_dbInfo"
[5] "MeSH_dbschema" "MeSHAAOR"      "MeSHAPCR"      "MeSHBAOR"
[9] "MeSHBPCR"       "MeSHCAOR"      "MeSHCPCR"      "MeSHDAOR"
[13] "MeSHDPCR"       "MeSHEAOR"      "MeSHEPCR"      "MeSHFAOR"
[17] "MeSHFPCR"       "MeSHGAOR"      "MeSHGPCR"      "MeSHHAOR"
[21] "MeSHHPCR"       "MeSHIAOR"      "MeSHIPCR"      "MeSHJAOR"
[25] "MeSHJPCR"       "MeSHKAOR"      "MeSHKPCR"      "MeSHLAOR"
[29] "MeSHLPCR"       "MeSHMAOR"      "MeSHMAPCOUNTS" "MeSHMPCR"
[33] "MeSHNAOR"       "MeSHNPCR"      "MeSHQUALIFIER" "MeSHSYNONYM"
[37] "MeSHTERM"       "MeSHVAOR"      "MeSHVPCR"      "MeSHZAOR"
[41] "MeSHZPCR"
```

Here we use columns, keytypes, keys and select against MeSHMAPCOUNTS.

columns returns the rows which you can retrieve in MeSHMAPCOUNTS.

```
> columns(MeSHMAPCOUNTS)
```

```
[1] "MAPNAME" "COUNT"
```

keytypes returns the rows which you can use as the optional parameter in keys and select functions against MeSHMAPCOUNTS.

```
> keytypes(MeSHMAPCOUNTS)
```

```
[1] "MAPNAME"
```

Here we will know that MAPNAME is available.

keys function specifies the value of keytype.

```
> k <- keys(MeSHMAPCOUNTS, keytype = "MAPNAME")
> head(k)
```

```
      MAPNAME
1      MeSHTERM
2      MeSHSYNONYM
3 MeSHQUALIFIER
4      MeSHAAOR
5      MeSHBAOR
6      MeSHCAOR
```

select method specifies the rows in particular columns having user-defined keys and retrieved data as single dataframe like SQL's SELECT statement. Now we retrieve the rows in which MAPNAME is equivalent to "MeSHTERM".

```
> select(MeSHMAPCOUNTS, keys = k[1, ], columns = c("MAPNAME", "COUNT"),
+       keytype = "MAPNAME")
```

```
      MAPNAME COUNT
1 MeSHTERM 28921
```

By the way, here we don't have to specify keytype as parameter against MeSHMAPCOUNTS, because MeSHMAPCOUNTS only has single column which is possible to be keytype and keytype is consequently specified.

```
> select(MeSHMAPCOUNTS, keys = k[1, ], columns = c("MAPNAME", "COUNT"))
```

```
      MAPNAME COUNT
1 MeSHTERM 28921
```

The same can be said of MeSHSYNONYM.

5.2 Annotation of *Leukemia*

Next we will annotate *Leukemia* by MeSH.

```
> columns(MeSHTERM)
```

```
[1] "MESHID"          "MESHTERM"        "MESHCATEGORY"
```

MESHID, MESHTERM and MESHCATEGORY can be retrieved from MeSHTERM.

```
> keytypes(MeSHTERM)
```

```
[1] "MESHID"          "MESHTERM"        "MESHCATEGORY"
```

All of them are available as a keytype's parameter.

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

```
> LEU <- select(MeSHTERM, keys = "Leukemia", columns = c("MESHID",  
+ "MESHTERM", "MESHCATEGORY"), keytype = "MESHTERM")  
> LEU
```

```
      MESHID MESHTERM MESHCATEGORY  
1 D007938 Leukemia           C
```

select function shows that MESHID of *Leukemia* is D007938 and *Leukemia* is in C (Diseases) category.

Using MeSHSYNONYM, we can also check whether *Leukemia* has some synonyms.

```
> select(MeSHSYNONYM, keys = LEU[1, 1], columns = c("MESHID", "MeSHSYNONYM"),  
+ keytype = "MESHTERM")
```

```
MESHID MeSHSYNONYM  
1 D007938 Leucocythaemias  
2 D007938 Leucocythaemia|T191|NON|EQV|NLM (2012)|110224|abcdef  
3 D007938 Leucocythemias  
4 D007938 Leucocythemia|T191|NON|EQV|NLM (2012)|110224|abcdef  
5 D007938 Leukemias
```

We will know that *Leukemia* has some synonyms like *Leucocythaemia*, *Leucocythaemias*, *Leucocythemias* and *Leukemias*.

MeSH also defines QUALIFIER, which is more rough category (SUBHEADING). We can also use select function against MeSHQUALIFIER.

```
> select(MeSHQUALIFIER, keys = LEU[1, 1], columns = c("QUALIFIERID",
+ "SUBHEADING", "MESHID"), keytype = "MESHID")
```

	QUALIFIERID	SUBHEADING	MESHID
1	Q000097	blood	D007938
2	Q000134	cerebrospinal fluid	D007938
3	Q000139	chemically induced	D007938
4	Q000145	classification	D007938
5	Q000150	complications	D007938
6	Q000151	congenital	D007938
7	Q000175	diagnosis	D007938
8	Q000178	diet therapy	D007938
9	Q000188	drug therapy	D007938
10	Q000191	economics	D007938
11	Q000196	embryology	D007938
12	Q000201	enzymology	D007938
13	Q000208	ethnology	D007938
14	Q000209	etiology	D007938
15	Q000235	genetics	D007938
16	Q000266	history	D007938
17	Q000276	immunology	D007938
18	Q000378	metabolism	D007938
19	Q000382	microbiology	D007938
20	Q000401	mortality	D007938
21	Q000451	nursing	D007938
22	Q000453	epidemiology	D007938
23	Q000469	parasitology	D007938
24	Q000473	pathology	D007938
25	Q000503	physiopathology	D007938
26	Q000517	prevention & control	D007938
27	Q000523	psychology	D007938
28	Q000530	radiography	D007938
29	Q000531	radionuclide imaging	D007938
30	Q000532	radiotherapy	D007938
31	Q000534	rehabilitation	D007938
32	Q000601	surgery	D007938
33	Q000628	therapy	D007938
34	Q000652	urine	D007938
35	Q000662	veterinary	D007938
36	Q000736	ultrasonography	D007938
37	Q000821	virology	D007938

As mentioned before, MeSH has hierarchical structures. AOR provides us upper (or lower) hierarchical MeSH Term. We already know *Leukemia* is categorized in C (Diseases), so MeSHCAOR is available.

```
> ANC <- select(MeSHCAOR, keys = LEU[1, 1], columns = c("ANCESTORMESHID",
+ "OFFSPRINGMESHID"), keytype = "OFFSPRINGMESHID")
> ANC
```

```
ANCESTORMESHID OFFSPRINGMESHID
1 D009370 D007938
```

There are D009370 above *Leukemia*.

We can translate these MeSH ID to MeSH Term.

```
> select(MeSHTERM, keys = ANC[, 1], columns = c("MESHTERM"), keytype = "MESHID")
```

```
MESHTERM
1 Neoplasms by Histologic Type
```

Once we set keytype to opposite direction (OFFSPRINGMESHID to ANCESTORMESHID), we can also retrieved MeSH ID of lower hierarchies.

```
> OFF <- select(MeSHCAOR, keys = LEU[1, 1], columns = c("ANCESTORMESHID",
+ "OFFSPRINGMESHID"), keytype = "ANCESTORMESHID")
> OFF
```

```
ANCESTORMESHID OFFSPRINGMESHID
1 D007938 D001353
2 D007938 D001752
3 D007938 D004915
4 D007938 D007939
5 D007938 D007940
6 D007938 D007941
7 D007938 D007942
8 D007938 D007943
9 D007938 D007945
10 D007938 D007946
11 D007938 D007947
12 D007938 D007948
13 D007938 D007951
14 D007938 D007952
15 D007938 D007953
16 D007938 D015448
17 D007938 D015451
18 D007938 D015452
19 D007938 D015456
20 D007938 D015458
21 D007938 D015459
22 D007938 D015461
23 D007938 D015463
```

24	D007938	D015464
25	D007938	D015465
26	D007938	D015466
27	D007938	D015470
28	D007938	D015471
29	D007938	D015472
30	D007938	D015473
31	D007938	D015477
32	D007938	D015479
33	D007938	D016582
34	D007938	D016583
35	D007938	D023981
36	D007938	D054066
37	D007938	D054198
38	D007938	D054218
39	D007938	D054403
40	D007938	D054429
41	D007938	D054438

There are a lot of MeSH ID, and it means *Leukemia* has many lower hierarchies.

PCR provides directly lower (or upper) hierarchy.

```
> CHI <- select(MeSHPCR, keys = LEU[1, 1], columns = c("PARENTMESHID",
+ "CHILDMESHID"), keytype = "PARENTMESHID")
> CHI
```

	PARENTMESHID	CHILDMESHID
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

We can also translate these MeSH ID to MeSH Term.

```
> select(MeSHTERM, keys = CHI[, 2], columns = c("MESHTERM"), keytype = "MESHID")
```

	MESHTERM
1	Leukemia, Experimental
3	Leukemia, Hairy Cell
4	Leukemia, Lymphoid
5	Leukemia, Mast-Cell

```

6           Leukemia, Myeloid
7           Leukemia, Plasma Cell
8 Leukemia, Radiation-Induced
9           Leukemia, Feline
10        Enzootic Bovine Leukosis

```

We will know *Leukemia* has a lot of subtypes like *Leukemia*, *Myeloid*, *Leukemia*, *PlasmaCell* and so on.

6 Setup

This vignette was built on:

```
> sessionInfo()
```

```

R Under development (unstable) (2013-08-27 r63742)
Platform: x86_64-apple-darwin10.8.0 (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] parallel stats      graphics  grDevices utils      datasets  methods
[8] base

```

```
other attached packages:
```

```

[1] MeSH.db_1.0           AnnotationForge_1.3.26 org.Hs.eg.db_2.9.0
[4] RSQLite_0.11.4        DBI_0.2-7             AnnotationDbi_1.23.23
[7] Biobase_2.21.7        BiocGenerics_0.7.5

```

```
loaded via a namespace (and not attached):
```

```
[1] IRanges_1.19.37 stats4_3.1.0    tools_3.1.0
```

References

- [1] S. J. Nelson and et al. The MeSH translation maintenance system: structure, interface design, and implementation. *Stud. Health Technol. Inform.*, 107: 67-69, 2004.
- [2] M. Ashburner and et al. Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nat. Genet.*, 25(1): 25-29, 2000.
- [3] T. Nakazato and et al. BioCompass: a novel functional inference tool that utilizes MeSH hierarchy to analyze groups of genes. *In Silico Biol.*, 8(1): 53-61, 2007.
- [4] T. Nakazato and et al. Nucleic Acids Res. *Gendoo: functional profiling of gene and disease features using MeSH vocabulary.*, 37: W166-W169, 2009.
- [5] D. J. Saurin and et al. GeneMeSH: a web-based microarray analysis tool for relating differentially expressed genes to MeSH terms. *BMC Bioinformatics*, 11: 166, 2010.
- [6] M. A. Sartor and et al. Metab2MeSH: annotating compounds with medical subject headings. *Bioinformatics*, 28(10): 1408-1410, 2012.