1 Introduction

1.0.1 General remarks

AnnotationDbi is used primarily to create maps that allow easy access from R to underlying annotation databases. AnnotationDbi introduces a new future for the Bioconductor annotation data packages by changing the paradigm that is used for exchanging annotations.

The largest difference between the older style of annotation packages and the newer ones is the decision to place a real database inside of each package. This is an improved design, because ultimately, the amount of annotation as well as the complexity of this information is likely to increase with time. And perhaps more importantly, this large amount of information needs to be organized in a flexible way in order to maximise its usefulness in a wide array of different circumstances. Since databases were created to solve problems just like this, the benefits of using real databases as the ultimate data structures for annotation packages is self evident.

For this remake of these classic annotation packages, the decision has been made to keep these databases gene centric rather than transcript centric or protein centric.

1.0.2 Database Schemas

For developers, a lot of the benefits of having the information loaded into a real database will require some knowledge about the database schema. For this reason the schemas that were used in the creation of each database type are included in AnnotationDbi. The currently supported schemas are listed in the DBschemas directory of AnnotationDbi. But it is also possible to simply print out the schema that a give package is currently using by using its ".dbschema" method.
Please note that there is one schema for each kind of package. These schemas specify which tables and indices will be present for each package of that type. The schema that a particular package is using is also listed when you type the name of the package as a function to obtain quality control information.

The code to make most kinds of the new database packages is also included in AnnotationDbi. Please see the vignette on SQLForge for more details on how to make additional database packages.

### 1.0.3 Internal Design

The current design of these packages is as deliberatly simple as it is gene centric. Each table in the database contains a unique kind of information and also an internal identifier called _id. The internal _id has no meaning outside of the context of a single database. But _id does connect all the data within a single database.

As an example if we wanted to connect the values in the genes table with the values in the kegg table, we could simply join the two tables using the internal _id column. It is very important to note however that _id does not have any absolute significance. That is, it has no meaning outside of the context of the database where it is used. It is tempting to think that an _id could have such significance because within a single database, it looks and behaves similarly to an entrez gene ID. But _id is definitely NOT an entrez gene ID. The entrez gene IDs are in another table entirely, and can be connected to using the internal _id just like all the other meaningful information inside these databases.

### 2 Examples

#### 2.0.4 Basic information

The *AnnotationDbi* package provides an interface to SQLite-based annotation packages. Each SQLite-based annotation package (identified by a “.db” suffix in the package name) contains a number of *AnnDbBimap* objects in place of the *environment* objects found in the old-style environment-based annotation packages. The API provided by *AnnotationDbi* allows you to treat the *AnnDbBimap* objects like *environment* instances. For example, the functions `[`, *get*, *mget*, and *ls* all behave the same as with the old-style packages. In addition, new methods like `[`, *toTable*, *subset* and others provide some additional flexibility in accessing the annotation data.
R> library("hgu95av2.db")

The same basic set of objects is provided with the db packages:

R> ls("package:hgu95av2.db")

[1] "hgu95av2"       "hgu95av2ACCNUM"
[3] "hgu95av2ALIAS2PROBE" "hgu95av2CHR"
[5] "hgu95av2CHRLENGTHS" "hgu95av2CHRLOC"
[7] "hgu95av2_dbconn"  "hgu95av2_dbfile"
[9] "hgu95av2_dbInfo"  "hgu95av2_dbschema"
[11] "hgu95av2ENSEMBL"  "hgu95av2ENSEMBL2PROBE"
[13] "hgu95av2ENTREZID" "hgu95av2ENZYME"
[15] "hgu95av2ENZYME2PROBE" "hgu95av2GENENAME"
[17] "hgu95av2GO"      "hgu95av2GO2ALLPROBES"
[19] "hgu95av2GO2PROBE" "hgu95av2MAP"
[21] "hgu95av2MAPCOUNTS" "hgu95av2OMIM"
[23] "hgu95av2ORGANISM" "hgu95av2PATH"
[25] "hgu95av2PATH2PROBE" "hgu95av2PFAM"
[27] "hgu95av2PMID"    "hgu95av2PMID2PROBE"
[29] "hgu95av2PROSITE" "hgu95av2REFSEQ"
[31] "hgu95av2SYMBOL"  "hgu95av2UNIGENE"

As before, it is possible to call the package name as a function to get some QC information about it.

R> qcdata = capture.output(hgu95av2())
R> head(qcdata, 20)

[1] "Quality control information for hgu95av2:
[2] ""[3] ""[4] "This package has the following mappings:
[5] ""[6] "hgu95av2ACCNUM has 12625 mapped keys (of 12625 keys)"
[7] "hgu95av2ALIAS2PROBE has 36833 mapped keys (of 36833 keys)"
[8] "hgu95av2CHR has 12117 mapped keys (of 12625 keys)"
[9] "hgu95av2CHRLENGTHS has 25 mapped keys (of 25 keys)"
[10] "hgu95av2CHRLOC has 11817 mapped keys (of 12625 keys)"
[11] "hgu95av2ENSEMBL has 11156 mapped keys (of 12625 keys)"
[12] "hgu95av2ENSEMBL2PROBE has 8286 mapped keys (of 8286 keys)"
Alternatively, you can get similar information on how many items are in each of the provided maps by looking at the MAPCOUNTs:

R> hgu95av2MAPCOUNTS

To demonstrate the environment API, we'll start with a random sample of probe set IDs.

R> all_probes <- ls(hgu95av2ENTREZID)
R> length(all_probes)
[1] 12625
R> set.seed(0xa1beef)
R> probes <- sample(all_probes, 5)
R> probes
[1] "31882_at"  "38780_at"  "37033_s_at"  "1702_at"  "31610_at"

The usual ways of accessing annotation data are also available.

R> hgu95av2ENTREZID[[probes[1]]]
[1] "9136"

R> hgu95av2ENTREZID$"31882_at"
[1] "9136"

R> syms <- unlist(mget(probes, hgu95av2SYMBOL))
R> syms
31882_at  38780_at  37033_s_at  1702_at  31610_at  "RRP9"  "AKR1A1"  "GPX1"  "IL2RA"  "PDZK1IP1"
2.0.5 Manipulating Bimap Objects

Many filtering operations on the annotation environment objects require conversion of the environment into a list. There is an as.list method for AnnDbBimap objects. In general, converting to lists will not be the most efficient way to filter the annotation data when using a SQLite-based package.

```r
R> zz <- as.list(hgu95av2SYMBOL)
```

In an environment-based package, each mapping is its own object. To save disk and memory resources, not all reverse mappings are included in the environment-based packages. Here is the common idiom for creating a list that serves as the reverse map of a given environment.

```r
R> library("hgu95av2", warn.conflicts=FALSE)
R> ## we load the environment so as not
R> ## to include the load time in the timing
R> class(hgu95av2SYMBOL)
[1] "environment"
R> system.time({
    p2sym <- as.list(hgu95av2SYMBOL)
    lens <- sapply(p2sym, length)
    nms <- rep(names(p2sym), lens)
    sym2p <- split(unlist(p2sym), nms)
})
user  system elapsed
0.096 0.012 0.111
R> ## in fact, there is a convenience function
R> ## for this operation in Biobase
R> system.time({
    p2sym <- as.list(hgu95av2SYMBOL)
    sym2p <- reverseSplit(p2sym)
})
user  system elapsed
0.088 0.000 0.085
```
The SQLite-based package provide the same reverse maps as objects in the package name space for backwards compatibility, but the reverse mappings of any map is available using **revmap**. Since the data are stored as tables, no extra disk space is needed to provide reverse mappings.

```r
R> system.time(sym2p <- revmap(hgu95av2SYMBOL))
    user  system elapsed
     0.004   0.000   0.000
R> unlist(mget(sym, revmap(hgu95av2SYMBOL)))
          RRP9  AKR1A1   GPX1  IL2RA  PDZK1IP1
      "31882_at" "38780_at" "37033_s_at" "1702_at" "31610_at"

So now that you know about the **revmap** function you might try something like this:

```r
R> as.list(revmap(hgu95av2PATH)["00300"])
$'00300'
[1] "34336_at" "35870_at" "35761_at"

But in the case of the PATH map, we don't need to use revmap(x) because hgu95av2.db already provides the PATH2PROBE map:

```r
R> x <- hgu95av2PATH
R> ## except for the name, this is exactly revmap(x)
R> revx <- hgu95av2PATH2PROBE
R> revx2 <- revmap(x, objName="PATH2PROBE")
R> revx2

PATH2PROBE map for chip hgu95av2 (object of class "AnnDbBimap")

R> identical(revx, revx2)
[1] TRUE
R> as.list(revx["00300"])
$'00300'
[1] "34336_at" "35870_at" "35761_at"

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2.0.6 Displaying the Contents and Structure of Bimap Objects

Sometimes you may just want to know what elements are in an individual map. A Bimap interface is available to access the data in table (data.frame) format using [ and toTable.

R> toTable(hgu95av2GO[probes[1:3]])

<table>
<thead>
<tr>
<th>probe_id</th>
<th>go_id</th>
<th>Evidence</th>
<th>Ontology</th>
</tr>
</thead>
<tbody>
<tr>
<td>31882_at</td>
<td>G0:0006364</td>
<td>TAS</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0001836</td>
<td>IMP</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0006749</td>
<td>IDA</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0006916</td>
<td>IMP</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0008631</td>
<td>IEA</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0009650</td>
<td>IMP</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0010269</td>
<td>IMP</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0030503</td>
<td>IDA</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0033599</td>
<td>IMP</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0040029</td>
<td>IDA</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0042744</td>
<td>IEA</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0043154</td>
<td>IMP</td>
<td>BP</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0060047</td>
<td>IMP</td>
<td>BP</td>
</tr>
<tr>
<td>38780_at</td>
<td>G0:0006006</td>
<td>TAS</td>
<td>BP</td>
</tr>
<tr>
<td>38780_at</td>
<td>G0:0019853</td>
<td>IEA</td>
<td>BP</td>
</tr>
<tr>
<td>38780_at</td>
<td>G0:0042840</td>
<td>IEA</td>
<td>BP</td>
</tr>
<tr>
<td>38780_at</td>
<td>G0:0046185</td>
<td>IEA</td>
<td>BP</td>
</tr>
<tr>
<td>31882_at</td>
<td>G0:0005634</td>
<td>IEA</td>
<td>CC</td>
</tr>
<tr>
<td>31882_at</td>
<td>G0:0005732</td>
<td>TAS</td>
<td>CC</td>
</tr>
<tr>
<td>31882_at</td>
<td>G0:0030532</td>
<td>TAS</td>
<td>CC</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0005737</td>
<td>IEA</td>
<td>CC</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0005739</td>
<td>IEA</td>
<td>CC</td>
</tr>
<tr>
<td>38780_at</td>
<td>G0:0005829</td>
<td>IEA</td>
<td>CC</td>
</tr>
<tr>
<td>38780_at</td>
<td>G0:0016324</td>
<td>IEA</td>
<td>CC</td>
</tr>
<tr>
<td>31882_at</td>
<td>G0:0003723</td>
<td>IEA</td>
<td>MF</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0004602</td>
<td>IEA</td>
<td>MF</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0008430</td>
<td>IEA</td>
<td>MF</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0008539</td>
<td>IDA</td>
<td>MF</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0016491</td>
<td>IEA</td>
<td>MF</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0017124</td>
<td>IPI</td>
<td>MF</td>
</tr>
<tr>
<td>37033_s_at</td>
<td>G0:0043295</td>
<td>IC</td>
<td>MF</td>
</tr>
<tr>
<td>38780_at</td>
<td>G0:0004032</td>
<td>TAS</td>
<td>MF</td>
</tr>
</tbody>
</table>
The `toTable` function will display all of the information in a `Bimap`. This includes both the left and right values along with any other attributes that might be attached to those values. The left and right keys of the `Bimap` can be extracted using `Lkeys` and `Rkeys`. If it is necessary to only display information that is directly associated with the left to right links in a `Bimap`, then the `links` function can be used. The `links` returns a data frame with one row for each link in the bimap that it is applied to. It only reports the left and right keys along with any attributes that are attached to the edge between these two values.

Note that the order of the cols returned by `toTable` does not depend on the direction of the map ("undirected method"):

\[
R> \text{toTable}(x)[1:6,] \\
\begin{array}{ll}
\text{probe_id} & \text{path_id} \\
1 & 38187\_at 00232 \\
2 & 38912\_at 00232 \\
3 & 36512\_at 00650 \\
4 & 36512\_at 00960 \\
5 & 36332\_at 00380 \\
6 & 36185\_at 00252 \\
\end{array}
\]

\[
R> \text{toTable}(\text{revx})[1:6,] \\
\begin{array}{ll}
\text{probe_id} & \text{path_id} \\
1 & 38187\_at 00232 \\
2 & 38912\_at 00232 \\
3 & 36512\_at 00650 \\
4 & 36512\_at 00960 \\
5 & 36332\_at 00380 \\
6 & 36185\_at 00252 \\
\end{array}
\]

Note however that the `Lkeys` are always on the left (1st col), the `Rkeys` always in the 2nd col.

There can be more than 2 columns in the returned data frame:

3 cols:
R> toTable(hgu95av2PFAM)[1:6, ]  # the right values are tagged

<table>
<thead>
<tr>
<th>probe_id</th>
<th>ipi_id</th>
<th>PfamId</th>
</tr>
</thead>
<tbody>
<tr>
<td>1000_at</td>
<td>IPI00018195</td>
<td>PF00069</td>
</tr>
<tr>
<td>1000_at</td>
<td>IPI00304111</td>
<td>PF00069</td>
</tr>
<tr>
<td>1000_at</td>
<td>IPI00742900</td>
<td>PF00069</td>
</tr>
<tr>
<td>1000_at</td>
<td>IPI00793141</td>
<td>PF00069</td>
</tr>
<tr>
<td>1001_at</td>
<td>IPI00019530</td>
<td>PF07714</td>
</tr>
<tr>
<td>1001_at</td>
<td>IPI00019530</td>
<td>PF00041</td>
</tr>
</tbody>
</table>

R> as.list(hgu95av2PFAM["1000_at"])

$`1000_at`
  IPI00018195  IPI00304111  IPI00742900  IPI00793141
  "PF00069"  "PF00069"  "PF00069"  "PF00069"

But the Rkeys are ALWAYS in the 2nd col.
For length() and keys(), the result does depend on the direction ("directed methods"):

R> length(x)
[1] 12625

R> length(revx)
[1] 199

R> allProbeSetIds <- keys(x)
R> allKEGGIds <- keys(revx)

There are more "undirected" methods listed below:

R> junk <- Lkeys(x)  # same for all maps in hgu95av2.db (except pseudo-map
R> # MAPCOUNTS)
R> Llength(x)  # nb of Lkeys

[1] 12625

R> junk <- Rkeys(x)  # KEGG ids for PATH/PATH2PROBE maps, GO ids for
R> # GO/GO2PROBE/GO2ALLPROBES maps, etc...
R> Rlength(x)  # nb of Rkeys

[1] 199

Notice how they give the same result for x and revmap(x)
2.0.7 Advantages of using revmap

Using revmap can be very efficient in some use cases:

```r
R> x <- hgu95av2CHR
R> Rkeys(x)

[1] "8" "14" "3" "2" "17" "16" "9" "X" "6" "1" "7" "12" "10"
[14] "11" "22" "19" "15" "20" "21" "5" "18" "4" "13" "Y"

R> chroms <- Rkeys(x)[23:24]
R> chroms

[1] "13" "Y"

R> Rkeys(x) <- chroms
R> toTable(x)[1:10,]

   probe_id chromosome
1   37303_at       13
2   37099_at       13
3  32991_f_at       Y
4   40435_at       Y
5   40436_g_at       Y
6   35447_s_at       Y
7   32482_at       13
8   32439_at       13
9   37930_at       13
10  1503_at       13

To get this in the classic named-list format:

R> z <- as.list(revmap(x)[chroms])
R> names(z)

[1] "13" "Y"

R> z["Y"][1:5]

[1] "32991_f_at" "40435_at" "40436_g_at" "35447_s_at" "33665_s_at"

Compare to what you need to do this with the current envi-based package:

```
```r
library(hgu95av2)

u <- unlist(as.list(hgu95av2CHR))
u <- u[u %in% chroms]
split(names(u), u)

A last example with cytogenetic locations:

x <- hgu95av2MAP
toTable(hgu95av2MAP)[1:6, ]

<table>
<thead>
<tr>
<th>probe_id</th>
<th>cytogenetic_location</th>
</tr>
</thead>
<tbody>
<tr>
<td>38187_at</td>
<td>8p23.1-p21.3</td>
</tr>
<tr>
<td>38912_at</td>
<td>8p22</td>
</tr>
<tr>
<td>33825_at</td>
<td>14q32.1</td>
</tr>
<tr>
<td>36512_at</td>
<td>3q21.3-q25.2</td>
</tr>
<tr>
<td>38434_at</td>
<td>2q35</td>
</tr>
<tr>
<td>36332_at</td>
<td>17q25</td>
</tr>
</tbody>
</table>

as.list(revmap(x)["8p22"])

$'8p22'
[1] "38912_at" "32372_at" "41209_at" "39981_at" "39982_r_at"
[6] "36850_at" "36851_g_at" "36852_at" "34553_at" "37363_at"
[11] "37951_at" "38013_at"

Are the probes in 'pbids' mapped to cytogenetic location "6p21.3"?

pbids <- c("38912_at", "41654_at", "907_at", "2053_at", "2054_g_at", "40781_at")
x <- subset(x, Lkeys=pbids, Rkeys="18q11.2")
toTable(x)

<table>
<thead>
<tr>
<th>probe_id</th>
<th>cytogenetic_location</th>
</tr>
</thead>
<tbody>
<tr>
<td>2053_at</td>
<td>18q11.2</td>
</tr>
<tr>
<td>2054_g_at</td>
<td>18q11.2</td>
</tr>
</tbody>
</table>

To coerce this map to a named vector:

pb2cyto <- as.character(x)
pb2cyto[pbids]

<NA> <NA> <NA> 2053_at 2054_g_at <NA> NA NA NA "18q11.2" "18q11.2" NA
```
The coercion of the reverse map works too but issues a warning because of the duplicated names:

```r
R> cyto2pb <- as.character(revmap(x))
```

### 2.0.8 Using SQL to speed things up

Another area where the SQLite-based packages provide some advantages is when one wishes to filter the available annotation data in a complex fashion. For example, consider the task of obtaining all gene symbols on which are probed on a chip that have at least one GO BP ID annotation with evidence code IMP, IGI, IPI, or IDA. Here is one way to extract this using the environment-based packages:

```r
R> ## Obtain SYMBOLS with at least one GO BP annotation with evidence IMP, IGI, IPI, or IDA.
R> probes <- sample(all_probes, 500)
R> library("hgu95av2", warn.conflicts=FALSE)
R> system.time({
  bpids <- eapply(hgu95av2GO, function(x) {
    if (length(x) == 1 && is.na(x))
      NA
    else {
      sapply(x, function(z) {
        if (z$Ontology == "BP")
          z$GOID
        else
          NA
      })
    }
  })
  bpids <- unlist(bpids)
  bpids <- unique(bpids[!is.na(bpids)])
  g2p <- mget(bpids, hgu95av2G2PROBE)
  wantedp <- lapply(g2p, function(x) {
    x[!is.na(c("IMP", "IGI", "IPI", "IDA"))]}
  })
  wantedp <- wantedp[sapply(wantedp, length) > 0]
  wantedp <- unique(unlist(wantedp))
  ans <- unlist(mget(wantedp, hgu95av2SYMBOL))
})
```
R> detach("package:hgu95av2")
R> length(ans)

[1] 1806
R> ans[1:10]

39970_at 35364_at 37778_at 38911_at 39024_at 39404_s_at
"NROB1" "NAE1" "KIN" "NUP98" "NUP98" "UPF1"
41293_at 41294_at 36891_at 37058_at
"KRT7" "KRT7" "MCAT" "UGT2B4"

All of the above code could have been reduced to a single SQL query with the SQLite-based packages. But to put together this query, you would need to look 1st at the schema to know what tables are present:

R> hgu95av2_dbschema()

This function will give you an output of all the create table statements that were used to generate the hgu5av2 database. Then you could assemble the sql query and use the helper function hgu95av2_dbconn to get a connection object for the database as follows:

R> system.time({
  SQL <- "SELECT symbol FROM go_bp INNER JOIN gene_info USING(_id)
  WHERE go_bp.evidence in ('IPI', 'IDA', 'IMP', 'IGI')"
  zz <- dbGetQuery(hgu95av2_dbconn(), SQL)
})

user    system   elapsed
0.064    0.000    0.066

2.0.9 Combining data from separate annotation packages

Sometimes a user may wish to combine data that is found in two different annotation packages. One nice thing about the new packages is a side benefit of the fact that they are sqlite databases. This means that they can be attached into the same session, allowing easy joining of tables across otherwise separate databases. Being able to select items from multiple tables
requires that their be a common value that can be used to identify those entries which are identical. It is also important to note that the internal IDs used in the AnnotatioDbi packages cannot be used to map between packages since they have no meaning outside of the databases where they are defined.

In this example, we will join tables from hgu95av2.db and GO.db. To do this, we will attach the GO database to the HGU95-Av2 database to allow access to tables from both databases. We can then use GO identifiers as the link across the two data packages to create the join. In this section we are using the term attach to mean attaching using the SQL function ATTACH, and not the R function, or concept, of attaching. Before we begin, it is important to understand a little about where the GO database is located and its name. We use this information with the system.file function to construct a path to that database. In contrast, the hgu95av2.db package is already attached and we can use our predefined AnnotationDbi connection to it, hgu95av2_dbconn() to pass the SQL query that will attach the other database.

\[
\text{R> goDBLoc = system.file("extdata", "GO.sqlite", package="GO.db")}
\]
\[
\text{R> attachSQL = paste("ATTACH ", goDBLoc, "," as goDB;", sep = ")}
\]
\[
\text{R> dbGetQuery(hgu95av2_dbconn(), attachSQL)}
\]
\[
\text{NULL}
\]

Next, we are going to select some data, based on the GO ID, from two tables, one table from the HGU95-Av2 database and one from the GO database. For brevity of output we will limit the query to 10 values. The WHERE clause on the last line of the SQL query specifies that the GO identifiers are the same. The first five lines of the query set up what variables to extract and what they will be named in the output.

\[
\text{R> selectSQL = paste("SELECT DISTINCT a.go_id AS 'hgu95av2.go_id',",}
\text{ "a._id AS 'hgu95av2._id',",}
\text{ "g.go_id AS 'GO.go_id', g._id AS 'GO._id',",}
\text{ "g.ontology",}
\text{ "FROM go_bp_all AS a, goDB.go_term AS g",}
\text{ "WHERE a.go_id = g.go_id LIMIT 10;")}
\]
\[
\text{R> dataOut = dbGetQuery(hgu95av2_dbconn(), selectSQL)}
\]
\[
\text{R> dataOut}
\]
\[
\begin{array}{cccc}
\text{hgu95av2.go_id} & \text{hgu95av2._id} & \text{GO.go_id} & \text{GO._id} & \text{ontology} \\
1 & 255 & 00000002 & 00000002 & 13 & BP
\end{array}
\]
This query combines the go_bp_all table from the HGU95-Av2 database with the go_term table from the GO database. They are joined based on their go_id columns. For illustration purposes, the internal ID _id and the go_id from both tables are included in the output. This demonstrates that the go_ids can be used to join these tables while the internal IDs cannot. The internal IDs, _id, are suitable for joins within a single database, but cannot be used across databases.