

Using Bioconductor's Annotation Libraries

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Overview

The Bioconductor project maintains a rich body of annotation data assembled into R libraries. The purpose of this vignette is to discuss the structure, contents, and usage of these annotation data libraries. Executable code is provided as examples.

Contents

Bioconductor's annotation data libraries are constructed by assembling data collected from various public data repositories using Bioconductor's *AnnotationDbi* package and distributed as regular R libraries that can be installed and loaded in the same way an R library is installed/loaded. Each annotation library is an independent unit that can be used alone or in conjunction with other annotation libraries. Platform specific libraries are a group annotation libraries assembled specifically for given platforms (e. g. Affymetrix HG_U95Av2). `org.XX.eg.db` are libraries containing data assembled at genome level for specific organisms such as human, mouse, fly, or rat. *KEGG.db* and *GO.db* are source specific libraries containing generic data for various genomes.

Each annotation library, when installed, contains a sqlite database contained within the `extdata` along with a `man` subdirectory filled with documentation about the data. The data can be accessed using the standard methods that would work for the classic environment objects (hash table with key-value pairs) and act as if they were simple associations of annotation values to a set of keys. For each of these emulated environment objects (which we will refer to as mappings), there is a corresponding help file in the `man` directory with detail descriptions of the data file and usage. In addition to the traditional access to these data, these databases can also be accessed directly by using DBI interfaces which allow for powerful new combinations of these data.

Each platform specific library creates a series of these mapping objects named by following the convention of package name plus mapping name. The package name is in lower case letters and the mapping names are in capital letters. When a given mapping maps platform specific keys to annotation data, only the name of the annotation data is used for the name of the mapping. Otherwise, the mapping names have a pattern of key name and value name joined by a "2" in between. For example, `hgu95av2ENTREZID` maps probe

ids on an Affymetrix human genome U95Av2 chip to EntrezGene IDs while *hgu95av2G02PROBE* maps Gene Ontology IDs to probe IDs. Names of the mappings available in a platform specific data package are not listed here to save space but are easily accessible as shown later in the section for usage.

Genome level annotation libraries are named in the form of *org.Xx.yy.db* where Xx represents an abbreviation of the genus and species. Each of the organism wide genome annotation packages is based upon some type of widely used gene based identifier (such as an Entrez Gene id) that is mapped onto all the other features in the package. The yy part of the name corresponds to this designation, where eg means a package is an entrez gene package and *sgd* is a package based on the *sgd* database etc. In many cases the *org* packages will contain more different kinds of information than the platform based ones, since not all types of information are as widely sought after.

The *KEGG.db* library contains mappings between ids such as Entrez Gene IDs and *GO* to *KEGG* pathway ids and thus also to pathway names. The *GO.db* library maintains the directed acyclic graph structure of the original data from Gene Ontology Consortium by providing mappings of *GO* ids to their direct parents or children for each of the three categories (molecular function, cellular component, and biological process). Mappings between Entrez Gene and *GO* ids are also available to complement the *GO.db* package. These mappings are found within the organism wide packages mentioned above. These mappings are provided with evidence code that specifies the type of evidence that supports the annotation of a gene to a particular *GO* term.

Usage

All the annotation libraries can be obtained from the Bioconductor web site (<http://www.bioconductor.org>). To illustrate their usages, we use the library for Affymetrix HG_U95Av2 chip (*hgu95av2.db*) as an example for platform specific data packages and the *GO.db* library for non-platform specific data packages. We assume that R (www.r-project.org) and Bioconductor's Biobase and annotation libraries have already been installed.

Package installation

After downloading libraries *hgu95av2.db* and *GO.db* by using *biocLite*, if the *reposTools* library has already been installed/loaded, typing `install.packages2(library name)` installs the library for both Unix and Windows.

Typing `library(library name)` in an R session will load the library into R. For example,

```
> library("annotate")
> library("hgu95av2.db")
> library("GO.db")
```

Documentations

Each library contains documentation for the library in general and each of the individual mapping objects contained by the library. Two documents at the library level can be accessed by typing a library basename proceeded by a question mark (e. g. `?hgu95av2`) and the library basename followed by a pair of brackets (e. g. `hgu95av2()`), respectively. The former explains what the package is and details how a user can get more information, while the latter lists all the mappings contained by a library and provides information on the total number of keys within each of the maps contained by the library and how many of these keys are annotated. In addition, the latter will indicate the sources for the information provided by the package as well as the date that these sources claim to have last been updated.

The documentation for a given mapping object can be accessed by typing the name of an mapping object proceeded by a question mark (e. g. `hgu95av2G0`). The resulting documentation provides detail explanations to the mapping object, data source used to build the object, and example code for accessing annotation data.

Accessing annotation data within a library

Annotation data of a given library are stored as mapping objects in the form of key (items to be annotated) and value (annotation for an key item) pairs. Each mapping object provides annotation for keys for a particular subject reflected by the name of the object. For example, `hgu95av2G0` annotates probes on the HGU95Av2 chip with ids of the Gene Ontology terms the probes correspond to.

The name of an mapping object consists of package basename (*hgu95av2.db*) and mapping name (*G0*) to avoid confusion when multiple libraries are loaded to the system at the same time. Data contained by an mapping can be accessed easily using Bioconductor's existing functions. For example, the following code stores all the keys contained by the `hgu95av2G0` mapping object to variable *temp* and displays the first five keys on the screen:

```
> as.list(hgu95av2G0[5])

$`1004_at`
$`1004_at`$`G0:0006928`
$`1004_at`$`G0:0006928`$GOID
[1] "G0:0006928"

$`1004_at`$`G0:0006928`$Evidence
[1] "TAS"

$`1004_at`$`G0:0006928`$Ontology
[1] "BP"
```

```

$`1004_at`$`GO:0032467`
$`1004_at`$`GO:0032467`$GOID
[1] "GO:0032467"

$`1004_at`$`GO:0032467`$Evidence
[1] "IMP"

$`1004_at`$`GO:0032467`$Ontology
[1] "BP"


$`1004_at`$`GO:0006935`
$`1004_at`$`GO:0006935`$GOID
[1] "GO:0006935"

$`1004_at`$`GO:0006935`$Evidence
[1] "IEA"

$`1004_at`$`GO:0006935`$Ontology
[1] "BP"


$`1004_at`$`GO:0006955`
$`1004_at`$`GO:0006955`$GOID
[1] "GO:0006955"

$`1004_at`$`GO:0006955`$Evidence
[1] "IEA"

$`1004_at`$`GO:0006955`$Ontology
[1] "BP"


$`1004_at`$`GO:0007186`
$`1004_at`$`GO:0007186`$GOID
[1] "GO:0007186"

$`1004_at`$`GO:0007186`$Evidence
[1] "IEA"

$`1004_at`$`GO:0007186`$Ontology
[1] "BP"


$`1004_at`$`GO:0048535`
$`1004_at`$`GO:0048535`$GOID

```

[1] "GO:0048535"

\$`1004_at`\$`GO:0048535`\$Evidence

[1] "IEA"

\$`1004_at`\$`GO:0048535`\$Ontology

[1] "BP"

\$`1004_at`\$`GO:0042113`

\$`1004_at`\$`GO:0042113`\$GOID

[1] "GO:0042113"

\$`1004_at`\$`GO:0042113`\$Evidence

[1] "IEA"

\$`1004_at`\$`GO:0042113`\$Ontology

[1] "BP"

\$`1004_at`\$`GO:0070098`

\$`1004_at`\$`GO:0070098`\$GOID

[1] "GO:0070098"

\$`1004_at`\$`GO:0070098`\$Evidence

[1] "IEA"

\$`1004_at`\$`GO:0070098`\$Ontology

[1] "BP"

\$`1004_at`\$`GO:0005886`

\$`1004_at`\$`GO:0005886`\$GOID

[1] "GO:0005886"

\$`1004_at`\$`GO:0005886`\$Evidence

[1] "TAS"

\$`1004_at`\$`GO:0005886`\$Ontology

[1] "CC"

\$`1004_at`\$`GO:0005887`

\$`1004_at`\$`GO:0005887`\$GOID

[1] "GO:0005887"

\$`1004_at`\$`GO:0005887`\$Evidence
[1] "TAS"

\$`1004_at`\$`GO:0005887`\$Ontology
[1] "CC"

\$`1004_at`\$`GO:0009897`
\$`1004_at`\$`GO:0009897`\$GOID
[1] "GO:0009897"

\$`1004_at`\$`GO:0009897`\$Evidence
[1] "IEA"

\$`1004_at`\$`GO:0009897`\$Ontology
[1] "CC"

\$`1004_at`\$`GO:0004930`
\$`1004_at`\$`GO:0004930`\$GOID
[1] "GO:0004930"

\$`1004_at`\$`GO:0004930`\$Evidence
[1] "TAS"

\$`1004_at`\$`GO:0004930`\$Ontology
[1] "MF"

\$`1004_at`\$`GO:0005515`
\$`1004_at`\$`GO:0005515`\$GOID
[1] "GO:0005515"

\$`1004_at`\$`GO:0005515`\$Evidence
[1] "IPI"

\$`1004_at`\$`GO:0005515`\$Ontology
[1] "MF"

\$`1004_at`\$`GO:0016494`
\$`1004_at`\$`GO:0016494`\$GOID
[1] "GO:0016494"

\$`1004_at`\$`GO:0016494`\$Evidence
[1] "IEA"

```
$`1004_at`$`GO:0016494`$Ontology
[1] "MF"
```

To obtain annotation for a given set of keys, one may use the `mget` function. Suppose we have run an experiment using the HG_U95Av2 chip and found three genes represented by Affymetrix probe ids *738_at*, *40840_at*, and *41668_r_at* interesting. To get the names of genes the three probe ids corresponding to, we do:

```
> mget(c("738_at", "40840_at", "41668_r_at"), hgu95av2GENENAME)

$`738_at`
[1] "5'-nucleotidase, cytosolic II"

$`40840_at`
[1] "peptidylprolyl isomerase F"

$`41668_r_at`
[1] "TDP-glucose 4,6-dehydratase"
```

Similarly, identifiers of Gene Ontology terms corresponding to the three probes can be obtained as shown below:

```
> temp <- mget(c("41561_s_at", "40840_at", "41668_r_at"), hgu95av2GO)
```

In this case, the function `mget` returns a list of pre-defined S4 objects containing data for the ids, ontology, and evidence code of Gene Ontology terms corresponding to the three keys. The following code shows how to access the GO id, evidence code and ontology of the Gene Ontology term corresponding to probe id *40840_at*:

```
> temp <- get("738_at", hgu95av2GO)
> names(temp)

[1] "GO:0006144" "GO:0006195" "GO:0016310" "GO:0016311" "GO:0017144"
[6] "GO:0044281" "GO:0055086" "GO:0008219" "GO:0016311" "GO:0016311"
[11] "GO:0005829" "GO:0050146" "GO:0005515" "GO:0000166" "GO:0046872"
[16] "GO:0008253"

> temp[["GO:0008253"]][["Evidence"]]

[1] "EXP"

> temp[["GO:0008253"]][["Ontology"]]

[1] "MF"
```

As shown above, probe *40840_at* can be annotated by three Gene Ontology terms identified by *GO:0005829*, *GO:0008253*, and *GO:0016787*. The evidence code for *GO:0008253* is *TAS* (traceable author statement) and it belongs to ontology *MF* (molecular function).

Accessing annotation data across libraries

Often, data available in a given data package alone may not be sufficient and need to be sought across packages. Bioconductor's annotation data packages are linked by common public data identifiers to allow traverse between packages (Fig. 1). Using the example above, we know that probe id *738_at* are annotated by three Gene Ontology ids *GO:0005829*, *GO:0008253*, and *GO:0016787*. The Gene Ontology terms for various Gene Ontology ids, however, are stored in another package named *GO.db*. AS package *hgu95av2.db* and *GO.db* are linked by *GO* ids, one can annotate probe id *738_at* with Gene Ontology terms by linking data in the two packages using *GO* id as shown below:

```
> mget(names(get("738_at", hgu95av2GO)), GOTERM)

$`GO:0006144`
GOID: GO:0006144
Term: purine nucleobase metabolic process
Ontology: BP
Definition: The chemical reactions and pathways involving
           purine nucleobases, one of the two classes of
           nitrogen-containing ring compounds found in DNA and RNA,
           which include adenine and guanine.
Synonym: purine base metabolic process
Synonym: purine base metabolism
Synonym: purine metabolic process
Synonym: purine metabolism

$`GO:0006195`
GOID: GO:0006195
Term: purine nucleotide catabolic process
Ontology: BP
Definition: The chemical reactions and pathways resulting in
           the breakdown of a purine nucleotide, a compound
           consisting of nucleoside (a purine base linked to a
           deoxyribose or ribose sugar) esterified with a phosphate
           group at either the 3' or 5'-hydroxyl group of the sugar.
Synonym: purine nucleotide breakdown
Synonym: purine nucleotide catabolism
Synonym: purine nucleotide degradation

$`GO:0016310`
GOID: GO:0016310
Term: phosphorylation
Ontology: BP
Definition: The process of introducing a phosphate group into
           a molecule, usually with the formation of a phosphoric
           ester, a phosphoric anhydride or a phosphoric amide.
```


\$`G0:0016311`
G0ID: G0:0016311
Term: dephosphorylation
Ontology: BP
Definition: The process of removing one or more phosphoric
(ester or anhydride) residues from a molecule.

\$`G0:0017144`
G0ID: G0:0017144
Term: drug metabolic process
Ontology: BP
Definition: The chemical reactions and pathways involving a
drug, a substance used in the diagnosis, treatment or
prevention of a disease; as used here antibiotic
substances (see antibiotic metabolism) are considered to
be drugs, even if not used in medical or veterinary
practice.
Synonym: drug metabolism

\$`G0:0044281`
G0ID: G0:0044281
Term: small molecule metabolic process
Ontology: BP
Definition: The chemical reactions and pathways involving
small molecules, any low molecular weight, monomeric,
non-encoded molecule.
Synonym: small molecule metabolism

\$`G0:0055086`
G0ID: G0:0055086
Term: nucleobase-containing small molecule metabolic process
Ontology: BP
Definition: The cellular chemical reactions and pathways
involving a nucleobase-containing small molecule: a
nucleobase, a nucleoside, or a nucleotide.
Synonym: nucleobase, nucleoside and nucleotide metabolic
process
Synonym: nucleobase, nucleoside and nucleotide metabolism

\$`G0:0008219`
G0ID: G0:0008219
Term: cell death
Ontology: BP
Definition: Any biological process that results in permanent
cessation of all vital functions of a cell. A cell should

be considered dead when any one of the following molecular or morphological criteria is met: (1) the cell has lost the integrity of its plasma membrane; (2) the cell, including its nucleus, has undergone complete fragmentation into discrete bodies (frequently referred to as "apoptotic bodies"); and/or (3) its corpse (or its fragments) have been engulfed by an adjacent cell in vivo.

Synonym: accidental cell death

Synonym: necrosis

\$`GO:0016311`
 GOID: GO:0016311
 Term: dephosphorylation
 Ontology: BP
 Definition: The process of removing one or more phosphoric (ester or anhydride) residues from a molecule.

\$`GO:0016311`
 GOID: GO:0016311
 Term: dephosphorylation
 Ontology: BP
 Definition: The process of removing one or more phosphoric (ester or anhydride) residues from a molecule.

\$`GO:0005829`
 GOID: GO:0005829
 Term: cytosol
 Ontology: CC
 Definition: The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes.

\$`GO:0050146`
 GOID: GO:0050146
 Term: nucleoside phosphotransferase activity
 Ontology: MF
 Definition: Catalysis of the reaction: a nucleotide + a 2'-deoxynucleoside = a nucleoside + a 2'-deoxynucleoside 5'-monophosphate.

Synonym: nonspecific nucleoside phosphotransferase activity

Synonym: nucleotide:2'-nucleoside 5'-phosphotransferase activity

Synonym: nucleotide:3'-deoxynucleoside 5'-phosphotransferase activity

Synonym: nucleotide:nucleoside 5'-phosphotransferase activity

\$`G0:0005515`
 GOID: G0:0005515
 Term: protein binding
 Ontology: MF
 Definition: Interacting selectively and non-covalently with any protein or protein complex (a complex of two or more proteins that may include other nonprotein molecules).
 Synonym: alpha-2 macroglobulin receptor-associated protein activity
 Synonym: protein amino acid binding
 Synonym: protein degradation tagging activity
 Synonym: protein folding chaperone
 Synonym: protein tagging activity
 Synonym: G0:0045308
 Secondary: G0:0045308

\$`G0:0000166`
 GOID: G0:0000166
 Term: nucleotide binding
 Ontology: MF
 Definition: Interacting selectively and non-covalently with a nucleotide, any compound consisting of a nucleoside that is esterified with (ortho)phosphate or an oligophosphate at any hydroxyl group on the ribose or deoxyribose.

\$`G0:0046872`
 GOID: G0:0046872
 Term: metal ion binding
 Ontology: MF
 Definition: Interacting selectively and non-covalently with any metal ion.
 Synonym: heavy metal binding
 Synonym: metal binding

\$`G0:0008253`
 GOID: G0:0008253
 Term: 5'-nucleotidase activity
 Ontology: MF
 Definition: Catalysis of the reaction: a 5'-ribonucleotide + H2O = a ribonucleoside + phosphate.
 Synonym: 5' nucleotidase activity
 Synonym: 5'-adenylic phosphatase
 Synonym: 5'-AMP nucleotidase
 Synonym: 5'-AMPase
 Synonym: 5'-mononucleotidase activity
 Synonym: 5'-ribonucleotide phosphohydrolase activity

Synonym: adenosine 5'-phosphatase
 Synonym: adenosine monophosphatase
 Synonym: AMP phosphatase
 Synonym: AMP phosphohydrolase
 Synonym: AMPase
 Synonym: snake venom 5'-nucleotidase
 Synonym: thimidine monophosphate nucleotidase
 Synonym: UMPase
 Synonym: uridine 5'-nucleotidase

It turns out that probe id *738.at* (corresponding to *GO:0008253*, and *GO:0016787*) has molecular function (MF) *5'-nucleotidase activity* and *hydrolase activity*.

1 Session Information

The version number of R and packages loaded for generating the vignette were:

R version 3.1.1 Patched (2014-09-25 r66681)
 Platform: x86_64-apple-darwin13.1.0 (64-bit)

locale:

[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

attached base packages:

[1]	grid	stats4	parallel	stats	graphics	grDevices
[7]	utils	datasets	methods	base		

other attached packages:

[1]	GO.db_3.0.0	hgu95av2.db_3.0.0	org.Hs.eg.db_3.0.0
[4]	RSQLite_0.11.4	DBI_0.3.1	Rgraphviz_2.10.0
[7]	graph_1.44.0	xtable_1.7-4	annotate_1.44.0
[10]	XML_3.98-1.1	AnnotationDbi_1.28.0	GenomeInfoDb_1.2.0
[13]	IRanges_2.0.0	S4Vectors_0.4.0	Biobase_2.26.0
[16]	BiocGenerics_0.12.0		

loaded via a namespace (and not attached):

[1] tools_3.1.1