

Package ‘GEOmetadb’

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Type Package

Title A compilation of metadata from NCBI GEO

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biocViews Infrastructure

Description The NCBI Gene Expression Omnibus (GEO) represents the largest public repository of microarray data. However, finding data of interest can be challenging using current tools. GEOmetadb is an attempt to make access to the metadata associated with samples, platforms, and datasets much more feasible. This is accomplished by parsing all the NCBI GEO metadata into a SQLite database that can be stored and queried locally. GEOmetadb is simply a thin wrapper around the SQLite database along with associated documentation. Finally, the SQLite database is updated regularly as new data is added to GEO and can be downloaded at will for the most up-to-date metadata. GEOmetadb paper: <http://bioinformatics.oxfordjournals.org/cgi/content/short/24/23/2798> .

URL <http://gbnci.abcc.ncifcrf.gov/geo/>

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GEOmetadb-package

Query NCBI GEO metadata from a local SQLite database

Description

The NCBI Gene Expression Omnibus (GEO) represents the largest public repository of microarray data. However, finding data of interest can be challenging using current tools. GEOmetadb is an attempt to make access to the metadata associated with samples, platforms, and datasets much more feasible. This is accomplished by parsing all the NCBI GEO metadata into a SQLite database that can be stored and queried locally. GEOmetadb is simply a thin wrapper around the SQLite database along with associated documentation. Finally, the SQLite database is updated regularly as new data is added to GEO and can be downloaded at will for the most up-to-date metadata.

Details

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Author(s)

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References

<http://meltzerlab.nci.nih.gov/apps/geo>, <http://gbnci.abcc.ncifcrf.gov/geo/>

Examples

```
if(file.exists(GEOmetadb.sqlite)) {  
  a <- columnDescriptions()[1:5,]  
  b <- geoConvert(GPL97,GSM)  
} else {  
  print("use getSQLiteFile() to get a copy of the GEOmetadb SQLite file  
and then rerun the example")  
}
```

columnDescriptions	<i>Get column descriptions for the GEOmetadb database</i>
--------------------	---

Description

Searching the GEOmetadb database requires a bit of knowledge about the structure of the database and column descriptions. This function returns those column descriptions for all columns in all tables in the database.

Usage

```
columnDescriptions(sqlite_db_name=GEOmetadb.sqlite)
```

Arguments

sqlite_db_name The filename of the GEOmetadb sqlite database file

Value

A three-column data.frame including TableName, FieldName, and Description.

Author(s)

Sean Davis <sdavis2@mail.nih.gov>

References

<http://meltzerlab.nci.nih.gov/apps/geo>

Examples

```
if(file.exists(GEOmetadb.sqlite)) {  
  columnDescriptions()[1:5,]  
} else {  
  print("You will need to use the getSQLiteFile() function to get a copy  
of the SQLite database file before this example will work")  
}
```

geoConvert

Cross-reference between GEO data types

Description

A common task is to find all the GEO entities of one type associated with another GEO entity (eg., find all GEO samples associated with GEO platform 'GPL96'). This function provides a very fast mapping between entity types to facilitate queries of this type.

Usage

```
geoConvert(in_list, out_type = c("gse", "gpl", "gsm", "gds", "smatrix"), sqlite_db_name = "GEOmetadb.s
```

Arguments

`in_list` Character vector of GEO entities to convert from.
`out_type` Character vector of GEO entity types to which to convert.
`sqlite_db_name` The filename of the GEOmetadb sqlite database file

Value

A list of data.frames.

Author(s)

Jack Zhu <zhujack@mail.nih.gov>

References

<http://meltzerlab.nci.nih.gov/apps/geo>, <http://gbnci.abcc.ncifcrf.gov/geo/>

Examples

```
if(file.exists("GEOmetadb.sqlite")) {  
  geoConvert(GPL96,out_type=GSM)  
} else {  
  print("Run getSQLiteFile() to get a copy of the GEOmetadb SQLite file  
and then rerun the example")  
}
```

getBiocPlatformMap	<i>Get mappings between GPL and Bioconductor microarray annotation packages</i>
--------------------	---

Description

Query the gpl table and get GPL information of a given list of Bioconductor microarray annotation packages. Note currently the GEOmetadb does not contains all the mappings, but we are trying to construct a relative complete list.

Usage

```
getBiocPlatformMap(con, bioc=all)
```

Arguments

con	Connection to the GEOmetadb.sqlite database
bioc	Character vector of Bioconductor microarray annotation packages, e.g. <code>c('hgu133plus2','hgu95av2')</code> . 'all' returns all mappings.

Value

A six-column data.frame including GPL title, GPL accession, bioc_package, manufacturer, organism, data_row_count.

Author(s)

Jack Zhu <zhujack@mail.nih.gov>, Sean Davis <sdavis2@mail.nih.gov>

References

<http://meltzerlab.nci.nih.gov/apps/geo>

Examples

```
if(file.exists(GEOmetadb.sqlite)) {
  con <- dbConnect(SQLite(), "GEOmetadb.sqlite")
  getBiocPlatformMap(con)[1:5,]
  getBiocPlatformMap(con, bioc=c(hgu133a,hgu95av2))
  dbDisconnect(con)
} else {
  print("You will need to use the getSQLiteFile() function to get a copy
of the SQLite database file before this example will work")
}
```

getSQLiteFile	<i>Download and unzip the most recent GEOmetadb SQLite file</i>
---------------	---

Description

This function is the standard method for downloading and unzipping the most recent GEOmetadb SQLite file from the server.

Usage

```
getSQLiteFile(destdir = getwd(), destfile = "GEOmetadb.sqlite.gz")
```

Arguments

destdir	The destination directory of the downloaded file
destfile	The filename of the downloaded file. This filename should end in ".gz" as the unzipping assumes that is the case

Value

Prints some diagnostic information to the screen.
Returns the local filename for use later.

Author(s)

Sean Davis <sdavis2@mail.nih.gov>

References

<http://meltzerlab.nci.nih.gov/apps/geo>, <http://gbnci.abcc.ncifcrf.gov/geo/>

Examples

```
## Not run: geometadbfile <- getSQLiteFile()
```

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