

# Using the GEOquery Package

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## Overview of GEO

The NCBI Gene Expression Omnibus (GEO) serves as a public repository for a wide range of high-throughput experimental data. These data include single and dual channel microarray-based experiments measuring mRNA, genomic DNA, and protein abundance, as well as non-array techniques such as serial analysis of gene expression (SAGE), mass spectrometry proteomic data, and high-throughput sequencing data.

At the most basic level of organization of GEO, there are four basic entity types. The first three (Sample, Platform, and Series) are supplied by users; the fourth, the dataset, is compiled and curated by GEO staff from the user-submitted data. See [the GEO home page](#) for more information.

### Platforms

A Platform record describes the list of elements on the array (e.g., cDNAs, oligonucleotide probesets, ORFs, antibodies) or the list of elements that may be detected and quantified in that experiment (e.g., SAGE tags, peptides). Each Platform record is assigned a unique and stable GEO accession number (GPLxxx). A Platform may reference many Samples that have been submitted by multiple submitters.

### Samples

A Sample record describes the conditions under which an individual Sample was handled, the manipulations it underwent, and the abundance measurement of each element derived from it. Each Sample record is assigned a unique and stable GEO accession number (GSMxxx). A Sample entity must reference only one Platform and may be included in multiple Series.

### Series

A Series record defines a set of related Samples considered to be part of a group, how the Samples are related, and if and how they are ordered. A Series provides a focal point and description of the experiment as a whole. Series records may also contain tables describing extracted data, summary conclusions, or analyses. Each Series record is assigned a unique and stable GEO accession number (GSExxx). Series records are available in a couple of formats which are handled by GEOquery independently. The smaller and new GSEMatrix files are quite fast to parse; a simple flag is used by GEOquery to choose to use GSEMatrix files (see below).

### Datasets

GEO DataSets (GDSxxx) are curated sets of GEO Sample data. A GDS record represents a collection of biologically and statistically comparable GEO Samples and forms the basis of GEO's suite of data display and analysis tools. Samples within a GDS refer to the same Platform, that is, they share a common set of probe elements. Value measurements for each Sample within a GDS are assumed to be calculated in an equivalent manner, that is, considerations such as background processing and normalization are consistent across the dataset. Information reflecting experimental design is provided through GDS subsets.

## Getting Started using GEOquery

Getting data from GEO is really quite easy. There is only one command that is needed, `getGEO`. This one function interprets its input to determine how to get the data from GEO and then parse the data into useful R data structures. Usage is quite simple. This loads the GEOquery library.

```
library(GEOquery)
```

Now, we are free to access any GEO accession. *Note that in the following, I use a file packaged with the GEOquery package. In general, you will use only the GEO accession, as noted in the code comments.*

```
# If you have network access, the more typical way to do this  
# would be to use this:  
# gds <- getGEO("GDS507")  
gds <- getGEO(filename=system.file("extdata/GDS507.soft.gz",package="GEOquery"))
```

Now, `gds` contains the R data structure (of class `GDS`) that represents the GDS507 entry from GEO. You'll note that the filename used to store the download was output to the screen (but not saved anywhere) for later use to a call to `getGEO(filename=...)`.

We can do the same with any other GEO accession, such as GSM11805, a GEO sample.

```
# If you have network access, the more typical way to do this  
# would be to use this:  
# gds <- getGEO("GSM11805")  
gsm <- getGEO(filename=system.file("extdata/GSM11805.txt.gz",package="GEOquery"))
```

## GEOquery Data Structures

The GEOquery data structures really come in two forms. The first, comprising `GDS`, `GPL`, and `GSM` all behave similarly and accessors have similar effects on each. The fourth GEOquery data structure, `GSE` is a composite data type made up of a combination of `GSM` and `GPL` objects. I will explain the first three together first.

### The GDS, GSM, and GPL classes

Each of these classes is comprised of a metadata header (taken nearly verbatim from the SOFT format header) and a `GEODDataTable`. The `GEODDataTable` has two simple parts, a `Columns` part which describes the column headers on the `Table` part. There is also a `show` method for each class. For example, using the `gsm` from above:

```
# Look at gsm metadata:  
head(Meta(gsm))  
  
## $channel_count  
## [1] "1"  
##  
## $comment  
## [1] "Raw data provided as supplementary file"  
##  
## $contact_address  
## [1] "715 Albany Street, E613B"  
##  
## $contact_city  
## [1] "Boston"  
##  
## $contact_country
```

```
## [1] "USA"
##
## $contact_department
## [1] "Genetics and Genomics"
```

```
# Look at data associated with the GSM:
# but restrict to only first 5 rows, for brevity
Table(gsm)[1:5,]
```

```
##          ID_REF  VALUE ABS_CALL
## 1 AFX-BioB-5_at  953.9         P
## 2 AFX-BioB-M_at 2982.8         P
## 3 AFX-BioB-3_at 1657.9         P
## 4 AFX-BioC-5_at 2652.7         P
## 5 AFX-BioC-3_at 2019.5         P
```

```
# Look at Column descriptions:
Columns(gsm)
```

```
##      Column
## 1   ID_REF
## 2   VALUE
## 3 ABS_CALL
##
##                                     Description
## 1
## 2                                     MAS 5.0 Statistical Algorithm (mean scaled to 500)
## 3 MAS 5.0 Absent, Marginal, Present call with Alpha1 = 0.05, Alpha2 = 0.065
```

The GPL class behaves exactly as the GSM class. However, the GDS class has a bit more information associated with the Columns method:

```
Columns(gds)[,1:3]
```

```
##      sample disease.state individual
## 1  GSM11815          RCC          035
## 2  GSM11832          RCC          023
## 3  GSM12069          RCC          001
## 4  GSM12083          RCC          005
## 5  GSM12101          RCC          011
## 6  GSM12106          RCC          032
## 7  GSM12274          RCC           2
## 8  GSM12299          RCC           3
## 9  GSM12412          RCC           4
## 10 GSM11810        normal          035
## 11 GSM11827        normal          023
## 12 GSM12078        normal          001
## 13 GSM12099        normal          005
## 14 GSM12269        normal           1
## 15 GSM12287        normal           2
## 16 GSM12301        normal           3
## 17 GSM12448        normal           4
```

## The GSE class

The GSE entity is the most confusing of the GEO entities. A GSE entry can represent an arbitrary number of samples run on an arbitrary number of platforms. The GSE class has a metadata section, just like the other classes. However, it doesn't have a GEODataTable. Instead, it contains two lists, accessible using the GPLList and GSMList methods, that are each lists of GPL and GSM objects. To show an example:

```
# Again, with good network access, one would do:
# gse <- getGEO("GSE781",GSEMatrix=FALSE)
gse <- getGEO(filename=system.file("extdata/GSE781_family.soft.gz",package="GEOquery"))
```

```
## Parsing....
```

```
head(Meta(gse))
```

```
## $contact_address
## [1] "715 Albany Street, E613B"
##
## $contact_city
## [1] "Boston"
##
## $contact_country
## [1] "USA"
##
## $contact_department
## [1] "Genetics and Genomics"
##
## $contact_email
## [1] "mlenburg@bu.edu"
##
## $contact_fax
## [1] "617-414-1646"
```

```
# names of all the GSM objects contained in the GSE
names(GSMList(gse))
```

```
## [1] "GSM11805" "GSM11810" "GSM11814" "GSM11815" "GSM11823" "GSM11827"
## [7] "GSM11830" "GSM11832" "GSM12067" "GSM12069" "GSM12075" "GSM12078"
## [13] "GSM12079" "GSM12083" "GSM12098" "GSM12099" "GSM12100" "GSM12101"
## [19] "GSM12105" "GSM12106" "GSM12268" "GSM12269" "GSM12270" "GSM12274"
## [25] "GSM12283" "GSM12287" "GSM12298" "GSM12299" "GSM12300" "GSM12301"
## [31] "GSM12399" "GSM12412" "GSM12444" "GSM12448"
```

```
# and get the first GSM object on the list
GSMList(gse)[[1]]
```

```
## An object of class "GSM"
## channel_count
## [1] "1"
## comment
## [1] "Raw data provided as supplementary file"
```

```

## contact_address
## [1] "715 Albany Street, E613B"
## contact_city
## [1] "Boston"
## contact_country
## [1] "USA"
## contact_department
## [1] "Genetics and Genomics"
## contact_email
## [1] "mleburg@bu.edu"
## contact_fax
## [1] "617-414-1646"
## contact_institute
## [1] "Boston University School of Medicine"
## contact_name
## [1] "Marc,E.,Lenburg"
## contact_phone
## [1] "617-414-1375"
## contact_state
## [1] "MA"
## contact_web_link
## [1] "http://gg.bu.edu"
## contact_zip/postal_code
## [1] "02130"
## data_row_count
## [1] "22283"
## description
## [1] "Age = 70; Gender = Female; Right Kidney; Adjacent Tumor Type = clear cell; Adjacent Tumor Fuhrm
## [2] "Keywords = kidney"
## [3] "Keywords = renal"
## [4] "Keywords = RCC"
## [5] "Keywords = carcinoma"
## [6] "Keywords = cancer"
## [7] "Lot batch = 2004638"
## geo_accession
## [1] "GSM11805"
## last_update_date
## [1] "May 28 2005"
## molecule_ch1
## [1] "total RNA"
## organism_ch1
## [1] "Homo sapiens"
## platform_id
## [1] "GPL96"
## series_id
## [1] "GSE781"
## source_name_ch1
## [1] "Trizol isolation of total RNA from normal tissue adjacent to Renal Cell Carcinoma"
## status
## [1] "Public on Nov 25 2003"
## submission_date
## [1] "Oct 20 2003"
## supplementary_file
## [1] "ftp://ftp.ncbi.nih.gov/pub/geo/DATA/supplementary/samples/GSM11nnn/GSM11805/GSM11805.CEL.gz"

```

```
## title
## [1] "N035 Normal Human Kidney U133A"
## type
## [1] "RNA"
## An object of class "GEODataTable"
## ***** Column Descriptions *****
##      Column
## 1  ID_REF
## 2  VALUE
## 3  ABS_CALL
##
##                                     Description
## 1
## 2                                     MAS 5.0 Statistical Algorithm (mean scaled to 500)
## 3 MAS 5.0 Absent, Marginal, Present call with Alpha1 = 0.05, Alpha2 = 0.065
## ***** Data Table *****
##      ID_REF  VALUE  ABS_CALL
## 1 AFFX-BioB-5_at  953.9      P
## 2 AFFX-BioB-M_at 2982.8      P
## 3 AFFX-BioB-3_at 1657.9      P
## 4 AFFX-BioC-5_at 2652.7      P
## 5 AFFX-BioC-3_at 2019.5      P
## 22278 more rows ...
```

```
# and the names of the GPLs represented
names(GPLList(gse))
```

```
## [1] "GPL96" "GPL97"
```

*See below for an additional, preferred method of obtaining GSE information.*

## Converting to BioConductor ExpressionSets and limma MALists

GEO datasets are (unlike some of the other GEO entities), quite similar to the `limma` data structure `MAList` and to the Biobase data structure `ExpressionSet`. Therefore, there are two functions, `GDS2MA` and `GDS2eSet` that accomplish that task.

### Getting GSE Series Matrix files as an ExpressionSet

GEO Series are collections of related experiments. In addition to being available as SOFT format files, which are quite large, NCBI GEO has prepared a simpler format file based on tab-delimited text. The `getGEO` function can handle this format and will parse very large GSEs quite quickly. The data structure returned from this parsing is a list of `ExpressionSets`. As an example, we download and parse GSE2553.

```
# Note that GSEMatrix=TRUE is the default
gse2553 <- getGEO('GSE2553', GSEMatrix=TRUE)
show(gse2553)
```

```
## $GSE2553_series_matrix.txt.gz
## ExpressionSet (storageMode: lockedEnvironment)
## assayData: 12600 features, 181 samples
```

```
## element names: exprs
## protocolData: none
## phenoData
## sampleNames: GSM48681 GSM48682 ... GSM48861 (181 total)
## varLabels: title geo_accession ... data_row_count (30 total)
## varMetadata: labelDescription
## featureData
## featureNames: 1 2 ... 12600 (12600 total)
## fvarLabels: ID PenAt ... Chimeric_Cluster_IDs (13 total)
## fvarMetadata: Column Description labelDescription
## experimentData: use 'experimentData(object)'
## Annotation: GPL1977
```

```
show(pData(phenoData(gse2553[[1]]))[1:5,c(1,6,8)])
```

```
## title
## GSM48681 Patient sample ST18, Dermatofibrosarcoma
## GSM48682 Patient sample ST410, Ewing Sarcoma
## GSM48683 Patient sample ST130, Sarcoma, NOS
## GSM48684 Patient sample ST293, Malignant Peripheral Nerve Sheath Tumor
## GSM48685 Patient sample ST367, Liposarcoma
## type source_name_ch1
## GSM48681 RNA Dermatofibrosarcoma
## GSM48682 RNA Ewing Sarcoma
## GSM48683 RNA Sarcoma, NOS
## GSM48684 RNA Malignant Peripheral Nerve Sheath Tumor
## GSM48685 RNA Liposarcoma
```

## Converting GDS to an ExpressionSet

Taking our `gds` object from above, we can simply do:

```
eset <- GDS2eSet(gds,do.log2=TRUE)
```

Now, `eset` is an `ExpressionSet` that contains the same information as in the GEO dataset, including the sample information, which we can see here:

```
eset
```

```
## ExpressionSet (storageMode: lockedEnvironment)
## assayData: 22645 features, 17 samples
## element names: exprs
## protocolData: none
## phenoData
## sampleNames: GSM11815 GSM11832 ... GSM12448 (17 total)
## varLabels: sample disease.state individual description
## varMetadata: labelDescription
## featureData
## featureNames: 200000_s_at 200001_at ... AFFX-TrpnX-M_at (22645
## total)
## fvarLabels: ID Gene title ... GO:Component ID (21 total)
## fvarMetadata: Column labelDescription
```

```
## experimentData: use 'experimentData(object)'
##   pubMedIds: 14641932
## Annotation:
```

```
pData(eset)[,1:3]
```

```
##           sample disease.state individual
## GSM11815 GSM11815         RCC         035
## GSM11832 GSM11832         RCC         023
## GSM12069 GSM12069         RCC         001
## GSM12083 GSM12083         RCC         005
## GSM12101 GSM12101         RCC         011
## GSM12106 GSM12106         RCC         032
## GSM12274 GSM12274         RCC          2
## GSM12299 GSM12299         RCC          3
## GSM12412 GSM12412         RCC          4
## GSM11810 GSM11810       normal         035
## GSM11827 GSM11827       normal         023
## GSM12078 GSM12078       normal         001
## GSM12099 GSM12099       normal         005
## GSM12269 GSM12269       normal          1
## GSM12287 GSM12287       normal          2
## GSM12301 GSM12301       normal          3
## GSM12448 GSM12448       normal          4
```

## Converting GDS to an MAList

No annotation information (called platform information by GEO) was retrieved from because `ExpressionSet` does not contain slots for gene information, typically. However, it is easy to obtain this information. First, we need to know what platform this GDS used. Then, another call to `getGEO` will get us what we need.

```
#get the platform from the GDS metadata
Meta(gds)$platform
```

```
## [1] "GPL97"
```

```
#So use this information in a call to getGEO
gpl <- getGEO(filename=system.file("extdata/GPL97.annot.gz",package="GEOquery"))
```

So, `gpl` now contains the information for GPL5 from GEO. Unlike `ExpressionSet`, the `limma MAList` does store gene annotation information, so we can use our newly created `gpl` of class `GPL` in a call to `GDS2MA` like so:

```
MA <- GDS2MA(gds,GPL=gpl)
class(MA)
```

```
## [1] "MAList"
## attr(,"package")
## [1] "limma"
```

Now, `MA` is of class `MAList` and contains not only the data, but the sample information and gene information associated with GDS507.

## Converting GSE to an ExpressionSet

First, make sure that using the method described above in the section “Getting GSE Series Matrix files as an ExpressionSet” for using GSE Series Matrix files is not sufficient for the task, as it is much faster and simpler. If it is not (i.e., other columns from each GSM are needed), then this method will be needed.

Converting a GSE object to an ExpressionSet object currently takes a bit of R data manipulation due to the varied data that can be stored in a GSE and the underlying GSM and GPL objects. However, using a simple example will hopefully be illustrative of the technique.

First, we need to make sure that all of the ‘GSMs’ are from the same platform:

```
gsmplatforms <- lapply(GSMList(gse),function(x) {Meta(x)$platform})
head(gsmplatforms)
```

```
## $GSM11805
## [1] "GPL96"
##
## $GSM11810
## [1] "GPL97"
##
## $GSM11814
## [1] "GPL96"
##
## $GSM11815
## [1] "GPL97"
##
## $GSM11823
## [1] "GPL96"
##
## $GSM11827
## [1] "GPL97"
```

Indeed, they all used GPL5 as their platform (which we could have determined by looking at the GPLList for gse, which shows only one GPL for this particular GSE.). So, now we would like to know what column represents the data that we would like to extract. Looking at the first few rows of the Table of a single GSM will likely give us an idea (and by the way, GEO uses a convention that the column that contains the single measurement for each array is called the VALUE column, which we could use if we don’t know what other column is most relevant).

```
Table(GSMList(gse)[[1]])[1:5,]
```

```
##           ID_REF  VALUE ABS_CALL
## 1 AFX-BioB-5_at  953.9         P
## 2 AFX-BioB-M_at 2982.8         P
## 3 AFX-BioB-3_at 1657.9         P
## 4 AFX-BioC-5_at 2652.7         P
## 5 AFX-BioC-3_at 2019.5         P
```

```
# and get the column descriptions
```

```
Columns(GSMList(gse)[[1]])[1:5,]
```

```
##           Column
```

```
## 1      ID_REF
## 2      VALUE
## 3      ABS_CALL
## NA      <NA>
## NA.1    <NA>
##
##                                     Description
## 1
## 2                                     MAS 5.0 Statistical Algorithm (mean scaled to 500)
## 3      MAS 5.0 Absent, Marginal, Present call with Alpha1 = 0.05, Alpha2 = 0.065
## NA                                     <NA>
## NA.1                                     <NA>
```

We will indeed use the VALUE column. We then want to make a matrix of these values like so:

```
# get the probeset ordering
probesets <- Table(GPLList(gse)[[1]])$ID
# make the data matrix from the VALUE columns from each GSM
# being careful to match the order of the probesets in the platform
# with those in the GSMs
data.matrix <- do.call('cbind',lapply(GSMList(gse),function(x)
  {tab <- Table(x)
    mymatch <- match(probesets,tab$ID_REF)
    return(tab$VALUE[mymatch])
  }))
data.matrix <- apply(data.matrix,2,function(x) {as.numeric(as.character(x))})
data.matrix <- log2(data.matrix)
data.matrix[1:5,]
```

```
##      GSM11805 GSM11810 GSM11814 GSM11815 GSM11823 GSM11827 GSM11830
## [1,] 10.926963      NA 11.105254      NA 11.275019      NA 11.438636
## [2,]  5.749534      NA  7.908092      NA  7.093814      NA  7.514122
## [3,]  7.066089      NA  7.750205      NA  7.244126      NA  7.962896
## [4,] 12.660353      NA 12.479755      NA 12.215897      NA 11.458355
## [5,]  6.195741      NA  6.061776      NA  6.565293      NA  6.583459
##      GSM11832 GSM12067 GSM12069 GSM12075 GSM12078 GSM12079 GSM12083
## [1,]      NA 11.424376      NA 11.222795      NA 11.469845      NA
## [2,]      NA  7.901470      NA  6.407693      NA  5.165912      NA
## [3,]      NA  7.337176      NA  6.569856      NA  7.477354      NA
## [4,]      NA 11.397568      NA 12.529870      NA 12.240046      NA
## [5,]      NA  6.877744      NA  6.652486      NA  3.981853      NA
##      GSM12098 GSM12099 GSM12100 GSM12101 GSM12105 GSM12106 GSM12268
## [1,] 10.823367      NA 10.835971      NA 10.810893      NA 11.062653
## [2,]  6.556123      NA  8.207014      NA  6.816344      NA  6.563768
## [3,]  7.708739      NA  7.428779      NA  7.754888      NA  7.126188
## [4,] 12.336534      NA 11.762839      NA 11.237509      NA 12.412490
## [5,]  5.501439      NA  6.247928      NA  6.017922      NA  6.525129
##      GSM12269 GSM12270 GSM12274 GSM12283 GSM12287 GSM12298 GSM12299
## [1,]      NA 10.323055      NA 11.181028      NA 11.566387      NA
## [2,]      NA  7.353147      NA  5.770829      NA  6.912889      NA
## [3,]      NA  8.742815      NA  7.339850      NA  7.602142      NA
## [4,]      NA 11.213408      NA 12.678380      NA 12.232901      NA
## [5,]      NA  6.683696      NA  5.918863      NA  5.837943      NA
##      GSM12300 GSM12301 GSM12399 GSM12412 GSM12444 GSM12448
```

```
## [1,] 11.078151      NA 11.535178      NA 11.105450      NA
## [2,]  4.812498      NA  7.471675      NA  7.488644      NA
## [3,]  7.383704      NA  7.432959      NA  7.381110      NA
## [4,] 12.090939      NA 11.421802      NA 12.172834      NA
## [5,]  6.281698      NA  5.419539      NA  5.469235      NA
```

Note that we do a match to make sure that the values and the platform information are in the same order. Finally, to make the `ExpressionSet` object:

```
require(Biobase)
# go through the necessary steps to make a compliant ExpressionSet
rownames(data.matrix) <- probesets
colnames(data.matrix) <- names(GSMList(gse))
pdata <- data.frame(samples=names(GSMList(gse)))
rownames(pdata) <- names(GSMList(gse))
pheno <- as(pdata, "AnnotatedDataFrame")
eset2 <- new('ExpressionSet', exprs=data.matrix, phenoData=pheno)
eset2
```

```
## ExpressionSet (storageMode: lockedEnvironment)
## assayData: 22283 features, 34 samples
## element names: exprs
## protocolData: none
## phenoData
## sampleNames: GSM11805 GSM11810 ... GSM12448 (34 total)
## varLabels: samples
## varMetadata: labelDescription
## featureData: none
## experimentData: use 'experimentData(object)'
## Annotation:
```

So, using a combination of `lapply` on the `GSMList`, one can extract as many columns of interest as necessary to build the data structure of choice. Because the GSM data from the GEO website are fully downloaded and included in the `GSE` object, one can extract foreground and background as well as quality for two-channel arrays, for example. Getting array annotation is also a bit more complicated, but by replacing “platform” in the `lapply` call to get platform information for each array, one can get other information associated with each array.

## Accessing Raw Data from GEO

NCBI GEO accepts (but has not always required) raw data such as `.CEL` files, `.CDF` files, images, etc. Sometimes, it is useful to get quick access to such data. A single function, `getGEOSuppFiles`, can take as an argument a GEO accession and will download all the raw data associate with that accession. By default, the function will create a directory in the current working directory to store the raw data for the chosen GEO accession. Combining a simple `sapply` statement or other loop structure with `getGEOSuppFiles` makes for a very simple way to get gobs of raw data quickly and easily without needing to know the specifics of GEO raw data URLs.

## Use Cases

`GEOquery` can be quite powerful for gathering a lot of data quickly. A few examples can be useful to show how this might be done for data mining purposes.

## Getting all Series Records for a Given Platform

For data mining purposes, it is sometimes useful to be able to pull all the GSE records for a given platform. GEOquery makes this very easy, but a little bit of knowledge of the GPL record is necessary to get started. The GPL record contains both the GSE and GSM accessions that reference it. Some code is useful to illustrate the point:

```
gpl97 <- getGEO('GPL97')
Meta(gpl97)$title
```

```
## [1] "[HG-U133B] Affymetrix Human Genome U133B Array"
```

```
head(Meta(gpl97)$series_id)
```

```
## [1] "GSE362" "GSE473" "GSE620" "GSE674" "GSE781" "GSE907"
```

```
length(Meta(gpl97)$series_id)
```

```
## [1] 151
```

```
head(Meta(gpl97)$sample_id)
```

```
## [1] "GSM3922" "GSM3924" "GSM3926" "GSM3928" "GSM3930" "GSM3932"
```

```
length(Meta(gpl97)$sample_id)
```

```
## [1] 6213
```

The code above loads the GPL97 record into R. The `Meta` method extracts a list of header information from the GPL record. The `title` gives the human name of the platform. The `series_id` gives a vector of series ids. Note that there are 151 series associated with this platform and 6213 samples. Code like the following could be used to download all the samples or series. I show only the first 5 samples as an example:

```
gsmids <- Meta(gpl97)$sample_id
gsmlist <- sapply(gsmids[1:5], getGEO)
names(gsmlist)
```

```
## [1] "GSM3922" "GSM3924" "GSM3926" "GSM3928" "GSM3930"
```

## Conclusion

The GEOquery package provides a bridge to the vast array resources contained in the NCBI GEO repositories. By maintaining the full richness of the GEO data rather than focusing on getting only the “numbers”, it is possible to integrate GEO data into current Bioconductor data structures and to perform analyses on that data quite quickly and easily. These tools will hopefully open GEO data more fully to the array community at large.

## Citing GEOquery

Please consider citing GEOquery if used in support of your own research:

```
citation("GEOquery")
```

```
##
## Please cite the following if utilizing the GEOquery software:
##
##   Davis, S. and Meltzer, P. S. GEOquery: a bridge between the Gene
##   Expression Omnibus (GEO) and BioConductor. Bioinformatics, 2007,
##   14, 1846-1847
##
## A BibTeX entry for LaTeX users is
##
##   @Article{,
##     author = {Sean Davis and Paul Meltzer},
##     title = {GEOquery: a bridge between the Gene Expression Omnibus (GEO) and BioConductor},
##     journal = {Bioinformatics},
##     year = {2007},
##     volume = {14},
##     pages = {1846--1847},
##   }
```

## Reporting problems or bugs

If you run into problems using GEOquery, the [Bioconductor Support site](#) is a good first place to ask for help. If you are convinced that there is a bug in GEOquery (this is pretty unusual, but not unheard of), feel free to submit an issue on the [GEOquery github site](#) or file a bug report directly from R (will open a new github issue):

```
bug.report(package='GEOquery')
```

## Session info

The following package and versions were used in the production of this vignette.

```
## R version 3.2.0 (2015-04-16)
## Platform: x86_64-unknown-linux-gnu (64-bit)
## Running under: Ubuntu 14.04.2 LTS
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
##  [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8    LC_NAME=C
##  [9] LC_ADDRESS=C            LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
```

```
## [1] parallel stats graphics grDevices utils datasets methods
## [8] base
##
## other attached packages:
## [1] limma_3.24.0 GEOquery_2.34.0 Biobase_2.28.0
## [4] BiocGenerics_0.14.0 knitr_1.9
##
## loaded via a namespace (and not attached):
## [1] codetools_0.2-11 XML_3.98-1.1 digest_0.6.8 bitops_1.0-6
## [5] formatR_1.1 evaluate_0.6 rmarkdown_0.5.1 tools_3.2.0
## [9] stringr_0.6.2 RCurl_1.95-4.5 yaml_2.1.13 htmltools_0.2.6
```