

Package 'KEGGandMetacoreDzPathwaysGEO'

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Type Package

Title Disease Datasets from GEO

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Description This is a collection of 18 data sets for which the phenotype is a disease with a corresponding pathway in either KEGG or metacore database. This collection of datasets were used as gold standard in comparing gene set analysis methods.

Depends R (>= 2.15.0)

Imports Biobase, BiocGenerics

biocViews ExperimentData, GEO

License GPL-2

NeedsCompilation no

R topics documented:

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KEGGandMetacoreDzPathwaysGEO-package

GEO Data Sets used to compare gene set analysis methods.

Description

This is a collection of 18 GEO datasets for which the phenotype is a disease with a corresponding pathway in either of the two popular gene to pathway annotation databases, KEGG and Metacore. These datasets were used as gold standard in comparing gene set analysis methods in the research article:

Tarca AL, Bhatti G, Romero R (2013) A Comparison of Gene Set Analysis Methods in Terms of Sensitivity, Prioritization and Specificity. PLoS ONE 8(11): e79217. doi:10.1371/journal.pone.0079217

| GEOID | Pubmed | Ref. | Disease/Target pathway | KEGGID |
|--------------------|----------|---------------------|---------------------------------------|--------------------------|
| GSE1145 | - | - | Dilated cardiomyopathy | hsa5414 |
| GSE11906 | 19852842 | <i>pmid19852842</i> | COPD | Chronic obstructive pulm |
| GSE14924_CD4 | 19710498 | <i>pmid19710498</i> | Acute myeloid leukemia | hsa5221 |
| GSE14924_CD8 | 19710498 | <i>pmid19710498</i> | Acute myeloid leukemia | hsa5221 |
| GSE16759 | 20126538 | <i>pmid20126538</i> | Alzheimer's disease | hsa5010 |
| GSE19420 | 22802091 | <i>pmid22802091</i> | Type II diabetes mellitus | hsa4930 |
| GSE20164 | 20926834 | <i>pmid20926834</i> | Parkinson's disease | hsa5012 |
| GSE23878 | 21281787 | <i>pmid21281787</i> | Colorectal cancer | hsa5210 |
| GSE24739_G0 | 21436996 | <i>pmid21436996</i> | Chronic myeloid leukemia | hsa5220 |
| GSE24739_G1 | 21436996 | <i>pmid21436996</i> | Chronic myeloid leukemia | hsa5220 |
| GSE30153 | 21886837 | <i>pmid21886837</i> | Lupus Erythematosus Systemic | Lupus Erythematosus Sy |
| GSE32676 | 22261810 | <i>pmid22261810</i> | Pancreatic cancer | hsa5212 |
| GSE38666_epithelia | 23762861 | <i>pmid23762861</i> | Ovarian cancer | Ovarian Neoplasms I |
| GSE38666_stroma | 23762861 | <i>pmid23762861</i> | Ovarian cancer | Ovarian Neoplasms I |
| GSE4183 | 19461970 | <i>pmid19461970</i> | Colorectal cancer | hsa5210 |
| GSE42057 | 23590301 | <i>pmid23590301</i> | Chronic obstructive pulmonary disease | Chronic obstructive pulm |
| GSE7305 | 17640886 | <i>pmid17640886</i> | Endometrial cancer | hsa5213 |
| GSE22780 | - | - | Pancreatic Neoplasms | Pancreatic Neoplasms |

Details

Package: KEGGandMetacoreDzPathwaysGEO
 Type: Package
 Version: 0.99.4
 Date: 2014-02-28
 License: GPL-2

Author(s)

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References

Tarca AL, Bhatti G, Romero R (2013) A Comparison of Gene Set Analysis Methods in Terms of Sensitivity, Prioritization and Specificity. PLoS ONE 8(11): e79217. doi:10.1371/journal.pone.0079217

See Also

<http://www.bioconductor.org/packages/release/data/experiment/html/KEGGdzPathwaysGEO.html>

Examples

```
mysets=data(package="KEGGandMetacoreDzPathwaysGEO")$results[, "Item"]
mysets
data(GSE1145)

set=mysets[1]
data(list=set, package="KEGGandMetacoreDzPathwaysGEO")
```

GSE1145

Data Set Id: GSE1145

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1145>

Usage

```
data(GSE1145)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE1145"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1145"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "05414"\$ disease : chr "Dilated cardiomyopathy"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x29f44c0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 26 obs. of 2 variables:\$ Sample: chr [1:26] "GSM18442" "GSM18443" "GSM18444" "GSM18445"\$ Group : chr [1:26] "c" "c" "c" "c"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 54675 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames"


```
"hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4
slots .. ..@ varMetadata :'data.frame': 0 obs. of 1 variable: .. .. ..$ labelDescription: chr(0)
.. .. ..@ data :'data.frame': 88 obs. of 0 variables .. .. ..@ dimLabels : chr [1:2] "sampleNames"
"sampleColumns" .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1
slots .. .. ..@ .Data:List of 1 .. .. .. ..$ : int [1:3] 1 1 0 ..@ .__classVersion__:Formal class
'Versions' [package "Biobase"] with 1 slots .. .. ..@ .Data:List of 4 .. .. .. ..$ : int [1:3] 3 0 0 .. ..
..$ : int [1:3] 2 20 0 .. .. .. ..$ : int [1:3] 1 3 0 .. .. .. ..$ : int [1:3] 1 0 0
```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE11906>

Examples

```
data(GSE11906)
```

GSE14924_CD4

Data Set Id: GSE14924_CD4

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14924>

Usage

```
data(GSE14924_CD4)
```

Format

```
The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData
:Formal class 'MIAME' [package "Biobase"] with 13 slots .. ..@ name : chr "GSE14924_CD4"
.. .. ..@ lab : chr "" .. .. ..@ contact : chr "" .. .. ..@ title : chr "" .. .. ..@ abstract : chr ""
.. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14924_CD4" .. .. ..@
pubMedIds : chr "" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls
: list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. .. ..$ design : chr "Not Paired"
.. .. ..$ targetGeneSets: chr "05221" .. .. ..$ disease : chr "Acute myeloid leukemia" .. .. ..@
.__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. .. ..@ .Data:List
of 2 .. .. .. ..$ : int [1:3] 1 0 0 .. .. .. ..$ : int [1:3] 1 1 0 ..@ assayData :<environment:
0x347bee0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. .. .. ..$ labelDescription: chr [1:2] NA
NA .. .. ..@ data :'data.frame': 20 obs. of 2 variables: .. .. .. ..$ Sample: chr [1:20] "GSM372721"
"GSM372722" "GSM372723" "GSM372724" ... .. .. ..$ Group : chr [1:20] "c" "c" "c" "c" ... ..
.. ..@ dimLabels : chr [1:2] "sampleNames" "sampleColumns" .. .. ..@ .__classVersion__:Formal
class 'Versions' [package "Biobase"] with 1 slots .. .. ..@ .Data:List of 1 .. .. .. ..$ : int
[1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. .. ..@ varMetadata :'data.frame': 0 obs. of 1 variable: .. .. .. ..$ labelDescription: chr(0) ..
.. ..@ data :'data.frame': 54675 obs. of 0 variables: .. .. ..@ dimLabels : chr [1:2] "featureNames"
"featureColumns" .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with
1 slots .. .. ..@ .Data:List of 1 .. .. .. ..$ : int [1:3] 1 1 0 ..@ annotation : chr
"hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4
slots .. .. ..@ varMetadata :'data.frame': 0 obs. of 1 variable: .. .. .. ..$ labelDescription: chr(0)
.. .. ..@ data :'data.frame': 20 obs. of 0 variables .. .. ..@ dimLabels : chr [1:2] "sampleNames"
```

```
"sampleColumns" .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1
slots .. ..@ .Data:List of 1 .. ..@ .$. : int [1:3] 1 1 0 ..@ .__classVersion__:Formal class
'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 4 .. ..@ .$. : int [1:3] 3 0 0 .. ..
..$. : int [1:3] 2 20 0 .. ..@ .$. : int [1:3] 1 3 0 .. ..@ .$. : int [1:3] 1 0 0
```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14924>

Examples

```
data(GSE14924_CD4)
```

GSE14924_CD8

Data Set Id: GSE14924_CD8

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14924>

Usage

```
data(GSE14924_CD8)
```

Format

```
The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData
:Formal class 'MIAME' [package "Biobase"] with 13 slots .. ..@ name : chr "GSE14924_CD8"
.. ..@ lab : chr "" .. ..@ contact : chr "" .. ..@ title : chr "" .. ..@ abstract : chr ""
.. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14924_CD8" .. ..@
pubMedIds : chr "" .. ..@ samples : list() .. ..@ hybridizations : list() .. ..@ normControls
: list() .. ..@ preprocessing : list() .. ..@ other :List of 3 .. ..@ design : chr "Not Paired"
.. ..@ targetGeneSets: chr "05221" .. ..@ disease : chr "Acute myeloid leukemia" .. ..@
.__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List
of 2 .. ..@ .$. : int [1:3] 1 0 0 .. ..@ .$. : int [1:3] 1 1 0 ..@ assayData :<environment:
0x3474e00> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..@ labelDescription: chr [1:2] NA
NA .. ..@ data :'data.frame': 21 obs. of 2 variables: .. ..@ Sample: chr [1:21] "GSM372731"
"GSM372732" "GSM372733" "GSM372734" .. ..@ Group : chr [1:21] "c" "c" "c" "c" .. ..
.. ..@ dimLabels : chr [1:2] "sampleNames" "sampleColumns" .. ..@ .__classVersion__:Formal
class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..@ .$. : int
[1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. ..@ varMetadata :'data.frame': 0 obs. of 1 variable: .. ..@ labelDescription: chr(0) .. ..
..@ data :'data.frame': 54675 obs. of 0 variables .. ..@ dimLabels : chr [1:2] "featureNames"
"featureColumns" .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with
1 slots .. ..@ .Data:List of 1 .. ..@ .$. : int [1:3] 1 1 0 ..@ annotation : chr
"hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4
slots .. ..@ varMetadata :'data.frame': 0 obs. of 1 variable: .. ..@ labelDescription: chr(0)
.. ..@ data :'data.frame': 21 obs. of 0 variables .. ..@ dimLabels : chr [1:2] "sampleNames"
"sampleColumns" .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1
slots .. ..@ .Data:List of 1 .. ..@ .$. : int [1:3] 1 1 0 ..@ .__classVersion__:Formal class
'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 4 .. ..@ .$. : int [1:3] 3 0 0 .. ..
..$. : int [1:3] 2 20 0 .. ..@ .$. : int [1:3] 1 3 0 .. ..@ .$. : int [1:3] 1 0 0
```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14924>

Examples

```
data(GSE14924_CD8)
```

GSE16759

Data Set Id: GSE16759

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16759>

Usage

```
data(GSE16759)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE16759"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16759"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "05010"\$ disease : chr "Alzheimer's disease"@ .._classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x3472060> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 8 obs. of 2 variables:\$ Sample: chr [1:8] "GSM420149" "GSM420150" "GSM420151" "GSM420152"\$ Group : chr [1:8] "c" "c" "c" "c"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .._classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 54675 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ .._classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 8 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .._classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ .._classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16759>

Examples

```
data(GSE16759)
```

GSE19420

Data Set Id: GSE19420

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19420>

Usage

```
data(GSE19420)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE19420"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19420"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "Diabetes Mellitus Type2"\$ disease : chr "Diabetes Mellitus Type2"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x3472418> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 24 obs. of 2 variables:\$ Sample: chr [1:24] "GSM482934" "GSM482938" "GSM482945" "GSM482947"\$ Group : chr [1:24] "c" "c" "c" "c"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 54675 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 24 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19420>

Examples

```
data(GSE19420)
```


GSE20164

*Data Set Id: GSE20164***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20164>

Usage

```
data(GSE20164)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE20164"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20164"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "Parkinson disease"\$ disease : chr "Parkinson disease"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x346d510> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 11 obs. of 2 variables:\$ Sample: chr [1:11] "GSM506013" "GSM506014" "GSM506019" "GSM506020"\$ Group : chr [1:11] "c" "c" "c" "c"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 22283 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ annotation : chr "hgu133a" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 11 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20164>

Examples

```
data(GSE20164)
```

GSE22780

*Data Set Id: GSE22780***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE22780>

Usage

```
data(GSE22780)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE22780"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE22780"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Paired"\$ targetGeneSets: chr "Pancreatic Neoplasms"\$ disease : chr "Pancreatic Neoplasms"@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x33b93f0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 3 obs. of 1 variable:\$ labelDescription: chr [1:3] NA NA NA@ data :'data.frame': 16 obs. of 3 variables:\$ Sample: chr [1:16] "GSM563305" "GSM563307" "GSM563309" "GSM563311"\$ Group : chr [1:16] "c" "c" "c" "c"\$ Block : chr [1:16] "1" "2" "3" "4"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 54675 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 16 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE22780>

Examples

```
data(GSE22780)
```

GSE23878

*Data Set Id: GSE23878***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE23878>

Usage

```
data(GSE23878)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE23878"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE23878"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Paired"\$ targetGeneSets: chr "05210"\$ disease : chr "Colorectal cancer"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x3466988> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 3 obs. of 1 variable:\$ labelDescription: chr [1:3] NA NA NA@ data :'data.frame': 38 obs. of 3 variables:\$ Sample: chr [1:38] "GSM588863" "GSM588864" "GSM588865" "GSM588867"\$ Group : chr [1:38] "c" "c" "c" "c"\$ Block : chr [1:38] "2" "3" "8" "11"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 54675 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 38 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE23878>

Examples

```
data(GSE23878)
```


GSE30153

*Data Set Id: GSE30153***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE30153>

Usage

```
data(GSE30153)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE30153"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE30153"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "Lupus Erythematosus Systemic"\$ disease : chr "Lupus Erythematosus Systemic"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0@ assayData :<environment: 0x345d438> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 26 obs. of 2 variables:\$ Sample: chr [1:26] "GSM746743" "GSM746744" "GSM746745" "GSM746746"\$ Group : chr [1:26] "c" "c" "c" "c"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 34853 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 26 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE30153>

Examples

```
data(GSE30153)
```

GSE32676

*Data Set Id: GSE32676***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32676>

Usage

```
data(GSE32676)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE32676"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32676"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "05212"\$ disease : chr "Pancreatic cancer"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x3456c68> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 32 obs. of 2 variables:\$ Sample: chr [1:32] "GSM811029" "GSM811030" "GSM811031" "GSM811032"\$ Group : chr [1:32] "c" "c" "c" "c"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 54675 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 32 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32676>

Examples

```
data(GSE32676)
```

GSE38666_epithelia *Data Set Id: GSE38666_epithelia*

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666>

Usage

```
data(GSE38666_epithelia)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE38666_epithelia"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets : chr "Ovarian Neoplasms1"\$ disease : chr "Ovarian Neoplasms1"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x3452868> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 30 obs. of 2 variables:\$ Sample: chr [1:30] "GSM947277" "GSM947278" "GSM947279" "GSM947280"\$ Group : chr [1:30] "c" "c" "c" "c"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 54675 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 30 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666>

Examples

```
data(GSE38666_epithelia)
```


GSE38666_stroma

*Data Set Id: GSE38666_stroma***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666>

Usage

```
data(GSE38666_stroma)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE38666_stroma"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666_epithelia"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "Not Paired"@ targetGeneSets: chr "Ovarian Neoplasms1"@ disease : chr "Ovarian Neoplasms1"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2@ : int [1:3] 1 0 0@ : int [1:3] 1 1 0 ..@ assayData :<environment: 0x33ff060> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:@ labelDescription: chr [1:2] NA NA@ data :'data.frame': 15 obs. of 2 variables:@ Sample: chr [1:15] "GSM947269" "GSM947270" "GSM947271" "GSM947272"@ Group : chr [1:15] "c" "c" "c" "c"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1@ : int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:@ labelDescription: chr(0)@ data :'data.frame': 54675 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1@ : int [1:3] 1 1 0 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:@ labelDescription: chr(0)@ data :'data.frame': 15 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1@ : int [1:3] 1 1 0 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4@ : int [1:3] 3 0 0@ : int [1:3] 2 20 0@ : int [1:3] 1 3 0@ : int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666>

Examples

```
data(GSE38666_stroma)
```

GSE4183

*Data Set Id: GSE4183***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4183>

Usage

```
data(GSE4183)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE4183"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4183"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "05210"\$ disease : chr "Colorectal cancer"@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x33fff38> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 23 obs. of 2 variables:\$ Sample: chr [1:23] "GSM95473" "GSM95474" "GSM95475" "GSM95476"\$ Group : chr [1:23] "c" "c" "c" "c"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 54675 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 23 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4183>

Examples

```
data(GSE4183)
```

GSE42057

*Data Set Id: GSE42057***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42057>

Usage

```
data(GSE42057)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE42057"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42057"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "Pulmonary Disease Chronic Obstructive"\$ disease : chr "Pulmonary Disease Chronic Obstructive"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x33eca48> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 136 obs. of 2 variables:\$ Sample: chr [1:136] "GSM1031553" "GSM1031554" "GSM1031555" "GSM1031564"\$ Group : chr [1:136] "c" "c" "c" "c"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 12531 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 136 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1\$: int [1:3] 1 1 0 ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 2 15 0\$: int [1:3] 2 16 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42057>

Examples

```
data(GSE42057)
```

GSE7305

*Data Set Id: GSE7305***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE7305>

Usage

```
data(GSE7305)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE7305"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE7305"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "Paired"@ targetGeneSets : chr "05213"@ disease : chr "Endometrial cancer"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2@ .\$. : int [1:3] 1 0 0@ .\$. : int [1:3] 1 1 0 ..@ assayData :<environment: 0x33e9dc0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 3 obs. of 1 variable:@ labelDescription: chr [1:3] NA NA NA@ data : 'data.frame': 20 obs. of 3 variables:@ Sample: chr [1:20] "GSM175776" "GSM175777" "GSM175778" "GSM175779"@ Group : chr [1:20] "c" "c" "c" "c"@ Block : chr [1:20] "1" "2" "3" "4"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1@ .\$. : int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 0 obs. of 1 variable:@ labelDescription: chr(0)@ data : 'data.frame': 54675 obs. of 0 variables@ dimLabels : chr [1:2] "featureNames" "featureColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1@ .\$. : int [1:3] 1 1 0 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 0 obs. of 1 variable:@ labelDescription: chr(0)@ data : 'data.frame': 20 obs. of 0 variables@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 1@ .\$. : int [1:3] 1 1 0 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4@ .\$. : int [1:3] 3 0 0@ .\$. : int [1:3] 2 20 0@ .\$. : int [1:3] 1 3 0@ .\$. : int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE7305>

Examples

```
data(GSE7305)
```

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