

Package 'KEGGandMetacoreDzPathwaysGEO'

August 26, 2025

Type Package

Title Disease Datasets from GEO

Version 1.28.0

Date 2014-04-25

Author Gaurav Bhatti

Maintainer Gaurav Bhatti <gbhatti@med.wayne.edu>

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

git_url <https://git.bioconductor.org/packages/KEGGandMetacoreDzPathwaysGEO>

git_branch RELEASE_3_21

git_last_commit fb4d093

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-08-26

Contents

KEGGandMetacoreDzPathwaysGEO-package	2
GSE1145	3
GSE11906	4
GSE14924_CD4	5
GSE14924_CD8	6
GSE16759	7

GSE19420	8
GSE20164	9
GSE22780	10
GSE23878	11
GSE24739_G0	12
GSE24739_G1	13
GSE30153	14
GSE32676	15
GSE38666_epithelia	16
GSE38666_stroma	17
GSE4183	18
GSE42057	19
GSE7305	20

Index	22
--------------	-----------

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 pulmona
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 Systemic
GSE32676	22261810	<i>pmid22261810</i>	Pancreatic cancer	hsa5212
GSE38666_epithelia	23762861	<i>pmid23762861</i>	Ovarian cancer	Ovarian Neoplasms1
GSE38666_stroma	23762861	<i>pmid23762861</i>	Ovarian cancer	Ovarian Neoplasms1
GSE4183	19461970	<i>pmid19461970</i>	Colorectal cancer	hsa5210
GSE42057	23590301	<i>pmid23590301</i>	Chronic obstructive pulmonary disease	Chronic obstructive pulmona
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)

Gaurav Bhatti <gbhatti@med.wayne.edu>

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" "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=GSE1145>

Examples

```
data(GSE1145)
```

GSE11906

Data Set Id: GSE11906

Description

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

Usage

```
data(GSE11906)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE11906"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE11906"@ 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: 0x3483a70> ..@ 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': 88 obs. of 2 variables:\$ Sample: chr [1:88] "GSM101095.CEL.gz" "GSM101097.CEL.gz" "GSM252799.CEL.gz" "GSM101098.CEL.gz"\$ Group : chr [1:88] "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': 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)
```

GSE24739_G0

Data Set Id: GSE24739_G0

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24739>

Usage

```
data(GSE24739_G0)
```


Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE24739_G1"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24739_G1"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "05220"\$ disease : chr "Chronic 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: 0x3460810> ..@ 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': 12 obs. of 2 variables:\$ Sample: chr [1:12] "GSM609366" "GSM609367" "GSM609368" "GSM609369"\$ Group : chr [1:12] "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': 54613 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': 12 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=GSE24739>

Examples

```
data(GSE24739_G1)
```

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	<i>Data Set Id: GSE38666_epithelia</i>
--------------------	--

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)
```

Index

* datasets

GSE1145, [3](#)
GSE11906, [4](#)
GSE14924_CD4, [5](#)
GSE14924_CD8, [6](#)
GSE16759, [7](#)
GSE19420, [8](#)
GSE20164, [9](#)
GSE22780, [10](#)
GSE23878, [11](#)
GSE24739_G0, [12](#)
GSE24739_G1, [13](#)
GSE30153, [14](#)
GSE32676, [15](#)
GSE38666_epithelia, [16](#)
GSE38666_stroma, [17](#)
GSE4183, [18](#)
GSE42057, [19](#)
GSE7305, [20](#)

* package

KEGGandMetacoreDzPathwaysGEO-package,
[2](#)

GSE7305, [20](#)

KEGGandMetacoreDzPathwaysGEO
(KEGGandMetacoreDzPathwaysGEO-package),
[2](#)
KEGGandMetacoreDzPathwaysGEO-package,
[2](#)

GSE1145, [3](#)
GSE11906, [4](#)
GSE14924_CD4, [5](#)
GSE14924_CD8, [6](#)
GSE16759, [7](#)
GSE19420, [8](#)
GSE20164, [9](#)
GSE22780, [10](#)
GSE23878, [11](#)
GSE24739_G0, [12](#)
GSE24739_G1, [13](#)
GSE30153, [14](#)
GSE32676, [15](#)
GSE38666_epithelia, [16](#)
GSE38666_stroma, [17](#)
GSE4183, [18](#)
GSE42057, [19](#)