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

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Contents

`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	*pmid19852842*	COPD	Chronic obstructive pulm
GSE14924_CD4	19710498	*pmid19710498*	Acute myeloid leukemia	hsa5221
GSE14924_CD8	19710498	*pmid19710498*	Acute myeloid leukemia	hsa5221
GSE16759	20126538	*pmid20126538*	Alzheimer's disease	hsa5010
GSE19420	22802091	*pmid22802091*	Type II diabetes mellitus	hsa4930
GSE20164	20926834	*pmid20926834*	Parkinson's disease	hsa5012
GSE23878	21281787	*pmid21281787*	Colorectal cancer	hsa5210
GSE24739_G0	21436996	*pmid21436996*	Chronic myeloid leukemia	hsa5220
GSE24739_G1	21436996	*pmid21436996*	Chronic myeloid leukemia	hsa5220
GSE30153	21886837	*pmid21886837*	Lupus Erythematosus Systemic	Lupus Erythematosus Sy
GSE32676	22261810	*pmid22261810*	Pancreatic cancer	hsa5212
GSE38666_epithelia	23762861	*pmid23762861*	Ovarian cancer	Ovarian Neoplasms1
GSE38666_stroma	23762861	*pmid23762861*	Ovarian cancer	Ovarian Neoplasms1
GSE4183	19461970	*pmid19461970*	Colorectal cancer	hsa5210
GSE42057	23590301	*pmid23590301*	Chronic obstructive pulmonary disease	Chronic obstructive pulm
GSE7305	17640886	*pmid17640886*	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" "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_G0" .. .. ..@ lab : chr "" .. .. ..@ contact : chr "" .. .. ..@ title : chr "" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24739_G0" .. .. ..@ 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: 0x34626d8> ..@ 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] "GSM609354" "GSM609355" "GSM609356" "GSM609357" ... .$ 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_G0)
```

`GSE24739_G1` *Data Set Id: GSE24739_G1*

Description

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

Usage

```
data(GSE24739_G1)
```

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` *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)
```

Index