Package 'KEGGdzPathwaysGEO'

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Type Package

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Description This is a collection of 24 data sets for which the phenotype is a disease with a corresponding pathway in the KEGG database.This collection of datasets were used as gold standard in comparing gene set analysis methods by the PADOG package.

Depends R (>= 2.13.0)

Imports Biobase, BiocGenerics

License GPL-2

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`KEGGdzPathwaysGEO-package`
GEO Data Sets used to compare gene set analysis methods by PADOG package

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Description

This is a collection of 24 data sets for which the phenotype is a disease with a corresponding pathway in the KEGG database. This collection of datasets were used as gold standard in comparing gene set analysis methods by the PADOG package.

GEOID	Pubmed	Ref.	Disease/Target pathway	KEGGID	Tissue
GSE1297	14769913	*pmid14769913*	Alzheimer's Disease	hsa05010	Hippocampal CA1
GSE5281	17077275	*pmid17077275*	Alzheimer's Disease	hsa05010	Brain, Entorhinal Cortex
GSE5281	17077275	*pmid17077275*	Alzheimer's Disease	hsa05010	Brain, hippocampus
GSE5281	17077275	*pmid17077275*	Alzheimer's Disease	hsa05010	Brain, Primary visual cortex
GSE20153	20926834	*pmid20926834*	Parkinson's disease	hsa05012	Lymphoblasts
GSE20291	15965975	*pmid15965975*	Parkinson's disease	hsa05012	Postmortem brain putamen
GSE8762	17724341	*pmid17724341*	Huntington's disease	hsa05016	Lymphocytes (blood)
GSE4107	17317818	*pmid17317818*	Colorectal Cancer	hsa05210	Mucosa
GSE8671	18171984	*pmid18171984*	Colorectal Cancer	hsa05210	Colon
GSE9348	20143136	*pmid20143136*	Colorectal Cancer	hsa05210	Colon
GSE14762	19252501	*pmid19252501*	Renal Cancer	hsa05211	Kidney
GSE781	14641932	*pmid14641932*	Renal Cancer	hsa05211	Kidney
GSE15471	19260470	*pmid19260470*	Pancreatic Cancer	hsa05212	Pancreas
GSE16515	19732725	*pmid19732725*	Pancreatic Cancer	hsa05212	Pancreas
GSE19728		-	Glioma	hsa05214	Brain

GSE21354		-	Glioma	hsa05214	Brain, Spine
GSE6956	18245496	*pmid18245496*	Prostate Cancer	hsa05215	Prostate
GSE6956	18245496	*pmid18245496*	Prostate Cancer	hsa05215	Prostate
GSE3467	16365291	*pmid16365291*	Thyroid Cancer	hsa05216	Thyroid
GSE3678		-	Thyroid Cancer	hsa05216	Thyroid
GSE9476	17910043	*pmid17910043*	Acute myeloid leukemia	hsa05221	Blood, Bone marrow
GSE18842	20878980	*pmid20878980*	Non-Small Cell Lung Cancer	hsa05223	Lung
GSE19188	20421987	*pmid20421987*	Non-Small Cell Lung Cancer	hsa05223	Lung
GSE3585	17045896	*pmid17045896*	Dilated cardiomyopathy	hsa05414	Heart

Details

Package:	KEGGdzPathwaysGEO
Type:	Package
Version:	1.0
Date:	2012-07-23
License:	GPL-2

Author(s)

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References

Tarca AL, Draghici S, Bhatti G, Romero R (2012) Down-weighting overlapping genes improves gene set analysis.BMC Bioinformatics 13:136.

Examples

```
mysets=data(package="KEGGdzPathwaysGEO")$results[,"Item"]
mysets
data(GSE8671)

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

GSE1297 *Gene Expression Omnibus (GEO) Data Set Id: GSE1297*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1297

Usage

```
data(GSE1297)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE1297" .. .. ..@ lab : chr "Landfield" .. .. ..@ contact : chr "emblal@uky.edu" .. .. ..@ title : chr "Incipient Alzheimer's Disease: Microarray Correlation Analyses" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1297" .. .. ..@ pubMedIds : chr "14769913" .. .. ..@ 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: 0x3f9e5268> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 16 obs. of 2 variables: .. ..$ Sample: chr [1:16] "GSM21215" "GSM21217" "GSM21218" "GSM21219" ... .$ Group : chr [1:16] "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': 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] 2 15 0 .. ..$: int [1:3] 2 16 0 .. ..$: int [1:3] 1 3 0 .. ..$: int [1:3] 1 0 0

Details

Samples belonging to the Severe and Control groups are included.The sample, GSM21207, was excluded during Quality Control.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1297

Examples

```
data(GSE1297)
```

GSE14762 *Gene Expression Omnibus (GEO) Data Set Id: GSE14762*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14762

Usage

```
data(GSE14762)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE14762" .. .. ..@ lab : chr "Lab of Computational Biology" .. .. ..@ contact : chr "NA" .. .. ..@ title : chr "Renal Cell Carcinoma: Hypoxia and Endocytosis" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14762" .. .. ..@ pubMedIds : chr "19252501" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Not Paired" .. ..$ targetGeneSets: chr "05211" .. ..$ disease : chr "Renal 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: 0x3f9eaa60> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 21 obs. of 2 variables: .. ..$ Sample: chr [1:21] "GSM368649" "GSM368650" "GSM368651" "GSM368652" ... .$ 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] 2 15 0 .. ..$: int [1:3] 2 16 0 .. ..$: int [1:3] 1 3 0 .. ..$: int [1:3] 1 0 0

Details

The sample, GSM368647, was excluded during Quality Control.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14762

Examples

```
data(GSE14762)
```

GSE15471 *Gene Expression Omnibus (GEO) Data Set Id: GSE15471*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE15471

Usage

```
data(GSE15471)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE15471" .. .. ..@ lab : chr "AI and Bioinformatics" .. .. ..@ contact : chr "badea.liviu@gmail.com" .. .. ..@ title : chr "Whole-Tissue Gene Expression Study of Pancreatic Ductal Adenocarcinoma" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE15471" .. .. ..@ pubMedIds : chr "19260470" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "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: 0x3f9f19b8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 3 obs. of 1 variable: .. ..$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID" .. .. ..@ data :'data.frame': 70 obs. of 3 variables: .. ..$ Sample: chr [1:70] "GSM388076" "GSM388078" "GSM388080" "GSM388082" ... .$ Group : chr [1:70] "c" "c" "c" "c" ... .$ Block : chr [1:70] "30162" "40728" "41027" "30057" ... .@ 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': 70 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

Details

Samples, GSM388077, GSM388079, GSM388081, GSM388116, GSM388118, GSM388120 were excluded because they were replicates. Samples, GSM388111 and GSM388150, were excluded during Quality Control.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE15471

Examples

```
data(GSE15471)
```

GSE16515 *Gene Expression Omnibus (GEO) Data Set Id: GSE16515*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16515

Usage

```
data(GSE16515)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE16515" .. .. ..@ lab : chr "NA" .. .. ..@ contact : chr "wang.liewei@mayo.edu" .. .. ..@ title : chr "Expression data from Mayo Clinic Pancreatic Tumor and Normal samples" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16515" .. .. ..@ pubMedIds : chr "19732725" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "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: 0x3f9f8150> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 3 obs. of 1 variable: .. ..$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID" .. .. ..@ data :'data.frame': 30 obs. of 3 variables: .. ..$ Sample: chr [1:30] "GSM414928" "GSM414930" "GSM414934" "GSM414938" ... .$ Group : chr [1:30] "c" "c" "c" "c" ... .$ Block : chr [1:30] "16" "53" "11" "54" ... .@ 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] 2 15 0 .. ..$: int [1:3] 2 16 0 .. ..$: int [1:3] 1 3 0 .. ..$: int [1:3] 1 0 0

Details

Only those samples that consisted of both tumor and normal expression data were included. Samples, GSM414931 and GSM414932, were excluded during Quality Control.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16515

Examples

```
data(GSE16515)
```

GSE18842 *Gene Expression Omnibus (GEO) Data Set Id: GSE18842*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE18842

Usage

```
data(GSE18842)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE18842" .. .. ..@ lab : chr "NA" .. .. ..@ contact : chr "efarez@ugr.es" .. .. ..@ title : chr "Gene expression analysis of human lung cancer and control samples" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE18842" .. .. ..@ pubMedIds : chr "20878980" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Paired" .. ..$ targetGeneSets: chr "05223" .. ..$ disease : chr "Non Small Cell Lung 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: 0x3f9fe140> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 3 obs. of 1 variable: .. ..$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID" .. .. ..@ data :'data.frame': 88 obs. of 3 variables: .. ..$ Sample: chr [1:88] "GSM466948" "GSM466950" "GSM466953" "GSM466955" ... .$ Group : chr [1:88] "c" "c" "c" "c" ... .$ Block : chr [1:88] "2" "3" "9" "10" ... .@ 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] 2 15 0 .. ..$: int [1:3] 2 16 0 .. ..$: int [1:3] 1 3 0 .. ..$: int [1:3] 1 0 0

Details

Only those samples were included that were paired.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE18842

Examples

```
data(GSE18842)
```

GSE19188 *Gene Expression Omnibus (GEO) Data Set Id: GSE19188*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19188

Usage

```
data(GSE19188)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE19188" .. .. ..@ lab : chr "NA" .. .. ..@ contact : chr "j.philipsen@erasmusmc.nl" .. .. ..@ title : chr "Expression data for early stage NSCLC" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19188" .. .. ..@ pubMedIds : chr "20421987" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Not Paired" .. ..$ targetGeneSets: chr "05223" .. ..$ disease : chr "Non Small Cell Lung 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: 0x3fa048d8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 153 obs. of 2 variables: .. ..$ Sample: chr [1:153] "GSM475657" "GSM475658" "GSM475660" "GSM475663" ... .$ Group : chr [1:153] "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': 153 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

Details

Samples, GSM475659, GSM475666 and GSM475781, were excluded during Quality Control.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19188

Examples

```
data(GSE19188)
```

GSE19728 *Gene Expression Omnibus (GEO) Data Set Id: GSE19728*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19728

Usage

```
data(GSE19728)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE19728" .. .. ..@ lab : chr "NA" .. .. ..@ contact : chr "yaozhq11@hotmail.com" .. .. ..@ title : chr "Expression data from different grades (WHO) of astrocytomas (ACM)" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19728" .. .. ..@ pubMedIds : chr "NA" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Not Paired" .. ..$ targetGeneSets: chr "05214" .. ..$ disease : chr "Glioma" .. .. ..@ .__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: 0x3fa0a8c8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 21 obs. of 2 variables: .. ..$ Sample: chr [1:21] "GSM492649" "GSM525014" "GSM525015" "GSM525016" ... .$ 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] 2 15 0 .. ..$: int [1:3] 2 16 0 .. ..$: int [1:3] 1 3 0 .. ..$: int [1:3] 1 0 0

Details

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19728

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19728

Examples

```
data(GSE19728)
```

GSE20153 *Gene Expression Omnibus (GEO) Data Set Id: GSE20153*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20153

Usage

```
data(GSE20153)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE20153" .. .. ..@ lab : chr "NA" .. .. ..@ contact : chr "middletf@upstate.edu" .. .. ..@ title : chr "Expression analysis of lymphoblast cells lines in Parkinson's disease" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20153" .. .. ..@ pubMedIds : chr "20926834" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Not Paired" .. ..$ targetGeneSets: chr "05012" .. ..$ disease : chr "Parkinson'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: 0x2cb8a330> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 16 obs. of 2 variables: .. ..$ Sample: chr [1:16] "GSM505297" "GSM505298" "GSM505299" "GSM505300" ... .$ Group : chr [1:16] "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': 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 .. ..$: int [1:3] 2 15 0 .. ..$: int [1:3] 2 16 0 .. ..$: int [1:3] 1 3 0 .. ..$: int [1:3] 1 0 0

Details

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20153

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20153

Examples

```
data(GSE20153)
```

GSE20291 *Gene Expression Omnibus (GEO) Data Set Id: GSE20291*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20291

Usage

```
data(GSE20291)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE20291" .. .. ..@ lab : chr "NA" .. .. ..@ contact : chr "middletf@upstate.edu" .. .. ..@ title : chr "Transcriptional analysis of putamen in Parkinson's disease" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20291" .. .. ..@ pubMedIds : chr "15965975" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Not Paired" .. ..$ targetGeneSets: chr "05012" .. ..$ disease : chr "Parkinson'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: 0x2cb9b7d8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 33 obs. of 2 variables: .. ..$ Sample: chr [1:33] "GSM508594" "GSM508683" "GSM508686" "GSM508687" ... .$ Group : chr [1:33] "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': 33 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

Details

Samples, GSM508611 and GSM606622, were excluded during Quality Control.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20291

Examples

```
data(GSE20291)
```

GSE21354 *Gene Expression Omnibus (GEO) Data Set Id: GSE21354*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE21354

Usage

```
data(GSE21354)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE21354" .. .. ..@ lab : chr "NA" .. .. ..@ contact : chr "yaozhq11@hotmail.com" .. .. ..@ title : chr "gene expression profiling of three type of grade II gliomas" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE21354" .. .. ..@ pubMedIds : chr "NA" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Not Paired" .. ..$ targetGeneSets: chr "05214" .. ..$ disease : chr "Glioma" .. .. ..@ .__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: 0x2cba1008> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 17 obs. of 2 variables: .. ..$ Sample:

chr [1:17] "GSM492649" "GSM525014" "GSM525015" "GSM525016" ... .$ Group : chr [1:17] "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': 17 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

Details

Sample, GSM492652, was excluded during Quality Control.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE21354

Examples

```
data(GSE21354)
```

GSE3467 *Gene Expression Omnibus (GEO) Data Set Id: GSE3467*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3467

Usage

```
data(GSE3467)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE3467" .. .. ..@ lab : chr "Davuluri Lab" .. .. ..@ contact : chr "sandya.liyanarachchi@osumc.edu" .. .. ..@ title : chr "The role of micro-RNA genes in papillary thyroid carcinoma" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3467" .. .. ..@ pubMedIds : chr "16365291" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@

normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Paired" .. ..$ targetGeneSets: chr "05216" .. ..$ disease : chr "Thyroid 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: 0x2cba7f60> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 3 obs. of 1 variable: .. ..$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID" .. .. ..@ data :'data.frame': 18 obs. of 3 variables: .. ..$ Sample: chr [1:18] "GSM77362" "GSM77364" "GSM77366" "GSM77368" ... .$ Group : chr [1:18] "c" "c" "c" "c" ... .$ Block : chr [1:18] "14" "26" "50" "69" ... .@ 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': 18 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

Details

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3467

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3467

Examples

```
data(GSE3467)
```

`GSE3585` *Gene Expression Omnibus (GEO) Data Set Id: GSE3585*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3585

Usage

```
data(GSE3585)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE3585" .. .. ..@ lab : chr "Unit Cancer Genome Research" .. .. ..@ contact : chr "r.kuner@dkfz.de" .. .. ..@ title : chr "Dilated Cardiomyopathy and Non Failing Biopsies" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3585" .. .. ..@ pubMedIds : chr "17045896" .. .. ..@ 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: 0x2cbaeeb8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 12 obs. of 2 variables: .. ..$ Sample: chr [1:12] "GSM82381" "GSM82382" "GSM82383" "GSM82384" ... .$ 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': 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': 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] 2 15 0 .. ..$: int [1:3] 2 16 0 .. ..$: int [1:3] 1 3 0 .. ..$: int [1:3] 1 0 0

Details

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3585

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3585

Examples

```
data(GSE3585)
```

GSE3678 *Gene Expression Omnibus (GEO) Data Set Id: GSE3678*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3678

Usage

```
data(GSE3678)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE3678" .. .. ..@ lab : chr "NA" .. .. ..@ contact : chr "ismael_reyes@nymc.edu" .. .. ..@ title : chr "PTC versus paired normal thyroid tissue" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3678" .. .. ..@ pubMedIds : chr "NA" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Paired" .. ..$ targetGeneSets: chr "05216" .. ..$ disease : chr "Thyroid 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: 0x2cbb46e8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 3 obs. of 1 variable: .. ..$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID" .. .. ..@ data :'data.frame': 14 obs. of 3 variables: .. ..$ Sample: chr [1:14] "GSM85215" "GSM85216" "GSM85217" "GSM85218" ... .$ Group : chr [1:14] "c" "c" "c" "c" ... .$ Block : chr [1:14] "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': 14 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

Details

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3678

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3678

Examples

```
data(GSE3678)
```

GSE4107 *Gene Expression Omnibus (GEO) Data Set Id: GSE4107*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4107

Usage

```
data(GSE4107)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE4107" .. .. ..@ lab : chr "CRC research lab" .. .. ..@ contact : chr "hong.yi@sgh.com.sg;fbap8570@yahoo.com" .. .. ..@ title : chr "Expression profiling in early onset colorectal cancer" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4107" .. .. ..@ pubMedIds : chr "17317818" .. .. ..@ 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: 0x41550490> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 22 obs. of 2 variables: .. ..$ Sample: chr [1:22] "GSM93938" "GSM93939" "GSM93941" "GSM93943" ... .$ Group : chr [1:22] "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': 22 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

Details

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4107

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4107

Examples

```
data(GSE4107)
```

`GSE5281_EC` *Gene Expression Omnibus (GEO) Data Set Id: GSE5281. GSE5281_EC contains data for Entorhinal cortex samples from the data set GSE5281.*

Description

GSE5281_EC contains data for Entorhinal cortex samples from the data set GSE5281. For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281

Usage

```
data(GSE5281_EC)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE5281_EC" .. .. ..@ lab : chr "NIH Neuroscience Microarray Consortium" .. .. ..@ contact : chr "bhamill@mednet.ucla.edu" .. .. ..@ title : chr "Alzheimer's disease and the normal aged brain (steph-affy-human-433773)" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281" .. .. ..@ pubMedIds : chr "17077275" .. .. ..@ 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: 0x415573e8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 21 obs. of 2 variables: .. ..$ Sample: chr [1:21] "GSM119615" "GSM119616" "GSM119617" "GSM119618" ... .$ 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] 2 15 0 .. ..$: int [1:3] 2 16 0 .. ..$: int [1:3] 1 3 0 .. ..$: int [1:3] 1 0 0

Details

GSE5281_EC contains data for Entorhinal cortex samples from the data set GSE5281. The samples, GSM119626 and GSM238763, were excluded during Quality Control.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281

Examples

```
data(GSE5281_EC)
```

GSE5281_HIP *Gene Expression Omnibus (GEO) Data Set Id: GSE5281.GSE5281_HIP contains data for hippocampus samples from the data set GSE5281.*

Description

GSE5281_HIP contains data for hippocampus samples from the data set GSE5281. For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281

Usage

```
data(GSE5281_HIP)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE5281_HIP" .. .. ..@ lab : chr "NIH Neuroscience Microarray Consortium" .. .. ..@ contact : chr "bhamill@mednet.ucla.edu" .. .. ..@ title : chr "Alzheimer's disease and the normal aged brain (steph-affy-human-433773)" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281"

.. .. ..@ pubMedIds : chr "17077275" .. .. ..@ 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: 0x4155cc18> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 23 obs. of 2 variables: .. ..$ Sample: chr [1:23] "GSM119628" "GSM119629" "GSM119630" "GSM119631" ... .$ 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] 2 15 0 .. ..$: int [1:3] 2 16 0 .. ..$: int [1:3] 1 3 0 .. ..$: int [1:3] 1 0 0

Details

GSE5281_HIP contains data for hippocampus samples from the data set GSE5281.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281

Examples

```
data(GSE5281_HIP)
```

`GSE5281_VCX` *Gene Expression Omnibus (GEO) Data Set Id: GSE5281. GSE5281_VCX contains data for Visual Cortex samples from the data set GSE5281.*

Description

GSE5281_VCX contains data for Visual Cortex samples from the data set GSE5281. For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281

Usage

```
data(GSE5281_VCX)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE5281_VCX" .. .. ..@ lab : chr "NIH Neuroscience Microarray Consortium" .. .. ..@ contact : chr "bhamill@mednet.ucla.edu" .. .. ..@ title : chr "Alzheimer's disease and the normal aged brain (steph-affy-human-433773)" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281" .. .. ..@ pubMedIds : chr "17077275" .. .. ..@ 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: 0x2cbb3168> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 31 obs. of 2 variables: .. ..$ Sample: chr [1:31] "GSM119677" "GSM119678" "GSM119679" "GSM119680" ... .$ Group : chr [1:31] "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': 31 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

Details

GSE5281_VCX contains data for Visual Cortex samples from the data set GSE5281.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281

Examples

```
data(GSE5281_VCX)
```

GSE6956AA *Gene Expression Omnibus (GEO) Data Set Id: GSE6956. GSE6956AA contains data for African-American Men from the data set GSE6956*

Description

GSE6956AA contains data for African-American Men from the data set GSE6956. For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE6956

Usage

```
data(GSE6956AA)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE6956AA" .. .. ..@ lab : chr "The Laboratory of Human Carcinogenesis" .. .. ..@ contact : chr "NA" .. .. ..@ title : chr "Tumor Immunobiological Differences in Prostate Cancer between African-American and European-American Men" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GS .. .. ..@ pubMedIds : chr "18245496" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Paired" .. ..$ targetGeneSets: chr "05215" .. ..$ disease : chr "Prostate 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: 0x2cb95870> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 3 obs. of 1 variable: .. ..$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID" .. .. ..@ data :'data.frame': 10 obs. of 3 variables: .. ..$ Sample: chr [1:10] "GSM160404" "GSM160424" "GSM160427" "GSM160428" ... .$ Group : chr [1:10] "c" "c" "c" "c" ... .$ Block : chr [1:10] "65" "51" "16" "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': 22277 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': 10 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

Details

GSE6956AA contains data for African-American Men from the data set GSE6956.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE6956

Examples

```
data(GSE6956AA)
```

GSE6956C — *Gene Expression Omnibus (GEO) Data Set Id: GSE6956. GSE6956C contains data for European-American Men from the data set GSE6956.*

Description

GSE6956C contains data for European-American Men from the data set GSE6956. For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE6956

Usage

```
data(GSE6956C)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE6956C" .. .. ..@ lab : chr "The Laboratory of Human Carcinogenesis" .. .. ..@ contact : chr "NA" .. .. ..@ title : chr "Tumor Immunobiological Differences in Prostate Cancer between African-American and European-American Men" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GS .. .. ..@ pubMedIds : chr "18245496" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Paired" .. ..$ targetGeneSets: chr "05215" .. ..$ disease : chr "Prostate 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: 0x3f9f5cd8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 3 obs. of 1 variable: .. ..$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID" .. .. ..@ data :'data.frame': 16 obs. of 3 variables: .. ..$ Sample: chr [1:16] "GSM160402" "GSM160407" "GSM160409" "GSM160411" ... .$ Group : chr [1:16] "c" "c" "c" "c" ... .$ Block : chr [1:16] "63" "68" "70" "72" ... .@ 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': 22277 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': 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] 2 15 0 .. ..$: int [1:3] 2 16 0 .. ..$: int [1:3] 1 3 0 .. ..$: int [1:3] 1 0 0

Details

GSE6956C contains data for European-American Men from the data set GSE6956.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE6956

Examples

```
data(GSE6956C)
```

GSE781 *Gene Expression Omnibus (GEO) Data Set Id: GSE781*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE781

Usage

```
data(GSE781)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE781" .. .. ..@ lab : chr "NA" .. .. ..@ contact : chr "mlenburg@bu.edu" .. .. ..@ title : chr "Normal and Renal Cell Carcinoma Kidney Tissue, Human" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE781" .. .. ..@ pubMedIds : chr "14641932" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Not Paired" .. ..$ targetGeneSets: chr "05211" .. ..$ disease : chr "Renal 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: 0x2a6cbd18> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample

ID" "Control/Disease status" .. .. ..@ data :'data.frame': 17 obs. of 2 variables: .. ..$ Sample: chr [1:17] "GSM11805" "GSM11823" "GSM12075" "GSM12098" ... .$ Group : chr [1:17] "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': 17 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

Details

Samples run on the chip, hgu133a, are included.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE781

Examples

```
data(GSE781)
```

`GSE8671` *Gene Expression Omnibus (GEO) Data Set Id: GSE8671*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8671

Usage

```
data(GSE8671)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE8671" .. .. ..@ lab : chr "NA" .. .. ..@ contact : chr "marra@imcr.uzh.ch" .. .. ..@ title : chr "Transcriptome profile of human colorectal adenomas." .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8671" .. .. ..@ pubMedIds : chr "18171984" .. .. ..@ 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: 0x383c9608> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 3 obs. of 1 variable: .. ..$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID" .. .. ..@ data :'data.frame': 64 obs. of 3 variables: .. ..$ Sample: chr [1:64] "GSM215051" "GSM215052" "GSM215053" "GSM215054" ... .$ Group : chr [1:64] "c" "c" "c" "c" ... .$ Block : chr [1:64] "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': 64 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

Details

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8671

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8671

Examples

```
data(GSE8671)
```

GSE8762 *Gene Expression Omnibus (GEO) Data Set Id: GSE8762*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8762

Usage

```
data(GSE8762)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE8762" .. .. ..@ lab : chr "Laboratory of Neurogenetics" .. .. ..@ contact : chr "kuhnam@mail.nih.gov" .. .. ..@ title : chr "Lymphocyte gene expression data from moderate stage HD patients and controls" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8762" .. .. ..@ pubMedIds : chr "17724341" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other :List of 3 .. ..$ design : chr "Not Paired" .. ..$ targetGeneSets: chr "05016" .. ..$ disease : chr "Huntington'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: 0x7e09e1f0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 22 obs. of 2 variables: .. ..$ Sample: chr [1:22] "GSM217766" "GSM217767" "GSM217768" "GSM217769" ... .$ Group : chr [1:22] "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': 22 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

Details

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8762

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8762

Examples

```
data(GSE8762)
```

GSE9348 *Gene Expression Omnibus (GEO) Data Set Id: GSE9348*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9348

Usage

```
data(GSE9348)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE9348" .. .. ..@ lab : chr "CRC research lab" .. .. ..@ contact : chr "hong.yi@sgh.com.sg;fbap8570@yahoo.com" .. .. ..@ title : chr "Expression data from healthy controls and early stage CRC patient's tumor" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9348" .. .. ..@ pubMedIds : chr "20143136" .. .. ..@ 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: 0x6239b018> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 82 obs. of 2 variables: .. ..$ Sample: chr [1:82] "GSM237984" "GSM237985" "GSM237986" "GSM237987" ... .$ Group : chr [1:82] "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': 82 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

Details

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9348

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9348

Examples

```
data(GSE9348)
```

GSE9476 *Gene Expression Omnibus (GEO) Data Set Id: GSE9476*

Description

For detailed description visit: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9476

Usage

```
data(GSE9476)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "GSE9476" .. .. ..@ lab : chr "Stirewalt Lab" .. .. ..@ contact : chr "dstirewa@fhcrc.org" .. .. ..@ title : chr "Abnormal Expression Changes in AML" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9476" .. .. ..@ pubMedIds : chr "17910043" .. .. ..@ 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: 0x6a5d4cd0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 2 obs. of 1 variable: .. ..$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. ..@ data :'data.frame': 63 obs. of 2 variables: .. ..$ Sample: chr [1:63] "GSM239170" "GSM239323" "GSM239324" "GSM239326" ... .$ Group : chr [1:63] "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': 63 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

Details

The sample, GSM240433, was excluded during Quality Control.

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9476

Examples

```
data(GSE9476)
```

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