

Package ‘MEALData’

April 20, 2016

Type Package

Title Example data of MEAL package

Version 1.0.0

Description The package contains methylation, expression and SNPs data obtained from GSE53261. It is used in MEAL case example to show MEAL functionalities.

License Artistic-2.0

LazyData TRUE

Depends R (>= 3.2.0)

biocViews Homo_sapiens_Data, MicroarrayData

NeedsCompilation no

Author Ruiz Carlos [aut, cre], Hernandez Carles [aut], Gonzalez JR [aut]

Maintainer Ruiz Carlos <cruiz@creal.cat>

R topics documented:

| | |
|----------|---|
| betavals | 1 |
| eset | 2 |
| MEALData | 2 |
| pheno | 3 |
| snps | 3 |

| | |
|--------------|----------|
| Index | 4 |
|--------------|----------|

| | |
|----------|--|
| betavals | <i>Methylation values for 62 individuals</i> |
|----------|--|

Description

A dataset containing the beta values of more than 450k cpgs and 62 samples.

Usage

betavals

Format

A matrix with 451448 rows and 62 columns.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52025>

| | |
|------|---------------------------------------|
| eset | <i>Expression data for 64 samples</i> |
|------|---------------------------------------|

Description

A dataset containing expression values for 21916 features and 64 samples, the annotation of the features and the phenotypic data of the samples.

Usage

eset

Format

An ExpressionSet

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE53243>

| | |
|----------|--|
| MEALData | <i>MEALData: Data package used to show functionalities of MEAL package</i> |
|----------|--|

Description

MEALData contains data from GEO GSE53261 adapted to show MEAL functionalities. There are four datasets in the package: betavals, pheno, eset and snps.

| | |
|-------|---|
| pheno | <i>Phenotype values for methylation individuals</i> |
|-------|---|

Description

A dataset containing phenotypic variables for the 62 samples with beta values.

Usage

pheno

Format

A data.frame with 62 rows and 2 columns.

gender gender of the donor of the fibroblast

source cell source of the fibroblast

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52025>

| | |
|------|---------------------------------|
| snps | <i>SNPs data for 98 samples</i> |
|------|---------------------------------|

Description

A dataset containing genotypes for 100000 SNPs and 98 samples and the annotation of these SNPs.

Usage

snps

Format

A list with elements:

genotypes matrix of 100000 rows and 98 columns with the genotypes in the numeric form

map data.frame of 100000 rows and 5 columns:

- Chromosome: SNP's chromosome
- snp.name: SNP's name
- position: SNP's position
- SNP: minor and major allele
- chromosome: SNP's chromosome with string "chr"

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52442>

Index

*Topic **datasets**

betavals, [1](#)

eset, [2](#)

pheno, [3](#)

snps, [3](#)

betavals, [1](#)

eset, [2](#)

MEALData, [2](#)

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

pheno, [3](#)

snps, [3](#)