

# Package ‘MEALData’

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**Type** Package

**Title** Example data of MEAL package

**Version** 1.9.1

**Description** The package contains methylation, expression and SNPs data obtained from GSE53261 and TCGA. 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

**RoxygenNote** 6.0.1

**Encoding** UTF-8

**PackageStatus** Deprecated

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betavals

*Methylation values for 62 individuals*

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**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>

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BRCAexpr

*Expression data of BRCA samples*

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**Description**

An ExpressionSet containing the expression values of 14779 features and 27 samples, the phenotypic data and the annotation. It is a subset of TCGA's breast cancer samples.

**Usage**

```
BRCAexpr
```

**Format**

An ExpressionSet

**Source**

<https://tcga-data.nci.nih.gov/tcga/dataAccessMatrix.htm>

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BRCAmeth	<i>Methylation data of BRCA samples</i>
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**Description**

A MethylationSet containing the methylation values of 384829 features and 27 samples, the phenotypic data and the annotation. It is a subset of TCGA's breast cancer samples.

**Usage**

BRCAmeth

**Format**

A MethylationSet

**Source**

<https://tcga-data.nci.nih.gov/tcga/dataAccessMatrix.htm>

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eset	<i>Expression data for 64 samples</i>
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**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>

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MEALData	<i>MEALData: Data package used to show functionalities of MEAL package</i>
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**Description**

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

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mset	<i>Methylation data for 64 samples #' A dataset containing the beta values of more than 450k cpgs and 62 samples. A dataset containing expression values for more than 450k cpgs features and 62 samples, the annotation of the features and the phenotypic data of the samples.</i>
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**Description**

Methylation data for 64 samples #' A dataset containing the beta values of more than 450k cpgs and 62 samples. A dataset containing expression values for more than 450k cpgs features and 62 samples, the annotation of the features and the phenotypic data of the samples.

**Usage**

mset

**Format**

A MethylationSet

**Source**

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

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pheno	<i>Phenotype values for methylation individuals</i>
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**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 donnor of the fibroblast

**source** cell source of the fibroblast

**inv** inversion 17q21.31 haplotype of the sample

**Source**

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

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snps

*SNPs data for 98 samples*

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### Description

A dataset containing genotypes for 29909 SNPs and 98 samples and the annotation of these SNPs. All the SNPs belong to chromosome 17. Probes not measuring SNPs or with only a genotype have been filtered out.

### Usage

snps

### Format

A list with elements:

**genotypes** matrix of 29909 rows and 98 columns with the genotypes in the numeric form

**map** data.frame of 29909 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>

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