Package ‘ChAMPdata’

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Type Package

Title Data Packages for ChAMP package

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Description

Provides datasets needed for ChAMP including a test dataset and blood controls for CNA analysis.

License GPL-3

Depends GenomicRanges (>= 1.22.4),BiocGenerics(>= 0.16.1),R (>= 3.2)

biocViews ExperimentData

NeedsCompilation no

R topics documented:

`ChAMPdata-package` *Data Packages to use with the ChAMP Chip Analysis Methylation Pipeline*

Description

This includes four data packages. ProbeInfoALL.lv includes annotation for the 450k array as required by the BMIQ normalization. probe.features includes probe annotations for the 450k array as included in the saved results files for the MVP and DMR functions. champBloodCtls provides reference control data for the champ.CNA function. testDataSet includes loaded and filtered (for detection) p-value of 6 arrays for the 450k array along with an accompanying samples sheet. This can be used to test the package. In addition, the raw IDAT files for these 6 arrays are available and can be accessed using system.file().

Details

Package:	ChAMPdata
Type:	Package
Version:	1.9.3
Date:	2016-03-22
License:	GPL-3

Three of the four packages are used internally by the ChAMP package. The testDataSet can be used to test the package.

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Examples

```
data(probeInfoALL.lv)
data(probe.features)
data(testDataSet)
data(champBloodCtls)
data(EPICSimData)
data(illumina450Gr)
data(illuminaEPICGr)
data(probeInfoALL.epic.lv)
data(probe.features.epic)
data(CellTypeMeans27K)
data(CellTypeMeans450K)
```

`bloodCtl` *Blood Control data*

Description

Blood control data for CNA analysis

Usage

```
data(bloodCtl)
```

Format

The format is: List of 6 $ mset :Formal class ’MethylSet’ [package "minfi"] with 8 slots .. ..@ preprocessMethod : Named chr [1:3] "Raw (no normalization or bg correction)" "1.8.9" "0.4.0" .. .. ..- attr(*, "names")= chr [1:3] "rg.norm" "minfi" "manifest" .. ..@ assayData :<environment: 0x105193308> .. ..@ phenoData :Formal class ’AnnotatedDataFrame’ [package "Biobase"] with 4 slots .. ..@ varMetadata :’data.frame’: 10 obs. of 1 variable: .. ..$ labelDescription: chr [1:10] NA NA NA NA ... .@ data :’data.frame’: 2 obs. of 10 variables: .. ..$ Sample_Name : chr [1:2] "blood_1" "blood_2" .. ..$ Sample_Plate: chr [1:2] "c" "c" .. ..$ Sample_Group: chr [1:2] "B" "B" .. ..$ Pool_ID : chr [1:2] "blood" "blood" .. ..$ Project : chr [1:2] "blood_pilot" "blood_pilot" .. ..$ Sample_Well : chr [1:2] "F01" "H01" .. ..$ Array : chr [1:2] "R06C01" "R02C02" .. ..$ Slide : num [1:2] 9.31e+09 9.31e+09 .. ..$ Basename : chr [1:2] "/Users/regmtmo/Desktop/Sync/ACTIVE work/Lotte_450k_twinStudy_9May2013/bloodPilot_Sept2013/MORRIS Meth450K 280813/champBlood/930"| __truncated__ "/Users/regmtmo/Desktop/Sync/ACTIVE work/Lotte_450k_twinStudy_9May2013/bloodPilot_S Meth450K 280813/champBlood/930"| __truncated__ .. ..$ filenames : chr [1:2] "/Users/regmtmo/Desktop/Sync/ACTIV work/Lotte_450k_twinStudy_9May2013/bloodPilot_Sept2013/MORRIS Meth450K 280813/champBlood/930"| __truncated__ "/Users/regmtmo/Desktop/Sync/ACTIVE work/Lotte_450k_twinStudy_9May2013/bloodPilot_S Meth450K 280813/champBlood/930"| __truncated__ .. ..@ 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’: 485512 obs. of 0 variables .. ..@ dimLabels : chr [1:2] "featureNames" "featureColumns" .. ..@ .__classVersion__:Formal class ’Versions’ [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..$: int [1:3] 1 1 0 .. ..@ experimentData :Formal class ’MIAME’ [package "Biobase"] with 13 slots .. ..@ name : chr "" .. ..@ lab : chr "" .. ..@ contact : chr "" .. ..@ title : chr "" .. ..@ abstract : chr "" .. ..@ url : chr "" .. ..@ pubMedIds : chr "" .. ..@ samples : list() .. ..@ hybridizations : list() .. ..@ normControls : list() .. ..@ preprocessing : list() .. ..@ other : list() .. ..@ .__classVersion__:Formal class ’Versions’ [package "Biobase"] with 1 slots .. ..@ .Data:List of 2 .. ..$: int [1:3] 1 0 0 .. ..$: int [1:3] 1 1 0 .. ..@ annotation : Named chr [1:2] "IlluminaHumanMethylation450k" "ilmn12.hg19" .. .. ..- attr(*, "names")= chr [1:2] "array" "annotation" .. ..@ protocolData :Formal class ’AnnotatedDataFrame’ [package "Biobase"] with 4 slots .. ..@ varMetadata :’data.frame’: 0 obs. of 1 variable: .. ..$ labelDescription: chr(0) .. ..@ data :’data.frame’: 2 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 2 .. .. .. .. ..$ : int [1:3] 2 22 0 .. .. .. .. ..$ : int [1:3] 1 3 0 .. .. .. .. ..$ :
int [1:3] 1 0 0 $ rgSet :Formal class 'RGChannelSetExtended' [package "minfi"] with 7 slots .. ..@
assayData :<environment: 0x105310db8> .. ..@ phenoData :Formal class 'AnnotatedDataFrame'
[package "Biobase"] with 4 slots .. .. .. ..@ varMetadata :'data.frame': 10 obs. of 1 variable: .. ..
.. .. ..$ labelDescription: chr [1:10] NA NA NA NA ... .. .. .. ..@ data :'data.frame': 2 obs. of 10
variables: .. .. .. .. ..$ Sample_Name : chr [1:2] "blood_1" "blood_2" .. .. .. .. ..$ Sample_Plate: chr
[1:2] "c" "c" .. .. .. .. ..$ Sample_Group: chr [1:2] "B" "B" .. .. .. .. ..$ Pool_ID : chr [1:2] "blood"
"blood" .. .. .. .. ..$ Project : chr [1:2] "blood_pilot" "blood_pilot" .. .. .. .. ..$ Sample_Well : chr
[1:2] "F01" "H01" .. .. .. .. ..$ Array : chr [1:2] "R06C01" "R02C02" .. .. .. .. ..$ Slide : num
[1:2] 9.31e+09 9.31e+09 .. .. .. .. ..$ Basename : chr [1:2] "/Users/regmtmo/Desktop/Sync/ACTIVE
work/Lotte_450k_twinStudy_9May2013/bloodPilot_Sept2013/MORRIS Meth450K 280813/champ-
Blood/930"| __truncated__ "/Users/regmtmo/Desktop/Sync/ACTIVE work/Lotte_450k_twinStudy_9May2013/bloodPilot_S
Meth450K 280813/champBlood/930"| __truncated__ .. .. .. .. ..$ filenames : chr [1:2] "/Users/regmtmo/Desktop/Sync/ACTI
work/Lotte_450k_twinStudy_9May2013/bloodPilot_Sept2013/MORRIS Meth450K 280813/champ-
Blood/930"| __truncated__ "/Users/regmtmo/Desktop/Sync/ACTIVE work/Lotte_450k_twinStudy_9May2013/bloodPilot_S
Meth450K 280813/champBlood/930"| __truncated__ .. .. .. ..@ dimLabels : chr [1:2] "sam-
pleNames" "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': 622399 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 .. ..@ experimentData
:Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. .. ..@ name : chr "" .. .. .. ..@ lab
: chr "" .. .. .. ..@ contact : chr "" .. .. .. ..@ title : chr "" .. .. .. ..@ abstract : chr "" .. .. .. ..@
url : chr "" .. .. .. ..@ pubMedIds : chr "" .. .. .. ..@ samples : list() .. .. .. ..@ hybridizations
: list() .. .. .. ..@ normControls : list() .. .. .. ..@ preprocessing : list() .. .. .. ..@ other : list()
.. .. .. ..@ .__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 ..
..@ annotation : Named chr [1:2] "IlluminaHumanMethylation450k" "ilmn12.hg19" .. .. ..- attr(*,
"names")= chr [1:2] "array" "annotation" .. ..@ protocolData :Formal class 'AnnotatedDataFrame'
[package "Biobase"] with 4 slots .. .. .. ..@ varMetadata :'data.frame': 0 obs. of 1 variable: .. .. .. ..
..$ labelDescription: chr(0) .. .. .. ..@ data :'data.frame': 2 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 2 .. .. .. .. ..$ : int [1:3] 2 22 0 .. .. .. .. ..$ : int [1:3] 1 3 0 .. .. .. .. ..$
: int [1:3] 1 0 0 $ pd :'data.frame': 2 obs. of 10 variables: ..$ Sample_Name : chr [1:2] "blood_1"
"blood_2" ..$ Sample_Plate: chr [1:2] "" "" ..$ Sample_Group: chr [1:2] "champCtls" "champCtls"
..$ Pool_ID : chr [1:2] "" "" ..$ Project : chr [1:2] "" "" ..$ Sample_Well : chr [1:2] "" "" ..$ Array :
chr [1:2] "R06C01" "R02C02" ..$ Slide : num [1:2] 9.31e+09 9.31e+09 ..$ Basename : chr [1:2] ""
"" ..$ filenames : chr [1:2] "" "" $ intensity: num [1:485512, 1:2] 12820 2714 1381 4083 3863 ... ..-
attr(*, "dimnames")=List of 2 .. ..$ : chr [1:485512] "cg00050873" "cg00212031" "cg00213748"
"cg00214611" ... .. ..$ : chr [1:2] "blood_1" "blood_2" $ beta : num [1:485512, 1:2] 0.8648 0.0924
0.7846 0.0323 0.7118 ... ..- attr(*, "dimnames")=List of 2 .. ..$ : chr [1:485512] "cg00050873"
```

"cg00212031" "cg00213748" "cg00214611" ... .$: chr [1:2] "blood_1" "blood_2" $ detP : num [1:485512, 1:2] 0 0 0 0 0 0 0 0 0 0 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:485512] "cg00050873" "cg00212031" "cg00213748" "cg00214611" ... .$: chr [1:2] "blood_1" "blood_2"

Examples

```
data(bloodCtl)
## maybe str(bloodCtl) ; plot(bloodCtl) ...
```

`CellTypeMeans27K` *Cell-type purified whole blood methylation CpG Sites for use with the RefBaseEWAS cell-type correction function.*

Description

This dataset contains 500 CpGs sites from cell type purified whole blood samples.

Usage

```
data(CellTypeMeans450K)
```

Format

The format is: num [1:500, 1:6] 0.901 0.9188 0.8503 0.8913 0.0436 ... - attr(*, "dimnames")=List of 2 ..$: chr [1:500] "cg00226923" "cg16698623" "cg14102807" "cg14127336" ... ..$: chr [1:6] "CD8T" "CD4T" "NK" "Bcell" ...

Examples

```
data(CellTypeMeans27K)
```

`CellTypeMeans450K` *Cell-type purified whole blood methylation CpG Sites for use with the RefBaseEWAS cell-type correction function.*

Description

This dataset contains 600 CpGs sites from cell type purified whole blood samples.

Usage

```
data(CellTypeMeans450K)
```

Format

The format is: num [1:600, 1:6] 0.125 0.2 0.178 0.284 0.226 ... - attr(*, "dimnames")=List of 2 ..$: chr [1:600] "cg25939861" "cg00219921" "cg08777095" "cg04329870" ... ..$: chr [1:6] "CD8T" "CD4T" "NK" "Bcell" ...

Examples

```
data(CellTypeMeans450K)
```

`EPICSimData` *Simulation EPIC beadarray Dataset.*

Description

This dataset is available to test ChAMP functions on EPIC array.

Usage

```
data(EPICSimData)
```

Format

List of 3 $ beta: num [1:780385, 1:16] 0.7382 0.8572 0.8624 0.4492 0.0751 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:780385] "cg14817997" "cg16269199" "cg13869341" "cg02404219" ... .$: chr [1:16] "HELA_Sim_1" "HELA_Sim_2" "HELA_Sim_3" "HELA_Sim_4" ... $ pd :'data.frame': 16 obs. of 10 variables: ..$ Sample_Name : chr [1:16] "HELA_Sim_1" "HELA_Sim_2" "HELA_Sim_3" "HELA_Sim_4" ... ..$ Sample_Plate: chr [1:16] "EPIC2" "EPIC2" "EPIC2" "EPIC2" ... ..$ Sample_Group: chr [1:16] "control" "control" "control" "control" ... ..$ Pool_ID : logi [1:16] NA NA NA NA NA NA ... ..$ Project : chr [1:16] "X" "X" "X" "X" ... ..$ Sample_Well : chr [1:16] "A01" "B01" "C01" "D01" ... ..$ Array : chr [1:16] "R01C01" "R02C01" "R03C01" "R04C01" ... ..$ Slide : chr [1:16] "200079600019" "200079600019" "200079600019" "200079600019" ... ..$ Basename : chr [1:16] "character(0)" "character(0)" "character(0)" "character(0)" ... ..$ filenames : chr [1:16] "./Demo/200079600019_R01C01" "./Demo/200079600019_R02C01" "./Demo/200079600019_R03C01" "./Demo/200079600019_R04C01" ... $ detP: num [1:780385, 1:16] 0 0 0 0 0 0 0 0 0 0 ... ..- attr(*, "dimnames")=List of 2 .. ..$: chr [1:780385] "cg18478105" "cg14361672" "cg01763666" "cg02115394" ... .$: NULL

Examples

```
data(EPICSimData)
```

`illumina450Gr` *GRange Struct of illumina 450K array.*

Description

This dataset will be used in champ.lasso functions.

Usage

```
data(illumina450Gr)
```

Format

..@ seqnames :Formal class 'Rle' [package "S4Vectors"] with 4 slots .. .. ..@ values : Factor w/ 24 levels "chr16","chr3",..: 1 2 3 4 5 1 4 3 6 7 ... .@ lengths : int [1:446018] 1 2 1 1 1 1 1 1 1 1 ... .@ elementMetadata: NULL .. .. ..@ metadata : list() ..@ ranges :Formal class 'IRanges' [package "IRanges"] with 6 slots .. .. ..@ start : int [1:485512] 53468112 37459206 171916037 91194674 42263294 69341139 28890100 41167802 230560793 23034447 ... .@ width : int [1:485512] 1 1 1 1 1 1 1 1 1 1 ... .@ NAMES : chr [1:485512] "cg00000029" "cg00000108" "cg00000109" "cg00000165" ... .@ elementType : chr "integer" .. .. ..@ elementMetadata: NULL .. .. ..@ metadata : list() ..@ strand :Formal class 'Rle' [package "S4Vectors"] with 4 slots .. .. ..@ values : Factor w/ 3 levels "+","-","*": 1 2 1 2 1 2 1 2 1 2 ... .@ lengths : int [1:242276] 3 2 2 1 2 1 1 1 3 2 ... .@ elementMetadata: NULL .. .. ..@ metadata : list() ..@ elementMetadata:Formal class 'DataFrame' [package "S4Vectors"] with 6 slots .. .. ..@ rownames : NULL .. .. ..@ nrows : int 485512 .. .. ..@ listData :List of 27 .. ..$ chrom_hg18 : Factor w/ 24 levels "chr1","chr10",..: 8 16 16 1 21 6 8 21 1 7 ... .$ MAPINFO_hg18 : int [1:485512] 52025613 37434210 173398731 90967262 42382451 68410892 28797601 41286959 228627416 20585888 ... .$ chrom_hg38 : Factor w/ 37 levels "chr1","chr1_KI270706v1_random",..: 13 26 26 1 32 8 13 32 1 11 ... .$ MAPINFO_hg38 : int [1:485512] 53434200 37417715 172198247 90729117 42405776 68874422 28878779 41310283 230425047 22838619 ... .$ arm : Factor w/ 2 levels "p","q": 2 1 2 1 1 2 1 1 2 2 ... .$ probeStrand : chr [1:485512] "+" "+" "+" "-" ... .$ ensemblID : chr [1:485512] "ENSG00000103479" "ENSG00000198590" "ENSG00000075420" "ENSG00000143032" ... .$ geneSymbol : chr [1:485512] "RBL2" "C3orf35" "FNDC3B" "BARHL2" ... .$ geneStrand : Factor w/ 48 levels "-","-;-","-;-;-",..: 24 24 24 1 24 1 24 1 1 1 ... .$ relationtoGene : Factor w/ 21 levels "downstream","inside",..: 3 2 2 3 2 2 2 3 2 3 ... .$ distancetoTSS : chr [1:485512] "-250" "31445" "158618" "-11880" ... .$ nearestGeneBoundary: chr [1:485512] "250" "17782" "158618" "11880" ... .$ feature : Factor w/ 7 levels "1stExon","3'UTR",..: 6 4 4 5 2 2 1 6 5 7 ... .$ cgi : Factor w/ 4 levels "island","open sea",..: 4 2 2 4 2 4 4 4 4 1 ... .$ cgiName : chr [1:485512] NA NA NA NA ... .$ featureCgi : Factor w/ 28 levels "1stExon - island",..: 24 14 14 20 6 8 4 24 20 25 ... .$ conservedTfsb : Factor w/ 815 levels "V$AHR_01","V$AHR_01;V$EGR1_01;V$EGR2_01;V$EGR3_01;V$NGFIC_01",..: NA NA NA 578 NA NA NA NA NA NA ... .$ bwaMultiMap : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... .$ promoterAssociated : Factor w/ 2 levels "0","1": 2 1 1 1 1 1 2 2 1 2 ... .$ asnCN : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... .$ afrCN : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 2 1 1 ... .$ amrCN : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... .$ eurCN : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 2 1 1 1 ... .$ asnLast4 : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... .$ afrLast4 : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... .$ amrLast4 : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... .$ eurLast4 : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ... .@ elementType : chr "ANY" .. .. ..@ elementMetadata: NULL .. .. ..@ metadata : list() ..@ seqinfo :Formal class 'Seqinfo' [package "GenomeInfoDb"] with 4 slots .. .. ..@ seqnames : chr [1:24] "chr16" "chr3" "chr1" "chr8" ... .@ seqlengths : int [1:24] NA NA NA NA NA NA NA NA NA NA ... .@ is_circular: logi [1:24] NA NA NA NA NA NA ... .@ genome : chr [1:24] NA NA NA NA ... ..@ metadata : list()

Examples

```
data(illumina450Gr)
```

`illuminaEPICGr` *GRange S4 Object of illumina EPIC array.*

Description

This dataset will be used in champ.lasso functions.

Usage

```
data(illuminaEPICGr)
```

Format

..@ seqnames :Formal class 'Rle' [package "S4Vectors"] with 4 slots .. .. ..@ values : Factor w/ 24 levels "chr19","chr20",..: 1 2 3 4 5 6 7 8 3 9 ... .@ lengths : int [1:822229] 1 1 1 1 1 1 1 1 1 1 ... .@ elementMetadata: NULL .. .. ..@ metadata : list() ..@ ranges :Formal class 'IRanges' [package "IRanges"] with 6 slots .. .. ..@ start : int [1:866836] 5236016 61847650 6841125 198303466 24072640 93581139 57865112 15248173 144921929 131463936 ... .@ width : int [1:866836] 2 2 2 2 2 2 2 2 2 2 ... .@ NAMES : chr [1:866836] "cg07881041" "cg18478105" "cg23229610" "cg03513874" ... .@ elementType : chr "integer" .. .. ..@ elementMetadata: NULL .. .. ..@ metadata : list() ..@ strand :Formal class 'Rle' [package "S4Vectors"] with 4 slots .. .. ..@ values : Factor w/ 3 levels "+","-","*": 2 1 2 1 2 1 2 1 2 1 ... .@ lengths : int [1:433990] 3 1 1 2 2 3 1 5 1 1 ... .@ elementMetadata: NULL .. .. ..@ metadata : list() ..@ elementMetadata:Formal class 'DataFrame' [package "S4Vectors"] with 6 slots .. .. ..@ rownames : NULL .. .. ..@ nrows : int 866836 .. .. ..@ listData : Named list() .. .. ..@ elementType : chr "ANY" .. .. ..@ elementMetadata: NULL .. .. ..@ metadata : list() ..@ seqinfo :Formal class 'Seqinfo' [package "GenomeInfoDb"] with 4 slots .. .. ..@ seqnames : chr [1:24] "chr19" "chr20" "chr1" "chr2" ... .@ seqlengths : int [1:24] NA NA NA NA NA NA NA NA NA NA ... .@ is_circular: logi [1:24] NA NA NA NA NA NA ... .@ genome : chr [1:24] NA NA NA NA ... ..@ metadata : list()

Examples

```
data(illuminaEPICGr)
```

`multi.hit` *multi.hit information.*

Description

This dataset contains 9341 multi hit CpGs.

Usage

```
data(multi.hit)
```

Format

The format is: 'data.frame': 9341 obs. of 38 variables: $ TargetID : Factor w/ 485577 levels "cg00000029","cg00000108",..: 30 92 234 246 294 325 358 374 402 418 ... $ INFINIUM_DESIGN_TYPE : Factor w/ 2 levels "I","II": 1 2 1 1 2 1 2 2 2 1 ... $ GENOME_BUILD : int 37 37 37 37 37 37 37 37 37 37 ... $ CHR : Factor w/ 25 levels "","1","10","11",..: 12 8 9 7 2 21 20 5 20 2 ... $ MAPINFO : int 54746945 82925333 33318910 81580765 149370974 74508806 58777304 54500832 7339455 149719536 ... $ CHROMOSOME_36 : Factor w/ 26 levels "","1","10","11",..: 12 8 9 7 2 21 20 5 20 2 ... $ COORDINATE_36 : Factor w/ 484739 levels "","100000057",..: 367785 440537 259149 440391 109936 419166 365930 343920 414240 110329 ... $ STRAND : Factor w/ 3 levels "","F","R": 3 2 3 2 3 3 3 2 2 3 ... $ UCSC_REFGENE_NAME : Factor w/ 42456 levels "","A1BG","A1CF;A1CF;A1CF",..: 19768 1 1 38813 13130 15618 1 13453 6037 1 ... $ UCSC_REFGENE_ACCESSION : Factor w/ 52670 levels "","NM_000014",..: 35153 1 1 598 51448 2129 1 50622 15082 1 ... $ UCSC_REFGENE_GROUP : Factor w/ 4165 levels "","1stExon","1stExon;1stExon",..: 2970 1 1 2035 2035 943 1 2035 2447 1 ... $ UCSC_CPG_ISLANDS_NAME : Factor w/ 27177 levels "","chr1:10003165-10003585",..: 1 8132 8895 1 1 23921 1 5852 1 400 ... $ RELATION_TO_UCSC_CPG_ISLAND: Factor w/ 6 levels "","Island","N_Shelf",..: 1 6 2 1 1 2 1 2 1 2 ... $ SNP : Factor w/ 139064 levels "","rs10000296",..: 88450 1 93755 1 94630 80342 79504 1 1 89545 ... $ SNP_DISTANCE : Factor w/ 11304 levels "","-1","-1;0",..: 10743 1 2655 1 3352 1938 10243 1 1 5664 ... $ snp.hit : int 0 0 0 0 1 0 0 0 0 0 ... $ bwa.multi.hit : int 1 1 1 1 1 1 1 1 1 1 ... $ analyzed : int 0 0 0 0 0 0 0 0 0 0 ... $ DNase : int 0 0 0 0 0 1 0 0 0 0 ... $ h3k4me3 : int 0 0 0 0 0 1 0 0 0 1 ... $ h3k36me3 : int 0 0 0 0 0 0 0 0 0 0 ... $ h3k27ac : int 0 0 0 0 0 1 1 0 0 0 ... $ h3k4me1 : int 0 0 0 0 0 0 0 0 0 0 ... $ bivalent : int 0 0 0 0 0 0 0 0 0 1 ... $ h3k27me3 : int 0 0 0 0 0 0 0 1 0 1 ... $ h3k9me3 : int 0 0 0 0 0 0 0 0 0 0 ... $ dmc.constitutive : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.relapse : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.T : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.MLL : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.dic920 : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.HeH : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.t119 : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.t1221 : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.t922 : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.iamp : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.undefined : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.nonrecurrent : int NA NA NA NA NA NA NA NA NA NA ...

Examples

```
data(multi.hit)
```

`probe.features` *probe.features*

Description

HumanMethylation450 probe annotations

Usage

```
data(probe.features)
```

Format

A data frame with 485577 observations on the following 9 variables.

`CHR` a factor with levels

`MAPINFO` a numeric vector

`arm` a character vector

`gene` The gene name related to this CpG site.

`distancetoGene` Distance of this CpG site to the gene.

`feature` a factor with levels `1stExon` `3'UTR} \code{5'UTR` `Body` `IGR` `TSS1500` `TSS200`

`cgi` a factor with levels `island` `open sea` `shelf` `shore`

`feat.cgi` a factor with levels `1stExon - island` `1stExon - open sea` `1stExon - shelf` `1stExon - shore` `3'UTR - island} \code{3'UTR - open sea` `3'UTR - shelf} \code{3'UTR - shore` `5'UTR - island} \code{5'UTR - open sea` `5'UTR - shelf} \code{5'UTR - shore` `Body - island` `Body - open sea` `Body - shelf` `Body - shore` `IGR - island` `IGR - open sea` `IGR - shelf` `IGR - shore` `TSS1500 - island` `TSS1500 - open sea` `TSS1500 - shelf` `TSS1500 - shore` `TSS200 - island` `TSS200 - open sea` `TSS200 - shelf` `TSS200 - shore`

`conserved_tfbs` Name for conserved Transcrtipy binding site.

Examples

```
data(probe.features)
```

`probe.features.epic` *probe.features.epic*

Description

HumanMethylationEPIC probe annotations

Usage

```
data(probe.features.epic)
```

Format

A data frame with 868565 observations on the following 14 variables.

`CHR` a factor with levels

`MAPINFO` a numeric vector

Examples

```
data(probe.features.epic)
```

`probeInfoALL.epic.lv` *Probe Info Data for use with the BMIQ normalization.*

Description

The probe details are formatted here for the BMIQ function.

Usage

```
data(probeInfoALL.epic.lv)
```

Format

The format is: List of 3 $ Design : num [1:867531] 2 1 2 2 1 2 2 2 2 1 ... $ CGI : num [1:867531] 0 1 0 0 1 1 0 0 0 0 ... $ probeID: chr [1:867531] "cg07881041" "cg18478105" "cg23229610" "cg03513874" ...

Examples

```
data(probeInfoALL.epic.lv)
```

`probeInfoALL.lv` *Probe Info Data for use with the BMIQ normalization.*

Description

The probe details are formatted here for the BMIQ function.

Usage

```
data(probeInfoALL.lv)
```

Format

The format is: List of 5 $ typeC : num [1:485577] 1 1 1 1 1 1 1 1 1 1 ... $ Design : num [1:485577] 2 2 2 2 2 2 2 2 2 1 ... $ GeneGroup: int [1:485577] 1 NA 5 NA 6 6 4 1 NA 2 ... $ CGI : num [1:485577] 1 0 0 1 0 1 1 1 1 1 ... $ probeID : chr [1:485577] "cg00000029" "cg00000108" "cg00000109" "cg00000165" ...

Examples

```
data(probeInfoALL.lv)
```

`snp.hit` *CpG site related to SNP sites information.*

Description

This dataset contains snp sites located into SNP related sites.

Usage

```
data(snp.hit)
```

Format

The format is: 'data.frame': 29481 obs. of 38 variables: $ TargetID : Factor w/ 485577 levels "cg00000029","cg00000108",..: 16 21 34 65 76 98 119 120 147 160 ... $ INFINIUM_DESIGN_TYPE : Factor w/ 2 levels "I","II": 2 1 2 1 2 2 2 2 2 2 ... $ GENOME_BUILD : int 37 37 37 37 37 37 37 37 37 37 ... $ CHR : Factor w/ 25 levels "","1","10","11",..: 13 2 2 10 2 13 18 17 3 8 ... $ MAPINFO : int 23913414 5937253 170490434 57839538 8739981 237027592 178364146 110612894 112068221 90066806 ... $ CHROMOSOME_36 : Factor w/ 26 levels "","1","10","11",..: 13 2 2 10 2 13 18 17 3 8 ... $ COORDINATE_36 : Factor w/ 484739 levels "","100000057",..: 206129 365300 143074 353467 452543 205188 156567 31100 30980 456465 ... $ STRAND : Factor w/ 3 levels "","F","R": 2 2 3 3 2 3 2 3 2 2 ... $ UCSC_REFGENE_NAME : Factor w/ 42456 levels "","A1BG","A1CF;A1CF;A1CF",..: 19016 25371 1 37783 30924 812 811 1 1 20318 ... $ UCSC_REFGENE_ACCESSION : Factor w/ 52670 levels "","NM_000014",..: 38959 27879 1 36493 25264 27559 26 1 1 51089 ... $ UCSC_REFGENE_GROUP : Factor w/ 4165 levels "","1stExon","1stExon;1stExon",..: 2035 2035 1 2035 1216 2348 2970 1 1 2496 ... $ UCSC_CPG_ISLANDS_NAME : Factor w/ 27177 levels "","chr1:10003165-10003585",..: 15329 2125 1 1 1 15292 19510 1 2598 1 ... $ RELATION_TO_UCSC_CPG_ISLAND: Factor w/ 6 levels "","Island","N_Shelf",..: 2 2 1 1 1 4 6 1 5 1 ... $ SNP : Factor w/ 139064 levels "","rs10000296",..: 17352 122999 51875 43171 103744 112856 35391 40027 21722 58062 ... $ SNP_DISTANCE : Factor w/ 11304 levels "","-1","-1;0",..: 1351 639 852 852 1410 5828 852 3352 14 508 ... $ snp.hit : int 1 1 1 1 1 1 1 1 1 1 ... $ bwa.multi.hit : int 0 0 0 0 0 0 0 0 0 0 ... $ analyzed : int 0 0 0 0 0 0 0 0 0 0 ... $ DNase : int 0 0 0 0 0 0 1 0 0 0 ... $ h3k4me3 : int 0 0 0 0 0 0 1 0 0 0 ... $ h3k36me3 : int 0 0 0 0 0 0 0 0 0 0 ... $ h3k27ac : int 0 0 0 0 0 0 1 0 0 0 ... $ h3k4me1 : int 0 0 0 0 0 0 1 0 0 0 ... $ bivalent : int 0 0 0 0 0 0 0 0 0 0 ... $ h3k27me3 : int 0 0 0 0 0 1 0 0 0 0 ... $ h3k9me3 : int 0 0 0 0 0 0 0 0 0 0 ... $ dmc.constitutive : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.relapse : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.T : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.MLL : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.dic920 : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.HeH : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.t119 : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.t1221 : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.t922 : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.iamp : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.undefined : int NA NA NA NA NA NA NA NA NA NA ... $ dmc.nonrecurrent : int NA NA NA NA NA NA NA NA NA NA ...

Examples

```
data(snp.hit)
```

`testDataSet` *Test dataset.*

Description

This dataset is available to test ChAMP functions.

Usage

```
data(testDataSet)
```

Format

The format is: List of 6 $ mset :Formal class 'MethylSet' [package "minfi"] with 8 slots $ rgSet :Formal class 'RGChannelSet' [package "minfi"] with 7 slots $ pd :'data.frame': 6 obs. of 9 variables: ..$ Sample_Name ..$ Sample_Well ..$ Sample_Plate ..$ Sample_Group ..$ Pool_ID ..$ Array ..$ Slide ..$ Basename $ intensity $ beta $ detP

Examples

```
data(testDataSet)
```

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