Package ‘ChAMPdata’

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Type Package

Title Data Packages for ChAMP package

Version 1.1.2

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

License GPL-3

Depends R (>= 3.0.1)

biocViews ExpressionData, IlluminaChip

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:	1.1.1
Date:	2014-06-24
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)
```

`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/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': 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) ...
```

`probe.features` *probe.features*

Description

HumanMethylation450 probe annotations

Usage

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

Format

A data frame with 485577 observations on the following 14 variables.

`CHR` a factor with levels

`MAPINFO` a numeric vector

`arm` a character vector

`gene.1` a factor with levels

`gene.2` a factor with levels

`gene.3` a factor with levels

`gene.4` a factor with levels

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

`feature.2` a factor with levels `1stExon` `3UTR} \code{5UTR` `Body` `TSS1500` `TSS200`

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

`feature.4` a factor with levels `1stExon` `3UTR} \code{5UTR` `Body` `TSS1500` `TSS200`

`feature` a factor with levels `1stExon` `3UTR} \code{5UTR` `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` `3UTR - island} \code{3UTR - open sea` `3UTR - shelf} \code{3UTR - shore` `5UTR - island} \code{5UTR - open sea` `5UTR - shelf} \code{5UTR - 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`

Examples

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

`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)
```

`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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