

Package ‘ChAMPdata’

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Type Package

Title Data Packages for ChAMP package

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Description Provides datasets needed for ChAMP and also a test dataset

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Depends R (>= 3.0.1)

biocViews ExpressionData, IlluminaChip

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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: 1.0.1
 Date: 2014-06-26
 License: GPL-3

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

Author(s)

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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/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/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__@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .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"@ .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()@ .Data:List of 1\$: int [1:3] 1 1 0@ .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"@ .Data:List of 1\$: int [1:3] 1 1 0@ .Data:List of 1@ .Data:List of 1@ .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/ACTIV
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) ...
```

```
probe.features      HumanMethylation450 probe annotations.
```

Description

This file includes the annotation for each probe on the 450k array

Usage

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

Examples

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

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

Description

The probe details are formatted here for the BMIQ function.

Usage

```
data(probeInfoALL.lvs)
```

Format

The format is: List of 5 \$ typeC : num [1:485577] 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.lvs)
```

testDataSet	<i>Test dataset.</i>
-------------	----------------------

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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