

Package ‘ChAMPdata’

April 20, 2016

Type Package

Title Data Packages for ChAMP package

Version 1.8.0

Date 2015-04-12

Author Tiffany Morris, Lee Butcher and Andrew Teschendorff

Maintainer Tiffany Morris <champ450k@gmail.com>

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 ExperimentData

NeedsCompilation no

R topics documented:

ChAMPdata-package	1
bloodCtl	2
probe.features	4
probeInfoALL.lv	6
testDataSet	6
Index	7

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.

Author(s)

Tiffany Morris, UCL Cancer Institute, Medical Genomics; Lee Butcher, UCL Cancer Institute, Medical Genomics; Andrew Teschendorff, UCL Cancer Institute, Statistical Genomics;

Maintainer: Tiffany Morris<tiffany.morris@ucl.ac.uk>

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"@ .__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/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 ... - 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) ...

```

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 3'UTR} \code{5'UTR Body IGR TSS1500 TSS200

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

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

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

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

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 ... \$ 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)
```

Index

*Topic **datasets**

bloodCtl, [2](#)

probe.features, [4](#)

probeInfoALL.lv, [6](#)

testDataSet, [6](#)

*Topic **package**

ChAMPdata-package, [1](#)

bloodCtl, [2](#)

ChAMPdata (ChAMPdata-package), [1](#)

ChAMPdata-package, [1](#)

probe.features, [4](#)

probeInfoALL.lv, [6](#)

testDataSet, [6](#)