Example data for use with the beadarray package

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1 Data Introduction

This package provides a lightweight dataset for those wishing to try out the examples within the *beadarray* package. The data in this package are a subset of the MAQC bead-level data available in the *beadarrayUseCases* package. 'Bead-level' refers to the availability of intensity and location information for each bead on each BeadArray in an experiment. In this dataset, BeadArrays were hybridized with either Universal Human Reference RNA (UHRR, Stratagene) or Brain Reference RNA (Ambion) as used in the MAQC project. This pacakge includes a representation of the bead-level data for 2 arrays in the data object `exampleBLdata`, which was created by beadarray. The summarised data for all 12 arrays are given in the `exampleSummaryData` object, which was creating by first reading the bead-level data for all 12 sections into *beadarray* and then summarising using the procedures described in the vignette for *BeadArrayUseCases*.

2 Loading the data

The example datasets can be loaded using the `data` function. The first dataset comprises two sections from the bead-level MAQC dataset generated at Cancer Research Uk (Cambridge Research Institute) that have been read in using the beadarray package. The second dataset is the summarised data of all sections from the same dataset.

```
> library(beadarrayExampleData)
> data(exampleBLData)
> exampleBLData
```

```


-----------------
Experiment information (@experimentData)
-----------------
$sdfFile
[1] "/home/dunnin01/software/R-devel/library/BeadArrayUseCases/extdata/BeadLevelBabFile

$platformClass
[1] "Slide"

$annotation
[1] "Humanv3"



-----------------
Per-section data (@sectionData)
-----------------
Targets

                                                                            directory
1 /home/dunnin01/software/R-devel/library/BeadArrayUseCases/extdata/BeadLevelBabFiles
2 /home/dunnin01/software/R-devel/library/BeadArrayUseCases/extdata/BeadLevelBabFiles
   sectionName         textFile greenImage        greenLocs greenxml
1 4613710017_B 4613710017_B.bab       <NA> 4613710017_B.bab     <NA>
2 4616494005_A 4616494005_A.bab       <NA> 4616494005_A.bab     <NA>
Metrics

                   Date     Matrix Section RegGrn FocusGrn SatGrn
1  3/13/2009 6:45:04 PM 4613710017       B   0.13     0.70      0
12       04/01/09 04:50 4616494005       A   0.13     0.59      0
   P95Grn P05Grn RegRed FocusRed SatRed P95Red P05Red
```

```
1     704     36      0         0       0       0       0
12    678     38      0         0       0       0       0
SampleGroup

[1] "4613710017_B" "4616494005_A"

numBeads

[1] 1088369 1100773


-----------------
Per-bead data (@beadData)
-----------------
Raw data from section 4613710017_B

     ProbeID      GrnX      GrnY Grn wts
[1,]   10008  900.6661 10781.320 355   1
[2,]   10008 1992.5400 11352.000 377   1
[3,]   10008 1257.4790  7559.513 452   1
[4,]   10008 1700.1600  6351.157 267   1
[5,]   10008 1814.5210  3299.495 431   1

... 1088364 more rows of data

... data for 1 more section/s
```

```
> data(exampleSummaryData)
> exampleSummaryData
```

```
ExpressionSetIllumina (storageMode: list)
assayData: 49576 features, 12 samples
  element names: exprs, se.exprs, nObservations
protocolData: none
phenoData
  rowNames: 4613710017_B 4613710052_B ... 4616494005_A (12
    total)
  varLabels: sampleID SampleFac
  varMetadata: labelDescription
featureData
  featureNames: ILMN_1802380 ILMN_1893287 ... ILMN_1846115
    (49576 total)
```

```
  fvarLabels: ArrayAddressID IlluminaID Status
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
Annotation: Humanv3
QC Information
 Available Slots:
  QC Items: Date, Matrix, ..., SampleGroup, numBeads
  sampleNames: 4613710017_B, 4613710052_B, ..., 4616443136_A, 4616494005_A
```

```
> pData(exampleSummaryData)
```

```
                 sampleID SampleFac
4613710017_B 4613710017_B      UHRR
4613710052_B 4613710052_B      UHRR
4613710054_B 4613710054_B      UHRR
4616443079_B 4616443079_B      UHRR
4616443093_B 4616443093_B      UHRR
4616443115_B 4616443115_B      UHRR
4616443081_B 4616443081_B     Brain
4616443081_H 4616443081_H     Brain
4616443092_B 4616443092_B     Brain
4616443107_A 4616443107_A     Brain
4616443136_A 4616443136_A     Brain
4616494005_A 4616494005_A     Brain
```

3 Data creation

The following commands were used to create the data included with this package.

```
> require(BeadArrayUseCases)
> targets <- read.table(system.file("extdata/BeadLevelBabFiles/targetsHT12.txt", packag
> sn <- paste(targets[,3], targets[,4], sep="_")
> babFilePath <- system.file("extdata/BeadLevelBabFiles", package = "BeadArrayUseCases'
> exampleBLData <- readIllumina(dir=babFilePath, sectionNames=sn[c(1,12)], useImages=FA
> bsh <- BASH(exampleBLData,array=c(1,2))
> exampleBLData <- setWeights(exampleBLData, wts = bsh$wts, array=1:2)
> data <- readIllumina(dir=babFilePath, sectionNames=sn, useImages=FALSE, illuminaAnnot
> grnchannel <- new("illuminaChannel", transFun = logGreenChannelTransform, outlierFun
> grnchannel.unlogged <- new("illuminaChannel", transFun = greenChannelTransform, outli
```

```
> exampleSummaryData <- summarize(data, list(grnchannel, grnchannel.unlogged), useSampl
> pData(exampleSummaryData)[,2] <- targets[,2]
>
>
```