

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 package 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 created 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/BeadLevelBabFiles"

$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	wt
[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", package = "BeadArrayUseCases"), as.is = TRUE)
> sn <- paste(targets[,3], targets[,4], sep="_")
> babFilePath <- system.file("extdata/BeadLevelBabFiles", package = "BeadArrayUseCases")
> exampleBLData <- readIllumina(dir=babFilePath, sectionNames=sn[c(1,12)], useImages=FALSE)
> bsh <- BASH(exampleBLData, array=c(1,2))
> exampleBLData <- setWeights(exampleBLData, wts = bsh$wts, array=1:2)
> data <- readIllumina(dir=babFilePath, sectionNames=sn, useImages=FALSE, illuminaAnnotation=targets[,5:11])
> grnchannel <- new("illuminaChannel", transFun = logGreenChannelTransform, outlierFun = logGreenChannelTransform)
> grnchannel.unlogged <- new("illuminaChannel", transFun = greenChannelTransform, outlierFun = greenChannelTransform)

```

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