

# Example data for use with the beadarray package

Mark Dunning

November 1, 2018

## Contents

<b>1</b>	<b>Data Introduction</b>	<b>1</b>
<b>2</b>	<b>Loading the data</b>	<b>2</b>
<b>3</b>	<b>Data creation</b>	<b>4</b>

## 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", pack
> sn <- paste(targets[,3], targets[,4], sep="_")
> babFilePath <- system.file("extdata/BeadLevelBabFiles", package = "BeadArrayUseCase
> exampleBLData <- readIllumina(dir=babFilePath, sectionNames=sn[c(1,12)], useImages=
> bsh <- BASH(exampleBLData, array=c(1,2))
> exampleBLData <- setWeights(exampleBLData, wts = bsh$wts, array=1:2)
> data <- readIllumina(dir=babFilePath, sectionNames=sn, useImages=FALSE, illuminaAnn
> grnchannel <- new("illuminaChannel", transFun = logGreenChannelTransform, outlierFu
> grnchannel.unlogged <- new("illuminaChannel", transFun = greenChannelTransform, out

```

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