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 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.

```r
library(beadarrayExampleData)
data(exampleBLData)
exampleBLData
```

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**Experiment information (@experimentData)**

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$sdfFile
[1] "/home/dunnin01/software/R-devel/library/BeadArrayUseCases/extdata/BeadLevelBabFiles/4613710017.sdf"

$platformClass
[1] "Slide"

$annotation
[1] "Humanv3"

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

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**Targets**

directory
1 /home/dunnin01/software/R-devel/library/BeadArrayUseCases/extdata/BeadLevelBabFiles
2 /home/dunnin01/software/R-devel/library/BeadArrayUseCases/extdata/BeadLevelBabFiles

<table>
<thead>
<tr>
<th>targets</th>
<th>directory</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>/home/dunnin01/software/R-devel/library/BeadArrayUseCases/extdata/BeadLevelBabFiles</td>
</tr>
<tr>
<td>2</td>
<td>/home/dunnin01/software/R-devel/library/BeadArrayUseCases/extdata/BeadLevelBabFiles</td>
</tr>
</tbody>
</table>

**Metrics**

<table>
<thead>
<tr>
<th>Date</th>
<th>Matrix</th>
<th>Section</th>
<th>RegGrn</th>
<th>FocusGrn</th>
<th>SatGrn</th>
<th>P95Grn</th>
<th>P05Grn</th>
<th>RegRed</th>
<th>FocusRed</th>
<th>SatRed</th>
<th>P95Red</th>
<th>P05Red</th>
</tr>
</thead>
<tbody>
<tr>
<td>3/13/2009</td>
<td>6:45:04</td>
<td>PM</td>
<td>4613710017</td>
<td>B</td>
<td>0.13</td>
<td>0.70</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>04/01/09</td>
<td>04:50</td>
<td>4616494005</td>
<td>A</td>
<td>0.13</td>
<td>0.59</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>P95Grn</td>
<td>P05Grn</td>
<td>RegRed</td>
<td>FocusRed</td>
<td>SatRed</td>
<td>P95Red</td>
<td>P05Red</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
SampleGroup

[1] "4613710017_B" "4616494005_A"

numBeads

[1] 1088369 1100773

Per-bead data (@beadData)

Raw data from section 4613710017_B

<table>
<thead>
<tr>
<th>ProbeID</th>
<th>GrnX</th>
<th>GrnY</th>
<th>Grn wts</th>
</tr>
</thead>
<tbody>
<tr>
<td>10008</td>
<td>900.6661</td>
<td>10781.320</td>
<td>355</td>
</tr>
<tr>
<td>10008</td>
<td>1992.5400</td>
<td>11352.000</td>
<td>377</td>
</tr>
<tr>
<td>10008</td>
<td>1257.4790</td>
<td>7559.513</td>
<td>452</td>
</tr>
<tr>
<td>10008</td>
<td>1700.1600</td>
<td>6351.157</td>
<td>267</td>
</tr>
<tr>
<td>10008</td>
<td>1814.5210</td>
<td>3299.495</td>
<td>431</td>
</tr>
</tbody>
</table>

... 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)

<table>
<thead>
<tr>
<th>sampleID</th>
<th>SampleFac</th>
</tr>
</thead>
<tbody>
<tr>
<td>4613710017_B</td>
<td>4613710017_B</td>
</tr>
<tr>
<td>4613710052_B</td>
<td>4613710052_B</td>
</tr>
<tr>
<td>4613710054_B</td>
<td>4613710054_B</td>
</tr>
<tr>
<td>4616443079_B</td>
<td>4616443079_B</td>
</tr>
<tr>
<td>4616443093_B</td>
<td>4616443093_B</td>
</tr>
<tr>
<td>4616443115_B</td>
<td>4616443115_B</td>
</tr>
<tr>
<td>4616443081_B</td>
<td>4616443081_B</td>
</tr>
<tr>
<td>4616443081_H</td>
<td>4616443081_H</td>
</tr>
<tr>
<td>4616443092_B</td>
<td>4616443092_B</td>
</tr>
<tr>
<td>4616443107_A</td>
<td>4616443107_A</td>
</tr>
<tr>
<td>4616443136_A</td>
<td>4616443136_A</td>
</tr>
<tr>
<td>4616494005_A</td>
<td>4616494005_A</td>
</tr>
</tbody>
</table>

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"), header=TRUE, sep="\t", 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, illuminaAnnotation="Humanv3")
> 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="Humanv3")
> grnchannel <- new("illuminaChannel", transFun = logGreenChannelTransform, outlierFun=illuminaOutlierMethod, exprFun = function(x) mean(x,na.rm=TRUE), varFun= function(x) sd(x, na.rm=TRUE),channelName= "G")
> grnchannel.unlogged <- new("illuminaChannel", transFun = greenChannelTransform, outlierFun=illuminaOutlierMethod, exprFun = function(x) mean(x,na.rm=TRUE), varFun= function(x) sd(x, na.rm=TRUE),channelName= "G.ul")
> exampleSummaryData <- summarize(data, list(grnchannel, grnchannel.unlogged), useSampleFac=FALSE)
> pData(exampleSummaryData)[,2] <- targets[,2]
>
>