Package ‘pumadata’

February 20, 2024

Type    Package
Title   Various data sets for use with the puma package
Version 2.38.0
Date    2019-09-04
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Depends R (>= 3.2.0), Biobase (>= 2.5.5), puma, oligo(>= 1.32.0)
Description This is a simple data package including various data sets derived from the estrogen data for use with the puma (Propagating Uncertainty in Microarray Analysis) package.
License LGPL
biocViews ExperimentData, MicroarrayData, SNPData
URL     http://umber.sbs.man.ac.uk/resources/puma
NeedsCompilation no
git_url https://git.bioconductor.org/packages/pumadata
git_branch RELEASE_3_18
git_last_commit da7fe7e
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-02-20

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The data from the estrogen package as an AffyBatch object

**Description**

This data is taken from the estrogen package. It was created to be used in the vignette for the puma package. It can be produced using the following code:

```r
library(estrogen)
datadir <- file.path(.find.package("estrogen"),"extdata")
estrogenFilenames <- c("low10-1.cel","low10-2.cel","high10-1.cel","high10-2.cel" ,"low48-1.cel","low48-2.cel","high48-1.cel","high48-2.cel")
affybatch.estrogen <- ReadAffy(
filenames=estrogenFilenames ,celfile.path=datadir)
pData(affybatch.estrogen) <- data.frame(
  "estrogen"=c("absent","absent","present","present" ,"absent","absent","present","present"),
  "time.h"=c("10","10","10","10","48","48","48","48"),
  row.names=rownames(pData(affybatch.estrogen)))
```

**Usage**

```r
data(affybatch.estrogen)
```

**Format**

An AffyBatch object containing 8 HG\_U95Av2 arrays, in a 2 x 2 factorial design, with 2 replicates for each combination of factors. The factors are estrogen (absent of present) and time.h (10 or 48).
eset_estrogen_comb

Description

This data is taken from the estrogen package. It was created to be used in the vignette for the puma package. It can be produced using the following code (note this could take a long time to run):

data(eset_estrogen_mmgmos)
eset_estrogen_mmgmos_normd <- PUMAnormalize(eset_estrogen_mmgmos, "median")
eset_estrogen_comb <- PUMAcomb(eset_estrogen_mmgmos_normd)

Usage

data(eset_estrogen_comb)

Format

An ExpressionSet object containing the expression levels and standard errors from combining the replicates for each combination of levels of factors from 8 HG_U95Av2 arrays, in a 2 x 2 factorial design, with 2 replicates for each combination of factors. The factors are estrogen (absent of present) and time.h (10 or 48).

See Also

eset_estrogen_mmgmos

Examples

data(eset_estrogen_comb)
exprs(eset_estrogen_comb)[1:3,1:3]
assayDataElement(eset_estrogen_comb,"se.exprs")[1:3,1:3]

eset_estrogen_mmgmos

Description

This data is taken from the estrogen package. It was created to be used in the vignette for the puma package. It can be produced using the following code (note this could take a long time to run):

data(oligo.estrogen)
eset_estrogen_mmgmos <- mmgmos(oligo.estrogen)
Usage

data(eset_estrogen_pmmmgmos)

Format

An exprReslt object containing expression levels and standard errors for 8 HG\_U95Av2 arrays, in a 2 x 2 factorial design, with 2 replicates for each combination of factors. The factors are estrogen (absent of present) and time.h (10 or 48).

See Also

oligo.estrogen eset_estrogen_rma

Examples

data(eset_estrogen_pmmmgmos)
show(eset_estrogen_pmmmgmos)
exprs(eset_estrogen_pmmmgmos)[1:3,1:3]
assayDataElement(eset_estrogen_pmmmgmos,"se.exprs")[1:3,1:3]

The data from the estrogen package processed using the multi-mgMOS
use PM intensities only

Description

This data is taken from the estrogen package. It was created to be used in the vignette for the puma package. It can be produced using the following code (note this could take a long time to run):

data(oligo.estrogen)
eset_estrogen_pmmmgmos <- pmmmgmos(oligo.estrogen)

Usage

data(eset_estrogen_pmmmgmos)

Format

An exprReslt object containing expression levels and standard errors for 8 HG\_U95Av2 arrays, in a 2 x 2 factorial design, with 2 replicates for each combination of factors. The factors are estrogen (absent of present) and time.h (10 or 48).

See Also

oligo.estrogen eset_estrogen_rma
**eset_estrogen_rma**

**Examples**

```r
data(eset_estrogen_pmmmgmos)
show(eset_estrogen_pmmmgmos)
exprs(eset_estrogen_pmmmgmos)[1:3,1:3]
assayDataElement(eset_estrogen_pmmmgmos,"se.exprs")[1:3,1:3]
```

---

**eset_estrogen_rma**  
*The data from the estrogen package processed using the RMA algorithm*

**Description**

This data is taken from the `estrogen` package. It was created to be used in the vignette for the `puma` package. It can be produced using the following code:

```r
data(oilogo.estrogen)
eset_estrogen_mmgmos <- rma(oilogo.estrogen)
```

**Usage**

```r
data(eset_estrogen_rma)
```

**Format**

An `ExpressionSet` object taining expression levels for 8 HG\_U95Av2 arrays, in a 2 x 2 factorial design, with 2 replicates for each combination of factors. The factors are estrogen (absent of present) and time.h (10 or 48).

**See Also**

`oligo.estrogen eset_estrogen_mmgmos`

**Examples**

```r
data(eset_estrogen_rma)
show(eset_estrogen_rma)
exprs(eset_estrogen_rma)[1:3,1:3]
assayDataElement(eset_estrogen_rma,"se.exprs")[1:3,1:3]
```
### HTA_Location

**The coordinates of probes and the mapped PM probes for hta2.0 chips**

**Description**

This data include the probes location for hta2.0 chips.

**Usage**

```r
data(HTA_Location)
```

**Format**

A 1*5118823 matrix including the location for unique probes in HTA_transcript_NO.

**Source**


---

### HTA_probes_transcripts

**The number of probes and the number of transcripts mapped to each gene for hta2.0 chips**

**Description**

This data is the number of probes and the number of transcripts mapped to each gene for hta2.0 chips.

**Usage**

```r
data(HTA_probes_transcripts)
```

**Format**

A 33394*2 matrix including the number of probes and the number of transcripts mapped to each of 33394 genes for hta20 chips.

**Source**


### Description

This data include the names of transcripts mapped to each gene for hta2.0 chips.

### Usage

```r
data(HTA_transcript_name)
```

### Format

A 225456*1 matrix including 225456 transcript names mapped to genes for hta2.0 chips.

### Source


---

### Description

This data include the coordinates of probes and the mapped transcripts for hta2.0 chips.

### Usage

```r
data(HTA_transcript_NO)
```

### Format

A 20626078*3 matrix including pos_x, pos_y and transcript_no. pos_x and pos_y are respectively X and Y coordinates of probes for hta2.0 chips. Transcript_no is the mapped transcripts for each probe.

### Source


Human probes transcripts

The number of probes and the number of transcripts mapped to each gene for human exon chips

Description
This data is the number of probes and the number of transcripts mapped to each gene for human exon chips.

Usage
data(Human_probes_transcripts)

Format
A 40174*2 matrix including the number of probes and the number of transcripts mapped to each of 40174 genes for human exon chips.

Source
**Human_transcript_name**

The names of transcripts mapped to each gene for human exon chips

**Description**

This data include the names of transcripts mapped to each gene for human exon chips.

**Usage**

```r
data(Human_transcript_name)
```

**Format**

A 121741*1 matrix including 121741 transcript names mapped to genes for human exon chips.

**Source**


---

**Human_transcript_NO**

The coordinates of probes and the mapped transcripts for human exon chips

**Description**

This data include the coordinates of probes and the mapped transcripts for human exon chips.

**Usage**

```r
data(Human_transcript_NO)
```

**Format**

A 4598850*3 matrix including pos_x,pos_y and transcript_no. pos_x and pos_y are respectively X and Y coordinates of probes for human exon chips. Transcript_no is the mapped transcripts for each probe.

**Source**

### Mouse_Location

**The coordinates of probes and the mapped PM for Mouse exon chips**

**Description**

This data include the probes location for Mouse exon chips.

**Usage**

```r
data(Mouse_Location)
```

**Format**

A 1*1278936 matrix including the location for unique probes in Mouse_transcript_NO.

**Source**


### Mouse_probes_transcripts

**The number of probes and the number of transcripts mapped to each gene for mouse exon chips**

**Description**

This data include the number of probes and the number of transcripts mapped to each gene for mouse exon chips.

**Usage**

```r
data(Mouse_probes_transcripts)
```

**Format**

A 27719*2 matrix including the number of probes and the number of transcripts mapped to each of 27719 genes for mouse exon chips.

**Source**

### Mouse_transcript_name

**The names of transcripts mapped to each gene for mouse exon chips**

**Description**

This data include the names of transcripts mapped to each gene for mouse exon chips.

**Usage**

```r
data(Mouse_transcript_name)
```

**Format**

A 75751*1 matrix including 75751 transcript names mapped to genes for mouse exon chips.

**Source**


### Mouse_transcript_NO

**The coordinates of probes and the mapped transcripts mapped for mouse exon chips**

**Description**

This data include the coordinates of probes and the mapped transcripts for mouse exon chips.

**Usage**

```r
data(Mouse_transcript_NO)
```

**Format**

A 2928848*3 matrix including pos_x, pos_y and transcript_no. pos_x and pos_y are respectively X and Y coordinates of probes for mouse exon chips. Transcript_no data is the mapped transcripts for each probe.

**Source**

oligo.estrogen  The data from the estrogen package as an ExpressionFeatureSet object

Description

This data is taken from the estrogen package. It was created to be used in the vignette for the puma package. It can be produced using the following code:

```r
library(estrogen)

datadir <- file.path(find.package("estrogen"),"extdata")
estrogenFilenames <- c("low10-1.cel","low10-2.cel","high10-1.cel","high10-2.cel","low48-1.cel","low48-2.cel","high48-1.cel","high48-2.cel")

datadir <- file.path(find.package("estrogen"),"extdata")
estrogenFilenames <- c("low10-1.cel","low10-2.cel","high10-1.cel","high10-2.cel","low48-1.cel","low48-2.cel","high48-1.cel","high48-2.cel")

data(oligo.estrogen) <- read.celfiles(
  filenames=estrogenFilenames
)

pData(oligo.estrogen) <- data.frame(
  "estrogen"=c("absent","absent","present","present","absent","absent","present","present"),
  "time.h"=c("10","10","10","10","48","48","48","48"),
  row.names=rownames(pData(oligo.estrogen))
)

Usage

data(oligo.estrogen)

Format

An ExpressionFeatureSet object containing 8 HG_U95Av2 arrays, in a 2 x 2 factorial design, with 2 replicates for each combination of factors. The factors are estrogen (absent of present) and time.h (10 or 48).

pumapca_estrogen  The data from the estrogen package processed using the pumaPCA algorithm

Description

This data is taken from the estrogen package. It was created to be used in the vignette for the puma package. It can be produced using the following code (note this could take a long time to run):

```r
data(eset_estrogen_mmgmos)
pumapca_estrogen <- pumaPCA(eset_estrogen_mmgmos)
```
Usage

data(pumapca_estrogen)

Format

An `pumaPCARes` object containing principal components (created using pumaPCA) of 8 HG\_U95Av2 arrays, in a 2 x 2 factorial design, with 2 replicates for each combination of factors. The factors are estrogen (absent of present) and time.h (10 or 48).

See Also

eset_estrogen_mmgmos

Examples

data(pumapca_estrogen)
plot(pumapca_estrogen,legend1pos="right",legend2pos="top")

---

**Rat_Location**

*The coordinates of probes and the mapped PM for Rat exon chips*

Description

This data include the probes location for Rat exon chips.

Usage

data(Rat_Location)

Format

A 1*931210 matrix including the location for unique probes in Rat_transcript_NO.

Source

Rat_probes_transcripts

Description
This data is the number of probes and the number of transcripts mapped to each gene for rat exon chips.

Usage
data(Rat_probes_transcripts)

Format
A 23585*2 matrix including the number of probes and the number of transcripts mapped to each of 23585 genes for rat exon chips.

Source

Rat_transcript_name

Description
This data is the names of transcripts mapped to each gene for rat exon chips.

Usage
data(Rat_transcript_name)

Format
A 334851*1 matrix including 334851 transcript names mapped to each gene for rat exon chips.

Source
Rat_transcript_NO

| Rat_transcript_NO | The coordinates of probes and the mapped transcripts for rat exon chips |

**Description**

This data include the coordinates of probes and the mapped transcripts for rat exon chips.

**Usage**

```r
data(Rat_transcript_NO)
```

**Format**

A 1491570*3 matrix including pos_x, pos_y and transcript_no. pos_x and pos_y are respectively X and Y coordinates of probes for rat exon chips. Transcript_no is the mapped transcripts for each probe.

**Source**

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