pumadata

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R topics documented:

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affybatch.estrogen *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** pacakge. It can be produced using the following code:

```
library(estrogen)
datadir <- file.path(.find.package("estrogen"),"extdata")
estrogenFilenames <- c("low10-1.cel","low10-2.cel","high10-1.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","4
        ,        row.names=rownames(pData(affybatch.estrogen))
)
```

Usage

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

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Format

An [AffyBatch](#) object containing 8 HG_U95Av2 arrays, in a 2 x 2 factorial design, with 2 repli-
cates for each combination of factors. The factors are estrogen (absent of present) and time.h (10 or
48).

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eset_estrogen_comb *The data from the estrogen package processed using the multi-mgMOS*
and PUMAcomb algorithms

Description

This data is taken from the **estrogen** package. It was created to be used in the vignette for the **puma**
pacakge. 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
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
```
The data from the estrogen package processed using the multi-mgMOS algorithm

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Description

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

```
data(affybatch.estrogen)
eset_estrogen_mmgmos <- mmgmos(affybatch.estrogen)
```

Usage

```
data(eset_estrogen_mmgmos)
```

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

`affybatch.estrogen` `eset_estrogen_rma`

Examples

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

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

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Description

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

```
data(affybatch.estrogen)
eset_estrogen_mmgmos <- rma(affybatch.estrogen)
```

Usage

```
data(eset_estrogen_rma)
```

Format

An [ExpressionSet](#) object containing 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

[affybatch.estrogen](#) [eset_estrogen_mmgmos](#)

Examples

```
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]
```

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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**
pacakge. It can be produced using the following code (note this could take a long time to run):

```
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")
```

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