

pumadata

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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** package. 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", "48")
, row.names=rowNames(pData(affybatch.estrogen))
)
```

Usage

```
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 *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** 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)
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

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

Usage

```
data(eset_estrogen_mmgmos)
```

Format

An `exprResult` 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 or 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

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:

```
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]
```

pumapca_estrogen	<i>The data from the estrogen package processed using the pumaPCA algorithm</i>
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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** package. 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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