

# pumadata

April 2, 2010

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`affybatch.estrogen` *The data from the estrogen package as an AffyBatch object*

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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:

```
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=row.names(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 or 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*

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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)
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]
```

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```
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** 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 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]
```

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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** 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 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**

[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*

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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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