

# Package ‘pumadata’

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**Type** Package

**Title** Various data sets for use with the puma package

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**Depends** R (>= 2.10.0), affy (>= 1.23.4), Biobase (>= 2.5.5), puma

**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

**URL** <http://umber.sbs.man.ac.uk/resources/puma>

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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", "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 of present) and time.h (10 or 48).

---

eset\_estrogen\_comb      *The data from the estrogen package processed using the multi-mgMOS and PUMAcmb 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, "median")
eset_estrogen_comb <- PUMAcmb(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 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_pmmgmos
```

*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(affybatch.estrogen)
eset_estrogen_pmmgmos <- pmmgmos(affybatch.estrogen)
```

### Usage

```
data(eset_estrogen_pmmgmos)
```

### 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_pmmgmos)
show(eset_estrogen_pmmgmos)
exprs(eset_estrogen_pmmgmos)[1:3,1:3]
assayDataElement(eset_estrogen_pmmgmos,"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 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]
```

---

Human\_Location

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

---

**Description**

This data include the probes location for human exon chips.

**Usage**

```
data(Human_Location)
```

**Format**

the location for probes

**Source**

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATEXplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

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**

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATEExplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

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**

data(Human\_transcript\_name)

**Format**

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

**Source**

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATEExplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

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**

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**

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATEExplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

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**

```
data(Mouse_Location)
```

**Format**

the location for probes

**Source**

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATEExplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

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**

```
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**

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATEExplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

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**

```
data(Mouse_transcript_name)
```

**Format**

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

**Source**

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATEplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

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**

```
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**

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATEplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.



---

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

---

### 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 or 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	<i>The coordinates of probes and the mapped PM for Rat exon chips</i>
--------------	---

---

### Description

This data include the probes location for Rat exon chips.

### Usage

```
data(Rat_Location)
```

### Format

the location for probes

### Source

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATEexplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

Rat\_probes\_transcripts

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

---

**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**

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATEXplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

Rat\_transcript\_name

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

---

**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**

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATEXplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

Rat_transcript_NO	<i>The coordinates of probes and the mapped transcripts for rat exon chips</i>
-------------------	--

---

**Description**

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

**Usage**

```
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**

Risueno A, Fontanillo C, Dinger ME, De Las Rivas J. GATExplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics. 2010 Apr 29;11:221.

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