

# Package ‘pumadata’

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**Type** Package

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

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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

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affybatch.estrogen	<i>The data from the estrogen package as an AffyBatch object</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:

```
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	<i>The data from the estrogen package processed using the multi-mgMOS and PUMAComb algorithms</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)
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	<i>The data from the estrogen package processed using the multi-mgMOS 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(oligo.estrogen)
eset_estrogen_mmgmos <- mmgmos(oligo.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**

[oligo.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(oligo.estrogen)
eset_estrogen_pmmgmos <- pmmgmos(oligo.estrogen)
```

**Usage**

```
data(eset_estrogen_pmmgmos)
```

**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**

[oligo.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	<i>The data from the estrogen package processed using the RMA 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:

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

[oligo.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]
```

---

HTA_Location	<i>The coordinates of probes and the mapped PM probes for hta2.0 chips</i>
--------------	--

---

### Description

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

### Usage

```
data(HTA_Location)
```

### Format

A 1\*5118823 matrix including the location for unique probes in HTA\_transcript\_NO.

**Source**

Danielle Thierry-Mieg ,Jean Thierry-Mieg. Aceview: a comprehensive cDNA-supported gene and transcripts annotaion. Genome Biology.2006,7(Suppl 1):S12

Manhong Dai, Pinglang Wang,Andrew D. Boyd. (2005) Evolving gene/transcript definitions significantly alter the interpretation of GeneChip data,Nucleic Acid Research 33(20):e175.

---

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**

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**

Danielle Thierry-Mieg ,Jean Thierry-Mieg. Aceview: a comprehensive cDNA-supported gene and transcripts annotaion Genome Biology.2006,7(Suppl 1):S12

Manhong Dai, Pinglang Wang,Andrew D. Boyd. (2005) Evolving gene/transcript definitions significantly alter the interpretation of GeneChip data,Nucleic Acid Research 33(20):e175.

---

HTA\_transcript\_name

*The names of transcripts mapped to each gene for hta2.0 chips*

---

**Description**

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

**Usage**

data(HTA\_transcript\_name)

**Format**

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

**Source**

Danielle Thierry-Mieg ,Jean Thierry-Mieg. Aceview: a comprehensive cDNA-supported gene and transcripts annotaion Genome Biology.2006,7(Suppl 1):S12

Manhong Dai, Pinglang Wang,Andrew D. Boyd. (2005) Evolving gene/transcript definitions significantly alter the interpretation of GeneChip data,Nucleic Acid Research 33(20):e175.

---

HTA\_transcript\_NO      *The coordinates of probes and the mapped transcripts for hta2.0 chips*

---

**Description**

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

**Usage**

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**

Danielle Thierry-Mieg ,Jean Thierry-Mieg. Aceview: a comprehensive cDNA-supported gene and transcripts annotaion Genome Biology.2006,7(Suppl 1):S12

Manhong Dai, Pinglang Wang,Andrew D. Boyd. (2005) Evolving gene/transcript definitions significantly alter the interpretation of GeneChip data,Nucleic Acid Research 33(20):e175.

---

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**

A 1\*1565476 matrix including the location for unique probes in Human\_transcript\_NO.

**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\_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	<i>The coordinates of probes and the mapped transcripts for human exon chips</i>
---------------------	--

---

**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	<i>The coordinates of probes and the mapped PM for Mouse exon chips</i>
----------------	---

---

**Description**

This data include the probes location for Mouse exon chips.

**Usage**

```
data(Mouse_Location)
```

**Format**

A 1\*1278936 matrix including the location for unique probes in Mouse\_transcript\_NO.

**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. GATEExplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

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

---

### 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. GATEExplorer: genomic and transcriptomic explorer; mapping expression probes to gene loci, transcripts, exons and ncRNAs. BMC Bioinformatics.2010 Apr 29;11:221.

---

oligo.estrogen	<i>The data from the estrogen package as an ExpressionFeatureSet object</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:

```
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")
setwd(datadir)
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=row.names(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	<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 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	<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**

A 1\*931210 matrix including the location for unique probes in Rat\_transcript\_NO.

**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_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	<i>The names of transcripts mapped to each gene for rat exon chips</i>
---------------------	--

---

**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. GATEExplorer: 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. GATEExplorer: 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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