Package ‘pumadata’

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Type Package

Title Various data sets for use with the puma package

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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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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:

```r
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"), "time.h"=c("10", "10", "10", "10", "48", "48", "48", "48"), row.names=rownames(pData(affybatch.estrogen)))
```

Usage

```r
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).

The data from the estrogen package processed using the multi-mmMOS 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):

```r
data(eset_estrogen_mmgmos)
eset_estrogen_mmgmos_normd <- PUMAnormalize(eset_estrogen_mmgmos, "median")
eset_estrogen_comb <- PUMAcomb(eset_estrogen_mmgmos_normd)
```
eset_estrogen_mmgmos

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(oligo.estrogen)
eset_estrogen_mmgmos <- mmgmos(oligo.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

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_pmmmgmos

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):

```r
data(oligo.estrogen)
eset_estrogen_pmmmgmos <- pmmmgmos(oligo.estrogen)
```

Usage

```r
data(eset_estrogen_pmmmgmos)
```

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

```r
data(eset_estrogen_pmmmgmos)
show(eset_estrogen_pmmmgmos)
exprs(eset_estrogen_pmmmgmos)[1:3,1:3]
assayDataElement(eset_estrogen_pmmmgmos,"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:

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

Usage

```r
data(eset_estrogen_rma)
```
**HTA_Location**

**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**

```r
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**

*The coordinates of probes and the mapped PM probes for hta2.0 chips*

**Description**

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

**Usage**

```r
data(HTA_Location)
```

**Format**

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

**Source**


---

**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 annotation Genome Biology.2006,7(Suppl 1):S12

Manhong Dai, Pinglang Wang, Andrew D. Boyd. (2005) Evolving gene/transcript definitions sig-
nificantly 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 annotation Genome Biology.2006,7(Suppl 1):S12

Manhong Dai, Pinglang Wang, Andrew D. Boyd. (2005) Evolving gene/transcript definitions sig-
nificantly 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)
**Human_Location**

**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**

<table>
<thead>
<tr>
<th>Human_Location</th>
<th>The coordinates of probes and the mapped PM for human exon chips</th>
</tr>
</thead>
</table>

**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**

<table>
<thead>
<tr>
<th>Human_probes_transcripts</th>
<th>The number of probes and the number of transcripts mapped to each gene for human exon chips</th>
</tr>
</thead>
</table>

**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)
**Human_transcript_NO**

**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**

---

**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**

---

**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.
**Mouse_Location**

**Source**

**Description**
This data include the probes location for Mouse exon chips.

**Usage**
```r
data(Mouse_Location)
```

**Format**
A 1*1278936 matrix including the location for unique probes in Mouse_transcript_NO.

**Source**

---

**Mouse_probes_transcripts**

**Description**
This data include the number of probes and the number of transcripts mapped to each gene for Mouse exon chips.

**Usage**
```r
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**
Mouse_transcript_NO

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

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
oligo.estrogen  

The data from the estrogen package as an ExpressionFeatureSet 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:

```r
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=rownames(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  
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 package. It can be produced using the following code (note this could take a long time to run):

```r
data(eset_estrogen_mmgmos)
pumapca_estrogen <- pumaPCA(eset_estrogen_mmgmos)
```

Usage

data(pumapca_estrogen)
Rat_probes_transcripts

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

The coordinates of probes and the mapped PM for Rat exon chips

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

---

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


---

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


---

Rat_transcript_NO

The coordinates of probes and the mapped transcripts for rat exon chips

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

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