Package 'pumadata'

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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

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

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

Usage

```
data(eset_estrogen_pmmmgmos)
```

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_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** pacakge. 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 *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

```
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. 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. GATExplorer: 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. GATExplorer: 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. GATExplorer: 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

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

`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** pacakge. 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=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** pacakge. 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 *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

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` *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` *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

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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