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.

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biocViews ExperimentData

URL `http://umber.sbs.man.ac.uk/resources/puma`

R topics documented:

`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(affybatch.estrogen)
eset_estrogen_mmgmos <- mmgmos(affybatch.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

`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_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(affybatch.estrogen)
eset_estrogen_pmmmgmos <- pmmmgmos(affybatch.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

`affybatch.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(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. 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

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.

`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.

`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

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.

`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.

Index