Package 'Ipsum'

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Type Package

Title Visualisation of gene and transcript expression levels from RNA-seq experiments

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Imports methods

Description Plot gene and transcript expression levels estimated from RNA-seq experiments using both sample-specific and summarised approaches.

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Ipsum-package	*Ipsum: visualisation of gene and transcript expression levels from RNA-seq experiments*

Description

Plot gene and transcript expression levels estimated from RNA-seq experiments using both sample-specific and summarised approaches.

Details

Package:	Ipsum
Type:	Package
Version:	1.0
Date:	2014-01-17
License:	GPLv2

Author(s)

Author: Mar Gonzàlez-Porta <mar@ebi.ac.uk>

References

https://github.com/mgonzalezporta/ipsum

biotypes	*Accessor function for the 'biotypes' slot of a TranscriptExpressionSet object.*

Description

The biotypes slot holds information on the different unique biotypes across all the transcripts annotated for a given gene. Such information has been previously loaded by the user when creating the TranscriptExpressionSet object.

Usage

```
## S4 method for signature TranscriptExpressionSet
biotypes(object)
```

Arguments

object   a TranscriptExpressionSet object.

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

conditions   *Accessor function for the 'conditions' slot of a TranscriptExpression-Set object.*

Description

The conditions slot contains information on the experimental conditions evaluated, as well as the list of samples corresponding to each one of them.

Usage

```
## S4 method for signature TranscriptExpressionSet
conditions(object)
```

Arguments

object   a `TranscriptExpressionSet` object.

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

dominance   *Accessor function for the 'dominance' slot of a TranscriptExpression-Set object.*

Description

The dominance slot contains information on major transcript dominance, calculated as the ratio of expression between the second vs. first most abundant transcripts for each gene.

Usage

```
## S4 method for signature TranscriptExpressionSet
dominance(object)
```

Arguments

object   a `TranscriptExpressionSet` object.

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

gexp	*Accessor function for the 'gexp' slot of a TranscriptExpressionSet object.*

Description

The gexp slot contains a list of gene expression levels in each sample. Gene expression is calculated as the sum of transcript expression.

Usage

```
## S4 method for signature TranscriptExpressionSet
gexp(object)
```

Arguments

object   a `TranscriptExpressionSet` object.

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

id	*Accessor function for the 'id' slot of a TranscriptExpressionSet object.*

Description

The id slot contains the id for the gene represented in a given TranscriptExpressionSet object.

Usage

```
## S4 method for signature TranscriptExpressionSet
id(object)
```

Arguments

object   a `TranscriptExpressionSet` object.

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

```
newTranscriptExpressionSet
```
Create a new TranscriptExpressionSet object from data files provided by the user

Description

Creates a new TranscriptExpressionSet object for further visualisation of the embedded expression data.

Usage

```
newTranscriptExpressionSet(
  gId=gId,
  rpkms=rpkms,
  biotypes=biotypes,
  significant_events=significant_events,
  cond1=cond1,
  cond2=cond2)
```

Arguments

gId   Id for the gene to be plotted.

rpkms   Matrix of transcript RPKM/FPKM values in each sample, loaded using the 'readExpressionData' function.

biotypes   Matrix of biotypes for each of the annotated transcripts within the gene, loaded using the 'readBiotypeData' function.

significant_events

                List of transcript ids that undergo differential usage across the studied conditions, loaded using the 'readSignificantEvents' function. Should be set to 'NA' in case such information is not available.

cond1   String indicating the range of columns (samples) that belong to the first condition. E.g: '3-6'.

cond2   String indicating the range of columns (samples) that belong to the second condition. E.g: '7-10'.

Value

A TranscriptExpressionSet object.

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

plotDistr	*Create a distribution plot for the specified TranscriptExpressionSet object.*

Description

A distribution plot contains information on the distribution of gene expression levels, major transcript dominance and transcript relative abundances in each condition. This plot contains three panels:

left - Distribution of gene expression levels (RPKMs or FPKMs).

middle - Distribution of major transcript dominance. Major transcript dominance is calculated in each condition as the ratio of expression of the second/first most abundant transcripts. Thus, a ratio close to 0 will indicate that the most abundant transcript is dominating the expression for that gene, while a ratio close to 1 indicates that the first and second most abundant transcripts are expressed at the same level.

right - Relative abundances for all the transcripts annotated within the gene. Considering that gene expression is the result of adding up transcript expression levels, relative abundance can be understood as the fraction of gene expression explained by each transcript.

Depending on the number of samples, the information in each panel will be displayed as boxplots (n >= 10 in each condition) or as dots + error bars (which correspond to the mean + SD across samples, respectively).

Usage

```
## S4 method for signature TranscriptExpressionSet
plotDistr(tes, outfile)
```

Arguments

tes	a `TranscriptExpressionSet` object.
outfile	ouput file (pdf).

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

plotStars	*Create a starplot for the specified TranscriptExpressionSet object.*

Description

A starplot provides information on the transcript RPKM quantifications in a sample specific manner. In this plot each sample is represented as a pie chart, where each of the slices corresponds to a transcript. The size of each slice is proportional to the transcript expression level, and the overall size of the plot is proportional to the gene expression level, thus allowing comparisons across samples.

Usage

```
## S4 method for signature TranscriptExpressionSet
plotStars(tes, outfile)
```

Arguments

tes   a TranscriptExpressionSet object.

outfile   ouput file (pdf).

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

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readBiotypeData   *Load transcript biotype data for a given gene from a system file.*

Description

Load transcript biotype data for a given gene from a system file.

Usage

```
readBiotypeData(gId=gId, infile=infile)
```

Arguments

gId   Id of the gene for which to load biotype data.

infile   Path to the file that contains the biotype data.

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

---

readExpressionData   *Create a matrix of RPKM/FPKM transcript expression levels for a*
                             given gene from a system file.

Description

Loads transcript expression data (RPKM/FPKM values) for a given gene from a system file. Each sample is represented as a column, and each transcript as a row.

Usage

```
readExpressionData(gId=gId, infile=infile, cond1=cond1, cond2=cond2)
```

Arguments

gId	Id of the gene for which to load expression data.
infile	Path to the file that contains the expression data.
cond1	String indicating the range of columns (samples) that belong to the first condition. E.g: '3-6'.
cond2	String indicating the range of columns (samples) that belong to the second condition. E.g: '7-10'.

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

---

readSignificantEvents	*For a given gene, load a list of transcripts that undergo differential usage across conditions.*

Description

For a given gene, load a list of transcripts that undergo differential usage across conditions.

Usage

```
readSignificantEvents(gId=gId, infile=infile)
```

Arguments

gId	Id of the gene for which to load the list of differentially used transcripts.
infile	Path to the file that contains the differential usage data.

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

---

rpkms	*Accessor function for the 'rpkms' slot of a TranscriptExpressionSet object.*

Description

The rpkms slot displays a matrix with the initial RPKM/FPKM values provided by the user. Each sample is represented as a column, and each transcript as a row.

Usage

```
## S4 method for signature TranscriptExpressionSet
rpkms(object)
```

Arguments

object   a `TranscriptExpressionSet` object.

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

---

significant_events   *Accessor function for the 'significant_events' slot of a TranscriptExpressionSet object.*

Description

The significant_events slot holds a list of transcript ids reported by the user as differentially used across the studied conditions. In the case that such information is not available, 'NA' will be assigned.

Usage

```
## S4 method for signature TranscriptExpressionSet
significant_events(object)
```

Arguments

object   a `TranscriptExpressionSet` object.

Author(s)

Mar Gonzàlez-Porta, <mar@ebi.ac.uk>

TranscriptExpressionSet

Class "TranscriptExpressionSet" – a container for transcript-level expression data from RNA-seq experiments

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Description

This is the main class for the present package.

Slots

gId Id for the gene to be plotted.

rpkms Matrix of transcript RPKM/FPKM values in each sample, loaded using the 'readExpressionData' function.

biotypes Matrix of biotypes for each of the annotated transcripts within the gene, loaded using the 'readBiotypeData' function.

significant_events List of transcript ids that undergo differential usage across the studied conditions, loaded using the 'readSignificantEvents' function. Should be set to 'NA' in case such information is not available.

cond1 String indicating the range of columns (samples) that belong to the first condition. E.g: '3-6'.

cond1 String indicating the range of columns (samples) that belong to the second condition. E.g: '7-10'.

Objects from the Class

Objects should be created with calls to `newTranscriptExpressionSet`.

Author(s)

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Index