

# Package ‘tviz’

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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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tviz-package	<i>tviz: visualisation of gene and transcript expression levels from RNA-seq experiments</i>
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### Description

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

### Details

Package: tviz  
Type: Package  
Version: 0.99.0  
Date: 2014-01-17  
License: GPLv2

### Author(s)

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

### References

<https://github.com/mgonzalezporta/tviz>

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biotypes	<i>Accessor function for the 'biotypes' slot of a TranscriptExpressionSet object.</i>
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### 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 González-Porta, <mar@ebi.ac.uk>

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conditions	<i>Accessor function for the 'conditions' slot of a TranscriptExpressionSet object.</i>
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### Description

The conditions slot contains information on the experimental conditions evaluated, as well as the list of samples corresponding to each one of them. This slot is automatically created from the header of the input file.

### Usage

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

### Arguments

object            a TranscriptExpressionSet object.

### Author(s)

Mar González-Porta, <mar@ebi.ac.uk>

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dominance	<i>Accessor function for the 'dominance' slot of a TranscriptExpressionSet object.</i>
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### 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 González-Porta, <mar@ebi.ac.uk>

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gexp	<i>Accessor function for the 'gexp' slot of a TranscriptExpressionSet object.</i>
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**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 González-Porta, <mar@ebi.ac.uk>

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id	<i>Accessor function for the 'id' slot of a TranscriptExpressionSet object.</i>
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**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 González-Porta, <mar@ebi.ac.uk>

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

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**Description**

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

**Usage**

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

**Arguments**

<code>gId</code>	Id for the gene to be plotted.
<code>texp</code>	Matrix of transcript expression values in each sample, loaded using the 'readExpressionData' function.
<code>biotypes</code>	Matrix of biotypes for each of the annotated transcripts within the gene, loaded using the 'readBiotypeData' function.
<code>significant_events</code>	List of transcript ids that undergo differential usage across the studied conditions, loaded using the 'readSignificantEvents' function. Must be set to 'NA' in case such information is not available.
<code>cond1</code>	String indicating the range of columns (samples) that belong to the first condition. E.g: '3-6'.
<code>cond2</code>	String indicating the range of columns (samples) that belong to the second condition. E.g: '7-10'.

**Value**

A TranscriptExpressionSet object.

**Author(s)**

Mar González-Porta, <mar@ebi.ac.uk>

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plotDistr	<i>Create a distribution plot for the specified TranscriptExpressionSet object.</i>
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### 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.

middle - Distribution of major transcript dominance. Major transcript dominance is calculated in each condition as the ratio of expression of the second v.s. 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 ( $n \geq 10$  in each condition) or as dots + error bars (which correspond to the mean + SD across samples, respectively).

### Usage

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

### Arguments

tes	a TranscriptExpressionSet object.
outfile	output file (pdf).

### Author(s)

Mar González-Porta, <mar@ebi.ac.uk>

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plotStars	<i>Create a starplot for the specified TranscriptExpressionSet object.</i>
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### Description

A starplot provides information on the transcript 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,character  
plotStars(tes, outfile)
```

**Arguments**

tes                    a TranscriptExpressionSet object.  
outfile                output file (pdf).

**Author(s)**

Mar González-Porta, <mar@ebi.ac.uk>

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readBiotypeData	<i>Load transcript biotype data for a given gene from a system file.</i>
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**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 González-Porta, <mar@ebi.ac.uk>

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readExpressionData	<i>Create a matrix of transcript expression levels for a given gene from the specified input file.</i>
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**Description**

Loads transcript expression data for a given gene from the specified input file. Each sample is represented as a column, and each transcript as a row. Columns with the same id will be treated as technical replicates. In this case, the median expression across all samples will be calculated for each transcript. Columns with different ids within the same condition will be treated as biological replicates. Those will be represented separately.

**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 González-Porta, <mar@ebi.ac.uk>

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

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**Description**

Loads a list of transcripts that undergo differential usage across conditions for the specified gene.

**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 González-Porta, <mar@ebi.ac.uk>

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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.

**Usage**

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



## Arguments

**object** a TranscriptExpressionSet object.

## Author(s)

Mar González-Porta, <mar@ebi.ac.uk>

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texp	<i>Accessor function for the 'texp' slot of a TranscriptExpressionSet object.</i>
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## Description

The `texp` slot displays a matrix with the initial expression values provided by the user. Each sample is represented as a column, and each transcript as a row.

## Usage

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

## Arguments

**object** a TranscriptExpressionSet object.

## Author(s)

Mar González-Porta, <mar@ebi.ac.uk>

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TranscriptExpressionSet-class	<i>Class "TranscriptExpressionSet" – a container for transcript-level expression data from RNA-seq experiments</i>
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## Description

This is the main class for the present package.

## Slots

**gId** Id for the gene to be plotted.

**texp** Matrix of transcript expression 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. Must 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'.

### **Objects from the Class**

Objects should be created with calls to [newTranscriptExpressionSet](#).

### **Author(s)**

Mar González-Porta, <mar@ebi.ac.uk>

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