oneChannelGUI
November 11, 2009

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**AptMidas**

*Graphical interface to APT midas*

### Description

This is a graphical interface to the midas program for detection of alternative splicing detection implemented in the Affymetrix APT tools.

### Usage

AptMidas()

### Note

For more information see Affymetrix Alternative Transcript Analysis Methods for Exon Arrays whitepaper. Before using MiDAS is strongly recommended to filter out gene level probe sets with low intensity values to avoid searching alternative splicing for probe sets which are not expressed. This can be done using filtering method implemented in oneChannelGUI which define a background intensity threshold on the basis of the intron exon signals of a set of housekeeping genes present in the exon arrays. However it is also possible to use a filter based on the dabg p-value calculated using Affymetrix APT tools. This function will also calculate Splice Index.

### Author(s)

Raffaele A Calogero

### See Also

erankProdAltSpl

**biomartFilter**

*Filtering only gene-level probe sets with multiple ensembl transcripts*

### Description

This function allows to filter exon array data to selected only those gene-level probe sets associated to multiple mRNAs annotated in ensembl database.

### Usage

biomartFilter()

### Author(s)

Raffaele A Calogero
**buildingLocalAnnotation**

*Updates local gene-level annotation data for gene and exon arrays using the netaffx database*

**Description**

Internal oneChannelGUI Gene/Exon gene-level annotation data can be upgraded using this function, which queries netaffx database. Annotation RDA files are saved in the data subdir of oneChannelGUI dir. Windows users need to exchange the older copies present in Rdata.zip, simply dragging them in the zip file.

**Usage**

```
buildingLocalAnnotation()
```

**Author(s)**

Raffaele A Calogero

---

**colExtract**

*Extract a column from a tab delimited file with header*

**Description**

This function allows to extract a specific column from a tab delimited file generated by oneChannelGUI. The file should contain an header. This function is useful to extract probe set ids to be used for ven diagram representations.

**Usage**

```
colExtract()
```

**Author(s)**

Raffaele A Calogero
combineGeoMSF

This function allows to combine GEO Matrix Series Files belonging to the same experiment.

Description
The function combines in a unique ExpressionSet the data derived from multiple Matrix Series Files belonging to a GEO experiment containing more than 255 arrays.

Usage
combineGeoMSF()

Note
see oneChannelGUI vignette for more info

Author(s)
Raffaele A Calogero

consistentFilters
This function allows filtering using the combination of multiple parameters, e.g. MiDAS p-values and Rank Product p-values

Description
This filter can be used to moderate multiple tests errors. E.g. finding the intersection between MiDAS p-values and Rank Product p-values user will remove some of the false positive produced by the two methods. A filter on the size of delta Splice Index associated to MiDAS p-values filter will will allow to remove statistical significant splicing events which are characterized by a very limited variation.

Usage
consistentFilters()

Note
This fuction needs the presence of Splice Index data, MiDAS p-values and RP p-values. It works for two groups only

Author(s)
Raffaele A Calogero

See Also
erankProdAltSpl, AptMidas
cosieHscore  
*Parameters precalculated for the Affymetrix core human annotation subgroup from FMI Bioinformatics group and needed to correct SI*

**Description**

The description of how these data were generated is described in Gaidatzis et al. Nucleic Acids Research, 2009, 1

**Usage**

`cosieHscore`

**Format**

A matrix with 7 observations: status, geneTrainFrom, geneTrainTo, a, b, c, d

**References**

[www.fmi.ch/groups/gbioinfo/cosie/cosie.html](http://www.fmi.ch/groups/gbioinfo/cosie/cosie.html)

---

cosieHsfull  
*Parameters precalculated for the Affymetrix full human annotation subgroup from FMI Bioinformatics group and needed to correct SI*

**Description**

The description of how these data were generated is described in Gaidatzis et al. Nucleic Acids Research, 2009, 1. Authors recommend the use of the core set since the full set is not as well characterized.

**Usage**

`cosieHsfull`

**Format**

A matrix with 7 observations: status, geneTrainFrom, geneTrainTo, a, b, c, d

**References**

[www.fmi.ch/groups/gbioinfo/cosie/cosie.html](http://www.fmi.ch/groups/gbioinfo/cosie/cosie.html)
**cosieMmcore**

Parameters precalculated for the Affymetrix core mouse annotation subgroup from FMI Bioinformatics group and needed to correct SI

**Description**

The description of how these data were generated is described in Gaidatzis et al. Nucleic Acids Research, 2009, 1

**Usage**

cosieMmcore

**Format**

A matrix with 7 observations: status, geneTrainFrom, geneTrainTo, a, b, c, d

**References**

www.fmi.ch/groups/gbioinfo/cosie/cosie.html

---

**cosieMmfull**

Parameters precalculated for the Affymetrix full mouse annotation subgroup from FMI Bioinformatics group and needed to correct SI

**Description**

The description of how these data were generated is described in Gaidatzis et al. Nucleic Acids Research, 2009, 1. Authors recommend the use of the core set since the full set is not as well characterized.

**Usage**

cosieMmfull

**Format**

A matrix with 7 observations: status, geneTrainFrom, geneTrainTo, a, b, c, d

**References**

www.fmi.ch/groups/gbioinfo/cosie/cosie.html
cosieWrapper

A wrapper to cosie, Corrected Splicing Indices for Exon arrays, that for any given set of new exon array experiments corrects for the observed bias and improves the detection of alternative splicing

Description

COSIE is a function that for a given set of exon arrays corrects for the observed bias and improves the detection of alternative splicing. It adjusts splicing indices for exons, especially for those that belong to differentially expressed genes. For this adjustment, COSIE uses parameters that are specific for each probeset which were trained from a large number of published exon arrays. The downside of this approach is that such parameters cannot be estimated for all probesets on the microarray. Based on our training set, COSIE corrects 95.1 percent of the probesets. Separate parameter files are provided for both the full and core sets, including all probesets that are linked to transcripts. We recommend the use of the core set that was also used in the cited study below. The full set is not as well characterized.

Usage

cosieWrapper()

Author(s)

Gaidatzis et al. Nucleic Acids Research, 2009, 1

See Also

cosieHscore, cosieMmcore, cosieHsfull, cosieMmfull

createGeoTarget

Creating a affylmGUI Target starting from a GEO Matrix series file

Description

The function extracts from GEO series matrix file all the information to create a Target file, that can be used to load the GEO series matrix file into oneChannelGUI.

Usage

createGeoTarget()

Note

see oneChannelGUI vignette for Target file description

Author(s)

Raffaele A Calogero
crosshybFilter

Removing from exon array gene/exon level probe sets characterized by cross hybridization with other transcripts

Description

XHYB field is mainly an indicator of weak assignment between a transcript cluster and the assigned mRNA, suggesting a potential crosshyb. CRSSHYB is a measure of the promiscuity of the probes within a probe set among transcribed sequences.

1. 1 unique. All probes in the probe set perfectly match only one sequence in the putatively transcribed array design content. The vast majority of probe sets are unique.
2. 2 similar. All the probes in the probe set perfectly match more than one sequence in the putatively transcribed array design content.
3. 3 mixed. The probes in the probe set either perfectly match or partially match more than one sequence in the putatively transcribed array design content.

XHYB and CRSSHYB are used to remove probe sets characterized by multiple hybridization of exon probes

Usage

crosshybFilter()

Author(s)

Raffaele A Calogero

crosshybhuex.annotation

Cross hybridization data for exon CORE subset of human exon array 1.0 ST

Description

These data are derived from Affymetrix annotation file huex10stv2na23hg18. XHYB field is mainly an indicator of weak assignment between a transcript cluster and the assigned mRNA, suggesting a potential crosshyb. CRSSHYB is a measure of the promiscuity of the probes within a probe set among transcribed sequences.

1. 1 unique. All probes in the probe set perfectly match only one sequence in the putatively transcribed array design content. The vast majority of probe sets are unique.
2. 2 similar. All the probes in the probe set perfectly match more than one sequence in the putatively transcribed array design content.
3. 3 mixed. The probes in the probe set either perfectly match or partially match more than one sequence in the putatively transcribed array design content.

XHYB and CRSSHYB are used to remove probe sets characterized by multiple hybridization of exon probes. Cross-hybridization potential of the probe set determined at the time of array design. This field is based on computational sequence alignment against all known and putatively transcribed array design content, which includes all potentially transcribed regions of the genome and other transcribed sequences that could not be mapped to the genome.
**Usage**
crosshybmoex.annotation

**Format**
A data frame with 9 observations: EPROBESETID, GPROBESETID, ACC, XHYB, CHR, STRAND, START, STOP, CROSSHYBTYPE

**References**
Affymetrix web site

---

crosshybmoex.annotation  
*Cross hybridization data for exon CORE subset of mouse exon array 1.0 ST*

**Description**
These data are derived from Affymetrix annotation file moex10stv1na24mm8. XHYB field is mainly an indictor of weak assignment between a transcript cluster and the assigned mRNA, suggesting a potential crosshyb, CRSSHYB is a measure of the promiscuity of the probes within a probe set among transcribed sequences.

1. 1 unique. All probes in the probe set perfectly match only one sequence in the putatively transcribed array design content. The vast majority of probe sets are unique.
2. 2 similar. All the probes in the probe set perfectly match more than one sequence in the putatively transcribed array design content.
3. 3 mixed. The probes in the probe set either perfectly match or partially match more than one sequence in the putatively transcribed array design content.

XHYB and CRSSHYB are used to remove probe sets characterized by multiple hybridization of exon probes. Cross-hybridization potential of the probe set determined at the time of array design. This field is based on computational sequence alignment against all known and putatively transcribed array design content, which includes all potentially transcribed regions of the genome and other transcribed sequences that could not be mapped to the genome.

**Usage**
crosshybmoex.annotation

**Format**
A data frame with 9 observations: EPROBESETID, GPROBESETID, ACC, XHYB, CHR, STRAND, START, STOP, CROSSHYBTYPE

**References**
Affymetrix web site
Cross hybridization data for exon CORE subset of rat exon array 1.0

Description

These data are derived from Affymetrix annotation file raex10stv1na24rn4. XHYB field is mainly an indictor of weak assignment between a transcript cluster and the assigned mRNA, suggesting a potential crosshyb, CRSSHYB is a measure of the promiscuity of the probes within a probe set among transcribed sequences.

1. 1 unique. All probes in the probe set perfectly match only one sequence in the putatively transcribed array design content. The vast majority of probe sets are unique.
2. 2 similar. All the probes in the probe set perfectly match more than one sequence in the putatively transcribed array design content.
3. 3 mixed. The probes in the probe set either perfectly match or partially match more than one sequence in the putatively transcribed array design content.

XHYB and CRSSHYB are used to remove probe sets characterized by multiple hybridization of exon probes Cross-hybridization potential of the probe set determined at the time of array design. This field is based on computational sequence alignment against all known and putatively transcribed array design content, which includes all potentially transcribed regions of the genome and other transcribed sequences that could not be mapped to the genome.

Usage
crosshybraex.annotation

Format

A data frame with 9 observations: EPROBESETID, GPROBESETID, ACC, XHYB, CHR, STRAND, START, STOP, CROSSHYBTYPE

References

Affymetrix web site

dfMAplot

MA and Volcano plots from data present in a limma derived topTable

Description

MA and Volcano plots can be generated starting from limma results summarized in a topTable. Specific subsets of the topTable defined by p-value below an user-defined threshold and/or log2 fold changes over an user-defined threshold can be saved. The subset of data can be saved as a tab delimited file
erankProdAltSplFilter

Usage

dfMAplot(table1)

Arguments

table1   topTable data.frame generate by affyImGUI

Note

To know more about topTable see limma help

Author(s)

Raffaele A Calogero

EG2probeset

This function allows to link GeneBank and Entrez Gene ids to gene-level probe set ids

Description

This function allows to link oneChannelGUI embedded Affymetrix annotated accession numbers to gene-level probe set ids. Using the ACC EG are linked using the Bioconductor human, mouse or rat LLMappings annotation library

Usage

EG2probeset()

Author(s)

Raffaele A Calogero

erankProdAltSplFilter

Filtering Rank Product results for the detection of alternative splicing events

Description

This is a graphical interface to filter data on the basis of p-value generated by rank product analysis applied for the detection of alternative splicing

Usage

erankProdAltSpl()

Author(s)

Raffaele A Calogero
Implementation of the Rank Product method for the detection of alternative splicing events

Description

This is a graphical interface to the RP function from RankProd package applied to detection of alternative splicing

Usage

erankProdAltSpl()

Details

Before using this method it is strongly suggested to perform a filter on the basis of DABG p-values using the filtering function available in the filtering menu. DABG values can be calculated if exon array probe set data are generated using the oneChannelGUI graphical implementation to APT tools. Affymetrix suggests to calculate probe set intensity at gene level using iterPlier and at exon level using plier. Subsequently SpliceIndex need to be calculated using the function available in the exon menu. Finally the Rank Product method could be applied exon by exon. For more details on the method see RankProd package. Selection of putative alternative splicing could be done using the filtering function available in the filtering menu of oneChannelGUI

Note

IMPORTANT we are still evaluating the efficacy of this method for detection of alternative splicing events. Use it being concios of this!

Author(s)

Raffaele A Calogero

See Also

inspecting.splice, spliceIndex
exonContrasts  **Defining t-test regularized p-values**

**Description**
This function constructs the contrasts as affyTmGUI but applied to exon-level. It also performs Bayes regularization. Raw p-values are plotted to see if BH or BY type I error correction can be applied. Corrected p-values are saved and used for extraction of alternative spliced exons.

**Usage**

```r
exonContrasts()
```

**Details**
It is important to note that if multiple contrasts should be considered after the calculation of each of them it is essential to extract the alternative spliced exons with exonTopTableExtract, because everytime exonContrasts is run it overwrites the previous results.

**Author(s)**
Raffaele A Calogero

---

exonsSpecific2as  **Defining the exons associated to the various alternative isoforms**

**Description**
This function uses the output derived from the function mapping2ensembl and produces a list of 1 and 0 for each of the alternative transcripts associated to a specific Entrez Gene. This function is useful to define which splicing events are not associated to exons conserved over all the possible isoforms.

**Usage**

```r
exonsSpecific2as()
```

**Author(s)**
Raffaele A Calogero
**exonTopTableExtract**

*Extracts data on the basis of a defined t-test regularized p-value*

**Description**

This function filters the data produced by exonContrasts to extract a list of alternative spliced exons that are saved in a file and they can be used for further analysis, i.e. extracting only variant exons. The function also filter the data present in the onechannelGUI project bot at gene and exon-level.

**Usage**

```r
exonTopTableExtract()
```

**Details**

It is important to note that if multiple contrasts should be considered after the calculation of each of them it is essential to extract the alternative spliced exons with exonTopTableExtract, because everytime exonContrasts is run it overwrites the previous results.

**Author(s)**

Raffaele A Calogero

---

**extractAffyids** *Extracting probe ids associated to a specific Gene Ontology term*

**Description**

It is possible to identify the affy ids associated to a specific GO term using the extractAffyids function.

**Usage**

```r
extractAffyids()
```

**Details**

The function asks to the user to select a file containing probe set ids separated by carriage return. The file should contain only one column and no header. The user is also asked to select a specific GO term. The probe sets associated to the specific GO term will be annotated ans saved in a HTML file.

**Note**

For the annotation the annotation library associated to the raw data loaded in the affyImGUI environment is used.

**Author(s)**

Raffaele A. Calogero
See Also

GOenrichment, plotGO

filteringTable  Filtering a tab delimited file

Description

This function allows to filter a tab delimited file using a vector of data present in an other file. The two files should have an header and the column name to be used for the filtering should be equal in both files

Usage

filteringTable()

Author(s)

Raffaele A Calogero

geneExonLibs  Download the Library files for gene and exon analysis

Description

Affymetrix Gene/Exon library files are necessary to APT tools to calculate probe set summaries. The versions downloaded from www.bioinformatica.unito.it, with this function, contain all informations needed to analyse gene exon arrays.

Usage

geneExonLibs()

Author(s)

Raffaele A Calogero
**geoVSbioc**

**linking GEO platforms to available BioC annotations libraries**

**Description**

This data file gives the link between GEO platforms and BioC annotation libraries. If the GEO BioC link exists the Bioconductor annotation lib is directly loaded in the annotation field of the SexpessionSet.

**Usage**

```
geoVSbioc
```

**Format**

A data frame with 4 observations: GEOAcc, Organisms, Title, BiocAnLib

**References**

GEO and Bioconductor

---

**GOenrichment**

*Searching for Gene Ontology enriched terms within a set of differentially expressed genes*

**Description**

In Bioconductor is available a library called GOstats, which allows the calculation of enriched GO terms within a set of differentially expressed probe sets. This is a graphical implementation of a function allowing the extraction of GO enriched term in a sub set of differentially expressed probe sets. To know more about it see GOstat library.

**Usage**

```
GOenrichment()
```

**Details**

The function asks to the user to select a file containing probe set ids separated by carriage return. The file should contain only one column and no header. The set of enriched terms are plotted in red over the graph of all GO term associated to the differentially expressed genes. GO enriched terms can be also saved in a tab delimited file.

**Author(s)**

Raffaele A Calogero

** References**

Robert Gentleman GOstat package
See Also
extractAffyids, plotGO

---

**huex.annotation**  
*Annotation data for CORE subset of human exon array 1.0 ST*

**Description**
These annotation data are derived from Affymetrix annotation file huex.annotation

**Usage**

`huex.annotation`

**Format**
A data frame with 5 observations: PROBESETID, SYMBOL, DESCRIPTION, CYTOBAND, ACC

**References**
Affymetrix web site

---

**huex.variantexons**  
*Table linking exon-level probe set ids to variant exons*

**Description**
The table is made integrating exon-level netaffx annotaiton with UCSC derived annotation. Specifically exon-level probesets are mapped on variant exons, i.e. those that are specific of only a subset of all isoforms associated to a gene. This table is used to filter differentially expressed exons to select only those associated to variant isoforms

**Usage**

`huex.variantexons`

**Format**
A data frame with 12 observations: affyname, affystart, affyend, affywidth, affystrand, vspname, vspstart, vspend, vspwidth, vspstrand, chr, genome

**References**
Affymetrix web site and UCSC database
Annotation data for human gene array 1.0 ST

Description

These annotation data are derived from Affymetrix annotation file hugene10stv1na24hg18.

Usage

hugene.annotation

Format

A data frame with 5 observations: PROBESETID, SYMBOL, DESCRIPTION, CYTOBAND, ACC

References

Affymetrix web site

inspecting.one.splice.index

Plotting on the profiles of splice indexes for a transcript cluster ID

Description

This function plots the splice index profiles for one transcript cluster ID

Usage

inspecting.one.splice.index( transcriptID, SpliceIndexDiff, PvalExon)

Arguments

class TranscriptID A character string indicating the featureName of the transcript cluster to be evaluate

SpliceIndexDiff a numerical value indicating the threshold to detect an alternative splicing. It represent the minimal absolute difference between the splice indexes measured for the same exon under two different experimental conditions

PvalExon The max p-value obtainable by a t-test done on the splice indexes measured for the same exon under two different experimental conditions

Author(s)

Raffaele A Calogero

See Also

spliceIndex
**inspecting.splice.index**

*Plotting on a pdf file the profiles of splice indexes*

**Description**

This function prints in a pdf file the splice index profiles of the available genes.

**Usage**

```r
inspecting.splice.index()
```

**Author(s)**

Raffaele A Calogero

**See Also**

spliceIndex

---

**intensityFilter**

*intensity filtering with a mouse click*

**Description**

This function removes all probe sets in which a certain percentage of experiments is below a user defined intensity threshold.

**Usage**

```r
intensityFilter()
```

**Details**

The aim of non specific filtering is to remove the genes that are unlikely to carry information about the phenotypes under investigation. This filtering remove genes that do not have a certain level of, user defined, intensities in a set of, user defined, experiments.

**Note**

Factor analysis will be limited by the problem of having fewer samples than genes. Therefore, preselecting a smaller set of genes is definitively helpful.

**Author(s)**

Raffaele A Calogero

**See Also**

iqrFilter, listFilter, IPAlistFilter
IPAlistFilter  Filtering an expression set using a set of Entrez genes extracted from Ingenuity Pathways analysis (IPA)

Description
It is possible to sub set an expression set loaded in the affylmGUI environment starting form a list of Entrez genes derived by IPA search tool.

Usage
IPAlistFilter()

Details
The function asks to the user to select a file containing Entrez genes separated by carriage return.
The file should contain only one column and no header.

Author(s)
Raffaele A Calogero

See Also
iqrFilter, listFilter, intensityFilter

iqrFilter  Interquantile filtering with a mouse click

Description
This function implements the interquantile filtering proposed by Heydebreck in 2004

Usage
iqrFilter()

Details
The aim of non specific filtering is to remove the genes that are unlikely to carry information about the phenotypes under investigation. This filtering remove genes that show little changes within the experimental points.

Note
Factor analysis will be limited by the problem of having fewer samples than genes. Therefore, preselecting a smaller set of genes is definitively helpful.

Author(s)
Raffaele A Calogero
References
Heydebreck et al. Bioconductor project Papers 2004

See Also
IPAlistFilter, listFilter, intensityFilter

limmaExons
graphical interface to limma for alternative splicing detection

Description
Applying the limma model fitting to exon-level data. Same implementation of AffylmGUI but applied to exon-level data. The first indication of alternative splicing detection using limma was proposed by Shah and Pallas in BMC Bioinformatics. 2009 Jan 20;10:26

Usage
limmaExons()

Details
The function fits the limma linear model to exon-level data

Author(s)
Raffaele A Calogero

listFilter
Subsetting an expression set using a list of Affymetrix ids

Description
This function subsets the normalized expression set present in the affylmGUI environment on the basis of a list of probe set ids passed via flat file.

Usage
listFilter()

Details
The function asks to the user to select a file containing probe set ids separated by carriage return. The file should contain only one column and no header.

Note
In transcriptional studies focusing on genes characterized by specific feature (i.e. transcription factor elements in promoters) the best filtering approach is selecting only those genes linked to the interesting biological feature.
**makeBED15**

Author(s)
Raffaele A Calogero

See Also
IPAlistFilter, iqrFilter, intensityFilter

---

### makeBED15

>This function creates files in BED15 format to be loaded on the UCSC browser

---

**Description**

This function creates files in BED15 format to be loaded on UCSC genome browser. The function uses the data derived by variantSI filter on the basis of chromosome annotation.

**Usage**

```r
makeBED15()
```

**Author(s)**
Raffaele A Calogero

**See Also**
variantSI, variantExons, plotVariantSI

---

**mapping2ensembl**

>Associating e-level probe sets to entrez gene exonic structure

---

**Description**

This function associates the statistical and expression data produced by a oneChannelGUI exon-level analysis to the exonic structure of Entrez Gene ID. This function uses biomaRt to retrieve the sequence of EG exons. RRE database is instead used to retrieve the exon-level target sequences. Any exon-level probe set id to be associated to the EG exonic sequence need to be a perfect matching substring of the exon. In the other case no exon is associated to the probe set.

**Usage**

```r
mapping2ensembl()
```

**Author(s)**
Raffaele A Calogero
mapping2exon

This function maps on exon-level Probe Selection Region (PSR) starting for the file produced by function oneChannelGUI: Mapping exon level probe sets to Reference Sequences

Description

This function retrieve from RRE the PSR sequences associated to the exon-level probe sets and all exons associated to the gene associated to PRS. Subsequently identify the exon where PSR maps and produces a fasta file were are located exon-level PSR and target exon. The mapping is done using the countPattern function of the Biostrings package. Up to three mismathces are allowed in PSR mapping on exonic sequence.

Usage

mapping2exon()

Author(s)

Raffaele A Calogero

mapping2RefSeq

This function maps on NCBI Reference sequences spliced exons detected by the function oneChannelGUI: Inspecting splice indexes

Description

This function retrieve from RRE the PSR sequences associated to the exon-level probe sets using blastn detects the best refseq associated to any of the exon-level probe sets retrieve from org.XX.eg.db the EG associated to any of the detected refseq and retrieves all the refseqs associated to the EG. Subsequently check if PSR maps on all the refseqs associated to the eg (conserved exon) or only some of them (isoform specific exon)

Usage

mapping2RefSeq()

Author(s)

Raffaele A Calogero
masigpro.edesign  The function creates an edesign object needed to run maSigPro

Description

The function creates an edesign object needed to run maSigPro. To know more about edesign object see maSigPro help. This function uses a specific configuration of Target column of the affylmGUI target file. To know more about target file see affylmGUI help. Each row of the column named Target, in the affylmGUI target file, describes the array on the basis of the experimental design. Each element needed for the construction of edesign is separated from the others by an underscore. The first three elements of the row are fixed and represent Time Replicate Control all separated by an underscore: Time_Replicate_Control. All the other elements refer to various experimental conditions. Considering two different conditions to be evaluated each row is made of 5 elements: Time_Replicate_Control_cond1_cond2 all separated by an underscore. Having an experiment made of 9 arrays, with two time points, 0h and 24h, in triplicate, and two different experimental conditions to be evaluated, the affylmGUI target file will look like:

<table>
<thead>
<tr>
<th>Name</th>
<th>FileName</th>
<th>Target</th>
</tr>
</thead>
<tbody>
<tr>
<td>mC1</td>
<td>M1.CEL</td>
<td>0_1_1_0_0</td>
</tr>
<tr>
<td>mC2</td>
<td>M4.CEL</td>
<td>0_1_1_0_0</td>
</tr>
<tr>
<td>mC3</td>
<td>M7.CEL</td>
<td>0_1_1_0_0</td>
</tr>
<tr>
<td>mE1</td>
<td>M3.CEL</td>
<td>24_2_0_1_0</td>
</tr>
<tr>
<td>mE2</td>
<td>M6.CEL</td>
<td>24_2_0_1_0</td>
</tr>
<tr>
<td>mE3</td>
<td>M9.CEL</td>
<td>24_2_0_1_0</td>
</tr>
<tr>
<td>mI1</td>
<td>M2.CEL</td>
<td>24_3_0_0_1</td>
</tr>
<tr>
<td>mI2</td>
<td>M5.CEL</td>
<td>24_3_0_0_1</td>
</tr>
<tr>
<td>mI3</td>
<td>M8.CEL</td>
<td>24_3_0_0_1</td>
</tr>
</tbody>
</table>

Usage

masigpro.edesign()

Author(s)

Raffaele A Calogero

See Also

masigpro, masigpro.view

masigpro  The function executes maSigPro analysis

Description

The function creates: 1. Create a regression matrix for the full regression model (make.design.matrix function). 2. Computes the p-value associated to the F-Statistic of the model, which is used to select significant genes (p.vector function). 3. Applies a variable selection procedure to find significant variables for each gene (T.fit function). This will ultimately be used to find which are the profile
differences between experimental groups. 4. Finally, it generates lists of significant genes according to R-squared of the models (get.siggenes function). To know more about the various steps see maSigPro help.

Usage

```r
masigpro()
```

Author(s)

Raffaele A Calogero

See Also

`masigpro.edesign`, `masigpro.view`

---

### `masigpro.view`

The function allows the visualization of maSigPro results

Description

The function is a graphical implementation of the maSigPro PlotGroups function. To know more about it see maSigPro help.

Usage

```r
masigpro.view()
```

Author(s)

Raffaele A Calogero

See Also

`masigpro.edesign`, `masigpro`

---

### `metaArrayIC`

Graphical interface to metaArray Integrative Correlation function

Description

The integrative correlation analysis (Parmigiani et al., 2004) is a convenient tool to monitor the interstudy concordance of within-study correlations of gene expression. The gene-specific reproducibility score takes the correlation between each gene and all other genes within individual study and calculate the average correlation of these correlations across all pairs of studies.

Usage

```r
metaArrayIC()
```
**metaArrayMerge**

Author(s)
Raffaele A Calogero

References
MergeMaid package and metaArray Package

---

**Description**

This function will create an ExpressionSet from a study starting from a tab delimit file and a target file this ExpressionSet will be merged with the NormalizedAffyData if they contain the same number of row and rownames in the same order. Data generated with this function could be analyzed using metaArrayIC function.

**Usage**

```r
metaArrayIC()
```

**Author(s)**
Raffaele A Calogero

**See Also**
metaArrayIC

---

**ML.edesign**

*The function creates an data frame containing the parameters useful for class prediction*

---

**Description**

This function uses a specific configuration of Target column of the affylmGUI target file. To know more about target file see affylmGUI help. Each row of the column named Target, in the affylmGUI target file, describes the array on the basis of the experimental design. Each element needed for the construction of the data frame is separated from the others by an underscore. All the other elements refer to experimental conditions or clinical parameters. The absence of a parameter NEEDS to be described in the Target file by NA Considering two different conditions to be evaluated each row is made of 5 elements: Time_Replicate_Control_cond1_cond2 all separated by an underscore. Having an experiment made of 9 arrays with 4 different experimental parameters the affylmGUI target file will look like:

<table>
<thead>
<tr>
<th>Name</th>
<th>FileName</th>
<th>Target</th>
</tr>
</thead>
<tbody>
<tr>
<td>mC1</td>
<td>M1.CEL</td>
<td>0_1_pos_0 NA</td>
</tr>
<tr>
<td>mC2</td>
<td>M4.CEL</td>
<td>0_1_pos_0 yes</td>
</tr>
<tr>
<td>mC3</td>
<td>M7.CEL</td>
<td>0_1_neg_0 no</td>
</tr>
</tbody>
</table>
moex.variantexons

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>mE1</td>
<td>M3.CEL</td>
<td>24_2_neg_1 NA</td>
</tr>
<tr>
<td>mE2</td>
<td>M6.CEL</td>
<td>24_2 NA 1 yes</td>
</tr>
<tr>
<td>mE3</td>
<td>M9.CEL</td>
<td>24_2_neg 1 yes</td>
</tr>
<tr>
<td>mI1</td>
<td>M2.CEL</td>
<td>12_3 0 pos yes</td>
</tr>
<tr>
<td>mI2</td>
<td>M5.CEL</td>
<td>12_3 0 pos no</td>
</tr>
<tr>
<td>mI3</td>
<td>M8.CEL</td>
<td>12_3 0 pos no</td>
</tr>
</tbody>
</table>

Usage

ML.edesign()

Author(s)

Raffaele A Calogero

---

moex.annotation  
Annotation data for CORE subset of mouse exon array 1.0 ST

Description

These annotation data are derived from Affymetrix annotation file moex10stv1na23mm8.

Usage

moex.annotation

Format

A data frame with 5 observations: PROBESETID, SYMBOL, DESCRIPTION, CYTOBAND, ACC

References

Affymetrix web site

---

moex.variantexons  
table linking exon-level probe set ids to variant exons

Description

The table is made integrating exon-level netaffx annotaiton with UCSC derived annotation. Specifically exon-level probesets are mapped on variant exons, i.e. those that are specific of only a subset of all isoforms associated to a gene. This table is used to filter differentially expressed exons to select only those associated to variant isoforms

Usage

moex.variantexons
Format
A data frame with 12 observations: affyname, affystart, affyend, affywidth, affystrand, vspname, vspstart, vspend, vspwidth, vspstrand, chr, genome

References
Affymetrix web site and UCSC database

mogene.annotation  Annotation data for mouse gene array 1.0 ST

Description
These annotation data are derived from Affymetrix annotation file mogene10stv1na24hg18.

Usage
mogene.annotation

Format
A data frame with 5 observations: PROBESETID, SYMBOL, DESCRIPTION, CYTOBAND, ACC

References
Affymetrix web site

myExpresso  Running the affy expresso function with the widget

Description
Various probe set intensity summary and normalization can be customized using the expresso function.

Usage
myExpresso()

Details
This function run expresso with the graphical interface for parameters selection. It is important to note that expresso is more slow than the C coded rma)

Author(s)
Raffaele A Calogero
normBoxplot

*Box plot of the arrays data available in NormalizeAffyData slot*

**Description**

Box plot visualization of normalized array data

**Usage**

```r
normBoxplot()
```

**Author(s)**

Raffaele A Calogero

---

ocPlotHist

*Gene/Exon level density plots*

**Description**

This function runs a modified version of the plotHist of the affycoretools to be used to check density distribution plots for gene and exon expression data generated by expression console.

**Usage**

```r
ocPlotHist()
```

**Author(s)**

Raffaele A Calogero

**See Also**

ocPlotPCA

---

ocPlotPCA

*Gene/Exon level density plots*

**Description**

This function runs a modified version of the plotPCA of the affycoretools to be used to check density distribution plots for gene and exon expression data.

**Usage**

```r
ocPlotPCA()
```
oneChannelGUI

Author(s)
Raffaele A Calogero

See Also
ocPlotHist

oneChannelGUI-package
Set of functions extending the capability of affylmGUI package

Description
This package is directed to Bioconductor beginners that have little or no experience in writing R code. The package implements, as simple functions accessible over the affylmGUI graphical interface, some code useful for QC, data filtering, data output manipulation and identification of GO enriched classes.

Details

<table>
<thead>
<tr>
<th>Package</th>
<th>oneChannelGUI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>Package</td>
</tr>
<tr>
<td>Version</td>
<td>1.0</td>
</tr>
<tr>
<td>Date</td>
<td>2006-12-16</td>
</tr>
<tr>
<td>License</td>
<td>GPL version 2 or newer</td>
</tr>
</tbody>
</table>

Author(s)
Author: Raffaele A Calogero Maintainer: Raffaele A Calogero <raffaele.calogero@unito.it>

Examples

```r
# library(oneChannelGUI)
# To start the oneChannelGUI with the modifications
# oneChannelGUI()
```

Description
Starting oneChannelGUI package. oneChannelGUI contains a set of functions extending the capabilities of affylmGUI package.
Usage

Aboutextendedaffy.lmGUI()
Aboutaffy.lmGUI()
oneChannelGUI()
oneChannelGUIHelp()
maSigProHelp()
siggenesHelp()
oneChannelGUIHelp()
initialize.ext.Affy.lmGUI()
OpenExon.andTargetsfiles()
GOstatsHelp()
NewLimmaFile()
OpenLimmaFile()
OpenALimmaFile(FileName)
OpenAFile(FileName)
OpenExonFile()
OpenLargeFile()
changeMenu()
oneChannelGUI.start()
libraryFilesDir()
whichKindOfArray()
intronicBg()
ExportNormalizedExpressionValues1()
ExportNormalizedExpressionValues()
Export.featureNames()
SaveAsLimmaFile()
addAnnLib()
OpenCDF.andTargets.files()
ComputeLinearModelFit()
GetNormalizationMethod()
NormalizeNow()
ComputeContrasts()
midasFilter()
dabgFilter()
largedatasetNorm()
RankProdHelp()
affyPLMHelp()
genefilterHelp()
pamrHelp()
pdmclassHelp()
size.powerHelp()
ssizeHelp()
OpenAGEoFile(FileName)
OpenGeoFile()
OpenGeoFiles()
recoverUnfiltered()
delete.ML()
affyPlotMA()
changes()
aptFolder()
deleteLocalData()
SetED()
chooseEDir()
.annotation(eset)
.myrk(x,df)

Arguments

FileName   Internal argument not to be set by the user
eset       Internal argument not to be set by the user
x          Internal argument not to be set by the user
df         Internal argument not to be set by the user

Details

This function launches a modify version of the Graphical User Interface by James Wettenhall for the limma package by Gordon Smyth. The GUI uses Tk widgets (via the R TclTk interface by Peter Dalgaard) in order to provide a simple interface to various tools for quality control and statistical analysis of Affymetrix gene chips.

Author(s)

Raffaele A Calogero

Examples

# library(oneChannelGUI)
## To start the affylmGUI with the modifications
#oneChannelGUI()

OpenBeadStudioFiles

Read BeadStudio expression data file

Description

Read BeadStudio expression data file

Usage

OpenBeadStudioFiles()

Details

Reads an Illumina intnesity data file produced by BeadStudio. Using BeadStudio version 'One' the file will have a 'gene profile.csv' extension and using version 'Two' the file will have a .txt extension. See package vignette for more information. Multiple filenames can be specified as a vector and the data are then combined into one output file. This function should only really be used for custom analysis as the beadAnalysis() function provides easier, flexible use.

Author(s)

Derived from readBead by Gareth Elvidge (gareth.elvidge@well.ox.ac.uk)
OpenLargefiles

This function loads large data set made from tab delimited files

Description

The function creates and expressionSet starting from a file containing the expression data in a tab delimited format. This file is loaded together with the description of the clinical parameters present in Target. This function uses a specific configuration of Target column of the affylmGUI target file. To know more about target file see affylmGUI help. Each row of the column named Target, in the affylmGUI target file, describes the clinical parameters. Each clinical parameter is separated from the others by an underscore. The affylmGUI target file will look like:

<table>
<thead>
<tr>
<th>Name</th>
<th>FileName</th>
<th>Target</th>
</tr>
</thead>
<tbody>
<tr>
<td>mC1</td>
<td>M1.CEL</td>
<td>pos_yes_1 NA_0</td>
</tr>
<tr>
<td>mC2</td>
<td>M4.CEL</td>
<td>pos_no_2 NA_0</td>
</tr>
<tr>
<td>mC3</td>
<td>M7.CEL</td>
<td>neg_no_3 pos_0</td>
</tr>
<tr>
<td>mE1</td>
<td>M3.CEL</td>
<td>neg_yes_3 neg_0</td>
</tr>
<tr>
<td>mE2</td>
<td>M6.CEL</td>
<td>neg_no NA_1_0</td>
</tr>
<tr>
<td>mE3</td>
<td>M9.CEL</td>
<td>neg_yes_3 pos_0</td>
</tr>
<tr>
<td>mI1</td>
<td>M2.CEL</td>
<td>pos_no_2 neg_1</td>
</tr>
<tr>
<td>mI2</td>
<td>M5.CEL</td>
<td>pos_yes_2 pos_1</td>
</tr>
<tr>
<td>mI3</td>
<td>M8.CEL</td>
<td>pos_no_2 pos_1</td>
</tr>
</tbody>
</table>

Usage

OpenLargefiles()

Author(s)

Raffaele A Calogero

plierToZero

Setting to 0 low log2 intensity values generated with plier

Description

The calculation of log2 of probe set intensity by mean of plier generates a set of intensities very low, this function will set to 0 all the log2 intensities below 1 produced by iter-plier or plier alghoritm

Usage

plierToZero()

Author(s)

Raffaele A Calogero
**plotGO**  
*Plotting parents of a GO term with few mouse click*

---

**Description**

To know more on the parents of a specific GO term you can use the `plotGO` function.

**Usage**

```r
plotGO()
```

**Details**

A GO term to be investigated for its parents has to be placed in the graphical window.

**Author(s)**

Raffaele A Calogero

**See Also**

`GOenrichment`, `extractAffyids`

---

**PlotOptionsv1**  
*A modified version of the function used in affyPLM library*

---

**Description**

As default the plots are generated on the R GUI to reduce RAM consumption.

**Usage**

```r
PlotOptionsv1()
```

**Author(s)**

Raffaele A Calogero
plotVariantSI

Description

This function plots on UCSC genome browser data derived by variantSI filter on the basis of chromosome annotation.

Usage

plotVariantSI()

Author(s)

Raffaele A Calogero

See Also

variantSI, variantExons, makeBED15

raex.annotation

Annotation data for CORE subset of rat exon array 1.0 ST

Description

These annotation data are derived from Affymetrix annotation file raex.annotation.

Usage

raex.annotation

Format

A data frame with 5 observations: PROBESETID, SYMBOL, DESCRIPTION, CYTOBAND, ACC

References

Affymetrix web site
**raex.variantexons**  
*table linking exon-level probe set ids to variant exons*

**Description**

The table is made integrating exon-level netaffx annotation with UCSC derived annotation. Specifically exon-level probesets are mapped on variant exons, i.e. those that are specific of only a subset of all isoforms associated to a gene. This table is used to filter differentially expressed exons to select only those associated to variant isoforms.

**Usage**

`raex.variantexons`

**Format**

A data frame with 12 observations: `affyname`, `affystart`, `affyend`, `affywidth`, `affystrand`, `vspname`, `vspstart`, `vspend`, `vspwidth`, `vspstrand`, `chr`, `genome`

**References**

Affymetrix web site and UCSC database

---

**ragene.annotation**  
*Annotation data for rat gene array 1.0 ST*

**Description**

These annotation data are derived from Affymetrix annotation file `ragene10stv1na24hg18`.

**Usage**

`ragene.annotation`

**Format**

A data frame with 5 observations: `PROBESETID`, `SYMBOL`, `DESCRIPTION`, `CYTOBAND`, `ACC`

**References**

Affymetrix web site


**rankingConversion**  
*This function transforms intensity data in normalized ranks*

**Description**
This function transforms intensity data in normalized ranks, i.e. high intensity genes will have a value near to 0 as instead low intensity genes a normalized rank near to 1.

**Usage**

```r
rankingConversion()
```

**Author(s)**

Raffaele A Calogero

---

**rankProd**  
*graphical interface to rank product method implemented in RankProd Bioconductor library.*

**Description**
To know more about rank product method see RankProd help.

**Usage**

```r
rankProd()
```

**Details**
The target file for the RankProd implementation contain the origin of the data as a number separated by an under score from the corresponding covariate. If all data are from the same origin the origin definition is not needed. Therefore target will contain only the covariates.

<table>
<thead>
<tr>
<th>Name</th>
<th>FileName</th>
<th>Target</th>
</tr>
</thead>
<tbody>
<tr>
<td>mC1</td>
<td>M1.CEL</td>
<td>CTRL_1</td>
</tr>
<tr>
<td>mC2</td>
<td>M4.CEL</td>
<td>CTRL_1</td>
</tr>
<tr>
<td>mC3</td>
<td>M7.CEL</td>
<td>CTRL_2</td>
</tr>
<tr>
<td>mE1</td>
<td>M3.CEL</td>
<td>CTRL_2</td>
</tr>
<tr>
<td>mE2</td>
<td>M6.CEL</td>
<td>CTRL_2</td>
</tr>
<tr>
<td>mE3</td>
<td>M9.CEL</td>
<td>TRT_1</td>
</tr>
<tr>
<td>mI1</td>
<td>M2.CEL</td>
<td>TRT_1</td>
</tr>
<tr>
<td>mI2</td>
<td>M5.CEL</td>
<td>TRT_2</td>
</tr>
<tr>
<td>mI3</td>
<td>M8.CEL</td>
<td>TRT_2</td>
</tr>
</tbody>
</table>

**Author(s)**

Raffaele A Calogero
**rawBoxplotPN**

Plotting raw log2 intensities from controls

**Description**

This function produces a box plot of the log2 raw intensities, extracted directly from CEL files, for positive and negative controls presente in XXXX.control.ps Affymetrix library file. Positive and negative controls are made of housekeeping exon and introns. It gives an idea of signal behaviour before data normalization both in the high and low intensity range

**Usage**

rawBoxplotPN()

**Author(s)**

Raffaele A Calogero

---

**rawpCheck**

Raw p-value distribution from limma analysis by a mouse click

**Description**

This function allow to visualize the histogram of raw p-value distribution generated by limma analysis.

**Usage**

rawpCheck()

**Details**

The histogram of raw p-value distribution will show if raw p-values are uniform in the non significant range and therefore the BH correction can be applied.

**Note**

BH is the most used method for the correction of type I errors in microarray analysis. However, it has some limitation due to the initial hypotheses: The gene expressions are independent from each other. The raw distribution of p values should be uniform in the non significant range.

**Author(s)**

Raffaele A Calogero

**References**

To know more see limma package help
reseqDownload | Retrieving Reference Sequences from NCBI ftp

Description
This function retrieves reference sequences from NCBI ftp. RefSeq are used for mapping exon-level probe sets to refseq specific isoforms.

Usage
reseqDownload()

Author(s)
Raffaele A Calogero

retrievePSRseq | This function, given a file containing exon-level probesets retrieves Probe selection Regions, PRS, from RRE db

Description
This function retrieve from RRE the PSR sequences associated to the exon-level probe sets

Usage
retrievePSRseq()

Author(s)
Raffaele A Calogero

reviqrFilter | Reverse interquantile filtering with a mouse click

Description
This function implements a reverse version of the interquantile filtering proposed by Heydebreck in 2004 to select low variance genelevel probe set. To be used to remove putative differentially expressed genes that will make more difficult the detection of alternative splicing events.

Usage
reviqrFilter()
**Details**

This function can be used in an analysis focused to the detection of alternative splicing events. The aim of this non specific filtering is to remove the genes that are likely to carry information about the phenotypes under investigation at gene level. This filtering remove genes that show strong changes within the experimental points at the gene level.

**Author(s)**

Raffaele A Calogero

**References**

Heydebreck et al. Bioconducotor project Papers 2004

**See Also**

dabgFilter, crosshybFilter

---

**runningJetta**  
_graphical interface to MADS/jetta R library._

---

**Description**

MADS, which stands for Microarray Analysis of Differential Splicing, is a tool to identify differential alternative splicing by exon array. The principle of MADS is to increase the precision of exon-level and gene-level expression estimates by correcting, as much as possible, noise in observed probe intensities due to background and cross-hybridization. MADS incorporates a series of novel algorithms motivated by the probe-rich design of exon-tiling arrays, such as background correction, iterative probe selection and removal of sequence-specific cross-hybridization to off-target transcripts. MADS was published in RNA, 2008, 14(8): 1470-1479. Junction and Exon array Toolkit for Transcriptome Analysis (JETTA) is a compacted version of MADS.

**Usage**

`runningJetta()`

**Details**

Expression indexes are calculated as the order of Background Correction, Normalization and Summarization. In the Summarization step, background corrected and normalized probe intensities of a meta probeset are summarized to expression of the meta probeset. Meta probesets can be defined as gene/transcript clust/exon level.

Background Correction JETTA estimates background signal using background probes and subtracts it from the probe intensity. If the probe intensity is less than the estimated background signal, the background subtracted signal is truncated to 1. Estimation of background signal is based on several models: Median GC: median of background probe signal of the same GC counts MAT: linear model of probe sequence with 80 parameters. see Kapur et al, 2007.

Normalization Normalization of JETTA is done for core probes defined in probeset annotation file. If the PSA file is not specified, it considers all probes in the MPS files as core probes. Median scaling: scaling each array so that its median is 100 Quantile: all probes of the same signal quantile have the same signal.
Summarization LiWong model: multiplication model of expression and probe effect, see Li and Wong, 2001
Probe selection: select probes based on cross-array correlation of signal. see Xing et al, 2006
Median-polish

Alternative Splicing Detection Detecting alternatively expressed PSR/Exon between two sample groups based on background corrected and normalized probe intensities. It has several criteria to filter out transcript clusters and probes from the analysis. TC expression level: excluding low-expressed transcript clusters TC expression fold change: excluding transcript clusters which have big fold change between two groups Extreme probe signal: excluding probes of which signal is extremely high Cross-hybridized probes: excluding cross hybridized probes, currently pre-calculated results are needed

Author(s)

jseok@stanford.edu

description

This function represents a tool for helping users to understand the trade off between sample size and statistical power. To know more about see ssize help.

Usage

sample.size.evaluation1()

details

see sizepower help

Author(s)

Raffaele A Calogero

description

This function represents a visual tool for helping users to understand the trade off between sample size and statistical power. To know more about see ssize help.

Usage

sample.size.evaluation()
Details

Both ssize and delta outputs are calculated using the BH type I error correction instead of the Bonferroni used as default in the ssize package. Furthermore, instead using the control group variance, this implementation uses the common variance described in Wei et al. BMC Genomics. 2004, 5:87

Main assumptions: A microarray experiment is set up to compare gene expressions between one treatment group and one control group. Microarray data has been normalized and transformed so that the data for each gene is sufficiently close to a normal distribution that a standard 2-sample pooled-variance t-test will reliably detect differentially expressed genes.

Author(s)

Raffaele A Calogero

showDataset

Grabbing info about the available expression set

Description

The size of the normalized expression set can change upon filtering. This function show info about the exact size of the data set.

Usage

showDataset()

Author(s)

Raffaele A Calogero

showTopTable

Modification of the function implemented in affylmGUI to generate a topTable

Description

Modification of the function implemented in affylmGUI to generate a topTable. To know more about topTable see limma package help

Usage

showTopTable(...,export=FALSE)

Arguments

export defining the possibility to export data
... Arguments to be passed to methods

Author(s)

Raffaele A Calogero
**siggenes**

*The function executes SAM analysis implemented in siggenes bioconductor library*

**Description**

To know more about SAM in Bioconductor see siggenes help.

**Usage**

`siggenes()`

**Author(s)**

Raffaele A Calogero

---

**simFilter**

*This function allows filtering on the basis of the average splice index mean or min difference between two groups*

**Description**

Filtering out gene/exon level probe sets associated to average splice index mean or min difference between two groups lower than user defined value

**Usage**

`simFilter()`

**Note**

This function needs the presence of Splice Index.

**Author(s)**

Raffaele A Calogero

**See Also**

`simFilter`
spliceIndex

This function converts the exon intensity data in a slice index

Description

Exons intensities are divided for the expression of the corresponding gene, as described by Clark et al. Science 2002 May 3;296(5569):907-10.

Usage

spliceIndex()

Details

The function is not yet optimized, therefore it could take quite a long time to compute spliceIndex if more than 1000 genes are used.

Author(s)

Raffaele A Calogero

See Also

inspecting.splice.index

targetWidget

Widget to create a target file to load .CEL files

Description

Widget to create a target file to load .CEL files to be used with NewLimmaFile function.

Usage

targetWidget()

Author(s)

Raffaele A Calogero
**templA**

*Generating a template A to be uploaded in Ingenuity Pathways analysis (IPA)*

**Description**

A template A file to be used in Ingenuity can be generated starting from a topTable containing the full array data.

**Usage**

```
templA()
```

**Note**

Template A file will contain a column with the gene ID, a column with fold change, a column with true p-value and a column with p-values for discriminating between the set of differentially expressed probe sets and the background. This column is needed to allow IPA to identify the set of enriched functional classes associated to the differentially expressed probe sets.

**Author(s)**

Raffaele A Calogero

**See Also**

IPAlistFilter

---

**trainTest**

*Creating a training set and a test set by a mouse click*

**Description**

This function allows the creation of a training set and a test set to be used for classification purposes.

**Usage**

```
trainTest()
```

**Details**

User will be asked to assign names to the available classification parameters. User will be asked to select the number associated to one of the available classification parameters. The training set will be made, using the selected classification parameter and it will be made of 2/3 of the original data set. The test set will be the remaining 1/3.

**Author(s)**

Raffaele A Calogero
updateLibs  

*This function allows to update the present installation of Bioconductor*

**Description**

The function allows the updating of local installation of Bioconductor. It might be quite long depending on the internet connection speed.

**Usage**

```r
updateLibs()
```

**Author(s)**

Raffaele A Calogero

---

**variantExons**  

*This function is used to generate a table containing exon-level probe set data linked to variant exons*

**Description**

Internal oneChannelGUI annotation data linking exon-level probesets to variant exons, i.e. those exons that are specific for a subgroup of the isoforms associated to a specific gene, can be upgraded using this function. Annotation RDA files need to be saved in the data subdir of oneChannelGUI dir. Windows users need to exchange the older copies present in Rdata.zip, simply dragging them in the zip file.

**Usage**

```r
variantExons()
```

**Author(s)**

Raffaele A Calogero

---

**variantSI**  

*This function allows filtering on the basis of variant exons*

**Description**

The function intersects a list of alternative splice exon-level probe sets detected by oneChannelGUI analysis and intersects it to the list of exon-level probe sets associated to variant exons, i.e. these exons that are associated only to a subset of all isoforms associated to a gene. The table of variant Exon is stored in RRE database and is retrieved by the function updating the UCSC tables linking probe set ids with variant exons, located in the General Tools menu. The variantSI function also attaches to the variant exons table the deltaSI associated exon-level probe set.
Usage

variantSI()

Note

This function needs the presence of Splice Index

Author(s)

Raffaele A Calogero

See Also

variantExons, plotVariantSI

VennDiagram

Venn diagrams using two or three lists

Description

Venn diagrams can be generated using probe sets ids or Entrez gene ids saved in flat files.

Usage

VennDiagram()

Details

The function asks to the user to select two/three files containing probe set ids or EGs separated by carriage return. Each file should contain only one column and no header.

Author(s)

Raffaele A Calogero
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