Package ‘oneChannelGUI’

January 15, 2017

Version 1.40.0
Date 2 April 2015
Title A graphical interface designed to facilitate analysis of microarrays and miRNA/RNA-seq data on laptops
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Depends Biobase, affyLmGUI, tkrplot, tkWidgets, IRanges, Rsamtools (>= 1.13.1), Biostrings, siggenes, chimera
Suggests annotate, genefilter, maSigPro, pamr, pdmclass, ChIPpeakAnno, chipseq, BSgenome, Rgraphviz, affy, anaffy, affyPLM, multtest, ssize, sizepower, RankProd, org.Hs.eG.db, org.Mm.eG.db, org.Rn.eG.db, edgeR, metaArray, MergeMaid, biomaRt, GenomeGraphs.AffyCompatible, rtracklayer, Genomina, EDASeq, limma, DESeq, DESeq2, goseq, huggene10sttranscriptcluster.db, mogene10sttranscriptcluster.db, ragnere10sttranscriptcluster.db, GOstats, AnnotationDbi, preprocessCore, baySeq, HuExExonProbesetLocation, MoExExonProbesetLocation, RaExExonProbesetLocation, snow, RmiR, RmiR.Hs.miRNA, BSgenome.Hsapiens.UCSC.hg19, R.utils, cummeRbund, BSgenome.Mmusculus.UCSC.mm9, BSgenome.Rnorvegicus.UCSC.rn4, DESeq2, GenomicAlignments, BiocParallel, KEGG.db, miRNAPath, miRNAatap, miRNAatap.db
Description This package was developed to simplify the use of Bioconductor tools for beginners having limited or no experience in writing R code. This library provides a graphical interface for microarray gene and exon level analysis as well as miRNA/mRNA-seq data analysis
License Artistic-2.0
URL http://www.bioinformatica.unito.it/oneChannelGUI/
bioView Sequencing, RNASeq, Microarray, OneChannel, DataImport, QualityControl, Preprocessing, StatisticalMethod, DifferentialExpression, GUI, MultipleComparison
NeedsCompilation no
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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

Package: oneChannelGUI
Type: Package
Version: 1.0
Date: 2006-12-16
License: GPL version 2 or newer
**adaptorTrimm**

**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()
```

---

adaptorTrimm  *Trimming 3,5 end primers for miRNAs NGS*

**Description**

A function to trim 3, 5 end primers for miRNAs NGS fastq files. The function is not very efficient. It takes about 5 minutes for 1 million reads file.

**Usage**

```r
adaptorTrimm()
```

**Author(s)**

Raffaele A Calogero

---

annotateNGSeset  *Associate annotation to NGS data loaded in oneChannelGUI*

**Description**

This function associates annotation to NGS data loaded in oneChannelGUI, using the information retrieved by genome annotation from ENSEMBL by ChIPpeakAnn package.

**Usage**

```r
annotateNGSeset()
```

**Author(s)**

Raffaele A Calogero
**AptMidas**

*Graphical interface to APT midas*

**Description**

This is a graphical interface to the midas program for detection of alternative splicing 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 recomanded 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

---

**bayseqInterface**

*graphical interface to baySeq library.*

**Description**

BaySeq provides statistical routines for determining differential expression in digital gene expression data. The routines can be applied equally to two groups experiments only.

**Usage**

bayseqInterface()

**Details**

This interfase reorganizes NGS data loaded in oneChannelGUI to be analysed by baySeq.

**Author(s)**

Raffaele A Calogero
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 data base

Usage
biomartFilter()

Author(s)
Raffaele A Calogero

bofa
Bovine microRNA data set

Description
microRNA data set fasta produced using miRbase B taurus precursors reformatted to have only miR name as descriptor of the fasta file

Usage
bofa

Format
Fasta file

bowtieBuilt
Downloading Bowtie prebuilt reference sets

Description
A function to download built reference sets for Human Mouse and Rat, available as precompiled at sourceforge oneChannelGUI.extras project.

Usage
bowtieBuilt()

Author(s)
Raffaele A Calogero
bowtieDownload  

*Description*

A function to download Bowtie and Picard tools for primary mapping of short reads and conversion of SAM to BAM format. Reference mapping for Bowtie are also generated using miRBase precursors sets for Human Mouse and Rat. Human, mouse and Rat gene-level scaffolds are also downloaded by sourceforge oneChannelGUI.extras

*Usage*

bowtieDownload()

*Author(s)*

Raffaele A Calogero

---

bowtieGenomes  

*Description*

A function to build Bowtie reference sets for short reads primary mapping.

*Usage*

bowtieGenomes()

*Author(s)*

Raffaele A Calogero

---

buildingLocalAnnotation  

*Description*

Internal oneChannelGUI Gene-level annotation data can be upgraded using this function, which queries netaffx database. The exon-level annotations are updated using UCSC golden path data. 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()
**chrLength**

**Author(s)**

Raffaele A Calogero

---

<table>
<thead>
<tr>
<th>chrLength</th>
<th>Chromosomes lengths</th>
</tr>
</thead>
</table>

**Description**

A list containing chromosome lengths for hg19, mm9 and rn4 genome releases

**Usage**

```r
chrLength
```

**Format**

A list with three observations: chromosome lengths for hg19, mm9 and rn4 genome releases

**Author(s)**

Raffaele A Calogero

---

<table>
<thead>
<tr>
<th>colExtract</th>
<th>Extract a column from a tab delimited file with header</th>
</tr>
</thead>
</table>

**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**

```r
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**

```r
combineGeoMSF()
```

**Note**

see oneChannelGUI vignette for more info

**Author(s)**

Raffaele A Calogero

---

**combining2eSet**

This function allows to combine two matrices extracted from oneChannelGUI.

**Description**

The function combines two matrices in one using column binding. This function is useful to combine two matrices generated for meV visualization.

**Usage**

```r
combining2eSet()
```

**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 allow to remove statistical significant splicing events which are characterized by a very limited variation.

Usage
consistentFilters()

Note
This function 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

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()
createGeoTarget

> **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**
> ```r
> createGeoTarget()
> ```

> **Note**
> see oneChannelGUI vignette for Target file description

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

---

crosshybFilter

> **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**
> ```r
> crosshybFilter()
> ```
**ctrtrtHeatmap**

**Author(s)**
Raffaele A Calogero

---

**Description**
This function needs a maSigPro target encompassing only one treatment condition. This function is ideal to visualize the expression data for putative mRNA targets upon miRNA expression perturbation with antagonir or mimics. Expression data reorganized as the average expression differences between treatment and untreated condition over the time course.

**Usage**

```r
catrtrtHeatmap()
```

**Author(s)**
Raffaele A Calogero

---

**desGenes**

**Description**
This function calculates differential gene expression for an RNA-seq experiment.

**Usage**

```r
desGenes()
```

**Details**
This function uses DESeq package to calculate differential expression at gene level starting from a gene table generated by DEXseq package. It returns an rda object called res.genes that can be used for further analysis.

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

**Description**

This function summarises counts using DEXseq python scripts.

**Usage**

dexCounts()

**Details**

This function uses the python scripts present in DEXseq package to summarise at the level of exons the reads derived by a sam file. The function needs to be run for each sample. It runs in background. It is necessary the installation of HTSeq python library

**Author(s)**

Raffaele A Calogero

---

**dexExons**

**Description**

This function calculates differential expression at exon level for an RNA-seq experiment.

**Usage**

dexExons()

**Details**

This function uses DEXseq package to calculate differential expression at exon level starting from a set of counts files located in different folders and generated by dexCounts function. The target file is the one used to run tophat in oneChannelGUI. it executes in background a batch file that returns two rda object called res.exons and ecs that can be used for further analysis. res.exons is contains all results descriing differential expression at exon level and ecs is the DEXseq object containg all info for the exons.

**Author(s)**

Raffaele A Calogero
**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.

**Usage**

```
dfMAplot(table1)
```

**Arguments**

- `table1`: topTable data.frame generate by affylmGUI

**Note**

To know more about topTable see limma help

**Author(s)**

Raffaele A Calogero

---

**EDANtFreq**

*Plotting Nts frequency for mapped reads extracted from BAM files*

**Description**

Plot the Nts frequency for mapped reads extracted from a BAM file.

**Usage**

```
EDANtFreq()
```

**Details**

Interface to the `plotNtFrequency` of EDASeq package

**Author(s)**

Raffaele A Calogero

**See Also**

EDAplotQuality, EDAreadNumber
EDAplotQuality

Plotting Quality scores for mapped reads extracted from BAM files

Description

Plotting the quality scores of mapped reads extracted from a BAM file

Usage

EDAplotQuality()

Details

Interface to the plotQuality of EDASeq package

Author(s)

Raffaele A Calogero

See Also

EDAreadNumber, EDAnFreq

EDAreadNumber

Plotting the number of mapped reads extracted from BAM files

Description

Plotting the number of mapped reads extracted from a BAM file

Usage

EDAreadNumber()

Details

Interface to the barplot of EDASeq package

Author(s)

Raffaele A Calogero

See Also

EDAplotQuality, EDAnFreq
edgerInterface

graphical interface to edgeR library.

Description

edgeR provides statistical routines for determining differential expression in digital gene expression data. The routines can be applied equally to SAGE, CAGE, Illumina, Solexa, 454 or ABI SOLiD experiments.

Usage

edgerInterface()

Details

This interface reorganizes NGS data loaded in oneChannelGUI to be analysed by edgeR.

Author(s)

Raffaele A Calogero

edgeRNorm

This function scale-normalize NGS raw data as described by Robinson and Oshlack Genome Biology 2010, 11:R25

Description

This function is scale-normalize NGS data using the normalization function provided in edgeR.

Usage

edgeRNorm()

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

---

**erankProdAltSpl**

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 conscious of this!

**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**

```r
erankProdAltSpl()
```

**Author(s)**

Raffaele A Calogero

**See Also**

`erankProdAltSpl`, `AptMidas`

---

**eSet4meV**

This function allows to reformat an eSet to be loaded in meV visualization software.

**Description**

The function allows to reformat an eSet to be loaded in meV visualization software. The eSet extracted from onechannelGUI exchanging array names, used for column names, with target Names.

**Usage**

```r
eSet4meV()
```

**Note**

see oneChannelGUI vignette for more info

**Author(s)**

Raffaele A Calogero
exonContrasts  

Defining t-test regularized p-values

Description

This function constructs the contrasts as affylmGUI 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

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

exonScaffold  

stand alone function to generate a scaffold containing only exon location from ENSEMBL

Description

The scaffold contains chr stand start and end position of exon. Ensembl geneID and exonID together with exon rank are also provided.

Usage

exonScaffold(genome)

Arguments

genome  
The genome code for H sapiens is hg19, for M musculus is mm9 and for R norvegicus is rn4

Details

The scaffold is used to map reads data into regions only associated to exons

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**
```
extractAffyids()
```

**Details**
The function asks 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 and saved in an HTML file.

**Note**
For the annotation the annotation library associated to the raw data loaded in the affylmGUI environment is used.

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

**See Also**
GOenrichment, plotGO

extractmirTargets

**Extract miRNA targets showing a opposite regulation with respect to miRNA**

**Description**
This function extract from a RmiR output the subset of genes showing a fold change variation inversely correlated to that of the miRNA selected by the user.

**Usage**
```
extractmirTargets()
```

**Details**
The output has the same structure of an RmiR output.

**Author(s)**
Raffaele A Calogero
### filteringmiRtargets

**Subsetting an expression set using a list of gene which are putative targets for a miRNA**

**Description**

This function subsets the normalized expression set present in the affylmGUI environment on the basis of a list of probe set ids extracted on the basis of the predicted gene targets for a microRNA. Extraction is based on predicted targets for miRNA in human.

**Usage**

```r
callingCommand()
```

**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.

**Author(s)**

Raffaele A Calogero

**See Also**

IPAlistFilter, iqrFilter, intensityFilter

---

### 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**

```r
callingCommand()
```

**Author(s)**

Raffaele A Calogero
geneExonLibs

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

genomePlot

Description

This function plots average intensity signals for two group experiment over the genes and transcripts structure mapped on ENSEMBL to identify a specific splicing event.

Usage

genoamePlot()

Author(s)

Raffaele A Calogero

See Also

variantSI, variantExons, makeBED15
genomeStudioReformat

The present function reformat an expression file exported by Genome Studio in a format that is compatible with oneChannelGUI

Description

The present function reformat an expression file exported by Genome Studio in a format that is compatible with oneChannelGUI

Usage

genomeStudioReformat()

Author(s)

Raffaele A Calogero

geoVSbioc

linking GEO platforms to available BioC annotations libraries

Description

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

Usage

geoVSbioc

Format

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

References

GEO and Bioconductor
getNGSannotation  Retrieving genome annotation from ENSEMBL

Description
This function retrieves genome annotation from ENSEMBL using ChIPpeakAnn package

Usage
getNGSannotation()

Author(s)
Raffaele A Calogero

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
hsfa

Human microRNA data set

Description

microRNA data set fasta produced using miRbase H sapiens precursors reformatted to have only
miR name as descriptor of the fasta file

Usage

hsfa

Format

Fasta file

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()

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

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

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**

_Filtration of expression sets using a set of Entrez genes extracted from Ingenuity Pathways analysis (IPA)_

**Description**

It is possible to subset an expression set loaded in the affyGUI environment starting from a list of Entrez genes derived by IPA search tool.

**Usage**

IPAlistFilter()

**Details**

The function asks 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 removes 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

limma2paired

graphical interface apply linear model to two sample groups with batch effect.

Description

This function allows to run Bayes regularized t-test on two groups with batch effects. Derived from the mailing list question: Paired samples and origin question, Limma 2006-05-11 13:45:41 GMT

Usage

limma2paired()

Details

This function allows to run Bayes regularized t-test on two groups with batch effects.

Author(s)

Raffaele A Calogero

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 fit 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**

```r
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.

**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
makeGeneScaffold

Description
A function to build a gene level scaffold to associate reads derived from bowtie mapping. The function is embedded in bowtieGenome function that build, at chromosome level, the reference genome for primary mapping. Built scaffolds are available as precompiled at sourceforge oneChannelGUI.extras project.

Usage
makeGeneScaffold(whichRef)

Arguments
whichRef The genome of interest to be used to create a gene-level scaffold

Author(s)
Raffaele A Calogero

See Also
makeGCcontent, wrapScaffold

makeGCcontent
Building a list of gene-level GC frequencies

Description
A function to build a gene-level GC frequencies associated to the genes generated by the makeGeneScaffold function. Built scaffolds with GC content are available as precompiled at sourceforge oneChannelGUI.extras project.

Usage
makeGCcontent(scaffold, whichRef)

Arguments
scaffold The GRange object created by makeGeneScaffold
whichRef The genome of interest to be used to create a gene-level scaffold

Author(s)
Raffaele A Calogero

See Also
makeGeneScaffold, wrapScaffold
**makeSam**

Description

This function uses samtools to convert a bam file in a sam file. It assumes that the bam file was generated by TopHat. Therefore it searches for accepted_hits.bam in the folder.

Usage

```r
makeSam()
```

Details

This function uses samtools to convert a bam file in a sam file. It assumes that the bam file was generated by TopHat. Therefore it searches for accepted_hits.bam in the folder. It produces a file named accepted_hits.sam.

Author(s)

Raffaele A Calogero

**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 perfct matching substring of the exon. In the otehr 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 procuces 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

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

masigpro()

Author(s)

Raffaele A Calogero

See Also

masigpro.edesign, masigpro.view

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`

---

**Description**

The function allows the visualization of maSigPro results.

**Usage**

`masigpro.view()`

**Author(s)**

Raffaele A Calogero

**See Also**

`masigpro.edesign`, `masigpro`

---

**Description**

Graphical interface to metaArray Integrative Correlation function

**Usage**

`metaArrayIC()`

**Author(s)**

Raffaele A Calogero

**References**

MergeMaid package and metaArray Package
metaArrayMerge

Tool to create a merge object for metaArray package

Description
This function will create an ExpressionSet from a study starting from a tab delimited 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
metaArrayIC()

Author(s)
Raffaele A Calogero

See Also
metaArrayIC

miRNAbowtieRun
Primary mapping of short reads with Bowtie/Picard for miRNA

Description
A function for primary mapping of short reads with bowtie and the conversion of the SAM output into BAM format In the actual implementation it is possible to run bowtie using single-end fastq files produced using Illumina platform. The available reference sets are derived by miRbase precursors and are available for human, hs, mouse, mm, rat, rn, and bovine, bo. It is strongly suggested to run a trimming of the 3 and 5 end linkers before performing the mapping with bowtie. In the present implementation bowtie runs with the following parameters: -a --best -k 1 -q -v 3 -S. Therefore only the first best alignment is shown, input files are in fastq format, alingement up to three mismatches are considered and the output is in SAM format. At the end of the mapping SAM files are converted in BAM files using picard tools.

Usage
miRNAbowtieRun()

Author(s)
Raffaele A Calogero
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 affyImGUI target file. To know more about target file see affyImGUI help. Each row of the column named Target, in the affyImGUI 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 affyImGUI 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_N</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>
<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_2NA_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

mmfa

Mouse microRNA data set

Description

microRNA data set fasta produced using miRbase M musculus precursors reformatted to have only miR name as descriptor of the fasta file

Usage

mmfa

Format

Fasta file
mRNAbowtieRun

| mRNAbowtieRun | Primary mapping of short reads with Bowtie/Picard for mRNA-seq |

**Description**

A function for primary mapping of short reads with bowtie and the conversion of the SAM output into BAM format. In the actual implementation it is possible to run bowtie using pair-end fastq files produced using Illumina platform. The available reference sets are built for human, hs, mouse, mm and rat, rn. Analysis is performed chromosome by chromosome to limit RAM consumption. In the present implementation bowtie runs with the following parameters: -a –best -k 1 -q -v 3 -S. Therefore only the first best alignment is shown, input files are in fastq format, alignment up to three mismatches are considered and the output is in SAM format. At the end of the mapping SAM files are converted in BAM files using picard tools.

**Usage**

mRNAbowtieRun()

**Author(s)**

Raffaele A Calogero

|mRNAmiRCor | Filtering by mean of correlation between expression data and miRNA expression changes |

**Description**

This function extract the subset of gene ids which are associated to the changes of expression on putative miRNA targets upon perturbation of miR expression.

**Usage**

mRNAmiRCor()

**Details**

To run this analysis a time course experiment suitable for maSigPro analysis is needed. Expression data need to have at least 3 time points for samples transfected with a scrambled and with an Antagomir or a Mimic. The expression changes at the same time points used for microarray data need to be measured also for miRNA. miRNA expression data need to be saved as table delimited file with two columns: column Name, which has to be organized exactly as the target file Name column, and a column named Value with expression of miRNA, e.g. deltaCt. Target file for mRNA data need to be organized as for maSigPro time course analysis. Output is a three column (gene level id, miRNA-mRNA correlation, mRNA untreated - mRNA treated correlation) tab delimited file with gene IDs and correlation coefficient between mRNA profile and miRNA profile upon treatment with antagonim, i.e. mRNA expression should rise due to the reduction of miRNA expression, or mimics, i.e. mRNA expression should be reduced due to the over-expression of the specific miRNA.
**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**

```r
myExpresso()
```

**Details**
This function runs `expresso` with the graphical interface for parameter selection. It is important to note that `expresso` is more slow than the C coded `rma`.

**Author(s)**
Raffaele A Calogero

---

**ncHs.data**  
*Subset of genomic regions with ncRNA of Homo sapiens*

**Description**
Two `IRanges` objects referring to the plus and minus strand of genomic regions encoding for ncRNAs. The ncRNAs considered are: miRNA, Mitochondrial rRNA, Mitochondrial tRNA, rRNA, snoRNA, snRNA.

**Usage**

```r
cchs.data
```

**Format**
A list with two observations: `IRanges` objects referring to the plus and minus strand of genomic region encoding for ncRNAs.

**Author(s)**
Raffaele A Calogero
**ncMm.data**  
*Subset of genomic regions with ncRNA of Mus musculus*

**Description**
Two IRanges object referring to the plus and minus strand of genomic region encoding ncRNAs. The ncRNAs taken in consideration are: miRNA, Mitochondrial rRNA, Mitochondrial tRNA, rRNA, snoRNA, snRNA

**Usage**
ncMm.data

**Format**
A list with two observations: IRanges object referring to the plus and minus strand of genomic regions encoding ncRNAs

**Author(s)**
Raffaele A Calogero

---

**ncRn.data**  
*Subset of genomic regions with ncRNA in Rattus norvegicus*

**Description**
Two IRanges object referring to the plus and minus strand of genomic region encoding ncRNAs. The ncRNAs taken in consideration are: miRNA, Mitochondrial rRNA, Mitochondrial tRNA, rRNA, snoRNA, snRNA

**Usage**
ncRn.data

**Format**
A list with two observations: IRanges object referring to the plus and minus strand of genomic region encoding ncRNAs

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

*stand alone function to generate a scaffold containing only ncRNA location from ENSEMBL*

---

**Description**

The scaffold contains chr stand start and end position of ncRNA. ENSEMBL retrieved species are miRNA,Mt_rRNA,Mt_tRNA,rRNA,snoRNA,snRNA

**Usage**

ncScaffold(genome, fasta)

**Arguments**

- **genome**
  The genome code for H sapiens is hg19, for M musculus is mm9 and for R norvegicus is rn4

- **fasta**
  If fasta is TRUE a fasta file with the sequences retrieved by ncScaffold will be produced

**Details**

The scaffold is used to map reads data into regions only associated to ncRNAs

**Author(s)**

Raffaele A Calogero

---

**NGSreformat**

*reforming output of NGS primary tools software*

---

**Description**

This function allows to reorganize the output files produced by SHRIMP, MicroRazerS in two files with the extension: bed and logos used by oneChannelGUI

**Usage**

NGSreformat()

**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**

`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**

`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**

`ocPlotPCA()`
Author(s)
Raffaele A Calogero

See Also
ocPlotHist

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

Usage

goseqInterface()
DESeqInterface()
EDAwithinLane()
EDAbetweenLane()
EDAbboxplot()
EDAbiasPlot()
AboutextendedaffylmGUI()
AboutaffylmGUI()
oneChannelGUI()
oneChannelGUIHelp() maSigProHelp()
siggenessHelp()
oneChannelGUIHelp()
initalize.extAffylmGUI()
OpenExonandTargetsfiles()
GOstatsHelp()
SaveLimmaFile()
NewLimmaFile()
NewLimmaFileNGS()
OpenLimmaFile()
OpenALimmaFile(FileName)
OpenFile(FileName)
OpenLargeFile()
changeMenu()
oneChannelGUI.start()
libraryFilesDir()
whichKindOfArray()
intronicBg()
ExportNormalizedExpressionValues1()
ExportNormalizedExpressionValues()
ExportfeatureNames()
SaveAsLimmaFile()
addAnnLib()
OpenCDFandTargetsfiles()
ComputeLinearModelFit()
GetNormalizationMethod()
NormalizeNow()
ComputeContrasts()
midasFilter()
dabgFilter()
largedatasetNorm()
RankProdHelp()
affyPLMHelp()
genefilterHelp()
pamrHelp()
pdmclassHelp()
sizelowerHelp()
sizeEffHelp()
OpenAGeoFile(FileName)
OpenGeoFile()
OpenGeoFiles()
OpenNgsfiles()
recoverUnfiltered()
delete.ML()
affyPlotMA()
changes()
aptFolder()
javaFolder()
deleteLocalData()
SetED()
chooseEDir()
.annotation(eset)
.myfindOverlaps(x,y)
log2Conversion()
.myrk(x,df)
exportFASTA()
OpenmiRanalyserfiles()
OpenmiRProfiles()
OpenmiRExpress()
OpenmiRShrimp()
OpenmiRBam()
ngsperlDownload()
meVDownload()
extPckInfo()
startmeV()
tuxedoMenu()
setBinDir()
fastQC()
openPdf()
closePdf()
plotDE.exons()
topTable.genes()
importfusions()
fusionNSf()
fusionfilter()
chimeraseq()
tophatrun()
addga()
fusionpeptides()
plotcoverage()
desCounts()
miRNAde()
downloadShrimp()
wrapperMirnaCounts(working.dir, out.dir, org = "hsa", threads = 1, cutadapt.path = "/usr/local/bin/cutadapt", parallel = FALSE, ...)
deseq2Processing()

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>FileName</td>
<td>Internal argument not to be set by the user</td>
</tr>
<tr>
<td>eset</td>
<td>Internal argument not to be set by the user</td>
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<tr>
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<td>Internal argument not to be set by the user</td>
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<tr>
<td>y</td>
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<td>group</td>
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<td>out.dir</td>
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</tr>
<tr>
<td>mirnaobj</td>
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</tr>
</tbody>
</table>
**OpenBeadStudioFiles**

**groups**  
Internal argument not to be set by the user

**format**  
Internal argument not to be set by the user

**Significance**  
Internal argument not to be set by the user

**na.char**  
Internal argument not to be set by the user

**pvalueTypes**  
Internal argument not to be set by the user

**maxStringLength**  
Internal argument not to be set by the user

**pathwaysNames**  
Internal argument not to be set by the user

**Composite**  
Internal argument not to be set by the user

**permutations**  
Internal argument not to be set by the user

**...**  
Internal argument not to be set by the user

**perm**  
Internal argument not to be set by the user

**expressioncol**  
Internal argument not to be set by the user

---

**Details**

This function launches a modified 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 intensity 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 an file containing the expression data in a tab delimited format. This file is loaded together with the description of the clinical parameter 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

OpenmRNABam

This function loads Bam files generated by local mapping with bowte in oneChannelGUI

Description

The function creates and expressionSet starting from the association of reads mapped by Bowtie using chromosome oriented mapping controlled by oneChannelGUI and associate those mapping to gene-level regions extracted by UCSC browser. IMPORTANT at the present time the expression set is base on gene-level data and not on exon-level data.

Usage

OpenmRNABam()
### plierToZero

**Author(s)**

Raffaele A Calogero

---

**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 algoritm

**Usage**

```r
plierToZero()
```

---

**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

Description

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

Usage

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
qcMDS

This function plots the sample relations based on multidimensional scaling using the plotMDS.dge edgeR function

Description

This function is a variation on the usual multidimensional scaling (or principle coordinate) plot, in that a distance measure particularly appropriate for the digital gene expression (DGE) context is used. The distance between each pair of samples (columns) is the square root of the common dispersion for the top genes which best distinguish that pair of samples. These top genes are selected according to the tagwise dispersion of all the samples.

Usage

qcMDS()

Author(s)

Raffaele A Calogero

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

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
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 allows 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

---

**Reads2logos**

*Extracting info on the counts associated to a differentially expressed ncRNA gene*

**Description**

This function allows to plot the raw counts associated to samples or experimental groups associated to a ncRNA found differentially expressed. Furthermore, it saves the count matrix for the mapped positions on the differentially expressed ncRNA.

**Usage**

`Reads2logos()`

**Author(s)**

Raffaele A Calogero
refiningPeaks  

**Description**

This function refines the structure of the genomics peaks, checking for the presence of nearby peaks that can be combined.

**Usage**

refiningPeaks()

**Author(s)**

Raffaele A Calogero

reformatGdl  

**Description**

This function reorganizes single NGS data in a matrix to be used for statistical analysis.

**Usage**

reformatGdl()

**Author(s)**

Raffaele A Calogero

refseqDownload  

**Description**

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

**Usage**

refseqDownload()
retrieveMirTargets

graphical interface to RmiR.Hs.miRNA library.

Description
This function retrieves putative targets from RmiR.Hs.miRNA given a specific microRNA.

Usage
retrieveMirTargets()

Details
This interface provides a graphical GUI to RmiR.Hs.miRNA.

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 retrieves from RRE the PSR sequences associated to the exon-level probe sets

Usage
retrievePSRseq()

Author(s)
Raffaele A Calogero

retrievePSRseq1gid
This function, given a gene-level probeset id, retrieves Probe selection Regions, PRS, from RRE db

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

Usage
retrievePSRseq1gid()

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 gene-level 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. Bioconductor project Papers 2004

See Also
dabgFilter, crosshybFilter

RmiRInterface  
graphical interface to RmiR library.

Description
RmiR package is to couple microRNA and gene expression data (coming from the same RNA). Input data are obtainable with limma interface (gene-level differential expression) in oneChannelGUI and baySeq interface (NGS microRNA differential expression).

Usage
RmiRInterface()

Details
This interface provides a graphical GUI to RmiR package. The output structure is described in RmiR package.
Author(s)
Raffaele A Calogero

rnfa  Rat microRNA data set

Description
microRNA data set fasta produced using miRbase R norvegicus precursors reformatted to have only miR name as descriptor of the fasta file

Usage
rnfa

Format
Fasta file
unningJetta  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-tilling 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 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 clusts and probes from the analysis. TC expression level: excluding low-expressed transcript clusts TC expression fold change: excluding transcript clusts 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

---

**sample.size.evaluation**

*The function executes and plots results from ssize and delta function from the ssize package*

---

**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
The function executes functions from the sizepower package

**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**

```r
sample.size.evaluation1()
```

**Details**

see sizepower help

**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**

```r
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**

```r
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 into 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**

```r
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`
standAloneAddingAnnotation

Attach to a data frame containing gene-level data derived from Affymetrix exon arrays the annotations derived by netaffx

Description

Standalone oneChannelGUI function attaches gene-level annotation to a data frame.

Usage

standAloneAddingAnnotation(annotationdf, df.tobe.annotated, ids.column)

Arguments

<table>
<thead>
<tr>
<th>annotationdf</th>
<th>An annotation data frame generated with standAloneBuildingLocalAnnotation function</th>
</tr>
</thead>
<tbody>
<tr>
<td>df.tobe.annotated</td>
<td>A data frame containing a gene-level data of any type. It is mandatory that one of the column contains gene-level ids</td>
</tr>
<tr>
<td>ids.column</td>
<td>the column of the df.tobe.annotated containing gene-level ids</td>
</tr>
</tbody>
</table>

Value

A data frame.

Author(s)

Raffaele A Calogero

---

standAloneBuildingLocalAnnotation

Creates a data frame with gene-level annotation data for exon arrays using the netaffx database

Description

Standalone oneChannelGUI function to create gene-level annotation data using netaffx database.

Usage

standAloneBuildingLocalAnnotation(libDirLocation = getwd(), netaffxUser = "myemail@somewhere.org", netaffxUserPw = "yourpassword", whichAnnotation = c("HuEx", "MoEx", "RaEx"))

Arguments

<table>
<thead>
<tr>
<th>libDirLocation</th>
<th>Folder where to save the annotation object</th>
</tr>
</thead>
<tbody>
<tr>
<td>netaffxUser</td>
<td>The email registered to Affymetrix netaffx web site</td>
</tr>
<tr>
<td>netaffxUserPw</td>
<td>The password to access to netaffx</td>
</tr>
<tr>
<td>whichAnnotation</td>
<td>Which annotation table should be used</td>
</tr>
</tbody>
</table>
**Value**
Location of the annotation data frame.

**Author(s)**
Raffaele A Calogero

---

**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
### topTable.exons

**Description**

This function generates a table of differentially expressed exons.

**Usage**

```r
topTable.exons()
```

**Details**

topTable.exons function uses the results produced by dexExons function to generate a table of differentially expressed exons.

**Author(s)**

Raffaele A Calogero

---

### 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**

```r
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
**tuxedoSetup**

---

**Description**

To be able to run Tuxedo Suite with oneChannelGUI it is necessary to make soft links for samtools, bowtie, tophat, cufflinks programs

**Usage**

```
tuxedoSetup()
```

**Details**

samtools need to be installed by the user, as instead bowtie, tophat and cufflinks are installed via oneChannelGUI

**Author(s)**

Raffaele A Calogero

---

**TuxedoSuite**

---

**Description**

TuxedoSuite contains a set of functions to run tophat, cufflinks, cuffmerge, cuffdiff and to extract gene, geneDiff, isoforms, isoDiff, and CDS, cdsDiff, differentially expressed between two experimental conditions. The present implementation works only on MAC and Linux, due to the absence of a windows implementation of the tuxedo suite. tophat, cufflinks, cuffmerge and cuffdiff create the line command to execute the corresponding program and all programs are run in background, since they might require quite a lot of computation time. One differential expression is obtained geneDiff, isoDiff and cdsDiff can be used to extract respectively differentially expressed genes, isoforms and CDSs

**Usage**

```
tophat()
createDir()
cufflinks()
cuffmerge()
cuffdiff()
geneDiff()
isoDiff()
cdsDiff()
chooseInDir()
chooseOutDir()
```
Details

tophat, cufflinks, samtools and bowtie need to be installed in the system and their folder installation inserted in the PATH variable. Also the genome of interest, as fasta file and as bowtie indexed files need to be previously installed together with a GTF file containing known annotations for the genome of interest. To run the pipeline a target file is needed. createDir generates folders, with the name extracted from the Name column in the target file. In each of these folders tophat will create the files used by cufflinks, cuffmerge, cuffdiff. cuffdiff will create a folder in which differentially expressed data are saved. Access to those data is done using the cummeRbund package.

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

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

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**

```r
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**

```r
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
wrapNGS

**Description**
A function to download all external software needed for NGS data analysis

**Usage**
```
wrapNGS()
```

**Author(s)**
Raffaele A Calogero

wrapScaffold

**Description**
A function to wrap the makeGCcontent, makeGeneScaffold functions. Built scaffolds are available as precompiled at sourceforge oneChannelGUIextras project.

**Usage**
```
wrapScaffold(whichRef)
```

**Arguments**
- `whichRef` The genome of interest to be used to create a gene-level scaffold

**Author(s)**
Raffaele A Calogero

**See Also**
makeGCcontent, makeGeneScaffold
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