

# Package ‘oneChannelGUI’

April 23, 2016

**Version** 1.36.0

**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, affyImlGUI, tkrplot, tkWidgets, IRanges, Rsamtools (>= 1.13.1), Biostrings, siggenes, chimera

**Suggests** annotate, genefilter, maSigPro, pamr, pdmclass, ChIPpeakAnno, chipseq, BSgenome, Rgraphviz, affy, annaffy, affyPLM, multtest, ssize, sizepower, RankProd, org.Hs.eg.db, org.Mm.eg.db, org.Rn.eg.db, edgeR, metaArray, MergeMaid, biomaRt, GenomeGraphs, AffyCompatible, rtracklayer, Genominator, EDASeq, limma, DESeq, DEXSeq, goseq, hugene10stranscriptcluster.db, mogene10stranscriptcluster.db, ragene10stranscriptcluster.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/>

**biocViews** Sequencing, RNASeq, Microarray, OneChannel, DataImport, QualityControl, Preprocessing, StatisticalMethod, DifferentialExpression, GUI, MultipleComparison

NeedsCompilation no

## R topics documented:

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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

## Author(s)

Author: Raffaele A Calogero Maintainer: Raffaele A Calogero <raffaele.calogeor@unito.it>

## Examples

```
# 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 nt very efficient. it takes about 5 minutes for 1 milion reads file

## Usage

```
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**

```
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 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
```

---

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 interface 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 *Downloading Bowtie and Picard tools*

---

**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	<i>Downloading and building chromosome level genomes references for bowtie</i>
---------------	--

---

**Description**

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

**Usage**

```
bowtieGenomes()
```

**Author(s)**

Raffaele A Calogero

---

buildingLocalAnnotation	<i>Updates local gene-level annotation data for gene and exon arrays using the netaffx database</i>
-------------------------	---

---

**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()
```

**Author(s)**

Raffaele A Calogero

---

chrLength	<i>Chromosomes lenghts</i>
-----------	----------------------------

---

**Description**

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

**Usage**

```
chrLength
```

**Format**

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

**Author(s)**

Raffaele A Calogero

---

colExtract	<i>Extract a column from a tab delimited file with header</i>
------------	---

---

**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 fro ven diagram representations

**Usage**

```
colExtract()
```

**Author(s)**

Raffaele A Calogero

---

combineGeoMSF	<i>This function allows to combine GEO Matrix Series Files belonging to the same experiment.</i>
---------------	--

---

**Description**

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

**Usage**

```
combineGeoMSF()
```

**Note**

see oneChannelGUI vignette for more info

**Author(s)**

Raffaele A Calogero

---

combining2eSet	<i>This function allows to combine two matrices extracted from oneChannelGUI.</i>
----------------	---

---

**Description**

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

**Usage**

```
combining2eSet()
```

**Note**

see oneChannelGUI vignette for more info

**Author(s)**

Raffaele A Calogero

---

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

---

### 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	<i>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</i>
--------------	---

---

### 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

---

ctrtrtHeatmap	<i>Creating heat map for maSigPro data with only one treatment condition</i>
---------------	--

---

#### 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 antagomir or mimics. Expression data reorganized as the average expression differences between treatment and untreated condition over the time course.

#### Usage

```
ctrtrtHeatmap()
```

#### Author(s)

Raffaele A Calogero

---

desGenes	<i>desGenes</i>
----------	-----------------

---

#### Description

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

#### Usage

```
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

*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

*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 describing differential expression at exon level and ecs is the DEXseq object containing 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 affyImGUI

**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**

EDApplotQuality, EDAREadNumber

---

`EDApplotQuality`*Plotting Quality scores for mapped reads extracted from BAM files*

---

**Description**

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

**Usage**

```
EDApplotQuality()
```

**Details**

Interface to the plotQuality of EDASeq package

**Author(s)**

Raffaele A Calogero

**See Also**

EDAREadNumber, EDANtFreq

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, EDANtFreq

---

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

---

**Description**

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

**Usage**

```
edgeRNorm()
```

**Author(s)**

Raffaele A Calogero

---

EG2probeset	<i>This function allows to link GeneBank and Entrez Gene ids to gene-level probe set ids</i>
-------------	--

---

**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 concious of this!

### **Author(s)**

Raffaele A Calogero

### **See Also**

inspecting.splice, spliceIndex

---

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

**See Also**

erankProdAltSpl, AptMidas

---

eSet4meV	<i>This function allows to reformat an eSet to be loaded in meV visualization software</i>
----------	--

---

**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**

```
eSet4meV()
```

**Note**

see oneChannelGUI vignette for more info

**Author(s)**

Raffaele A Calogero

---

exonContrasts	<i>Defining t-test regularized p-values</i>
---------------	---

---

**Description**

This function constructs the contrasts as affyImGUI 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	<i>stand alone function to generate a scaffold containing only exon location from ENSEMBL</i>
--------------	---

---

**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**

```
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**

```
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	<i>Extracting probe ids associated to a specific Gene Ontology term</i>
----------------	---

---

**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 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 and saved in a 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	<i>Extract miRNA targets showing a opposite regulation with respect to miRNA</i>
-------------------	--

---

**Description**

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

**Usage**

```
extractmirTargets()
```



**Details**

The output as 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 affyImGUI 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**

```
filteringmiRtargets()
```

**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	<i>Filtering a tab delimited file</i>
----------------	---------------------------------------

---

**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	<i>Download the Library files for gene and exon analysis</i>
--------------	--

---

**Description**

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

**Usage**

```
geneExonLibs()
```

**Author(s)**

Raffaele A Calogero

---

genomePlot	<i>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</i>
------------	--

---

**Description**

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

**Usage**

```
genomePlot()
```

**Author(s)**

Raffaele A Calogero

**See Also**

variantSI, variantExons, makeBED15

---

genomeStudioReformat	<i>The present function reformat an expression file exported by Genome Studio in a format that is compatible with oneChannelGUI</i>
----------------------	---

---

**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 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 `SespressionSet`

**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	<i>Searching for Gene Ontology enriched terms within a set of differentially expressed genes</i>
--------------	--

---

**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	<i>Human microRNA data set</i>
------	--------------------------------

---

**Description**

microRNA data set fasta produced using miRbase H sapiens precursors reformated 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	<i>intensity filtering with a mouse click</i>
-----------------	---

---

**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	<i>Filtering an expression set using a set of Entrez genes extracted from Ingenuity Pathways analysis (IPA)</i>
---------------	---

---

**Description**

It is possible to sub set an expression set loaded in the affyImGUI 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



---

limma2paired	<i>graphical interface apply linear model to two sample groups with batch effect.</i>
--------------	---

---

**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	<i>graphical interface to limma for alternative splicing detection</i>
------------	--

---

**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	<i>Subsetting an expression set using a list of Affymetrix ids</i>
------------	--

---

**Description**

This function subsets the normalized expression set present in the affyImGUI 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.

**Author(s)**

Raffaele A Calogero

**See Also**

IPAlistFilter, iqrFilter, intensityFilter

---

makeBED15	<i>This function creates files in BED15 format to be loaded on the UCSC browser</i>
-----------	---

---

**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**

```
makeBED15()
```

**Author(s)**

Raffaele A Calogero

**See Also**

variantSI, variantExons, plotVariantSI

---

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 GRRange 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

---

makeGeneScaffold

*Building a GRRange object at chromosome level on UCSC genome data*

---

**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

---

makeSam

*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**

```
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 oneChannleGUI 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 otehr case no exon is associated to the probe set

**Usage**

```
mapping2ensembl()
```

**Author(s)**

Raffaele A Calogero

---

mapping2exon	<i>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</i>
--------------	---

---

**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 where are located exon-level PSR and target exon. The mapping is done using the countPattern function of the Biostrings package. Up to three mismatches are allowed in PSR mapping on exonic sequence.

**Usage**

```
mapping2exon()
```

**Author(s)**

Raffaele A Calogero

---

mapping2RefSeq	<i>This function maps on NCBI Reference sequences spliced exons detected by the function oneChannelGUI: Inspecting splice indexes</i>
----------------	---

---

**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 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 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 affyImGUI target file will look like:

Name	FileName	Target
mC1	M1.CEL	0_1_1_0_0
mC2	M4.CEL	0_1_1_0_0

mC3	M7.CEL	0_1_1_0_0
mE1	M3.CEL	24_2_0_1_0
mE2	M6.CEL	24_2_0_1_0
mE3	M9.CEL	24_2_0_1_0
mI1	M2.CEL	24_3_0_0_1
mI2	M5.CEL	24_3_0_0_1
mI3	M8.CEL	24_3_0_0_1

**Usage**

```
masigpro.edesign()
```

**Author(s)**

Raffaele A Calogero

**See Also**

masigpro, 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**

```
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**

```
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 rows 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, 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**

```
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 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:

Name	FileName	Target
mC1	M1.CEL	0_1_pos_0_NA
mC2	M4.CEL	0_1_pos_0_yes
mC3	M7.CEL	0_1_neg_0_no
mE1	M3.CEL	24_2_neg_1_NA
mE2	M6.CEL	24_2_NA_1_yes

mE3	M9.CEL	24_2_neg_1_yes
mI1	M2.CEL	12_3_0_pos_yes
mI2	M5.CEL	12_3_0_pos_no
mI3	M8.CEL	12_3_0_pos_no

**Usage**

```
ML.edesign()
```

**Author(s)**

Raffaele A Calogero

---

mmfa

*Mouse microRNA data set*

---

**Description**

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

**Usage**

```
mmfa
```

**Format**

Fasta file

---

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	<i>Filtering by mean of correlation between expression data and miRNA expression changes</i>
------------	--

---

**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 antagomir, 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.

**Author(s)**

Raffaele A Calogero

**See Also**

IPAlistFilter, iqrFilter, intensityFilter

---

`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 runs `expresso` with the graphical interface for parameter selection. It is important to note that `expresso` is slower 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 region encoding for ncRNAs. The ncRNAs taken into consideration are: miRNA, Mitochondrial rRNA, Mitochondrial tRNA, rRNA, snoRNA, snRNA.

**Usage**

```
ncHs.data
```

**Format**

A list with two observations: `IRanges` object 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	<i>stand alone function to generate a scaffold containing only ncRNA location from ENSEMBL</i>
------------	--

---

**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	<i>reformatting output of NGS primary tools software</i>
-------------	--

---

**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	<i>Box plot of the arrays data available in NormalizeAffyData slot</i>
-------------	--

---

**Description**

Box plot visualization of normalized array data

**Usage**

```
normBoxplot()
```

**Author(s)**

Raffaele A Calogero

---

ocPlotHist	<i>Gene/Exon level density plots</i>
------------	--------------------------------------

---

**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

---

oneChannelGUI                      *Starting oneChannelGUI package*

---

**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()
siggenesHelp()
oneChannelGUIHelp()
initialize.extAffylmGUI()
OpenExonandTargetsfiles()
GOstatsHelp()
```



```
SaveLimmaFile()
NewLimmaFile()
NewLimmaFileNGS()
OpenLimmaFile()
OpenALimmaFile(FileName)
OpenAFile(FileName)
OpenExonFile()
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()
sizepowerHelp()
ssizeHelp()
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()
fusionNS()
fusionfilter()
chimeraseq()
tophatrun()
addga()
fusionpeptides()
plotcoverage()
desCounts()
miRNAd()
downloadShrimp()
wrapperMirnaCounts(working.dir, out.dir, org = "hsa", threads = 1, cutadapt.path = "/usr/local/bin/cu
deseq2Processing()
enrich(group, permutations = permutations)
loadmirnopath(mirnafile = "mirna_input.txt", mirnacol = "miRNA.id",
              assayidcol = "ASSAYID", groupcol = "GROUP",
              filterflagcol = "FILTERFLAG", expressioncol = NA,
              foldchangeacol = NA, pvaluecol = NA)
mirPath()
mirnaTable(mirnaobj, groups = NULL, format = "Tall", Significance
           = 0.2, na.char = NA, pvalueTypes = c("pvalues",
           "permpvalues"), maxStringLength = NA, pathwaysNames =
           hs.path.name)
permuting(perm)
runEnrichment(Composite = TRUE, groups = NULL, permutations = 0)
```

**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
y	Internal argument not to be set by the user
df	Internal argument not to be set by the user
group	Internal argument not to be set by the user
working.dir	Internal argument not to be set by the user
out.dir	Internal argument not to be set by the user
org	Internal argument not to be set by the user
threads	Internal argument not to be set by the user
cutadapt.path	Internal argument not to be set by the user
parallel	Internal argument not to be set by the user
mirnafile	Internal argument not to be set by the user
mirnacol	Internal argument not to be set by the user
assayidcol	Internal argument not to be set by the user
groupcol	Internal argument not to be set by the user
filterflagcol	Internal argument not to be set by the user
foldchange	Internal argument not to be set by the user
pvaluecol	Internal argument not to be set by the user
mirnaobj	Internal argument not to be set by the user
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 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 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 an 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:

Name	FileName	Target
mC1	M1.CEL	pos_yes_1_NA_0

mC2	M4.CEL	pos_no_2_NA_0
mC3	M7.CEL	neg_no_3_pos_0
mE1	M3.CEL	neg_yes_3_neg_0
mE2	M6.CEL	neg_no_NA_1_0
mE3	M9.CEL	neg_yes_3_pos_0
mI1	M2.CEL	pos_no_2_neg_1
mI2	M5.CEL	pos_yes_2_pos_1
mI3	M8.CEL	pos_no_2_pos_1

**Usage**

```
OpenLargefiles()
```

**Author(s)**

Raffaele A Calogero

---

OpenmRNABam

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

---

**Description**

The function creates an 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 based on gene-level data and not on exon-level data.

**Usage**

```
OpenmRNABam()
```

**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 algorithm

**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**

```
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	<i>A modified version of the function used in affyPLM library</i>
---------------	---

---

**Description**

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

**Usage**

```
PlotOptionsv1()
```

**Author(s)**

Raffaele A Calogero

---

plotVariantSI	<i>This function plots on UCSC genome browser data derived by variantSI filter</i>
---------------	--

---

**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	<i>graphical interface to rank product method implemented in RankProd Bioconductor library.</i>
----------	---

---

**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.

Name	FileName	Target
mC1	M1.CEL	CTRL_1
mC2	M4.CEL	CTRL_1
mC3	M7.CEL	CTRL_2
mE1	M3.CEL	CTRL_2
mE2	M6.CEL	CTRL_2
mE3	M9.CEL	TRT_1
mI1	M2.CEL	TRT_1
mI2	M5.CEL	TRT_2
mI3	M8.CEL	TRT_2

**Author(s)**

Raffaele A Calogero

---

rawBoxplotPN	<i>Plotting raw log2 intensities from controls</i>
--------------	--

---

**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

---

Reads2logos

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

---

**Description**

This function allow 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	<i>This function refines the structure of the genomics peaks, checking for the presence nearby peaks that can be combined</i>
---------------	---

---

**Description**

This function allows the user to define a threshold for peaks merging. if threshold is set to 0 non merging is provided.

**Usage**

```
refiningPeaks()
```

**Author(s)**

Raffaele A Calogero

---

reformatGdl	<i>This function reorganizes single NGS data in a matrix to be used for statistical analysis.</i>
-------------	---

---

**Description**

This function reorganizes the raw NGS data saved in a GenomeDataList object in a matrix. Matrix rows are peaks containing multiple reads. For peak detection, user has to indicate the amount of extension of each read, e.g. 200 nt in chipseq experiments, and the number of reads due by random events, e.g. 8.

**Usage**

```
reformatGdl()
```

**Author(s)**

Raffaele A Calogero

---

refseqDownload      *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**

```
refseqDownload()
```

**Author(s)**

Raffaele A Calogero

---

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	<i>This function, given a file containing exon-level probesets retrieves Probe selection Regions, PRS, from RRE db</i>
----------------	--

---

**Description**

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

**Usage**

```
retrievePSRseq()
```

**Author(s)**

Raffaele A Calogero

---

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

---

**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 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 a 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	<i>Rat microRNA data set</i>
------	------------------------------

---

**Description**

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

**Usage**

```
rnfa
```

**Format**

Fasta file

---

runningJetta	<i>graphical interface to MADS/jetta R library.</i>
--------------	---

---

**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 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 fulction from the ssize packahe*

---

## Description

This function represents avisual 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

---

sample.size.evaluation1

*The function executes functions from the sizepower packahe*

---

**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

---

showDataset	<i>Grabbing info about the available expression set</i>
-------------	---

---

**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	<i>Modification of the function implemented in affyLmGUI to generate a topTable</i>
--------------	---

---

**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	<i>The function executes SAM analysis implemented in siggenes bioconductor library</i>
----------	--

---

**Description**

To know more about SAM in Bioconductor see siggenes help.

**Usage**

```
siggenes()
```

**Author(s)**

Raffaele A Calogero

---

simFilter	<i>This function allows filtering on the basis of the average splice index mean or min difference between two groups</i>
-----------	--

---

**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 fuction needs the presence of Splice Index.

**Author(s)**

Raffaele A Calogero

**See Also**

simFilter

---

spliceIndex	<i>This function covers the exon intensity data in a slice index</i>
-------------	--

---

**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

---

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**

annotationdf	An annotation data frame generated with standAloneBuildingLocalAnnotation function
df.tobe.annotated	A data frame containing a gene-level data of any type. It is mandatory that one of the column contains gene-level ids
ids.column	the column of the df.tobe.annotated containing gene-level ids

**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",
```

**Arguments**

libDirLocation Folder where to save the annotation object  
netaffxUser The email registered to Affymetrix netaffx web site  
netaffxUserPw The password to access to netaffx  
whichAnnotation Which annotation table should be used

**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	<i>topTable.exons</i>
----------------	-----------------------

---

**Description**

This function generates a tables of differentially expressed exons.

**Usage**

```
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	<i>Creating a training set and a test set by a mouse click</i>
-----------	--

---

**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

tuxedoSetup                      *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                      *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 correponding 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**`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

---

`wrapNGS`*Downloading software for NGS*

---

**Description**

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

**Usage**`wrapNGS()`**Author(s)**

Raffaele A Calogero

---

`wrapScaffold`*A wrapper for makeGCcontent, makeGeneScaffold*

---

**Description**

A function to wrap the makeGCcontent, makeGeneScaffold functions Built scaffolds are available as precompiled at sourceforge oneChannelGUI.extras 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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