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Description Provides a Graphical User Interface for Analysing DNA Microarray Data. It performs functional enrichment on genes of interest, identifies gene symbols and also builds co-expression network.

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maGUI-package

A Graphical User Interface for Microarray Data Analysis and Annotation

Description

Provides a comprehensive graphical user interface for analysis of Affymetrix, Agilent, Illumina, Nimblegen and other microarray data. It can perform miscellaneous tasks such gene set enrichment and test analysis, identifying gene symbols and building co-expression network. It can also estimate sample size for atleast two-fold expression change. Further, it can identify protein-protein associations from two normalized microarray data.

Details

Package: maGUI
Type: Package
Version: 2.3
Date: 2019-03-21
License: GPL-2

Author(s)

Dhammapal Bharne, Vaibhav Vindal

Maintainer: Dhammapal Bharne <dhammapalb@uohyd.ac.in>

affym

Preprocessing and Analysis of Loaded Affymetrix Data

Description

Performs pre-processing and analysis of loaded microarray data automatically. It includes normalization, quality check, filtering, statistical significance, differential gene expression, principal component analysis, clustering and classification.

Details

Function performs pre-processing and analysis of loaded Affymetrix data automatically if exists object datAffy of Affymetrix data.

Author(s)

Dhammapal Bharne

agone

Preprocessing and Analysis of Loaded Agilent_OneColor Data

Description

Performs pre-processing and analysis of loaded microarray data automatically. It includes normalization, quality check, filtering, statistical significance, differential gene expression, principal component analysis, clustering and classification.

Details

Function performs pre-processing and analysis of loaded Agilent_OneColor data automatically if exists object datAgOne of Agilent OneColor data.

Author(s)

Dhammapal Bharne

agtwo

Preprocessing and Analysis of Loaded Agilent_TwoColor Data

Description

Performs pre-processing and analysis of loaded microarray data automatically. It includes normalization, quality check, filtering, statistical significance, differential gene expression, principal component analysis, clustering and classification.

Details

Function performs pre-processing and analysis of loaded Agilent_TwoColor data automatically if exists object datAgTwo of Agilent TwoColor data.

Author(s)

Dhammapal Bharne

clas

Classification of Differentially Expression Genes

Description

Performs Classification of Differentially Expression Genes

Details

Function can perform classification of differentially expressed genes based on filtered data if exists object of Affymetrix, Agilent_OneColor, Agilent_TwoColor, Illumina_Beadarray, Illumina_Lumi, Nimblegen, Series_Matrix and Online as .f data. It maps differentially expressed genes to corresponding normalized .m or .m2 data and classify the genes. The outputs are Clas_Affy for Affymetrix, Clas_Ag1 for Agilent_OneColor, Clas_Ag2 for Agilent_TwoColor, Clas_II_B for Illumina_Beadarray, Clas_II_L for Illumina_Lumi, Clas_N for Nimblegen, Clas_S for Series_Matrix and Clas_O for Online procedures.

Author(s)

Dhammapal Bharne

`clust`*Clustering of Normalized Microarray Data*

Description

Performs Clustering of normalized microarray data

Details

Function can perform clustering on normalized microarray data if exists object of Affymetrix data as `dat2Affy.m`, Agilent_OneColor as `datAgOne2.m`, Agilent_TwoColor as `datAgTwo2.m`, Illumina_Beadarray as `datIIBA2.m2`, Illumina_Lumi as `lumi_NQ.m`, Nimblegen as `data.matrix.Nimblegen2.m`, Series_Matrix as `data.matrixNorm.m` and Online_Data as `data.matrix_onlineNorm.m`. The outputs are `sample.dist_Affy` and `sample.clust_Affy` for Affymetrix, `sample.dist_Ag1` and `sample.clust_Ag1` for Agilent_OneColor, `sample.dist_Ag2` and `sample.clust_Ag2` for Agilent_TwoColor, `sample.dist_II_B` and `sample.clust_II_B` for Illumina_Beadarray, `sample.dist_II_L` and `sample.clust_II_L` for Illumina_Lumi, `sample.dist_N` and `sample.clust_N` for Nimblegen, `sample.dist_S` and `sample.clust_S` for Series_Matrix and `sample.dist_O` and `sample.clust_O` for Online procedures.

Author(s)

Dhammapal Bharne

`dge`*Differential Gene Expression of Filtered Data*

Description

Performs differential gene expression of filtered microarray data. Parameters such as top differentially expressed genes or a set of genes of interest, number of genes to list, the amount of log fold change, p-value cut off, adjustment method and sort order can be set from the dialog box.

Details

Function can perform differential gene expression on filtered microarray data if exists object of Affymetrix data as `dat2Affy.f`, Agilent_OneColor as `datAgOne2.f`, Agilent_TwoColor as `datAgTwo2.f`, Illumina_Beadarray as `datIIBA2.f`, Illumina_Lumi as `lumi_NQ.f`, Nimblegen as `data.matrix.Nimblegen2.f`, Series_Matrix as `data.matrixNorm.f` and Online_Data as `data.matrix_onlineNorm.f`. The outputs are `DE_Affy` for Affymetrix, `DE_Ag1` for Agilent_OneColor, `DE_Ag2` for Agilent_TwoColor, `DE_II_B` for Illumina_Beadarray, `DE_II_L` for Illumina_Lumi, `DE_N` for Nimblegen, `DE_S` for Series_Matrix and `DE_O` for Online procedures.

Author(s)

Dhammapal Bharne

dmo

Preprocessing and Analysis of Loaded Online Data

Description

Performs pre-processing and analysis of loaded microarray data automatically. It includes normalization, quality check, filtering, statistical significance, differential gene expression, principal component analysis, clustering and classification.

Details

Function performs pre-processing and analysis of loaded Online data automatically if exists object `data.matrix_onlineImp` of `Online_Data`.

Author(s)

Dhammapal Bharne

dmsm

Preprocessing and Analysis of Loaded Series_Matrix Data

Description

Performs pre-processing and analysis of loaded microarray data automatically. It includes normalization, quality check, filtering, statistical significance, differential gene expression, principal component analysis, clustering and classification.

Details

Function performs pre-processing and analysis of loaded `Series_Matrix` data automatically if exists object `data.matrixImp` of `Series_Matrix` data.

Author(s)

Dhammapal Bharne

`filter_sp2`*Specific Filtering on Normalized Microarray Data*

Description

Performs specific filtering on normalized microarray data. It takes control and test sample names of one or multiple groups as input.

Details

Function can perform specific filtering on normalized microarray data if exists object new of Affymetrix data as `use.dat2Affy.m`, Agilent_OneColor as `use.datAgOne2.m`, Agilent_TwoColor as `use.datAgTwo2.m`, Illumina_Beadarray as `use.datIIBA2.m2`, Illumina_Lumi as `use.lumi_NQ.m`, Nimblegen as `use.data.matrix_Nimblegen2.m`, Series_Matrix as `use.data.matrixNorm.m` and Online_Data as `use.data.matrix_onlineNorm.m`. The outputs are as `.f` object to the normalized data. It also generates data with p-value less than 0.01 as statistically significant genes.

Author(s)

Dhammapal Bharne

`filter_unsp`*UnSpecific Filtering on Normalized Microarray Data*

Description

Performs UnSpecific filtering on normalized microarray data. It includes Standard Deviation and Expression filtering.

Details

Function can perform UnSpecific filtering on normalized microarray data if exists object of Affymetrix data as `dat2Affy.m`, Agilent_OneColor as `datAgOne2.m`, Agilent_TwoColor as `datAgTwo2.m`, Illumina_Beadarray as `datIIBA2.m2`, Illumina_Lumi as `lumi_NQ.m`, Nimblegen as `data.matrix_Nimblegen2.m`, Series_Matrix as `data.matrixNorm.m` and Online_Data as `data.matrix_onlineNorm.m`. The outputs are as `.f` to the normalized data. It also generates data with p-value less than 0.01 as statistically significant genes.

Author(s)

Dhammapal Bharne

graph_gsea_goBP

Plots Graph of GO Terms for Biological Process of GSEA

Description

Plots a network graph of GO terms for Biological Process obtained from gene set enrichment analysis.

Details

Function can plot a graph for GO terms obtained from gene set enrichment analysis. It is a network of GO terms of Biological Process as nodes and links as directed lines. It is performed if exists object GOresultBP_Affy for Affymetrix, GOresultBP_Ag1 for Agilent_OneColor, GOresultBP_Ag2 for Agilent_TwoColor, GOresultBP_IL_B for Illumina_Beadarray, GOresultBP_IL_L for Illumina_Lumi, GOresultBP_N for Nimblegen, GOresultBP_S for Series_Matrix and GOresultBP_O for Online procedures.

Author(s)

Dhammapal Bharne

graph_gsea_goCC

Plots Graph of GO Terms for Cellular Component of GSEA

Description

Plots a network graph of GO terms for Cellular Component obtained from gene set enrichment analysis.

Details

Function can plot a graph for GO terms obtained from gene set enrichment analysis. It is a network of GO terms of Cellular Component as nodes and links as directed lines. It is performed if exists object GOresultCC_Affy for Affymetrix, GOresultCC_Ag1 for Agilent_OneColor, GOresultCC_Ag2 for Agilent_TwoColor, GOresultCC_IL_B for Illumina_Beadarray, GOresultCC_IL_L for Illumina_Lumi, GOresultCC_N for Nimblegen, GOresultCC_S for Series_Matrix and GOresultCC_O for Online procedures.

Author(s)

Dhammapal Bharne

`graph_gsea_goMF`*Plots Graph of GO Terms for Molecular Function of GSEA*

Description

Plots a network graph of GO terms for Molecular Function obtained from gene set enrichment analysis.

Details

Function can plot a graph for GO terms obtained from gene set enrichment analysis. It is a network of GO terms of Molecular Function as nodes and links as directed lines. It is performed if exists object `GOresultMF_Affy` for Affymetrix, `GOresultMF_Ag1` for Agilent_OneColor, `GOresultMF_Ag2` for Agilent_TwoColor, `GOresultMF_IL_B` for Illumina_Beadarray, `GOresultMF_IL_L` for Illumina_Lumi, `GOresultMF_N` for Nimblegen, `GOresultMF_S` for Series_Matrix and `GOresultMF_O` for Online procedures.

Author(s)

Dhammapal Bharne

`graph_gsea_kegg`*Plots Graph of Pathways for a KEGG ID from GSEA*

Description

Plots a network graph of KEGG pathways for a KEGG ID obtained from gene set enrichment analysis.

Details

Function can plot a graph of KEGG Pathways for KEGG ID obtained from gene set enrichment analysis. It is a network of genes as nodes and links as directed lines. It is performed if exists object `KEGGresult_Affy` for Affymetrix, `KEGGresult_Ag1` for Agilent_OneColor, `KEGGresult_Ag2` for Agilent_TwoColor, `KEGGresult_IL_B` for Illumina_Beadarray, `KEGGresult_IL_L` for Illumina_Lumi, `KEGGresult_N` for Nimblegen, `KEGGresult_S` for Series_Matrix and `KEGGresult_O` for Online procedures.

Author(s)

Dhammapal Bharne

`graph_gsta_goBP`*Plots Graph of GO Terms for Biological Process of GSTA*

Description

Plots a network graph of GO terms for Biological Process obtained from gene set test analysis.

Details

Function can plot a graph for GO terms obtained from gene set test analysis. It is a network of GO terms of Biological Process as nodes and links as directed lines. It is performed if exists object `GOTable.outBP_Affy` for Affymetrix, `GOTable.outBP_Ag1` for Agilent_OneColor, `GOTable.outBP_Ag2` for Agilent_TwoColor, `GOTable.outBP_IL_B` for Illumina_Beadarray, `GOTable.outBP_IL_L` for Illumina_Lumi, `GOTable.outBP_N` for Nimblegen, `GOTable.outBP_S` for Series_Matrix and `GOTable.outBP_O` for Online procedures.

Author(s)

Dhammapal Bharne

`graph_gsta_goCC`*Plots Graph of GO Terms for Cellular Component of GSTA*

Description

Plots a network graph of GO terms for Cellular Component obtained from gene set test analysis.

Details

Function can plot a graph for GO terms obtained from gene set test analysis. It is a network of GO terms of Cellular Component as nodes and links as directed lines. It is performed if exists object `GOTable.outCC_Affy` for Affymetrix, `GOTable.outCC_Ag1` for Agilent_OneColor, `GOTable.outCC_Ag2` for Agilent_TwoColor, `GOTable.outCC_IL_B` for Illumina_Beadarray, `GOTable.outCC_IL_L` for Illumina_Lumi, `GOTable.outCC_N` for Nimblegen, `GOTable.outCC_S` for Series_Matrix and `GOTable.outCC_O` for Online procedures.

Author(s)

Dhammapal Bharne

`graph_gsta_goMF`*Plots Graph of GO Terms for Molecular Function of GSTA*

Description

Plots a network graph of GO terms for Molecular Function obtained from gene set test analysis.

Details

Function can plot a graph for GO terms obtained from gene set test analysis. It is a network of GO terms of Molecular Function as nodes and links as directed lines. It is performed if exists object `GOTable.outMF_Affy` for Affymetrix, `GOTable.outMF_Ag1` for Agilent_OneColor, `GOTable.outMF_Ag2` for Agilent_TwoColor, `GOTable.outMF_II_B` for Illumina_Beadarray, `GOTable.outMF_II_L` for Illumina_Lumi, `GOTable.outMF_N` for Nimblegen, `GOTable.outMF_S` for Series_Matrix and `GOTable.outMF_O` for Online procedures.

Author(s)

Dhammapal Bharne

`graph_gsta_kegg`*Plots Graph of Pathways for a KEGG ID from GSTA*

Description

Plots a network graph of KEGG pathways for a KEGG ID obtained from gene set test analysis.

Details

Function can plot a graph of KEGG Pathways for KEGG ID obtained from gene set test analysis. It is a network of genes as nodes and links as directed lines. It is performed if exists object `KEGGtable.out_Affy` for Affymetrix, `KEGGtable.out_Ag1` for Agilent_OneColor, `KEGGtable.out_Ag2` for Agilent_TwoColor, `KEGGtable.out_II_B` for Illumina_Beadarray, `KEGGtable.out_II_L` for Illumina_Lumi, `KEGGtable.out_N` for Nimblegen, `KEGGtable.out_S` for Series_Matrix and `KEGGtable.out_O` for Online procedures.

Author(s)

Dhammapal Bharne

gsea_goBP

Gene Set Enrichment Analysis for Biological Process

Description

Performs Gene Set Enrichment Analysis on statistically significant microarray data to obtain GO terms of Biological Process.

Details

Function can perform gene set enrichment analysis of statistical significant microarray data if exists object of Affymetrix, Agilent_OneColor, Agilent_TwoColor, Illumina_Beadarray, Illumina_Lumi, Nimblegen, Series_Matrix and Online as .s data. It needs GEOMETADB.sqlite database file or internet connection. The outputs are GOresultBP_Affy for Affymetrix, GOresultBP_Ag1 for Agilent_OneColor, GOresultBP_Ag2 for Agilent_TwoColor, GOresultBP_IL_B for Illumina_Beadarray, GOresultBP_IL_L for Illumina_Lumi, GOresultBP_N for Nimblegen, GOresultBP_S for Series_Matrix and GOresultBP_O for Online procedures.

Author(s)

Dhammapal Bharne

gsea_goCC

Gene Set Enrichment Analysis for Cellular Component

Description

Performs Gene Set Enrichment Analysis on statistically significant microarray data to obtain GO terms of Cellular Component.

Details

Function can perform gene set enrichment analysis of statistical significant microarray data if exists object of Affymetrix, Agilent_OneColor, Agilent_TwoColor, Illumina_Beadarray, Illumina_Lumi, Nimblegen, Series_Matrix and Online as .s data. It needs GEOMETADB.sqlite database file or internet connection. The outputs are GOresultCC_Affy for Affymetrix, GOresultCC_Ag1 for Agilent_OneColor, GOresultCC_Ag2 for Agilent_TwoColor, GOresultCC_IL_B for Illumina_Beadarray, GOresultCC_IL_L for Illumina_Lumi, GOresultCC_N for Nimblegen, GOresultCC_S for Series_Matrix and GOresultCC_O for Online procedures.

Author(s)

Dhammapal Bharne

gsea_goMF

Gene Set Enrichment Analysis for Molecular Function

Description

Performs Gene Set Enrichment Analysis on statistically significant microarray data to obtain GO terms of Molecular Function.

Details

Function can perform gene set enrichment analysis of statistical significant microarray data if exists object of Affymetrix, Agilent_OneColor, Agilent_TwoColor, Illumina_Beadarray, Illumina_Lumi, Nimblegen, Series_Matrix and Online as .s data. It needs GEOmetadb.sqlite database file or internet connection. The outputs are GOresultMF_Affy for Affymetrix, GOresultMF_Ag1 for Agilent_OneColor, GOresultMF_Ag2 for Agilent_TwoColor, GOresultMF_IL_B for Illumina_Beadarray, GOresultMF_IL_L for Illumina_Lumi, GOresultMF_N for Nimblegen, GOresultMF_S for Series_Matrix and GOresultMF_O for Online procedures.

Author(s)

Dhammapal Bharne

gsea_kegg

Gene Set Enrichment Analysis for KEGG Pathways

Description

Performs Gene Set Enrichment Analysis on statistically significant microarray data to obtain KEGG pathways.

Details

Function can perform gene set enrichment analysis of statistical significant microarray data if exists object of Affymetrix, Agilent_OneColor, Agilent_TwoColor, Illumina_Beadarray, Illumina_Lumi, Nimblegen, Series_Matrix and Online as .s data. It needs GEOmetadb.sqlite database file or internet connection. The outputs are KEGGresult_Affy for Affymetrix, KEGGresult_Ag1 for Agilent_OneColor, KEGGresult_Ag2 for Agilent_TwoColor, KEGGresult_IL_B for Illumina_Beadarray, KEGGresult_IL_L for Illumina_Lumi, KEGGresult_N for Nimblegen, KEGGresult_S for Series_Matrix and KEGGresult_O for Online procedures.

Author(s)

Dhammapal Bharne

gsta_goBP

Gene Set Test Analysis for Biological Process

Description

Performs Gene Set Test Analysis on normalized microarray data to obtain GO terms of Biological Process.

Details

Function can perform gene set test analysis of normalized microarray data if exists object of Affymetrix, Agilent_OneColor, Agilent_TwoColor, Illumina_Beadarray, Illumina_Lumi, Nimblegen, Series_Matrix and Online as .m or m2 data. It needs GEOMETADB.sqlite database file or internet connection. The outputs are GTable.outBP_Affy for Affymetrix, GTable.outBP_Ag1 for Agilent_OneColor, GTable.outBP_Ag2 for Agilent_TwoColor, GTable.outBP_IL_B for Illumina_Beadarray, GTable.outBP_IL_L for Illumina_Lumi, GTable.outBP_N for Nimblegen, GTable.outBP_S for Series_Matrix and GTable.outBP_O for Online procedures.

Author(s)

Dhammapal Bharne

gsta_goCC

Gene Set Test Analysis for Cellular Component

Description

Performs Gene Set Test Analysis on normalized microarray data to obtain GO terms of Cellular Component.

Details

Function can perform gene set test analysis of normalized microarray data if exists object of Affymetrix, Agilent_OneColor, Agilent_TwoColor, Illumina_Beadarray, Illumina_Lumi, Nimblegen, Series_Matrix and Online as .m or m2 data. It needs GEOMETADB.sqlite database file or internet connection. The outputs are GTable.outCC_Affy for Affymetrix, GTable.outCC_Ag1 for Agilent_OneColor, GTable.outCC_Ag2 for Agilent_TwoColor, GTable.outCC_IL_B for Illumina_Beadarray, GTable.outCC_IL_L for Illumina_Lumi, GTable.outCC_N for Nimblegen, GTable.outCC_S for Series_Matrix and GTable.outCC_O for Online procedures.

Author(s)

Dhammapal Bharne

gsta_goMF

Gene Set Test Analysis for Molecular Function

Description

Performs Gene Set Test Analysis on normalized microarray data to obtain GO terms of Molecular Function.

Details

Function can perform gene set test analysis of normalized microarray data if exists object of Affymetrix, Agilent_OneColor, Agilent_TwoColor, Illumina_Beadarray, Illumina_Lumi, Nimblegen, Series_Matrix and Online as .m or m2 data. It needs GEOMETADB.sqlite database file or internet connection. The outputs are GOTable.outMF_Affy for Affymetrix, GOTable.outMF_Ag1 for Agilent_OneColor, GOTable.outMF_Ag2 for Agilent_TwoColor, GOTable.outMF_IL_B for Illumina_Beadarray, GOTable.outMF_IL_L for Illumina_Lumi, GOTable.outMF_N for Nimblegen, GOTable.outMF_S for Series_Matrix and GOTable.outMF_O for Online procedures.

Author(s)

Dhammapal Bharne

gsta_kegg

Gene Set Test Analysis for KEGG Pathways

Description

Performs Gene Set Test Analysis on normalized microarray data to obtain KEGG pathways.

Details

Function can perform gene set test analysis of normalized microarray data if exists object of Affymetrix, Agilent_OneColor, Agilent_TwoColor, Illumina_Beadarray, Illumina_Lumi, Nimblegen, Series_Matrix and Online as .m or m2 data. It needs GEOMETADB.sqlite database file or internet connection. The outputs are KEGGtable.out_Affy for Affymetrix, KEGGtable.out_Ag1 for Agilent_OneColor, KEGGtable.out_Ag2 for Agilent_TwoColor, KEGGtable.out_IL_B for Illumina_Beadarray, KEGGtable.out_IL_L for Illumina_Lumi, KEGGtable.out_N for Nimblegen, KEGGtable.out_S for Series_Matrix and KEGGtable.out_O for Online procedures.

Author(s)

Dhammapal Bharne

`illbead`*Preprocessing and Analysis of Loaded Illumina_Beadarray Data*

Description

Performs pre-processing and analysis of loaded microarray data automatically. It includes normalization, quality check, filtering, statistical significance, differential gene expression, principal component analysis, clustering and classification.

Details

Function performs pre-processing and analysis of loaded Illumina_Beadarray data automatically if exists object of Illumina_Beadarray as `datIllBA`.

Author(s)

Dhammapal Bharne

`illlumi`*Preprocessing and Analysis of Loaded Illumina_Lumi Data*

Description

Performs pre-processing and analysis of loaded microarray data automatically. It includes normalization, quality check, filtering, statistical significance, differential gene expression, principal component analysis, clustering and classification.

Details

Function performs pre-processing and analysis of loaded Illumina_Lumi data automatically if exists object of Illumina_Lumi as `lumi_data`.

Author(s)

Dhammapal Bharne

maGUI

A Graphical User Interface for Microarray Data Analysis and Annotation

Description

Provides a comprehensive graphical user interface for analysis of Affymetrix, Agilent, Illumina, Nimblegen and other microarray data. It can perform miscellaneous tasks such gene set enrichment and test analysis, identifying gene symbols and building co-expression network. It can also estimate sample size for atleast two-fold expression change. Further, it can identify protein-protein associations from two normalized microarray data.

Details

Loading of Affymetrix data requires raw files with .CEL extension, Agilent-OneColor requires raw files with foreground mean signal and background median signal values, Agilent-TwoColor requires raw files with Agilent source, Nimblegen require raw files with .xys or .pair extensions, Illumina Beadarray and Lumi data requires non-normalized files, Series Matrix requires platform file and series matrix file and Online data requires a GSE number. The loaded microarray data can pre-processed and analyzed. Miscellaneous applications such as gene set enrichment analysis, gene set test analysis, annotations and gene symbol can also be performed online or through GEO metadata SQLite database. Other miscellaneous applications include sample size estimation and co-regulation network. Protein-protein associations can also be predicted from two normalized microarray data.

Author(s)

Dhammapal Bharne

Examples

```
maGUI:::maGUI()
```

nimblg

Preprocessing and Analysis of Loaded Nimblegen Data

Description

Performs pre-processing and analysis of loaded microarray data automatically. It includes normalization, quality check, filtering, statistical significance, differential gene expression, principal component analysis, clustering and classification.

Details

Function performs pre-processing and analysis of loaded Nimblegen data automatically if exists object of Nimblegen as data.matrix_Nimblegen.

Author(s)

Dhammapal Bharne

ntwk

*Co-regulated Network for Differentially Expressed Genes***Description**

Builds Co-regulated Network for Differentially Expressed Genes.

Details

Function can build co-regulated network for differentially expressed genes if exists object of Affymetrix data as DE_Affy, Agilent_OneColor as DE_Ag1, Agilent_TwoColor as DE_Ag2, Illumina_Beadarray as DE_Il_B, Illumina_Lumi as DE_Il_L, Nimblegen as DE_N, Series_Matrix as DE_S and On-line_Data as DE_O. It maps differentially expressed genes to corresponding normalized .m or .m2 data, create adjacency matrix and builds the co-regulated newtwork.

Author(s)

Dhammapal Bharne

pca

*Pricipal Component Analysis on Normalized Microarray Data***Description**

Performs Principal Component Analysis on normalized microarray data

Details

Function can perform pricipal component analysis on normalized microarray data if exists object of Affymetrix data as dat2Affy.m, Agilent_OneColor as datAgOne2.m, Agilent_TwoColor as datAgTwo2.m, Illumina_Beadarray as datIllBA2.m2, Illumina_Lumi as lumi_NQ.m, Nimblegen as data.matrix_Nimblegen2.m, Series_Matrix as data.matrixNorm.m and Online_Data as data.matrix_onlineNorm.m. The outputs are pca_Affy for Affymetrix, pca_Ag1 for Agilent_OneColor, pca_Ag2 for Agilent_TwoColor, pca_Il_B for Illumina_Beadarray, pca_Il_L for Illumina_Lumi, pca_N for Nimblegen, pca_S for Series_Matrix and pca_O for Online procedures.

Author(s)

Dhammapal Bharne

ppis

Protein-Protein Interactions Prediction from Microarray Data

Description

Predicts-protein protein interactions from two normalized microarray data

Details

Function can predict protein-protein interactions from two normalized microarray data if exists Affymetrix data as dat2Affy.m, Agilent_OneColor as datAgOne2.m, Agilent_TwoColor as datAgTwo2.m, Illumina_Beadarray as datIllBA2.m2, Illumina_Lumi as lumi_NQ.m, Nimblegen as data.matrix_Nimblegen2.m, Series_Matrix as data.matrixNorm.m and Online_Data as data.matrix_onlineNorm.m. The outputs are protein-protein pairs written to a file.

Author(s)

Dhammapal Bharne

sse

Sample Size Estimation on Normalized Microarray Data

Description

Performs Sample Size Estimation on Normalized Microarray Data

Details

Function can perform estimation of sample size for atleast two-fold expression change, on normalized microarray data if exists object of Affymetrix data as dat2Affy.m, Agilent_OneColor as datAgOne2.m, Agilent_TwoColor as datAgTwo2.m, Illumina_Beadarray as datIllBA2.m2, Illumina_Lumi as lumi_NQ.m, Nimblegen as data.matrix_Nimblegen2.m, Series_Matrix as data.matrixNorm.m and Online_Data as data.matrix_onlineNorm.m. The outputs are size_Affy for Affymetrix, size_Ag1 for Agilent_OneColor, size_Ag2 for Agilent_TwoColor, size_Il_B for Illumina_Beadarray, size_Il_L for Illumina_Lumi, size_N for Nimblegen, size_S for Series_Matrix and size_O for Online procedures.

Author(s)

Dhammapal Bharne

`stat_sign`*Statistical Significance of Filtering Data*

Description

Performs Statistical Significance of Filtering Data.

Details

Function can perform statistical significance test of filtered data if exists object of Affymetrix, Agilent_OneColor, Agilent_TwoColor, Illumina_Beadarray, Illumina_Lumi, Nimblegen, Series_Matrix and Online as .f data. It maps toptable genes with p-value cut of 0.01 to corresponding normalized .m or .m2 data. The output data objects are the substitution of .m or .m2 to .s.

Author(s)

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`symbol`*Mapping of Identifiers of Microarray Data to Genes*

Description

Maps Identifiers of Microarray Data to Genes

Details

Function can perform mapping of genes for identifiers of normalized microarray data if exists object of Affymetrix, Agilent_OneColor, Agilent_TwoColor, Illumina_Beadarray, Illumina_Lumi, Nimblegen, Series_Matrix and Online as .m or .m2 data. It needs GEOMETADB.sqlite database file or internet connection.

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