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**Description**

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

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

Author(s)

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

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

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

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agt\textino\textsuperscript{two}

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

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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_Il_B for Illumina_Beadarray, Clas_Il_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 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 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_Il_B and sample.clust_Il_B for Illumina_Beadarray, sample.dist_Il_L and sample.clust_Il_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 datILLBA2.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_Il_B for Illumina_Beadarray, DE_Il_L for Illumina_Lumi, DE_N for Nimblegen, DE_S for Series_Matrix and DE_O for Online procedures.

Author(s)

Dhammapal Bharne
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

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.datIIlBA2.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

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**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 datIIlBA2.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

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**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

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**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

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

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_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.

Dhammapal Bharne

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

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_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.

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

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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 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

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**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 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
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

illumi  
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
Description

Provides a comprehensive graphical user interface for analysis of Affymetrix, Agilent, Illumina, Nimblegen and other microarray data. It can perform miscellaneous tasks such as gene set enrichment and test analysis, identifying gene symbols and building co-expression network. It can also estimate sample size for at least 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 Online_Data as DE_O. It maps differentially expressed genes to corresponding normalized .m or .m2 data, create adjacency matrix and builds the co-regulated network.

Author(s)
Dhammapal Bharne

pca
Principal Component Analysis on Normalized Microarray Data

Description
Performs Principal Component Analysis on normalized microarray data

Details
Function can perform principal 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 datIlIBA2.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
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

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 at least 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)**

Dhammapal Bharne

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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.

**Author(s)**

Dhammapal Bharne
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