Package 'RNAinteractMAPK'

October 18, 2017

Type Package

Title Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi

Version 1.14.0

Author Bernd Fischer <b.fischer@dkfz.de>

Maintainer Bernd Fischer <b.fischer@dkfz.de>

Description
This package includes all data used in the paper -Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi- by Horn, Sandmann, Fischer et al.., Nat. Methods, 2011. The package vignette shows the R code to reproduce all figures in the paper.

License Artistic-2.0

LazyLoad yes

Imports grid, gdata, MASS, genefilter

Depends R (>= 2.12.0), methods, fields, sparseLDA, RNAinteract

Suggests qvalue, lattice

biocViews ExperimentData, MicrotitrePlateAssayData, Drosophila_melanogaster_Data, CellCulture

NeedsCompilation no

R topics documented:

RNAinteractMAPK-package *Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi.*

Description

The package contains the data and the source code to reproduce the results and figures from the paper

T. Horn, T. Sandmann, B. Fischer, W. Huber, M. Boutros. Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi. Nature Methods, 2011.

Details

See vignette("RNAinteractMAPK") for details.

Package content

See vignette("RNAinteractMAPK") for more detail on how to obtain the data used for specific figures. In addition this vignette contains the complete analysis and the generation of all figures.

The main screen can be loaded by `data("Dmel2PPMAPK", package="RNAinteractMAPK")`. Access to the pairwise interaction data is done via the `getData` function from the `RNAinteract`-package. See example below.

The following datasets are provided with this package:

`Dmel2PPMAPK`	interaction data of main screen. See example below.
`ElpB1phenotype`	in vivo experiment on ectopic wing vein formation (used in Figure 5f)
`mRNAdoubleKDefficiency`	mRNA level after double gene knockdown (used in Figure S1)
`mRNAsingleKDefficiency`	mRNA level after single gene knockdown (used in Figure S2)
`singleKDphenotype`	single knockdown phenotypes (used in Figure S3)
`dsRNAiDilutionSeries`	dsRNA dilution series (used in Figure S5)
`Networks`	known interactions from DroID (used in Figure S12)
`pathwayMembership`	pathway membership of genes (used in Figure S13)
`PhysicalInteractions`	Known physical interactions (used in Figure S13)
`cellTiterGlo`	cellTiterGlo viability data (used in Figure S15)

Within this package a number of specialized functions is defined written for the analysis of the MAPK interaction screen and additional experiments shown in the paper. These functions are not intended to be general purpose analysis functions, but should document the steps of analysis of the paper. Therefore, these functions are not exported. A list of functions is given below. A general purpose package for the analysis of genetic interaction screens is the package `RNAinteract`.

The following functions are provided within this package.

Functions used for the classification: `MAPK.predict.classification`, `MAPK.cv.classifier`, `MAPK.getCV`, `MAPK.ternary.plot`, `MAPK.getXY`, `MAPK.plot.classification`.

Functions for the analysis of the interaction surfaces: `MAPK.plot.TPS.single`, `MAPK.plot.TPS.all`, `MAPK.estimate.TPS`, `MAPK.cv.TPS`, `MAPK.screen.as.array`.

A function to write the hit list: `MAPK.report.gene.lists.paper`.

A function to plot a heatmap: `MAPK.plot.heatmap.raster`.

A function to plot smaooth scatters: `MAPK.smooth.scatter`.

Author(s)

Bernd Fischer

Maintainer: Bernd Fischer <bernd.fischer@embl.de>

References

T. Horn, T. Sandmann, B. Fischer, W. Huber, M. Boutros. Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi. Nature Methods, 2011.

See Also

`RNAinteractMAPK-package`

Examples

```
data(Dmel2PPMAPK)
Dmel2PPMAPK

# Obtain the pairwise interaction matrix
PI <- getData(Dmel2PPMAPK, type="pi", format="targetMatrix", screen="mean", withoutgroups = c("pos", "neg"))
```

---

cellTiterGlo *Comparison of interaction experiment with an cellTiterGlo viability assay*

Description

For ten gene pairs genetic interactions are measured. The experiment contains 24 different conditions. These are repeated in each row of the three 384 mutli well plates. The data.frame contains the plate annotation as well as the viability readout for the three plates.

Usage

```
data(cellTiterGlo)
```

Format

A data frame with 384 observations on the following 6 variables.

`Well` a character vector

`dsRNA_1` a character vector

`dsRNA_2` a character vector

`plate1` a numeric vector

`plate2` a numeric vector

`plate3` a numeric vector

Source

Horn, Sandmann, Fischer, Huber, Boutros, Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi, Nature Methods, 2011, Figure S15.

Examples

```
data(cellTiterGlo)
head(cellTiterGlo)
```

Dmel2PPMAPK *The interaction data of the main screen*

Description

Dmel2PPMAPK is an object of class RNAinteract. It contains the raw data, the computed main effects, pairwise interaction scores, p-values and q-values computed by a t-test. The package vignette vontains the complete code and documentation for the statistical analysis.

Usage

```
data(Dmel2PPMAPK)
```

Format

An object of class RNAinteract.

Source

Horn, Sandmann, Fischer, Huber, Boutros, Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi, Nature Methods, 2011, main interaction screen.

Examples

```
data(Dmel2PPMAPK)
Dmel2PPMAPK

# Obtain the pairwise interaction matrix
PI <- getData(Dmel2PPMAPK, type="pi", format="targetMatrix", screen="mean", withoutgroups = c("pos", "neg"))
```

dsRNAiDilutionSeries *dsRNA dilution series*

Description

A dilution series for 6 x 6 gene. For each gene pair all combinations of 8 different concentrations of dsRNA reagent are screened. Three readout channels (nrCells, area, intensity) are available in the data.frame dsRNAiDilutionSeries. The plate annotation is given in the data.frame dsRNAiDilutionSeriesAnno and precomputed degrees of freedom for thin plate splines are available in the matrix dsRNAiDilutionSeriesDF.

Usage

```
data(dsRNAiDilutionSeries)
```

Format

- dsRNAiDilutionSeries: A data frame with 2688 observations on the following 3 variables.

  nrCells a numeric vector representing the number of cells readout.

  area a numeric vector representing the are readout.

  intensity a numeric vector representing the intensity readout.

- dsRNAiDilutionSeriesAnno: A data frame with 2688 observations on the following 7 variables.

  plate a numeric vector representing the plate number.

  well a numeric vector representing the well.

  row a numeric vector representing the row on plate.

  col a numeric vector representing the column on plate.

  targetID1 a numeric vector representing the target number of the first reagent (see targets).

  targetID2 a numeric vector representing the target number of the second reagent (see targets).

  targets a data.frame representing the 49 target reagents For each target reagent the gene name and the dsRNAi concentration is given.

- dsRNAiDilutionSeriesDF: A 6 x 6 matrix with degrees of freedom for thin-plate spline regression.

Source

Horn, Sandmann, Fischer, Huber, Boutros, Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi, Nature Methods, 2011, Figure 1abc and Figure S5.

Examples

```
data(dsRNAiDilutionSeries)
head(dsRNAiDilutionSeries)
head(dsRNAiDilutionSeriesAnno)
head(dsRNAiDilutionSeriesDF)
```

ElpB1phenotype *Ectopic wing vein formation phenotype caused by the EgfrElpB1.*

Description

Partial suppression of ectopic wing vein formation (in vivo fly phenotpye) caused by the EgfrElpB1 in Cka heterozygous mutant backgrounds. The wing vein formation phenotype is classified as strong and notstrong. It is tested for three fly mutants.

Usage

```
data(ElpB1phenotype)
```

Format

A data frame with 3 observations on the following 2 variables.

`strong` a numeric vector

`notstrong` a numeric vector

Source

Horn, Sandmann, Fischer, Huber, Boutros, Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi, Nature Methods, 2011, Figure 5f.

Examples

```
data(ElpB1phenotype)
ElpB1phenotype
```

MAPK.cv.classifier *A classifier for genetic interaction data.*

Description

These functions implement a classifier to classify three classes of pathway membership of the RasMAPK and JNK pathway. For each sample and each channel a sparse linear discriminat classifier is trained. The posterior probabilities are averaged over all single classifiers. The classification posterior probabilities of three classes are plotted as a ternary plot (ternary plot adapted from CRAN package vcd).

Usage

```
MAPK.cv.classifier(sgi, traingroups)
MAPK.predict.classification(sgi, traingroups)
MAPK.plot.classification(posterior,
                         classes = NULL, classnames = NULL,
         col = "darkgray", y = NULL,
                         classcol = NULL,
         main = "predicted classification probabilities",
                         pop = TRUE, threshText = 0.3,
 textToLeft = NULL, textToRight = NULL)
```

Arguments

sgi	An object of class RNAinteract
traingroups	A list of gene names for the training examples. For each class there should be a vector of gene names.
posterior	A matrix of posterior probabilities. Each row represents one gene, each column represents one class.
classes	The three classes to be displayed on the ternary plot.
classnames	The class names to be displayed.
col	The color used for the text labels.
y	A factor representing the class label for each gene in posterior.
classcol	The color used for the three classes.
main	The title of the plot.
pop	If TRUE, all viewports are popped before finishing the function.
threshText	A threshold for the posterior probability of the three classes. Only genes that are assigned with a larger probability to the three classes are shown.
textToLeft	These text labels will be shown on the left hand side.
textToRight	These text labels will be shown on the right hand side.

Details

The code for the ternary plot (used by MAPK.plot.classification) is adapted from the function ternaryplot in the CRAN package vcd Author of the original code is David Meyer (David.Meyer@R-project.org). References: M. Friendly (2000), Visualizing Categorical Data. SAS Institute, Cary, NC. This code is specialized for the publication "Mapping Signalling Networks by RNAi ..." in Nat. Methods. It is highly recommended to use the original code by David Meyer.

Value

MAPK.cv.classifier returns a list with the cross validated class assignment probability, as well as the results of the single classifiers.

MAPK.predict.classifier returns the predicted posterior probabilities of new genes as well as the classification results of the single classifier.

MAPK.plot.classifier returns nothing.

Author(s)

Bernd Fischer

References

function ternaryplot, CRAN package vdc. M. Friendly (2000), Visualizing Categorical Data. SAS Institute, Cary, NC.

See Also

RNAinteract, RNAinteractMAPK

MAPK.estimate.TPS *genetic interaction surfaces*

Description

Genetic interaction surfaces are estimated from a dilution experiment. Cells are treated with two RNAi's. The concentration of the RNAi reagent is changed in 8 steps. All 8 x 8 combinations of concentrations are tested for 6 x 6 gene pairs.

Usage

```
MAPK.screen.as.array(data, Anno)
MAPK.estimate.TPS   (A, DF, n.out = 8, channel = 1)
MAPK.cv.TPS         (A, range.df = 6:56, channel = 1)
MAPK.plot.TPS.all   (TPSmodel, range = c(-6, 6), fill = c("cornflowerblue",
                     "cornflowerblue", "black", "#777700", "yellow"),
     channel = 1)
MAPK.plot.TPS.single(gene1, gene2, TPSmodel, range = c(-6, 6),
                      fill = c("cornflowerblue", "cornflowerblue", "black",
     "#777700", "yellow"), channel = 1)
```

Arguments

data, Anno	
	A data.frame containing the read.out of the dilution screen. Each row is one well. Each column one feature.
Anno	A data.frame containing the plate configuration. For each row in data there should a row in Anno.
A	An array of dimension concentration x concentration x genes x genes x channel as returned by MAPK.screen.as.array.
DF	A 6 x 6 matrix of degrees of freedom for the thin spline plate regression.
n.out	number of points for sampling from the regression function.
channel	The channel used.
range.df	The range of degrees of freedom that is considered for cross validation.
range	The range of pairwise interaction scores that is shown by the colorbar.
gene1, gene2	The genes for which the interaction surface is plotted.
TPSmodel	The TPS model estimated by MAPK.estimate.TPS
fill	The range of colors used for the color code.

Details

The screen readout can be reshaped as an array with dimensions concentration x concentration x genes x genes x channel by the function MAPK.screen.as.array. Then the function MAPK.estimate.TPS fits a regression in the 8 x 8 pairwise dilution series. The degrees of freedom for the regression can be estimated automatically by cross validation with the function MAPK.cv.TPS. Finally one can plot the interaction surface for a single gene or an overview of interaction surfaces for all genes with the functions MAPK.plot.TPS.single or MAPK.plot.TPS.all.

Value

- `MAPK.screen.as.array` returns an array of dimensions concentration x concentration x genes x genes x channel with the screen data.
- `MAPK.estimate.TPS` returns a regression model estimated by thin plate splines for each pair of genes and subsampled matrices.
- `MAPK.cv.TPS.all` returns
  - `DF` a matrix with degrees of freedom.
  - `CVerror` The prediction error estimated by cross validation.
  - `CVerrorSD` The standard deviation of the prediction error estimated by cross validation.
- `MAPK.plot.TPS.single`,`MAPK.plot.TPS.all`: An object of class "trellis". See `levelplot` for details.

Author(s)

Bernd Fischer

See Also

`RNAinteract-package`, `RNAinteractMAPK-package`

`MAPK.plot.heatmap.raster`

Plots a heatmap using grid.raster

Description

This functions provides a grid plot that displays the raster image of a heatmap without any axis or label. This function is adapted from the function `grid.sgiHeatmap` from the package `RNAinteract-package`. It is highly recommended to use the original function `grid.sgiHeatmap`.

Usage

```
MAPK.plot.heatmap.raster(X, subset = NULL,
                         hc.row = NULL, hc.col = NULL,
                         pi.max = NULL)
```

Arguments

`X`	A matrix of pairwise interaction scores.
`subset`	A subset of genes that are displayed in the rows.
`hc.row`	A hclust object.
`hc.col`	A hclust object.
`pi.max`	The maximum interaction score of the colorbar. All interaction scores larger than this value will be displayed in the same color.

Value

Nothing is returned.

Author(s)

Bernd Fischer

See Also

RNAinteract-package, RNAinteractMAPK-package

`MAPK.report.gene.lists.paper` *A hitlist report.*

Description

Reports the hitlist of genetic interactions, with p-values from a t-test with pooled variance estimate, from limma, and from Hotelling T^2 test.

Usage

```
MAPK.report.gene.lists.paper(sgi, sgilimma, sgi3T2, screen = "mean")
```

Arguments

`sgi`	An object of class `RNAinteract` containing p-values from a t-test with pooled variance estimate.
`sgilimma`	An object of class `RNAinteract` containing p-values from limma.
`sgi3T2`	An object of class `RNAinteract` containing p-values from a Hotelling T^2 test.
`screen`	The screen name for which the report should be written.

Details

Writes tab-separated lists for each single test as well as a joint table with all three tests.

Value

Nothing is returned.

Author(s)

Bernd Fischer

See Also

RNAinteract-package, RNAinteractMAPK-package

MAPK.smooth.scatter *smooth scatter using grid raster*

Description

This function is a reimplementation of smoothScatter. For nicer graphics output the background image is written by grid.raster. It is recommended to use the smoothScatter function from the graphics package.

Usage

```
MAPK.smooth.scatter(x, y, n = 75,
                    nrpoints = 100, col = "blue",
    pch = 20, size = unit(0.3, "char"), cex = 1.2,
   colramp = colorRampPalette(c("white", "blue", "green", "yellow", "red"))(256),
    xlab = "", ylab = "", respect = FALSE)
```

Arguments

x	x-values.
y	y-values. Has to be the same length as x.
n	nr of bins used for the kernel density estimation.
nrpoints	nrpoints points in the lowest density region will be plotted. This allows the identification of outliers.
col	color of points.
pch	symbol to plot points.
size	The size of the points.
cex	The size of the label text.
colramp	color ramp for the density plot.
xlab,ylab	axis labels.
respect	A logical value indicating if the height and width of the axis scales should respect each other.

Details

Plots a density plot with grid graphics.

Author(s)

Bernd Fischer

See Also

RNAinteractMAPK-package, smoothScatter

mRNAdoubleKDefficiency

mRNA levels for double knock downs

Description

qPCR measurements for the mRNA level after a double gene knock down (ratio relative to wild type control). The experiments tests the knock down efficiency in the presence of a second gene knock down.

Usage

```
data(mRNAdoubleKDefficiency)
```

Format

A data frame with 320 observations on the following 5 variables.

`template` an ordered factor with levels `Fluc` < `CG10417` < `CG13197` < `CG9391` < `egr` < `lic` < `PRL-1` < `Rho1` < `Tak1`

`query` a factor with levels `CG10417 [query dsRNA]` `CG13197 [query dsRNA]` `CG9391 [query dsRNA]` `egr [query dsRNA]` `lic [query dsRNA]` `PRL-1 [query dsRNA]` `Rho1 [query dsRNA]` `Tak1 [query dsRNA]`

`qPCR.target` a factor with levels `CG10417` `CG13197` `CG9391` `egr` `lic` `PRL-1` `Rho1` `Tak1`

`passage` a factor with levels `passage 4` `passage 42`

`RNAi` a numeric vector

Source

Horn, Sandmann, Fischer, Huber, Boutros, Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi, Nature Methods, 2011, Figure S2.

Examples

```
data(mRNAdoubleKDefficiency)
head(mRNAdoubleKDefficiency)
```

mRNAsingleKDefficiency

mRNA levels for single gene knock downs

Description

qPCR measurements for the mRNA level after a single gene knock down (ratio relative to wild type control). The experiments is done for two independent designs of RNAi reagents.

Usage

```
data(mRNAsingleKDefficiency)
```

Format

A data frame with 89 observations on the following 5 variables.

`Symbol` a character vector

`MeanDesign1` a numeric vector

`StderrDesign1` a numeric vector

`MeanDesign2` a numeric vector

`StderrDesign2` a numeric vector

Source

Horn, Sandmann, Fischer, Huber, Boutros, Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi, Nature Methods, 2011, Figure S1.

Examples

```
data(mRNAsingleKDefficiency)
head(mRNAsingleKDefficiency)
```

`Networks` *Knock interaction networks*

Description

This dataset is a subset of the DroID database. It contains the known (genetic) interactions between the genes regarded in the main screen.

Usage

```
data(Networks)
```

Format

A data frame with 402 observations on the following 5 variables.

`gene1` a character vector

`gene2` a character vector

`correlation` a numeric vector

`genetic` a numeric vector

`human` a numeric vector

Source

Data as used in Horn, Sandmann, Fischer, Huber, Boutros, Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi, Nature Methods, 2011, Figure S12.

The data is a subset from the drosophila interactions database (DroID), http://www.droidb.org, Data version 2010_10 updated 20 October 2010.

Murali T, Pacifico S, Yu J, Guest S, Roberts GG 3rd, Finley RL Jr . DroID 2011: a comprehensive, integrated resource for protein, transcription factor, RNA and gene interactions for Drosophila. Nucleic Acids Res. 2010 Oct 29.

Examples

```
data(Networks)
head(Networks)
```

`pathwayMembership` *Pathway membership of genes.*

Description

The membership of the tested genes in the four pathways JAK/STAT, RasMAPK, JNK, and p38.

Usage

```
data(pathwayMembership)
```

Format

The format is: chr "pathwayMembership"

Source

Horn, Sandmann, Fischer, Huber, Boutros, Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi, Nature Methods, 2011, Figure S13.

Examples

```
data(pathwayMembership)
head(pathwayMembership)
```

`PhysicalInteractions` *Known physical interactions*

Description

This dataset contains a collection of known physical interactions assembled from the literature. It contains the known pathway structure of the RasMAPK and the JNK pathway.

Usage

```
data(PhysicalInteractions)
```

Format

A data frame with 29 observations on the following 2 variables.

`V1` a character vector

`V2` a character vector

Source

Horn, Sandmann, Fischer, Huber, Boutros, Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi, Nature Methods, 2011, Figure S13.

Examples

```
data(PhysicalInteractions)
head(PhysicalInteractions)
```

`singleKDphenotype` *Single knockdown phenotype*

Description

This data.frame `singleKDphenotype` contains a screen assessing the single knock down phenotypes (nrCells, intensity, and area) of the tested genes. `singleKDphenotypeAnno` is a data.frame describing the plate annotation.

Usage

```
data(singleKDphenotype)
```

Format

The format is: chr "singleKDphenotype" chr "singleKDphenotypeAnno"

Source

Horn, Sandmann, Fischer, Huber, Boutros, Mapping of Signalling Networks through Synthetic Genetic Interaction Analysis by RNAi, Nature Methods, 2011, Figure S3.

Examples

```
data(singleKDphenotype)
head(singleKDphenotype)
head(singleKDphenotypeAnno)
```

Index