DTA

March 24, 2012

`DTA-package` *Dynamic Transcriptome Analysis*

Description

The `DTA` package implements all methods of the quantitative kinetic modeling approach belonging to DTA (Dynamic Transcriptome Analysis) to estimate mRNA synthesis and decay rates from individual time point measurements.

Author(s)

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References

C. Miller, B. Schwalb, K. Maier, D. Schulz, S. Duemcke, B. Zacher, A. Mayer, J. Sydow, L. Marcinowski, L. Dolken, D. E. Martin, A. Tresch, and P. Cramer. Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Mol Syst Biol, 7:458, 2011.

Examples

```
## see vignette
```

`DTA.dynamic.estimate`
Estimation of synthesis and decay rates upon perturbation

Description

DTA.dynamic.estimate uses an experiment, given by a phenotype matrix, data matrix and the number of uridines for each gene to estimate synthesis and decay rate of the genes.

Usage

```
DTA.dynamic.estimate(phenomat = NULL,datamat = NULL,tnumber = NULL,ccl = NULL,mR
```

Arguments

phenomat	A phenotype matrix, containing the design of the experiment as produced by DTA.phenomat. Columns are name, fraction (U=unlabebeld, L=labeled, T=total), time and nr (=replicate number). Rows represent individual experiments.
datamat	A matrix, containing the measurements from U, L and T, according to the design given in phenomat. Matrix should only contain the rows of phenomat as columns.
tnumber	Integer vector, containing the numbers of uridines. Elements should have the rownames of datamat.
ccl	The cell cycle length of the cells.
mRNAs	Estimated number of mRNAs in a cell (optional).
reliable	Vector of 'reliable' genes, which are used for parameter estimation.
mediancenter	Should the quotient Labeled/Total resp. Unlabeled/Total be rescaled to a common median over it's replicates before building the genewise median.
usefractions	From which fractions should the decay rate be calculated: "LandT", "UandT" or "both".
LtoTratio	Coefficient to rescale Labeled/Total. Is estimated from the data, if not specified. See ratiomethod.
ratiomethod	Choose the regression method to be used, possible methods are: "tls", "bias" and "lm". For details, see the vignette.
largest	Percentage of largest residues from the first regression not to be used in the second regression step. For details, see the vignette.
weighted	Should the regression be weighted with 1/(Total^2 + median(Total))?
relevant	Choose the arrays to be used for halflives calculation, vector due to nr (=replicate number) in phenomat.
check	If check=TRUE, control messages and plots will be generated.
regression	Should the regression results be plotted?
labeling	Should the labeling bias be plotted?
correctedlabeling	Should the corrected labeling bias be plotted?
rankpairs	Should the ranks of decayrates be compared in pairs be plotted (based on Labeled/Total)?
assessment	Should 1-L/T, U/T or (1-L/T+U/T)/2 be assessed due to limitations of the decay rate formula?
correlation	Should the correlation of half-lives, decay rates and synthesis rates vs Total, Labeled and the number of uridines be plotted as color-coded squares?
error	Should the standard deviations and coefficients of variation be calculated?
bicor	Should the labeling bias be corrected?
condition	String, to be added to the plotnames.
upper	Upper bound for labeling bias estimation. For details, see the vignette.
lower	Lower bound for labeling bias estimation. For details, see the vignette.
plots	If plots=TRUE, control plots will be saved.
folder	Path to the folder, where to save the plots.

addformat	Additional fileformat for plots to be saved. See plotit function (LSD package).
totaloverwt	Will be available in the very near future for comparative DTA data.
folds	should the dr vs sr folds be plotted
folds.lims	limits of the folds plot
clusters	should the dr vs sr folds be plotted with clusters, choose 'sr', 'dr' for cluster selection or 'none' to omit it
ranktime	at which time should the rankgain be calculated, default is the last column
upperquant	upper quantile for cluster selection
lowerquant	lower quantile for cluster selection
notinR	Should plots be not plotted in R.
simulation	True, if data was generated by DTA.generate.
sim.object	Simulation object created by DTA.generate.

Value

DTA.dynamic.estimate returns a list, where each entry contains the estimation results for all replicates of one timecourse timepoint. Each result contains the following entries

triples	Mapping of each fraction and experiment to its corresponding column in the data matrix.
plabel	The labeling efficiency. For details, see the vignette.
LtoTratio	Estimated ratio of labeled to total fraction.
UtoTratio	Estimated ratio of unlabeled to total fraction.
LtoUratio	Estimated ratio of labeled to unlabeled fraction.
correcteddatamat	Labeling bias corrected data matrix.
drmat	Decay rates for each replicate. The last column gives the median decay rates.
hlmat	Half-lives for each replicate. The last column gives the median half-lifes.
dr	Median decay rates. The last column of drmat.
hl	Median half-lives. The last column of hlmat.
dr.sd	Standard deviations of decay rates.
dr.cv	Coefficients of variation of decay rates.
hl.sd	Standard deviations of half-lives.
hl.cv	Coefficients of variation of half-lives.
TEmat	Total expression for each replicate. The last column gives the median total expression values.
TE	Median total expression values. The last column of TEmat.
TE.sd	Standard deviations of total expression values.
TE.cv	Coefficients of variation of total expression values.
LEmat	Labeled expression for each replicate. The last column gives the median labeled expression values.
LE	Median labeled expression values. The last column of LEmat.
LE.sd	Standard deviations of labeled expression values.

LE.cv	Coefficients of variation of labeled expression values.
UEmat	Unlabeled expression for each replicate. The last column gives the median unlabeled expression values. (Only if unlabeled values exist in the experiment)
UE	Median unlabeled expression values. The last column of UEmat. (Only if unlabeled values exist in the experiment)
UE.sd	Standard deviations of unlabeled expression values.
UE.cv	Coefficients of variation of unlabeled expression values.
srmat	Synthesis rates for each replicate. The last column gives the median synthesis rates.
sr	Median synthesis rates. The last column of srmat.
sr.sd	Standard deviations of synthesis rates.
sr.cv	Coefficients of variation of synthesis rates.
LTmat	Labeled to total ratio for each replicate. The last column gives the median labeled to total ratios.
LT	Median labeled to total ratios. The last column of LTmat.
UTmat	Unlabeled to total ratio for each replicate. The last column gives the median unlabeled to total ratios.
UT	Median unlabeled to total ratios. The last column of UTmat.
Rsrmat	Rescaled synthesis rates for each replicate, if parameter mRNAs is specified. The last column gives the median synthesis rates.
Rsr	Rescaled median synthesis rates. The last column of Rsrmat.
globaldrmat	Decay rate for each replicate. Reciprocally weighted by the total expression. Last element contains (weighted) median decay rate.
globaldr	(Weighted) median decay rate.

Author(s)

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References

C. Miller, B. Schwalb, K. Maier, D. Schulz, S. Duemcke, B. Zacher, A. Mayer, J. Sydow, L. Marcinowski, L. Dolken, D. E. Martin, A. Tresch, and P. Cramer. Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Mol Syst Biol, 7:458, 2011.

See Also

heatscatter, plotit, tls

Examples

```
dataPath = system.file("data", package="DTA")
load(file.path(dataPath, "tDTAdatamat.RData"))
load(file.path(dataPath, "tDTAphenomat.RData"))
load(file.path(dataPath, "tDTAtnumber.RData"))
load(file.path(dataPath, "tDTAreliable.RData"))

res = DTA.dynamic.estimate(tDTAphenomat,tDTAdatamat,tDTAtnumber,ccl = 150,mRNAs = 60000,r

dev.off()
```

DTA.dynamic.generate

Simulation of DTA experiments upon perturbation

Description

DTA.dynamic.generate produces the phenotype matrix and the matrix containing the simulated data according to the given parameters.

Usage

```
DTA.dynamic.generate(duration = 60,lab.duration = 6,tnumber = NULL,plabel = NULL
```

Arguments

duration	duration of the whole time course (min)
lab.duration	labeling duration for single experiments (min)
tnumber	Integer vector containing the number of uridine residues for each gene. If NULL, tnumber is sampled from an F-distribution within the function.
plabel	The labeling efficiency. If NULL, plabel is set to 0.005 within the function. For details, see the vignette.
nrgenes	The number of genes the simulated experiment will have (will be cropped if it exceeds the length of tnumber).
mediantime.halflives	the median of the half life distribution
mediantime.synthesisrates	the median of the synthesis rates distribution (counts/cell/cellcycle)
n	the number of cells N(0)
ccl	The cell cycle length (in minutes).
check	if check=TRUE, control messages will be generated
plots	if plots = TRUE, control plots will be plotted
save.plots	if save.plots = TRUE, control plots will be saved
folder	folder, where to save the plots
condition	to be added to the plotnames
addformat	additional fileformat for plots to be saved
sdnoise	The amount of measurement noise (proportional to expression strength).
nobias	Should a labeling bias be added?
unspecific.LtoU	Proportion of labeled RNAs that unspecifically end up in the unlabeled fraction.
unspec.LtoU.weighted	Should unspecific proportion of labeled to unlabeled depend linearly on the length of the RNA?
unspecific.UtoL	Proportion of unlabeled RNAs that unspecifically end up in the labeled fraction.

`unspec.UtoL.weighted`
: Should unspecific proportion of unlabeled to labeled depend linearly on the length of the RNA?

`mu.values.mat`
: if the data should be generated using given synthesis rates, this matrix must contain the respective values for each gene

`mu.breaks.mat`
: timepoints of synthesis rate changes, this matrix must contain the respective values for each gene, only needed when mu.values.mat is given (one column less than mu.values.mat)

`lambda.values.mat`
: if the data should be generated using given decay rates, this matrix must contain the respective values for each gene

`lambda.breaks.mat`
: timepoints of decay rate changes, this matrix must contain the respective values for each gene, only needed when lambda.values.mat is given (one column less than lambda.values.mat)

`truehalflives`
: If the data should be generated using a given half-life distribution, this vector must contain the respective values for each gene.

`truesynthesisrates`
: If the data should be generated using a given synthesis rates distribution, this vector must contain the respective values for each gene

`genenames`
: An optional list of gene names.

Value

DTA.dynamic.generate returns a list, containing the following entries

`phenomat`
: A matrix, containing the design of the experiment as produced by `DTA.phenomat`.

`datamat`
: A matrix, containing the simulated measurements from U, L and T, according to the design given in phenomat.

`tnumber`
: Integer vector containing the number of uridine residues for each gene.

`ccl`
: The cell cycle length (in minutes).

`truemus`
: A vector, containing the true synthesis rates.

`truemusaveraged`
: A vector, containing the true synthesis rates, averaged over the labeling period.

`truelambdas`
: A vector, containing the true decay rates.

`truelambdasaveraged`
: A vector, containing the true decay rates, averaged over the labeling period.

`truehalflives`
: A vector, containing the true half-lives.

`truehalflivesaveraged`
: A vector, containing the true half-lives, averaged over the labeling period.

`trueplabel`
: The true labeling efficiency. For details, see the vignette.

`truecomplete`
: A vector, containing the true amount of total RNA.

`truelambdas`
: A vector, containing the true decay rates.

`truemus`
: A vector, containing the true synthesis rates.

`truehalflives`
: A vector, containing the true half-lives.

`trueplabel`
: The true labeling efficiency. For details, see the vignette.

`truear`
: The true parameter ar. For details, see the vignette.

`truebr`
: The true parameter br. For details, see the vignette.

`truecr`
: The true parameter cr. For details, see the vignette.

`truecrbyar`
: The true parameter cr/ar. For details, see the vignette.

`truecrbybr`
: The true parameter cr/br. For details, see the vignette.

`truebrbyar`
: The true parameter br/ar. For details, see the vignette.

`trueLasymptote`
: The true parameter asymptote (labeled bias). For details, see the vignette.

`trueUasymptote`
: The true parameter asymptote (unlabeled bias). For details, see the vignette.

Author(s)

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References

C. Miller, B. Schwalb, K. Maier, D. Schulz, S. Duemcke, B. Zacher, A. Mayer, J. Sydow, L. Marcinowski, L. Dolken, D. E. Martin, A. Tresch, and P. Cramer. Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Mol Syst Biol, 7:458, 2011.

Examples

```
nrgenes = 1000
truesynthesisrates = rf(nrgenes,5,5)*18
steady = rep(1,nrgenes)
shock = 1/pmax(rnorm(nrgenes,mean = 8,sd = 4),1)
induction = pmax(rnorm(nrgenes,mean = 8,sd = 4),1)
changes.mat = cbind(steady,shock,shock*induction)
mu.values.mat = changes.mat*truesynthesisrates
mu.breaks.mat = cbind(rep(12,nrgenes),rep(18,nrgenes))
truehalflives = rf(nrgenes,15,15)*12
truelambdas = log(2)/truehalflives
changes.mat = cbind(steady,shock,shock*induction,steady)
lambda.values.mat = changes.mat*truelambdas
lambda.breaks.mat = cbind(rep(12,nrgenes),rep(18,nrgenes),rep(27,nrgenes))

# it takes 2 min to build sim.object

sim.object = DTA.dynamic.generate(duration = 36,lab.duration = 6,nrgenes = nrgenes,mu.val

res = DTA.dynamic.estimate(simulation = TRUE,sim.object = sim.object,labeling = FALSE,ran

dev.off()
```

DTA.estimate *Estimation of synthesis and decay rates*

Description

DTA.estimate uses an experiment, given by a phenotype matrix, data matrix and the number of uridines for each gene to estimate synthesis and decay rate of the genes.

Usage

```
DTA.estimate(phenomat = NULL, datamat = NULL, tnumber = NULL, ccl = NULL, mRNAs
```

Arguments

phenomat	A phenotype matrix, containing the design of the experiment as produced by DTA.phenomat. Columns are name, fraction (U=unlabebeld, L=labeled, T=total), time and nr (=replicate number). Rows represent individual experiments.
datamat	A matrix, containing the measurements from U, L and T, according to the design given in phenomat. Matrix should only contain the rows of phenomat as columns.
tnumber	Integer vector, containing the numbers of uridines. Elements should have the rownames of datamat.
ccl	The cell cycle length of the cells.
mRNAs	Estimated number of mRNAs in a cell (optional).
reliable	Vector of 'reliable' genes, which are used for parameter estimation.
mediancenter	Should the quotient Labeled/Total resp. Unlabeled/Total be rescaled to a common median over it's replicates before building the genewise median.
usefractions	From which fractions should the decay rate be calculated: "LandT", "UandT" or "both".
LtoTratio	Coefficient to rescale Labeled/Total. Is estimated from the data, if not specified. See ratiomethod.
ratiomethod	Choose the regression method to be used, possible methods are: "tls", "bias" and "lm". For details, see the vignette.
largest	Percentage of largest residues from the first regression not to be used in the second regression step. For details, see the vignette.
weighted	Should the regression be weighted with 1/(Total^2 + median(Total))?
relevant	Choose the arrays to be used for halflives calculation, vector due to nr (=replicate number) in phenomat.
check	If check=TRUE, control messages and plots will be generated.
regression	Should the regression results be plotted?
labeling	Should the labeling bias be plotted?
correctedlabeling	Should the corrected labeling bias be plotted?
rankpairs	Should the ranks of decayrates be compared in pairs be plotted (based on Labeled/Total)?

assessment	Should 1-L/T, U/T or (1-L/T+U/T)/2 be assessed due to limitations of the decay rate formula?
correlation	Should the correlation of half-lives, decay rates and synthesis rates vs Total, Labeled and the number of uridines be plotted as color-coded squares?
error	Should the standard deviations and coefficients of variation be calculated?
bicor	Should the labeling bias be corrected?
condition	String, to be added to the plotnames.
upper	Upper bound for labeling bias estimation. For details, see the vignette.
lower	Lower bound for labeling bias estimation. For details, see the vignette.
plots	If plots=TRUE, control plots will be saved.
notinR	Should plots be not plotted in R.
folder	Path to the folder, where to save the plots.
addformat	Additional fileformat for plots to be saved. See `plotit` function (`LSD` package).
totaloverwt	Will be available in the very near future for comparative DTA data.
simulation	True, if data was generated by `DTA.generate`.
sim.object	Simulation object created by `DTA.generate`.

Value

`DTA.estimate` returns a list, where each entry contains the estimation results for all replicates of one labeling time. Each result contains the following entries

triples	Mapping of each fraction and experiment to its corresponding column in the data matrix.
plabel	The labeling efficiency. For details, see the vignette.
LtoTratio	Estimated ratio of labeled to total fraction.
UtoTratio	Estimated ratio of unlabeled to total fraction.
LtoUratio	Estimated ratio of labeled to unlabeled fraction.
correcteddatamat	Labeling bias corrected data matrix.
drmat	Decay rates for each replicate. The last column gives the median decay rates.
hlmat	Half-lives for each replicate. The last column gives the median half-lifes.
dr	Median decay rates. The last column of drmat.
hl	Median half-lives. The last column of hlmat.
dr.sd	Standard deviations of decay rates.
dr.cv	Coefficients of variation of decay rates.
hl.sd	Standard deviations of half-lives.
hl.cv	Coefficients of variation of half-lives.
TEmat	Total expression for each replicate. The last column gives the median total expression values.
TE	Median total expression values. The last column of TEmat.
TE.sd	Standard deviations of total expression values.
TE.cv	Coefficients of variation of total expression values.

LEmat	Labeled expression for each replicate. The last column gives the median labeled expression values.
LE	Median labeled expression values. The last column of LEmat.
LE.sd	Standard deviations of labeled expression values.
LE.cv	Coefficients of variation of labeled expression values.
UEmat	Unlabeled expression for each replicate. The last column gives the median unlabeled expression values. (Only if unlabeled values exist in the experiment)
UE	Median unlabeled expression values. The last column of UEmat. (Only if unlabeled values exist in the experiment)
UE.sd	Standard deviations of unlabeled expression values.
UE.cv	Coefficients of variation of unlabeled expression values.
srmat	Synthesis rates for each replicate. The last column gives the median synthesis rates.
sr	Median synthesis rates. The last column of srmat.
sr.sd	Standard deviations of synthesis rates.
sr.cv	Coefficients of variation of synthesis rates.
LTmat	Labeled to total ratio for each replicate. The last column gives the median labeled to total ratios.
LT	Median labeled to total ratios. The last column of LTmat.
UTmat	Unlabeled to total ratio for each replicate. The last column gives the median unlabeled to total ratios.
UT	Median unlabeled to total ratios. The last column of UTmat.
Rsrmat	Rescaled synthesis rates for each replicate, if parameter mRNAs is specified. The last column gives the median synthesis rates.
Rsr	Rescaled median synthesis rates. The last column of Rsrmat.
globaldrmat	Decay rate for each replicate. Reciprocally weighted by the total expression. Last element contains (weighted) median decay rate.
globaldr	(Weighted) median decay rate.

Author(s)

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References

C. Miller, B. Schwalb, K. Maier, D. Schulz, S. Duemcke, B. Zacher, A. Mayer, J. Sydow, L. Marcinowski, L. Dolken, D. E. Martin, A. Tresch, and P. Cramer. Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Mol Syst Biol, 7:458, 2011.

See Also

heatscatter, plotit, tls

Examples

```
dataPath = system.file("data", package="DTA")
load(file.path(dataPath, "datamat.RData"))
load(file.path(dataPath, "phenomat.RData"))
load(file.path(dataPath, "tnumber.RData"))
load(file.path(dataPath, "reliable.RData"))

res = DTA.estimate(phenomat,datamat,tnumber,ccl = 150,mRNAs = 60000,reliable = reliable,a

dev.off()
```

DTA.generate *Simulation of DTA experiments*

Description

DTA.generate produces the phenotype matrix and the matrix containing the simulated data according to the given parameters.

Usage

```
DTA.generate(timepoints, tnumber = NULL, plabel = NULL, nrgenes = 5000, medianti
```

Arguments

timepoints	Integer vector containing the labeling times for which the samples should be generated.
tnumber	Integer vector containing the number of uridine residues for each gene. If NULL, tnumber is sampled from an F-distribution within the function.
plabel	The labeling efficiency. If NULL, plabel is set to 0.005 within the function. For details, see the vignette.
nrgenes	The number of genes the simulated experiment will have (will be cropped if it exceeds the length of tnumber).
mediantime	The median of the randomly drawn half-life distribution.
ccl	The cell cycle length (in minutes).
delaytime	Estimates the delay between the moment of 4sU/4tU labeling and actual incorporation of it into mRNA.
sdnoise	The amount of measurement noise (proportional to expression strength).
nobias	Should a labeling bias be added?
unspecific.LtoU	Proportion of labeled RNAs that unspecifically end up in the unlabeled fraction.
unspec.LtoU.weighted	Should unspecific proportion of labeled to unlabeled depend linearly on the length of the RNA?
unspecific.UtoL	Proportion of unlabeled RNAs that unspecifically end up in the labeled fraction.
unspec.UtoL.weighted	Should unspecific proportion of unlabeled to labeled depend linearly on the length of the RNA?

truehalflives
: If the data should be generated using a given half-life distribution, this vector must contain the respective values for each gene.

truecomplete
: If the data should be generated using a given expression distribution, this vector must contain the respective values for each gene.

genenames
: An optional list of gene names.

Value

DTA.generate returns a list, containing the following entries

phenomat
: A matrix, containing the design of the experiment as produced by `DTA.phenomat`.

datamat
: A matrix, containing the simulated measurements from U, L and T, according to the design given in phenomat.

tnumber
: Integer vector containing the number of uridine residues for each gene.

ccl
: The cell cycle length (in minutes).

truecomplete
: A vector, containing the true amount of total RNA.

truelambdas
: A vector, containing the true decay rates.

truemus
: A vector, containing the true synthesis rates.

truehalflives
: A vector, containing the true half-lives.

trueplabel
: The true labeling efficiency. For details, see the vignette.

truear
: The true parameter ar. For details, see the vignette.

truebr
: The true parameter br. For details, see the vignette.

truecr
: The true parameter cr. For details, see the vignette.

truecrbyar
: The true parameter cr/ar. For details, see the vignette.

truecrbybr
: The true parameter cr/br. For details, see the vignette.

truebrbyar
: The true parameter br/ar. For details, see the vignette.

trueLasymptote
: The true parameter asymptote (labeled bias). For details, see the vignette.

trueUasymptote
: The true parameter asymptote (unlabeled bias). For details, see the vignette.

Author(s)

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References

C. Miller, B. Schwalb, K. Maier, D. Schulz, S. Duemcke, B. Zacher, A. Mayer, J. Sydow, L. Marcinowski, L. Dolken, D. E. Martin, A. Tresch, and P. Cramer. Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Mol Syst Biol, 7:458, 2011.

Examples

```
sim.object = DTA.generate(timepoints=rep(c(6,12),2))

res.sim = DTA.estimate(ratiomethod = "bias",simulation = TRUE,sim.object = sim.object,lab

dev.off()
```

DTA.phenomat *Create a phenomat that suits your experiment*

Description

`DTA.phenomat` creates a phenomat for a given experimental design, i.e. used labeling times.

Usage

```
DTA.phenomat(timepoints, timecourse = NULL)
```

Arguments

`timepoints`	The respective labeling times of the measured samples.
`timecourse`	Vector giving the order for timecourse DTA data.

Value

A matrix, containing the design of the experiment. Columns are name, fraction (U=unlabebeld, L=labeled, T=total), time and nr (=replicate number). Rows represent individual experiments.

Author(s)

Bjoern Schwalb `<schwalb@lmb.uni-muenchen.de>`

Examples

```
DTA.phenomat(c(6,12))
```

DTA.plot.it *Plots in any format and any quality*

Description

`DTA.plot.it` can save plots in any format and any quality in addition to show them in R devices

Usage

```
DTA.plot.it(filename,sw = 1,sh = 1,sres = 1,plotsfkt,ww = 7,wh = 7,pointsize = 1
```

Arguments

`filename`	Name of the plot to be saved with the format type suffix.
`sw`	Scaling factor of weight.
`sh`	Scaling factor of height.
`sres`	Scaling factor of the resolution.
`plotsfkt`	Function of plots to be plotted.
`ww`	Width of window. Needed only for plotting in R or if filformat = "pdf" or "ps"

wh	Height of window. Needed only for plotting in R or if filformat = "pdf" or "ps"
pointsize	The default pointsize of plotted text, interpreted as big points (1/72 inch) for plots to be saved.
paper	Needed only if filformat = "pdf" or "ps".
quality	Needed only if filformat = "jpeg".
units	Needed only if filformat = "jpeg", "png", "bmp" or "tiff".
bg	Backgroundcolor.
fileformat	Save the plot as jpeg, png, bmp, tiff, ps or pdf.
saveit	Should plot be saved.
notinR	Should plot be not plotted in R.
addformat	Should plot be saved additionally in another format.

Author(s)

Bjoern Schwalb <schwalb@lmb.uni-muenchen.de>

Examples

```
plotsfkt = function(){
par(mfrow = c(1,2))
plot(1:10)
plot(10:1)
}
DTA.plot.it(filename = "test",plotsfkt = plotsfkt,saveit = TRUE)

dev.off()
```

RPdatamat *DTA RPdatamat*

Description

Gene expression profiles of rpb1-N488D (Slow Polymerase) cDTA.

Usage

```
RPdatamat
```

Format

This matrix contains the RNA intensity values for each gene across each RNA fraction and their replicate measurements. The column names of the matrix give the cel-file name and the row names the ORF identifier.

Source

M. Sun, B. Schwalb, D. Schulz, N. Pirkl, L. Lariviere, K. Maier, A. Tresch, P. Cramer. Mutual feedback between mRNA synthesis and degradation buffers transcript levels in a eukaryote. submitted.

RPphenomat *cDTA RPphenomat*

Description

Design of a rpb1-N488D (Slow Polymerase) cDTA experiment.

Usage

```
RPphenomat
```

Format

The phenomat is comprised of the file name, the type of RNA fraction mesasured (T, U or L), the labeling time and the replicate number. Rows in this matrix represent the individual experiments.

Source

M. Sun, B. Schwalb, D. Schulz, N. Pirkl, L. Lariviere, K. Maier, A. Tresch, P. Cramer. Mutual feedback between mRNA synthesis and degradation buffers transcript levels in a eukaryote. submitted.

WTdatamat *cDTA WTdatamat*

Description

Gene expression profiles of wild-type cDTA.

Usage

```
WTdatamat
```

Format

This matrix contains the RNA intensity values for each gene across each RNA fraction and their replicate measurements. The column names of the matrix give the cel-file name and the row names the ORF identifier.

Source

M. Sun, B. Schwalb, D. Schulz, N. Pirkl, L. Lariviere, K. Maier, A. Tresch, P. Cramer. Mutual feedback between mRNA synthesis and degradation buffers transcript levels in a eukaryote. submitted.

WTphenomat *cDTA WTphenomat*

Description

Design of a wild-type cDTA experiment.

Usage

```
WTphenomat
```

Format

The phenomat is comprised of the file name, the type of RNA fraction mesasured (T, U or L), the labeling time and the replicate number. Rows in this matrix represent the individual experiments.

Source

M. Sun, B. Schwalb, D. Schulz, N. Pirkl, L. Lariviere, K. Maier, A. Tresch, P. Cramer. Mutual feedback between mRNA synthesis and degradation buffers transcript levels in a eukaryote. submitted.

cDTAreliable *cDTA reliable ORFs*

Description

S.cerevisiae genes, that passed certain criteria to be considered valid for parameter estimation. (see publication)

Usage

```
cDTAreliable
```

Format

Vector of ORF identifiers.

Source

M. Sun, B. Schwalb, D. Schulz, N. Pirkl, L. Lariviere, K. Maier, A. Tresch, P. Cramer. Mutual feedback between mRNA synthesis and degradation buffers transcript levels in a eukaryote. submitted.

cDTAtnumber *cDTA tnumber*

Description

The amount of thymines in the cDNA of each transcript.

Usage

```
cDTAtnumber
```

Format

Vector gives the number of uridine residues for every ORF identifiers.

Source

J. M. Cherry, C. Adler, C. Ball, S. A. Chervitz, S. S. Dwight, E. T. Hester, Y. Jia, G. Juvik, T. Roe, M. Schroeder, S. Weng, and D. Botstein. Sgd: Saccharomyces genome database. Nucleic Acids Res, 26(1):73-79, 1998.

datamat *DTA datamat*

Description

Gene expression profiles of wild-type yeast for DTA.

Usage

```
datamat
```

Format

This matrix contains the RNA intensity values for each gene across each RNA fraction and their replicate measurements. The column names of the matrix give the cel-file name and the row names the ORF identifier.

Source

C. Miller, B. Schwalb, K. Maier, D. Schulz, S. Duemcke, B. Zacher, A. Mayer, J. Sydow, L. Marcinowski, L. Dolken, D. E. Martin, A. Tresch, and P. Cramer. Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Mol Syst Biol, 7:458, 2011.

orfs_ribig *Ribosome biogenesis genes*

Description

ORF identifiers found to be associated with ribosome biogenesis, rRNA processing etc.

Usage

```
orfs_ribig
```

Format

Vector of ORF identifiers.

Source

P. Jorgensen, I. RupeAi, J. R. Sharom, L. Schneper, J. R. Broach, and M. Tyers. A dynamic transcriptional network communicates growth potential to ribosome synthesis and critical cell size. Genes & Development, 18(20):2491-2505, October 2004.

orfs_rpg *Ribosomal protein genes*

Description

ORF identifiers encoding for ribosomal protein genes.

Usage

```
orfs_rpg
```

Format

Vector of ORF identifiers.

Source

A. Nakao, M. Yoshihama, and N. Kenmochi. RPG: the Ribosomal Protein Gene database. Nucleic acids research, 32(Database issue), January 2004.

orfs_stress *ISA stress module*

Description

ORF identifiers found to be associated with stress response by the iterative signature algorithm.

Usage

```
orfs_stress
```

Format

Vector of ORF identifiers.

Source

J. Ihmels, G. Friedlander, S. Bergmann, O. Sarig, Y. Ziv, and N. Barkai. Revealing modular organization in the yeast transcriptional network. Nature genetics, 31(4):370-377, August 2002.

orfs_tf *Transcription factors*

Description

ORF identifiers encoding for transcription factors.

Usage

```
orfs_tf
```

Format

Vector of ORF identifiers.

Source

K. D. MacIsaac, T. Wang, D. B. Gordon, D. K. Gifford, G. D. Stormo, and E. Fraenkel. An improved map of conserved regulatory sites for saccharomyces cerevisiae. BMC Bioinformatics, 7:113, 2006.

phenomat *DTA phenomat*

Description

Design of a wild-type yeast DTA experiment.

Usage

```
phenomat
```

Format

The phenomat is comprised of the file name, the type of RNA fraction mesasured (T, U or L), the labeling time and the replicate number. Rows in this matrix represent the individual experiments.

Source

C. Miller, B. Schwalb, K. Maier, D. Schulz, S. Duemcke, B. Zacher, A. Mayer, J. Sydow, L. Marcinowski, L. Dolken, D. E. Martin, A. Tresch, and P. Cramer. Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Mol Syst Biol, 7:458, 2011.

reliable *DTA reliable ORFs*

Description

4490 genes, that passed certain criteria to be considered valid for parameter estimation (see vignette for details).

Usage

```
reliable
```

Format

Vector of ORF identifiers.

Source

C. Miller, B. Schwalb, K. Maier, D. Schulz, S. Duemcke, B. Zacher, A. Mayer, J. Sydow, L. Marcinowski, L. Dolken, D. E. Martin, A. Tresch, and P. Cramer. Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Mol Syst Biol, 7:458, 2011.

tDTAdatamat *tDTA datamat*

Description

Gene expression profiles of wild-type tDTA.

Usage

```
tDTAdatamat
```

Format

This matrix contains the RNA intensity values for each gene across each RNA fraction and their replicate measurements. The column names of the matrix give the cel-file name and the row names the ORF identifier.

Source

M. Sun, B. Schwalb, D. Schulz, N. Pirkl, L. Lariviere, K. Maier, A. Tresch, P. Cramer. Mutual feedback between mRNA synthesis and degradation buffers transcript levels in a eukaryote. submitted.

tDTAphenomat *tDTA phenomat*

Description

Design of a wild-type tDTA experiment.

Usage

```
tDTAphenomat
```

Format

The phenomat is comprised of the file name, the type of RNA fraction mesasured (T, U or L), the labeling time and the replicate number. Rows in this matrix represent the individual experiments.

Source

M. Sun, B. Schwalb, D. Schulz, N. Pirkl, L. Lariviere, K. Maier, A. Tresch, P. Cramer. Mutual feedback between mRNA synthesis and degradation buffers transcript levels in a eukaryote. submitted.

tDTAreliable *tDTA reliable ORFs*

Description

S.cerevisiae genes, that passed certain criteria to be considered valid for parameter estimation. (see publication)

Usage

```
tDTAreliable
```

Format

Vector of ORF identifiers.

Source

M. Sun, B. Schwalb, D. Schulz, N. Pirkl, L. Lariviere, K. Maier, A. Tresch, P. Cramer. Mutual feedback between mRNA synthesis and degradation buffers transcript levels in a eukaryote. submitted.

tDTAtnumber *tDTA tnumber*

Description

The amount of thymines in the cDNA of each transcript.

Usage

```
tDTAtnumber
```

Format

Vector gives the number of uridine residues for every ORF identifiers.

Source

J. M. Cherry, C. Adler, C. Ball, S. A. Chervitz, S. S. Dwight, E. T. Hester, Y. Jia, G. Juvik, T. Roe, M. Schroeder, S. Weng, and D. Botstein. Sgd: Saccharomyces genome database. Nucleic Acids Res, 26(1):73-79, 1998.

`tls` *Weighted Total Least Square Regression*

Description

Weigthed total least square regression according to Golub and Van Loan (1980) in SIAM J.Numer.Anal Vol 17 No.6

Usage

```
tls(formula, D = NULL, T = NULL, precision = .Machine$double.eps)
```

Arguments

`formula`	An object of class formula.
`D`	Diagonal weigth matrix. Default weights are set to 1.
`T`	Diagonal weigth matrix. Default weights are set to 1.
`precision`	Smallest possible numeric value on this machine (default).

Value

`tls` returns a lm object.

Author(s)

Sebastian Duemcke <duemcke@lmb.uni-muenchen.de>

References

Golub, G.H. and Van Loan, C.F. (1980). An analysis of the total least squares problem. SIAM J. Numer. Anal., 17:883-893.

Examples

```
f = 1.5 # true ratio
a = rnorm(5000)
b = f*a
a = a + rnorm(5000,sd=0.5)
b = b + rnorm(5000,sd=0.5)

coeff.tls = coef(tls(b ~ a + 0))
coeff.lm1 = coef(lm(b ~ a + 0))
coeff.lm2 = 1/coef(lm(a ~ b + 0))

heatscatter(a,b)
abline(0,coeff.lm1,col="red",pch=19,lwd=2)
abline(0,coeff.lm2,col="orange",pch=19,lwd=2)
abline(0,coeff.tls,col="green",pch=19,lwd=2)
abline(0,f,col="grey",pch=19,lwd=2,lty=2)
legend("topleft", c("Least-squares regr. (y ~ x + 0)", "Least-squares regr. (x ~ y + 0)",

results = c(coeff.tls,coeff.lm1,coeff.lm2)
names(results) = c("coeff.tls","coeff.lm1","coeff.lm2")
print(results)
```

`tnumber` *DTA tnumber*

Description

The amount of thymines in the cDNA of each transcript.

Usage

```
tnumber
```

Format

Vector gives the number of uridine residues for every ORF identifiers.

Source

J. M. Cherry, C. Adler, C. Ball, S. A. Chervitz, S. S. Dwight, E. T. Hester, Y. Jia, G. Juvik, T. Roe, M. Schroeder, S. Weng, and D. Botstein. Sgd: Saccharomyces genome database. Nucleic Acids Res, 26(1):73-79, 1998.

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