

rama

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<code>arrange.row</code>	<i>Reorder a dataset by increasing row order.</i>
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Description

The functions could be used to reorder a dataset to make sure that all the genes are in the same row before fitting any model. The `arrange.row` function is also used by the `weight.plot` function to map all the genes to their position on the slide.

Usage

```
arrange.row(data)
```

Arguments

<code>data</code>	A dataset containing the row indices in the first column and the column indices in the second column. The row indices should all be distinct. All indices should start at zero!
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Value

The ordered dataset.

Author(s)

Raphael Gottardo

References

Robust Estimation of cDNA Microarray Intensities with Replicates Raphael Gottardo, Adrian E. Raftery, Ka Yee Yeung, and Roger Bumgarner Department of Statistics, University of Washington, Box 354322, Seattle, WA 98195-4322

See Also

`weight.plot`

Examples

```

data(hiv)
### Put the indices in the first two columns and
### reorder the first 4 replicates
new.data<-cbind(hiv[,9:10],hiv[,1:4])
ordered.data<-arrange.row(new.data)

```

`est.shift`*Estimate the shift used in the log transformation*

Description

Estimate the shift in the log transformation when fitting the Hierarchical model as in `bayes.rob`.

Usage

```
est.shift(sample1, sample2, B=1000, min.iter=0, batch=10, mcmc.obj=NULL, dye.swap=FALSE)
```

Arguments

<code>sample1</code>	The matrix of intensity from the sample 1. Each row corresponds to a different gene.
<code>sample2</code>	The matrix of intensity from the sample 2. Each row corresponds to a different gene.
<code>B</code>	The number of iteration used the MCMC algorithm.
<code>min.iter</code>	The length of the burn-in period in the MCMC algorithm. <code>min.iter</code> should be less than <code>B</code> .
<code>batch</code>	The thinning value to be used in the MCMC. Only every <code>batch</code> -th iteration will be stored.
<code>mcmc.obj</code>	An object of type <code>mcmc.shift</code> , as returned by <code>est.shift</code> . If no <code>mcmc.obj</code> , the MCMC is initialized to the least squares estimates.
<code>dye.swap</code>	A logical value indicating if the experiment was a dye swap experiment.
<code>nb.coll</code>	An integer value corresponding to the number of arrays (columns) in the first group of the dye swap experiment. In other words, the number of replicates before the dyes have been swapped.
<code>all.out</code>	A logical value indicating if all the parameters should be outputted. If <code>all.out</code> is <code>FALSE</code> , only the posterior mean is outputted. This could be used to save memory.
<code>verbose</code>	A logical value indicating if the current MCMC iteration number should be printed out.

Details

The estimation is done by fitting the same model (as in `fit.model`) with constant variance, Gaussian errors and a prior for the shift. The main purpose of this function is to estimate the shift in the log transformation. Parameter estimation is carried out using Markov Chain Monte Carlo. The shift is estimated with the posterior mean.

Value

An object of type `mcmc.est` containing the sampled values from the posterior distribution.

<code>mu</code>	A vector containing the sampled values from <code>mu</code> , the baseline intensity.
<code>alpha2</code>	A vector containing the sampled values from <code>alpha2</code> , the sample effect.
<code>beta2</code>	A vector containing the sampled values from <code>beta2</code> , the dye effect.
<code>delta22</code>	A vector containing the sampled values from <code>delta_22</code> , the dye*sample interaction.
<code>eta</code>	A matrix, each row contains the sampled values from the corresponding array effect.
<code>gamma1</code>	A matrix, each row contains the sampled values from the corresponding gene effect in sample 1.
<code>gamma2</code>	A matrix, each row contains the sampled values from the corresponding gene effect in sample 1.
<code>lambda.gamma1</code>	A vector containing the sampled values for the precision of the gene effect prior in sample 1.
<code>lambda.gamma2</code>	A vector containing the sampled values for the precision of the gene effect prior in sample 2.
<code>rho</code>	A vector containing the sampled values from between sample correlation coefficient <code>rho</code>
<code>lambda_eps1</code>	A vector containing the sampled values from the gene precision in sample 1.
<code>lambda_eps2</code>	A vector containing the sampled values from the gene precision in sample 2.
<code>shift</code>	A vector containing the sampled values from the shift.

Author(s)

Raphael Gottardo

References

Robust Estimation of cDNA Microarray Intensities with Replicates Raphael Gottardo, Adrian E. Raftery, Ka Yee Yeung, and Roger Bumgarner Department of Statistics, University of Washington, Box 354322, Seattle, WA 98195-4322

See Also

`fit.model`

Examples

```
data(hiv)
### Initialize the proposals
mcmc.hiv<-est.shift(hiv[1:10,c(1:4)],hiv[1:10,c(5:8)],B=2000,min.iter=000,batch=1,mcmc.ob
```

fit.model

*Robust estimation of microarray intensities with replicates***Description**

Estimate the log transformed intensities of each sample of a replicated microarray experiment. The estimation is done via Hierarchical Bayesian Modeling.

Usage

```
fit.model(sample1, sample2, B=1000, min.iter=0, batch=10, shift=NULL, mcmc.obj=NULL, dye.swap=FALSE, verbose=FALSE)
```

Arguments

sample1	The matrix of intensity from the sample 1. Each row corresponds to a different gene.
sample2	The matrix of intensity from the sample 2. Each row corresponds to a different gene.
B	The number of iteration used the MCMC algorithm.
min.iter	The length of the burn-in period in the MCMC algorithm. <code>min.iter</code> should be less than B.
batch	The thinning value to be used in the MCMC. Only every <code>batch</code> -th iteration will be stored.
mcmc.obj	An object of type <code>mcmc</code> , as returned by <code>fit.model</code> . <code>mcmc.obj</code> is used to initialize the MCMC. If no <code>mcmc.obj</code> , the MCMC is initialized to the least squares estimates.
shift	The shift to be used in the log transformation. If <code>shift=NULL</code> is specified (default), it is estimated using <code>est.shift</code> .
dye.swap	A logical value indicating if the experiment was a dye swap experiment.
nb.coll	An integer value corresponding to the number of arrays (columns) in the first group of the dye swap experiment. In other words, the number of replicates before the dyes have been swapped.
all.out	A logical value indicating if all the parameters should be outputted. If <code>all.out</code> is <code>FALSE</code> , only the posterior mean is outputted. This could be used to save memory.
ci	A number between 0 and 1 corresponding to the level used when computing log ratio credible intervals. If <code>all.out</code> is <code>FALSE</code> , this option is ignored.
verbose	A logical value indicating if the current MCMC iteration number should be printed out.

Details

The function fits a hierarchical Bayesian model for robust estimation of cDNA microarray intensities. Our model addresses classical issues such as design effects, normalization and transformation. Outliers are modeled explicitly using a t-distribution. Parameter estimation is carried out using Markov Chain Monte Carlo.

Value

An object of type `mcmc` containing the sampled values from the posterior distribution.

<code>mu</code>	A vector containing the sampled values from <code>mu</code> , the baseline intensity.
<code>alpha2</code>	A vector containing the sampled values from <code>alpha2</code> , the sample effect.
<code>beta2</code>	A vector containing the sampled values from <code>beta2</code> , the dye effect.
<code>delta22</code>	A vector containing the sampled values from <code>delta_22</code> , the dye*sample interaction.
<code>eta</code>	A matrix, each row contains the sampled values from the corresponding array effect.
<code>gamma1</code>	A matrix, each row contains the sampled values from the corresponding gene effect in sample 1.
<code>gamma2</code>	A matrix, each row contains the sampled values from the corresponding gene effect in sample 1.
<code>q.low</code>	A vector containing the lower bounds for the log ratio credible intervals, i.e. the credible intervals for <code>gamma1-gamma2</code> .
<code>q.up</code>	A vector containing the upper bounds for the log ratio credible intervals, i.e. the credible intervals for <code>gamma1-gamma2</code> .
<code>lambda.gamma1</code>	A vector containing the sampled values for the precision of the gene effect prior in sample 1.
<code>lambda.gamma2</code>	A vector containing the sampled values for the precision of the gene effect prior in sample 2.
<code>rho</code>	A vector containing the sampled values from between sample correlation coefficient <code>rho</code>
<code>lambda_eps1</code>	A matrix, each row contains the sampled values from the corresponding gene precision in sample 1.
<code>lambda_eps2</code>	A matrix, each row contains the sampled values from the corresponding gene precision in sample 2.
<code>a.eps</code>	A vector containing the sampled values for the mean of the prior of the genes precision.
<code>b.eps</code>	A vector containing the sampled values for the variance of the prior of the genes precision.
<code>w</code>	A matrix, each element (i,j) correspond to the posterior mean of the sampled weights of replicate j in gene i. To save memory, we only store the posterior means of the weights.
<code>shift</code>	The value of the shift.

Author(s)

Raphael Gottardo

References

Robust Estimation of cDNA Microarray Intensities with Replicates Raphael Gottardo, Adrian E. Raftery, Ka Yee Yeung, and Roger Bumgarner Department of Statistics, University of Washington, Box 354322, Seattle, WA 98195-4322

See Also

`est.shift`

Examples

```
data(hiv)
mcmc.hiv<-fit.model(hiv[1:10,c(1:4)],hiv[1:10,c(5:8)],B=2000,min.iter=000,batch=1,shift=3
```

hiv	<i>Cellular gene expression upon human immunodeficiency virus type 1</i>
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Description

This data set consists of 4 experiments using the same RNA preparation on 4 different slides. The expression levels of ~7000 cellular RNA transcripts were assessed in CD4-T-cell lines at time $t=24$ hour after infection with HIV virus type 1. The first 4 columns correspond to the first treatment state (hiv infected). The second four represent the control state. The experiment is a balanced dye swap experiment. Finally, the last two columns contain the row and column positions of each gene on the array (slide).

Usage

```
data(hiv)
```

Source

<http://expression.microslu.washington.edu/expression/vantwoutjvi2002.html>

References

van't Wout, A. B., Lehrma, G. K., Mikheeva, S. A., O'Keeffe, G. C., Katze, M. G., Bumgarner, R. E., Geiss, G. K. and Mullins, J. I. Cellular gene expression upon human immunodeficiency virus type 1 infection of CD4+-T-Cell lines *Journal of Virology*, 2003. 77(2):1392-1402.

is.row.na	<i>Test if a matrix contains missing values</i>
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Description

The function returns a vector of logical variables, one for each row of the matrix. The variable is TRUE if the row does not contain any missing values and FALSE otherwise.

Usage

```
is.row.na(data)
```

Arguments

`data` The data matrix.

Value

The vector of logical variable

Author(s)

Raphael Gottardo

See Also

is.na

Examples

```
### Generate a matrix
M<-matrix(rnorm(100),10,10)
M[1,1]<-NA
M[1,2]<- -Inf
M[3,10]<-NA

### Indices of the rows without missing values
ind<-is.row.na(M)

### Submatrix of M with finite values
M.finite<-M[ind,]
```

ls.effect

Compute the least squares estimates of the all the effects of the

Description

Compute the least squares estimates of the all the effects of the general model.

Usage

```
ls.effect(sample1, sample2, dye.swap=FALSE, nb.col1=NULL)
```

Arguments

sample1	The matrix of intensity from the sample 1. Each row corresponds to a different gene.
sample2	The matrix of intensity from the sample 2. Each row corresponds to a different gene.
dye.swap	A logical value indicating if the experiment was a dye swap experiment.
nb.col1	An integer value corresponding to the number of arrays (columns) in the first group of the dye swap experiment. In other words, the number of replicates before the dyes have been swapped.

Value

mu	The baseline intensity
alpha2	The sample effect
beta2	The dye effect
delta22	The dye*sample interaction
eta	The array effects
gamma1	The genes effects in sample 1
gamma2	The genes effect in sample 2
M1	The main effects in sample 1
M2	The main effects in sample 2
R1	The residuals from the sample 1
R2	The residuals from the sample 2

Author(s)

Raphael Gottardo

References

Robust Estimation of cDNA Microarray Intensities with Replicates Raphael Gottardo, Adrian E. Raftery, Ka Yee Yeung, and Roger Bumgarner Department of Statistics, University of Washington, Box 354322, Seattle, WA 98195-4322

See Also

`fit.model`

Examples

```
### Compute the least squares effects on the log scale
data(hiv)
ls.fx<-ls.effect(log2(hiv[,c(1:4)]),log2(hiv[,c(5:8)]),dye.swap=TRUE,nb.col1=2)
```

`mat.mean`

Compute the mean and standard deviation of each row in a data matrix

Description

This function computes the mean and standard deviation of each row in a data matrix. The source code is written in C. As a consequence, the computation is quite fast.

Usage

```
mat.mean(data)
```

Arguments

`data` The data matrix.

Value

A matrix, the first columns contain the means, the second the standard deviations.

Author(s)

Raphael Gottardo

See Also

[mean.sd](#)

Examples

```
data(hiv)
sample1<-hiv[,1:4]
ms1<-mat.mean(sample1)
```

ratio.plot

Plot the estimated log ratios against the overall intensities

Description

Plot the estimated $\log_2(\gamma_1/\gamma_2)$ against $\log_2(\gamma_1*\gamma_2)/2$.

Usage

```
ratio.plot(mcmc.obj, col=1, pch=1)
```

Arguments

mcmc.obj	An object of class mcmc as returned by fit.model
col	The color to be used for the symbols
pch	The type of symbols to be used.

Value

The graph!

Author(s)

Raphael Gottardo

References

Robust Estimation of cDNA Microarray Intensities with Replicates Raphael Gottardo, Adrian E. Raftery, Ka Yee Yeung, and Roger Bumgarner Department of Statistics, University of Washington, Box 354322, Seattle, WA 98195-4322

See Also

[fit.model](#)

Examples

```
data(hiv)
### Initialize the proposals
mcmc.hiv<-fit.model(hiv[1:10,c(1:4)],hiv[1:10,c(5:8)],B=2000,min.iter=000,batch=1,shift=3)
ratio.plot(mcmc.hiv,col=1,pch=1)
```

```
weight.plot
```

Plot the weights of a given array using the spatial location of the

Description

Plot the weights of a given array using the spatial location of the genes on the slide. This function is a useful diagnostic tool.

Usage

```
weight.plot(mcmc.obj, coordinate, array=1)
```

Arguments

mcmc.obj	An object of class mcmc as returned by fit.model
coordinate	The coordinate of each gene on the corresponding array. The coordinates should be a two column integer valued matrix containing the row indices (column 1) and the column indices (column 2). The row indices should all be distinct. All indices should start at zero!
array	An integer corresponding to the array number to be plotted.

Value

The image plot of the weights. A small weight (bright color) correspond to an outlier.

Author(s)

Raphael Gottardo

References

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See Also

```
arrange.row
```

Examples

```
data(hiv)
### Initialize the proposals
mcmc.hiv<-fit.model(hiv[1:640,c(1:4)],hiv[1:640,c(5:8)],B=1000,min.iter=500,batch=1,shift=3)
weight.plot(mcmc.hiv,hiv[1:640,9:10],array=3)
```

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