Package ‘LTR’

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Title Perform LTR analysis on microarray data
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Author Paul C. Boutros
Maintainer Paul C. Boutros <Paul.Boutros@oicr.on.ca>
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Description A set of functions to execute the linear-transformation of replicate (LTR) algorithm for preprocessing of microarray data
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LazyLoad yes
Repository CRAN
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NeedsCompilation no

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apply.LTR         Apply a fitted LTR model to a new dataset

Description

Map a gene-expression matrix into the space encoded by a linear-transformation of replicates (LTR) fit object.
Usage
apply.LTR(x, model.fit);

Arguments

x  A matrix with samples as columns and genes as rows; must have the same number of rows as the model in model.fit

model.fit  A list with components rownames, intercepts, slopes, r.squared, and residuals. Exactly such a list is generated by fit.LTR

Details
x must have the same number of rows (and in the same order) as the components of model.fit – no validation of this is performed.

Value
A gene-expression matrix of dim(x) in the space of model.fit

Author(s)
Paul C. Boutros

References
The LTR paper, once published

Examples
x <- matrix(nrow = 100, ncol = 10, data = rnorm(1000));
y <- matrix(nrow = 100, ncol = 10, data = rnorm(1000));
model.fit <- fit.LTR(x, y);

z <- apply.LTR(
x = y + matrix(nrow = 100, ncol = 10, data = rnorm(1000) / 10),
model.fit = model.fit
);

fit.and.apply.LTR One-step fit and apply an LTR model

Description
Take two datasets that define a relationship between two gene-expression spaces, fit the relationship, and apply to map a third gene-expression matrix from one space to the other.
Usage

fit.and.apply.LTR(x, dataset1, dataset2);

Arguments

x A matrix with samples as columns and genes as rows; must have the same number of rows as the model in model.fit

dataset1 A matrix with samples as columns and probes as rows corresponding to the space we want to map expression values into

dataset2 A matrix with samples as columns and probes as rows corresponding to the space we want to map expression values out of

Details

x, dataset1, and dataset2 must all have the same number of rows (and in the same order). dataset1 and dataset2 must have the same number of columns (samples) and in the same order.

Value

A gene-expression matrix of dim(x) in the space of model.fit

Author(s)

Paul C. Boutros

References

The LTR paper, once published

Examples

x <- matrix(nrow = 100, ncol = 10, data = rnorm(1000));
y <- matrix(nrow = 100, ncol = 10, data = rnorm(1000));
z <- y + matrix(nrow = 100, ncol = 10, data = rnorm(1000) / 10)

tmp <- fit.and.apply.LTR(
x = x,
dataset1 = y,
dataset2 = z
);

fit.LTR  

Fit a linear-transformation of replicates model

Description

Fit probe-wise linear models using replicates samples on two different platforms or batches and return the fit in a format suitable for application to smoothing other data.

Usage

fit.LTR(dataset1, dataset2);

Arguments

dataset1 A matrix with samples as columns and probes as rows corresponding to the space we want to map expression values *out of*
dataset2 A matrix with samples as columns and probes as rows corresponding to the space we want to map expression values *into*

Details

dataset1 and dataset2 must have the same number of rows and columns, and must be identically ordered. Some gentle checking on the equivalence of rownames is done, but users must do proper assessment themselves. The model fitted is, for each probe $\text{Expression}(\text{dataset2}) = \text{intercept} + \text{slope} \times \text{Expression}(\text{dataset1})$. Thus we are learning a transform from the space of dataset1 into the space of dataset2.

Value

Returns a list with components: rownames vector, length nrow(dataset1), taken from dataset1 and components intercepts vector, length nrow(dataset1), taken from the LTR fit slopes vector, length nrow(dataset1), taken from the LTR fit r.squared vector, length nrow(dataset1), taken from the LTR fit residuals matrix nrow(dataset1) x ncol(dataset1) that gives for each gene/sample tuple in dataset2 the residual of the fit

Author(s)

Paul C. Boutros

References

This would be the LTR paper if/when it gets published

Examples

```r
x <- matrix(nrow = 100, ncol = 10, data = rnorm(1000));
y <- matrix(nrow = 100, ncol = 10, data = rnorm(1000));
model.fit <- fit.LTR(x, y);
```
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apply.LTR.1

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