

Package ‘agce’

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Title analysis of growth curve experiments

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Depends nlme

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Description This package contains some simple functions for the analysis of growth curve experiments.

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ano.difference *Performs a simple anova on a vector of measurement (or differences).*

Description

This function is a particular case of the `manova.growth`, the `manova` reduces to an ANOVA when the matrix of measurement is a vector. If an initial time is specified (see `initial`), the anova is performed on the differences and rates of growth might be computed.

Usage

```
ano.difference(data, initial=NULL, final="last", C=NULL, U=NULL, normal=TRUE, B=100)
```

Arguments

<code>data</code>	The data matrix or data frame, where the first column correspond to the group ids, the second to the animal ids, the remaining columns are the measurements at each time.
<code>initial</code>	An integer corresponding to the index of the initial time. If <code>initial</code> is specified, the anova is performed on the differences. Otherwise only the 'final' measurements are used.
<code>final</code>	An integer corresponding to the index of the final time. By default <code>final</code> is equal to "last" which correspond to the last measurement.
<code>C</code>	The left contrast matrix. Default to the matrix to test equal means in each group.
<code>U</code>	The right contrast matrix. Default to the identity.
<code>normal</code>	A logical value, if <code>normal</code> is true the standard deviations of the rates are computed based on normal assumption of the measurements, otherwise computed by bootstrapping. Default to TRUE.
<code>B</code>	A numeric value, the number of bootstraps. Only used if <code>normal</code> is FALSE.
<code>rate</code>	A logical value, if TRUE, the rates are computed. Default to TRUE. The rate can not be computed if <code>initial</code> is not specified.
<code>time</code>	A vector of numeric values corresponding to the time points at which the measurements were effectued. Time is absolutely required.

Value

<code>Ftest</code>	The value of the F-test used to test the hypothesis based on <code>C</code> and <code>U</code> .
<code>df1</code>	The numerator degrees of freedom for the F-test
<code>df2</code>	The denominator degrees of freedom for the F-test
<code>p</code>	The p-value associated to the F-test
<code>mean</code>	The estimate of the mean
<code>std.mean</code>	The standard deviation associated to the mean
<code>rate</code>	The rate of growth. Set to NULL if <code>rate</code> is FALSE
<code>std.rate</code>	The standard deviation of the rates. Set to NULL if <code>rate</code> is FALSE

Author(s)

Raphael Gottardo

See Also

[manova.growth,growth.curve](#)

Examples

```
data(Bt20)
ano.difference(Bt20, initial=1, final="last", C=NULL, U=NULL, normal=TRUE, rate=TRUE, time=c(0, 3, 7, 10, 14, 16))
```

Bt20

Effect of DFMO on breast cancer tumors

Description

The data are the result of an experiment, that we will refer to as the Bt-20 experiment. The goal of the experiment was to determine whether hormone-independent human breast cancer cells growing in nude mice manifest sensitivity to the polyamine-biosynthetic inhibitor DFMO. Mice bearing established tumors to one of six groups: 0% (control), 0.5%, 1%, 2% and 3%. Tumors in each group were measured at day 0, 3, 7, 10, 14 and 16.

Usage

```
data(Bt20)
```

Format

A matrix, the first column contains the group ids (which dose), the second column contains the animal ids. Columns 3 to 8 contains the measurements at the time points 0, 3, 7, 10, 14 and 16, respectively.

Source

Daniel F. Heitjan, Andrea Manni and Richard J. Santen. Statistical Analysis of in Vivo Tumor Growth Experiments. *Cancer Research* 1993.53:6042-6050.

References

Daniel F. Heitjan, Andrea Manni and Richard J. Santen. Statistical Analysis of in Vivo Tumor Growth Experiments. *Cancer Research* 1993.53:6042-6050.

<code>design.matrix</code>	<i>Create the design matrix associated to the data.</i>
----------------------------	---

Usage

```
design.matrix(factors)
```

Arguments

<code>factors</code>	The vector (first column of the data) of group ids.
----------------------	---

Value

The design matrix X.

Author(s)

Raphael Gottardo

Examples

```
data(Bt20)
### Remove the missing values (if any)
Bt20<-remove.NA(Bt20)
X<-design.matrix(Bt20[,1])
```

<code>graph.curve</code>	<i>Graph the medians tumor volumes at each time point and for each group.</i>
--------------------------	---

Description

Estimate the growth curve for each group. All curves are graphed on the same figure.

Usage

```
graph.curve(data, time, legend=TRUE)
```

Arguments

<code>data</code>	The data matrix or data frame, where the first column correspond to the group ids, the second to the animal ids, the remaining columns are the measurements at each time.
<code>time</code>	A vector of numeric values corresponding to the time points at which the measurements were effectued.
<code>legend</code>	A logical value, if TRUE legends using the group ids, are added to the graph.

Value

The graph added to the current plotting device.

Author(s)

Raphael Gottardo

Examples

```
data(Bt20)
graph.curve(Bt20, c(0,3,7,10,14,16), legend=TRUE)
```

growth.curve	<i>Perform an anova on slopes.</i>
--------------	------------------------------------

Description

This function is particular a case of the manova.growth, the manova reduces to an ANOVA when the a particular growth curve is linear.

Usage

```
growth.curve(data, C=NULL, U=NULL, normal=TRUE, B=1000, time=NULL)
```

Arguments

data	The data matrix or data frame, where the first column correspond to the group ids, the second to the animal ids, the remaining columns are the measurements at each time.
C	The left contrast matrix. Default to test same rate of growth in each group.
U	The right contrast matrix. Default to test same rate of growth in each group.
normal	A logical value, if <code>normal</code> is true the standard deviations of the rates are computed based on normal assumption of the measurements, otherwise computed by bootstraping. Default to TRUE.
B	A numeric value, the number of bootstraps. Only used if <code>normal</code> is FALSE.
time	A vector of numeric values corresponding to the time points at which the measurements were effected. Time is absolutely required.

Details

In this function, we assume that the mean is of the form $A+B*t$. Where A, B are estimated . Therefore the mean is just a function (matrix multiplication) of the rates.

Value

<code>Ftest</code>	The value of the F-test used to test the hypothesis based on C and U.
<code>df1</code>	The numerator degrees of freedom for the F-test
<code>df2</code>	The denominator degrees of freedom for the F-test
<code>p</code>	The p-value associated to the F-test
<code>mean</code>	The estimate of the mean
<code>std.mean</code>	The standard deviation associated to the mean
<code>rate</code>	The rate of growth. Set to NULL if <code>rate</code> is FALSE
<code>std.rate</code>	The standard deviation of the rates. Set to NULL if <code>rate</code> is FALSE

Author(s)

Raphael Gottardo

References

Daniel F. Heitjan, Andrea Manni and Richard J. Santen Statistical Analysis of in Vivo Tumor Growth Experiments Cancer Research 53:6042-6050, 1993.

See Also

[manova.growth](#)

Examples

```
data(Bt20)
growth.curve(Bt20, C=NULL, U=NULL, normal=TRUE, time=c(0,3,7,10,14,16))
```

`hotelling.trace` *Compute the hotteling trace statistics.*

Description

The trace statistic is computed by matrix multiplication. It depends on the contrast matrices, the design matrix and the observations.

Usage

```
hotelling.trace(X, Y, C, U)
```

Arguments

<code>X</code>	The design matrix.
<code>Y</code>	The matrix of observations.
<code>C</code>	The left contrast matrix.
<code>U</code>	The right contrast matrix.

Value

The hotelling trace statistic.

Author(s)

Raphael Gottardo

References

- 1 Steven F. Arnold. The Theory of Linear Models and Multivariate Analysis. John Wiley & Sons. New York, 1981.
- 2 Daniel F. Heitjan, Andrea Manni and Richard J. Santen. Statistical Analysis of in Vivo Tumor Growth Experiments. Cancer Research 1993.53:6042-6050.

Examples

```
data(Bt20)
### Remove the missing values (if any)
Bt20<-remove.NA(Bt20)
### Create the design matrix
X<-design.matrix(Bt20[,1])
### Convert as numeric the measurement
Y<-as.matrix(Bt20[,3:dim(Bt20)[2]])
### Number of groups
p<-dim(X)[2]
### Default contrast matrices
C<-cbind(rep(1,p-1),-diag(p-1))
U<-rbind(rep(1,p),-diag(p))
### Compute the Lawley Hotteling trace statistics
tr<-hotelling.trace(X,Y,C,U)
```

manova.estimate *Compute the mean estimates.*

Description

A simple matrix multiplication to compute the mean estimate.

Usage

```
manova.estimate(Y, X)
```

Arguments

Y	The matrix of observations.
X	The design matrix.

Value

The matrix of estimates.

Author(s)

Raphael Gottardo

References

Steven F. Arnold. The Theory of Linear Models and Multivariate Analysis. John Wiley & Sons. New York, 1981.

Examples

```
data(Bt20)
### Remove the missing values (if any)
Bt20<-remove.NA(Bt20)
### Create the design matrix
X<-design.matrix(Bt20[,1])
### Convert as numeric the measurement
Y<-as.matrix(Bt20[,3:dim(Bt20)[2]])
manova.estimate(Y, X)
```

manova.growth	<i>Performs a multivariate analysis of variance for growth curve experiments.</i>
---------------	---

Description

Performs a multivariate analysis of variance for growth curves experiments. By default we test the hypothesis of no group*time interactions.

Usage

```
manova.growth(data, C=NULL, U=NULL, normal=TRUE, B=1000)
```

Arguments

data	The data matrix or data frame, where the first column correspond to the group ids, the second to the animal ids, the remaining columns are the measurements at each time.
C	The left contrast matrix. Default to test no time*group interactions.
U	The right contrast matrix. Default to test no time*group interactions.
normal	A logical value, if <code>normal</code> is true the standard deviations of the rates are computed based on normal assumption of the measurements, otherwise computed by bootstrapping. Default to TRUE.
B	A numeric value, the number of bootstraps. Only used if <code>normal</code> is FALSE.

Value

<code>Ftest</code>	The value of the F-test used to test the hypothesis based on C and U.
<code>df1</code>	The numerator degrees of freedom for the F-test
<code>df2</code>	The denominator degrees of freedom for the F-test
<code>p</code>	The p-value associated to the F-test
<code>mean</code>	The estimate of the mean
<code>std.mean</code>	The standard deviation associated to the mean
<code>rate</code>	The rate of growth. Set to NULL if <code>rate</code> is FALSE
<code>std.rate</code>	The standard deviation of the rates. Set to NULL if <code>rate</code> is FALSE

Author(s)

Raphael Gottardo

References

Daniel F. Heitjan, Andrea Manni and Richard J. Santen Statistical Analysis of in Vivo Tumor Growth Experiments Cancer Research 53:6042-6050, 1993.

See Also

[growth.curve](#), [ano.difference](#)

Examples

```
data(Bt20)
manova.growth(Bt20, C=NULL, U=NULL, normal=TRUE)
```

REAR

Fit a autoregressive model with random errors

Description

This function fits two different models using the nlme library and then compares them using a likelihood ratio test. The first model is an autoregressive random errors model with a linear mean assuming different slope in each group. The second model is an autoregressive random errors model with a linear mean assuming same slope in each group.

Usage

```
REAR(data, time)
```

Arguments

<code>data</code>	The data matrix or data frame, where the first column correspond to the group id, the second to the animal id, the remaining columns are the measurement at each time.
<code>time</code>	A vector of numeric values corresponding to the time points at which the measurements were effected.

Details

The data are reshaped in a longitudinal dataset and then the models are fit using the `lme` function of the `nlme` library.

Value

<code>Chi</code>	The value of the Chisquare test used to test the hypothesis of equal slopes
<code>df</code>	The degrees of freedom for the Chisquare test
<code>p</code>	The p-value associated to the Chisquare test
<code>sum.fit.full</code>	The summary on the fit of the full model
<code>std.fit.reduced</code>	The summary on the fit of the reduced model

Author(s)

Raphael Gottardo

References

Daniel F. Heitjan, Andrea Manni and Richard J. Santen Statistical Analysis of in Vivo Tumor Growth Experiments Cancer Research 53:6042-6050, 1993.

Examples

```
data(Bt20)
REAR(Bt20, c(0, 3, 7, 10, 14, 16))
```

```
remove.NA
```

Remove the rows with missing values.

Description

If one row of the data matrix contains missing measurements, the row is delete.

Usage

```
remove.NA(data)
```

Arguments

`data` The matrix of measurements

Value

The data matrix (missing values removed).

Author(s)

Raphael Gottardo

Examples

```
data(Bt20)
remove.NA(Bt20)
```

```
resamp.std            Compute the standard deviation by bootstrap.
```

Description

Bootstrap a new data set from the original data set by keeping the general structure of the groups. Then compute the standard deviation based on the bootstrap estimates.

Usage

```
resamp.std(factors, Y, X, B=1000)
```

Arguments

`factors` A vector (character or numeric) containing the group ids.
`Y` The matrix of measurements.
`X` The design matrix.
`B` A numeric value, the number of bootstraps.

Value

The matrix of standard deviation.

Author(s)

Raphael Gottardo

Examples

```
data(Bt20)
###Create the design matrix
X<-design.matrix(Bt20[,1])
###Convert as numeric the measurement
Y<-as.matrix(Bt20[,3:dim(Bt20)[2]])
### Number of groups
p<-dim(X)[2]
### Compute the standard deviation associated with the mean
std<-resamp.std(Bt20[,1],Y,X,B=1000)
```

reshape.long	<i>Reshape the data set in a longitudinal data set in order to use the lme function.</i>
--------------	--

Usage

```
reshape.long(data, time)
```

Arguments

data	The data matrix or data frame, where the first column correspond to the group ids, the second to the animal ids, the remaining columns are the measurements at each time.
time	A vector of numeric values corresponding to the time points at which the measurements were effected.

Value

The reshaped data.

Author(s)

Raphael Gottardo

Examples

```
data(Bt20)
long.data<-reshape.long(Bt20,c(0,3,7,10,14,16))
```

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