Package 'asremlPlus'

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Version 4.1-29

Date 2019-07-08

Title Augments 'ASReml-R' in Fitting Mixed Models and Packages Generally in Exploring Prediction Differences

Depends R (>= 3.1.0)

Imports dae, ggplot2, stats, methods, utils, reshape, plyr, dplyr, stringr, RColorBrewer, grDevices, foreach, parallel, doParallel

Suggests testthat, lattice, emmeans, lmerTest, pbkrtest, R.rsp

Enhances asreml

VignetteBuilder R.rsp

SystemRequirements asreml-R 2.x

Description Assists in automating the testing of terms in mixed models when 'asreml' is used to fit the models. Also used to display, in tables and graphs, predictions obtained using any model fitting function and to explore differences between predictions. The content falls into the following natural groupings: (i) Data, (ii) Object manipulation functions, (iii) Model modification functions, (iv) Model testing functions, (v) Model diagnostics functions, (vi) Prediction production and presentation functions, (vii) Response transformation functions, and (viii) Miscellaneous functions. A history of the fitting of a sequence of models is kept in a data frame. Procedures are available for choosing models that conform to the hierarchy or marginality principle and for displaying predictions for significant terms in tables and graphs. The 'asreml' package provides a computationally efficient algorithm for fitting mixed models using Residual Maximum Likelihood. It is a commercial packages that can be purchased from 'VSNi' <http://www.vsni.co.uk/> as 'asreml-R', who will supply a zip file for local installation/updating. It is not needed for functions that are methods for 'alldiffs' and 'data.frame' objects. The package 'asremPlus' can also be installed from <http://chris.brien.name/rpackages/>.

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URL http://chris.brien.name

NeedsCompilation no

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R topics documented:

`asremlPlus-package` *Augments 'ASReml-R' in Fitting Mixed Models and Packages Generally in Exploring Prediction Differences*

Description

Assists in automating the testing of terms in mixed models when 'asreml' is used to fit the models. Also used to display, in tables and graphs, predictions obtained using any model fitting function and to explore differences between predictions. The content falls into the following natural groupings: (i) Data, (ii) Object manipulation functions, (iii) Model modification functions, (iv) Model testing functions, (v) Model diagnostics functions, (vi) Prediction production and presentation functions, (vii) Response transformation functions, and (viii) Miscellaneous functions. A history of the fitting of a sequence of models is kept in a data frame. Procedures are available for choosing models that conform to the hierarchy or marginality principle and for displaying predictions for significant terms in tables and graphs. The 'asreml' package provides a computationally efficient algorithm for fitting mixed models using Residual Maximum Likelihood. It is a commercial packages that can be purchased from 'VSNi' <http://www.vsni.co.uk/> as 'asreml-R', who will supply a zip file for local installation/updating. It is not needed for functions that are methods for 'alldiffs' and 'data.frame' objects. The package 'asremPlus' can also be installed from <http://chris.brien.name/rpackages/>.

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(i) Data

`Wheat.dat`	Data for an experiment to investigate 25 varieties of wheat.
`WaterRunoff.dat`	Data for an experiment to investigate the quality of water runoff over time

(ii) Object manipulation

`as.alldiffs`	Forms an `alldiffs.object` from the supplied predictions, along with those statistics, associated with the

	predictions and their pairwise differnces, that have been supplied.
asrtests	Pseudonym for as.asrtests.
as.asrtests	Forms an asrtests.object that stores (i) a fitted asreml object, (ii) a pseudo-anova table for the fixed terms and (iii) a history of changes and hypthesis testing used in obtaining the model.
as.predictions.frame	Forms a predictions.frame from a data.frame, ensuring that the correct columns are present.
facCombine.alldiffs	Combines several factors into one in the components of an alldiffs.object.
is.alldiffs	A single-line function that tests whether an object is of class alldiffs.
is.asrtests	A single-line function that tests whether an object is of class asrtests.
is.predictions.frame	A single-line function that tests whether an object is of classes predictions.frame and data.frame.
print.alldiffs	Prints the values in an alldiffs.object in a nice format.
print.asrtests	Prints the values in an asrtests.object.
print.predictions.frame	Prints the values in a predictions.frame, with or without title and heading
print.wald.tab	Prints a Wald or pseudoanova table.
sort.alldiffs	Sorts the components of an alldiffs.object according to the predicted values associated with a factor.
subset.alldiffs	Subsets the components in an alldiffs.object according to the supplied condition.
validAlldiffs	Checks that an object is a valid alldiffs.object.
validAsrtests	Checks that an object is a valid asrtests.object.
validPredictionsFrame	Checks that an object is a valid predictions.frame.

(iii) Model modification

changeTerms.asrtests	Adds and drops the specified sets of terms from one or both of the fixed or random model and/or replaces the residual (rcov) model with a new model.
newfit.asreml	Refits an asreml model with modified model formula using either a call to 'update.asreml' or a direct call to 'asreml'.
reparamSigDevn.asrtests	Reparamterizes each random (deviations) term involving 'devn.fac' to a fixed term and ensures that the same term, with 'trend.num' replacing 'devn.fac', is included if any other term with 'trend.num' is included in 'terms'.
rmboundary.asrtests	Removes any boundary or singular variance components from the fit stored in 'asreml.obj' and records their removal in an asrtests.object.
setvarianceterms.call	Allows the setting of bounds and initial values for terms in the 'random' and 'residual' arguments of an 'asreml' call.

(iv) Model testing

chooseModel.asrtests	Determines the set of significant terms taking into account hierarchy or marginality relations and records

	the tests performed in an asrtests.object.
getTestPvalue.asrtests	Gets the p-value for a test recorded in the test.summary data.frame of an asrtests.object.
infoCriteria.asreml	Computes AIC and BIC for a model.
recalcWaldTab.asrtests	Recalculates the denDF, F.inc and P values for a table of Wald test statistics obtained using 'wald.asreml'.
REMLRT.asreml	Performs a REML ratio test.
bootREMLRT.asreml	Performs a REML ratio test using the parametric bootstrap.
testranfix.asrtests	Tests for a single fixed or random term in model fitted using 'asreml' and records the result in an asrtests.object.
testresidual.asrtests	Fits a new residual formula using 'asreml', tests whether the change is significant and records the result in an asrtests.object.
testswapran.asrtests	Tests, using a REMLRT, the significance of the difference between the current random model and one in which oldterms are dropped and newterms are added. The result is recorded in an asrtests.object.

(v) Model diagnostics and simulation

plotVariofaces	Plots empirical variogram faces, including envelopes, from supplied residuals as described by Stefanova, Smith & Cullis (2009).
variofaces.asreml	Calculates and plots empirical variogram faces, including envelopes, as described by Stefanova, Smith & Cullis (2009).
estimateV.asreml	Forms the estimated variance, random or residual matrix for the observations from the variance parameter estimates.
simulate.asreml	Produce sets of simulated data from a multivariate normal distribtion and save quantites related to the simulated data.

(vi) Prediction production and presentation

addBacktransforms.alldiffs	Adds or recalculates the backtransforms component of an alldiffs.object.
allDifferences.data.frame	Using supplied predictions and standard errors of pairwise differences or the variance matrix of predictions, forms all pairwise differences between the set of predictions, and p-values for the differences.
linTransform.alldiffs	Calculates a linear transformation of the predictions stored in an alldiffs.object.
plotPredictions.data.frame	Plots the predictions for a term, possibly with error bars.
plotPvalues.alldiffs	Plots the p-values in the p.differences components of an alldiffs.object as a heat map.
plotPvalues.data.frame	Plots the p-values in data.frame as a heat map.
predictPlus.asreml	Forms the predictions and associated statistics for a term, using an asreml object and a wald.tab and taking into account that a numeric vector and a factor having parallel values may occur in the model. It stores the results in an object of class

	'alldifffs' and may print the results. It can be when there are not parallel values.
predictPresent.asreml	Forms the predictions for each of one or more terms and presents them in tables and/or graphs.
recalcLSD.alldiffs	Adds or recalculates the LSD component of an alldiffs.object.
redoErrorIntervals.alldiffs	Adds or replaces the error intervals stored in the prediction component of an alldiffs.object.
renewClassify.alldiffs	Renews the components in an alldiffs.object according to a new classify.
sort.alldiffs	Sorts the components in an alldiffs.object according to the predicted values associated with a factor.
subset.alldiffs	Subsets the components in an alldiffs.object according to the supplied condition.

(vii) Response transformation

angular	Applies the angular transformation to proportions.
angular.mod	Applies the modified angular transformation to a vector of counts.
powerTransform	Performs a combination of a linear and a power transformation on a variable. The transformed variable is stored in the 'data.frame data'.

(viii) Miscellaneous

getASRemlVersionLoaded	Finds the version of asreml that is loaded and returns the initial characters in version.
loadASRemlVersion	Ensures that a specific version of asreml is loaded.
num.recode	Recodes the unique values of a vector using the values in a new vector.
permute.square	Permutes the rows and columns of a square matrix.
permute.to.zero.lowertri	Permutes a square matrix until all the lower triangular elements are zero.

The functions whose names end in 'alldiffs" utilize an alldiffs.object that stores: (i) a predictions.frame, being a data frame containing predicted values, variables indexing them and their standard errores and estimability status; the lower and upper limits of error intervals will be included when these are requested, (ii) optionally, square matrices containing all pairwise differences, the standard errors and p-values of the differences, and a summary of the LSD values, (iii) optionally, the variance matrix of the predictions, and (iv) if the response was trandformed for analysis, a data frame with backtransforms of the predicted values.

The functions whose names end in 'asrtests', which are most of the model functions, utilize an asrtests.object that stores: (i) the currently fitted model in asreml.obj, (ii) the table of test statistics for the fixed effects in wald.tab, and (iii) a data frame that contains a history of the changes made to the model in test.summary.

Author(s)

NA

Maintainer: NA

References

Butler, D. G., Cullis, B. R., Gilmour, A. R., Gogel, B. J. and Thompson, R. (2018). *ASReml-R Reference Manual Version 4.* VSN International Ltd, http://asreml.org.

Stefanova, K. T., Smith, A. B. & Cullis, B. R. (2009) Enhanced diagnostics for the spatial analysis of field trials. *Journal of Agricultural, Biological, and Environmental Statistics*, **14**, 392–410.

See Also

asreml

Examples

```
## Not run:
## Analyse wheat dat using asreml and asremlPlus (see also the Wheat Vignette)
## Set up for analysis
library(dae)
library(asreml)
library(asremlPlus)
## use ?Wheat.dat for data set details
data(Wheat.dat)

# Fit initial model
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)
summary(current.asr)

# Intialize a testing sequence by loading the current fit into an asrtests object
current.asrt <- as.asrtests(current.asr, NULL, NULL)

# Check for and remove any boundary terms
current.asrt <- rmboundary(current.asrt)

#Unbind Rep, Row and Column components and reload into an asrtests object
current.asr <- setvarianceterms(current.asr$call,
                                terms = c("Rep", "Rep:Row", "Rep:Column"),
                                bounds = "U")
current.asrt <- as.asrtests(current.asr, NULL, NULL)
current.asrt <- rmboundary(current.asrt)
summary(current.asrt$asreml.obj)$varcomp
print(current.asrt, which = "testsummary")
print(current.asrt, which = "pseudoanova")

# Check term for within Column pairs (a post hoc covariate)
current.asrt <- testranfix(current.asrt, "WithinColPairs", drop.fix.ns=TRUE)

# Test nugget term
current.asrt <- testranfix(current.asrt, "units", positive=TRUE)

# Test Row autocorrelation
current.asrt <- testresidual(current.asrt, "~ Row:ar1(Column)",
                             label="Row autocorrelation", simpler=TRUE)

# Test Col autocorrelation (depends on whether Row autocorrelation retained)
(p <- getTestPvalue(current.asrt, label = "Row autocorrelation"))
```

```
{ if (p <= 0.05)
    current.asrt <- testresidual(current.asrt, "~ ar1(Row):Column",
                                 label="Col autocorrelation",
                                 simpler=TRUE, update=FALSE)
  else
    current.asrt <- testresidual(current.asrt, "~ Row:Column",
                                 label="Col autocorrelation",
                                 simpler=TRUE, update=FALSE)
}

# Output the results
print(current.asrt, which = "test")
info <- infoCriteria(current.asrt$asreml.obj)
summary(current.asrt$asreml.obj)$varcomp

# Get current fitted asreml object and update to include standardized residuals
current.asr <- current.asrt$asreml.obj
current.asr <- update(current.asr, aom=TRUE)
Wheat.dat$res <- residuals(current.asr, type = "stdCond")
Wheat.dat$fit <- fitted(current.asr)

#### Do diagnostic checking
# Do residuals-versus-fitted values plot
with(Wheat.dat, plot(fit, res))

#Produce variogram and variogram faces plot (Stefanaova et al, 2009)
plot.varioGram(varioGram(current.asr))
faces <- variofaces(current.asr, V=NULL, units="addtores",
                    maxiter=50, update = FALSE)

#Get Variety predictions, sorted in increasing order for the predicted values,
#and all pairwise prediction differences and p-values
Var.diffs <- predictPlus(classify = "Variety",
                         asreml.obj=current.asr,
                         error.intervals="halfLeast",
                         wald.tab=current.asrt$wald.tab,
                         sortFactor = "Variety",
                         tables = "predictions")
print(Var.diffs, which = c("differences", "p.differences"))

# Plot the Variety predictions, with halfLSD intervals, and the p-values
plotPredictions(Var.diffs$predictions,
                classify = "Variety", y = "predicted.value",
                error.intervals = "half")
plotPvalues(Var.diffs)

## End(Not run)
```

`addBacktransforms.alldiffs` *Adds or recalculates the backtransforms component of an* `alldiffs.object`.

Description

Given an `alldiffs.object`, adds or recalculate its `backtransforms` component.

Usage

```
## S3 method for class 'alldiffs'
addBacktransforms(alldiffs.obj, transform.power = 1,
                  offset = 0, scale = 1, ...)
```

Arguments

alldiffs.obj	An alldiffs.object.
transform.power	A numeric specifying the power of a transformation, if one has been applied to the response variable. Unless it is equal to 1, the default, back-transforms of the predictions will be obtained and presented in tables or graphs as appropriate. The back-transformation raises the predictions to the power equal to the reciprocal of transform.power, unless it equals 0 in which case the exponential of the predictions is taken.
offset	A numeric that has been added to each value of the response after any scaling and before applying any power transformation.
scale	A numeric by which each value of the response has been multiplied before adding any offset and applying any power transformation.
...	Provision for passsing arguments to functions called internally - not used at present.

Value

An alldiffs.object with components predictions, vcov, differences, p.differences, sed, LSD and backtransforms.

Author(s)

Chris Brien

See Also

asremlPlus-package, as.alldiffs, sort.alldiffs, subset.alldiffs, print.alldiffs, renewClassify.alldiffs, redoErrorIntervals.alldiffs, plotPredictions.data.frame, predictPlus.asreml, predictPresent.asreml

Examples

```
data(WaterRunoff.dat)

##Use asreml to get predictions and associated statistics

## Not run:
asreml.options(keep.order = TRUE) #required for asreml-R4 only
current.asr <- asreml(fixed = log.Turbidity ~ Benches + (Sources * (Type + Species)),
                      random = ~ Benches:MainPlots,
                      keep.order=TRUE, data= WaterRunoff.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
TS.diffs <- predictPlus(classify = "Sources:Type",
                        asreml.obj = current.asr,
                        wald.tab = current.asrt$wald.tab,
                       present = c("Sources", "Type", "Species"))
```

```
## End(Not run)

## Use lmeTest and emmmeans to get predictions and associated statistics

if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  m1.lmer <- lmerTest::lmer(log.Turbidity ~ Benches + (Sources * (Type + Species)) +
                              (1|Benches:MainPlots),
                            data=na.omit(WaterRunoff.dat))
  TS.emm <- emmeans::emmeans(m1.lmer, specs = ~ Sources:Species)
  TS.preds <- summary(TS.emm)
  den.df <- min(TS.preds$df, na.rm = TRUE)
  ## Modify TS.preds to be compatible with a predictions.frame
  TS.preds <- as.predictions.frame(TS.preds, predictions = "emmean",
                                   se = "SE", interval.type = "CI",
                                   interval.names = c("lower.CL", "upper.CL"))

  ## Form an all.diffs object and check its validity
  TS.vcov <- vcov(TS.emm)
  TS.diffs <- allDifferences(predictions = TS.preds, classify = "Sources:Species",
                             vcov = TS.vcov, tdf = den.df)
  validAlldiffs(TS.diffs)
}

## Plot p-values for predictions obtained using asreml or lmerTest
if (exists("TS.diffs"))
{
  ##Recalculate the LSD values for predictions obtained using asreml or lmerTest
  TS.diffs <- addBacktransforms.alldiffs(TS.diffs, transform.power = 0)
}
```

`allDifferences.data.frame` *Using supplied predictions and standard errors of pairwise differences or the variance matrix of predictions, forms all pairwise differences between the set of predictions, and p-values for the differences.*

Description

Uses supplied predictions and standard errors of pairwise differences, or the variance matrix of predictions to form, in an `alldiffs.object`, for those components not already present, (i) a table of all pairwise differences of the predictions, (ii) the p-value of each pairwise difference, and (iii) the minimum, mean and maximum LSD values. Predictions that are aliased (or nonestimable) are removed from the `predictions` component of the `alldiffs.object` and standard errors of differences involving them are removed from the `sed` component.

If necessary, the order of the columns of the variables in the `predictions` component are changed to be the initial columns of the `predictions.frame` and to match their order in the `classify`. Also, the rows of `predictions` component are ordered so that they are in standard order for the variables in the `classify`. That is, the values of the last variable change with every row, those of the second-last variable only change after all the values of the last variable have been traversed; in general, the values of a variable are the same for all the combinations of the values to the variables

to its right in the classify. The sortFactor or sortOrder arguments can be used to order of the values for the classify variables, which is achieved using sort.alldiffs.

Each p-value is computed as the probability of a t-statistic as large as or larger than the absolute value of the observed difference divided by its standard error. The p-values are stored in the p.differences component. The degrees of freedom of the t-distribution is the degrees of freedom stored in the tdf attribute of the alldiffs.object. This t-distibrution is also used in calculating the LSD statistics stored in the alldiffs.object.

Usage

```
## S3 method for class 'data.frame'
allDifferences(predictions, classify, vcov = NULL,
               differences = NULL, p.differences = NULL, sed = NULL,
               LSD = NULL, meanLSD.type = "overall", LSDby = NULL,
               backtransforms = NULL,
               response = NULL, response.title = NULL,
               term = NULL, tdf = NULL,
               x.num = NULL, x.fac = NULL,
               level.length = NA,
               pairwise = TRUE, alpha = 0.05,
               transform.power = 1, offset = 0, scale = 1,
               inestimable.rm = TRUE,
               sortFactor = NULL, sortWithinVals = NULL,
               sortOrder = NULL, decreasing = FALSE, ...)
```

Arguments

predictions	A predictions.frame, or a data.frame, beginning with the variables classifying the predictions and also containing columns named predicted.value, standard.error and est.status; each row contains a single predicted value. It may also contain columns for the lower and upper limits of error intervals for the predictions. Note that the names standard.error and est.status have been changed to std.error and status in the pvals component produced by asreml-R4; if the new names are in the data.frame supplied to predictions, they will be returned to the previous names.
classify	A character string giving the variables that define the margins of the multiway table that has been predicted. Multiway tables are specified by forming an interaction type term from the classifying variables, that is, separating the variable names with the : operator.
vcov	A matrix containing the variance matrix of the predictions; it is used in computing the variance of linear transformations of the predictions.
differences	A matrix containing all pairwise differences between the predictions; it should have the same number of rows and columns as there are rows in predictions.
p.differences	A matrix containing p-values for all pairwise differences between the predictions; each p-value is computed as the probability of a t-statistic as large as or larger than the observed difference divided by its standard error. The degrees of freedom of the t distribution for computing it are computed as the denominator degrees of freedom of the F value for the fixed term, if available; otherwise, the degrees of freedom stored in the attribute tdf are used; the matrix should be of the same size as that for differences.
sed	A matrix containing the standard errors of all pairwise differences between the predictions; they are used in computing the p-values.

LSD — A data.frame containing the mean, minimum and maximum LSD for determining the significance of pairwise differences, the mean LSD being calculated using the square root of the mean of the variances of pairwise differences. If factor.combination was specified for meanLSD.type when the LSDs were being calculated, then LSD contains an LSD for each factor.combination of the factors specified by LSDby. Each LSD is calculated from the square root of the mean of the variances for all pairwise differences for each factor combination, unless there is only one predicted value for each factor.combination, when it is based on the standard error of the prediction multiplied by the square root of two. If LSD is not NULL then the overall mean LSD will be added as an attribute named meanLSD of the alldiffs.object, as will the values of meanLSD.type and LSDby. The LSD for a single prediction assumes that any predictions to be compared are independent; this is not the case if residual errors are correlated.

meanLSD.type — A character string determining whether the mean LSD stored is (i) the overall mean, based on the square root of the mean of the variances of all pairwise variances, (ii) the mean for each factor.combination of the factors specified by LSDby, which is based on the square root of the mean of the variances for all pairwise differences for each factor combination, unless there is only one prediction for a factor.combination, when notional LSDs are calculated that are based on the standard error of the prediction multiplied by the square root of two, or (iii) the per.prediction mean, based, for each prediction, on the square root of the mean of the variances for all pairwise differences involving that prediction. If LSD is not NULL then meanLSD.type will be added as an attribute of the alldiffs.object.

LSDby — A character (vector) of variables names, being the names of the factors or numerics in the classify for each combination of which a mean LSD, minLSD and max LSD is stored in the LSD component of the alldiffs.object when meanLSD.type is factor.combinatons.

backtransforms — A data.frame containing the backtransformed values of the predicted values that is consistent with the predictions component, except that the column named predicted.value is replaced by one called backtransformed.predictions. Any error.interval values will also be the backtransformed values. Each row contains a single predicted value.

response — A character specifying the response variable for the predictions. It is stored as an attribute to the alldiffs.object.

response.title — A character specifying the title for the response variable for the predictions. It is stored as an attribute to the alldiffs.object.

term — A character string giving the variables that define the term that was fitted using asreml and that corresponds to classify. It is often the same as classify. It is stored as an attribute to the alldiffs.object.

tdf — an integer specifying the degrees of freedom of the standard error. It is used as the degrees of freedom for the t-distribution on which p-values and confidence intervals are based. It is stored as an attribute to the alldiffs.object.

x.num — A character string giving the name of the numeric covariate that corresponds to x.fac, is potentially included in terms in the fitted model and which corresponds to the x-axis variable. It should have the same number of unique values as the number of levels in x.fac.

x.fac — A character string giving the name of the factor that corresponds to x.num, is potentially included in terms in the fitted model and which corresponds to the x-axis variable. It should have the same number of levels as the number of unique

values in x.num. The levels of x.fac must be in the order in which they are to be plotted - if they are dates, then they should be in the form yyyymmdd, which can be achieved using as.Date. However, the levels can be non-numeric in nature, provided that x.num is also set.

level.length — The maximum number of characters from the the levels of factors to use in the row and column labels of the tables of pairwise differences and their p-values and standard errors.

pairwise — A logical indicating whether all pairwise differences of the predictions and their standard errors and p-values are to be computed and stored. If FALSE, the components differences and p.differences will be NULL in the returned alldiffs.object.

alpha — The significance level for an LSD to compare a pair of predictions.

transform.power — A numeric specifying the power of a transformation, if one has been applied to the response variable. Unless it is equal to 1, the default, back-transforms of the predictions will be obtained and presented in tables or graphs as appropriate. The back-transformation raises the predictions to the power equal to the reciprocal of transform.power, unless it equals 0 in which case the exponential of the predictions is taken.

offset — A numeric that has been added to each value of the response after any scaling and before applying any power transformation.

scale — A numeric by which each value of the response has been multiplied before adding any offset and applying any power transformation.

inestimable.rm — A logical indicating whether rows for predictions that are not estimable are to be removed from the components of the alldiffs.object.

sortFactor — A character containing the name of the factor that indexes the set of predicted values that determines the sorting of each component of the the alldiffs.object by sort.alldiffs. If NULL then sorting is not carried out. If there is more than one variable in the classify term then sortFactor is sorted for the predicted values within each combination of the values of the sortWithin variables: the classify variables, excluding the sortFactor. There should be only one predicted value for each unique value of sortFactor within each set defined by a combination of the values of the sortWithin variables.

sortWithinVals — A list with a component named for each factor and numeric that is a classify variable for the predictions, excluding sortFactor. Each component should contain a single value that is a value of the variable. The combination of this set of values will be used to define a subset of the predicted values whose order will define the order of sortFactor to be used for all combinations of the sortWithinVals variables. If sortWithinVals is NULL then the first value of each sortWithin variable in predictions component is used to define sortWithinVals. If there is only one variable in the classify then sortWithinVals is ignored.

sortOrder — A character vector whose length is the same as the number of levels for sortFactor in the predictions component of the alldiffs.object. It specifies the desired order of the levels in the reordered components of the alldiffs.object. The argument sortWithinVals is ignored.

The following creates a sortOrder vector levs for factor f based on the values in x:
levs <-levels(f)[order(x)].

decreasing	A logical passed to order that detemines whether the order for sorting the components of the alldiffs.object is for increasing or decreasing magnitude of the predicted values.
...	provision for passsing arguments to functions called internally - not used at present.

Value

An alldiffs.object with components predictions, vcov, differences, p.differences sed, and LSD.

The name of the response, the response.title, the term, the classify, tdf, sortFactor and the sortOrder will be set as attributes to the object. Note that the classify in an alldiffs.object is based on the variables indexing the predictions, which may differ from the classify used to obtain the original predictions (for example, when the alldiffs.objects stores a linear transformation of predictions.

Also, see predictPlus.asreml for more information.

Author(s)

Chris Brien

See Also

asremlPlus-package, as.alldiffs, as.predictions.frame, sort.alldiffs, subset.alldiffs, print.alldiffs, renewClassify.alldiffs, redoErrorIntervals.alldiffs, recalcLSD.alldiffs, plotPredictions.data.frame, predictPlus.asreml, predictPresent.asreml

Examples

```
data(Oats.dat)

## Use asreml to get predictions and associated statistics

## Not run:
m1.asr <- asreml(Yield ~ Nitrogen*Variety,
                 random=~Blocks/Wplots,
                 data=Oats.dat)
current.asrt <- as.asrtests(m1.asr)
Var.pred <- asreml::predict.asreml(m1.asr, classify="Nitrogen:Variety",
                                   sed=TRUE)
if (getASRemlVersionLoaded(nchar = 1) == "3")
  Var.pred <- Var.pred$predictions
Var.preds <- Var.pred$pvals
Var.sed <- Var.pred$sed
Var.vcov <- NULL
wald.tab <-  current.asrt$wald.tab
den.df <- wald.tab[match("Variety", rownames(wald.tab)), "denDF"]

## End(Not run)

## Use lmerTest and emmmeans to get predictions and associated statistics
if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
```

```
{
  m1.lmer <- lmerTest::lmer(Yield ~ Nitrogen*Variety + (1|Blocks/Wplots),
                            data=Oats.dat)
  Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
  Var.preds <- summary(Var.emm)
  den.df <- min(Var.preds$df)
  ## Modify Var.preds to be compatible with a predictions.frame
  Var.preds <- as.predictions.frame(Var.preds, predictions = "emmean",
                                    se = "SE", interval.type = "CI",
                                    interval.names = c("lower.CL", "upper.CL"))
  Var.vcov <- vcov(Var.emm)
  Var.sed <- NULL
}

## Use the predictions obtained with either asreml or lmerTest
if (exists("Var.preds"))
{
  ## Order the Varieties in decreasing order for the predictions values in the
  ## first N level
  Var.diffs <- allDifferences(predictions = Var.preds,
                              classify = "Nitrogen:Variety",
                              sed = Var.sed, vcov = Var.vcov, tdf = den.df,
                              sortFactor = "Variety", decreasing = TRUE)
  print.alldiffs(Var.diffs, which="differences")

  ## Change the order of the factors in the alldiffs object and reorder components
  Var.reord.diffs <- allDifferences(predictions = Var.preds,
                              classify = "Variety:Nitrogen",
                              sed = Var.sed, vcov = Var.vcov, tdf = den.df)
  print.alldiffs(Var.reord.diffs, which="predictions")
}
```

`alldiffs.object` *Description of an alldiffs object*

Description

An object of S3-class `alldiffs` that that stores the predictions for a model, along with supplied statistics for all pairwise differences. While `alldiffs.object` can be constructed by defining a `list` with the appropriate components, it can be formed by passing the components to `as.alldiffs`, or from a `predictions` `data.frame` using `allDifferences.data.frame`.

`as.alldiffs` is function that assembles an object of this class from supplied components.

`is.alldiffs` is the membership function for this class; it tests that an object is of class `alldiffs`.

`validAlldiffs(object)` can be used to test the validity of an object with this class.

`allDifferences.data.frame` is the function that constructs an object of this class by calculating components from statistics supplied via its arguments and then using `as.alldiffs` to make the object.

Value

A `list` of class `alldiffs` containing the following components: `predictions`, `vcov`, `differences`, `p.differences`, `sed`, `LSD` and `backtransforms`. Except for `predictions`, the components are optional and can be set to `NULL`.

An alldiffs.object also has attributes response, response.title, term, classify, tdf, sortFactor and sortOrder, which may be set to NULL.

The details of the components are as follows:

1. predictions: A predictions.frame, being a data.frame beginning with the variables classifying the predictions, in the same order as in the classify, and also containing columns named predicted.value, standard.error and est.status; each row contains a single predicted value. The number of rows should equal the number of unique combinations of the classify variables and will be in standard order for the classify variables. That is, the values of the last variable change with every row, those of the second-last variable only change after all the values of the last variable have been traversed; in general, the values of a variable are the same for all the combinations of the values to the variables to its right in the classify.

   The data.frame may also include columns for the lower and upper values of error intervals, either standard error, confidence or half-LSD intervals. The names of these columns will consist of three parts separated by full stops: 1) the first part will be lower or upper; 2) the second part will be one of Confidence, StandardError or halfLeastSignificant; 3) the third component will be limits.

   Note that the names standard.error and est.status have been changed to std.error and status in the pvals component produced by asreml-R4; if the new names are in the data.frame supplied to predictions, they will be returned to the previous names.

2. differencesA matrix containing all pairwise differences between the predictions; it should have the same number of rows and columns as there are rows in predictions.

3. p.differences: A matrix containing p-values for all pairwise differences between the predictions; each p-value is computed as the probability of a t-statistic as large as or larger than the observed difference divided by its standard error. The degrees of freedom of the t distribution for computing it are computed as the denominator degrees of freedom of the F value for the fixed term, if available; otherwise, the degrees of freedom stored in the attribute tdf are used; the matrix should be of the same size as that for differences.

4. sed: A matrix containing the standard errors of all pairwise differences between the predictions; they are used in computing the p-values in p.differences.

5. vcov: A matrix containing the variance matrix of the predictions; it is used in computing the variance of linear transformations of the predictions.

6. LSD: A data.frame containing the mean, minimum and maximum LSD for determining the significance of pairwise differences, the mean LSD being calculated using the square root of the mean of the variances of pairwise differences. If factor.combination was specified for meanLSD.type when the LSDs were being calculated, then LSD contains an LSD for each factor.combination of the factors specified by LSDby. Each LSD is calculated from the square root of the mean of the variances for all pairwise differences for each factor combination, unless there is only one prediction for a factor.combination, when notional LSDs are calculated that are based on the standard error of the prediction multiplied by the square root of two. If LSD is not NULL then the overall mean LSD will be added as an attribute named meanLSD of the alldiffs.object, as will the values of meanLSD.type and LSDby. The LSD for a single prediction assumes that any predictions to be compared are independent; this is not the case if residual errors are correlated.

7. backtransforms: When the response values have been transformed for analysis, a data.frame containing the backtransformed values of the predicted values is added to the alldiffs.object. This data.frame is consistent with the predictions component, except that the column named predicted.value is replaced by one called backtransformed.predictions. Any error.interval values will also be the backtransformed values. Each row contains a single predicted value.

The details of the attributes of an alldiffs.object are:

1. response: A character specifying the response variable for the predictions.
2. response.title: A character specifying the title for the response variable for the predictions.
3. term: A character string giving the variables that define the term that was fitted using asreml and that corresponds to classify. It is often the same as classify.
4. classify: A character string giving the variables that define the margins of the multiway table used in the prediction. Multiway tables are specified by forming an interaction type term from the classifying variables, that is, separating the variable names with the : operator.
5. tdf: An integer specifying the degrees of freedom of the standard error. It is used as the degrees of freedom for the t-distribution on which p-values and confidence intervals are based.
6. meanLSD: If the LSD component is not NULL then the mean LSD is added as an attribute, calculated using the square root of the mean of the variances of pairwise differences.
7. meanLSD.type: If the LSD component is not NULL then meanLSD.type is added as an attribute.
8. LSDby: If the LSD component is not NULL then LSDby is added as an attribute.
9. sortFactor: A character containing the name of the factor that indexes the set of predicted values that determined the sorting of the components.
10. sortOrder: A character vector that is the same length as the number of levels for sortFactor in the predictions component of the alldiffs.object. It specifies the order of the levels in the reordered components of the alldiffs.object.

    The following creates a sortOrder vector levs for factor f based on the values in x: levs <-levels(f)[order(x)].

See predictPlus.asreml for more information.

Author(s)

Chris Brien

See Also

is.alldiffs, as.alldiffs, validAlldiffs, allDifferences.data.frame

Examples

```
data(Oats.dat)

## Use asreml to get predictions and associated statistics

## Not run:
m1.asr <- asreml(Yield ~ Nitrogen*Variety,
                 random=~Blocks/Wplots,
                 data=Oats.dat)
current.asrt <- as.asrtests(m1.asr)
Var.pred <- asreml::predict.asreml(m1.asr, classify="Nitrogen:Variety",
                                   sed=TRUE)
if (getASRemlVersionLoaded(nchar = 1) == "3")
  Var.pred <- Var.pred$predictions
Var.preds <- Var.pred$pvals
Var.sed <- Var.pred$sed
Var.vcov <- NULL
```

```
## End(Not run)

  ## Use lmerTest and emmmeans to get predictions and associated statistics
  if (requireNamespace("lmerTest", quietly = TRUE) &
      requireNamespace("emmeans", quietly = TRUE))
  {
    m1.lmer <- lmerTest::lmer(Yield ~ Nitrogen*Variety + (1|Blocks/Wplots),
                              data=Oats.dat)
    Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
    Var.preds <- summary(Var.emm)
    den.df <- min(Var.preds$df)
    ## Modify Var.preds to be compatible with a predictions.frame
    Var.preds <- as.predictions.frame(Var.preds, predictions = "emmean",
                                      se = "SE", interval.type = "CI",
                                      interval.names = c("lower.CL", "upper.CL"))
    Var.vcov <- vcov(Var.emm)
    Var.sed <- NULL
  }

  ## Use the predictions obtained with either asreml or lmerTest
  if (exists("Var.preds"))
  {
    ## Form an all.diffs object
     Var.diffs <- as.alldiffs(predictions = Var.preds, classify = "Nitrogen:Variety",
                              sed = Var.sed, vcov = Var.vcov, tdf = den.df)

    ## Check the class and validity of the alldiffs object
    is.alldiffs(Var.diffs)
    validAlldiffs(Var.diffs)
  }
```

`angular` *Applies the angular transformation to proportions.*

Description

Applies the angular transformation to numeric values. It is given by $\sin^{-1}(\sqrt{proportions})$

Usage

```
angular(proportions, n)
```

Arguments

`proportions`	The proportions.
`n`	The divisor(s) for each proportion

Value

A numeric.

Author(s)

Chris Brien

See Also

angular.mod, powerTransform.

Examples

```
n <-25
y <- rbinom(10, n, 0.5)
y <- c(y,0,n)
p <- y/n
p.ang <- angular(p, n)
```

---

angular.mod *Applies the modified angular transformation to a vector of counts.*

Description

Applies the angular transformation to a vector of counts. A modified transformation is used that is appropriate when N < 50 and the proportion is not between 0.3 and 0.7. The transformation is given by $\sin^{-1} \frac{count+0.375}{n+0.75}$ arcsin(sqrt((count + 0.375) / (n + 0.75))).

Usage

```
angular.mod(count, n)
```

Arguments

count	The numeric vector of counts.
n	The number(s) of observations from which the count(s) were obtained.

Value

A numeric vector.

Author(s)

Chris Brien

See Also

angular, powerTransform.

Examples

```
n <-25
y <- rbinom(10, n, 0.5)
y <- c(y,0,n)
p.ang.mod <- angular.mod(y, n)
```

`as.alldiffs` *Forms an* `alldiffs.object` *from the supplied predictions, along with those statistics, associated with the predictions and their pairwise differences, that have been supplied.*

Description

Creates an `alldiffs.object` that consists of a `list` containing the following components: `predictions`, `vcov`, `differences`, `p.differences`, `sed`, `LSD` and `backtransforms`. Predictions must be supplied to the function while the others will be set only if they are supplied; those not supplied are set to `NULL`. It also has attributes `response`, `response.title`, `term`, `classify`, `tdf`, `sortFactor` and `sortOrder`. which will be set to the values supplied or `NULL` if none are supplied.

Usage

```
as.alldiffs(predictions, vcov = NULL, differences = NULL,
            p.differences = NULL, sed = NULL, LSD = NULL,
            backtransforms = NULL,
            response = NULL, response.title = NULL,
            term = NULL, classify = NULL, tdf = NULL,
            sortFactor = NULL, sortOrder = NULL)
```

Arguments

`predictions`	A `predictions.frame`, being a `data.frame` beginning with the variables classifying the predictions and also containing columns named `predicted.value`, `standard.error` and `est.status`; each row contains a single predicted value. It may also contain columns for the lower and upper limits of error intervals for the predictions. Note that the names `standard.error` and `est.status` have been changed to `std.error` and `status` in the `pvals` component produced by `asreml-R4`; if the new names are in the `data.frame` supplied to `predictions`, they will be returned to the previous names.
`differences`	A `matrix` containing all pairwise differences between the predictions; it should have the same number of rows and columns as there are rows in `predictions`.
`p.differences`	A `matrix` containing p-values for all pairwise differences between the predictions; each p-value is computed as the probability of a t-statistic as large as or larger than the observed difference divided by its standard error. The degrees of freedom of the t distribution for computing it are computed as the denominator degrees of freedom of the F value for the fixed term, if available; otherwise, the degrees of freedom stored in the attribute `tdf` are used; the matrix should be of the same size as that for `differences`.
`sed`	A `matrix` containing the standard errors of all pairwise differences between the predictions; they are used in computing the p-values.
`vcov`	A `matrix` containing the variance matrix of the predictions; it is used in computing the variance of linear transformations of the predictions.
`LSD`	A `data.frame` containing the mean, minimum and maximum LSD for determining the significance of pairwise differences, the mean LSD being calculated using the square root of the mean of the variances of pairwise differences. If `factor.combination` was specified for `meanLSD.type` when the LSDs were

being calculated, then LSD contains an LSD for each factor.combination of the factors specified by LSDby. Each LSD is calculated from the square root of the mean of the variances for all pairwise differences for each factor combination, unless there is only one prediction for a factor.combination, when notional LSDs are calculated that are based on the standard error of the prediction multiplied by the square root of two. If LSD is not NULL then the overall mean LSD will be added as an attribute named meanLSD of the alldiffs.object, as will the values of meanLSD.type and LSDby. The LSD for a single prediction assumes that any predictions to be compared are independent; this is not the case if residual errors are correlated.

backtransforms A data.frame containing the backtransformed values of the predicted values that is consistent with the predictions component, except that the column named predicted.value is replaced by one called backtransformed.predictions. Any error.interval values will also be the backtransformed values. Each row contains a single predicted value.

response A character specifying the response variable for the predictions. It is stored as an attribute to the alldiffs.object.

response.title A character specifying the title for the response variable for the predictions. It is stored as an attribute to the alldiffs.object.

term A character string giving the variables that define the term that was fitted using asreml and that corresponds to classify. It is often the same as classify. It is stored as an attribute to the alldiffs.object.

classify A character string giving the variables that define the margins of the multiway table used in the prediction. Multiway tables are specified by forming an interaction type term from the classifying variables, that is, separating the variable names with the : operator. It is stored as an attribute to the alldiffs.object.

tdf an integer specifying the degrees of freedom of the standard error. It is used as the degrees of freedom for the t-distribution on which p-values and confidence intervals are based. It is stored as an attribute to the alldiffs.object.

sortFactor A character containing the name of the factor that indexes the set of predicted values that determined the sorting of the components.

sortOrder A character vector that is the same length as the number of levels for sortFactor in the predictions component of the alldiffs.object. It specifies the order of the levels in the reordered components of the alldiffs.object.

The following creates a sortOrder vector levs for factor f based on the values in x: levs <-levels(f)[order(x)].

Value

An S3-class alldiffs.object. Also, see predictPlus.asreml for more information.

Author(s)

Chris Brien

See Also

asremlPlus-package, alldiffs.object, is.alldiffs, as.alldiffs, print.alldiffs, sort.alldiffs, subset.alldiffs, allDifferences.data.frame, renewClassify.alldiffs, redoErrorIntervals.alldiffs, recalcLSD.alldiffs, predictPlus.asreml, plotPredictions.data.frame, predictPresent.asreml

Examples

```
data(Oats.dat)

## Use asreml to get predictions and associated statistics

## Not run:
m1.asr <- asreml(Yield ~ Nitrogen*Variety,
                 random=~Blocks/Wplots,
                 data=Oats.dat)
current.asrt <- as.asrtests(m1.asr)
Var.pred <- asreml::predict.asreml(m1.asr, classify="Nitrogen:Variety",
                                   sed=TRUE)
if (getASRemlVersionLoaded(nchar = 1) == "3")
  Var.pred <- Var.pred$predictions
Var.preds <- Var.pred$pvals
Var.sed <- Var.pred$sed
Var.vcov <- NULL

## End(Not run)

## Use lmerTest and emmmeans to get predictions and associated statistics
if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  m1.lmer <- lmerTest::lmer(Yield ~ Nitrogen*Variety + (1|Blocks/Wplots),
                            data=Oats.dat)
  Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
  Var.preds <- summary(Var.emm)
  den.df <- min(Var.preds$df)
  ## Modify Var.preds to be compatible with a predictions.frame
  Var.preds <- as.predictions.frame(Var.preds, predictions = "emmean",
                                    se = "SE", interval.type = "CI",
                                    interval.names = c("lower.CL", "upper.CL"))
  Var.vcov <- vcov(Var.emm)
  Var.sed <- NULL
}

## Use the predictions obtained with either asreml or lmerTest
if (exists("Var.preds"))
{
  ## Form an all.diffs object
   Var.diffs <- as.alldiffs(predictions = Var.preds, classify = "Nitrogen:Variety",
                            sed = Var.sed, vcov = Var.vcov, tdf = den.df)

  ## Check the class and validity of the alldiffs object
  is.alldiffs(Var.diffs)
  validAlldiffs(Var.diffs)
}
```

`as.asrtests` *Forms an asrtests object that stores (i) a fitted asreml object, (ii) a pseudo-anova table for the fixed terms and (iii) a history of changes and hypthesis testing used in obtaining the model.*

Description

An asrtests.object that is a list consisting of the components asreml.obj, wald.tab and test.summary.

A call to as.asrtests with test.summary = NULL re-initializes the test.summary data.frame.

If there is no wald.tab, wald.asreml is called. In all cases, recalcWaldTab is called and any changes made as specified by the the recalcWaldTab arguments supplied via ....

Usage

```
as.asrtests(asreml.obj, wald.tab = NULL, test.summary = NULL,
            denDF = "numeric", ...)
asrtests(asreml.obj, wald.tab = NULL, test.summary = NULL,
         denDF = "numeric", ...)
```

Arguments

asreml.obj	an asreml object for a fitted model.
wald.tab	A data.frame containing a pseudo-anova table for the fixed terms produced by wald.asreml; it should have 4 or 6 columns. Sometimes wald.asreml returns a data.frame and at other times a list. For example, it may return a list when denDF is used. In this case, the Wald component of the list is to be extracted and stored. It is noted that, as of asreml version 4, wald.asreml has a kenadj argument.
test.summary	A data.frame with columns term, DF, denDF, p and action containing the results of previous hypothesis tests.
denDF	Specifies the enthod to use in computing approximate denominator degrees of freedom when wald.asreml is called. Can be none to suppress the computations, numeric for numerical methods, algebraic for algebraic methods or default, the default, to autommatically choose numeric or algebraic computations depending on problem size. The denominator degrees of freedom are calculated according to Kenward and Roger (1997) for fixed terms in the dense part of the model.
...	further arguments passed to wald.asreml and recalcWaldTab.

Value

An object of S3-class asrtests.

Author(s)

Chris Brien

See Also

asremlPlus-package, is.alldiffs, as.alldiffs, recalcWaldTab, testranfix.asrtests, chooseModel.asrtests, rmboundary.asrtests, reparamSigDevn.asrtests

Examples

```
## Not run:
data(Wheat.dat)

# Fit initial model
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)

# Load current fit into an asrtests object
current.asrt <- as.asrtests(current.asr, NULL, NULL)

# Check for and remove any boundary terms
current.asrt <- rmboundary(current.asrt)

## End(Not run)
```

---

as.predictions.frame *Forms a* predictions.frame *from a* data.frame*, ensuring that the correct columns are present.*

Description

Creates a predictions.frame from a data.frame by adding the class predictions.frame to it, and renaming the columns containing the predictions, se, est.status and error.intervals.

Usage

```
as.predictions.frame(data, predictions = NULL, se = NULL, est.status = NULL,
                     interval.type = NULL, interval.names = NULL)
```

Arguments

data	A data.frame containing columns giving the variables that uniquely index the predicted values and columns with the predicted values, their standard errors and, optionally, their estimation status (est.status).
predictions	A character giving the name of the column in data that contains the predicted values. This column will be renamed to predicted.value.
se	A character giving the name of the column in data that contains the standard errors of the predicted values. This column will be renamed to standard.error.
est.status	A character giving the name of the column in data that contains the estimation status of the predicted values. It will have a value Estimable for predicted values that have been estimated and a value Aliased for predicted values that are NA. If a column named est.status is not present in data and est.status is NULL, a column est.status will be generated.
interval.type	A character specifying the type of error.intervals stored in data that require renaming. If NULL, error.intervals will not be renamed, even if they are present. Otherwise, interval.type should be set to one of "CI", "SE" or "halfLSD".

`interval.names` A character specifying the column names of the lower and upper limits stored in data that are to be renamed. The character must be of length two, with the first element being the name of the 'lower' limit and the second element being the name of the 'upper' limit.

Value

An S3-class predictions.frame.

Author(s)

Chris Brien

See Also

asremlPlus-package, predictions.frame, is.predictions.frame, as.predictions.frame

Examples

```
  data(Oats.dat)

  ## Use asreml to get predictions and associated statistics

  ## Not run:
  m1.asr <- asreml(Yield ~ Nitrogen*Variety,
                   random=~Blocks/Wplots,
                   data=Oats.dat)
  current.asrt <- as.asrtests(m1.asr)
  Var.pred <- asreml::predict.asreml(m1.asr, classify="Nitrogen:Variety",
                                     sed=TRUE)
  if (getASRemlVersionLoaded(nchar = 1) == "3")
    Var.pred <- Var.pred$predictions
 #Form predictions.frame changing asreml-R4 names to the standard names, if these are present
  Var.preds <- as.predictions.frame(Var.pred$pvals, se = "std.error",
                                    est.status = "status")

## End(Not run)

  ## Use lmerTest and emmmeans to get predictions and associated statistics
  if (requireNamespace("lmerTest", quietly = TRUE) &
      requireNamespace("emmeans", quietly = TRUE))
  {
    m1.lmer <- lmerTest::lmer(Yield ~ Nitrogen*Variety + (1|Blocks/Wplots),
                              data=Oats.dat)
    Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
    Var.preds <- summary(Var.emm)
    Var.preds <- as.predictions.frame(Var.preds, predictions = "emmean",
                                      se = "SE", interval.type = "CI",
                                      interval.names = c("lower.CL", "upper.CL"))
  }

  ## Check the class and validity of the alldiffs object
  if (exists("Var.preds"))
  {
    is.predictions.frame(Var.preds)
    validPredictionsFrame(Var.preds)
  }
```

asremlPlus-deprecated *Deprecated Functions in the Package asremlPlus*

Description

These functions have been renamed and deprecated in asremlPlus:

1. addrm.terms.asreml and addrm.terms.asrtests -> changeTerms.asrtests,
2. alldiffs -> as.alldiffs,
3. choose.model.asreml and choose.model.asrtests -> chooseModel.asrtests,
4. info.crit and info.crit.asreml -> infoCriteria.asreml,
5. newrcov.asrtests -> changeTerms.asrtests,
6. plotvariofaces.asreml -> plotVariofaces.data.frame,
7. power.transform -> powerTransform,
8. predictiondiffs.asreml -> allDifferences.data.frame,
9. predictionplot.asreml -> plotPredictions.data.frame,
10. predictparallel.asreml -> predictPlus.asreml,
11. pred.present.asreml -> predictPresent.asreml,
12. recalc.wald.tab.asreml and recalc.wald.tab.asrtests -> recalcWaldTab.asrtests,
13. reorderClassify and reorderClassify.alldiffs -> renewClassify.alldiffs,
14. reml.lrt and reml.lrt.asreml -> REMLRT.asreml,
15. rmboundary.asreml -> rmboundary.asrtests,
16. setvarianceterms.asreml -> setvarianceterms.call,
17. sig.devn.reparam.asreml and sig.devn.reparam.asrtests -> reparamSigDevn.asrtests,
18. testranfix.asreml -> testranfix.asrtests,
19. testrcov.asreml and testrcov.asrtests -> testresidual.asrtests,
20. testswapran.asreml -> testswapran.asrtests

Usage

```
addrm.terms.asreml(...)
addrm.terms.asrtests(...)
alldiffs(...)
choose.model.asreml(...)
choose.model.asrtests(...)
info.crit(...)
info.crit.asreml(...)
newrcov.asrtests(...)
plotvariofaces.asreml(...)
power.transform(...)
predictiondiffs.asreml(...)
predictionplot.asreml(...)
predictparallel.asreml(...)
pred.present.asreml(...)
recalc.wald.tab.asreml(...)
```

```
recalc.wald.tab.asrtests(...)
reml.lrt(...)
reml.lrt.asreml(...)
## S3 method for class 'alldiffs'
reorderClassify(...)
## S3 method for class 'asreml'
rmboundary(...)
setvarianceterms.asreml(...)
sig.devn.reparam.asreml(...)
sig.devn.reparam.asrtests(...)
testranfix.asreml(...)
testrcov.asreml(...)
testrcov.asrtests(...)
## S3 method for class 'asreml'
testswapran(...)
```

Arguments

...	absorbs arguments passed from the old functions of the style foo.bar().

Author(s)

Chris Brien

---

asremlPlusTips *The randomly-presented, startup tips.*

Description

The intermittent, randomly-presented, startup tips.

Startup tips

Need help? The manual is a vignette and is in the vignettes subdirectory of the package's install directory.

Find out what has changed in asremlPlus: enter news(package = 'asremlPlus').

Need help getting started? Enter vignette(package = 'asremlPlus').

To avoid start-up message that ASReml-R is needed, load asreml before asremlPlus.

The methods for alldiffs and data.frame do not require asreml

Use suppressPackageStartupMessages() to eliminate all package startup messages.

To see all the intermittent, randomly-presented, startup tips enter ?asremlPlusTips.

To install the latest version: go to http://chris.brien.name/rpackages.

For versions between CRAN releases (and more) go to http://chris.brien.name/rpackages.

Author(s)

Chris Brien

asrtests.object *Description of an asrtests object*

Description

An object of S3-class asrtests that contains information derived from the fits of a mixed model using asreml.

as.asrtests is function that makes an object of this class.

is.list is the membership function for this class; it tests that an object is of class list.

validAsrtests can be used to test the validity of an asrtests.object.

Value

A list that contains three components:

1. asreml.obj: an object of class asreml that contains the fit of a model;
2. wald.tab: A data.frame containing a pseudo-anova table for the fixed terms produced by wald.asreml. It has rownames that corresond to the fixed terms that were fitted and four columns. If denominator degrees of freedom were calculated then the columns are Df, denDF, F.inc, Pr; otherwise the columns are Df, Sum of Sq, Wald statistic, and Pr(Chisq).
3. test.summary: A data.frame with columns term, DF, denDF, p and action. A row is added to it for each term that is dropped, added or tested or a note that several terms have been added or removed. A row contains the name of the term, the DF, the p-value and the action taken. Possible codes are: Dropped, Retained, Swapped, Unswapped, Significant, Nonsignificant, Absent, Added, Removed and Boundary. If the changed model did not converge, Unconverged will be added to the code. Note that the logical asreml.obj$converge also reflects whether there is convergence.

Author(s)

Chris Brien

See Also

as.asrtests, as.asrtests, validAsrtests

bootREMLRT.asreml *Uses the parametric bootstrap to calculate the p-value for a REML ratio test to compare two models.*

Description

Extracts the REML log likelihood for two asreml objects and forms the observed REML ratio statistic. It assumes that the second asreml object is the result of fitting a model that is a reduced version of the model for the first object and is considered to the null model. Using the mean and V, nboot bootstrap samples of simulated response values are generated in parallel; that is, ncores cores are used and each is used to generate and analyse a sample. The full and reduced models are fitted to the data and if either analysis fails to converge another sample is generated and analysed using the current core, with a maximum of max.retries attempts to obtain a sample that converges for both analysis. Thus the maximum number of data sets that will be generated is nboot * max.retries. If a bootstrap sample converges for both analyses, the REML ratio test statistic is formed for it. The p-value is then calculated as $(k+1)/(b+1)$ where k is the number of simulated ratio test statistics greater than the observed test statistic and s is the number of bootstrap samples that were returned.

The function checks that the models do not differ in either their fixed or sparse models. It also check the difference in the number of variance parameters between the two fits to the models, taking into account the bound.exclusions.

Usage

```
## S3 method for class 'asreml'
bootREMLRT(h0.asreml.obj, h1.asreml.obj,
           nboot = 100, max.retries = 5, seed = NULL,
           means=NULL, V = NULL, extra.matrix = NULL, ignore.terms = NULL,
           fixed.spline.terms = NULL,
           bound.exclusions = c("F","B","S","C"),
           tolerance = 1E-10, update = TRUE, trace = FALSE,
           ncores = detectCores(), ...)
```

Arguments

h0.asreml.obj	asreml object containing the fit under the model for the null hypothesis.
h1.asreml.obj	asreml object containing the fit under the model for the alternative hypothesis.
nboot	The number of bootstrap samples to be generated.
max.retries	The maximum number of attempts to generate a sample whose analyses converge for both models.
seed	A single value, interpreted as an integer, that specifies the starting value of the random number generator. The "L'Ecuyer-CMRG" random generator is used and nextRNGStream is used to seed each core from the original seed.
means	The vector of means to be used in generating simulated bootstrap samples. If it is NULL, the fitted values based on object are used. It must be the same length as the response variable for object.
V	The fitted variance matrix, i.e. having the pattern and values that conform to the model fit stored in the supplied object. If it is NULL, estimateV.asreml is used to estimate the variance matrix for the observations from the variance parameter estimates from the reduced.asreml.obj.
extra.matrix	A matrix of order equal to the number of observations that is to be added to the variance matrix, the latter based on the information in asreml.obj. It is assumed that the sigma-parameterized values of the variance parameter estimates, such as is given in the varcomp component of summary.asreml, have been used in calculating extra.matrix; the values in the vparameters component of G.param and R.param may be either gamma- or sigma-parameterized.

The argument extra.matrix can be used in conjunction with ignore.terms as a workaround to include components of the variance matrix for variance functions that have not been implemented in estimateV.

ignore.terms A character giving terms from either the random or residual models that are to be ignored in that their contributions to the variance is not to be included in the estimated matrix. The term names are those given in the vparameters component of the asreml object or the varcomp component produced by summary.asreml, but only up to the first exclamation mark (!). This can be used in conjunction with estimateV.asreml as a workaround to include components of the variance matrix for variance functions that have not been implemented in estimateV.

fixed.spline.terms
A character vector giving one or mor spline terms in the random model that are regarded as fixed and so are to be ignored because they are not regarded as contributing to the variance. The term names are those given in the vparameters component of the asreml object or the varcomp component produced by summary.asreml, but only up to the first exclamation mark (!).

bound.exclusions
A character specifying one or more bound codes that will result in a variance parameter in the random model being excluded from contributing to the variance. If set to NULL then none will be excluded.

tolerance The value such that eigenvalues less than it are considered to be zero.

update If TRUE then the arguments R.param and G.param are set to those in the asreml object supplied in object so that the values from the original model are used as starting values. If FALSE then calls are made to asreml in which the only changes from the previous call are (i) the model is fitted to simulated data and (ii) modifications specified via ... are made, except that changes cannot be made to any of the models.

trace If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.

ncores A numeric specifying the number of cores to use in doing the simulations.

... Other arguments that are passed down to the function asreml. Changes to the models are not allowed. Other changes are dangerous and generally should be avoided.

Value

A list with the following components:

1. **REMLRT:** the observed REML ratio statistic.
2. **p:** the bootstrap p-value for the observed test statistic.
3. **DF:** the calculated difference in DF for the variance parameters in the two models.
4. **totalunconverged:** the total number of unconverged analyses over the simulations.
5. **REMLRT.sim:** a numeric containing the values of the ratio statistics for the simulated data. It has an attribute called na.action that can be retrieved using attr(REMLRT.sim,which = "na.action"); it contains a list of the simulation numbers that were abandoned because max.retries failed to converge for both models.
6. **nunconverged:** the number of unconverged analyses for each bootstap sample, the maximum being max.retries.

Note

A boostrap sample is generated using a multivariate normal distribution with expected value as specified by `means` and variance matrix given by `V`. Each simulated sample is analysed according to the reduced model and, provided this analysis converges, according to the full.model. If one of these analyses fails to converge, it is abandoned and another sample is generated for this simulation. As many as `max.retries` attempts are made to generate a data set for which both analyses converge. If data set that converges for both analyses is not generated for a simulation, `NA` is returned for that bootstrap sample. Hence, the maximum number of data sets that will be generated is `nboot` * `max.retries` and less than `nboot` samples will be generated if a data set that converges for both analyses is not obtained within `max.retries` attempts.

If a bootstrap sample converges for both analyses, the REML ratio test statistic is calculated as $2(log(REML)_F - log(REML)_R)$.

The `DF` is calculated from the information in `full.asreml.obj` and `reduced.asreml.obj`. The degrees of freedom are computed as the difference between the two models in the number of variance parameters whose estimates do not have a code for bound specified in `bound.exclusions`.

If ASReml-R version 4 is being used then the codes specified in `bound.exclusions` are not restricted to a subset of the default codes, but a warning is issued if a code other than these is specified. For ASReml-R version 3, only a subset of the default codes are allowed: `F` (`Fixed`), `B` (`Boundary`), `C` (`Constrained`) and `S` (`Singular`).

Author(s)

Chris Brien

See Also

`REMLRT.asreml`, `infoCriteria.asreml`, `testranfix.asrtests`

Examples

```
## Not run:
    bootREMLRT(ICV.max, ICV.red, ncores = 2)

## End(Not run)
```

`changeTerms.asrtests` *Adds and drops the specified sets of terms from one or both of the fixed or random model and/or replaces the residual (rcov) model with a new model.*

Description

The specified terms are simply added or dropped, without testing, from either the fixed or random model and/or the residual (rcov) model replaced. No hypothesis testing is performed, but a check is made for boundary or singular terms. A row is added to the `test.summary` `data.frame` using the supplied `label` and stating which models have been changed. Convergence in fitting the model is checked and a note included in the action if there was not. All components of the `asrtests.object` are updated.

Usage

```
## S3 method for class 'asrtests'
changeTerms(asrtests.obj,
            dropFixed = NULL, addFixed = NULL,
            dropRandom = NULL,  addRandom = NULL,
            newResidual = NULL, label = "Changed terms",
            allow.unconverged = TRUE, checkboundaryonly = FALSE,
            trace = FALSE, update = TRUE, denDF = "numeric",
            set.terms = NULL, ignore.suffices = TRUE,
            bounds = "P", initial.values = NA, ...)
```

Arguments

asrtests.obj	An asrtests.object containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary.
dropFixed	A single character string in the form of a formula which, after addition of ". ~ . -" and after expansion, specifies the sum of a set of terms to be dropped from the fixed formula.
addFixed	A single character string in the form of a formula which, after addition of ". ~ . +" and expansion, specifies the sum of a set of terms to be added to the fixed formula.
dropRandom	A single character string in the form of a formula which, after addition of " ~ . -" and expansion, specifies the sum of a set of terms to be dropped from the random formula.
addRandom	A single character string in the form of a formula which, after addition of " ~ . +"and expansion, specifies the sum of a set of terms to be added to the random formula.
newResidual	A single character string in the form of a formula which, after addition of " ~ ", specifies the residual (or rcov) model. To remove the model, enter "-(.)".
label	A character string to use as the label in test.summary and which indicates what is being tested.
allow.unconverged	A logical indicating whether to accept a new model even when it does not converge. If FALSE and the fit does not converge, the supplied asreml object is returned.
checkboundaryonly	If TRUE then boundary and singular terms are not removed by rmboundary.asrtests; a warning is issued instead.
trace	If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.
update	If TRUE then update.asreml is called to fit the model to be tested. In doing this the arguments R.param and G.param are set to those in the asreml object stored in asrtests.obj so that the values from the previous model are used as starting values. If FALSE then a call is made to asreml in which the only changes from the previous call are that (i) models are modifed as specified and (ii) modifications specified via ... are made.
denDF	Specifies the enthod to use in computing approximate denominator degrees of freedom when wald.asreml is called. Can be none to suppress the computations, numeric for numerical methods, algebraic for algebraic methods or

default, the default, to autommatically choose numeric or algebraic computations depending on problem size. The denominator degrees of freedom are calculated according to Kenward and Roger (1997) for fixed terms in the dense part of the model.

set.terms A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting.

ignore.suffices
A logical vector specifying whether the suffices of the asreml-assigned names of the variance terms (i.e. the information to the right of an "!", other than "R!") is to be ignored in matching elements of terms. If TRUE for an element of terms, the suffices are stripped from the asreml-assigned names. If FALSE for an element of terms, the element must exactly match an asreml-assigned name for a variance term. This vector must be of length one or the same length as terms. If it is of length one then the same action is applied to the asreml-assigned suffices for all the terms in terms.

bounds A character vector specifying the bounds to be applied to the terms specified in set.terms. This vector must be of length one or the same length as set.terms. If it is of length one then the same constraint is applied to all the terms in set.terms. If any of the bounds are equal to NA then they are left unchanged for those terms.

initial.values A character vector specifying the initial values for the terms specified in terms. This vector must be of length one or the same length as terms. If it is of length one then the same initial value is applied to all the terms in terms. If any of the initial.values are equal to NA then they are left unchanged for those terms.

... Further arguments passed to asreml, wald.asreml and as.asrtests.

Value

An asrtests.object containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary.

Author(s)

Chris Brien

See Also

as.asrtests, rmboundary.asrtests, testranfix.asrtests, testresidual.asrtests, newfit.asreml, reparamSigDevn.asrtests, chooseModel.asrtests

Examples

```
## Not run:
terms <- "(Date/(Sources * (Type + Species)))"
current.asrt <- changeTerms(current.asrt, addFixed = terms)

current.asrt <- changeTerms(current.asrt, dropFixed = "A + B", denDF = "algebraic")

data(Wheat.dat)
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
```

```
current.asrt <- rmboundary(current.asrt)
# Add and drop both fixed and random terms
current.asrt <- changeTerms(current.asrt,
                            addFixed = "vRow", dropFixed = "WithinColPairs",
                            addRandom = "spl(vRow)", dropRandom = "units",
                            checkboundaryonly = TRUE)
# Replace residual with model without Row autocorrelation
current.asrt <- changeTerms(current.asrt,
                            newResidual = "Row:ar1(Column)",
                            label="Row autocorrelation")


## End(Not run)
```

`chooseModel.asrtests` *Determines the set of significant terms taking into account the hierarchy or marginality relations and records the tests performed in an* `asrtests.object`.

Description

Performs a series of hypothesis tests taking into account the marginality of terms. In particular, a term will not be tested if it is marginal to (or nested in) one that is significant. For example, if A:B is significant, then neither A nor B will be tested. For a random term, the term is removed from the model fit, any boundary terms are removed using `rmboundary.asrtests` and a REML likelihood ratio test is performed using `REMLRT.asreml`. If it is not significant and `drop.ran.ns` is TRUE, the term is permanently removed from the model. Note that if boundary terms are removed, the reduced model may not be nested in the full model in which case the test is not valid. For fixed terms, the Wald tests are performed and the p-value for the term obtained. If it is not significant and `drop.fix.ns` is TRUE, the term is permanently removed from the model. A row is added to `test.summary` for each term that is tested.

Usage

```
## S3 method for class 'asrtests'
chooseModel(asrtests.obj, terms.marginality=NULL,
            alpha = 0.05, allow.unconverged = TRUE,
            checkboundaryonly = FALSE, drop.ran.ns=TRUE,
            positive.zero = FALSE, bound.test.parameters = "none",
            drop.fix.ns=FALSE, denDF = "numeric",  dDF.na = "none",
            dDF.values = NULL, trace = FALSE, update = TRUE,
            set.terms = NULL, ignore.suffices = TRUE,
            bounds = "P", initial.values = NA, ...)
```

Arguments

`asrtests.obj` an `asrtests.object` containing the components (i) `asreml.obj`, (ii) `wald.tab`, and (iii) `test.summary`.

`terms.marginality`
A square matrix of ones and zeros with row and column names being the names of the terms. The diagonal elements should be one, indicating that a term is marginal to itself. Elements should be one if the row term is marginal to the column term. All other elements should be zero.

alpha The significance level for the test.

allow.unconverged
A logical indicating whether to accept a new model even when it does not converge. If FALSE and a fit when a term is removed does not converge, the term will not be removed.

checkboundaryonly
If TRUE then boundary and singular terms are not removed by rmboundary.asrtests; a warning is issued instead.

drop.ran.ns A logical indicating whether to drop nonsignificant random terms from the model.

positive.zero Indicates whether the hypothesized values for the variance components being tested are on the boundary of the parameter space. For example, this is true for positively-constrained variance components that, under the reduced model, are zero. This argument does not need to be set if bound.test.parameters is set.

bound.test.parameters
Indicates whether for the variance components being tested, at least some of the hypothesized values are on the boundary of the parameter space. The possibilities are "none", "onlybound" and "one-and-one". The default is "none", although if it is set to "none" and positive.zero is TRUE then bound.test.parameters is taken to be "onlybound". When bound.test.parameters is set to "one-and-one", it signifies that there are two parameters being tested, one of which is bound and the other is not. For example, the latter is true for testing a covariance and a positively-constrained variance component that, under the reduced model, are zero.

drop.fix.ns A logical indicating whether to drop a fixed term from the model when it is nonsignificant

denDF Specifies the enthod to use in computing approximate denominator degrees of freedom when wald.asreml is called. Can be none to suppress the computations, numeric for numerical methods, algebraic for algebraic methods or default, the default, to autommatically choose numeric or algebraic computations depending on problem size. The denominator degrees of freedom are calculated according to Kenward and Roger (1997) for fixed terms in the dense part of the model.

dDF.na The method to use to obtain substitute denominator degrees of freedom. when the numeric or algebraic methods produce an NA. If dDF.na = "none", no substitute denominator degrees of freedom are employed; if dDF.na = "residual", the residual degrees of freedom from asreml.obj$nedf are used; if dDF.na = "maximum", the maximum of those denDF that are available, excluding that for the Intercept, is used; if all denDF are NA, asreml.obj$nedf is used. If dDF.na = "supplied", a vector of values for the denominator degrees of freedom is to be supplied in dDF.values. Any other setting is ignored and a warning message produced. Generally, substituting these degrees of freedom is anticonservative in that it is likely that the degrees of freedom used will be too large.

dDF.values A vector of values to be used when dDF.na = "supplied". Its values will be used when denDF in a test for a fixed effect is NA. This vector must be the same length as the number of fixed terms, including (Intercept) whose value could be NA.

trace If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.

update If TRUE then update.asreml is called in testing models. In doing this the arguments R.param and G.param are set to those in the asreml object stored in

asrtests.obj so that the values from the previous model are used as starting values. If FALSE then a call is made to asreml in which the only changes to the asreml.obj stored in the supplied asrtests.obj are (i) to the terms in the fixed and random models corresponding to terms in terms.marginality and (ii) those modifications specified via ....

set.terms — A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting.

ignore.suffices — A logical vector specifying whether the suffices of the asreml-assigned names of the variance terms (i.e. the information to the right of an "!", other than "R!") is to be ignored in matching elements of terms. If TRUE for an element of terms, the suffices are stripped from the asreml-assigned names. If FALSE for an element of terms, the element must exactly match an asreml-assigned name for a variance term. This vector must be of length one or the same length as terms. If it is of length one then the same action is applied to the asreml-assigned suffices for all the terms in terms.

bounds — A character vector specifying the bounds to be applied to the terms specified in set.terms. This vector must be of length one or the same length as set.terms. If it is of length one then the same constraint is applied to all the terms in set.terms. If any of the bounds are equal to NA then they are left unchanged for those terms.

initial.values — A character vector specifying the initial values for the terms specified in terms. This vector must be of length one or the same length as terms. If it is of length one then the same initial value is applied to all the terms in terms. If any of the initial.values are equal to NA then they are left unchanged for those terms.

... — further arguments passed to asreml, wald.asreml and as.asrtests via testranfix.asrtests.

Value

A list containing:

1. asrtests.obj: an asrtests.object containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary.;
2. sig.tests: a character vector whose elements are the the significant terms amongst those tested.

Author(s)

Chris Brien

See Also

as.asrtests, testranfix.asrtests, testresidual.asrtests, REMLRT.asreml, rmboundary.asrtests, newfit.asreml, changeTerms.asrtests, reparamSigDevn.asrtests

Examples

```
## Not run:
data(WaterRunoff.dat)
asreml.options(keep.order = TRUE) #required for asreml-R4 only
current.asr <- asreml(log.Turbidity ~ Benches + (Sources * (Type + Species)) * Date,
                      random = ~Benches:MainPlots:SubPlots:spl(xDay),
```

```
                      data = WaterRunoff.dat, keep.order = TRUE)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
terms.treat <- c("Sources", "Type", "Species",
                 "Sources:Type", "Sources:Species")
terms <- sapply(terms.treat,
                FUN=function(term){paste("Date:",term,sep="")},
                simplify=TRUE)
terms <- c("Date", terms)
terms <- unname(terms)
marginality <-  matrix(c(1,0,0,0,0,0, 1,1,0,0,0,0,  1,0,1,0,0,0,
                         1,0,1,1,0,0, 1,1,1,0,1,0, 1,1,1,1,1,1), nrow=6)
rownames(marginality) <- terms
colnames(marginality) <- terms
choose <- chooseModel(current.asrt, marginality)
current.asrt <- choose$asrtests.obj
sig.terms <- choose$sig.terms

## End(Not run)
```

`estimateV.asreml` *Forms the estimated variance, random or residual matrix for the observations from the variance parameter estimates.*

Description

Forms the estimated variance (**V**), random (**G**) or (**R**) matrix for the observations, a square symmetric matrix of order equal to the number of observations. The estimates of the variance parameters and the information about the `random` and `residual` models for which they were estimated are obtained from the `asreml` object. This function is not available in ASReml-R version 3.

Usage

```
## S3 method for class 'asreml'
estimateV(asreml.obj, which.matrix = "V",
          extra.matrix = NULL, ignore.terms = NULL, fixed.spline.terms = NULL,
          bound.exclusions = c("F","B","S","C"), ...)
```

Arguments

`asreml.obj`	An `asreml` object from a call to `asreml` in which the `data` argument has been set.
`which.matrix`	A `character` giving the matrix that is to be formed. It must be one of `"V"`, to produce the variance matrix $\mathbf{V} = \mathbf{G} + \mathbf{R}$, `"G"` to produce the matrix **G**, corresponding to the `random` formula, or `"R"` to produce the matrix **R**, corresponding to the `residual` formula.
`extra.matrix`	A `matrix` of order equal to the number of observations that is to be added to the `matrix` specified by `which.matrix`, the latter based on the information in `asreml.obj`. It is assumed that the sigma-parameterized values of the variance parameter estimates, such as is given in the `varcomp` component of `summary.asreml`, have been used in calculating `extra.matrix`; the values in the `vparameters` component of `G.param` and `R.param` may be either gamma-

or sigma-parameterized. The argument `extra.matrix` can be used in conjunction with `ignore.terms` as a workaround to include components of the variance matrix for variance functions that have not been implemented in `estimateV`.

`ignore.terms` A `character` giving terms from either the `random` or `residual` models that are to be ignored in that their contributions to the variance is not to be included in the estimated matrix. The term names are those given in the `vparameters` component of the `asreml` object or the `varcomp` component produced by `summary.asreml`, but only up to the first exclamation mark (`!`). This can be used in conjunction with `estimateV.asreml` as a workaround to include components of the variance matrix for variance functions that have not been implemented in `estimateV`.

`fixed.spline.terms`
A `character` vector giving one or mor spline terms in the `random` model that are regarded as fixed and so are to be ignored because they are not regarded as contributing to the variance. The term names are those given in the `vparameters` component of the `asreml` object or the `varcomp` component produced by `summary.asreml`, but only up to the first exclamation mark (`!`).

`bound.exclusions`
A `character` specifying one or more bound codes that will result in a variance parameter in the `random` model being excluded from contributing to the variance. If set to `NULL` then none will be excluded.

`...` Provision for passsing arguments to functions called internally - not used at present.

Details

The information about the variance parameters in the fitted mixed model are obtained from the `G.param` and `R.param` components of the `asreml` object. The function can deal with the following variance functions in either the `random` or `residual` models: `id`, `diag`, `us`, `ar1`, `ar2`, `ar3`, `sar`,`sar2`, `ma1`, `ma2`, `arma`, `exp`, `gau`, `cor`, `corb` and `corg`. All of these functions, except `us`, can be combined with either `v` or `h`. It will also cope with the following functions in the `random` model: `at`, `str`, `spl`, `dev`, `grp`, `fa` and `rr`. Additionally, it can deal with the function `dsum` in the `residual` model. For further information see the ASReml-R User Guide Version 4 (Butler et al., 2018).

Value

A `matrix` containing the estimated variance matrix.

Author(s)

Chris Brien

References

Butler, D. G., Cullis, B. R., Gilmour, A. R., Gogel, B. J. and Thompson, R. (2018). *ASReml-R Reference Manual Version 4.* VSN International Ltd, http://asreml.org.

See Also

`asreml`, `simulate.asreml`, `variofaces.asreml`.

Examples

```
## Not run:
data(Wheat.dat)
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)
# Form variance matrix based on estimated variance parameters
V <- estimateV(current.asr)


## End(Not run)
```

---

facCombine.alldiffs *Combines several factors into one in the components of an alldiffs.object*

Description

Combines several factors, in the prediction component of object, into one whose levels are the combinations of the used levels of the individual factors. The matching changes are made to the other components of the alldiffs.object. The levels of the factors are combined using fac.combine from the dae package.

Usage

```
## S3 method for class 'alldiffs'
facCombine(object, factors, order="standard",
           combine.levels=TRUE, sep="_", level.length = NA, ...)
```

Arguments

object	An alldiffs.object.
factors	A character containing the names of factors in the prediction component of object whose levels are to be combined.
order	Either standard or yates. The order in which the levels combinations of the factors are to be considered as numbered when forming the levels of the combined factor; standard numbers them as if they are arranged in standard order, that is with the levels of the first factor moving slowest and those of the last factor moving fastest; yates numbers them as if they are arranged in Yates order, that is with the levels of the first factor moving fastest and those of the last factor moving slowest.
combine.levels	A logical specifying whether the levels labels of the new factor are to be combined from those of the factors being combined. The default is to use the integers from 1 to the product of the numbers of combinations of used levels of the individual factors, numbering the levels according to order.
sep	A character string to separate the levels when combine.levels = TRUE.
level.length	The maximum number of characters from the the levels of factors to use in the row and column labels of the tables of pairwise differences and their p-values and standard errors.
...	Further arguments passed to the factor call creating the new factor.

Value

A factor whose levels are formed form the observed combinations of the levels of the individual factors.

Author(s)

Chris Brien

See Also

as.alldiffs, allDifferences.data.frame, print.alldiffs, sort.alldiffs, renewClassify.alldiffs, fac.combine in package **dae**.

Examples

```
  data("Ladybird.dat")

  ## Use asreml to get predictions and associated statistics

  ## Not run:
  m1.asr <- asreml(logitP ~ Host*Cadavers*Ladybird,
                   random = ~ Run,
                   data = Ladybird.dat)
  current.asrt <- as.asrtests(m1.asr)
  HCL.pred <- asreml::predict.asreml(m1.asr, classify="Host:Cadavers:Ladybird",
                                     sed=TRUE)
  HCL.preds <- HCL.pred$pvals
  HCL.sed <- HCL.pred$sed
  HCL.vcov <- NULL
  wald.tab <-  current.asrt$wald.tab
  den.df <- wald.tab[match("Host:Cadavers:Ladybird", rownames(wald.tab)), "denDF"]

## End(Not run)

  ## Use lmeTest and emmmeans to get predictions and associated statistics
  if (requireNamespace("lmerTest", quietly = TRUE) &
      requireNamespace("emmeans", quietly = TRUE))
  {
    m1.lmer <- lmerTest::lmer(logitP ~ Host*Cadavers*Ladybird + (1|Run),
                              data=Ladybird.dat)
    HCL.emm <- emmeans::emmeans(m1.lmer, specs = ~ Host:Cadavers:Ladybird)
    HCL.preds <- summary(HCL.emm)
    den.df <- min(HCL.preds$df)
    ## Modify HCL.preds to be compatible with a predictions.frame
    HCL.preds <- as.predictions.frame(HCL.preds, predictions = "emmean",
                                      se = "SE", interval.type = "CI",
                                      interval.names = c("lower.CL", "upper.CL"))
    HCL.vcov <- vcov(HCL.emm)
    HCL.sed <- NULL
  }

  ## Use the predictions obtained with either asreml or lmerTest
  if (exists("HCL.preds"))
  {
    ## Form an all.diffs object
   HCL.diffs <- as.alldiffs(predictions = HCL.preds, classify = "Host:Cadavers:Ladybird",
```

```
                              sed = HCL.sed, vcov = HCL.vcov, tdf = den.df)

  ## Check the class and validity of the alldiffs object
  is.alldiffs(HCL.diffs)
  validAlldiffs(HCL.diffs)

  ## Combine Cadavers and Ladybird
  HCL.diffs <- facCombine(HCL.diffs, factors = c("Cadavers","Ladybird"))

  ## Check the validity of HCL.diffs
  validAlldiffs(HCL.diffs)
}
```

`getASRemlVersionLoaded` *Finds the version of asreml that is loaded and returns the initial characters in version.*

Description

Checks that `asreml` is loaded and, if it is, returns the first `nchar` characters of the version that is loaded.

Usage

```
getASRemlVersionLoaded(nchar = NULL, notloaded.fault = FALSE)
```

Arguments

`nchar`	The number of characters in the asreml version to get.
`notloaded.fault`	A `logical` indicating whether a fault is to occur if `asreml` is not loaded.

Value

A character, being the first `nchar` characters of the version of `asreml` that is loaded.

Author(s)

Chris Brien

See Also

`loadASRemlVersion`.

Examples

```
## Not run:
getASRemlVersionLoaded()
## End(Not run)
```

`getTestPvalue.asrtests` *Gets the p-value for a test recorded in the test.summary data.frame of an* `asrtests.object`

Description

Matches the `label` in the `term` column of the supplied `asrtests.object` and extracts the its p-value. It only matches the first occurence of `label`.

Usage

```
## S3 method for class 'asrtests'
getTestPvalue(asrtests.obj, label, ...)
```

Arguments

`asrtests.obj`	An `asrtests.object` containing the components (i) `asreml.obj`, (ii) `wald.tab`, and (iii) `test.summary`.
`label`	A `character` specifying the `label` of the test for which the p-value is required. If `testranfix.asrtests` was used for the test of interest, then the `label` will be the value of the `term` argument supplied to `testranfix.asrtests`.
`...`	provision for passsing arguments to functions called internally - not used at present.

Value

An `numeric` containing the p-value. It can be `NA`, for example when a p-value could not be calculated.

Author(s)

Chris Brien

See Also

`as.asrtests`, `testranfix.asrtests`, `testswapran.asrtests`, `testresidual.asrtests`, `changeTerms.asrtests`, `chooseModel.asrtests`

Examples

```
## Not run:
data(Wheat.dat)
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
current.asrt <- rmboundary(current.asrt)
# Test nugget term
current.asrt <- testranfix(current.asrt, "units", positive=TRUE)
getTestPvalue(current.asrt, label = "units")
```

```
## End(Not run)
```

`infoCriteria.asreml` *Computes AIC and BIC for a model.*

Description

Computes Akiake and Bayesian (Schwarz) Information Criteria for a model.

Usage

```
## S3 method for class 'asreml'
infoCriteria(asreml.obj, DF = NULL,
            bound.exclusions = c("F","B","S","C"), ...)
```

Arguments

`asreml.obj`	An `asreml` object resulting from the fitting of a model using REML.
`DF`	A `numeric` giving the number of estimated variance parameters. If `NULL` then this is determined from the information in `asreml.obj`.
`bound.exclusions`	A `character` specifying the bound (constraint) codes that will result in a variance parameter being excluded from the count of estimated variance parameters. If set to `NULL` then none will be excluded.
`...`	Provision for passsing arguments to functions called internally - not used at present.

Details

The degrees of freedom (DF) are the number of number of variance parameters that have been estimated, excluding those whose estimates have a code for bound specified in `bound.exclusions`. If `DF` is not `NULL`, the supplied value is used. Otherwise `DF` is determined from the information in `asreml.obj`.

If ASReml-R version 4 is being used then the codes specified in `bound.exclusions` are not restricted to a subset of the default codes, but a warning is issued if a code other than these is specified. For ASReml-R version 3, only a subset of the default codes are allowed: `F` (`Fixed`), `B` (`Boundary`), `C` (`Constrained`) and `S` (`Singular`).

The AIC is calculated as $-2 \times log(REML) + 2 \times DF$ and the BIC as $-2 \times log(REML) + DF \times (n - p)$, where n is the number of observations and r is the rank of the fixed effects design matrix.

Value

A data frame containing the degrees of freedom, number of bound parameters, AIC, BIC and log of the REML value.

Author(s)

Chris Brien

See Also

REMLRT.asreml

Examples

```
## Not run:
   data(Wheat.dat)
   current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                         random = ~ Row + Column + units,
                         residual = ~ ar1(Row):ar1(Column),
                         data=Wheat.dat)
    infoCriteria(current.asr)

## End(Not run)
```

---

is.alldiffs *Tests whether an object is of class alldiffs*

Description

A single-line function that tests whether an object is of class alldiffs.

Usage

```
is.alldiffs(object)
```

Arguments

object	An object to be tested.

Value

A logical.

Author(s)

Chris Brien

See Also

asremlPlus-package, alldiffs.object, is.alldiffs, as.alldiffs

Examples

```
  data(Oats.dat)

  ## Use lmerTest and emmmeans to get predictions and associated statistics
  if (requireNamespace("lmerTest", quietly = TRUE) &
      requireNamespace("emmeans", quietly = TRUE))
  {
    m1.lmer <- lmerTest::lmer(Yield ~ Nitrogen*Variety + (1|Blocks/Wplots),
                              data=Oats.dat)
    Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
```

```
  Var.preds <- summary(Var.emm)
  den.df <- min(Var.preds$df)
  ## Modify Var.preds to be compatible with a predictions.frame
  Var.preds <- as.predictions.frame(Var.preds, predictions = "emmean",
                                    se = "SE", interval.type = "CI",
                                    interval.names = c("lower.CL", "upper.CL"))
  Var.vcov <- vcov(Var.emm)
  Var.sed <- NULL

## Form an all.diffs object
 Var.diffs <- as.alldiffs(predictions = Var.preds, classify = "Nitrogen:Variety",
                          sed = Var.sed, vcov = Var.vcov, tdf = den.df)

## check the class of Var.diffs
is.alldiffs(Var.diffs)
}
```

`is.asrtests` *Tests whether an object is of class asrtests*

Description

A single-line `function` that tests whether an object is of `class` `asrtests`.

Usage

```
is.asrtests(object)
```

Arguments

`object`	An `object` to be tested.

Value

A `logical`.

Author(s)

Chris Brien

See Also

`asremlPlus-package`, `asrtests.object`, `is.asrtests`, `as.asrtests`

Examples

```
## Not run:
library(dae)
library(asreml)
library(asremlPlus)
## use ?Wheat.dat for data set details
data(Wheat.dat)

# Fit initial model
```

```
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)

# Load current fit into an asrtests object
current.asrt <- as.asrtests(current.asr, NULL, NULL)

# check the class of current.asrt
is.asrtests(current.asrt)

## End(Not run)
```

`is.predictions.frame` *Tests whether an object is of class predictions.frame*

Description

A single-line `function` that tests whether an object is of `class` `predictions.frame`.

Usage

```
is.predictions.frame(object)
```

Arguments

`object`	An `object` to be tested.

Value

A `logical`.

Author(s)

Chris Brien

See Also

`asremlPlus-package`, `predictions.frame`, `is.predictions.frame`, `as.predictions.frame`

Examples

```
data(Oats.dat)

## Use asreml to get predictions and associated statistics

## Not run:
m1.asr <- asreml(Yield ~ Nitrogen*Variety,
                 random=~Blocks/Wplots,
                 data=Oats.dat)
current.asrt <- as.asrtests(m1.asr)
Var.pred <- asreml::predict.asreml(m1.asr, classify="Nitrogen:Variety",
                                   sed=TRUE)
if (getASRemlVersionLoaded(nchar = 1) == "3")
```

```
  Var.pred <- Var.pred$predictions
Var.preds <- as.predictions.frame(Var.pred$pvals, se = "std.error",
                                  est.status = "status")

## End(Not run)

  ## Use lmerTest and emmmeans to get predictions and associated statistics
  if (requireNamespace("lmerTest", quietly = TRUE) &
      requireNamespace("emmeans", quietly = TRUE))
  {
    m1.lmer <- lmerTest::lmer(Yield ~ Nitrogen*Variety + (1|Blocks/Wplots),
                              data=Oats.dat)
    Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
    Var.preds <- summary(Var.emm)
    Var.preds <- as.predictions.frame(Var.preds, predictions = "emmean",
                                      se = "SE", interval.type = "CI",
                                      interval.names = c("lower.CL", "upper.CL"))
  }

  if (exists("Var.preds"))
  {
    ## Check the class and validity of the alldiffs object
    is.predictions.frame(Var.preds)
  }
```

`Ladybird.dat` *Data for an experiment to investigate whether ladybirds transfer aphids*

Description

Welham et al. (2015, Example 8.2) describe a three-factor factorial experiment to investigate whether ladybirds transfer fungus to live aphids on plants. The three factors are Host plant (beans, trefoil), infected Cadavers (5, 10, 20), and Ladybird (-, +). A generalized randomized complete-block design is used to assign the three factors to 2 Runs, each of which involves 36 containers with a plant and live aphids. The response to be analyzed is the logit of the proportion of live aphids that were infected.

The columns in the data frame are: ID, Run, Plant, Host, Ladybird, Cadavers, Live, Infected, logitP, Prop. The column ID numbers the observations. Live, Infected, logitP, Prop are response variables.

Usage

```
data(Ladybird.dat)
```

Format

A data.frame containing 72 observations of 10 variables.

Author(s)

Chris Brien

Source

Welham, S. J., Gezan, S. A., Clark, S. J., \& Mead, A. (2015). *Statistical Methods in Biology: Design and Analysis of Experiments and Regression*. Boca Raton: Chapman and Hall/CRC..

`linTransform.alldiffs` *Calculates a linear transformation of the predictions stored in an* `alldiffs.object`.

Description

Effects the linear transformation of the predictions in the supplied `alldiffs.object`, the transformation being specified by a `matrix` or a `formula`. The values of the transformed values are stored in an `alldiffs.object`. A `matrix` might be a contrast `matrix` or a `matrix` of weights for the levels of a `factor` used to obtain the weighted average over the levels of that `factor`. A `formula` gives rise to a projection `matrix` that linearly transforms the predictions so that they conform to the model specified by the `formula`, this model being a submodel of that inherent in the `classify`.

If `pairwise = TRUE`, all pairwise differences between the linear transforms of the `predictions`, their standard errors, p-values and LSD statistics are computed as using `allDifferences.data.frame`. This adds them to the `alldiffs.object` as additional `list` components named `differences`, `sed`, `p.differences` and `LSD`.

If a transformation has been applied (any one of `transform.power` is not one, `scale` is not one and `offset` is nonzero), the backtransforms of the transformed values and their lower and upper confidence intervals are added to a `data.frame` that is consistent with a `predictions.frame`. If `transform.power` is other than one, the `standard.error` column of the `data.frame` is set to `NA`. This `data.frame` is added to the `alldiffs.object` as a `list` component called `backtransforms`.

The printing of the components produced is controlled by the `tables` argument. The order of plotting the levels of one of the factors indexing the predictions can be modified and is achieved using `sort.alldiffs`.

Usage

```
## S3 method for class 'alldiffs'
linTransform(alldiffs.obj, classify = NULL, term = NULL,
             linear.transformation = NULL, Vmatrix = FALSE,
             error.intervals = "Confidence", avsed.tolerance = 0.25,
             meanLSD.type = "overall", LSDby = NULL,
             response = NULL, response.title = NULL,
             x.num = NULL, x.fac = NULL,
             tables = "all", level.length = NA,
             pairwise = TRUE, alpha = 0.05,
             inestimable.rm = TRUE, ...)
```

Arguments

`alldiffs.obj`	An `alldiffs.object`.
`classify`	A `character` string giving the variables that define the margins of the multiway table to be predicted. Multiway tables are specified by forming an interaction type term from the classifying variables, that is, separating the variable names with the : operator.

`term` A character string giving the variables that define the term that was fitted using `asreml` and that corresponds to `classify`. It only needs to be specified when it is different to `classify`.

`linear.transformation`
A formula or a matrix. If a formula is given then it is taken to be a submodel of the model term corresponding to the `classify`. The projection matrix that transforms the `predictions` so that they conform to the submodel is obtained; the submodel should involving the variables in the `classify`. For example, for `classify` set to `"A:B"`, the submodel `~ A + B` will result in the `predictions` for the combinations of `A` and `B` being made additive for the factors `A` and `B`.

If a matrix is provided then it will be used to apply the linear transformation to the `predictions`. The number of rows in the matrix should equal the number of linear combinations of the `predictions` desired and the number of columns should equal the number of `predictions`.

In either case, as well as the values of the linear combinations, their standard errors, pairwise differences and associated statistics are returned.

`Vmatrix` A logical indicating whether the variance matrix of the `predictions` will be stored as a component of the `alldiffs.object` that is returned. If `linear.transformation` is set, it will be stored irrespective of the value of `Vmatrix`.

`error.intervals`
A character string indicating the type of error interval, if any, to calculate in order to indicate uncertainty in the results. Possible values are `"none"`, `"StandardError"`, `"Confidence"` and `"halfLeastSignificant"`. The default is for confidence limits to be used. The `"halfLeastSignificant"` option results in half the Least Significant Difference (LSD) being added and subtracted to the predictions, the LSD being calculated using the square root of the mean of the variances of all or a subset of pairwise differences between the predictions. If `meanLSD.type` is set to `overall`, the `avsed.tolerance` is not `NA` and the range of the SEDs divided by the average of the SEDs exceeds `avsed.tolerance` then the `error.intervals` calculations and the plotting will revert to confidence intervals.

`avsed.tolerance`
A numeric giving the value of the SED range, the range of the SEDs divided by the square root of the mean of the variances of all or a subset of the pairwise differences, that is considered reasonable in calculating `error.intervals`. It should be a value between 0 and 1. The following rules apply:

1. If `avsed.tolerance` is `NA` then mean LSDs of the type specified by `meanLSD.type` are calculated and used in `error.intervals` and plots.
2. Irrespective of the setting of `meanLSD.type`, if `avsed.tolerance` is not exceeded then the mean LSDs are used in `error.intervals` and plots.
3. If `meanLSD.type` is set to `overall`, `avsed.tolerance` is not `NA`, and `avsed.tolerance` is exceeded then `error.intervals` and plotting revert to confidence intervals.
4. If `meanLSD.type` is set to `factor.combinations` and `avsed.tolerance` is not exceeded for any factor combination then the half LSDs are used in `error.intervals` and plots; otherwise, `error.intervals` and plotting revert to confidence intervals.
5. If `meanLSD.type` is set to `per.prediction` and `avsed.tolerance` is not exceeded for any prediction then the half LSDs are used in `error.intervals` and plots; otherwise, `error.intervals` and plotting revert to confidence intervals.

meanLSD.type	A character string determining whether the mean LSD stored is (i) the overall mean, based on the square root of the mean of the variances of all pairwise variances, (ii) the mean for each factor.combination of the factors specified by LSDby, which is based on the square root of the mean of the variances for all pairwise differences for each factor combination, or (iii) the per.prediction mean, based, for each prediction, on the square root of the mean of the variances for all pairwise differences involving that prediction, unless there is only one prediction for a factor.combination, when notional LSDs are calculated that are based on the standard error of the prediction multiplied by the square root of two. It also determines, in conjunction with avsed.tolerance, which LSD will be used in calculating error.intervals and, hence, is used for plots.
LSDby	A character (vector) of variables names, being the names of the factors or numerics in the classify for each combination of which a mean LSD, minLSD and max LSD is stored in the LSD component of the alldiffs.object when meanLSD.type is factor.combinatons.
response	A character specifying the response variable for the predictions. It is stored as an attribute to the alldiffs.object .
response.title	A character specifying the title for the response variable for the predictions. It is stored as an attribute to the alldiffs.object.
x.num	A character string giving the name of the numeric covariate that (i) corresponds to x.fac, (ii) is potentially included in terms in the fitted model, and (iii) which corresponds to the x-axis variable. It should have the same number of unique values as the number of levels in x.fac.
x.fac	A character string giving the name of the factor that (i) corresponds to x.num, (ii) is potentially included in terms in the fitted model, and (iii) which corresponds to the x-axis variable. It should have the same number of levels as the number of unique values in x.num. The levels of x.fac must be in the order in which they are to be plotted - if they are dates, then they should be in the form yyyymmdd, which can be achieved using as.Date. However, the levels can be non-numeric in nature, provided that x.num is also set.
tables	A character vector containing a combination of none, predictions, vcov, backtransforms, differences, p.differences, sed, LSD and all. These nominate which components of the alldiffs.object to print.
level.length	The maximum number of characters from the the levels of factors to use in the row and column labels of the tables of pairwise differences and their p-values and standard errors.
pairwise	A logical indicating whether all pairwise differences of the predictions and their standard errors and p-values are to be computed and stored. If tables is equal to "differences" or "all" or error.intervals is equal to "halfLeastSignificant", they will be stored irrespective of the value of pairwise.
alpha	A numeric giving the significance level for LSDs or one minus the confidence level for confidence intervals.
inestimable.rm	A logical indicating whether rows for predictions that are not estimable are to be removed from the components of the alldiffs.object.
...	further arguments passed to redoErrorIntervals.alldiffs.

Details

For a matrix $\mathbf{L}$, vector of predictions $\mathbf{p}$ and variance matrix of the predictions $\mathbf{V}_p$, the linear transformed predictions are given by $\mathbf{Lp}$ with variance matrix $\mathbf{LV}_p\mathbf{L}^{\mathrm{T}}$. The last matrix is used to compute the variance of pairwise differences between the transformed values.

The matrix $\mathbf{L}$ is directly specified by setting linear.transformation to it. If linear.transformation is a formula then $\mathbf{L}$ is formed as the sum of the orthogonal projection matrices obtained using pstructure.formula from the package dae; grandMean is set to TRUE and orthogonalize to "eigenmethods".

Value

A alldiffs.object with the linear transformation of the predictions and their standard errors and all pairwise differences between the linear transforms of their predictions, their standard errors and p-values and LSD statistics.

If the supplied alldiffs.object contained a backtransforms componnent, then the returned alldiffs.object will contain a backtransforms component with the backtransformed linear transformation of the predictions. The backtransformation will, after backtransforming for any power transformation, subtract the offset and then divide by the scale.

If error.intervals is not "none", then the predictions component and, if present, the backtransforms component will contain columns for the lower and upper values of the limits for the interval. The names of these columns will consist of three parts separated by full stops: 1) the first part will be lower or upper; 2) the second part will be one of Confidence, StandardError or halfLeastSignificant; 3) the third component will be limits.

The name of the response, the response.title, the term, the classify, tdf, sortFactor and the sortOrder will be set as attributes to the object.

Author(s)

Chris Brien

See Also

predictPlus.asreml, as.alldiffs, print.alldiffs, sort.alldiffs, subset.alldiffs, allDifferences.data.frame, redoErrorIntervals.alldiffs, recalcLSD.alldiffs, predictPresent.asreml, plotPredictions.data.frame, as.Date, predict.asreml

Examples

```
data(WaterRunoff.dat)

##Use asreml to get predictions and associated statistics

## Not run:
asreml.options(keep.order = TRUE) #required for asreml-R4 only
current.asr <- asreml(fixed = pH ~ Benches + (Sources * (Type + Species)),
                      random = ~ Benches:MainPlots,
                      keep.order=TRUE, data= WaterRunoff.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
#Get additive predictions directly using predictPlus
diffs.sub <- predictPlus.asreml(classify = "Sources:Species", Vmatrix = TRUE,
                                linear.transformation = ~ Sources + Species,
                                asreml.obj = current.asr, tables = "none",
                                wald.tab = current.asrt$wald.tab,
                                present = c("Type","Species","Sources"))

## End(Not run)

## Use lmeTest and emmmeans to get predictions and associated statistics
```

```
if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  m1.lmer <- lmerTest::lmer(pH ~ Benches + (Sources * Species) +
                              (1|Benches:MainPlots),
                            data=na.omit(WaterRunoff.dat))
  SS.emm <- emmeans::emmeans(m1.lmer, specs = ~ Sources:Species)
  SS.preds <- summary(SS.emm)
  den.df <- min(SS.preds$df, na.rm = TRUE)
  ## Modify SS.preds to be compatible with a predictions.frame
  SS.preds <- as.predictions.frame(SS.preds, predictions = "emmean",
                                   se = "SE", interval.type = "CI",
                                   interval.names = c("lower.CL", "upper.CL"))

  ## Form an all.diffs object and check its validity
  SS.vcov <- vcov(SS.emm)
  SS.diffs <- allDifferences(predictions = SS.preds, classify = "Sources:Species",
                             vcov = SS.vcov, tdf = den.df)
  validAlldiffs(SS.diffs)

  #Get additive predictions
  diffs.sub <- linTransform(SS.diffs, classify = "Sources:Species",
                            linear.transformation = ~ Sources + Species,
                            Vmatrix = TRUE, tables = "none")
}

##Calculate contrasts from prediction obtained using asreml or lmerTest
if (exists("diffs.sub"))
{
  #Contrast matrix for differences between each species and non-planted for the last source
  L <- cbind(matrix(rep(0,7*32), nrow = 7, ncol = 32),
             diag(1, nrow = 7),
             matrix(rep(-1, 7), ncol = 1))
  rownames(L) <- as.character(diffs.sub$predictions$Species[33:39])
  diffs.L <- linTransform(diffs.sub,
                          classify = "Sources:Species",
                          linear.transformation = L,
                          tables = "predictions")
}
```

`loadASRemlVersion` *Ensures that a specific version of* `asreml` *is loaded.*

Description

Loads the specified version of `asreml`, provided that it is not already loaded. If the version of `asreml` is not the required version, then the loaded version is unloaded first.

Usage

```
loadASRemlVersion(version = 4, ...)
```

Arguments

version	The version that is to be loaded, the vesion consisting of just the initial characters that are significant in the version that should be loaded. For example, the default value of 4 implies that any version that begins with "4" is acceptable. It is used to check that the required version is loaded.
...	Other library/require arguments that are needed to load the specified version of asreml.

Value

A character, being all characters in the version of asreml that is loaded on exit from the function.

Author(s)

Chris Brien

See Also

getASRemlVersionLoaded.

Examples

```
## Not run:
loadASRemlVersion(3, lib.loc = "D:\Analyses\R asreml3")
## End(Not run)
```

---

newfit.asreml *Refits an asreml model with modified model formula using either a call to* update.asreml *or a direct call to* asreml.

Description

Extracts the call from the asreml.obj and evaluates that call, replacing any arguments with changed values. If update is TRUE and set.terms is not set, the call is evaluated using update.asreml; otherwise, it is evaluated using a direct call to asreml. The principal difference is that the latter does not enforce the use of previous values of the variance parameters as initial values; it sets G.param and R.param to NULL or to values as specified for set.terms. The ... argument can be used to pass G.param and/or R.param, provided update is FALSE and set.terms is not set.

Usage

```
## S3 method for class 'asreml'
newfit(asreml.obj, fixed., random., sparse.,
       residual., rcov., update = TRUE,
       allow.unconverged = TRUE, keep.order = TRUE,
       set.terms = NULL, ignore.suffices = TRUE, bounds = "P",
       initial.values = NA, ...)
```

Arguments

asreml.obj	A valid asreml object with with a component named call (from a previous call to either asreml or update.asreml).
fixed.	A character or formula specifying changes to the fixed formula. This is a two-sided formula where "." is substituted for existing components in the fixed component of asreml.obj$call.
random.	A character or formula specifying changes to the random formula. This is a one-sided formula where "." is substituted for existing components in the random component of asreml.obj$call.
sparse.	A character or formula specifying changes to the sparse formula. This is a one-sided formula where "." is substituted for existing components in the sparse component of asreml.obj$call.
residual.	A character or formula specifying changes to the error formula, used when version 4 or later of ASReml-R is loaded. This is a one-sided formula where "." is substituted for existing components in the residual component of asreml.obj$call.
rcov.	A character or formula specifying changes to the error formula, used when version 3 of ASReml-R is loaded. This is a one-sided formula where "." is substituted for existing components in the residual component of asreml.obj$call.
update	A logical indicated whether to use update.asreml or asreml to evaluate the modified call. If TRUE, use update.asreml to evaluate the modified call. In doing this the arguments R.param and G.param are set to those in the asreml.obj so that the values from the previous model are used as starting values. If FALSE then a call is made to asreml itself, in which the only changes from the previous call are those specified in the arguments to newfit.asreml.
allow.unconverged	A logical indicating whether to accept a new model even when it does not converge. If FALSE and the fit does not converge, the supplied asreml object is returned.
keep.order	A logical value indicating whether the terms should keep their positions. If FALSE the terms are reordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on. Effects of a given order are kept in the order specified.
set.terms	A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting.
ignore.suffices	A logical vector specifying whether the suffices of the asreml-assigned names of the variance terms (i.e. the information to the right of an "!", other than "R!") is to be ignored in matching elements of terms. If TRUE for an element of terms, the suffices are stripped from the asreml-assigned names. If FALSE for an element of terms, the element must exactly match an asreml-assigned name for a variance term. This vector must be of length one or the same length as terms. If it is of length one then the same action is applied to the asreml-assigned suffices for all the terms in terms.
bounds	A character vector specifying the bounds to be applied to the terms specified in set.terms. This vector must be of length one or the same length as set.terms. If it is of length one then the same constraint is applied to all the terms in set.terms. If any of the bounds are equal to NA then they are left unchanged for those terms.

initial.values — A character vector specifying the initial values for the terms specified in terms. This vector must be of length one or the same length as terms. If it is of length one then the same initial value is applied to all the terms in terms. If any of the initial.values are equal to NA then they are left unchanged for those terms.

... — additional arguments to the call, or arguments with changed values.

Value

An asreml object.

Author(s)

Chris Brien

References

Butler, D. G., Cullis, B. R., Gilmour, A. R., Gogel, B. J. and Thompson, R. (2018). *ASReml-R Reference Manual Version 4.* VSN International Ltd, http://asreml.org.

See Also

update.asreml, setvarianceterms.call

Examples

```
## Not run:
    m2.asreml <- newfit(m1.asreml, random. = "~ . - Blocks:Plots", maxiter=75)

## End(Not run)
```

---

num.recode — *Recodes the unique values of a vector using the values in a new vector.*

Description

Recodes the unique values of a variate using the value in position i of the new.values vector to replace the ith sorted unique values of x. The new levels do not have to be unique.

Usage

```
num.recode(x, new.values)
```

Arguments

x — The vector to be recoded.

new.values — A vector of length unique(x) containing values to use in the recoding.

Value

A vector.

Author(s)

Chris Brien

See Also

`dae::fac.recode`.

Examples

```
## set up a factor with labels
x <- rep(c(-42, -14, 14, 42), 4)

## recode x
b <- num.recode(x, c(0, 28, 56, 84))
```

Oats.dat — *Data for an experiment to investigate nitrogen response of 3 oats varieties*

Description

Yates (1937) describes a split-plot experiment that investigates the effects of three varieties of oats and four levels of Nitrogen fertilizer. The varieties are assigned to the main plots using a randomized complete block design with 6 blocks and the nitrogen levels are randomly assigned to the subplots in each main plot.

The columns in the data frame are: Blocks, Wplots, Subplots, Variety, Nitrogen, xNitrogen, Yield. The column xNitrogen is a numeric version of the factor Nitrogen. The response variable is Yield.

Usage

```
data(Oats.dat)
```

Format

A data.frame containing 72 observations of 7 variables.

Author(s)

Chris Brien

Source

Yates, F. (1937). The Design and Analysis of Factorial Experiments. *Imperial Bureau of Soil Science, Technical Communication*, **35**, 1-95.

permute.square *Permutes the rows and columns of a square matrix.*

Description

Permutes the rows and columns of a square matrix.

Usage

```
permute.square(x, permutation)
```

Arguments

x	A square matrix.
permutation	A vector specifying the new order of rows and columns.

Value

A square matrix.

Author(s)

Chris Brien

See Also

permute.to.zero.lowertri

Examples

```
terms.marginality <-  matrix(c(1,0,0,0,0,  0,1,0,0,0, 0,1,1,0,0,
                               1,1,1,1,0, 1,1,1,1,1), nrow=5)
permtn <- c(1,3,2,4,5)
terms.marginality <- permute.square(terms.marginality, permtn)
```

permute.to.zero.lowertri *Permutes a square matrix until all the lower triangular elements are zero.*

Description

Permutes a square matrix until all the lower triangular elements are zero.

Usage

```
permute.to.zero.lowertri(x)
```

Arguments

x	A square matrix of order n with at least n*(n-1)/2 zero elements.

Value

A square matrix.

Author(s)

Chris Brien

See Also

permute.square

Examples

```
terms.marginality <-  matrix(c(1,0,0,0,0,  0,1,0,0,0, 0,1,1,0,0,
                               1,1,1,1,0, 1,1,1,1,1), nrow=5)
terms.marginality <- permute.to.zero.lowertri(terms.marginality)
```

---

plotPredictions.data.frame

Plots the predictions for a term, possibly with error bars.

Description

This function plots the predictions y that are based on classify and stored in the data.frame data. The package ggplot2 is used to produce the plots. Line plots are produced when variables involving x.num or x.fac are involved in classify for the predictions; otherwise, bar charts are produced. Further, for line charts, the argument panels determines whether a single plot or multiple plots in a single window are produced; for bar charts, the argument panels is ignored.

Usage

```
## S3 method for class 'data.frame'
plotPredictions(data, classify, y,
                x.num = NULL, x.fac = NULL, nonx.fac.order = NULL,
                colour.scheme = "colour", panels = "multiple",
                graphics.device = NULL,
                error.intervals = "Confidence",  titles = NULL,
                y.title = NULL, filestem = NULL, ggplotFuncs = NULL, ...)
```

Arguments

data	A predictions.frame, or data.frame, containing the values of the variables to be plotted. Generally, it should contain the variables classifying the predictions and include a column with the name specified in the y argument, usually predicted.value or backtransformed.predictions; each row contains a single predicted value. It should also include columns for the standard.error and est.status. The number of rows should equal the number of unique combinations of the classifying variables. While such a data.frame can be constructed from the beginning, the pvals component of the value produced by predict.asreml is a suitable value to supply for this argument. Note that the names standard.error and est.status have been changed to std.error and

status in the pvals component produced by asreml-R4; if the new names are in the data.frame supplied to predictions, they will be returned to the previous names.

If error.intervals is not "none", then the predictions component and, if present, the backtransforms component should contain columns for the lower and upper values of the limits for the interval with names that begin with lower and upper, respectively. The second part of the name must be one of Confidence, StandardError or halfLeastSignificant. The last part needs to be consistent between the lower and upper limits.

classify — A character string giving the combinations of the independent variables on which the predictions are based. It is an interaction type term formed from the independent variables, that is, separating the variable names with the : operator. To predict the overall mean, set the classify to "(Intercept)".

y — A character string giving the name of the variable that is to be plotted on the Y axis.

x.num — A character string giving the name of the numeric covariate that corresponds to x.fac, is potentially included in terms in the fitted model and which corresponds to the x-axis variable. It should have the same number of unique values as the number of levels in x.fac.

x.fac — A character string giving the name of the factor that corresponds to x.num, is potentially included in terms in the fitted model and which corresponds to the x-axis variable. It should have the same number of levels as the number of unique values in x.num. The levels of x.fac must be in the order in which they are to be plotted - if they are dates, then they should be in the form yyyymmdd, which can be achieved using as.Date. However, the levels can be non-numeric in nature, provided that x.num is also set.

nonx.fac.order — A character vector giving the order in which factors other than x.fac are to be plotted in facetted plots (i.e. where the number of non x factors is greater than 1). The first factor in the vector will be plotted on the X axis (if there is no x.num or x.fac. Otherwise, the order of plotting the factors is in columns (X facets) and then rows (Y facets). By default the order is in decreasing order for the numbers of levels of the non x factors.

colour.scheme — A character string specifying the colour scheme for the plots. The default is "colour" which produces coloured lines and bars, a grey background and white gridlines. A value of "black" results in black lines, grey bars and gridlines and a white background.

panels — Possible values are "single" and "multiple". When line plots are to be produced, because variables involving x.num or x.fac are involved in classify for the predictions, panels determines whether or not a single panel or multiple panels in a single window are produced. The panels argument is ignored for bar charts.

graphics.device

A character specifying a graphics device for plotting. The default is graphics.device = NULL, which will result in plots being produced on the current graphics device. Setting it to "windows", for example, will result in a windows graphics device being opened.

error.intervals

A character string indicating the type of error interval, if any, to plot in order to indicate uncertainty in the results. Possible values are "none", "StandardError", "Confidence" and "halfLeastSignificant". Here, any option other than "none" will result in the interval limits contained in data being plotted.

titles	A list, each component of which is named for a column in the data.frame for the asreml.obj used in making the predictions and contains a character string giving a title to use in output (e.g. tables and graphs). Here they will be used for axis labels for nonresponse variables. For response variable labels see y.title.
filestem	A character sting giving the beginning of the name of the file in which to save the plot. If filestem = NULL, the plot is not saved. The remainder of the file name will be generated automatically and consists of the following elements separated by full stops: the classify term, Bar or Line and, if error.intervals is not "none", one of SE, CI or LSI. The file will be saved as a 'png' file in the current work directory.
y.title	The title to be displayed on the y axis of any plot.
ggplotFuncs	A list, each element of which contains the results of evaluating a ggplot function. It is created by calling the list function with a ggplot function call for each element.
...	further arguments passed to ggplot.

Value

no values are returned.

Author(s)

Chris Brien

See Also

allDifferences.data.frame, predictPresent.asreml, redoErrorIntervals.alldiffs, recalcLSD.alldiffs, ggplot, Devices

Examples

```
## Not run:
data(WaterRunoff.dat)
asreml.options(keep.order = TRUE) #required for asreml-R4 only
current.asr <- asreml(fixed = log.Turbidity ~ Benches + Sources + Type + Species +
                                Sources:Type + Sources:Species +
                                Sources:xDay + Species:xDay + Species:Date,
                      data = WaterRunoff.dat, keep.order = TRUE)
current.asrt <- as.asrtests(current.asr, NULL, NULL)

#### Get the observed combinations of the factors and variables in classify
class.facs <- c("Species","Date","xDay")
levs <- as.data.frame(table(WaterRunoff.dat[class.facs]))
levs <- as.list(levs[levs$Freq != 0, class.facs])
levs$xDay <- as.numfac(levs$xDay)

predictions <- predict(current.asr, classify="Species:Date:xDay",
                       parallel = TRUE, levels = levs,
                       present = c("Type","Species","Sources"))
#### for asreml-R3
predictions <- predictions$predictions$pvals
predictions <- predictions[predictions$est.status == "Estimable",]
#### for asreml-R4
```

```
predictions <- predictions$pvals
predictions <- predictions[predictions$status == "Estimable",]
#### end
plotPredictions(classify="Species:Date:xDay", y = "predicted.value",
                data = predictions,
                x.num = "xDay", x.fac = "Date",
                x.title = "Days since first observation",
                y.title = "Predicted log(Turbidity)",
                present = c("Type","Species","Sources"),
                error.intervals = "none",
                ggplotFuncs = list(ggtitle("Transformed turbidity over time")))

diffs <- predictPlus(classify="Species:Date:xDay",
                     present=c("Type","Species","Sources"),
                     asreml.obj = current.asr, tables = "none",
                     x.num = "xDay", x.fac = "Date",
                     parallel = TRUE, levels = levs,
                     x.plot.values=c(0,28,56,84),
                     wald.tab = current.asrt$wald.tab)
x.title <- "Days since first observation"
names(x.title) <- "xDay"
plotPredictions(classify="Species:Date:xDay", y = "predicted.value",
               data = diffs$predictions,
               x.num = "xDay", x.fac = "Date",
               titles = x.title,
               y.title = "Predicted log(Turbidity)")

## End(Not run)

## Use lmerTest and emmmeans to get predictions and associated statistics
if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  data(Ladybird.dat)
  m1.lmer <- lmerTest::lmer(logitP ~ Host*Cadavers*Ladybird + (1|Run),
                            data=Ladybird.dat)
  HCL.emm <- emmeans::emmeans(m1.lmer, specs = ~ Host:Cadavers:Ladybird)
  HCL.preds <- summary(HCL.emm)
  den.df <- min(HCL.preds$df)
  ## Modify HCL.preds to be compatible with a predictions.frame
  HCL.preds <- as.predictions.frame(HCL.preds, predictions = "emmean",
                                    se = "SE", interval.type = "CI",
                                    interval.names = c("lower.CL", "upper.CL"))
  ## Plot the predictions
  plotPredictions(HCL.preds, y = "predicted.value", "Host:Cadavers:Ladybird")
}
```

`plotPvalues.alldiffs` *Plots a heat map of p-values for pairwise differences between predictions.*

Description

Produces a heat-map plot of the p-values for pairwise differences between predictions that is stored in the `p.differences` component of an `all.diffs` object. This is generally a matrix whose rows

and columns are labelled by the levels of one or more factors, the set of labels being the same for rows and columns. The `sections` argument allows multiple plots to be produced, one for each combination of the levels of the factors listed in `sections`. Otherwise, a single plot is produced for all observed combinations of the levels of the factors in the `classify` for the `alldiffs.object`. The plots are produced using `plotPvalues.data.frame`. The order of plotting the levels of one of the factors indexing the predictions can be modified and is achieved using `sort.alldiffs`.

Usage

```
plotPvalues(object, ...)
## S3 method for class 'alldiffs'
plotPvalues(object, sections = NULL,
            gridspacing = 0, factors.per.grid = 0,
            show.sig = FALSE, triangles = "both",
            title = NULL, axis.labels = TRUE, sep=",",
            colours = RColorBrewer::brewer.pal(3, "Set2"),
            ggplotFuncs = NULL, sortFactor = NULL,
            sortWithinVals = NULL, sortOrder = NULL,
            decreasing = FALSE, ...)
```

Arguments

`object`	An `alldiffs.object` with a `p.differences` component that is not `NULL`.
`sections`	A `character` listing the names of the factors that are to be used to break the plot into sections. A separate plot will be produced for each observed combination of the levels of these factors.
`gridspacing`	A `numeric` specifying the number(s) of rows and columns that form groups in the grid of differences. An alternative is to specify the `factors.per.grid` argument to have the grid spacings automatically calculated. Grids are most useful when two or more factors index the rows and columns. If a single, nonzero number, *k* say, is given then a grid line is placed after every *k*th row and column. If a vector of values is given then the number of grid lines is the length of the vector and the spacing between each is specified by the elements of the vector.
`factors.per.grid`	A `numeric` specifying the number of factors to include within each grid of differences. The `gridspacing` will then be computed based on the numbers of combinations observed within the levels of the remaining factors in a single plot. The `gridspacing` argument to this function will be ignored if `factors.per.grid` is greater than zero. Grids are most useful when two or more factors index the rows and columns of each plot.
`show.sig`	A `logical` that specifies whether asterisks indicating the level of significance are to be added to the plot. If they are then '***' indicates that $p \leq 0.001$, '**' that $0.001 < p \leq 0.01$, '*' that $0.01 < p \leq 0.05$ '.' that $0.05 < p \leq 0.10$.
`triangles`	A `character` indicating whether the plot should include the `lower`, `upper` or `both` traingle(s).
`title`	A `character` string giving the main title for the plot and to which is appended the levels combination of the sectioning factors, if any, for each plot.
`axis.labels`	A `logical` indicating whether a label is to be added to the x- and y-axes. If TRUE, the label is the comma-separated list of factors whose levels combinations are involved in the prediction differences for which the p-values are calculated.

colours	A vector of of colours to be passed to the ggplot function scale_colour_gradientn.
sep	A character giving the characters separating the levels of different factors in the row and column names of the p.differences component.
ggplotFuncs	A list, each element of which contains the results of evaluating a ggplot function. It is created by calling the list function with a ggplot function call for each element. It is passed to ggplot via plotPvalues.data.frame.
sortFactor	A character containing the name of the factor that indexes the set of predicted values that determines the sorting of the components of the alldiffs.object by sort.alldiffs. If NULL then sorting is not carried out. If there is more than one variable in the classify term then sortFactor is sorted for the predicted values within each combination of the values of the sortWithin variables: the classify variables, excluding the sortFactor. There should be only one predicted value for each unique value of sortFactor within each set defined by a combination of the values of the sortWithin variables.
sortWithinVals	A list with a component named for each factor and numeric that is a classify variable for the predictions, excluding sortFactor. Each component should contain a single value that is a value of the variable. The combination of this set of values will be used to define a subset of the predicted values whose order will define the order of sortFactor to be used for all combinations of the sortWithinVals variables. If sortWithinVals is NULL then the first value of each sortWithin variable in predictions component is used to define sortWithinVals. If there is only one variable in the classify then sortWithinVals is ignored.
sortOrder	A character vector whose length is the same as the number of levels for sortFactor in the predictions component of the alldiffs.object. It specifies the desired order of the levels in the reordered components of the alldiffs.object. The argument sortWithinVals is ignored. The following creates a sortOrder vector levs for factor f based on the values in x: levs <-levels(f)[order(x)].
decreasing	A logical passed to order that detemines whether the order for sorting the alldiffs.object components is for increasing or decreasing magnitude of the predicted values.
...	Provision for passsing arguments to functions called internally - not used at present.

Value

A data.frame with the columns X1, X2, p, sections1 and sections2. This data.frame is formed from the p.differences component of object and is used in producng the plot.

Author(s)

Chris Brien

See Also

plotPvalues.data.frame, allDifferences.data.frame, sort.alldiffs, subset.alldiffs, ggplot

Examples

```
data(WaterRunoff.dat)

##Use asreml to get predictions and associated statistics

## Not run:
asreml.options(keep.order = TRUE) #required for asreml-R4 only
current.asr <- asreml(fixed = pH ~ Benches + (Sources * (Type + Species)),
                      random = ~ Benches:MainPlots,
                      keep.order=TRUE, data= WaterRunoff.dat))
current.asrt <- as.asrtests(current.asr, NULL, NULL)
SS.diffs <- predictPlus.asreml(classify = "Sources:Type",
                               asreml.obj = current.asr, tables = "none",
                               wald.tab = current.asrt$wald.tab,
                               present = c("Type","Species","Sources"))

## End(Not run)

## Use lmeTest and emmmeans to get predictions and associated statistics

if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  m1.lmer <- lmerTest::lmer(pH ~ Benches + (Sources * (Type + Species)) +
                              (1|Benches:MainPlots),
                            data=na.omit(WaterRunoff.dat))
  TS.emm <- emmeans::emmeans(m1.lmer, specs = ~ Sources:Species)
  TS.preds <- summary(TS.emm)
  den.df <- min(TS.preds$df, na.rm = TRUE)
  ## Modify TS.preds to be compatible with a predictions.frame
  TS.preds <- as.predictions.frame(TS.preds, predictions = "emmean",
                                   se = "SE", interval.type = "CI",
                                   interval.names = c("lower.CL", "upper.CL"))

  ## Form an all.diffs object and check its validity
  TS.vcov <- vcov(TS.emm)
  TS.diffs <- allDifferences(predictions = TS.preds, classify = "Sources:Species",
                             vcov = TS.vcov, tdf = den.df)
  validAlldiffs(TS.diffs)
}

## Plot p-values for predictions obtained using asreml or lmerTest
if (exists("TS.diffs"))
{
  plotPvalues(TS.diffs, gridspacing = rep(c(3,4), c(4,2)), show.sig = TRUE)
  plotPvalues(TS.diffs, sections = "Sources", show.sig = TRUE, axis.labels = TRUE)
}
```

`plotPvalues.data.frame` *Plots a heat map of p-values for pairwise differences between predictions.*

Description

Produces a heat-map plot of the p-values for pairwise differences between predictions that is in a `data.frame`. The `data.frame` includes two factors whose levels specify, for each p-value, which factor levels are being compared.

Usage

```
## S3 method for class 'data.frame'
plotPvalues(object, p = "p", x, y,
            gridspacing = 0, show.sig = FALSE, triangles = "both",
            title = NULL, axis.labels = NULL,
            colours = RColorBrewer::brewer.pal(3, "Set2"),
            ggplotFuncs = NULL, ...)
```

Arguments

`object`	A `data.frame` containing the three columns specified by `p`, `x` and `y`.
`p`	A `character` giving the name of the column in `object` that contains the p-values to be plotted.
`x`	A `character` giving the name of the column in `object` that contains the factor whose levels index the p-values that are to be plotted in the same column.
`y`	A `character` giving the name of the column in `object` that contains the labels of the the p-values that are to be plotted as the rows.
`gridspacing`	A `numeric` specifying the number(s) of rows and columns that form groups in the grid of differences. This is most useful when two or more factors index the rows and columns. If a single, nonzero number, *k* say, is given then a grid line is placed after every *k*th row and column. If a vector of values is given then the number of grid lines is the length of the vector and the spacing between each is specified by the elements of the vector.
`show.sig`	A `logical` that specifies whether asterisks indicating the level of significance are to be added to the plot. If they are then '***' indicates that $p \leq 0.001$, '**' that $0.001 < p \leq 0.01$, '*' that $0.01 < p \leq 0.05$ '.' that $0.05 < p \leq 0.10$.
`triangles`	A `character` indicating whether the plot should include the `lower`, `upper` or `both` traingle(s). Here it is only used to adjust gridlines for the omission of the diagonal.
`title`	A `character` string giving the main title for the plot.
`axis.labels`	A `character` string giving the label to use for both the x- and y-axis.
`colours`	A vector of of colours to be passed to the `ggplot` function `scale_colour_gradientn`.
`ggplotFuncs`	A `list`, each element of which contains the results of evaluating a `ggplot` function. It is created by calling the `list` function with a `ggplot` function call for each element. It is passed to `ggplot`.
`...`	Provision for passsing arguments to functions called internally - not used at present.

Value

No values are returned, but a plot is printed.

Author(s)

Chris Brien

See Also

plotPvalues.alldiffs, allDifferences.data.frame, ggplot

Examples

```
data(WaterRunoff.dat)

##Use asreml to get predictions and associated statistics

## Not run:
asreml.options(keep.order = TRUE) #required for asreml-R4 only
current.asr <- asreml(fixed = pH ~ Benches + (Sources * (Type + Species)),
                      random = ~ Benches:MainPlots,
                      keep.order=TRUE, data= WaterRunoff.dat))
current.asrt <- as.asrtests(current.asr, NULL, NULL)
SS.diffs <- predictPlus.asreml(classify = "Sources:Type",
                               asreml.obj = current.asr, tables = "none",
                               wald.tab = current.asrt$wald.tab,
                               present = c("Type","Species","Sources"))

## End(Not run)

## Use lmeTest and emmmeans to get predictions and associated statistics

if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  m1.lmer <- lmerTest::lmer(pH ~ Benches + (Sources * (Type + Species)) +
                              (1|Benches:MainPlots),
                            data=na.omit(WaterRunoff.dat))
  TS.emm <- emmeans::emmeans(m1.lmer, specs = ~ Sources:Species)
  TS.preds <- summary(TS.emm)
  den.df <- min(TS.preds$df, na.rm = TRUE)
  ## Modify TS.preds to be compatible with a predictions.frame
  TS.preds <- as.predictions.frame(TS.preds, predictions = "emmean",
                                   se = "SE", interval.type = "CI",
                                   interval.names = c("lower.CL", "upper.CL"))

  ## Form an all.diffs object and check its validity
  TS.vcov <- vcov(TS.emm)
  TS.diffs <- allDifferences(predictions = TS.preds, classify = "Sources:Species",
                             vcov = TS.vcov, tdf = den.df)
  validAlldiffs(TS.diffs)
}

## Plot p-values for predictions obtained using asreml or lmerTest
if (exists("TS.diffs"))
{
  p <- within(reshape::melt(TS.diffs$p.differences),
              {
                X1 <- factor(X1, levels=dimnames(TS.diffs$p.differences)[[1]])
                X2 <- factor(X2, levels=levels(X1))
```

```
            })
  names(p)[match("value", names(p))] <- "p"
  plotPvalues(p, x = "X1", y = "X2",
              gridspacing = rep(c(3,4), c(4,2)), show.sig = TRUE)
}
```

`plotVariofaces.data.frame` *Plots empirical variogram faces, including envelopes, from supplied residuals as described by Stefanova, Smith & Cullis (2009).*

Description

Produces a plot for each face of an empirical 2D `variogram` based on supplied residuals from both an observed data set and simulated data sets. Those from simulated data sets are used to produce confidence envelopes If the data consists of sections, such as separate experiments, the two variogram faces are produced for each section. This function is less efficient in storage terms than `variofaces.asreml`, because here the residuals from all simulated data sets must be saved, in addition to the values for the variogram faces; in `variofaces.asreml`, the residuals for each simulated data set are discarded after the variogram has been calculated. On the other hand, the present function is more flexible, because there is no restriction on how the residuals are obtained.

Usage

```
## S3 method for class 'data.frame'
plotVariofaces(data, residuals, restype="Residuals", ...)
```

Arguments

`data`	A `data.frame` with either 3 or 4 columns. Only if there are 4 columns, the first should be a factor indexing sections for which separate variogram plots are to be produced. In either case, the other 3 columns should be, in order, (i) a factor indexing the x-direction, (ii) a factor indexing the y-direction, and (iii) the residuals for the observed response.
`residuals`	A `data.frame`, with either 2 or 3 initial columns followed by columns, each of which are the residuals from a simulated data set.
`restype`	A `character` describing the type of residuals that have been supplied. It will be used in the plot titles.
`...`	Other arguments that are passed down to the function `asreml.variogram`.

Details

For each set of residuals, `asreml.variogram` is used to obtain the empirical variogram, from which the values for its faces are obtained. Plots are produced for each face and include the observed residuals and the 2.5%, 50% & 97.5% quantiles.

Value

A `list` with the following components:

1. **face1:** a `data.frame` containing the variogram values on which the plot for the first dimension is based.
2. **face2:** a `data.frame` containing the variogram values on which the plot for the second dimension is based.

Author(s)

Chris Brien

References

Stefanova, K. T., Smith, A. B. & Cullis, B. R. (2009) Enhanced diagnostics for the spatial analysis of field trials. *Journal of Agricultural, Biological, and Environmental Statistics*, **14**, 392–410.

See Also

`asremlPlus-package`, `asreml`, `asreml.variogram`, `variofaces.asreml`, `simulate.asreml`.

Examples

```
## Not run:
data(Wheat.dat)
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
current.asrt <- rmboundary.asrtests(current.asrt)
# Form variance matrix based on estimated variance parameters
s2 <- current.asr$sigma2
gamma.Row <- current.asr$gammas[1]
gamma.unit <- current.asr$gammas[2]
rho.r <- current.asr$gammas[4]
rho.c <- current.asr$gammas[5]
row.ar1 <- mat.ar1(order=10, rho=rho.r)
col.ar1 <- mat.ar1(order=15, rho=rho.c)
V <- gamma.Row * fac.sumop(Wheat.dat$Row) +
  gamma.unit * diag(1, nrow=150, ncol=150) +
  mat.dirprod(col.ar1, row.ar1)
V <- s2*V

#Produce variogram faces plot (Stefanaova et al, 2009)
resid <- simulate(current.asr, V=V, which="residuals")
resid$residuals <- cbind(resid$observed[c("Row","Column")],
                         resid$residuals)
plotVariofaces(data=resid$observed[c("Row","Column","residuals")],
               residuals=resid$residuals,
               restype="Standardized conditional residuals")

## End(Not run)
```

`powerTransform` *Performs a combination of a linear and a power transformation on a variable. The transformed variable is stored in the* `data.frame` `data`.

Description

Perform a combination of a linear and a power transformation on a variable whose name is given as a character string in `var.name`. The transformed variable is stored in the `data.frame` `data`. The name of the transformed variable is made by prepending to the original `var.name` a combination of (i) `.offset`, if `offset` is nonzero, (ii) `neg.`, if `scale` is -1, or `scaled.`, if `abs(scale)` is other than one, and (iii) either `log.`, `sqrt.`, `recip.` or `power.`, if `power` is other than one. No action is taken if there is no transformation (i.e. `offset` = `0`, `scale` = `1` and `power` = `1`). Also, the `titles` list is extended to include a component with a generated title for the transformed variable with text indicating the transformation prepended to the `title` for the `var.name` obtained from the `titles` `list`. For nonzero `offset`, 'Offset ' is prepended, For `scaled` not equal to one, the possible prepends are 'Negative of ' and 'Scaled '. The possible prepended texts for `power` not equal to one are 'Logarithm of', 'Square root of ', 'Reciprocal of ' and 'Power nnnn of ', where nnn is the power used.

Usage

```
powerTransform(var.name, power = 1, offset = 0, scale = 1, titles = NULL, data)
```

Arguments

`var.name`	A `character` `string` specifying the name of the variable in the `data.frame` `data` that is to be transformed.
`power`	A number specifying the power to be used in the transformation. If equal to 1, the default, no power transformation is applied. Otherwise, the variable is raised to the specified `power`, after scaling and applying any nonzero `offset`. If `power` = `0`, the natural logarithm is used to transform the response; however, if the smallest value to be log-transformed is less than 1e-04, an error is generated. A log-transformation in this situation may be possible if a nonzero `offset` and/or a `scale` not equal to one is used.
`offset`	A number to be added to each value of the variable, after any scaling and before applying any power transformation.
`scale`	A number to multiply each value of the variable, before adding any offset and applying any power transformation.
`titles`	A `character` `vector`, each element of which is named for a variable in `data` and is a `character` `string` giving a title to use in output (e.g. tables and graphs) involving the variable. If titles are not supplied, the column name of the variable in `data` is used.
`data`	A `data.frame` containing the variable to be transformed and to which the transformed variable is to be appended.

Value

A `list` with a component named `data` that is the `data.frame` containing the transformed variable, a component named tvar.name that is a `character` `string` that is the name of the transformed variable in `data`, and a component named `titles` that extends the `list` supplied in the `titles`

argument to include a generated title for the transformed title, the name of the new component being tvar.name.

Author(s)

Chris Brien

See Also

angular, angular.mod.

Examples

```
## set up a factor with labels
x.dat <- data.frame(y = c(14, 42, 120, 150))

## transform y to logarithms
trans <- powerTransform("y", power = 0, titles=list(y = "Length (cm)"), data = x.dat)
x.dat <- trans$data
tvar.name <- trans$tvar.name

## transform y to logarithms after multiplying by -1 and adding 1.
z.dat <- data.frame( y = c(-5.25, -4.29, -1.22, 0.05))
trans <- powerTransform("y", power = 0, scale = -1, offset = 1 ,
                        titles=list(y = "Potential"), data = z.dat)
z.dat <- trans$data
tvar.name <- trans$tvar.name
```

---

predictions.frame *Description of a predictions object*

Description

A data.frame of S3-class predictions.frame that stores the predictions for a fitted model.

as.predictions.frame is function that converts a data.frame to an object of this class.

is.predictions.frame is the membership function for this class; it tests that an object has class predictions.frame.

validPredictionsFrame can be used to test the validity of a predictions.frame.

Value

A data.frame being a data.frame beginning with the variables classifying the predictions, in the same order as in the classify, and also containing columns named standard.error and est.status; each row contains a single predicted value. The usual name of the column containing the predictions is predicted.value or backtransformed.predictions. The number of rows should equal the number of unique combinations of the classifying variables. While such a data.frame can be constructed from the beginning, the pvals component of the value produced by predict.asreml is a suitable value to supply for this argument. Note that the names standard.error and est.status have been changed to std.error and status in the pvals component produced by asreml-R4; if the new names are in the data.frame supplied to predictions, they will be returned to the previous names.

The `data.frame` may also include columns for the lower and upper values of error intervals, either standard error, confidence or half-LSD intervals. The names of these columns will consist of three parts separated by full stops: 1) the first part will be `lower` or `upper`; 2) the second part will be one of `Confidence`, `StandardError` or `halfLeastSignificant`; 3) the third component will be `limits`.

See `predictPlus.asreml` for more information.

Author(s)

Chris Brien

See Also

`predictPlus.asreml`, `is.predictions.frame`, `as.predictions.frame`, `validPredictionsFrame`

Examples

```
data(Oats.dat)

## Use asreml to get predictions and associated statistics

## Not run:
m1.asr <- asreml(Yield ~ Nitrogen*Variety,
                 random=~Blocks/Wplots,
                 data=Oats.dat)
current.asrt <- as.asrtests(m1.asr)
Var.pred <- asreml::predict.asreml(m1.asr, classify="Nitrogen:Variety",
                                   sed=TRUE)
if (getASRemlVersionLoaded(nchar = 1) == "3")
  Var.pred <- Var.pred$predictions
Var.preds <- as.predictions.frame(Var.pred$pvals, se = "std.error",
                                  est.status = "status")

## End(Not run)

## Use lmerTest and emmmeans to get predictions and associated statistics
if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  m1.lmer <- lmerTest::lmer(Yield ~ Nitrogen*Variety + (1|Blocks/Wplots),
                            data=Oats.dat)
  Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
  Var.preds <- summary(Var.emm)
  Var.preds <- as.predictions.frame(Var.preds, predictions = "emmean",
                                    se = "SE", interval.type = "CI",
                                    interval.names = c("lower.CL", "upper.CL"))
}

if (exists("Var.preds"))
{
  ## Check the class and validity of the alldiffs object
  is.predictions.frame(Var.preds)
  validPredictionsFrame(Var.preds)
}
```

predictPlus.asreml *Forms the predictions for a term, their pairwise differences and associated statistics. A factor having parallel values may occur in the model and a linear transformation of the predictions can be specified. It results in an object of class alldifffs.*

Description

This function forms the predictions for `term` using `classify` and the supplied `asreml` object and stores them in an `alldiffs.object`. If `x.num` is supplied, the predictions will be obtained for the values supplied in `x.pred.values` and, if supplied, `x.plot.values` will replace them in the `alldiffs.object` that is returned. If `x.fac`, but not `x.num`, is specified, predictions will involve it and, if supplied, `x.plot.values` will replace the levels of `x.fac` in the `alldiffs.object` that is returned. In order to get the correct predictions you may need to supply additional arguments to `predict.asreml` through `...` e.g. `present`, `parallel`, `levels`. Any aliased predictions will be removed, as will any standard error of pairwise differences involving them.

Also calculated are the approximate degrees of freedom of the standard errors of the predictions. If the deominator degrees of freedom for `term` are available in `wald.tab`, they are used. Otherwise the residual degrees of freedom or the maximum of the denominator degrees in `wald.tab`, excluding the Intercept, are used. Which is used depends on the setting of `dDF.na`. These degrees of freedom are used for the t-distribution on which p-values and confidence intervals are based. It is stored as an attribute to the `alldiffs.object`. The degrees of freedom are also used in calculating the minimum, mean and maximum LSD for comparing pairs of predictions, which are also stored in the `alldiffs.object`.

If `pairwise = TRUE`, all pairwise differences between the `predictions`, their standard errors, p-values and LSD statistics are computed using `allDifferences.data.frame`. This adds them to the `alldiffs.object` as additional `list` components named `differences`, `sed`, `p.differences` and `LSD`.

If a linear transformation of the predictions is specified then the values of this linear transformation are returned, instead of the original predictions, along with their standard errors and the pairwise differences and associated statistics.

If a transformation has been applied in the analysis (any one of `transform.power` is not one, `scale` is not one and `offset` is nonzero), the backtransforms of the transformed values and their lower and upper error intervals are added to a `data.frame` that is consistent with the `predictions` `data.frame`.

If `transform.power` is other than one, the `standard.error` column of the `data.frame` is set to `NA`. This `data.frame` is added to the `alldiffs.object` as a `list` component called `backtransforms`.

The printing of the components produced is controlled by the `tables` argument. The order of plotting the levels of one of the factors indexing the predictions can be modified and is achieved using `sort.alldiffs`.

Usage

```
## S3 method for class 'asreml'
predictPlus(asreml.obj, classify, term = NULL,
            linear.transformation = NULL, titles = NULL,
            x.num = NULL, x.fac = NULL,
            x.pred.values = NULL, x.plot.values = NULL,
            error.intervals = "Confidence", avsed.tolerance = 0.25,
```

```
meanLSD.type = "overall", LSDby = NULL,
pairwise = TRUE, Vmatrix = FALSE,
tables = "all" , level.length = NA,
transform.power = 1, offset = 0, scale = 1,
inestimable.rm = TRUE,
sortFactor = NULL, sortWithinVals = NULL,
sortOrder = NULL, decreasing = FALSE,
wald.tab = NULL, alpha = 0.05,
dDF.na = "residual",  dDF.values = NULL,
trace = FALSE, ...)
```

Arguments

asreml.obj	asreml object for a fitted model.
classify	A character string giving the variables that define the margins of the multiway table to be predicted. Multiway tables are specified by forming an interaction type term from the classifying variables, that is, separating the variable names with the : operator. To predict the overall mean, set the classify to "(Intercept)".
term	A character string giving the variables that define the term that was fitted using asreml and that corresponds to classify. It only needs to be specified when it is different to classify.
linear.transformation	A formula or a matrix. If a formula is given then it is taken to be a submodel of the model term corresponding to the classify. The projection matrix that transforms the predictions so that they conform to the submodel is obtained; the submodel should involving the variables in the classify. For example, for classify set to "A:B", the submodel ~ A + B will result in the predictions for the combinations of A and B being made additive for the factors A and B. If a matrix is provided then it will be used to apply the linear transformation to the predictions. It might be a contrast matrix or a matrix of weights for a factor used to obtain the weighted average over that factor. The number of rows in the matrix should equal the number of linear combinations of the predictions desired and the number of columns should equal the number of predictions. In either case, as well as the values of the linear combinations, their standard errors, pairwise differences and associated statistics are returned.
titles	A list, each component of which is named for a column in the data.frame for asreml.obj and contains a character string giving a title to use in output (e.g. tables and graphs). Here they will be used for table headings.
x.num	A character string giving the name of the numeric covariate that (i) corresponds to x.fac, (ii) is potentially included in terms in the fitted model, and (iii) which corresponds to the x-axis variable. It should have the same number of unique values as the number of levels in x.fac.
x.fac	A character string giving the name of the factor that (i) corresponds to x.num, (ii) is potentially included in terms in the fitted model, and (iii) which corresponds to the x-axis variable. It should have the same number of levels as the number of unique values in x.num. The levels of x.fac must be in the order in which they are to be plotted - if they are dates, then they should be in the form yyyymmdd, which can be achieved using as.Date. However, the levels can be non-numeric in nature, provided that x.num is also set.

x.pred.values The values of x.num for which predicted values are required. If levels is set for passing to predict.asreml, x.pred.values is ignored. Note that while levels is and alternative to x.pred.values, it allows more general setting of the levels to be predicted.

x.plot.values The actual values to be plotted on the x axis. They are needed when values different to those in x.num are to be plotted or x.fac is to be plotted because there is no x.num term corresponding to the same term with x.fac.

error.intervals

A character string indicating the type of error interval, if any, to calculate in order to indicate uncertainty in the results. Possible values are "none", "StandardError", "Confidence" and "halfLeastSignificant". The default is for confidence limits to be used. The "halfLeastSignificant" option results in half the Least Significant Difference (LSD) being added and subtracted to the predictions, the LSD being calculated using the square root of the mean of the variances of all or a subset of pairwise differences between the predictions. If meanLSD.type is set to overall, the avsed.tolerance is not NA and the range of the SEDs divided by the average of the SEDs exceeds avsed.tolerance then the error.intervals calculations and the plotting will revert to confidence intervals.

avsed.tolerance

A numeric giving the value of the SED range, the range of the SEDs divided by the square root of the mean of the variances of all or a subset of the pairwise differences, that is considered reasonable in calculating error.intervals. It should be a value between 0 and 1. The following rules apply:

1. If avsed.tolerance is NA then mean LSDs of the type specified by meanLSD.type are calculated and used in error.intervals and plots.
2. Irrespective of the setting of meanLSD.type, if avsed.tolerance is not exceeded then the mean LSDs are used in error.intervals and plots.
3. If meanLSD.type is set to overall, avsed.tolerance is not NA, and avsed.tolerance is exceeded then error.intervals and plotting revert to confidence intervals.
4. If meanLSD.type is set to factor.combinations and avsed.tolerance is not exceeded for any factor combination then the half LSDs are used in error.intervals and plots; otherwise, error.intervals and plotting revert to confidence intervals.
5. If meanLSD.type is set to per.prediction and avsed.tolerance is not exceeded for any prediction then the half LSDs are used in error.intervals and plots; otherwise, error.intervals and plotting revert to confidence intervals.

meanLSD.type A character string determining whether the mean LSD stored is (i) the overall mean, based on the square root of the mean of the variances of all pairwise variances, (ii) the mean for each factor.combination of the factors specified by LSDby, which is based on the square root of the mean of the variances for all pairwise differences for each factor combination, unless there is only one predction for a factor.combination, when notional LSDs are calculated that are based on the standard error of the prediction multiplied by the square root of two, or (iii) the per.prediction mean, based, for each prediction, on the square root of the mean of the variances for all pairwise differences involving that prediction. It also determines, in conjunction with avsed.tolerance, which LSD will be used in calculating error.intervals and, hence, is used for plots.

LSDby — A character (vector) of variables names, being the names of the factors or numerics in the classify for each combination of which a mean LSD, minLSD and max LSD is stored in the LSD component of the alldiffs.object when meanLSD.type is factor.combinatons.

pairwise — A logical indicating whether all pairwise differences of the predictions and their standard errors and p-values are to be computed and stored. If tables is equal to "differences" or "all" or error.intervals is equal to "halfLeastSignificant", they will be stored irrespective of the value of pairwise.

Vmatrix — A logical indicating whether the variance matrix of the predictions will be stored as a component of the alldiffs.object that is returned. If linear.transformation is set, it will be stored irrespective of the value of Vmatrix.

tables — A character vector containing a combination of none, predictions, vcov, backtransforms, differences, p.differences, sed, LSD and all. These nominate which components of the alldiffs.object to print.

level.length — The maximum number of characters from the the levels of factors to use in the row and column labels of the tables of pairwise differences and their p-values and standard errors.

transform.power — A numeric specifying the power of a transformation, if one has been applied to the response variable. Unless it is equal to 1, the default, back-transforms of the predictions will be obtained and presented in tables or graphs as appropriate. The back-transformation raises the predictions to the power equal to the reciprocal of transform.power, unless it equals 0 in which case the exponential of the predictions is taken.

offset — A numeric that has been added to each value of the response after any scaling and before applying any power transformation.

scale — A numeric by which each value of the response has been multiplied before adding any offset and applying any power transformation.

inestimable.rm — A logical indicating whether rows for predictions that are not estimable are to be removed from the components of the alldiffs.object.

sortFactor — A character containing the name of the factor that indexes the set of predicted values that determines the sorting of the components of the alldiffs.object by sort.alldiffs. If NULL then sorting is not carried out. If there is more than one variable in the classify term then sortFactor is sorted for the predicted values within each combination of the values of the sortWithin variables: the classify variables, excluding the sortFactor. There should be only one predicted value for each unique value of sortFactor within each set defined by a combination of the values of the sortWithin variables.

sortWithinVals — A list with a component named for each factor and numeric that is a classify variable for the predictions, excluding sortFactor. Each component should contain a single value that is a value of the variable. The combination of this set of values will be used to define a subset of the predicted values whose order will define the order of sortFactor to be used for all combinations of the sortWithinVals variables. If sortWithinVals is NULL then the first value of each sortWithin variable in predictions component is used to define sortWithinVals. If there is only one variable in the classify then sortWithinVals is ignored.

sortOrder — A character vector whose length is the same as the number of levels for sortFactor in the predictions component of the alldiffs.object. It specifies the desired order of the levels in the reordered components of the alldiffs.object. The argument sortWithinVals is ignored.

The following creates a sortOrder vector levs for factor f based on the values in x: levs <-levels(f)[order(x)].

decreasing — A logical passed to order that detemines whether the order for sorting the components of the alldiffs.object is for increasing or decreasing magnitude of the predicted values.

wald.tab — A data.frame containing the pseudo-anova table for the fixed terms produced by a call to wald.asreml. The main use of it here is in determinining the degrees of freedom of the standard errors of the predictions. denominator degrees of freedom when p-values or confidence intervals are to be calculated.

alpha — A numeric giving the significance level for LSDs or one minus the confidence level for confidence intervals.

dDF.na — A character specifying the method to use to obtain approximate denominator degrees of freedom. when the numeric or algebraic methods produce an NA. Consistent with when no denDF are available, the default is "residual" and so the residual degrees of freedom from asreml.obj$nedf are used. If dDF.na = "none", no subtitute denominator degrees of freedom are employed; if dDF.na = "maximum", the maximum of those denDF that are available, excluding that for the Intercept, is used; if all denDF are NA, asreml.obj$nedf is used. If dDF.na = "supplied", a vector of values for the denominator degrees of freedom is to be supplied in dDF.values. Any other setting is ignored and a warning message produced. Generally, substituting these degrees of freedom is anticonservative in that it is likely that the degrees of freedom used will be too large.

dDF.values — A vector of values to be used when dDF.na = "supplied". Its values will be used when denDF in a test for a fixed effect is NA. This vector must be the same length as the number of fixed terms, including (Intercept) whose value could be NA.

trace — A logical that control output from ASReml-R. If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.

... — further arguments passed to predict.asreml.

Value

For linear.transformations set to NULL, an S3-class alldiffs.object with predictions and their standard errors and, depending on the settings of the arguments, all pairwise differences between predictions, their standard errors and p-values and LSD statistics. Also, unless the sortFactor or sortOrder arguments are invoked, the rows of predictions component are ordered so that they are in standard order for the variables in the classify. That is, the values of the last variable change with every row, those of the second-last variable only change after all the values of the last variable have been traversed; in general, the values of a variable are the same for all the combinations of the values to the variables to its right in the classify. In addition, if necessary, the order of the columns of the variables in the predictions component are changed to match their order in the classify.

If transform.power or scale is not one or offset is not zero, it will contain a data.frame with the backtransformed linear transformation of the predictions. The backtransformation will, after backtransforming for any power transformation, subtract the offset and then divide by the scale.

If error.intervals is not "none", then the predictions component and, if present, the backtransforms component will contain columns for the lower and upper values of the limits for the interval.

The name of the response, the response.title, the term, the classify, tdf, sortFactor and the sortOrder will be set as attributes to the object. Note that the classify in an alldiffs.object

is based on the variables indexing the predictions, which may differ from the classify used to obtain the original predictions (for example, when the alldiffs.objects stores a linear transformation of predictions.

For linear.transformations set to other than NULL, an alldiffs.object with the linear.transformation applied to the predictions and their standard errors and, depending on the settings of the arguments, all pairwise differences between the linearly transformed predictions, their standard errors and p-values and LSD statistics. (See also linTransform.alldiffs.)

Author(s)

Chris Brien

See Also

alldiffs.object, as.alldiffs, print.alldiffs, linTransform.alldiffs, sort.alldiffs, subset.alldiffs, allDifferences.data.frame, redoErrorIntervals.alldiffs, recalcLSD.alldiffs, predictPresent.asreml, plotPredictions.data.frame, as.Date, predict.asreml

Examples

```
## Not run:
data(WaterRunoff.dat)
asreml.options(keep.order = TRUE) #required for asreml-R4 only
current.asr <- asreml(fixed = pH ~ Benches + (Sources * (Type + Species)),
                      random = ~ Benches:MainPlots,
                      keep.order=TRUE, data= WaterRunoff.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
diffs <- predictPlus(classify = "Sources:Type",
                     asreml.obj = current.asr,
                     wald.tab = current.asrt$wald.tab,
                     present = c("Sources", "Type", "Species"))

## End(Not run)
```

---

predictPresent.asreml *Forms the predictions for each of one or more terms and presents them in tables and/or graphs.*

Description

This function forms the predictions for each term in terms using a supplied asreml object and predictPlus.asreml. Tables are produced using predictPlus.asreml, in conjunction with allDifferences.data.frame, with the argument tables specifying which tables are printed. The argument plots, along with transform.power, controls which plots are produced. The plots are produced using plotPredictions.data.frame, with line plots produced when variables involving x.num or x.fac are involved in classify for the predictions and bar charts otherwise. In order to get the correct predictions you may need to supply additional arguments to predict.asreml through ... e.g. present, parallel, levels.

The order of plotting the levels of one of the factors indexing the predictions can be modified and is achieved using sort.alldiffs.

Usage

```
## S3 method for class 'asreml'
predictPresent(asreml.obj, terms,
               linear.transformation = NULL,
               wald.tab = NULL, dDF.na = "residual", dDF.values = NULL,
               x.num = NULL, x.fac = NULL, nonx.fac.order = NULL,
               x.pred.values = NULL, x.plot.values = NULL,
               plots = "predictions", panels = "multiple",
               graphics.device = NULL,
               error.intervals = "Confidence", meanLSD.type = "overall",
               LSDby = NULL, avsed.tolerance = 0.25, titles = NULL,
               colour.scheme = "colour", save.plots = FALSE,
               transform.power = 1, offset = 0, scale = 1,
               pairwise = TRUE, Vmatrix = FALSE,
               tables = "all", level.length = NA,
               alpha = 0.05, inestimable.rm = TRUE,
               sortFactor = NULL, sortWithinVals = NULL,
               sortOrder = NULL, decreasing = FALSE,
               trace = FALSE, ggplotFuncs = NULL, ...)
```

Arguments

`asreml.obj` `asreml` object for a fitted model.

`terms` A `character` `vector` giving the terms for which predictions are required.

`linear.transformation`

A `formula` or a `matrix` specifying a linear transformation to be applied to the predictions. If a `formula` is given then it is taken to be a submodel of the model term corresponding to the `classify`. The projection matrix that transforms the `predictions` so that they conform to the submodel is obtained; the submodel should involving the variables in the `classify`. For example, for `classify` set to `"A:B"`, the submodel `~ A + B` will result in the `predictions` for the combinations of `A` and `B` being made additive for the `factor`s `A` and `B`.

If a `matrix` is provided then it will be used to apply the linear transformation to the `predictions`. It might be a contrast `matrix` or a `matrix` of weights for a factor used to obtain the weighted average over that factor. The number of rows in the `matrix` should equal the number of linear combinations of the `predictions` desired and the number of columns should equal the number of `predictions`.

In either case, as well as the values of the linear combinations, their standard errors, pairwise differences and associated statistics are returned in the `alldiffs.object`.

`wald.tab` A `data frame` containing the pseudo-anova table for the fixed terms produced by a call to `wald.asreml`. The main use of it here is in getting denominator degrees of freedom when confidence intervals are to be plotted.

`dDF.na` The method to use to obtain approximate denominator degrees of freedom. when the numeric or algebraic methods produce an `NA`. Consistent with when no denDF are available, the default is `"residual"` and so the residual degrees of freedom from `asreml.obj$nedf` are used. If `dDF.na = "none"`, no subtitute denominator degrees of freedom are employed; if `dDF.na = "maximum"`, the maximum of those denDF that are available, excluding that for the Intercept, is used; if all denDF are `NA`, `asreml.obj$nedf` is used. If `dDF.na = "supplied"`, a `vector` of values for the denominator degrees of freedom is to be supplied

in dDF.values. Any other setting is ignored and a warning message produced. Generally, substituting these degrees of freedom is anticonservative in that it is likely that the degrees of freedom used will be too large.

dDF.values A vector of values to be used when dDF.na = "supplied". Its values will be used when denDF in a test for a fixed effect is NA. This vector must be the same length as the number of fixed terms, including (Intercept) whose value could be NA.

x.num A character string giving the name of the numeric covariate that corresponds to x.fac, is potentially included in terms in the fitted model and which corresponds to the x-axis variable. It should have the same number of unique values as the number of levels in x.fac.

x.fac A character string giving the name of the factor that corresponds to x.num, is potentially included in terms in the fitted model and which corresponds to the x-axis variable. It should have the same number of levels as the number of unique values in x.num. The levels of x.fac must be in the order in which they are to be plotted - if they are dates, then they should be in the form yyyymmdd, which can be achieved using as.Date. However, the levels can be non-numeric in nature, provided that x.num is also set.

nonx.fac.order A character vector giving the order in which factors other than x.fac are to be plotted in plots with multiple panels (i.e. where the number of non-x factors is greater than 1). The first factor in the vector will be plotted on the X axis (if there is no x.num or x.fac. Otherwise, the order of plotting the factors is in columns (X facets) and then rows (Y facets). By default the order is in decreasing order for the numbers of levels of the non x factors.

x.pred.values The values of x.num for which predicted values are required.

x.plot.values The actual values to be plotted on the x axis or in the labels of tables. They are needed when values different to those in x.num are to be plotted or x.fac is to be plotted because there is no x.num term corresponding to the same term with x.fac.

plots Possible values are "none", "predictions", "backtransforms" and "both". Plots are not produced if the value is "none". If data are not transformed for analysis (transform.power = 1), a plot of the predictions is produced provided plots is not "none". If the data are transformed, the value of plots determines what is produced.

panels Possible values are "single" and "multiple". When line plots are to be produced, because variables involving x.num or x.fac are involved in classify for the predictions, panels determines whether or not a single panel or multiple panels in a single window are produced. The panels argument is ignored for for bar charts.

graphics.device

A character specifying a graphics device for plotting. The default is graphics.device = NULL, which will result in plots being produced on the current graphics device. Setting it to "windows", for example, will result in a windows graphics device being opened.

error.intervals

A character string indicating the type of error interval, if any, to calculate in order to indicate uncertainty in the results. Possible values are "none", "StandardError", "Confidence" and "halfLeastSignificant". The default is for confidence limits to be used. The "halfLeastSignificant" option results in half the Least Significant Difference (LSD) being added and subtracted

to the predictions, the LSD being calculated using the square root of the mean of the variances of all or a subset of pairwise differences between the predictions. If meanLSD.type is set to overall, the avsed.tolerance is not NA and the range of the SEDs divided by the average of the SEDs exceeds avsed.tolerance then the error.intervals calculations and the plotting will revert to confidence intervals.

avsed.tolerance

A numeric giving the value of the SED range, the range of the SEDs divided by the square root of the mean of the variances of all or a subset of the pairwise differences, that is considered reasonable in calculating error.intervals. It should be a value between 0 and 1. The following rules apply:

1. If avsed.tolerance is NA then mean LSDs of the type specified by meanLSD.type are calculated and used in error.intervals and plots.
2. Irrespective of the setting of meanLSD.type, if avsed.tolerance is not exceeded then the mean LSDs are used in error.intervals and plots.
3. If meanLSD.type is set to overall, avsed.tolerance is not NA, and avsed.tolerance is exceeded then error.intervals and plotting revert to confidence intervals.
4. If meanLSD.type is set to factor.combinations and avsed.tolerance is not exceeded for any factor combination then the half LSDs are used in error.intervals and plots; otherwise, error.intervals and plotting revert to confidence intervals.
5. If meanLSD.type is set to per.prediction and avsed.tolerance is not exceeded for any prediction then the half LSDs are used in error.intervals and plots; otherwise, error.intervals and plotting revert to confidence intervals.

meanLSD.type A character string determining whether the mean LSD stored is (i) the overall mean, based on the square root of the mean of the variances of all pairwise variances, (ii) the mean for each factor.combination of the factors specified by LSDby, which is based on the square root of the mean of the variances for all pairwise differences for each factor combination, unless there is only one predction for a factor.combination, when notional LSDs are calculated that are based on the standard error of the prediction multiplied by the square root of two, or (iii) the per.prediction mean, based, for each prediction, on the square root of the mean of the variances for all pairwise differences involving that prediction. It also determines, in conjunction with avsed.tolerance, which LSD will be used in calculating error.intervals and, hence, is used for plots.

LSDby A character (vector) of variables names, being the names of the factors or numerics in the classify for each combination of which a mean LSD, minLSD and max LSD is stored in the LSD component of the alldiffs.object when meanLSD.type is factor.combinatons.

titles A list, each component of which is named for a column in the data.frame for asreml.obj and contains a character string giving a title to use in output (e.g. tables and graphs). Here they will be used for axis labels.

colour.scheme A character string specifying the colour scheme for the plots. The default is "colour" which produces coloured lines and bars, a grey background and white gridlines. A value of "black" results in black lines, grey bars and gridlines and a white background.

save.plots A logical that determines whether any plots will be saved. If they are to be saved, a file name will be generated that consists of the following elements separated by full stops: the response variable name with .back if backtransformed

values are being plotted, the classify term, Bar or Line and, if error.intervals is not "none", one of SE, CI or LSI. The file will be saved as a 'png' file in the current work directory.

transform.power
: A number specifying the power of a transformation, if one has been applied to the response variable. Unless it is equal to 1, the default, back-transforms of the predictions will be obtained and presented in tables or graphs as appropriate. The back-transform will raise the predictions to the power equal to the reciprocal of transform.power, unless it equals 0 in which case the exponential will be taken. Any scaling and offsetting will also be taken into account in the backtransformation.

offset
: A number that has been added to each value of the response after any scaling and before applying any power transformation. Unless it is equal to 0, the default, back-transforms of the predictions will be obtained and presented in tables or graphs as appropriate. The backtransformation will, after backtransforming for any power transformation, subtract the offset.

scale
: A number by which each value of the response has been multiply before adding any offset and applying any power transformation. Unless it is equal to 1, the default, back-transforms of the predictions will be obtained and presented in tables or graphs as appropriate. The backtransformation will, after backtransforming for any power transformation and then subtracting the offset, divide by the scale.

pairwise
: A logical indicating whether all pairise differences of the predictions and their standard errors and p-values are to be computed and stored. If tables is equal to "differences" or "all" or error.intervals is equal to "halfLeastSignificant", they will be stored irrespective of the value of pairwise.

Vmatrix
: A logical indicating whether the variance matrix of the predictions will be stored as a component of the alldiffs.object that is returned. If linear.transformation is set, it will be stored irrespective of the value of Vmatrix.

tables
: A character vector containing a combination of predictions, vcov, backtransforms, differences, p.differences, sed, LSD and all. These nominate which components of the alldiffs.object to print.

level.length
: The maximum number of characters from the the levels of factors to use in the row and column labels of the tables produced by allDifferences.data.frame.

alpha
: The significance level for LSDs or 1 - alpha is the confidence level for confidence intervals.

inestimable.rm
: A logical indicating whether rows for predictions that are not estimable are to be removed from the components of the alldiffs.object.

sortFactor
: A character containing the name of the factor that indexes the set of predicted values that determines the sorting of the components of the alldiffs.object by sort.alldiffs. If NULL then sorting is not carried out. If there is more than one variable in the classify term then sortFactor is sorted for the predicted values within each combination of the values of the sortWithin variables: the classify variables, excluding the sortFactor. There should be only one predicted value for each unique value of sortFactor within each set defined by a combination of the values of the sortWithin variables.

sortWithinVals
: A list with a component named for each factor and numeric that is a classify variable for the predictions, excluding sortFactor. Each component should contain a single value that is a value of the variable. The combination of this

set of values will be used to define a subset of the predicted values whose order will define the order of sortFactor to be used for all combinations of the sortWithinVals variables. If sortWithinVals is NULL then the first value of each sortWithin variable in predictions component is used to define sortWithinVals. If there is only one variable in the classify then sortWithinVals is ignored.

sortOrder — A character vector whose length is the same as the number of levels for sortFactor in the predictions component of the alldiffs.object. It specifies the desired order of the levels in the reordered components of the alldiffs.object. The argument sortWithinVals is ignored.

The following creates a sortOrder vector levs for factor f based on the values in x: levs <-levels(f)[order(x)].

decreasing — A logical passed to order that detemines whether the order for sorting the components of the alldiffs.object is for increasing or decreasing magnitude of the predicted values.

trace — If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.

ggplotFuncs — A list, each element of which contains the results of evaluating a ggplot function. It is created by calling the list function with a ggplot function call for each element. It is passed to plotPredictions.data.frame.

... — further arguments passed to predict.asreml via predictPlus.asreml and to ggplot via plotPredictions.data.frame.

Value

A list containing an alldiffs.object for each term for which tables are produced. The names of the components of this list are the terms with full-stops (.) replacing colons (:). Plots are also preduced depending on the setting of the plot argument.

Author(s)

Chris Brien

See Also

predictPlus.asreml, allDifferences.data.frame, sort.alldiffs, subset.alldiffs, redoErrorIntervals.alldiffs, recalcLSD.alldiffs, plotPredictions.data.frame, print.alldiffs, as.Date, Devices

Examples

```
## Not run:
data(WaterRunoff.dat)
titles <- list("Days since first observation", "Days since first observation",
               "pH", "Turbidity (NTU)")
names(titles) <- names(WaterRunoff.dat)[c(5,7,11:12)]
asreml.options(keep.order = TRUE) #required for asreml-R4 only
current.asr <- asreml(fixed = log.Turbidity ~ Benches + Sources + Type + Species +
                                Sources:Type + Sources:Species + Sources:Species:xDay +
                                Sources:Species:Date,
                      data = WaterRunoff.dat, keep.order = TRUE)
current.asrt <- as.asrtests(current.asr, NULL, NULL)

#### Get the observed combinations of the factors and variables in classify
```

```
class.facs <- c("Sources","Species","Date","xDay")
levs <- as.data.frame(table(WaterRunoff.dat[class.facs]))
levs <- levs[do.call(order, levs), ]
levs <- as.list(levs[levs$Freq != 0, class.facs])
levs$xDay <- as.numfac(levs$xDay)

#### parallel and levels are arguments from predict.asreml
diff.list <- predictPresent.asreml(asreml.obj = current.asrt$asreml.obj,
                                   terms = "Date:Sources:Species:xDay",
                                   x.num = "xDay", x.fac = "Date",
                                   parallel = TRUE, levels = levs,
                                   wald.tab = current.asrt$wald.tab,
                                   plots = "predictions",
                                   error.intervals = "StandardError",
                                   titles = titles,
                                   transform.power = 0,
                                   present = c("Type","Species","Sources"),
                                   tables = "none",
                                   level.length = 6)

## End(Not run)
```

`print.alldiffs` *Prints the values in an* `alldiffs.object` *in a nice format.*

Description

Prints the predictions and standard errors from a fitted model, including the attributes of the `predictions.frame`. Also prints out all pairwise differences between the predictions to 2 signigicant figures, along with their p-values and standard errors to 4 decimal places. If LSDs are requested the mean, minimum and maximum LSDs will be printed.

Usage

```
## S3 method for class 'alldiffs'
print(x, which = "all", colourise = FALSE, ...)
```

Arguments

`x`	An `alldiffs.object`.
`which`	A `character vector` containing a combination of `predictions`, `vcov`, `backtransforms`, `differences`, `p.differences`, `sed`, `LSD` and `all`. These nominate which components of the `alldiffs.object` to print.
`colourise`	A `logical` which, if `TRUE`, results in the header text produced by `predict.asreml` being displayed in a different colour, if supported by the output terminal device. It overrides the `TRUE` setting of the `colourise` argument of `asreml::asreml.options`.
`...`	further arguments passed to `print.predictions.frame`.

Value

No value is returned, but the components of `x` are printed.

Author(s)

Chris Brien

See Also

print.predictions.frame, as.alldiffs, allDifferences.data.frame

Examples

```
## Not run:
print.alldiffs(diffs, which = "predictions")

## End(Not run)
```

---

print.asrtests *Prints the values in an asrtests.object*

Description

Prints a summary of the asreml object, the pseusdanova and the test.summary data.frame that are stored in the asrtests.object.

Usage

```
## S3 method for class 'asrtests'
print(x, which = "all", colourise = FALSE, ...)
```

Arguments

x	An asrtests.object.
which	Which elements of the asrtests.object to print. Possible values are some combination of asremlsummary, pseudoanova, wald.tab, testsummary and all. The option wald.tab is a synonym for pseudoanova.
colourise	A logical which, if TRUE, results in the header text produced by wald.asreml being displayed in a different colour, if supported by the output terminal device. It overrides the TRUE setting of the colourise argument of asreml::asreml.options.
...	further arguments passed to print and print.wald.tab.

Value

No value is returned, but the elements of the list in x are printed.

Author(s)

Chris Brien

See Also

print.wald.tab, as.asrtests, asremlPlus-package

Examples

```
## Not run:
data(Wheat.dat)
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
current.asrt <- rmboundary.asrtests(current.asrt)
# Test Row autocorrelation
current.asrt <- testresidual(current.asrt, , "~ Row:ar1(Column)",
                             label="Row autocorrelation", simpler=TRUE)
print(current.asrt)

## End(Not run)
```

`print.predictions.frame` *Prints the values in a* `predictions.frame`*, with or without title and heading.*

Description

Prints the predictions from a fitted model, along with their standard errors and, if present, their error intervals, with or without title and headings.

Usage

```
## S3 method for class 'predictions.frame'
print(x, title = NULL,
      which.predictions = c("title", "heading", "table"),
      colourise = FALSE, ...)
```

Arguments

`x`	An object that, ideally, is of class `predictions.frame`.
`title`	A `character` giving a title to be printed out before the `heading` and `table` for the `predictions.frame`,
`which.predictions`	what Which elements of the `predictions.frame` to print. Possible values are some combination of `title`, `heading`, `table` and `all`. The `heading` is an attribute of `x`.
`colourise`	A `logical` which, if `TRUE`, results in the header text produced by `predict.asreml` being displayed in a different colour, if supported by the output terminal device. It overrides the `TRUE` setting of the `colourise` argument of `asreml::asreml.options`, but is only operational when the `table` is also printed.
`...`	further arguments passed to `print.predictions.frame`.

Value

No value is returned, but the components of `x` are printed.

Author(s)

Chris Brien

See Also

print.alldiffs, as.alldiffs, allDifferences.data.frame

Examples

```
## Not run:
print.predictions.frame(diffs$predictions, which = "all")

## End(Not run)
```

---

print.wald.tab *Prints a Wald or pseudoanova table.*

Description

Prints a wald.tab with or without title and/or heading.

Usage

```
## S3 method for class 'wald.tab'
print(x, which.wald = c("title", "heading", "table"),
      colourise = FALSE, ...)
```

Arguments

x	A object that, ideally, is of class wald.tab.
which.wald	Which elements of the wald.tab to print. Possible values are some combination of title, heading, table and all. The heading is an attribute of x.
colourise	A logical which, if TRUE, results in the header text produced by wald.asreml being displayed in a different colour, if supported by the output terminal device. It overrides the TRUE setting of the colourise argument of asreml::asreml.options.
...	further arguments passed to print and print.wald.tab, but is only operational when the table is also printed.

Value

No value is returned, but the elements of the list in x are printed.

Author(s)

Chris Brien

See Also

print.asrtests, as.asrtests, asremlPlus-package

Examples

```
## Not run:
data(Wheat.dat)
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
current.asrt <- rmboundary.asrtests(current.asrt)
# Test Row autocorrelation
current.asrt <- testresidual(current.asrt, , "~ Row:ar1(Column)",
                             label="Row autocorrelation", simpler=TRUE)
print(current.asrt$wald.tab)

## End(Not run)
```

`recalcLSD.alldiffs` *Adds or recalculates the LSD component of an* `alldiffs.object`.

Description

Given an `alldiffs.object`, adds or recalculate its LSD component.

Usage

```
## S3 method for class 'alldiffs'
recalcLSD(alldiffs.obj, meanLSD.type = "overall", LSDby = NULL,
          alpha = 0.05, ...)
```

Arguments

`alldiffs.obj`	An `alldiffs.object`.
`meanLSD.type`	A `character` string determining whether the mean LSD stored is (i) the `overall` mean, based on the square root of the mean of the variances of all pairwise variances, (ii) the mean for each `factor.combination` of the `factors` specified by `LSDby`, which is based on the square root of the mean of the variances for all pairwise differences for each factor combination, unless there is only one predction for a `factor.combination`, when notional LSDs are calculated that are based on the standard error of the prediction multiplied by the square root of two, or (iii) the `per.prediction` mean, based, for each prediction, on the square root of the mean of the variances for all pairwise differences involving that prediction. It also determines, in conjunction with `avsed.tolerance`, which LSD will be used in calculating `error.intervals` and, hence, is used for plots.
`LSDby`	A `character` (vector) of variables names, being the names of the `factors` or `numerics` in the `classify` for each combination of which a mean LSD, minLSD and max LSD is stored in the `LSD` component of the `alldiffs.object` when `meanLSD.type` is `factor.combinatons`.
`alpha`	The significance level for an LSD to compare a pair of predictions.
`...`	further arguments passed to `allDifferences.data.frame`.

Value

An alldiffs.object with components predictions, vcov, differences, p.differences sed, LSD and, if present in alldiffs.obj, backtransforms.

Author(s)

Chris Brien

See Also

asremlPlus-package, as.alldiffs, sort.alldiffs, subset.alldiffs, print.alldiffs, renewClassify.alldiffs, redoErrorIntervals.alldiffs, plotPredictions.data.frame, predictPlus.asreml, predictPresent.asreml

Examples

```
data(WaterRunoff.dat)

##Use asreml to get predictions and associated statistics

## Not run:
asreml.options(keep.order = TRUE) #required for asreml-R4 only
current.asr <- asreml(fixed = pH ~ Benches + (Sources * (Type + Species)),
                      random = ~ Benches:MainPlots,
                      keep.order=TRUE, data= WaterRunoff.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
TS.diffs <- predictPlus(classify = "Sources:Type",
                        asreml.obj = current.asr,
                        wald.tab = current.asrt$wald.tab,
                       present = c("Sources", "Type", "Species"))

## End(Not run)

## Use lmeTest and emmmeans to get predictions and associated statistics

if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  m1.lmer <- lmerTest::lmer(pH ~ Benches + (Sources * (Type + Species)) +
                              (1|Benches:MainPlots),
                            data=na.omit(WaterRunoff.dat))
  TS.emm <- emmeans::emmeans(m1.lmer, specs = ~ Sources:Species)
  TS.preds <- summary(TS.emm)
  den.df <- min(TS.preds$df, na.rm = TRUE)
  ## Modify TS.preds to be compatible with a predictions.frame
  TS.preds <- as.predictions.frame(TS.preds, predictions = "emmean",
                                   se = "SE", interval.type = "CI",
                                   interval.names = c("lower.CL", "upper.CL"))

  ## Form an all.diffs object and check its validity
  TS.vcov <- vcov(TS.emm)
  TS.diffs <- allDifferences(predictions = TS.preds, classify = "Sources:Species",
                             vcov = TS.vcov, tdf = den.df)
  validAlldiffs(TS.diffs)
}
```

```
## Plot p-values for predictions obtained using asreml or lmerTest
if (exists("TS.diffs"))
{
  ##Recalculate the LSD values for predictions obtained using asreml or lmerTest
  TS.diffs <- recalcLSD.alldiffs(TS.diffs, meanLSD.type = "factor.combinations",
                                 LSDby = "Sources")
}
```

`recalcWaldTab.asrtests` *Recalculates the denDF, F.inc and P values for a table of Wald test statistics obtained using* `wald.asreml`

Description

If some or all denDF are not available, either because they are NA or because F.inc values were not calculated, this function allows the user to specify how approximate denDF values are to be obtained. This is done through the `dDF.na` and `dDF.values` arguments. Note that if denDF values are available in the Wald table then only those that are `NA` will be replaced. The P values are recalculated using F.con, if present in the `wald.tab`, otherwise F.inc is used. It is noted that, as of asreml version 4, `wald.asreml` has a `kenadj` argument.

Usage

```
## S3 method for class 'asrtests'
recalcWaldTab(asrtests.obj, recalc.wald = FALSE,
              denDF="numeric", dDF.na = "none",
              dDF.values = NULL, trace = FALSE, ...)
```

Arguments

`asrtests.obj`	an `asrtests.object` containing the components (i) `asreml.obj`, (ii) `wald.tab`, and (iii) `test.summary`.
`recalc.wald`	A `logical` indicating whether to call `wald.asreml` to recalculate the pseudoanova table for the model fit stored in the `asreml` object contained in `asrtests.obj`.
`denDF`	Specifies the method to use in computing approximate denominator degrees of freedom when `wald.asreml` is called. Can be `none` to suppress the computations, `numeric` for numerical methods, `algebraic` for algebraic methods or `default`, the default, to autommatically choose numeric or algebraic computations depending on problem size. The denominator degrees of freedom are calculated according to Kenward and Roger (1997) for fixed terms in the dense part of the model.
`dDF.na`	The method to use to obtain substitute denominator degrees of freedom. when the numeric or algebraic methods produce an `NA`. If `dDF.na = "none"`, no substitute denominator degrees of freedom are employed; if `dDF.na = "residual"`, the residual degrees of freedom from `asreml.obj$nedf` are used; if `dDF.na = "maximum"`, the maximum of those denDF that are available, excluding that for the Intercept, is used; if all denDF are `NA`, `asreml.obj$nedf` is used. If `dDF.na = "supplied"`, a `vector` of values for the denominator degrees of freedom is to be supplied in `dDF.values`. Any other setting is ignored and a warning message produced. Generally, substituting these degrees of freedom is anticonservative in that it is likely that the degrees of freedom used will be too large.

dDF.values	A vector of values to be used when dDF.na = "supplied". Its values will be used when denDF in a test for a fixed effect is NA. This vector must be the same length as the number of fixed terms, including (Intercept) whose value could be NA.
trace	If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.
...	further arguments passed to asreml and to wald.asreml.

Value

A wald.tab: a 4- or 6-column data.frame containing a pseudo-anova table for the fixed terms produced by wald.asreml.

Author(s)

Chris Brien

See Also

as.asrtests, testranfix.asrtests

Examples

```
## Not run:
  wald.tab <- recalcWaldTab(current.asrt,
                            dDF.na = "supplied",
                            dDF.values = c(NA,rep(c(330,346), c(4,3))))

## End(Not run)
```

---

redoErrorIntervals.alldiffs

Adds or replaces the error intervals stored in a prediction component of an alldiffs.object.

Description

Given an alldiffs.object, adds or replaces error.intervals for its prediction component. If the backtransforms component is present, the transform.power, offset and scale will be retieved from the backtransforms attributes, ignoring the values for the function's arguments, and the backtransformed error.intervals will also be calculated.

Usage

```
## S3 method for class 'alldiffs'
redoErrorIntervals(alldiffs.obj, error.intervals = "Confidence",
                   alpha = 0.05, avsed.tolerance = 0.25,
                   meanLSD.type = NULL, LSDby = NULL, ...)
```

Arguments

alldiffs.obj	An alldiffs.object.
error.intervals	A character string indicating the type of error interval, if any, to calculate in order to indicate uncertainty in the predicted values. Possible values are "none", "StandardError", "Confidence" and "halfLeastSignificant". The default is for confidence limits to be used. The "halfLeastSignificant" option results in half the Least Significant Difference (LSD) being added and subtracted to the predictions, the LSD being calculated using the square root of the mean of the variances of all or a subset of pairwise differences between the predictions. If meanLSD.type is set to overall, the avsed.tolerance is not NA and the range of the SEDs divided by the average of the SEDs exceeds avsed.tolerance then the error.intervals calculations and the plotting will revert to confidence intervals.
alpha	The significance level for an LSD to compare a pair of predictions.
avsed.tolerance	A numeric giving the value of the SED range, the range of the SEDs divided by the square root of the mean of the variances of all or a subset of the pairwise differences, that is considered reasonable in calculating error.intervals. It should be a value between 0 and 1. The following rules apply: 1. If avsed.tolerance is NA then mean LSDs of the type specified by meanLSD.type are calculated and used in error.intervals and plots. 2. Irrespective of the setting of meanLSD.type, if avsed.tolerance is not exceeded then the mean LSDs are used in error.intervals and plots. 3. If meanLSD.type is set to overall, avsed.tolerance is not NA, and avsed.tolerance is exceeded then error.intervals and plotting revert to confidence intervals. 4. If meanLSD.type is set to factor.combinations and avsed.tolerance is not exceeded for any factor combination then the half LSDs are used in error.intervals and plots; otherwise, error.intervals and plotting revert to confidence intervals. 5. If meanLSD.type is set to per.prediction and avsed.tolerance is not exceeded for any prediction then the half LSDs are used in error.intervals and plots; otherwise, error.intervals and plotting revert to confidence intervals.
meanLSD.type	A character string determining whether the mean LSD stored is (i) the overall mean, based on the square root of the mean of the variances of all pairwise variances, (ii) the mean for each factor.combination of the factors specified by LSDby, which is based on the square root of the mean of the variances for all pairwise differences for each factor combination, or (iii) the per.prediction mean, based, for each prediction, on the square root of the mean of the variances for all pairwise differences involving that prediction. If NULL, the attributes meanLSD.type and LSDby of the alldiffs.obj will be used to determine the LSDs to be calculated. If the meanLSD.type attribute is NULL then meanLSD.type will be set to overall. The meanLSD.type also determines, in conjunction with avsed.tolerance, which LSD will be usedin calculating error.intervals and, hence, is used for plots.
LSDby	A character (vector) of variables names, being the names of the factors or numerics in the classify for each combination of which a mean LSD, minLSD and max LSD is stored in the LSD component of the alldiffs.object when meanLSD.type is factor.combinatons.

... pass transform.power, offset and scale as required - for further information see predictPlus.asreml.

Value

An alldiffs.object with components predictions, vcov, differences, p.differences sed, LSD and, if present in alldiffs.obj, backtransforms.

If error.intervals is not "none", then the predictions component and, if present, the backtransforms component will contain columns for the lower and upper values of the limits for the interval. The names of these columns will consist of three parts separated by full stops: 1) the first part will be lower or upper; 2) the second part will be one of Confidence, StandardError or halfLeastSignificant; 3) the third component will be limits.

The name of the response, the term, the classify and tdf, as well as the degrees of freedom of the standard error, will be set as attributes to the object.

Author(s)

Chris Brien

See Also

as.alldiffs, print.alldiffs, sort.alldiffs, subset.alldiffs, allDifferences.data.frame, recalcLSD.alldiffs, predictPresent.asreml, plotPredictions.data.frame, as.Date, predict.asreml

Examples

```
data(WaterRunoff.dat)

##Use asreml to get predictions and associated statistics

## Not run:
asreml.options(keep.order = TRUE) #required for asreml-R4 only
current.asr <- asreml(fixed = pH ~ Benches + (Sources * (Type + Species)),
                      random = ~ Benches:MainPlots,
                      keep.order=TRUE, data= WaterRunoff.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
TS.diffs <- predictPlus(classify = "Sources:Type",
                        asreml.obj = current.asr,
                        wald.tab = current.asrt$wald.tab,
                       present = c("Sources", "Type", "Species"))

## End(Not run)

## Use lmeTest and emmmeans to get predictions and associated statistics

if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  m1.lmer <- lmerTest::lmer(pH ~ Benches + (Sources * (Type + Species)) +
                              (1|Benches:MainPlots),
                            data=na.omit(WaterRunoff.dat))
  TS.emm <- emmeans::emmeans(m1.lmer, specs = ~ Sources:Species)
  TS.preds <- summary(TS.emm)
  den.df <- min(TS.preds$df, na.rm = TRUE)
```

```
  ## Modify TS.preds to be compatible with a predictions.frame
  TS.preds <- as.predictions.frame(TS.preds, predictions = "emmean",
                                   se = "SE", interval.type = "CI",
                                   interval.names = c("lower.CL", "upper.CL"))

  ## Form an all.diffs object and check its validity
  TS.vcov <- vcov(TS.emm)
  TS.diffs <- allDifferences(predictions = TS.preds,
                             classify = "Sources:Species",
                             vcov = TS.vcov, tdf = den.df)
  validAlldiffs(TS.diffs)
}

## Plot p-values for predictions obtained using asreml or lmerTest
if (exists("TS.diffs"))
{
  ##Recalculate the LSD values for predictions obtained using asreml or lmerTest
  TS.diffs <- redoErrorIntervals.alldiffs(TS.diffs,
                                          error.intervals = "halfLeastSignificant")

}
```

`REMLRT.asreml` *Performs a REML ratio test to compare two models.*

Description

Extracts the REML log likelihood and the number of variance parameters from two `asreml` objects. It assumes that that the first `asreml` object corresponds to the null hypothesis and the second `asreml` object to the alternative hypothesis for the test being conducted. That is, the second `asreml` object is the result of fitting a model that is a reduced version of the model for the first object. In the case where the reduced model is obtained by setting positively-constrained variance parameters in the full model to zero, the `positive.zero` argument should be set to `TRUE` so that the p-value is computed using a mixture of chi-square distributions as described in Self and Liang (1987).

The function checks that the models do not differ in either their fixed or sparse models.

Usage

```
## S3 method for class 'asreml'
REMLRT(h0.asreml.obj, h1.asreml.obj,
       positive.zero = FALSE, bound.test.parameters = "none",
       DF = NULL, bound.exclusions = c("F","B","S","C"), ...)
```

Arguments

`h0.asreml.obj`	`asreml` object containing the fit under the model for the null hypothesis.
`h1.asreml.obj`	`asreml` object containing the fit under the model for the alternative hypothesis.
`positive.zero`	Indicates whether the hypothesized values for the variance components being tested are on the boundary of the parameter space. For example, this is true for positively-constrained variance components that, under the reduced model, are zero. This argument does not need to be set if `bound.test.parameters` is set.

`bound.test.parameters`
: Indicates whether for the variance components being tested, at least some of the hypothesized values are on the boundary of the parameter space. The possibilities are `"none"`, `"onlybound"` and `"one-and-one"`. The default is `"none"`, although if it is set to `"none"` and `positive.zero` is `TRUE` then `bound.test.parameters` is taken to be `"onlybound"`. When `bound.test.parameters` is set to `"one-and-one"`, it signifies that there are two parameters being tested, one of which is bound and the other is not. For example, the latter is true for testing a covariance and a positively-constrained variance component that, under the reduced model, are zero.

`DF`
: A `numeric` giving the difference between the two models in the number of variance parameters whose estimates are not of the type specified in `bound.exclusions`. If `NULL` then this is determined from the information in `full.asreml.obj` and `reduced.asreml.obj`.

`bound.exclusions`
: A `character` specifying one or more bound (constraint) codes that will result in a variance parameter being excluded from the count of estimated variance parameters. If set to `NULL` then none will be excluded.

`...`
: Provision for passsing arguments to functions called internally - not used at present.

Value

A `data.frame` containing the log of the likelihood ratio, its degrees of freedom, its p-value and the number of bound parameters in each of the two models being compared.

Note

If `DF` is not `NULL`, the supplied value is used. Otherwise `DF` is determined from the information in `h1.asreml.obj` and `h0.asreml.obj`. In this case, the degrees of freedom for the test are computed as the difference between the two models in the number of variance parameters whose estimates do not have a code for bound specified in `bound.exclusions`.

If ASReml-R version 4 is being used then the codes specified in `bound.exclusions` are not restricted to a subset of the default codes, but a warning is issued if a code other than these is specified. For ASReml-R version 3, only a subset of the default codes are allowed: `F` (`Fixed`), `B` (`Boundary`), `C` (`Constrained`) and `S` (`Singular`).

The test statistic is calculated as $2(log(REML)_1 - log(REML)_0)$.

This procedure is only approriate when the null hypothesis is that (i) all parameters are on the boundary of the parameter space (ii) all parameters are in the interior of the parameter space, or (iii) there are two parameters, one of which is on the boundary and the other is not. Other cases have been discussed by Self and Liang (1987), but are not implemented here.

Author(s)

Chris Brien

References

Self, S.G., and Liang, K-Y. (1987) Asymptotic Properties of Maximum Likelihood Estimators and Likelihood Ratio Tests Under Nonstandard Conditions. *Journal of the American Statistical Association*, **82**, 605-10.

See Also

infoCriteria.asreml, testranfix.asrtests

Examples

```
## Not run:
    REMLRT(ICV.max, ICV.red, bound.test.parameters = "onlybound")

## End(Not run)
```

---

renewClassify.alldiffs *Renews the components in an* alldiffs.object *according to a new classify.*

Description

The classify is an attribute of an alldiffs.object and determines the order within the components of an unsorted alldiffs.object. This function resets the classify attribute and re-orders the components of alldiffs.object to be in standard order for the variables in a newclassify, using allDifferences.data.frame. The newclassify may be just a re-ordering of the variable names in the previous classify, or be based on a new set of variable names. The latter is particularly useful when linTransform.alldiffs has been used with a matrix and it is desired to replace the resulting Combination classify with a newclassify comprised of a more meaningful set of variables that have replaced Combination in the predictions component.

Usage

```
## S3 method for class 'alldiffs'
renewClassify(alldiffs.obj, newclassify,
              sortFactor = NULL, sortWithinVals = NULL,
              sortOrder = NULL, decreasing = FALSE, ...)
```

Arguments

alldiffs.obj	An alldiffs.object.
newclassify	A character string giving the variables that define the margins of the multiway table that was predicted, but ordered so that the predictions are in the desired order when they are arranged in standard order for the newclassify. Multiway tables are specified by forming an interaction type term from the classifying variables, that is, separating the variable names with the : operator. The number of combined values of the set of variable name(s) must equal the number of rows in the predictions component.
sortFactor	A character containing the name of the factor that indexes the set of predicted values that determines the sorting of the components. If there is only one variable in the classify term then sortFactor can be NULL and the order is defined by the complete set of predicted values. If there is more than one variable in the classify term then sortFactor must be set. In this case the sortFactor is sorted for the predicted values within each combination of the values of the sortWithin variables: the classify variables, excluding the sortFactor. There should be only one predicted value for each unique value of sortFactor within each set defined by a combination of the values of the sortWithin variables.

sortWithinVals	A list with a component named for each factor and numeric that is a classify variable for the predictions, excluding sortFactor. Each component should contain a single value that is a value of the variable. The combination of this set of values will be used to define a subset of the predicted values whose order will define the order of sortFactor to be used for all combinations of the sortWithinVals variables. If sortWithinVals is NULL then the first value of each sortWithin variable in predictions component is used to define sortWithinVals. If there is only one variable in the classify then sortWithinVals is ignored.
sortOrder	A character vector whose length is the same as the number of levels for sortFactor in the predictions component of the alldiffs.object. It specifies the desired order of the levels in the reordered components of the alldiffs.object. The argument sortWithinVals is ignored. The following creates a sortOrder vector levs for factor f based on the values in x: levs <-levels(f)[order(x)].
decreasing	A logical passed to order that detemines whether the order is for increasing or decreasing magnitude of the predicted values.
...	further arguments passed to allDifferences.data.frame.

Details

First, the components of the alldiffs.object is arranged in standard order for the newclassify. Then predictions are reordered according to the settings of sortFactor, sortWithinVals, sortOrder and decreasing (see sort.alldiffs for details).

Value

The alldiffs.object supplied with the following components, if present, sorted: predictions, vcov, backtransforms, differences, p.differences and sed. Also, the sortFactor and sortOrder attributes are set.

Author(s)

Chris Brien

See Also

as.alldiffs, allDifferences.data.frame, print.alldiffs, sort.alldiffs, redoErrorIntervals.alldiffs, recalcLSD.alldiffs, predictPlus.asreml, predictPresent.asreml

Examples

```
data(WaterRunoff.dat)

##Use asreml to get predictions and associated statistics

## Not run:
#Analyse pH
m1.asr <- asreml(fixed = pH ~ Benches + (Sources * (Type + Species)),
                 random = ~ Benches:MainPlots,
                 keep.order=TRUE, data= WaterRunoff.dat)
current.asrt <- as.asrtests(m1.asr, NULL, NULL)
current.asrt <- as.asrtests(m1.asr)
current.asrt <- rmboundary(current.asrt)
```

```
m1.asr <- current.asrt$asreml.obj

#Get predictions and associated statistics
TS.diffs <- predictPlus.asreml(classify = "Sources:Type",
                               asreml.obj = m1.asr, tables = "none",
                               wald.tab = current.asrt$wald.tab,
                               present = c("Type","Species","Sources"))

## End(Not run)

## Use lmeTest and emmmeans to get predictions and associated statistics

if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  #Analyse pH
  m1.lmer <- lmerTest::lmer(pH ~ Benches + (Sources * (Type + Species)) +
                            (1|Benches:MainPlots),
                          data=na.omit(WaterRunoff.dat))
  TS.emm <- emmeans::emmeans(m1.lmer, specs = ~ Sources:Type)
  TS.preds <- summary(TS.emm)
  den.df <- min(TS.preds$df, na.rm = TRUE)
  ## Modify TS.preds to be compatible with a predictions.frame
  TS.preds <- as.predictions.frame(TS.preds, predictions = "emmean",
                                   se = "SE", interval.type = "CI",
                                   interval.names = c("lower.CL", "upper.CL"))

  ## Form an all.diffs object and check its validity
  TS.vcov <- vcov(TS.emm)
  TS.diffs <- allDifferences(predictions = TS.preds,
                             classify = "Sources:Type",
                             vcov = TS.vcov, tdf = den.df)
  validAlldiffs(TS.diffs)
}

#Re-order predictions from asreml or lmerTest so all Sources for the same Type are together
#for each combination of A and B
if (exists("TS.diffs"))
{
  TS.diffs.reord <- renewClassify(TS.diffs, newclassify = "Type:Sources")
  validAlldiffs(TS.diffs.reord)
}
```

`reparamSigDevn.asrtests` *Reparamterizes each random (deviations) term involving* `devn.fac` *to a fixed term and ensures that the same term, with* `trend.num` *replacing* `devn.fac`*, is included if any other term with* `trend.num` *is included in* `terms`*.*

Description

This function reparamterizes each random (deviations) term involving `devn.fac` to a fixed term and ensures that the same term with `trend.num` replacing `devn.fac` is included if any other term

with trend.num is included in terms. It also ansures that any term with spl{trend.num} replacing devn.fac in a term being reparameterized is removed from the model.

Usage

```
## S3 method for class 'asrtests'
reparamSigDevn(asrtests.obj,terms = NULL,
               trend.num = NULL, devn.fac = NULL,
               allow.unconverged = TRUE, checkboundaryonly = FALSE,
               denDF = "numeric", trace = FALSE, update = TRUE,
               set.terms = NULL, ignore.suffices = TRUE,
               bounds = "P", initial.values = NA,...)
```

Arguments

asrtests.obj	an asrtests.object containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary.
terms	A character string vector giving the terms that are to be reparameterized.
trend.num	A character string giving the name of the numeric covariate that corresponds to devn.fac and is potentially included in terms in the fitted model.
devn.fac	A character string giving the name of the factor that corresponds to trend.num and is included in terms in the fitted model.
allow.unconverged	A logical indicating whether to accept a new model even when it does not converge. Initially all changes are made with allow.unconverged set to TRUE. If allow.unconverged has been set to FALSE in the call and the final fit does not converge, an attempt is made to achieve convergence by removing any boundary terms. If this is unsuccessful, the supplied asrtsts object is returned.
checkboundaryonly	If TRUE then boundary and singular terms are not removed by rmboundary.asrtests; a warning is issued instead.
denDF	Specifies the enthod to use in computing approximate denominator degrees of freedom when wald.asreml is called. Can be none to suppress the computations, numeric for numerical methods, algebraic for algebraic methods or default, the default, to autommatically choose numeric or algebraic computations depending on problem size. The denominator degrees of freedom are calculated according to Kenward and Roger (1997) for fixed terms in the dense part of the model.
trace	If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.
update	If TRUE then update.asreml is called in removing and adding terms to the model. In doing this the arguments R.param and G.param are set to those in the asreml object stored in the supplied asrtests.obj so that the values from the previous model are used as starting values. If FALSE then calls are made to asreml in which the only changes from the previous call are (i) that the models are updated and (ii) modifications specified via ... are made.
set.terms	A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting.
ignore.suffices	A logical vector specifying whether the suffices of the asreml-assigned names of the variance terms (i.e. the information to the right of an "!", other than

	"R!") is to be ignored in matching elements of terms. If TRUE for an element of terms, the suffices are stripped from the asreml-assigned names. If FALSE for an element of terms, the element must exactly match an asreml-assigned name for a variance term. This vector must be of length one or the same length as terms. If it is of length one then the same action is applied to the asreml-assigned suffices for all the terms in terms.
bounds	A character vector specifying the bounds to be applied to the terms specified in set.terms. This vector must be of length one or the same length as set.terms. If it is of length one then the same constraint is applied to all the terms in set.terms. If any of the bounds are equal to NA then they are left unchanged for those terms.
initial.values	A character vector specifying the initial values for the terms specified in terms. This vector must be of length one or the same length as terms. If it is of length one then the same initial value is applied to all the terms in terms. If any of the initial.values are equal to NA then they are left unchanged for those terms.
...	further arguments passed to asreml via changeTerms.asrtests and as.asrtests.

Value

An asrtests.object containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary.

Author(s)

Chris Brien

See Also

as.asrtests, changeTerms.asrtests, testranfix.asrtests, testresidual.asrtests, newfit.asreml, chooseModel.asrtests

Examples

```
## Not run:
  data(WaterRunoff.dat)
  asreml.options(keep.order = TRUE) #required for asreml-R4 only
  current.asr <- asreml(fixed = log.Turbidity ~ Benches + Sources + Type + Species +
                              Sources:Type + Sources:Species + Sources:Species:xDay +
                              Sources:Species:Date,
                        data = WaterRunoff.dat, keep.order = TRUE)
  current.asrt <- as.asrtests(current.asr, NULL, NULL)

  #Examine terms that describe just the interactions of Date and the treatment factors
  terms.treat <- c("Sources", "Type", "Species", "Sources:Type", "Sources:Species")
  date.terms <- sapply(terms.treat,
                       FUN=function(term){paste("Date:",term,sep="")},
                       simplify=TRUE)
  date.terms <- c("Date", date.terms)
  date.terms <- unname(date.terms)
  treat.marginality <-  matrix(c(1,0,0,0,0,0, 1,1,0,0,0,0,  1,0,1,0,0,0,
                                 1,0,1,1,0,0, 1,1,1,0,1,0, 1,1,1,1,1,1), nrow=6)
  rownames(treat.marginality) <- date.terms
  colnames(treat.marginality) <- date.terms
  choose <- chooseModel(current.asrt, treat.marginality, denDF="algebraic")
  current.asrt <- choose$asrtests.obj
```

```
current.asr <- current.asrt$asreml.obj
sig.date.terms <- choose$sig.terms

#Remove all Date terms left in the fixed model
terms <- "(Date/(Sources * (Type + Species)))"
current.asrt <- changeTerms(current.asrt, dropFixed = terms)
#if there are significant date terms, reparameterize to xDays + spl(xDays) + Date
if (length(sig.date.terms) != 0)
{ #add lin + spl + devn for each to fixed and random models
  trend.date.terms <- sapply(sig.date.terms,
                             FUN=function(term){sub("Date","xDay",term)},
                             simplify=TRUE)
  trend.date.terms <- paste(trend.date.terms,  collapse=" + ")
  current.asrt <- changeTerms(current.asrt, addFixed=trend.date.terms)
  trend.date.terms <- sapply(sig.date.terms,
                             FUN=function(term){sub("Date","spl(xDay)",term)},
                             simplify=TRUE)
  trend.date.terms <- c(trend.date.terms, sig.date.terms)
  trend.date.terms <- paste(trend.date.terms,  collapse=" + ")
  current.asrt <- changeTerms(current.asrt, addRandom = trend.date.terms)
  current.asrt <- rmboundary(current.asrt)
}

#Now test terms for sig date terms
spl.terms <- sapply(terms.treat,
                    FUN=function(term){paste("spl(xDay):",term,sep="")},
                    simplify=TRUE)
spl.terms <- c("spl(xDay)",spl.terms)
lin.terms <- sapply(terms.treat,
                    FUN=function(term){paste(term,":xDay",sep="")},
                    simplify=TRUE)
lin.terms <- c("xDay",lin.terms)
systematic.terms <- c(terms.treat, lin.terms, spl.terms, date.terms)
systematic.terms <- unname(systematic.terms)
treat.marginality <-  matrix(c(1,0,0,0,0,0, 1,1,0,0,0,0,  1,0,1,0,0,0,
                               1,0,1,1,0,0, 1,1,1,1,1,0, 1,1,1,1,1,1), nrow=6)
systematic.marginality <- kronecker(matrix(c(1,0,0,0, 1,1,0,0,
                                             1,1,1,0, 1,1,1,1), nrow=4),
                                    treat.marginality)
systematic.marginality <- systematic.marginality[-1, -1]
rownames(systematic.marginality) <- systematic.terms
colnames(systematic.marginality) <- systematic.terms
choose <- chooseModel(current.asrt, systematic.marginality,
                      denDF="algebraic", pos=TRUE)
current.asrt <- choose$asrtests.obj

#Check if any deviations are significant and, for those that are, go back to
#fixed dates
current.asrt <- reparamSigDevn(current.asrt, choose$sig.terms,
                               trend.num = "xDay", devn.fac = "Date",
                               denDF = "algebraic")

## End(Not run)
```

`rmboundary.asrtests` *Removes any boundary or singular variance components from the fit stored in* `asrtests.obj` *and records their removal in an* `asrtests.object`.

Description

Any terms specified in the random model that are estimated on the boundary or are singular and can be removed are removed from the fit stored in the `asreml` object stored in the `asrtests.object`. Terms that specify multiple parameters in the random model cannot be removed (e.g. terms specified using the `at` function with more than one level of the factor) and terms in `residual` model are not removed. Terms that can be removed are selected for removal in the following order based on whether they involve: (i) a `dev` function, (ii) only factors, (iii) an `spl` function, (iv) a `pol` function and (v) a `lin` function or a variable that is an `integer` or a `numeric`. It should be noted that this order of removal presumes that random deviation terms are specified via the `dev` function rather than via a random factor. Once the earliest of the above classes with a boundary term is identified, a term within this class is selected for removal. For all classes, except for factor-only terms, the smallest term with the largest number of variables/factors is removed. Amongst factor-only terms, the smallest term with the smallest number of variables/factors is removed. After each variance component is removed, a row for it is added to the `test.summary` `data.frame` and the model refitted. If there are further boundary or singular terms, one is removed using the above strategy. This process continues until there are no further boundary or singular variance components that are removable. Other types of boundary or singular terms, which cannot be removed, are reported in warning messages.

Usage

```
## S3 method for class 'asrtests'
rmboundary(asrtests.obj, checkboundaryonly = FALSE,
           trace = FALSE, update = TRUE,
           set.terms = NULL, ignore.suffices = TRUE,
           bounds = "P", initial.values = NA, ...)
```

Arguments

`asrtests.obj`	an `asrtests.object` containing the components (i) `asreml.obj`, (ii) `wald.tab`, and (iii) `test.summary`.
`checkboundaryonly`	If `TRUE` then boundary and singular terms are not removed by `rmboundary.asrtests`; a warning is issued instead.
`trace`	If `TRUE` then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.
`update`	If `TRUE` then `update.asreml` is called to fit the model with any boundary terms removed. In doing this the arguments `R.param` and `G.param` are set to those in the `asreml` object stored in `asrtests.obj` so that the values from the previous model are used as starting values. If `FALSE` then a call is made to `asreml` in which the only changes from the previous call are that (i) the terms for boundary variance components are removed from the models and (ii) modifications specified via `...` are made.
`set.terms`	A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting.

ignore.suffices
: A logical vector specifying whether the suffices of the asreml-assigned names of the variance terms (i.e. the information to the right of an "!", other than "R!") is to be ignored in matching elements of terms. If TRUE for an element of terms, the suffices are stripped from the asreml-assigned names. If FALSE for an element of terms, the element must exactly match an asreml-assigned name for a variance term. This vector must be of length one or the same length as terms. If it is of length one then the same action is applied to the asreml-assigned suffices for all the terms in terms.

bounds
: A character vector specifying the bounds to be applied to the terms specified in set.terms. This vector must be of length one or the same length as set.terms. If it is of length one then the same constraint is applied to all the terms in set.terms. If any of the bounds are equal to NA then they are left unchanged for those terms.

initial.values
: A character vector specifying the initial values for the terms specified in terms. This vector must be of length one or the same length as terms. If it is of length one then the same initial value is applied to all the terms in terms. If any of the initial.values are equal to NA then they are left unchanged for those terms.

...
: further arguments passed to asreml.

Value

An asrtests.object containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary.

Author(s)

Chris Brien

See Also

as.asrtests, changeTerms.asrtests, testranfix.asrtests, testresidual.asrtests, newfit.asreml, reparamSigDevn.asrtests, chooseModel.asrtests

Examples

```
## Not run:
current.asrt <- rmboundary(current.asrt)

## End(Not run)
```

---

setvarianceterms.call *allows the setting of bounds and initial values for terms in the* random *and* residual *arguments of an* asreml *call, with the resulting call being evaluated.*

Description

Takes an unevaluated call and evaluates the call after setting the bounds and initial values for the terms specified in terms. The elements of terms are matched with those generated by asreml and used, for example, in the varcomp component of a summary.asreml object. These names generally include descriptive suffices. To match an element of terms that includes such a suffix, set ignore.suffices to FALSE so that a literal match between the element and the assigned names is sought.

Usage

```
## S3 method for class 'call'
setvarianceterms(call, terms, ignore.suffices = TRUE,
                 bounds = "P", initial.values = NA, ...)
```

Arguments

call	an unevaluated call to asreml. One way to create such a call is to use the call function with its name argument set to "asreml". Another is to obtain it from the call component of an asreml object (e.g. call <-asreml.obj$call).
terms	A character vector specifying the terms that are to have bounds and/or initial values specified.
ignore.suffices	A logical vector specifying whether the suffices of the asreml-assigned names of the variance terms (i.e. the information to the right of an "!", other than "R!") is to be ignored in matching elements of terms. If TRUE for an element of terms, the suffices are stripped from the asreml-assigned names. If FALSE for an element of terms, the element must exactly match an asreml-assigned name for a variance term. This vector must be of length one or the same length as terms. If it is of length one then the same action is applied to the asreml-assigned suffices for all the terms in terms.
bounds	A character vector specifying the bounds to be applied to the terms specified in set.terms. This vector must be of length one or the same length as set.terms. If it is of length one then the same constraint is applied to all the terms in set.terms. If any of the bounds are equal to NA then they are left unchanged for those terms. The codes used by ASReml are: • B - fixed at a boundary; • F - fixed by the user; • P - positive definite; • C - Constrained by user; • U - unbounded.
initial.values	A character vector specifying the initial values for the terms specified in terms. This vector must be of length one or the same length as terms. If it is of length one then the same initial value is applied to all the terms in terms. If any of the initial.values are equal to NA then they are left unchanged for those terms.
...	additional arguments to be added to the call, or arguments in the call with changed values.

Value

An asreml object.

Author(s)

Chris Brien

References

Butler, D. G., Cullis, B. R., Gilmour, A. R., Gogel, B. J. and Thompson, R. (2018). *ASReml-R Reference Manual Version 4*. VSN International Ltd, http://asreml.org.

See Also

update.asreml

Examples

```
## Not run:
   m1.call <- call("asreml",
                   fixed = Height ~ (Block + Irrig)*csDay.num,
                   random= ~ spl(csDay.num)/(Irrig+Block)
                             + dev(csDay.num)
                             + str(~Block:Plot/csDay.num, ~us(2):id(20))
                             + Block:Plot:spl(csDay.num),
                   data=quote(dat)) ##use quote to stop evaluation of dat here
   terms <- c("Block:Plot+Block:Plot:csDay.num!us(2).2:1", "R!variance")
   m1.asreml <- setvarianceterms(m1.call, terms, bounds=c("U","P"),
                                 initial=c(NA,3), ignore.suffices=c(FALSE,TRUE))
   summary(m1.asreml)

## End(Not run)
```

---

simulate.asreml *Produce sets of simulated data from a multivariate normal distribtion and save quantites related to the simulated data*

Description

Produce in parallel sets of simulated data corresponding to an asreml model, along with its fitted values and residuals. A variance matrix V, corresponding to the random and residual models must be supplied. What to save is specified by the which argument.

Usage

```
## S3 method for class 'asreml'
simulate(object, nsim=100, seed = NULL, means=NULL, V, tolerance = 1E-10,
         update = TRUE, trace = FALSE, which="data", units = "ignore",
         ncores = detectCores(), ...)
```

Arguments

object	An asreml object from a call to asreml in which the data argument has been set.
means	The vector of means to be used in generating simulated data sets. If it is NULL, the fitted values based on object are used. It must be the same length as the response variable for object.
V	The fitted variance matrix, i.e. having the pattern and values that conform to the model fit stored in the supplied object.
nsim	The number of data sets to be simulated.
seed	A single value, interpreted as an integer, that specifies the starting value of the random number generator. The "L'Ecuyer-CMRG" random generator is used and nextRNGStream is used to seed each core from the original seed.

tolerance	The value such that eigenvalues less than it are considered to be zero.
update	If TRUE then the arguments R.param and G.param are set to those in the asreml object supplied in object so that the values from the original model are used as starting values. If FALSE then calls are made to asreml in which the only changes from the previous call are (i) the model is fitted to simulated data and (ii) modifications specified via ... are made, except that changes cannot be made to any of the models.
trace	If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.
which	The quantites from the simulated data set to be stored. Any combination of "response", "residuals" and "fitted", or "all". If residuals and/or fitted is specified, those for the analysis stored in object will be added to the data.frame nominated in the data argument of object and the modified data.frame added as a component named data in the list that is the value returned by the function.
units	A character indicating whether the BLUPs for units are added to the residuals when this reserved factor is included in the random model. Possible values are addtoresiduals and ignore.
ncores	A numeric specifying the number of cores to use in doing the simulations.
...	Other arguments that are passed down to the function asreml. Changes to the models are not allowed. Other changes are dangerous and generally should be avoided.

Details

Generate nsim sets of data and analyse them using asreml using the model in object, performing the generation and analysis of several sets in parallel. Note, if the analysis for a data set does not converge in maxiter iterations, it is discarded and a replacement data set generated. The value of maxiter can be specified in the call to simulate.asreml. The fitted values and residuals are extracted as required. If aom = TRUE when the simulated data are analysed, standardised conditional residuals are stored. If which includes residuals or fitted, the specified quantities for the observed data are added to the data.frame on which the fit in object is based.

Value

A list with the following components whose presence depends on the setting of which:

1. **observed:** present if which includes residuals or fitted, in which case it will be the data.frame on which the fit in object is based, with residuals and/or fitted.
2. **data:** present if which includes data, a data.frame containing the simulated data sets.
3. **fitted:** present if which includes fitted, a data.frame containing the fitted values from the analyses of the simulated data sets.
4. **residuals:** present if which includes residuals, a data.frame containing the residuals from the analyses of the simulated data sets.

Author(s)

Chris Brien

See Also

asreml, variofaces.asreml, plotVariofaces.data.frame, set.seed.

Examples

```
## Not run:
data(Wheat.dat)
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
current.asrt <- rmboundary.asrtests(current.asrt)
# Form variance matrix based on estimated variance parameters
s2 <- current.asr$sigma2
gamma.Row <- current.asr$gammas[1]
gamma.unit <- current.asr$gammas[2]
rho.r <- current.asr$gammas[4]
rho.c <- current.asr$gammas[5]
row.ar1 <- mat.ar1(order=10, rho=rho.r)
col.ar1 <- mat.ar1(order=15, rho=rho.c)
V <- gamma.Row * fac.sumop(Wheat.dat$Row) +
     gamma.unit * diag(1, nrow=150, ncol=150) +
     mat.dirprod(col.ar1, row.ar1)
V <- s2*V

#Produce residuals from 100 simulated data sets
resid <- simulate(current.asr, V=V, which="residuals", ncores = 2)

## End(Not run)
```

`sort.alldiffs` *Sorts the components in an* `alldiffs.object` *according to the predicted values associated with a factor.*

Description

Sorts the rows of the components in an `alldiffs.object` (see `as.alldiffs`) that are `data.frames` and the rows and columns of those that are `matrices` according to the predicted values in the `predictions` component. These predicted values are generally obtained using `predict.asreml` by specifying a `classify` term comprised of one or more variables. Generally, the values associated with one variable are sorted in parallel within each combination of values of the other variables. When there is more than one variable in the `classify` term, the sorting is controlled using one or more of `sortFactor`, `sortWithinVals` and `sortOrder`. If there is only one variable in the `classify` then all components are sorted according to the order of the complete set of predictions.

Note that reordering the `classify` variables in the `alldiffs.object` and changing the order of the rows and columns of the components so that they are in standard order for the new variable order can be achieved using either `renewClassify.alldiffs` or `allDifferences.data.frame`.

Usage

```
## S3 method for class 'alldiffs'
sort(x, decreasing = FALSE, classify = NULL,
     sortFactor = NULL, sortWithinVals = NULL, sortOrder = NULL, ...)
```

Arguments

x	An alldiffs.object.
decreasing	A logical passed to order that detemines whether the order is for increasing or decreasing magnitude of the predicted values.
classify	A character string giving the variables that define the margins of the multiway table that was predicted. Multiway tables are specified by forming an interaction type term from the classifying variables, that is, separating the variable names with the : operator. If NULL, it will be obtained from the classify attribute of the as.alldiffs object supplied through x.
sortFactor	A character containing the name of the factor that indexes the set of predicted values that determines the sorting of the components. If there is only one variable in the classify term then sortFactor can be NULL and the order is defined by the complete set of predicted values. If there is more than one variable in the classify term then sortFactor must be set. In this case the sortFactor is sorted in the same order within each combination of the values of the sortWithin variables: the classify variables, excluding the sortFactor. There should be only one predicted value for each unique value of sortFactor within each set defined by a combination of the values of the sortWithin variables. The order to use is determined by either sortWithinVals or sortOrder.
sortWithinVals	A list with a component named for each factor and numeric that is a classify variable for the predictions, excluding sortFactor. Each component should contain a single value that is a value of the variable. The combination of this set of values will be used to define a subset of the predicted values whose order will define the order of sortFactor to be used for all combinations of the sortWithinVals variables. If sortWithinVals is NULL then the first value of each sortWithin variable in predictions component is used to define sortWithinVals. If there is only one variable in the classify then sortWithinVals is ignored.
sortOrder	A character vector whose length is the same as the number of levels for sortFactor in the predictions component of the alldiffs.object. It specifies the desired order of the levels in the reordered components of the alldiffs.object. The argument sortWithinVals is ignored. The following creates a sortOrder vector levs for factor f based on the values in x: levs <-levels(f)[order(x)].
...	further arguments passed to or from other methods. Not used at present.

Details

The basic technique is to change the order of the levels of the sortFactor within the predictions and, if present, backtransforms components so that they are ordered for a subset of predicted values, one for each levels of the sortFactor. When the classify term consists of more than one variable then a subset of one combination of the values of variables other than the sortFactor, the sortWithin set, must be chosen for determining the order of the sortFactor levels. Then the sorting of the rows (and columns) will be in parallel within each combination of the values of sortWithin variables: the classify term, excluding the sortFactor.

Value

The alldiffs.object supplied with the following components, if present, sorted: predictions, vcov, backtransforms, differences, p.differences and sed. Also, the sortFactor and sortOrder attributes are set.

Author(s)

Chris Brien

See Also

as.alldiffs, allDifferences.data.frame, print.alldiffs, renewClassify.alldiffs, redoErrorIntervals.alldiffs, recalcLSD.alldiffs, predictPlus.asreml, predictPresent.asreml

Examples

```
data(WaterRunoff.dat)

##Use asreml to get predictions and associated statistics

## Not run:
#Analyse pH
m1.asr <- asreml(fixed = pH ~ Benches + (Sources * (Type + Species)),
                 random = ~ Benches:MainPlots,
                 keep.order=TRUE, data= WaterRunoff.dat)
current.asrt <- as.asrtests(m1.asr, NULL, NULL)
current.asrt <- as.asrtests(m1.asr)
current.asrt <- rmboundary(current.asrt)
m1.asr <- current.asrt$asreml.obj

#Get predictions and associated statistics
TS.diffs <- predictPlus.asreml(classify = "Sources:Type",
                               asreml.obj = m1.asr, tables = "none",
                               wald.tab = current.asrt$wald.tab,
                               present = c("Type","Species","Sources"))

#Use sort.alldiffs and save order for use with other response variables
TS.diffs.sort <- sort(diffs, sortFactor = "Sources", sortWithinVals = list(Type = "Control"))
sort.order <- attr(TS.diffs.sort, which = "sortOrder")

#Analyse Turbidity
m2.asr <- asreml(fixed = Turbidity ~ Benches + (Sources * (Type + Species)),
                 random = ~ Benches:MainPlots,
                 keep.order=TRUE, data= WaterRunoff.dat)
current.asrt <- as.asrtests(m2.asr)
#Use pH sort.order to sort Turbidity alldiffs object
diffs2.sort <- predictPlus(m2.asr, classify = "Sources:Type",
                           pairwise = FALSE, error.intervals = "Stand",
                           tables = "none", present = c("Type","Species","Sources"),
                           sortFactor = "Sources",
                           sortOrder = sort.order)

## End(Not run)

## Use lmeTest and emmmeans to get predictions and associated statistics

if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  #Analyse pH
  m1.lmer <- lmerTest::lmer(pH ~ Benches + (Sources * (Type + Species)) +
```

```
                            (1|Benches:MainPlots),
                           data=na.omit(WaterRunoff.dat))
  TS.emm <- emmeans::emmeans(m1.lmer, specs = ~ Sources:Type)
  TS.preds <- summary(TS.emm)
  den.df <- min(TS.preds$df, na.rm = TRUE)
  ## Modify TS.preds to be compatible with a predictions.frame
  TS.preds <- as.predictions.frame(TS.preds, predictions = "emmean",
                                   se = "SE", interval.type = "CI",
                                   interval.names = c("lower.CL", "upper.CL"))

  ## Form an all.diffs object and check its validity
  TS.vcov <- vcov(TS.emm)
  TS.diffs <- allDifferences(predictions = TS.preds,
                             classify = "Sources:Type",
                             vcov = TS.vcov, tdf = den.df)
  validAlldiffs(TS.diffs)

  #Use sort.alldiffs and save order for use with other response variables
  TS.diffs.sort <- sort(TS.diffs, sortFactor = "Sources",
                        sortWithinVals = list(Type = "Control"))
  sort.order <- attr(TS.diffs.sort, which = "sortOrder")

  #Analyse Turbidity
  m2.lmer <- lmerTest::lmer(Turbidity ~ Benches + (Sources * (Type + Species)) +
                              (1|Benches:MainPlots),
                            data=na.omit(WaterRunoff.dat))
  TS.emm <- emmeans::emmeans(m2.lmer, specs = ~ Sources:Type)
  TS.preds <- summary(TS.emm)
  den.df <- min(TS.preds$df, na.rm = TRUE)
  ## Modify TS.preds to be compatible with a predictions.frame
  TS.preds <- as.predictions.frame(TS.preds, predictions = "emmean",
                                   se = "SE", interval.type = "CI",
                                   interval.names = c("lower.CL", "upper.CL"))

  ## Form an all.diffs object, sorting it using the pH sort.order and check its validity
  TS.vcov <- vcov(TS.emm)
  TS.diffs2.sort <- allDifferences(predictions = TS.preds,
                                   classify = "Sources:Type",
                                   vcov = TS.vcov, tdf = den.df,
                                   sortFactor = "Sources",
                                   sortOrder = sort.order)
  validAlldiffs(TS.diffs2.sort)
}
```

`subset.alldiffs` *Subsets the components in an* `alldiffs.object` *according to the supplied condition.*

Description

Subsets each of the components of an `alldiffs.object`. The subset is determined by applying the condition to the `prediction` component to determine which of its rows are to be included in the subset. Then, if present, this subset is applied to the rows of `backtransforms` and to the rows and columns of `differences`, `p.differences` and `sed` components. In addition, if `sed` is present,

recalcLSD.alldiffs is called to recalculate the values in the LSD component, with any arguments supplied via the ... argument passed ot it.

Usage

```
## S3 method for class 'alldiffs'
subset(x, subset, rmClassifyVars = NULL, ...)
```

Arguments

x	An alldiffs.object.
subset	A logical that detemines rows of the predictions component of x to be included in the subset.
rmClassifyVars	A character that contains the names of the variables in the classify attribute of x that are to be removed from the predictions data.frame and the names of the dimensions of the other components of x. In doing this, the combinations of the remaining classify variables must uniquely index the predictions. This will be the case when the combinations of the rmClassifyVars have only a single unique value.
...	further arguments passed to recalcLSD.alldiffs.

Value

An alldiffs.object with the following components of the supplied alldiffs.object subsetted, if present in the original object: predictions, vcov, backtransforms, differences, p.differences and sed. In addition, if sed is present, the LSD component will be recalculated.

Author(s)

Chris Brien

See Also

as.alldiffs, allDifferences.data.frame, print.alldiffs, sort.alldiffs, redoErrorIntervals.alldiffs, recalcLSD.alldiffs, predictPlus.asreml, predictPresent.asreml

Examples

```
data(WaterRunoff.dat)

##Use asreml to get predictions and associated statistics

## Not run:
asreml.options(keep.order = TRUE) #required for asreml-R4 only
current.asr <- asreml(fixed = pH ~ Benches + (Sources * (Type + Species)),
                      random = ~ Benches:MainPlots,
                      keep.order=TRUE, data= WaterRunoff.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
TS.diffs <- predictPlus.asreml(classify = "Sources:Type",
                               asreml.obj = current.asr, tables = "none",
                               wald.tab = current.asrt$wald.tab,
                               present = c("Type","Species","Sources"))
```

```
## End(Not run)

## Use lmeTest and emmmeans to get predictions and associated statistics

if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  m1.lmer <- lmerTest::lmer(pH ~ Benches + (Sources * (Type + Species)) +
                              (1|Benches:MainPlots),
                            data=na.omit(WaterRunoff.dat))
  TS.emm <- emmeans::emmeans(m1.lmer, specs = ~ Sources:Type)
  TS.preds <- summary(TS.emm)
  den.df <- min(TS.preds$df, na.rm = TRUE)
  ## Modify TS.preds to be compatible with a predictions.frame
  TS.preds <- as.predictions.frame(TS.preds, predictions = "emmean",
                                   se = "SE", interval.type = "CI",
                                   interval.names = c("lower.CL", "upper.CL"))

  ## Form an all.diffs object and check its validity
  TS.vcov <- vcov(TS.emm)
  TS.diffs <- allDifferences(predictions = TS.preds, classify = "Sources:Type",
                             vcov = TS.vcov, tdf = den.df)
  validAlldiffs(TS.diffs)
}

## Plot p-values for predictions obtained using asreml or lmerTest
if (exists("TS.diffs"))
{
  ##Use subset.alldiffs to select a subset of the alldiffs object
  TS.diffs.subs <- subset(TS.diffs,
                          subset = grepl("R", Sources, fixed = TRUE) &
                                   Type %in% c("Control","Medicinal"))
}
```

`testranfix.asrtests` *Tests for a single fixed or random term in model fitted using* `asreml` *and records the result in an* `asrtests.object`.

Description

Tests for a single term, using a REML LRT for a random term or based on Wald statistics for a fixed term. The term must be in the fitted model. A random term is removed from the model fit and a REML likelihood ratio test is performed using `REMLRT.asreml`. It compares the fit of the model in `asreml.obj` and the newly fitted model without the `term`. If the newly fitted model is retained, any boundary terms are then removed using `rmboundary.asrtests`. For a fixed term, the probability of the Wald statistics is extracted from the pseudo-anova table produced by `wald.asreml`. If this is available in the `asrtests.object`, it is used; otherwise `wald.asreml` is called to add it to the `asrtests.object`. Whether nonsignificant terms are dropped is controlled by `drop.ran.ns` for random terms and `drop.fix.ns` for fixed terms. A row is added to the `test.summary` `data.frame` for the term that is tested.

Usage

```
## S3 method for class 'asrtests'
```

```
testranfix(asrtests.obj, term=NULL, alpha = 0.05,
           allow.unconverged = TRUE, checkboundaryonly = FALSE,
           drop.ran.ns = TRUE, positive.zero = FALSE,
           bound.test.parameters = "none",
           bound.exclusions = c("F","B","S","C"), REMLDF = NULL,
           drop.fix.ns = FALSE, denDF="numeric", dDF.na = "none",
           dDF.values = NULL, trace = FALSE, update = TRUE,
           set.terms = NULL, ignore.suffices = TRUE,
           bounds = "P", initial.values = NA, ...)
```

Arguments

asrtests.obj	An asrtests.object containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary.
term	A single model term that is valid in asreml, stored as a character.
alpha	The significance level for the test.
allow.unconverged	A logical indicating whether to accept a new model even when it does not converge. If FALSE, it will be checked whether convergence can be achieved with the removal of any boundary random terms; random terms will be retested if terms are removed. Also, if FALSE and the fit of the new model has converged, but that of the old model has not, the new model will be accepted.
checkboundaryonly	If TRUE then boundary and singular terms are not removed by rmboundary.asrtests; a warning is issued instead.
drop.ran.ns	A logical indicating whether to drop a random term from the model when it is nonsignificant.
positive.zero	Indicates whether the hypothesized values for the variance components being tested are on the boundary of the parameter space. For example, this is true for positively-constrained variance components that, under the reduced model, are zero. This argument does not need to be set if bound.test.parameters is set.
bound.test.parameters	Indicates whether for the variance components being tested, at least some of the hypothesized values are on the boundary of the parameter space. The possibilities are "none", "onlybound" and "one-and-one". The default is "none", although if it is set to "none" and positive.zero is TRUE then bound.test.parameters is taken to be "onlybound". When bound.test.parameters is set to "one-and-one", it signifies that there are two parameters being tested, one of which is bound and the other is not. For example, the latter is true for testing a covariance and a positively-constrained variance component that, under the reduced model, are zero.
bound.exclusions	A character specifying one or more bound (constraint) codes that will result in a variance parameter being excluded from the count of estimated variance parameters in using REMLRT.asreml. If set to NULL then none will be excluded.
REMLDF	A numeric giving the difference in the number of variance parameters whose estimates are not of the type specified in bound.exclusions for two models being compared in a REML ratio test using REMLRT.asreml. If NULL then this is determined from the information in the asreml object for the two models.
drop.fix.ns	A logical indicating whether to drop a fixed term from the model when it is nonsignificant

denDF — Specifies the enthod to use in computing approximate denominator degrees of freedom when wald.asreml is called. Can be none to suppress the computations, numeric for numerical methods, algebraic for algebraic methods or default, the default, to autommatically choose numeric or algebraic computations depending on problem size. The denominator degrees of freedom are calculated according to Kenward and Roger (1997) for fixed terms in the dense part of the model.

dDF.na — The method to use to obtain substitute denominator degrees of freedom. when the numeric or algebraic methods produce an NA. If dDF.na = "none", no substitute denominator degrees of freedom are employed; if dDF.na = "residual", the residual degrees of freedom from asreml.obj$nedf are used; if dDF.na = "maximum", the maximum of those denDF that are available, excluding that for the Intercept, is used; if all denDF are NA, asreml.obj$nedf is used. If dDF.na = "supplied", a vector of values for the denominator degrees of freedom is to be supplied in dDF.values. Any other setting is ignored and a warning message produced. Generally, substituting these degrees of freedom is anticonservative in that it is likely that the degrees of freedom used will be too large.

dDF.values — A vector of values to be used when dDF.na = "supplied". Its values will be used when denDF in a test for a fixed effect is NA. This vector must be the same length as the number of fixed terms, including (Intercept) whose value could be NA.

trace — If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.

update — If TRUE then update.asreml is called to fit the model to be tested. In doing this the arguments R.param and G.param are set to those in the asreml object stored in asrtests.obj so that the values from the previous model are used as starting values. If FALSE then a call is made to asreml in which the only changes from the previous call are that (i) models are modifed for the supplied terms and (ii) modifications specified via ... are made.

set.terms — A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting.

ignore.suffices — A logical vector specifying whether the suffices of the asreml-assigned names of the variance terms (i.e. the information to the right of an "!", other than "R!") is to be ignored in matching elements of terms. If TRUE for an element of terms, the suffices are stripped from the asreml-assigned names. If FALSE for an element of terms, the element must exactly match an asreml-assigned name for a variance term. This vector must be of length one or the same length as terms. If it is of length one then the same action is applied to the asreml-assigned suffices for all the terms in terms.

bounds — A character vector specifying the bounds to be applied to the terms specified in set.terms. This vector must be of length one or the same length as set.terms. If it is of length one then the same constraint is applied to all the terms in set.terms. If any of the bounds are equal to NA then they are left unchanged for those terms.

initial.values — A character vector specifying the initial values for the terms specified in terms. This vector must be of length one or the same length as terms. If it is of length one then the same initial value is applied to all the terms in terms. If any of the initial.values are equal to NA then they are left unchanged for those terms.

... — Further arguments passed to asreml, wald.asreml and as.asrtests.

Value

An asrtests.object containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary. If the term is not in the model, then the supplied asreml object will be returned. Also, reml.test will have the likelihood ratio and the p-value set to NA and the degrees of freedom to zero. Similarly, the row of test.summary for the term will have its name, DF set to NA, p-value set to NA, and action set to Absent.

Author(s)

Chris Brien

See Also

asremlPlus-package, as.asrtests, chooseModel.asrtests, REMLRT.asreml, rmboundary.asrtests, newfit.asreml, reparamSigDevn.asrtests, changeTerms.asrtests

Examples

```
## Not run:
data(Wheat.dat)
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
current.asrt <- rmboundary(current.asrt)
# Test nugget term
current.asrt <- testranfix(current.asrt, "units", positive=TRUE)

## End(Not run)
```

---

testresidual.asrtests *Fits a new residual formula, tests whether the change is significant and records the result in an asrtests.object.*

Description

Fits a new residual formula using asreml-R4 (replaces the rcov formula of asreml-R3) and tests whether the change is significant. If simpler = FALSE the model to be fitted must be more complex than the one whose fit has been stored in asrtests.obj. That is, the new model must have more parameters. However, if simpler = TRUE the model to be fitted must be simpler than the one whose fit has been stored in asrtests.obj in that it must have fewer parameters. Any boundary terms are removed using rmboundary.asrtests, which may mean that the models are not nested. The test is a REML likelihood ratio test that is performed using REMLRT.asreml, which is only valid if the models are nested. It compares the newly fitted model with the fit of the model in asrtest.obj. A row is added to the test.summary data.frame using the supplied label.

Usage

```
## S3 method for class 'asrtests'
testresidual(asrtests.obj, terms=NULL, label = "R model",
             simpler = FALSE, alpha = 0.05, allow.unconverged = TRUE,
             checkboundaryonly = FALSE, positive.zero = FALSE,
             bound.test.parameters = "none",
             bound.exclusions = c("F","B","S","C"), REMLDF = NULL,
             denDF="numeric", update = TRUE, trace = FALSE,
             set.terms = NULL, ignore.suffices = TRUE,
             bounds = "P", initial.values = NA, ...)
```

Arguments

asrtests.obj	an asrtests.object for a fitted model that is a list containing the componets (i) asreml.obj, (ii) wald.tab (iii) test.summary.
terms	A model for the residual argument in asreml-R4 (the rcov formula in older versions of asreml), stored as a character.
label	A character string to use as the label in test.summary and which indicates what is being tested.
simpler	A logical indicating whether the new model to be fitted is simpler than the already fitted model whose fit is stored in asrtests.obj.
alpha	The significance level for the test.
allow.unconverged	A logical indicating whether to accept a new model even when it does not converge. If FALSE and the fit of the new model does not converge, the supplied asreml object is returned. Also, if FALSE and the fit of the new model has converged, but that of the old model has not, the new model will be accepted.
checkboundaryonly	If TRUE then boundary and singular terms are not removed by rmboundary.asrtests; a warning is issued instead.
positive.zero	Indicates whether the hypothesized values for the variance components being tested are on the boundary of the parameter space. For example, this is true for positively-constrained variance components that, under the reduced model, are zero. This argument does not need to be set if bound.test.parameters is set.
bound.test.parameters	Indicates whether for the variance components being tested, at least some of the hypothesized values are on the boundary of the parameter space. The possibilities are "none", "onlybound" and "one-and-one". The default is "none", although if it is set to "none" and positive.zero is TRUE then bound.test.parameters is taken to be "onlybound". When bound.test.parameters is set to "one-and-one", it signifies that there are two parameters being tested, one of which is bound and the other is not. For example, the latter is true for testing a covariance and a positively-constrained variance component that, under the reduced model, are zero.
bound.exclusions	A character specifying one or more bound (constraint) codes that will result in a variance parameter being excluded from the count of estimated variance parameters in using REMLRT.asreml. If set to NULL then none will be excluded.
REMLDF	A numeric giving the difference in the number of variance parameters whose estimates are not of the type specified in bound.exclusions for two models

being compared in a REML ratio test using REMLRT.asreml. If NULL then this is determined from the information in the asreml object for the two models.

denDF — Specifies the method to use in computing approximate denominator degrees of freedom when wald.asreml is called. Can be none to suppress the computations, numeric for numerical methods, algebraic for algebraic methods or default, the default, to autommatically choose numeric or algebraic computations depending on problem size. The denominator degrees of freedom are calculated according to Kenward and Roger (1997) for fixed terms in the dense part of the model.

update — If TRUE then update.asreml is called to fit the model with the residual (rcov) model supplied in terms. In doing this the arguments R.param and G.param are set to those in the asreml object stored in asrtests.obj so that the values from the previous model are used as starting values. If FALSE then a call is made to asreml in which the only changes from the previous call are that (i) residual (rcov) model is that specified in terms and (ii) modifications specified via ... are made.

trace — If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.

set.terms — A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting.

ignore.suffices — A logical vector specifying whether the suffices of the asreml-assigned names of the variance terms (i.e. the information to the right of an "!", other than "R!") is to be ignored in matching elements of terms. If TRUE for an element of terms, the suffices are stripped from the asreml-assigned names. If FALSE for an element of terms, the element must exactly match an asreml-assigned name for a variance term. This vector must be of length one or the same length as terms. If it is of length one then the same action is applied to the asreml-assigned suffices for all the terms in terms.

bounds — A character vector specifying the bounds to be applied to the terms specified in set.terms. This vector must be of length one or the same length as set.terms. If it is of length one then the same constraint is applied to all the terms in set.terms. If any of the bounds are equal to NA then they are left unchanged for those terms.

initial.values — A character vector specifying the initial values for the terms specified in terms. This vector must be of length one or the same length as terms. If it is of length one then the same initial value is applied to all the terms in terms. If any of the initial.values are equal to NA then they are left unchanged for those terms.

... — Further arguments passed to asreml, wald.asreml and as.asrtests.

Value

An asrtests.object containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary. If the term is not in the model, then the supplied asreml.obj will be returned. Also, reml.test will have the likelihood ratio and the p-value set to NA and the degrees of freedom to zero. Similarly, the row of test.summary for the term will have its name, a p-value set to NA, and action set to Absent.

Author(s)

Chris Brien

See Also

asremlPlus-package, as.asrtests, changeTerms.asrtests, chooseModel.asrtests, REMLRT.asreml, rmboundary.asrtests, newfit.asreml, testswapran.asrtests, changeTerms.asrtests, reparamSigDevn.asrtests

Examples

```
## Not run:
data(Wheat.dat)
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
current.asrt <- rmboundary(current.asrt)
# Test Row autocorrelation
current.asrt <- testresidual(current.asrt, "~ Row:ar1(Column)",
                             label="Row autocorrelation", simpler=TRUE)
print(current.asrt)

## End(Not run)
```

---

testswapran.asrtests *Tests, using a REMLRT, the significance of the difference between the current random model and one in which oldterms are dropped and newterms are added. The result is recorded in an* asrtests.object.

Description

Fits a new random model using asreml by removing oldterms and adding newterms. If simpler = FALSE the model to be fitted must be more complex than the one whose fit has been stored in asrtests.obj. That is, the new model must have more parameters. However, if simpler = TRUE the model to be fitted must be simpler than the one whose fit has been stored in asrtests.obj in that it must have fewer parameters. The test is a REML ratio test that is performed using REMLRT.asreml, which is only valid if the models are nested. It compares the newly fitted model with the fit of the model in asrtest.obj. A row is added to the test.summary data.frame using the supplied label. If the newly fitted model is retained, any boundary terms are then removed using rmboundary.asrtests.

Usage

```
## S3 method for class 'asrtests'
testswapran(asrtests.obj, oldterms = NULL, newterms = NULL,
            label = "Swap in random model", simpler = FALSE,
            alpha = 0.05, allow.unconverged = TRUE, checkboundaryonly = FALSE,
            positive.zero = FALSE, bound.test.parameters = "none",
            bound.exclusions = c("F","B","S","C"), REMLDF = NULL,
            denDF="numeric", trace = FALSE, update = TRUE,
            set.terms = NULL, ignore.suffices = TRUE,
            bounds = "P", initial.values = NA, ...)
```

Arguments

asrtests.obj	an asrtests.object for a fitted model that is a list containing the componets (i) asreml.obj, (ii) wald.tab (iii) test.summary.
oldterms	Terms, stored as a character, that are to be removed from the random model using asreml.
newterms	Terms, stored as a character, that are to be added to the random model using asreml.
simpler	A logical indicating whether the new model to be fitted. after the changes made as a result of swapping oldterms for newterms, is simpler than the already fitted model whose fit is stored in asrtests.obj.
alpha	The significance level for the test.
allow.unconverged	A logical indicating whether to accept a new model even when it does not converge. If FALSE and the fit of the new model does not converge, the supplied asreml object is returned. Also, if FALSE and the fit of the new model has converged, but that of the old model has not, the new model will be accepted.
checkboundaryonly	If TRUE then boundary and singular terms are not removed by rmboundary.asrtests; a warning is issued instead.
label	A character string to use as the label in test.summary and which indicates what is being tested.
positive.zero	Indicates whether the hypothesized values for the variance components being tested are on the boundary of the parameter space. For example, this is true for positively-constrained variance components that, under the reduced model, are zero. This argument does not need to be set if bound.test.parameters is set.
bound.test.parameters	Indicates whether for the variance components being tested, at least some of the hypothesized values are on the boundary of the parameter space. The possibilities are "none", "onlybound" and "one-and-one". The default is "none", although if it is set to "none" and positive.zero is TRUE then bound.test.parameters is taken to be "onlybound". When bound.test.parameters is set to "one-and-one", it signifies that there are two parameters being tested, one of which is bound and the other is not. For example, the latter is true for testing a covariance and a positively-constrained variance component that, under the reduced model, are zero.
bound.exclusions	A character specifying one or more bound (constraint) codes that will result in a variance parameter being excluded from the count of estimated variance parameters in using REMLRT.asreml. If set to NULL then none will be excluded.
REMLDF	A numeric giving the difference in the number of variance parameters whose estimates are not of the type specified in bound.exclusions for two models being compared in a REML ratio test using REMLRT.asreml. If NULL then this is determined from the information in the asreml object for the two models.
denDF	Specifies the enthod to use in computing approximate denominator degrees of freedom when wald.asreml is called. Can be none to suppress the computations, numeric for numerical methods, algebraic for algebraic methods or default, the default, to autommatically choose numeric or algebraic computations depending on problem size. The denominator degrees of freedom are calculated according to Kenward and Roger (1997) for fixed terms in the dense part of the model.

trace — If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.

update — If TRUE then update.asreml is called to change the model. In doing this the arguments R.param and G.param are set to those in the asreml object stored in asrtests.obj so that the values from the previous model are used as starting values. If FALSE then a call is made to asreml in which the only changes from the previous call are that (i) models are modifed for the supplied oldterms and newterms, and (ii) modifications specified via ... are made.

set.terms — A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting.

ignore.suffices — A logical vector specifying whether the suffices of the asreml-assigned names of the variance terms (i.e. the information to the right of an "!", other than "R!") is to be ignored in matching elements of terms. If TRUE for an element of terms, the suffices are stripped from the asreml-assigned names. If FALSE for an element of terms, the element must exactly match an asreml-assigned name for a variance term. This vector must be of length one or the same length as terms. If it is of length one then the same action is applied to the asreml-assigned suffices for all the terms in terms.

bounds — A character vector specifying the bounds to be applied to the terms specified in set.terms. This vector must be of length one or the same length as set.terms. If it is of length one then the same constraint is applied to all the terms in set.terms. If any of the bounds are equal to NA then they are left unchanged for those terms.

initial.values — A character vector specifying the initial values for the terms specified in terms. This vector must be of length one or the same length as terms. If it is of length one then the same initial value is applied to all the terms in terms. If any of the initial.values are equal to NA then they are left unchanged for those terms.

... — Further arguments passed to asreml, wald.asreml and as.asrtests.

Value

An asrtests.object for a fitted model that is a list containing the componets (i) asreml.obj, (ii) wald.tab (iii) test.summary. If the term is not in the model, then the supplied asreml object will be returned. Also, reml.test will have the likelihood ratio and the p-value set to NA and the degrees of freedom to zero. Similarly, the row of test.summary for the term will have its name, a p-value set to NA, and action set to Absent.

Author(s)

Chris Brien

See Also

as.asrtests, chooseModel.asrtests, REMLRT.asreml, rmboundary.asrtests, newfit.asreml, testresidual.asrtests, changeTerms.asrtests, reparamSigDevn.asrtests

Examples

```
## Not run:
current.asrt <- testswapran(current.asrt, oldterms = "str(~ Cart/xDays, ~us(2):id(184))",
                            newterms = "Cart/xDays", pos = FALSE,
```

```
                            label = "Intercept/Slope correlation",
                            simpler = TRUE)
  print(current.asrt)

## End(Not run)
```

---

validAlldiffs *Checks that an object is a valid alldiffs object.*

Description

Checks that an object is an alldiffs.object of S3-class alldiffs containing the components asreml.obj, wald.tab and test.summary.

Usage

```
validAlldiffs(object)
```

Arguments

object	an alldiffs.object.

Value

TRUE or a character describing why the object is not a valid alldiffs.object.

Author(s)

Chris Brien

See Also

alldiffs.object, is.alldiffs, as.alldiffs, validPredictionsFrame, validAsrtests

Examples

```
data(Oats.dat)

## Use lmerTest and emmmeans to get predictions and associated statistics
if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  m1.lmer <- lmerTest::lmer(Yield ~ Nitrogen*Variety + (1|Blocks/Wplots),
                            data=Oats.dat)
  Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
  Var.preds <- summary(Var.emm)
  den.df <- min(Var.preds$df)
  ## Modify Var.preds to be compatible with a predictions.frame
  Var.preds <- as.predictions.frame(Var.preds, predictions = "emmean",
                                    se = "SE", interval.type = "CI",
                                    interval.names = c("lower.CL", "upper.CL"))
  Var.vcov <- vcov(Var.emm)
  Var.sed <- NULL
```

```
  ## Form an all.diffs object
   Var.diffs <- as.alldiffs(predictions = Var.preds, classify = "Nitrogen:Variety",
                            sed = Var.sed, vcov = Var.vcov, tdf = den.df)

  ## check the validity of Var.diffs
  validAlldiffs(Var.diffs)
}
```

---

validAsrtests *Checks that an object is a valid asrtests object.*

Description

Checks that an object is an asrtests.object of S3-class asrtests containing the components asreml.obj, wald.tab and test.summary.

Usage

```
validAsrtests(object)
```

Arguments

object	an asrtests.object.

Value

TRUE or a character describing why the object is not a valid asrtests.object.

Author(s)

Chris Brien

See Also

asrtests.object, is.asrtests, as.asrtests, validPredictionsFrame, validAlldiffs

Examples

```
## Not run:
library(dae)
library(asreml)
library(asremlPlus)
## use ?Wheat.dat for data set details
data(Wheat.dat)

# Fit initial model
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
                      data=Wheat.dat)

# Load current fit into an asrtests object
```

```
current.asrt <- as.asrtests(current.asr, NULL, NULL)

# check validity of current.asrt
validAsrtests(current.asrt)

## End(Not run)
```

---

validPredictionsFrame *Checks that an object is a valid predictions.frame.*

Description

Checks that an object is a predictions.frame of S3-class data.frame that contains the columns predicted.value, standard.error and est.status.

Usage

```
validPredictionsFrame(object)
```

Arguments

object	an predictions.frame.

Value

TRUE or a character describing why the object is not a valid predictions.frame.

Author(s)

Chris Brien

See Also

predictions.frame, validAsrtests, validAlldiffs

Examples

```
data(Oats.dat)

## Use asreml to get predictions and associated statistics

## Not run:
m1.asr <- asreml(Yield ~ Nitrogen*Variety,
                 random=~Blocks/Wplots,
                 data=Oats.dat)
current.asrt <- as.asrtests(m1.asr)
Var.pred <- asreml::predict.asreml(m1.asr, classify="Nitrogen:Variety",
                                   sed=TRUE)
if (getASRemlVersionLoaded(nchar = 1) == "3")
  Var.pred <- Var.pred$predictions
Var.preds <- as.predictions.frame(Var.pred$pvals, se = "std.error",
                                  est.status = "status")
```

```
## End(Not run)

  ## Use lmerTest and emmmeans to get predictions and associated statistics
  if (requireNamespace("lmerTest", quietly = TRUE) &
      requireNamespace("emmeans", quietly = TRUE))
  {
    m1.lmer <- lmerTest::lmer(Yield ~ Nitrogen*Variety + (1|Blocks/Wplots),
                              data=Oats.dat)
    Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
    Var.preds <- summary(Var.emm)
    Var.preds <- as.predictions.frame(Var.preds, predictions = "emmean",
                                      se = "SE", interval.type = "CI",
                                      interval.names = c("lower.CL", "upper.CL"))
  }

  if (exists("Var.preds"))
  {
    ## Check the class and validity of the predictions.frame
    is.predictions.frame(Var.preds)
    validPredictionsFrame(Var.preds)
  }
```

`variofaces.asreml` *Plots empirical variogram faces, including envelopes, as described by Stefanova, Smith & Cullis (2009).*

Description

A function that produces a plot for each face of an empirical 2D `variogram` based on residuals produced after the fitting of a model using the function `asreml`. It also adds envelopes to the plot by simulating data sets in parallel from a multivariate normal distribution with expectation equal to the fitted values obtained from the fixed and spline terms and variance matrix equal to the fitted variance matrix (Stefanova, Smith & Cullis, 2009). The plot is controlled by the `residual` model, which must consist of two factors corresponding to the two physical dimensions underlying the data. It can also have a third term involving the `at` or `dsum` function that defines sections of the data, such as experiments in different environments. In this case, the two variogram faces are produced for each section.

Usage

```
## S3 method for class 'asreml'
variofaces(asreml.obj, means=NULL, V=NULL, nsim=100, seed = NULL,
           extra.matrix = NULL, ignore.terms = NULL, fixed.spline.terms = NULL,
           bound.exclusions = c("F","B","S","C"), tolerance=1E-10,
           units = "ignore", update = TRUE, trace = FALSE,
           graphics.device=NULL, ncores = detectCores(), ...)
```

Arguments

`asreml.obj`	An `asreml` object from a call to `asreml` in which the `data` argument has been set.

means — The vector of means to be used in generating simulated data sets. If it is NULL, the fitted values based on object are used. It must be the same length as the response variable for object.

V — The fitted variance matrix, i.e. having the appropriate pattern and values given the model fitted to the observed data and the estimates of the parameters obtained. If V is NULL then estimateV.asreml is called to obtain it from asreml.obj

nsim — The number of data sets to be simulated in obtaining the envelopes.

seed — A single value, interpreted as an integer, that specifies the starting value of the random number generator. The "L'Ecuyer-CMRG" random generator is used and nextRNGStream is used to seed each core from the original seed.

extra.matrix — A matrix of order equal to the number of observations that is to be added to the varaince matrix, the latter based on the information in asreml.obj. It is assumed that the sigma-parameterized values of the variance parameter estimates, such as is given in the varcomp component of summary.asreml, have been used in calculating extra.matrix; the values in the vparameters component of G.param and R.param may be either gamma- or sigma-parameterized. The argument extra.matrix can be used in conjunction with ignore.terms as a workaround to include components of the variance matrix for variance functions that have not been implemented in estimateV.

ignore.terms — A character giving terms from either the random or residual models that are to be ignored in that their contributions to the variance is not to be included in the estimated matrix. The term names are those given in the vparameters component of the asreml object or the varcomp component produced by summary.asreml, but only up to the first exclamation mark (!). This can be used in conjunction with estimateV.asreml as a workaround to include components of the variance matrix for variance functions that have not been implemented in estimateV.

fixed.spline.terms — A character vector giving one or mor spline terms in the random model that are regarded as fixed and so are to be ignored because they are not regarded as contributing to the variance. The term names are those given in the vparameters component of the asreml object or the varcomp component produced by summary.asreml, but only up to the first exclamation mark (!).

bound.exclusions — A character specifying one or more bound codes that will result in a variance parameter in the random model being excluded from contributing to the variance. If set to NULL then none will be excluded.

tolerance — The value such that eigenvalues less than it are considered to be zero.

units — A character indicating whether the BLUPs for units are added to the residuals when this reserved factor is included in the random model. Possible values are addtoresiduals and ignore. If standardized conditional residuals are plotted and the BLUPs for units are to be added then it is the standardized BLUPs that are added.

update — If TRUE then the arguments R.param and G.param are set to those in the asreml object supplied in object so that the values from the original model are used as starting values. If FALSE then calls are made to asreml in which the only changes from the previous call are (i) the model is fitted to simulated data and (ii) modifications specified via ... are made, except that changes cannot be made to any of the models.

trace — If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.

graphics.device
: A character specifying a graphics device for plotting. The default is graphics.device = NULL, which will result in plots being produced on the current graphics device. Setting it to "windows", for example, will result in a windows graphics device being opened.

ncores
: A numeric specifying the number of cores to use in doing the simulations.

...
: Other arguments that are passed down to the function asreml. Changes to the models are not allowed. Other changes are dangerous and generally should be avoided.

Details

The residual model is scanned to ensure that it involves only two factors not included in the at function, and to see if it has a third factor in an at function. If so, the faces of the 2D variogram, each based on one of the two non-at factors, are derived from the residuals in the supplied asreml object using asreml.variogram, this yielding the observed variogram faces. If aom was set to TRUE for the asreml object, the standardized consitional residuals are used. Then nsim data sets are generated by adding the fitted.values, extracted from the asreml object, to a vector of values randomly generated from a normal distribution with expectation zero and variance matrix V. Each data set is analyzed using the model in object and several sets are generated and analyzed in parallel. The variogram values for the faces are obtained using asreml.variogram stored. Note, if the analysis for a data set does not converge in maxiter iterations, it is discarded and a replacement data set generated. The value of maxiter can be specified in the call to variofaces.asreml. Plots are produced for each face and include the observed values and the 2.5%, 50% & 97.5% quantiles.

Value

A list with the following components:

1. **face1:** a data.frame containing the variogram values on which the plot for the first dimension is based.
2. **face2:** a data.frame containing the variogram values on which the plot for the second dimension is based.

Author(s)

Chris Brien

References

Stefanova, K. T., Smith, A. B. & Cullis, B. R. (2009) Enhanced diagnostics for the spatial analysis of field trials. *Journal of Agricultural, Biological, and Environmental Statistics*, **14**, 392–410.

See Also

asremlPlus-package, asreml, plotVariofaces.data.frame, simulate.asreml, set.seed.

Examples

```
## Not run:
data(Wheat.dat)
current.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
                      random = ~ Row + Column + units,
                      residual = ~ ar1(Row):ar1(Column),
```

```
                      data=Wheat.dat)
current.asrt <- as.asrtests(current.asr, NULL, NULL)
current.asrt <- rmboundary.asrtests(current.asrt)
# Form variance matrix based on estimated variance parameters
s2 <- current.asr$sigma2
gamma.Row <- current.asr$gammas[1]
gamma.unit <- current.asr$gammas[2]
rho.r <- current.asr$gammas[4]
rho.c <- current.asr$gammas[5]
row.ar1 <- mat.ar1(order=10, rho=rho.r)
col.ar1 <- mat.ar1(order=15, rho=rho.c)
V <- gamma.Row * fac.sumop(Wheat.dat$Row) +
     gamma.unit * diag(1, nrow=150, ncol=150) +
     mat.dirprod(col.ar1, row.ar1)
V <- s2*V

#Produce variogram faces plot (Stefanaova et al, 2009)
variofaces(current.asr, V=V, ncores = 2)

## End(Not run)
```

`WaterRunoff.dat` *Data for an experiment to investigate the quality of water runoff over time*

Description

This data is from an experiment to investigate the quality of water runoff. However, it has been modified to hide the true identity of the Species and Sources. It is used to provide executable examples of the functions listed under **Examples**.

Usage

```
data(WaterRunoff.dat)
```

Format

A data.frame containing 440 observations of 13 variables.

Author(s)

Chris Brien

Source

Kazemi, F. (pers. comm.)

See Also

`chooseModel.asrtests`, `reparamSigDevn.asrtests`, `plotPredictions.data.frame`, `predictPlus.asreml`, `predictPresent.asreml`

`Wheat.dat` *Data for an experiment to investigate 25 varieties of wheat*

Description

The data appears in Gilmour et al. [1995] and is from a field experiment designed to compare the performance of 25 varieties of wheat. An analysis of it using asreml is presented by Butler et al. (2018, Section 7.6), although they suggest that it is a barley experiment. It is used in `asremlPlus-package` as an executable example of the use of the `asremlPlus` to analyse a data set.

The experiment was conducted at Slate Hall Farm, UK, in 1976 and was designed as a balanced lattice square with 6 replicates laid out in a 10×15 rectangular grid. The columns in the data frame are: Rep, Row, Column, WithinColPairs, Variety, yield. The response variable is the grain yield.

Usage

```
data(Wheat.dat)
```

Format

A data.frame containing 150 observations of 6 variables.

Author(s)

Chris Brien

Source

Butler, D. G., Cullis, B. R., Gilmour, A. R., Gogel, B. J. and Thompson, R. (2018). *ASReml-R Reference Manual Version 4*. VSN International Ltd, `http://asreml.org`.

Gilmour, A. R., et al. (1995) Average Information REML: An efficient algorithm for variance parameter estimation in linear mixed models. *Biometrics*, **51**, 1440-1450.

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