

# Package ‘asremlPlus’

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

**Depends** R (>= 3.5.0)

**Imports** dae, doParallel, dplyr, ggplot2, foreach, grDevices, graphics,  
methods, parallel, reshape2, RColorBrewer, rlang, stats,  
stringr, sticky, utils

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

**Enhances** asreml

**VignetteBuilder** R.rsp

**SystemRequirements** asreml-R 4.x

**LazyData** true

**Description** Assists in automating the selection of terms to include 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 (for further details see 'asremlPlus-package' in help). 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 package that can be purchased from 'VSNi' <<https://vsni.co.uk/>> as 'asreml-R', who will supply a zip file for local installation/updating (see <<https://asreml.kb.vsn.co.uk/>>). It is not needed for functions that are methods for 'alldiffs' and 'data.frame' objects. The package 'asremlPlus' 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:**

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asremlPlus-package	<i>Augments 'ASReml-R' in Fitting Mixed Models and Packages Generally in Exploring Prediction Differences</i>
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## Description

Assists in automating the selection of terms to include 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 (for further details see 'asremlPlus-package' in help). 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 package that can be purchased from 'VSNi' <<https://vsni.co.uk/>> as 'asreml-R', who will supply a zip file for local installation/updating (see <<https://asreml.kb.vsn.co.uk/>>). It is not needed for functions that are methods for 'alldiffs' and 'data.frame' objects. The package 'asremlPlus' can also be installed from <<http://chris.brien.name/rpackages/>>.

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## Index

### (i) Data

<a href="#">Oats.dat</a>	Data for an experiment to investigate nitrogen response of 3 oats varieties.
<a href="#">Wheat.dat</a>	Data for an experiment to investigate 25 varieties of wheat.
<a href="#">WaterRunoff.dat</a>	Data for an experiment to investigate the quality of water runoff over time

### (ii) Object manipulation

<a href="#">as.alldiffs</a>	Forms an <a href="#">alldiffs.object</a> from the supplied predictions, along with those statistics, associated with the predictions and their pairwise differences, that have been supplied.
<a href="#">asrtests</a>	Pseudonym for <a href="#">as.asrtests</a> .
<a href="#">as.asrtests</a>	Forms an <a href="#">asrtests.object</a> that stores (i) a fitted asreml object, (ii) a pseudo-anova table for the fixed terms and (iii) a history of changes and hypothesis testing used in obtaining the model.
<a href="#">as.predictions.frame</a>	Forms a <a href="#">predictions.frame</a> from a data.frame, ensuring that the correct columns are present.
<a href="#">facCombine.alldiffs</a>	Combines several factors into one in the components of an <a href="#">alldiffs.object</a> .

<code>facRecast.alldiffs</code>	Reorders and/or revises the factor levels using the order of old levels in <code>levels.order</code> and the new labels for the levels given in <code>newlabels</code> .
<code>facRename.alldiffs</code>	Renames <code>factors</code> in the prediction component of an <code>alldiffs.object</code> .
<code>getFormulae.asreml</code> <code>is.alldiffs</code>	Gets the formulae from an <code>asreml</code> object. A single-line function that tests whether an object is of class <code>alldiffs</code> .
<code>is.asrtests</code>	A single-line function that tests whether an object is of class <code>asrtests</code> .
<code>is.predictions.frame</code>	A single-line function that tests whether an object is of classes <code>predictions.frame</code> and <code>data.frame</code> .
<code>makeTPPSplineMats.data.frame</code>	Make the spline basis matrices and data needed to fit Tensor Product P-Splines.
<code>print.alldiffs</code> <code>print.asrtests</code> <code>print.LSDdata</code>	Prints the values in an <code>alldiffs.object</code> in a nice format. Prints the values in an <code>asrtests.object</code> . Prints the components of a list containing data on the LSDs for all pairwise differences of predictions.
<code>print.predictions.frame</code> <code>print.test.summary</code> <code>print.wald.tab</code> <code>printFormulae.asreml</code> <code>sort.alldiffs</code>	Prints the values in a <code>predictions.frame</code> , with or without title and heading. Prints a <code>data.frame</code> containing a test.summary. Prints a <code>data.frame</code> containing a Wald or pseudoanova table. Prints the formulae from an <code>asreml</code> object. Sorts the components of an <code>alldiffs.object</code> according to the predicted values associated with a factor.
<code>subset.alldiffs</code>	Subsets the components in an <code>alldiffs.object</code> according to the supplied condition.
<code>subset.list</code>	Forms a list that contains a subset of the components of the supplied <code>list</code> .
<code>validAlldiffs</code> <code>validAsrtests</code> <code>validPredictionsFrame</code>	Checks that an object is a valid <code>alldiffs.object</code> . Checks that an object is a valid <code>asrtests.object</code> . Checks that an object is a valid <code>predictions.frame</code> .
(iii) Model modification	
<code>addSpatialModel.asrtests</code>	Adds, to a supplied model, a spatial model that accounts for local spatial variation.
<code>addSpatialModelOnIC.asrtests</code>	Uses information criteria to decide whether to add a spatial model to account for local spatial variation.
<code>changeTerms.asrtests</code>	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.
<code>iterate.asrtests</code>	Subject the fitted <code>asreml.obj</code> stored in an <code>asrtests.object</code> to further iterations of the fitting process.
<code>newfit.asreml</code>	Refits an <code>asreml</code> model with modified model formula using either a call to <code>'update.asreml'</code> or a direct call to <code>'asreml'</code> .
<code>reparamSigDevn.asrtests</code>	Reparamterizes each random (deviations) term involving <code>'devn.fac'</code> to a fixed term and ensures that the same term, with <code>'trend.num'</code> replacing <code>'devn.fac'</code> , is included if any other term with <code>'trend.num'</code> is included in <code>'terms'</code> .
<code>rmboundary.asrtests</code>	Removes any boundary or singular variance components from the fit stored in <code>'asreml.obj'</code> and records their

`setvarianceterms.call`

removal in an `asrtests.object`.

Allows the setting of bounds and initial values for terms in the 'random' and 'residual' arguments of an 'asreml' call.

#### (iv) Model selection

`addto.test.summary`

Adds a row to a `test.summary` data.frame.

`changeModelOnIC.asrtests`

Uses information criteria to decide whether to change an already fitted model.

`chooseModel.asrtests`

Determines and records the set of significant terms using an `asrtests.object`, taking into account the hierarchy or marginality relations of the terms..

`chooseModel.data.frame`

Determines the set of significant terms from results stored in a data.frame, taking into account the marginality relations of terms and recording the tests used in a data.frame.

`chooseSpatialModelOnIC.asrtests`

Uses information criteria to choose the best fitting spatial model for accounting for local spatial variation.

`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 models.

`infoCriteria.list`

Computes AIC and BIC for models.

`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 distribution and save quantites related to the simulated data.

#### (vi) Prediction production and presentation

<code>addBacktransforms.alldiffs</code>	Adds or recalculates the backtransforms component of an <code>alldiffs.object</code> .
<code>allDifferences.data.frame</code>	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.
<code>exploreLSDs</code>	Explores the computed LSD values for pairwise differences between predictions.
<code>linTransform.alldiffs</code>	Calculates a linear transformation of the predictions stored in an <code>alldiffs.object</code> .
<code>pairediffsTransform.alldiffs</code>	Calculates the differences between nominated pairs of predictions stored in an <code>alldiffs.object</code>
<code>pickLSDstatistics</code>	Pick LSDstatistics whose values minimize the number of errors in pairwise comparisons of predictions.
<code>plotLSDerrors.data.frame</code>	Plots a map of the supplied errors that occur in using the computedLSD values for pairwise differences between predictions.
<code>plotLSDerrors.alldiffs</code>	Plots a map of the errors that occur in using the computed LSD values for pairwise differences between predictions.
<code>plotLSDs.data.frame</code>	Plots a heat map of computed LSD values for pairwise differences between predictions.
<code>plotLSDs.alldiffs</code>	Plots a heat map of computed LSD values for pairwise differences between predictions.
<code>plotPredictions.data.frame</code>	Plots the predictions for a term, possibly with error bars.
<code>plotPvalues.alldiffs</code>	Plots the p-values in the p.differences components of an <code>alldiffs.object</code> as a heat map.
<code>plotPvalues.data.frame</code>	Plots the p-values in data.frame as a heat map.
<code>predictPlus.asreml</code>	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 'alldiffs' and may print the results. It can be when there are not parallel values.
<code>predictPresent.asreml</code>	Forms the predictions for each of one or more terms and presents them in tables and/or graphs.
<code>ratioTransform.alldiffs</code>	Calculates the ratios of noinated pairs of predictions stored in an <code>alldiffs.object</code> .
<code>recalcLSD.alldiffs</code>	Adds or recalculates the <code>LSD.frame</code> that is a component of an <code>alldiffs.object</code> .
<code>redoErrorIntervals.alldiffs</code>	Adds or replaces the error intervals stored in the prediction component of an <code>alldiffs.object</code> .
<code>renewClassify.alldiffs</code>	Renews the components in an <code>alldiffs.object</code> according to a new classify.
<code>sort.alldiffs</code>	Sorts the components in an <code>alldiffs.object</code> according to the predicted values associated with a factor.
<code>subset.alldiffs</code>	Subsets the components in an <code>alldiffs.object</code> according to the supplied condition.
<code>sort.predictions.frame</code>	Sorts a <code>predictions.frame</code> according to the predicted values. associated with a factor.

## (vii) Response transformation

<code>angular</code>	Applies the angular transformation to proportions.
<code>angular.mod</code>	Applies the modified angular transformation to a vector of counts.
<code>powerTransform</code>	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

<code>getASRemlVersionLoaded</code>	Finds the version of asreml that is loaded and returns the initial characters in version.
<code>loadASRemlVersion</code>	Ensures that a specific version of asreml is loaded.
<code>num.recode</code>	Recodes the unique values of a vector using the values in a new vector.
<code>permute.square</code>	Permutes the rows and columns of a square matrix.
<code>permute.to.zero.lowertri</code>	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 errors 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 `data.frame` containing LSD values and their summary statistics, (iii) optionally, the variance matrix of the predictions, and (iv) if the response was transformed 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`.

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**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, <https://asreml.kb.vsnl.co.uk/>.

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)

# Initialize 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", simplr=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",
                              simplr=TRUE, update=FALSE)
  else
    current.asrt <- testresidual(current.asrt, "~ Row:Column",
                                label="Col autocorrelation",
                                simplr=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. The values of transform.power, offset, scale and transform.function from the backtransforms component will be used, unless this component is NULL when the values supplied in the call will be used.

## Usage

```

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

```

**Arguments**

<code>alldiffs.obj</code>	An <a href="#">alldiffs.object</a> .
<code>transform.power</code>	A <a href="#">numeric</a> 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 <code>transform.power</code> , unless it equals 0 in which case the exponential of the predictions is taken.
<code>offset</code>	A <a href="#">numeric</a> that has been added to each value of the response after any scaling and before applying any power transformation.
<code>scale</code>	A <a href="#">numeric</a> by which each value of the response has been multiplied before adding any offset and applying any power transformation.
<code>transform.function</code>	A <a href="#">character</a> giving the name of a function that specifies the scale on which the predicted values are defined. This may be the result of a transformation of the data using the function or the use of the function as a link function in the fitting of a generalized linear (mixed) model (GL(M)M). The possible <code>transform.functions</code> are <code>identity</code> , <code>log</code> , <code>inverse</code> , <code>sqrt</code> , <code>logit</code> , <code>probit</code> , and <code>cloglog</code> . The <code>predicted.values</code> and <code>error.intervals</code> , if not <code>StandardError</code> intervals, will be back-transformed using the inverse function of the <code>transform.function</code> . The <code>standard.error</code> column will be set to NA, unless (i) <code>asreml</code> returns columns named <code>transformed.value</code> and <code>approx.se</code> , as well as those called <code>predicted.values</code> and <code>standard.error</code> (such as when a GLM is fitted) and (ii) the values in <code>transformed.value</code> are equal to those obtained by backtransforming the <code>predicted.values</code> using the inverse function of the <code>transform.function</code> . Then, the <code>approx.se</code> values will be saved in the <code>standard.error</code> column of the <code>backtransforms</code> component of the returned <code>alldiffs.obj</code> . Also, the <code>transformed.value</code> and <code>approx.se</code> columns are removed from both the <code>predictions</code> and <code>backtransforms</code> components of the <code>alldiffs.obj</code> . Note that the values that end up in the <code>standard.errors</code> column are approximate for the backtransformed values and are not used in calculating <code>error.intervals</code> .
<code>...</code>	Provision for passing arguments to functions called internally - not used at present.

**Value**

An [alldiffs.object](#) with components `predictions`, `vcov`, `differences`, `p.differences`, `sed`, `LSD` and `backtransforms`.

The `backtransforms` component will have the attributes (i) `LSDtpe`, `LSDby` and `LSDstatistic` added from the `predictions` component and (ii) `transform.power`, `offset`, `scale`, and `link`.

**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**

```

##Subset WaterRunoff data to reduce time to execute
data(WaterRunoff.dat)
tmp <- subset(WaterRunoff.dat, Date == "05-18" & Benches != "3")

##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= tmp)
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 emmeans 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=tmp)
  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
  els <- as.numeric(rownames(TS.preds))
  TS.vcov <- vcov(TS.emm)[els,els]
  TS.diffs <- allDifferences(predictions = TS.preds, classify = "Sources:Species",
    vcov = TS.vcov, tdf = den.df)

  validAlldiffs(TS.diffs)
}

## Recalculate the back-transforms of the predictions obtained using asreml or lmerTest
if (exists("TS.diffs"))
{
  TS.diffs <- addBacktransforms.alldiffs(TS.diffs, transform.power = 0)
}

```

---

addSpatialModel.asrtests

*Adds, to a supplied model, a spatial model that accounts for local spatial variation.*

---

## Description

Adds either a correlation, two-dimensional tensor-product natural cubic smoothing spline (TP-NCSS), or a two-dimensional tensor-product penalized P-spline model (TPPS) to account for the local spatial variation exhibited by a response variable measured on a potentially irregular grid of rows and columns of the units. The data may be arranged in sections, for each of which there is a grid and for which the model is to be fitted separately. Also, the rows and columns of a grid are not necessarily one observational unit wide.

No hypothesis testing or comparison of information criteria is made. To only change the terms based on a comparison of information criteria use [chooseSpatialModelOnIC.asrtests](#).

The model fit supplied in the `asrtests.obj` should not include terms that will be included in the local spatial model. All spatial model terms are fitted as fixed or random. Consequently, the residual model does not have to be iid.

One or more rows is added for each section to the `test.summary.data.frame`. Convergence and the occurrence of fixed correlations 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 for the new model.

## Usage

```
## S3 method for class 'asrtests'
addSpatialModel(asrtests.obj, spatial.model = "TPPS",
  sections = NULL,
  row.covar = "cRow", col.covar = "cCol",
  row.factor = NULL, col.factor = NULL,
  nsegs = NULL, nestorder = c(1,1),
  degree = c(3,3), difforder = c(2,2),
  asreml.option = "mbf", tpps4mbf.obj = NULL,
  allow.unconverged = FALSE, allow.fixedcorrelation = FALSE,
  checkboundaryonly = FALSE, update = FALSE,
  IClikelihood = "full", ...)
```

## Arguments

<code>asrtests.obj</code>	An <a href="#">asrtests.object</a> containing the components (i) <code>asreml.obj</code> , (ii) <code>wald.tab</code> , and (iii) <code>test.summary</code> .
<code>spatial.model</code>	A single character string nominating the type of spatial model to fit. Possible values are <code>corr</code> , <code>TPNCSS</code> and <code>TPPS</code> .
<code>sections</code>	A single character string that species the name of the column in the <a href="#">data.frame</a> that contains the <a href="#">factor</a> that identifies different sections of the data to which separate spatial models are to be fitted.
<code>row.covar</code>	A single character string nominating a <a href="#">numeric</a> column in the <a href="#">data.frame</a> that contains the values of a centred covariate indexing the rows of the grid.
<code>col.covar</code>	A single character string nominating a <a href="#">numeric</a> column in the <a href="#">data.frame</a> that contains the values of a centred covariate indexing the columns of the grid.
<code>row.factor</code>	A single character string nominating a <a href="#">factor</a> in the <a href="#">data.frame</a> that has as many levels as there are unique values in <code>row.covar</code> . This argument is required for <code>spatial.model</code> set to <code>TPNCSS</code> or <code>TPPS</code> . It is used to remove a term corresponding to the <code>row.factor</code> and a random row deviations term based on <code>row.covar</code> will be included in the model. If the argument is <code>NULL</code> , it is assumed that such a term is not included in the fitted model stored in <code>asrtests.obj</code> .

<code>col.factor</code>	A single character string nominating a <a href="#">factor</a> in the <a href="#">data.frame</a> that has as many levels as there are unique values in <code>col.covar</code> . This argument is required for <code>spatial.model</code> set to <code>TPNCSS</code> or <code>TPPS</code> . It is used to remove a term corresponding to the <code>col.factor</code> and a random column deviations term based on <code>col.covar</code> will be included in the model. If the argument is <code>NULL</code> , it is assumed that such a term is not included in the fitted model stored in <code>asrtests.obj</code> .
<code>nsegs</code>	A pair of <a href="#">numeric</a> values giving the number of segments into which the column and row ranges are to be split, respectively (each value specifies the number of internal knots + 1). If only one number is specified, that value is used in both dimensions. If not specified, then (number of unique values - 1) is used in each dimension; for a grid layout with equal spacing, this gives a knot at each data value.
<code>nestorder</code>	A <a href="#">character</a> of length 2. The order of nesting for column and row dimensions, respectively; default=1 (no nesting). A value of 2 generates a spline with half the number of segments in that dimension, etc. The number of segments in each direction must be a multiple of the order of nesting.
<code>degree</code>	A <a href="#">character</a> of length 2. The degree of polynomial spline to be used for column and row dimensions respectively; default=3.
<code>difforder</code>	A <a href="#">character</a> of length 2. The order of differencing for column and row dimensions, respectively; default=2.
<code>asreml.option</code>	A single character string specifying whether the <code>grp</code> or <code>mbf</code> methods are to be used to supply externally formed covariate matrices to <code>asreml</code> . If the <code>mbf</code> methods is to be used, then <a href="#">makeTPPSplineMats.data.frame</a> must be used before calling <code>addSpatialModel.asrtests</code> . Compared to the <code>mbf</code> method, the <code>grp</code> method creates large <code>asreml</code> objects, but is faster. The <code>grp</code> method adds columns to the <a href="#">data.frame</a> containing the data; the <code>mbf</code> method adds only fixed covariate to data and stores the random covariates externally.
<code>tps4mbf.obj</code>	An object made with <a href="#">makeTPPSplineMats.data.frame</a> and which contains the spline basis information, extra to that created by <a href="#">makeTPPSplineMats.data.frame</a> , that is needed to fit a <code>TPPS</code> model using the <code>mbf</code> method of <code>asreml</code> .
<code>allow.unconverged</code>	A logical indicating whether to accept a new model even when it does not converge. If <code>FALSE</code> and the fit of the new model does not converge, the supplied <code>asrtests.obj</code> is returned. Also, if <code>FALSE</code> and the fit of the new model has converged, but that of the old model has not, the new model will be accepted.
<code>allow.fixedcorrelation</code>	A logical indicating whether to accept a new model even when it contains correlations in the model whose values have been designated as fixed, bound or singular. If <code>FALSE</code> and the new model contains correlations whose values have not been able to be estimated, the supplied <code>asrtests.obj</code> is returned. The fit in the <code>asreml.obj</code> component of the supplied <code>asrtests.obj</code> will also be tested and a warning issued if both fixed correlations are found in it and <code>allow.fixedcorrelation</code> is <code>FALSE</code> .
<code>checkboundaryonly</code>	If <code>TRUE</code> then boundary and singular terms are not removed by <a href="#">rmboundary.asrtests</a> ; a warning is issued instead.
<code>update</code>	If <code>TRUE</code> then <code>update.asreml</code> is called to fit the model to be tested. In doing this the arguments <code>R.param</code> and <code>G.param</code> are set to those in the <code>asreml</code> object stored in <code>asrtests.obj</code> so that the values from the previous model are used as starting values. If <code>FALSE</code> then a call is made to <code>asreml</code> in which the only

changes from the previous call are that (i) models are modified as specified and (ii) modifications specified via ... are made.

IClikelihood	A character that controls both the occurrence and the type of likelihood for information criterion in the <code>test.summary</code> of the new <code>asrtests.object</code> . If <code>none</code> , none are included. Otherwise, if <code>REML</code> , then the AIC and BIC based on the Restricted Maximum Likelihood are included; if <code>full</code> , then the AIC and BIC based on the full likelihood are included. (See also <code>infoCriteria.asreml</code> .)
...	Further arguments passed to <code>changeModelOnIC.asrtests</code> , <code>asreml</code> and <code>tpsmmb</code> .

## Details

The model to which the spatial models is to be added is supplied in the `asrtests.obj`. It should not include terms that will be included in the local spatial model. All spatial model terms are fitted as fixed or random. Consequently, the residual model does not have to be iid. The improvement in the fit resulting from the addition of a spatial model to the supplied model is evaluated.

For the corr spatial model, an exponential model (`exp`) is used for each dimension to model the spatial correlation. A series of models are tried, beginning with the addition of row correlation and followed by the addition of column correlation. Only if the model fit is improved is a correlation retained. Finally, if any correlation term is retained, the improvement to the fit of a nugget term is assessed. In this model, the correlation between observations from different rows is the correlation between observations in adjacent rows raised to the power equal to the absolute value of the difference in their `row.covar` values; similarly for the correlation in the column dimension.

The TPNCSS spatial model is as described by Verbyla et al. (2018) and the TPPS model is as described by Rodriguez-Alvarez et al. (2018). However, for the TPPS model, the degree of the polynomial and the order of differencing can be varied. The defaults of 3 and 2, respectively, fit a cubic spline with second order differencing, while setting both the degree and order of differencing to 1 will fit a type of linear variance model (Piepho, Boer and Williams, 2022). The fixed terms for these models are `row.covar + col.covar + row.covar:col.covar` and the random terms are `spl(row.covar) + spl(col.covar) + dev(row.covar) + dev(col.covar) + spl(row.covar):col.covar + row.covar:spl(col.covar) + spl(row.covar):spl(col.covar)`. The supplied model should not include any of these terms. However, any fixed or random main-effect term for either `row.factor` or `col.factor` will be removed from the fit.

The TPPS model is fitted using the function `tpsmmb` from the R package `TPSbits` authored by Sue Welham (2022). There are two methods for supplying the spline basis information produced by `tpsmmb` to `asreml`. The `grp` method adds the it to the `data.frame` holding the information for the analysis. The `mbf` method requires the spline basis information to be in the same environment as the function that is called to make a fit using `asreml`. To this end and prior to invoking the calling function, `makeTPPSplineMats.data.frame` must be used produce the `data.frames`.

All models utilize the function `changeTerms.asrtests` to fit the spatial model. Arguments from `tpsmmb` and `changeTerms.asrtests` can be supplied in calls to `addSpatialModel.asrtests` and will be passed on to the relevant function through the ellipses argument (...).

The data for experiment can be divided sections and the same spatial model fitted separately to each. The fit over all of the sections is assessed.

Each combination of a `row.coords` and a `col.coords` does not have to specify a single observation; for example, to fit a local spatial model to the main units of a split-unit design, each combination would correspond to a main unit and all subunits of the main unit would have the same combination.

**Value**

An `asrtests.object` containing the components (i) `asreml.obj`, (ii) `wald.tab`, and (iii) `test.summary` for the model that includes the spatial model, unless the spatial model fails to be fitted when `allow.unconverged` and/or `allow.fixedcorrelation` is set to `FALSE`.

**Author(s)**

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**References**

- Piepho, H.-P., Boer, M. P., & Williams, E. R. (2022). Two-dimensional P-spline smoothing for spatial analysis of plant breeding trials. *Biometrical Journal*, **64**, 835-857.
- Rodriguez-Alvarez, M. X., Boer, M. P., van Eeuwijk, F. A., & Eilers, P. H. C. (2018). Correcting for spatial heterogeneity in plant breeding experiments with P-splines. *Spatial Statistics*, **23**, 52-71.
- Verbyla, A. P., De Faveri, J., Wilkie, J. D., & Lewis, T. (2018). Tensor Cubic Smoothing Splines in Designed Experiments Requiring Residual Modelling. *Journal of Agricultural, Biological and Environmental Statistics*, **23**(4), 478-508.
- Welham, S. J. (2022) *TPSbits: Creates Structures to Enable Fitting and Examination of 2D Tensor-Product Splines using ASReml-R*. Version 1.0.0 <https://mmade.org/tpsbits/>

**See Also**

`as.asrtests`, `rmboundary.asrtests`, `addSpatialModelOnIC.asrtests`, `testranfix.asrtests`, `testresidual.asrtests`, `newfit.asreml`, `reparamSigDevn.asrtests`, `changeTerms.asrtests`, `chooseSpatialModelOnIC.asrtests`, `changeTerms.asrtests`, `infoCriteria.asreml`

**Examples**

```
## Not run:

data(Wheat.dat)

#Add row and column covariates
Wheat.dat <- within(Wheat.dat,
{
  cColumn <- dae::as.numfac(Column)
  cColumn <- cColumn - mean(unique(cColumn))
  cRow <- dae::as.numfac(Row)
  cRow <- cRow - mean(unique(cRow))
})

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

#Create an asrtests object, removing boundary terms
current.asrt <- as.asrtests(current.asr, NULL, NULL,
  label = "Random Row and Column effects")
current.asrt <- rmboundary(current.asrt)

current.asrt <- addSpatialModel(current.asrt, spatial.model = "TPPS",
  row.covar = "cRow", col.covar = "cColumn",
```



```

                                row.factor = "Row", col.factor = "Column",
                                asreml.option = "grp")
infoCriteria(current.asrt$asreml.obj)

## End(Not run)

```

---

```
addSpatialModelOnIC.asrtests
```

*Uses information criteria to decide whether to add a spatial model to account for local spatial variation.*

---

## Description

Adds either a correlation, two-dimensional tensor-product natural cubic smoothing spline (TP-NCSS), or a two-dimensional tensor-product penalized P-spline model (TPPS) to account for the local spatial variation exhibited by a response variable measured on a potentially irregular grid of rows and columns of the units. The data may be arranged in sections for each of which there is a grid and for which the model is to be fitted separately. Also, the rows and columns of a grid are not necessarily one observational unit wide. The spatial model is only added if the information criterion of the supplied model is decreased with the addition of the local spatial model.

A row is added for each section to the test.summary data.frame of the `asrtests.object` stating whether or not the new model has been swapped for a model in which the spatial model has been add to the supplied model. Convergence and the occurrence of fixed correlations 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 to exhibit the differences between the supplied and the new model, if a spatial model is added.

## Usage

```

## S3 method for class 'asrtests'
addSpatialModelOnIC(asrtests.obj, spatial.model = "TPPS",
                    sections = NULL,
                    row.covar = "cRow", col.covar = "cCol",
                    row.factor = NULL, col.factor = NULL,
                    nsegs = NULL, nestorder = c(1,1),
                    degree = c(3,3), difforder = c(2,2),
                    asreml.option = "mbf", tpps4mbf.obj = NULL,
                    allow.unconverged = FALSE, allow.fixedcorrelation = FALSE,
                    checkboundaryonly = FALSE, update = FALSE,
                    IClikelihood = "full", which.IC = "AIC", ...)

```

## Arguments

- |                            |  |
|----------------------------|--|
| <code>asrtests.obj</code>  | An <code>asrtests.object</code> containing the components (i) <code>asreml.obj</code> , (ii) <code>wald.tab</code> , and (iii) <code>test.summary</code> .   |
| <code>spatial.model</code> | A single character string nominating the type of spatial model to fit. Possible values are <code>corr</code> , <code>TPNCSS</code> and <code>TPPS</code> .   |
| <code>sections</code>      | A single character string that species the name of the column in the <code>data.frame</code> that contains the <code>factor</code> that identifies different sections of the data to which separate spatial models are to be fitted. |

row.covar	A single character string nominating a <a href="#">numeric</a> column in the <a href="#">data.frame</a> that contains the values of a centred covariate indexing the rows of the grid.
col.covar	A single character string nominating a <a href="#">numeric</a> column in the <a href="#">data.frame</a> that contains the values of a centred covariate indexing the columns of the grid.
row.factor	A single character string nominating a <a href="#">factor</a> in the <a href="#">data.frame</a> that has as many levels as there are unique values in row.covar. This argument is required for spatial.model set to TPNCSS or TPPS. It is used to remove a term corresponding to the row.factor and a random row deviations term based on row.covar will be included in the model. If the argument is NULL, it is assumed that such a term is not included in the fitted model stored in asrtests.obj.
col.factor	A single character string nominating a <a href="#">factor</a> in the <a href="#">data.frame</a> that has as many levels as there are unique values in col.covar. This argument is required for spatial.model set to TPNCSS or TPPS. It is used to remove a term corresponding to the col.factor and a random column deviations term based on col.covar will be included in the model. If the argument is NULL, it is assumed that such a term is not included in the fitted model stored in asrtests.obj.
nsegs	A pair of <a href="#">numeric</a> values giving the number of segments into which the column and row ranges are to be split, respectively (each value specifies the number of internal knots + 1). If only one number is specified, that value is used in both dimensions. If not specified, then (number of unique values - 1) is used in each dimension; for a grid layout with equal spacing, this gives a knot at each data value.
nestorder	A <a href="#">character</a> of length 2. The order of nesting for column and row dimensions, respectively; default=1 (no nesting). A value of 2 generates a spline with half the number of segments in that dimension, etc. The number of segments in each direction must be a multiple of the order of nesting.
degree	A <a href="#">character</a> of length 2. The degree of polynomial spline to be used for column and row dimensions respectively; default=3.
difforder	A <a href="#">character</a> of length 2. The order of differencing for column and row dimensions, respectively; default=2.
asrem1.option	A single character string specifying whether the grp or mbf methods are to be used to supply externally formed covariate matrices to asrem1. If the mbf methods is to be used, then <a href="#">makeTPPSplineMats.data.frame</a> must be used before calling addSpatialModelOnIC.asrtests. Compared to the mbf method, the grp method creates large asrem1 objects, but is faster. The grp method adds columns to the <a href="#">data.frame</a> containing the data; the mbf method adds only fixed covariate to data and stores the random covariates externally.
tps4mbf.obj	An object made with <a href="#">makeTPPSplineMats.data.frame</a> and which contains the spline basis information, extra to that created by <a href="#">makeTPPSplineMats.data.frame</a> , that is needed to fit a TPPS model using the mbf method of asrem1.
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 asrtests.obj 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.
allow.fixedcorrelation	A logical indicating whether to accept a new model even when it contains correlations in the model whose values have been designated as fixed, bound or singular. If FALSE and the new model contains correlations whose values

	have not been able to be estimated, the supplied <code>asrtests.obj</code> is returned. The fit in the <code>asreml.obj</code> component of the supplied <code>asrtests.obj</code> will also be tested and a warning issued if both fixed correlations are found in it and <code>allow.fixedcorrelation</code> is FALSE.
<code>checkboundaryonly</code>	If TRUE then boundary and singular terms are not removed by <code>rmboundary.asrtests</code> ; a warning is issued instead.
<code>update</code>	If TRUE then <code>update.asreml</code> is called to fit the model to be tested. In doing this the arguments <code>R.param</code> and <code>G.param</code> are set to those in the <code>asreml</code> object stored in <code>asrtests.obj</code> so that the values from the previous model are used as starting values. If FALSE then a call is made to <code>asreml</code> in which the only changes from the previous call are that (i) models are modified as specified and (ii) modifications specified via <code>...</code> are made.
<code>which.IC</code>	A character specifying the information criterion to be used in selecting the best model. Possible values are AIC and BIC. The values of the criterion for supplied model must exceed that for changed model for the changed model to be returned.
<code>IClikelihood</code>	A character specifying whether Restricted Maximum Likelihood (REML) or the full likelihood ( <code>full</code> ) are to be used in calculating the information criteria.
<code>...</code>	Further arguments passed to <code>changeModelOnIC.asrtests</code> , <code>asreml</code> and <code>tpsmmb</code> .

## Details

A fitted spatial model is only returned if it improves the fit over and above that of achieved with the model fit supplied in the `asrtests.obj`. To fit the spatial model without any hypotheses testing or comparison of information criteria use `addSpatialModel.asrtests`. The model fit supplied in the `asrtests.obj` should not include terms that will be included in the local spatial model. All spatial model terms are fitted as fixed or random. Consequently, the residual model does not have to be iid.

For the corr spatial model, an exponential model (`exp`) is used for each dimension to model the spatial correlation. A series of models are tried, beginning with the addition of row correlation and followed by the addition of column correlation. Only if the model fit is improved is a correlation retained. Finally, if any correlation is retained, the improvement to the fit of a nugget term is assessed. In this model, the correlation between observations from different rows is the correlation between observations in adjacent rows raised to the power equal to the absolute value of the difference in their `row.covar` values; similarly for the correlation in the column dimension.

The TPNCSS spatial model is as described by Verbyla et al. (2018) and the TPPS model is as described by Rodriguez-Alvarez et al. (2018). However, for the TPPS model, the degree of the polynomial and the order of differencing can be varied. The defaults of 3 and 2, respectively, fit a cubic spline with second order differencing, while setting both the degree and order of differencing to 1 will fit a type of linear variance model (Piepho, Boer and Williams, 2022). The fixed terms for these models are `row.covar + col.covar + row.covar:col.covar` and the random terms are `spl(row.covar) + spl(col.covar) + dev(row.covar) + dev(col.covar) + spl(row.covar):col.covar + row.covar:spl(col.covar) + spl(row.covar):spl(col.covar)`. The supplied model should not include any of these terms. However, any fixed or random main-effect term for either `row.factor` or `col.factor` will be removed from the fit.

The TPPS model is fitted using the function `tpsmmb` from the R package `TPSbits` authored by Sue Welham (2022). There are two methods for supplying the spline basis information produced by `tpsmmb` to `asreml`. The `grp` method adds it to the `data.frame` holding the information for the analysis. The `mbf` method requires the spline basis information to be in the same environment as the function that is called to make a fit using `asreml`. To this end and prior to invoking the calling function, `makeTPPSplineMats.data.frame` must be used to produce the `data.frames`.

All models utilize the function `changeModelOnIC.asrtests` to assess the model fit, the information criteria used in assessing the fit being calculated using `infoCriteria`. Arguments from `tpsmmb` and `changeModelOnIC.asrtests` can be supplied in calls to `addSpatialModelOnIC.asrtests` and will be passed on to the relevant function through the ellipses argument (...).

The data for experiment can be divided sections and the same spatial model fitted separately to each. The fit over all of the sections is assessed.

Each combination of a row.coords and a col.coords does not have to specify a single observation; for example, to fit a local spatial model to the main units of a split-unit design, each combination would correspond to a main unit and all subunits of the main unit would have the same combination.

### Value

An `asrtests.object` containing the components (i) `asreml.obj`, (ii) `wald.tab`, and (iii) `test.summary` for the model whose fit has the smallest information criterion between the supplied and spatial model. The values of the degrees of freedom and the information criteria in the `test.summary` are differences between those of the changed model and those of the model supplied to `addSpatialModelOnIC`.

### Author(s)

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### References

- Piepho, H.-P., Boer, M. P., & Williams, E. R. (2022). Two-dimensional P-spline smoothing for spatial analysis of plant breeding trials. *Biometrical Journal*, **64**, 835-857.
- Rodriguez-Alvarez, M. X., Boer, M. P., van Eeuwijk, F. A., & Eilers, P. H. C. (2018). Correcting for spatial heterogeneity in plant breeding experiments with P-splines. *Spatial Statistics*, **23**, 52-71.
- Verbyla, A. P., De Faveri, J., Wilkie, J. D., & Lewis, T. (2018). Tensor Cubic Smoothing Splines in Designed Experiments Requiring Residual Modelling. *Journal of Agricultural, Biological and Environmental Statistics*, **23**(4), 478-508.
- Welham, S. J. (2022) *TPSbits: Creates Structures to Enable Fitting and Examination of 2D Tensor-Product Splines using ASReML-R*. Version 1.0.0 <https://mmade.org/tpsbits/>

### See Also

`as.asrtests`, `rmboundary.asrtests`, `testtranfix.asrtests`, `testresidual.asrtests`, `newfit.asreml`, `reparamSigDevn.asrtests`, `addSpatialModel.asrtests`, `changeModelOnIC.asrtests`, `chooseSpatialModelOnIC.asrtests`, `changeModelOnIC.asrtests`, `infoCriteria.asreml`

### Examples

```
## Not run:

data(Wheat.dat)

#Add row and column covariates
Wheat.dat <- within(Wheat.dat,
  {
    cColumn <- dae::as.numfac(Column)
    cColumn <- cColumn - mean(unique(cColumn))
    cRow <- dae::as.numfac(Row)
```

```

        cRow <- cRow - mean(unique(cRow))
    })

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

#Create an asrtests object, removing boundary terms
current.asrt <- as.asrtests(current.asr, NULL, NULL,
                          label = "Random Row and Column effects")
current.asrt <- rmboundary(current.asrt)

current.asrt <- addSpatialModelOnIC(current.asrt, spatial.model = "TPPS",
                                   row.covar = "cRow", col.covar = "cColumn",
                                   row.factor = "Row", col.factor = "Column",
                                   asreml.option = "grp")

infoCriteria(current.asrt$asreml.obj)

## End(Not run)

```

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addto.test.summary	Adds a row to a test.summary data.frame.
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## Description

A row that summarizes the result of a proposed change to a model is added to a test.summary data.frame. Only the values of those arguments for which there are columns in test.summary will be included in the row.

## Usage

```

addto.test.summary(test.summary, terms, DF = 1, denDF = NA,
                  p = NA, AIC = NA, BIC = NA,
                  action = "Boundary")

```

## Arguments

test.summary	A <a href="#">data.frame</a> whose columns are a subset of terms, DF, denDF, p, AIC, BIC and action. Each row summarizes the results of proposed changes to the fitted model. See <a href="#">asrtests.object</a> for more information.
terms	A <a href="#">character</a> giving the name of a term that might be added to or removed from the model or a label indicating a change that might be made to the model.
DF	A <a href="#">numeric</a> giving the numerator degrees of freedom for a Wald F-statistic or the number of variance parameters in the current model minus the number in the proposed model.
denDF	A <a href="#">numeric</a> giving the denominator degrees of freedom for a Wald F-statistic.
p	A <a href="#">numeric</a> giving the p-value for a Wald F-statistic or REML ratio test.
AIC	A <a href="#">numeric</a> giving Akaike Information Criterion (AIC) for a model or the difference between the AIC values for the current and proposed models.

BIC A [numeric](#) giving Bayesian (Schwarz) Information Criterion for a model or the difference between the AIC values for the current and proposed models.

action A [character](#) giving what action was taken with respect to the proposed change. See [asrtests.object](#) for more information.

### Value

A [data.frame](#).

### Author(s)

Chris Brien

### See Also

[asremlPlus-package](#), [asrtests.object](#), [print.test.summary](#)

### Examples

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

## Fit an autocorrelation model
ar1.asr <- asreml(yield ~ Rep + WithinColPairs + Variety,
  random = ~ Row + Column + units,
  residual = ~ ar1(Row):ar1(Column),
  data=Wheat.dat)
ar1.asrt <- as.asrtests(ar1.asr, NULL, NULL,
  label = "Autocorrelation model")
ar1.asrt <- rmboundary.asrtests(ar1.asrt)

## Fit a tensor spline
Wheat.dat <- within(Wheat.dat,
  {
    cRow <- dae::as.numfac(Row)
    cRow <- cRow - mean(unique(cRow))
    cColumn <- dae::as.numfac(Column)
    cColumn <- cColumn - mean(unique(cColumn))
  })
ts.asr <- asreml(yield ~ Rep + cRow + cColumn + WithinColPairs +
  Variety,
  random = ~ spl(cRow) + spl(cColumn) +
    dev(cRow) + dev(cColumn) +
    spl(cRow):cColumn + cRow:spl(cColumn) +
    spl(cRow):spl(cColumn),
  residual = ~ Row:Column,
  data=Wheat.dat)
ts.asrt <- as.asrtests(ts.asr, NULL, NULL,
  label = "Tensor spline model")
ts.asrt <- rmboundary.asrtests(ts.asrt)
ar1.ic <- infoCriteria(ar1.asrt$asreml.obj)
ts.ic <- infoCriteria(ts.asrt$asreml.obj)
if (ar1.ic$AIC < ts.ic$AIC)
{
  ic.diff <- ar1.ic - ts.ic
  new.asrt <- ar1.asrt
}
```

```

new.asrt$test.summary <- addto.test.summary(ar1.asrt$test.summary,
                                           terms = "Compare ar1 to ts",
                                           DF = ic.diff$varDF,
                                           AIC = ic.diff$AIC, BIC = ic.diff$BIC,
                                           action = "Chose ar1")
} else
{
  ic.diff <- ts.ic - ar1.ic
  new.asrt <- ts.asrt
  new.asrt$test.summary <- addto.test.summary(ts.asrt$test.summary,
                                              terms = "Compare ar1 to ts",
                                              DF = ic.diff$varDF,
                                              AIC = ic.diff$AIC, BIC = ic.diff$BIC,
                                              action = "Chose ts")
}

## End(Not run)

```

---

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, maximum and accuracy of LSD values. Predictions that are aliased (or non-estimable) 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-distribution is also used in calculating the LSD statistics stored in the `LSD` component of the `alldiffs.object`.

## Usage

```

## S3 method for class 'data.frame'
allDifferences(predictions, classify, vcov = NULL,
               differences = NULL, p.differences = NULL, sed = NULL,
               LSD = NULL, LSDtype = "overall", LSDsupplied = NULL,

```

```

LSDby = NULL, LSDstatistic = "mean",
LSDaccuracy = "maxAbsDeviation",
retain.zeroLSDs = FALSE,
zero.tolerance = .Machine$double.eps ^ 0.5,
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,
transform.function = "identity",
inestimable.rm = TRUE,
sortFactor = NULL, sortParallelToCombo = NULL,
sortNestingFactor = NULL, sortOrder = NULL,
decreasing = FALSE, ...)

```

### Arguments

predictions	A <a href="#">predictions.frame</a> , 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	An <a href="#">LSD.frame</a> containing the mean, minimum and maximum LSD for determining the significance of pairwise differences, as well as an assigned LSD and a measure of the accuracy of the LSD. If LSD is NULL then the <a href="#">LSD.frame</a> stored in the LSD component will be calculated and the values of LSDtype, LSDby and LSDstatistic added as attributes of the <a href="#">alldiffs.object</a> . 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.



LSDtype	<p>A <a href="#">character</a> string that can be overall, factor.combinations, per.prediction or supplied. It determines whether the values stored in a row of a <a href="#">LSD.frame</a> are the values calculated (i) overall from the LSD values for all pairwise comparison2, (ii) the values calculated from the pairwise LSDs for the levels of each factor.combination, unless there is only one prediction for a level of the factor.combination, when a notional LSD is calculated, (iii) per.prediction, being based, for each prediction, on all pairwise differences involving that prediction, or (iv) as supplied values of the LSD, specified with the LSDsupplied argument; these supplied values are to be placed in the assignedLSD column of the <a href="#">LSD.frame</a> stored in an <a href="#">alldiffs.object</a> so that they can be used in LSD calculations.</p> <p>See <a href="#">LSD.frame</a> for further information on the values in a row of this data.frame and how they are calculated.</p>
LSDsupplied	<p>A <a href="#">data.frame</a> or a named <a href="#">numeric</a> containing a set of LSD values that correspond to the observed combinations of the values of the LSDby variables in the <a href="#">predictions.frame</a> or a single LSD value that is an overall LSD. If a <a href="#">data.frame</a>, it may have (i) a column for the LSDby variable and a column of LSD values or (ii) a single column of LSD values with rownames being the combinations of the observed values of the LSDby variables. Any name can be used for the column of LSD values; assignedLSD is sensible, but not obligatory. Otherwise, a <a href="#">numeric</a> containing the LSD values, each of which is named for the observed combination of the values of the LSDby variables to which it corresponds. (Applying the function <code>dac::fac.combine</code> to the predictions component is one way of forming the required combinations for the (row) names.) The values supplied will be incorporated into assignedLSD column of the <a href="#">LSD.frame</a> stored as the LSD component of the <a href="#">alldiffs.object</a>.</p>
LSDby	<p>A <a href="#">character</a> (vector) of variables names, being the names of the <a href="#">factors</a> or <a href="#">numerics</a> in the <a href="#">classify</a>; for each combination of their levels and values, there will be or is a row in the <a href="#">LSD.frame</a> stored in the LSD component of the <a href="#">alldiffs.object</a> when LSDtype is factor.combinations.</p>
LSDstatistic	<p>A <a href="#">character</a> nominating one or more of minnum, q10, q25, mean, median, q75, q90 or maximum as the value(s) to be stored in the assignedLSD column in an <a href="#">LSD.frame</a>; the values in the assignedLSD column are used in computing halfLeastSignificant error.intervals. Here q10, q25, q75 and q90 indicate the sample quantiles corresponding to probabilities of 0.1, 0.25, 0.75 and 0.9 for the group of LSDs from which a single LSD value is calculated. The function <a href="#">quantile</a> is used to obtain them. The mean LSD is calculated as the square root of the mean of the squares of the LSDs for the group. The median is calculated using the <a href="#">median</a> function. Multiple values are only produced for LSDtype set to factor.combination, in which case LSDby must not be NULL and the number of values must equal the number of observed combinations of the values of the variables specified by LSDby. If LSDstatistic is NULL, it is reset to mean.</p>
LSDaccuracy	<p>A <a href="#">character</a> nominating one of maxAbsDeviation, maxDeviation, q90Deviation or RootMeanSqDeviation as the statistic to be calculated as a measure of the accuracy of assignedLSD. The option q90Deviation produces the sample quantile corresponding to a probability of 0.90. The deviations are the differences between the LSDs used in calculating the LSD statistics and each assigned LSD and the accuracy is expressed as a proportion of the assigned LSD value. The calculated values are stored in the column named accuracyLSD in an <a href="#">LSD.frame</a>.</p>
retain.zeroLSDs	<p>A <a href="#">logical</a> indicating whether to retain or omit LSDs that are zero when calcu-</p>

	lating the summaries of LSDs.
zero.tolerance	A <b>numeric</b> specifying the value such that if an LSD is less than it, it will be considered to be zero.
backtransforms	A <code>data.frame</code> containing the backtransformed values of the predicted values that is consistent with the predictions component, except that the column named <code>predicted.value</code> is replaced by one called <code>backtransformed.predictions</code> . Any <code>error.interval</code> 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 <code>alldiffs.object</code> .
response.title	A character specifying the title for the response variable for the predictions. It is stored as an attribute to the <code>alldiffs.object</code> .
term	A <b>character</b> string giving the variables that define the term that was fitted using <code>asreml</code> and that corresponds to <code>classify</code> . It only needs to be specified when it is different to <code>classify</code> ; it is stored as an attribute of the <code>alldiffs.object</code> . It is likely to be needed when the fitted model includes terms that involve both a <b>numeric</b> covariate and a <b>factor</b> that parallel each other; the <code>classify</code> would include the covariate and the term would include the factor.
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 <code>alldiffs.object</code> .
x.num	A character string giving the name of the numeric covariate that corresponds to <code>x.fac</code> , 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 <code>x.fac</code> .
x.fac	A character string giving the name of the factor that corresponds to <code>x.num</code> , 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 <code>x.num</code> . The levels of <code>x.fac</code> must be in the order in which they are to be plotted - if they are dates, then they should be in the form <code>yyyymmdd</code> , which can be achieved using <code>as.Date</code> . However, the levels can be non-numeric in nature, provided that <code>x.num</code> is also set.
level.length	The maximum number of characters from 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 <code>FALSE</code> , the components <code>differences</code> and <code>p.differences</code> will be <code>NULL</code> in the returned <code>alldiffs.object</code> .
alpha	A <b>numeric</b> giving the significance level for LSDs or one minus the confidence level for confidence intervals. It is stored as an attribute to the <code>alldiffs.object</code> .
transform.power	A <b>numeric</b> 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 <code>transform.power</code> , unless it equals 0 in which case the exponential of the predictions is taken.

offset	A <b>numeric</b> that has been added to each value of the response after any scaling and before applying any power transformation.
scale	A <b>numeric</b> by which each value of the response has been multiplied before adding any offset and applying any power transformation.
transform.function	A <b>character</b> giving the name of a function that specifies the scale on which the predicted values are defined. This may be the result of a transformation of the data using the function or the use of the function as a link function in the fitting of a generalized linear (mixed) model (GL(M)M). The possible transform.functions are identity, log, inverse, sqrt, logit, probit, and cloglog. The predicted.values and error.intervals, if not StandardError intervals, will be back-transformed using the inverse function of the transform.function. The standard.error column will be set to NA, unless (i) asreml returns columns named transformed.value and approx.se, as well as those called predicted.values and standard.error (such as when a GLM is fitted) and (ii) the values in transformed.value are equal to those obtained by backtransforming the predicted.values using the inverse function of the transform.function. Then, the approx.se values will be saved in the standard.error column of the backtransforms component of the returned alldiffs.obj. Also, the transformed.value and approx.se columns are removed from both the predictions and backtransforms components of the alldiffs.obj. Note that the values that end up in the standard errors column are approximate for the backtransformed values and are not used in calculating error.intervals.
inestimable.rm	A logical indicating whether rows for predictions that are not estimable are to be removed from the components of the <b>alldiffs.object</b> .
sortFactor	A <b>character</b> 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 sortParallelToCombo 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 classify variables, excluding the sortFactor factor. The order to use is determined by either sortParallelToCombo or sortOrder.
sortParallelToCombo	A <b>list</b> that specifies a combination of the values of the factors and numerics, excluding sortFactor, that are in classify. Each of the components of the supplied <b>list</b> is named for a classify variable and specifies a single value for it. 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. Each of the other combinations of the values of the factors and numerics will be sorted in parallel. If sortParallelToCombo is NULL then the first value of each classify variable, except for the sortFactor factor, in the predictions component is used to define sortParallelToCombo. If there is only one variable in the classify then sortParallelToCombo is ignored.
sortNestingFactor	A <b>character</b> containing the name of the factor that defines groups of the sortFactor within which the predicted values are to be ordered. If there is only one variable in the classify then sortNestingFactor is ignored.

sortOrder	<p>A character vector whose length is the same as the number of levels for sortFactor in the predictions component of the <code>alldiffs.object</code>. It specifies the desired order of the levels in the reordered components of the <code>alldiffs.object</code>. The argument <code>sortParallelToCombo</code> is ignored.</p> <p>The following creates a <code>sortOrder</code> vector <code>levs</code> for factor <code>f</code> based on the values in <code>x</code>:</p> <pre>levs &lt;- levels(f)[order(x)].</pre>
decreasing	A logical passed to <code>order</code> that determines whether the order for sorting the components of the <code>alldiffs.object</code> is for increasing or decreasing magnitude of the predicted values.
...	provision for passing 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`, `alpha`, `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`, `pickLSDstatistics.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 emmeans 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 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`, `alpha`, `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. `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`.
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`: An `LSD.frame` containing (i) `c`, the number of pairwise predictions comparisons for each LSD value and the mean, minimum, maximum and assigned LSD, (ii) the column `accuracyLSD` that gives a measure of the accuracy of the assigned LSD, given the variation in LSD values, and (iii) the columns `false.pos` and `false.neg` that contain the number of false positives and negatives if the assignedLSD value(s) is(are) used to determine the significance of the pairwise predictions differences. The LSD values in the `assignedLSD` column is used to determine the significance of pairwise differences that involve predictions for the combination of levels given by a row name. The value in the `assignedLSD` column is specified using the `LSDstatistic` argument.

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 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 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. `alpha`: An integer specifying the significance level. It is used as the significance level calculating LSDs.
7. `LSDtype`: If the LSD component is not NULL then `LSDtype` is added as an attribute. A character nominating the type of grouping of seds to be used in combining LSDs.
8. `LSDby`: If the LSD component is not NULL then `LSDby` is added as an attribute. A character vector containing the names of the factors and numerics within whose combinations the LSDs are to be summarized.
9. `LSDstatistic`: If the LSD component is not NULL then `LSDstatistic` is added as an attribute. A character nominating what statistic to use in summarizing a set of LSDs.
10. `LSDaccuracy`: If the LSD component is not NULL then `LSDaccuracy` is added as an attribute. A character nominating the method of calculating a measure of the accuracy of the LSDs stored in the `assignedLSD` column of the `LSD.frame`.
11. `sortFactor`: factor that indexes the set of predicted values that determined the sorting of the components.
12. `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 emmeans 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 alldiffs 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  $\sin^{-1}(\sqrt{\text{proportions}})$



**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	<i>Applies the modified angular transformation to a vector of counts.</i>
-------------	---

---

**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  $\sin^{-1} \frac{\text{count} + 0.375}{n + 0.75} \arcsin(\sqrt{(\text{count} + 0.375) / (n + 0.75)})$ .

**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, tdf, alpha, 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, alpha = 0.05,
             sortFactor = NULL, sortOrder = NULL)
```

**Arguments**

- |             |   |
|-------------|---|
| predictions | A <a href="#">predictions.frame</a> , 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	An <code>LSD.frame</code> containing the mean, minimum and maximum LSD for determining the significance of pairwise differences, as well as an assigned LSD and a measure of the accuracy of the LSD. If LSD is NULL then the <code>LSD.frame</code> stored in the LSD component will be calculated and the values of <code>LSDtype</code> , <code>LSDby</code> and <code>LSDstatistic</code> added as attributes of the <code>alldiffs.object</code> . 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 <code>data.frame</code> containing the backtransformed values of the predicted values that is consistent with the predictions component, except that the column named <code>predicted.value</code> is replaced by one called <code>backtransformed.predictions</code> . Any <code>error.interval</code> 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 <code>alldiffs.object</code> .
response.title	A character specifying the title for the response variable for the predictions. It is stored as an attribute to the <code>alldiffs.object</code> .
term	A <code>character</code> string giving the variables that define the term that was fitted using <code>asreml</code> and that corresponds to <code>classify</code> . It only needs to be specified when it is different to <code>classify</code> ; it is stored as an attribute of the <code>alldiffs.object</code> . It is likely to be needed when the fitted model includes terms that involve both a <code>numeric</code> covariate and a <code>factor</code> that parallel each other; the <code>classify</code> would include the covariate and the term would include the factor.
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 <code>:</code> operator. It is stored as an attribute to the <code>alldiffs.object</code> .
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 <code>alldiffs.object</code> .
alpha	A <code>numeric</code> giving the significance level for LSDs or one minus the confidence level for confidence intervals. It is stored as an attribute to the <code>alldiffs.object</code> .
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 <code>sortFactor</code> in the predictions component of the <code>alldiffs.object</code> . It specifies the order of the levels in the reordered components of the <code>alldiffs.object</code> . The following creates a <code>sortOrder</code> vector <code>levs</code> for factor <code>f</code> based on the values in <code>x</code> : <code>levs &lt;- levels(f)[order(x)]</code> .

**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 emmeans 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	<i>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 hypothesis testing used in obtaining the model.</i>
-------------	--

---

## 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 `recalcWaldTab` arguments supplied via ...

The `label` argument can be used to include an entry in `test.summary` for the starting model. If a label is included, (i) the information criteria calculated using the `asreml.obj` will be added to the `test.summary`, if `IClikelihood` is not set to none and (ii) the number of variance parameters is included in the `denDF` column, if `IClikelihood` is set to none.

## Usage

```

as.asrtests(asreml.obj, wald.tab = NULL, test.summary = NULL,
            denDF = "numeric", label = NULL,
            IClikelihood = "none", bound.exclusions = c("F", "B", "S", "C"), ...)

```

## 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 <code>wald.asreml</code> ; it should have 4 or 6 columns. Sometimes <code>wald.asreml</code> returns a data.frame and at other times a list. For example, it may return a list when <code>denDF</code> 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, <code>wald.asreml</code> has a <code>kenadj</code> argument.
test.summary	A data.frame with columns <code>term</code> , <code>DF</code> , <code>denDF</code> , <code>p</code> and <code>action</code> containing the results of previous hypothesis tests.
denDF	Specifies the method to use in computing approximate denominator degrees of freedom when <code>wald.asreml</code> is called. Can be none to suppress the computations, numeric for numerical methods, algebraic for algebraic methods or default, the default, to automatically 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.

label	A character to use as an entry in the terms column in <code>test.summary</code> to indicate as far as is possible the nature of the model that has been fitted. The action column in <code>test.summary</code> will be Starting model.
IClikelihood	A character that controls both the occurrence and the type of likelihood for information criterion in the <code>test.summary</code> of the new <code>asrtests.object</code> . If none, none are included. Otherwise, if REML, then the AIC and BIC based on the Restricted Maximum Likelihood are included; if full, then the AIC and BIC based on the full likelihood are included. (See also <code>infoCriteria.asreml</code> .)
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 in calculating information criteria. If set to NULL then none will be excluded.
...	further arguments passed to <code>wald.asreml</code> and <code>recalcWaldTab</code> .

**Value**

An object of S3-class `asrtests`.

**Author(s)**

Chris Brien

**References**

Kenward, M. G., & Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics*, **53**, 983-997.

**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, classify = NULL,
                     predictions = NULL, se = NULL, est.status = NULL,
                     interval.type = NULL, interval.names = NULL)
```

## Arguments

data	A <code>data.frame</code> 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).
classify	A <code>character</code> 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 <code>:</code> operator. For predicting the overall mean, the classify is set to "(Intercept)".
predictions	A <code>character</code> giving the name of the column in data that contains the predicted values. This column will be renamed to predicted.value.
se	A <code>character</code> 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 <code>character</code> 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 <code>character</code> 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 <code>character</code> 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](#), [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$predictions
#Form predictions.frame changing asreml-R4 names to the standard names, if these are present
Var.preds <- as.predictions.frame(Var.pred$pvals, se = "std.error",
                                  est.status = "status")

## End(Not run)

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

## Usage

```

addrm.terms.asreml(...)
addrm.terms.asrtests(...)
alldiffs(...)
asrtests(...)
choose.model.asreml(...)
choose.model.asrtests(...)
facRecode(...)
facRecode.alldiffs(...)
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	<i>Description of an asrtests object</i>
-----------------	--

---

## 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 correspond 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 `terms`, `DF`, `denDF`, `p`, `AIC`, `BIC` and `action`, each row of which summarizes the results of proposed changes to the fitted model.  
Possible codes for `action` are: `Dropped`, `Retained`, `Swapped`, `Unswapped`, `Unchanged`, `Significant`, `Nonsignificant`, `Absent`, `Added`, `Removed` and `Boundary`. If the either of the models did not converge, `unconverged` will be added to the code. `Unchanged` is used when `allow.unconverged` is `FALSE`. Note that the logical `asreml.obj$converge` also reflects whether there is convergence.  
A row is added to the `test.summary` for each term that is dropped, added or tested or a note that several terms have been added or removed. When values for the `AIC` and `BIC` are included in the row, then the `DF` are the number of fixed parameters in the model and `denDF` are the numbers of variance parameters. When `changeModelOnIC` adds a row then the values of the degrees of freedom and information criteria are differences between those for the model that is supplied and the model changed by `changeModelOnIC`.

## Author(s)

Chris Brien

## See Also

`as.asrtests`, `as.asrtests`, `validAsrtests`

---

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

## 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

<code>h0.asreml.obj</code>	<code>asreml</code> object containing the fit under the model for the null hypothesis.
<code>h1.asreml.obj</code>	<code>asreml</code> object containing the fit under the model for the alternative hypothesis.
<code>nboot</code>	The number of bootstrap samples to be generated.
<code>max.retries</code>	The maximum number of attempts to generate a sample whose analyses converge for both models.
<code>seed</code>	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 <code>nextRNGStream</code> is used to seed each core from the original seed.
<code>means</code>	The vector of means to be used in generating simulated bootstrap samples. If it is <code>NULL</code> , the fitted values based on object are used. It must be the same length as the response variable for object.
<code>V</code>	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 <code>NULL</code> , <a href="#">estimateV.asreml</a> is used to estimate the variance matrix for the observations from the variance parameter estimates from the <code>reduced.asreml.obj</code> .

<code>extra.matrix</code>	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 <code>asreml.obj</code> . It is assumed that the sigma-parameterized values of the variance parameter estimates, such as is given in the <code>varcomp</code> component of <code>summary.asreml</code> , have been used in calculating <code>extra.matrix</code> ; the values in the <code>vparameters</code> component of <code>G.param</code> and <code>R.param</code> may be either gamma- or sigma-parameterized. The argument <code>extra.matrix</code> can be used in conjunction with <code>ignore.terms</code> as a workaround to include components of the variance matrix for variance functions that have not been implemented in <code>estimateV</code> .
<code>ignore.terms</code>	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 <code>vparameters</code> component of the <code>asreml</code> object or the <code>varcomp</code> component produced by <code>summary.asreml</code> , but only up to the first exclamation mark (!). This can be used in conjunction with <code>estimateV.asreml</code> as a workaround to include components of the variance matrix for variance functions that have not been implemented in <code>estimateV</code> .
<code>fixed.spline.terms</code>	A character vector giving one or more 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 <code>vparameters</code> component of the <code>asreml</code> object or the <code>varcomp</code> component produced by <code>summary.asreml</code> , but only up to the first exclamation mark (!).
<code>bound.exclusions</code>	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.
<code>tolerance</code>	The value such that eigenvalues less than it are considered to be zero.
<code>update</code>	If TRUE then the arguments <code>R.param</code> and <code>G.param</code> are set to those in the <code>asreml</code> object supplied in <code>object</code> so that the values from the original model are used as starting values. If FALSE then calls are made to <code>asreml</code> in which the only changes from the previous call are (i) the model is fitted to simulated data and (ii) modifications specified via <code>...</code> are made, except that changes cannot be made to any of the models.
<code>trace</code>	If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.
<code>ncores</code>	A numeric specifying the number of cores to use in doing the simulations.
<code>...</code>	Other arguments that are passed down to the function <code>asreml</code> . 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 bootstrap sample, the maximum being `max.retries`.

### Note

A bootstrap 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)
```

---

changeModelOnIC.asrtests

*Uses information criteria to decide whether to change an already fitted model.*

---

## Description

Uses information criteria to decide whether to change the fitted model stored in the supplied `asrtests.object` according to the specified modifications. The function `changeTerms` is used to change the model. Thus, the model can be modified using a combination of adding and removing sets of terms from one or both of the fixed or random models and replacing the residual model. The model will be unchanged if terms specified in `dropFixed` or `dropRandom` are not in the fitted model.

A row is added to the `test.summary` data.frame of the `asrtests.object` using the supplied label and stating whether or not the new model has been swapped for the supplied model. 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 to exhibit the differences between the supplied and new model.

To obtain a list of the information criteria for a set of models use `changeTerms.asrtests` with `IClikelihood` set to `REML` or `full`, or use `infoCriteria.asreml`.

## Usage

```
## S3 method for class 'asrtests'
changeModelOnIC(asrtests.obj,
                dropFixed = NULL, addFixed = NULL,
                dropRandom = NULL, addRandom = NULL,
                newResidual = NULL, label = "Changed terms",
                allow.unconverged = TRUE, allow.fixedcorrelation = TRUE,
                checkboundaryonly = FALSE,
                trace = FALSE, update = TRUE, denDF = "numeric",
                set.terms = NULL, ignore.suffices = TRUE,
                bounds = "P", initial.values = NA,
                which.IC = "AIC", IClikelihood = "REML",
                fixedDF = NULL, varDF = NULL,
                bound.exclusions = c("F", "B", "S", "C"),
                ...)
```

## Arguments

<code>asrtests.obj</code>	An <code>asrtests.object</code> containing the components (i) <code>asreml.obj</code> , (ii) <code>wald.tab</code> , and (iii) <code>test.summary</code> .
<code>dropFixed</code>	A single character string in the form of a formula which, after addition of <code>" ~ . -"</code> and after expansion, specifies the sum of a set of terms to be dropped from the fixed formula. The names must match those in the <code>wald.tab</code> component of the <code>asrtests.obj</code> . The fixed terms will be reordered so that single-variable terms come first, followed by two-variable terms and so on. Note that multiple terms specified using a single <code>asreml::at</code> function can only be dropped as a whole. If the term was specified using an <code>asreml::at</code> function with a single level, then it can be removed and either the level itself or its <code>numeric</code> position in the levels returned by the <code>levels</code> function can be specified.
<code>addFixed</code>	A single character string in the form of a formula which, after addition of <code>" ~ . +"</code> and expansion, specifies the sum of a set of terms to be added to the fixed formula. The fixed terms will be reordered so that single-variable terms come first, followed by two-variable terms and so on.
<code>dropRandom</code>	A single character string in the form of a formula which, after addition of <code>" ~ . -"</code> and expansion, specifies the sum of a set of terms to be dropped from the random formula. The names must match those in the <code>vparameters</code> component

	of the <code>asreml.obj</code> component in the <code>asrtests.obj</code> . Note that multiple terms specified using a single <code>asreml::at</code> function can only be dropped as a whole. If the term was specified using an <code>asreml::at</code> function with a single level, then it can be removed and either the level itself or its <code>numeric</code> position in the levels returned by the <code>levels</code> function can be specified.
<code>addRandom</code>	A single character string in the form of a formula which, after addition of " <code>~</code> " and expansion, specifies the sum of a set of terms to be added to the random formula.
<code>newResidual</code>	A single character string in the form of a formula which, after addition of " <code>~</code> ", specifies the residual (or <code>rcov</code> ) model. To remove the model, enter " <code>-(.)</code> ".
<code>label</code>	A character to use as an entry in the terms column in <code>test.summary</code> to indicate as far as is possible the terms that are being manipulated.
<code>allow.unconverged</code>	A logical indicating whether to accept a new model even when it does not converge. If <code>FALSE</code> and the fit of the new model does not converge, the supplied <code>asrtests.obj</code> is returned. Also, if <code>FALSE</code> and the fit of the new model has converged, but that of the old model has not, the new model will be accepted.
<code>allow.fixedcorrelation</code>	A logical indicating whether to accept a new model even when it contains correlations in the model whose values have been designated as fixed, bound or singular. If <code>FALSE</code> and the new model contains correlations whose values have not been able to be estimated, the supplied <code>asrtests.obj</code> is returned. The fit in the <code>asreml.obj</code> component of the supplied <code>asrtests.obj</code> will also be tested and a warning issued if both fixed correlations are found in it and <code>allow.fixedcorrelation</code> is <code>FALSE</code> .
<code>checkboundaryonly</code>	If <code>TRUE</code> then boundary and singular terms are not removed by <code>rmboundary.asrtests</code> ; a warning is issued instead.
<code>trace</code>	If <code>TRUE</code> then partial iteration details are displayed when <code>ASReml-R</code> functions are invoked; if <code>FALSE</code> then no output is displayed.
<code>update</code>	If <code>TRUE</code> then <code>update.asreml</code> is called to fit the model to be tested. In doing this the arguments <code>R.param</code> and <code>G.param</code> are set to those in the <code>asreml</code> object stored in <code>asrtests.obj</code> so that the values from the previous model are used as starting values. If <code>FALSE</code> then a call is made to <code>asreml</code> in which the only changes from the previous call are that (i) models are modified as specified and (ii) modifications specified via <code>...</code> are made.
<code>denDF</code>	Specifies the method to use in computing approximate denominator degrees of freedom when <code>wald.asreml</code> is called. Can be <code>none</code> to suppress the computations, <code>numeric</code> for numerical methods, <code>algebraic</code> for algebraic methods or <code>default</code> , the default, to automatically 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.
<code>set.terms</code>	A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting. The names must match those in the <code>vparameters</code> component of the <code>asreml.obj</code> component in the new <code>asrtests.object</code> .
<code>ignore.suffices</code>	A logical vector specifying whether the suffices of the <code>asreml</code> -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 <code>TRUE</code> 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 <a href="#">character</a> 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.
which.IC	A character specifying the information criterion to be used in selecting the best model. Possible values are AIC and BIC. The values of the criterion for supplied model must exceed that for changed model for the changed model to be returned.
IClikelihood	A character specifying whether Restricted Maximum Likelihood (REML) or the full likelihood (full) are to be used in calculating the information criteria for family set to asr_gaussian. For family set to asr_binomial or asr_poisson and with dispersion set to 1, the deviance is extracted from object and used to calculate the AIC and BIC (as suggested by Damian Collins); the setting of IClikelihood is ignored and the log-likelihood set to NA. The information criteria are not valid for other settings of family and dispersion.
fixedDF	A numeric giving the number of estimated fixed parameters. If NULL then this is determined from the information in asreml.obj.
varDF	A numeric giving the number of estimated variance parameters. If NULL then this is determined from the information in asreml.obj. It replaces the varDF argument.
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.
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 in calculating the information criteria. If set to NULL then none will be excluded.
...	Further arguments passed to asreml, wald.asreml and <a href="#">as.asrtests</a> .

**Value**

An [asrtests.object](#) containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary. The values of the degrees of freedom and the information criteria are differences between those of the changed model and those of the model supplied to changeModelOnIC.

**Author(s)**

Chris Brien

**See Also**

[as.asrtests](#), [rmboundary.asrtests](#), [testranfix.asrtests](#), [testresidual.asrtests](#), [newfit.asreml](#), [reparamSigDevn.asrtests](#), [chooseModel.asrtests](#), [changeTerms.asrtests](#), [infoCriteria.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,
                          label = "Maximal model")
current.asrt <- rmboundary(current.asrt)

# Drop both Row and Column terms
current.asrt <- changeModelOnIC(current.asrt,
                              dropRandom = "Row + Column",
                              checkboundaryonly = TRUE,
                              which.IC = "AIC", IClikelihood = "full")
current.asrt <- iterate(current.asrt)

# Add and drop both fixed and random terms
current.asrt <- changeModelOnIC(current.asrt,
                              addFixed = "vRow", dropFixed = "WithinColPairs",
                              addRandom = "spl(vRow)", dropRandom = "units",
                              checkboundaryonly = TRUE,
                              which.IC = "AIC", IClikelihood = "full")

# Replace residual with model without Row autocorrelation
current.asrt <- changeModelOnIC(current.asrt,
                              newResidual = "Row:ar1(Column)",
                              label="Row autocorrelation",
                              IClikelihood = "full")

## End(Not run)
```

---

changeTerms.asrtests	<i>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.</i>
----------------------	---

---

## 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 of the `asrtests.object` using the supplied label and stating which models have been changed. Information criteria can be included in the row of the `test.summary`. 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.

To only change the terms based on a comparison of information criteria use `changeModelOnIC.asrtests`.

## 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, allow.fixedcorrelation,
            checkboundaryonly = FALSE,
            trace = FALSE, update = TRUE, denDF = "numeric",
            set.terms = NULL, ignore.suffices = TRUE,
            bounds = "P", initial.values = NA,
            ICl likelihood = "none", bound.exclusions = c("F","B","S","C"),
            ...)
```

## Arguments

asrtests.obj	An <a href="#">asrtests.object</a> containing the components (i) <code>asreml.obj</code> , (ii) <code>wald.tab</code> , and (iii) <code>test.summary</code> .
dropFixed	A single character string in the form of a formula which, after addition of <code>" ~ . -"</code> and after expansion, specifies the sum of a set of terms to be dropped from the fixed formula. The names must match those in the <code>wald.tab</code> component of the <code>asrtests.obj</code> . The fixed terms will be reordered so that single-variable terms come first, followed by two-variable terms and so on. Note that multiple terms specified using a single <code>asreml::at</code> function can only be dropped as a whole. If the term was specified using an <code>asreml::at</code> function with a single level, then it can be removed and either the level itself or its <a href="#">numeric</a> position in the levels returned by the <a href="#">levels</a> function can be specified.
addFixed	A single character string in the form of a formula which, after addition of <code>" ~ . +"</code> and expansion, specifies the sum of a set of terms to be added to the fixed formula. The fixed terms will be reordered so that single-variable terms come first, followed by two-variable terms and so on.
dropRandom	A single character string in the form of a formula which, after addition of <code>" ~ . -"</code> and expansion, specifies the sum of a set of terms to be dropped from the random formula. The terms must match those in the <code>vparameters</code> component of the <code>asreml.obj</code> component in the <code>asrtests.obj</code> . Note that multiple terms specified using a single <code>asreml::at</code> function can only be dropped as a whole. If the term was specified using an <code>asreml::at</code> function with a single level, then it can be removed and either the level itself or its <a href="#">numeric</a> position in the levels returned by the <a href="#">levels</a> function can be specified.
addRandom	A single character string in the form of a formula which, after addition of <code>" ~ . +"</code> 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 <code>" ~ "</code> , specifies the residual (or <code>rcov</code> ) model. To remove the model, enter <code>"-(.)"</code> .
label	A character to use as an entry in the <code>terms</code> column in <code>test.summary</code> to indicate as far as is possible the terms that are being manipulated.
allow.unconverged	A logical indicating whether to accept a new model even when it does not converge. If <code>FALSE</code> and the fit does not converge, the supplied <code>asrtests.obj</code> is returned.

`allow.fixedcorrelation`

A logical indicating whether to accept a new model even when it contains correlations in the model whose values have been designated as fixed, bound or singular. If FALSE and the new model contains correlations whose values have not been able to be estimated, the supplied `asrtests.obj` is returned. The fit in the `asreml.obj` component of the supplied `asrtests.obj` will also be tested and a warning issued if both fixed correlations are found in it and `allow.fixedcorrelation` is FALSE.

`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 modified as specified and (ii) modifications specified via `...` are made.

`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 automatically 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. The names must match those in the `vparameters` component of the `asreml.obj` component in the `asrtests.object`.

`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.

`IClikelihood`

A character that controls both the occurrence and the type of likelihood for information criterion in the `test.summary` of the new `asrtests.object`. If none, none are included. Otherwise, if REML and family is set to `asr_gaussian` (the



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

---

ChickpeaEnd.dat	<i>A large data set comprising the end of imaging data from a chick pea experiment conducted in high-throughput greenhouses</i>
-----------------	---

---

## Description

The data collected after imaging had been completed on the 1056 plants in the experiment reported by Atieno et al. (2017). The design employed for the experiment was a split-plot design in which two consecutive carts formed a main plot. The split-plot design assigned 245 genotypes to main plots, the genotypes being unequally replicated 2 or 3 times. Treatments (non-saline, saline) were randomized to the two subplots (carts) within each main plot.

The columns in the `data.frame` are: `Smarthouse`, `Lane`, `Position`, `Zone`, `Mainplot`, `Subplot`, `Replicate`, `xLane`, `xPosition`, `Genotypes`, `Treatments`, `Biomass`, `PlantHeight`, `SenescenceRank`, `TotalPods`, `FilledPods`, `EmptyPods`, `SeedNo`, `TotalSeedWt`, `SeedWt100`.

The columns `Smarthouse`, `Lane` and `Position` uniquely identify the rows of observations. Zones are groups of 4 Lanes, Mainplots are the 44 pairs of consecutive Subplots within each Zone, and a Subplot is a cart containing a single plant. The columns `xLane` and `xPosition` are numeric covariates for location within a Smarthouse. Genotypes and Treatments indicate the genotype and treatment that each plant was allocated. The response variables are Biomass, PlantHeight, SenescenceRank, TotalPods, FilledPods, EmptyPods, SeedNo, TotalSeedWt and SeedWt100.

## Usage

```
data(ChickpeaEnd.dat)
```

## Format

A `data.frame` with 1056 rows by 20 columns.

## References

Atieno, J., Li, Y., Langridge, P., Dowling, K., Brien, C., Berger, B., Varshney, R. K., and Sutton, T. (2017). Exploring genetic variation for salinity tolerance in chickpea using image-based phenotyping. *Scientific Reports*, 7, 1300. doi:10.1038/s41598017012117

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chooseModel	<i>Determines the set of significant terms using p-values and records the tests performed in a <code>data.frame</code>, taking into account the marginality relations of terms.</i>
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## Description

Using p-values from hypothesis tests, determines the set of significant terms, taking into account the hierarchy or 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. The tests conducted in choosing selected model are listed in a summary `data.frame`.

**Usage**

```
chooseModel(object, ...)
```

**Arguments**

`object`            an object using which p-values can be obtained for use in model selection.

`...`            further arguments passed to or from other methods.

**Details**

`chooseModel` is the generic function for the `chooseModel` method. Use `methods("chooseModel")` to get all the methods for the `chooseModel` generic.

`chooseModel.asrtests` is a method for an `asrtests.object`. It uses `testranfix.asrtests` to conduct tests to determine the p-values used in the model selection.

`chooseModel.data.frame` is a method for a `data.frame`. It uses the p-values stored in the `data.frame` in the model selection.

**Author(s)**

Chris Brien

**See Also**

`chooseModel.asrtests`, `chooseModel.asrtests`, `changeModelOnIC.asrtests`, `testranfix.asrtests`

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<code>chooseModel.asrtests</code>	<i>Determines and records the set of significant terms using an <code>asrtests.object</code>, taking into account the hierarchy or marginality relations of the terms.</i>
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**Description**

Performs a series of hypothesis tests on a set of fixed and/or random terms 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.asrem1`. 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 that records the outcome of a test is added to `test.summary` for each term that is tested.

## Usage

```
## S3 method for class 'asrtests'
chooseModel(object, terms.marginality=NULL,
            alpha = 0.05, allow.unconverged = TRUE,
            allow.fixedcorrelation = 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,
            IClkelihood = "none", ...)
```

## Arguments

- |                        |  |
|------------------------|--|
| object                 | an <a href="#">asrtests.object</a> containing the components (i) <code>asreml.obj</code> , (ii) <code>wald.tab</code> , and (iii) <code>test.summary</code> .  |
| terms.marginality      | A square matrix of ones and zeros with row and column names being the names of the terms to be tested. The names of fixed terms must match those in the <code>wald.tab</code> component of the object, while the names of random terms must match those in the <code>vparameters</code> component of the <code>asreml.obj</code> component in the object. The diagonal elements of the matrix 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.  |
| allow.fixedcorrelation | A logical indicating whether to accept a new model even when it contains correlations in the model whose values have been designated as fixed, bound or singular. If FALSE and the new model contains correlations whose values have not been able to be estimated, the supplied <code>asrtests.obj</code> is returned. The fit in the <code>asreml.obj</code> component of the supplied <code>asrtests.obj</code> will also be tested and a warning issued if both fixed correlations are found in it and <code>allow.fixedcorrelation</code> is FALSE.             |
| checkboundaryonly      | If TRUE then boundary and singular terms are not removed by <a href="#">rmboundary.asrtests</a> ; 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 <code>bound.test.parameters</code> 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 <code>positive.zero</code> is TRUE then <code>bound.test.parameters</code>  |



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.

<code>drop.fix.ns</code>	A logical indicating whether to drop a fixed term from the model when it is nonsignificant
<code>denDF</code>	Specifies the method to use in computing approximate denominator degrees of freedom when <code>wald.asreml</code> is called. Can be none to suppress the computations, numeric for numerical methods, algebraic for algebraic methods or default, the default, to automatically 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.
<code>dDF.na</code>	The method to use to obtain substitute denominator degrees of freedom. when the numeric or algebraic methods produce an NA. If <code>dDF.na = "none"</code> , no substitute denominator degrees of freedom are employed; if <code>dDF.na = "residual"</code> , the residual degrees of freedom from <code>asreml.obj\$nedf</code> are used; if <code>dDF.na = "maximum"</code> , the maximum of those <code>denDF</code> that are available, excluding that for the Intercept, is used; if all <code>denDF</code> are NA, <code>asreml.obj\$nedf</code> is used. If <code>dDF.na = "supplied"</code> , a vector of values for the denominator degrees of freedom is to be supplied in <code>dDF.values</code> . 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.
<code>dDF.values</code>	A vector of values to be used when <code>dDF.na = "supplied"</code> . Its values will be used when <code>denDF</code> 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.
<code>trace</code>	If TRUE then partial iteration details are displayed when ASReml-R functions are invoked; if FALSE then no output is displayed.
<code>update</code>	If TRUE then <code>update.asreml</code> is called in testing models. In doing this the arguments <code>R.param</code> and <code>G.param</code> are set to those in the <code>asreml</code> object stored in object so that the values from the previous model are used as starting values. If FALSE then a call is made to <code>asreml</code> in which the only changes to the <code>asreml.obj</code> stored in the supplied object are (i) to the terms in the fixed and random models corresponding to terms in <code>terms.marginality</code> and (ii) those modifications specified via ....
<code>set.terms</code>	A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting. The names must match those in the <code>vparameters</code> component of the <code>asreml.obj</code> component in the new <a href="#">asrtests.object</a> .
<code>ignore.suffices</code>	A logical vector specifying whether the suffices of the <code>asreml</code> -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 <code>asreml</code> -assigned names. If FALSE for an element of terms, the element must exactly match an <code>asreml</code> -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 <code>asreml</code> -assigned suffices for all the terms in terms.

bounds	A <a href="#">character</a> vector specifying the bounds to be applied to the terms specified in <code>set.terms</code> . This vector must be of length one or the same length as <code>set.terms</code> . If it is of length one then the same constraint is applied to all the terms in <code>set.terms</code> . 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 <code>terms</code> . This vector must be of length one or the same length as <code>terms</code> . If it is of length one then the same initial value is applied to all the terms in <code>terms</code> . If any of the <code>initial.values</code> are equal to NA then they are left unchanged for those terms.
IClikelihood	A character that controls both the occurrence and the type of likelihood for information criterion in the <code>test.summary</code> of the new <a href="#">asrtests.object</a> . If none, none are included. Otherwise, if REML, then the AIC and BIC based on the Restricted Maximum Likelihood are included; if full, then the AIC and BIC based on the full likelihood are included. (See also <a href="#">infoCriteria.asreml</a> .)
...	further arguments passed to <code>asreml</code> , <code>wald.asreml</code> and <a href="#">as.asrtests</a> via <a href="#">testranfix.asrtests</a> .

### 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

### References

Kenward, M. G., & Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics*, **53**, 983-997.

### See Also

[chooseModel](#), [chooseModel.data.frame](#), [as.asrtests](#), [testranfix.asrtests](#), [testresidual.asrtests](#), [REMLRT.asreml](#), [rmboundary.asrtests](#), [newfit.asreml](#), [changeModelOnIC.asrtests](#), [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)

```

---

chooseModel.data.frame

*Determines the set of significant terms from results stored in a data.frame, taking into account the marginality relations of terms and recording the tests used in a [data.frame](#).*

---

## Description

Uses the p.values from a set of hypothesis tests that are stored in the supplied [data.frame](#) to choose a model to describe the effects of the terms corresponding to the p-values, taking into account the hierarchy or 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. The tests used in choosing the selected model are listed in the [data.frame](#) choose.summary.

No change is made to the p.values, the DF and denDF being for information only.

## Usage

```

## S3 method for class 'data.frame'
chooseModel(object, terms=NULL, p.values = "Pr",
            DF = "Df", denDF = "denDF", omit.DF = FALSE,
            terms.marginality=NULL, alpha = 0.05, ...)

```

## Arguments

object	a <a href="#">data.frame</a> object containing the results of hypothesis tests for a set of terms. It components should include terms, p.values, and, if not set to NA, DF and denDF.
terms	A character giving the name of the column in object containing the terms corresponding to the p.values. If NULL, it is assumed that the row names of object give the terms.
p.values	A character giving the name of the column in object containing the p-values to use in deciding whether or not terms are significant.
DF	Can be a character or a numeric that specifies the numerator degrees of freedom for the tests. If it is a character, it must be the name of a column in object containing the numerator degrees of freedom that are to be included in the choose.summary data.frame. if it is a numeric, its length must equal 1 or the number of rows in object. In either case, a column labelled DF will be included in the choose.summary data.frame. It will contain either the replicated single value (which can be NA) or the values supplied.

denDF	Can be a character or a numeric that specifies the denominator degrees of freedom for the tests. If it is a character, it must be the name of a column in object containing the denominator degrees of freedom that are to be included in the choose.summary data.frame. If it is a numeric, its length must equal 1 or the number of rows in object. In either case, a column labelled denDF will be included in the choose.summary data.frame. It will contain either the replicated single value (which can be NA) or the values supplied.
omit.DF	A logical indicating whether or not both the numerator and denominator degrees of freedom are to be omitted from choose.summary. Doing so will mean that the choose.summary no longer has the same columns as a test.summary from an <a href="#">asrtests.object</a> .
terms.marginality	A square matrix of ones and zeros with row and column names being the names of the those terms in the terms column of object that are to be tested. 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. The names of the rows and columns should match the those elements of terms that are to be tested.
alpha	The significance level for the hypothesis testing.
...	Provision for passing arguments to functions called internally - not used at present.

### Value

A list containing:

1. choose.summary: a [data.frame](#) summarizing the tests carried out in choosing the significant terms; provided omit.DF = FALSE, it has the same columns as a test.summary from an [asrtests.object](#)
2. sig.tests: a character vector whose elements are the the significant terms amongst those tested.

### Author(s)

Chris Brien

### See Also

[chooseModel](#), [chooseModel.asrtests](#)

### Examples

```
data("Ladybird.dat")

## Use asrem1 to get the table of p-values

## Not run:
m1.asr <- asrem1(logitP ~ Host*Cadavers*Ladybird,
                 random = ~ Run,
                 data = Ladybird.dat)
current.asrt <- as.asrtests(m1.asr)
fixed.tab <- current.asrt$wald.tab
col.p <- "Pr"
```

```

df = "Df"
den.df = "denDF"

## End(Not run)

## Use lmeTest to get the table of p-values
if (requireNamespace("lmerTest", quietly = TRUE) &
    requireNamespace("emmeans", quietly = TRUE))
{
  m1.lmer <- lmerTest::lmer(logitP ~ Host*Cadavers*Ladybird + (1|Run),
                          data=Ladybird.dat)
  fixed.tab <- anova(m1.lmer, type = "II")
  col.p <- "Pr(>F)"
  df = "NumDF"
  den.df = "DenDF"
}

## Select a model using the table of p-values obtained with either asreml or lmerTest
if (exists("fixed.tab"))
{
  term.marg <- dae::marginality(dae::pstructure(~ Host*Cadavers*Ladybird,
                                              data = Ladybird.dat))
  chosen <- chooseModel(fixed.tab, p.values = col.p, DF = df, denDF = den.df,
                      terms.marginality = term.marg)
}

```

---

chooseSpatialModelOnIC.asrtests

*Uses information criteria to choose the best fitting spatial model for accounting for local spatial variation.*

---

## Description

For a response variable measured on a potentially irregular grid of rows and columns of the units, uses information criteria to decide whether to add to the fitted model stored in the supplied `asrtests.object` either a two-dimensional exponential correlation model, a two-dimensional tensor-product natural cubic smoothing spline model (TPNCSS), a two-dimensional tensor-product penalized P-spline model (TPPCS) model, or a two-dimensional tensor-product penalized linear spline model with first-difference penalties (TPPILS) to account for the local spatial variation. The models from which to select can be reduced to a subset of these four models. The data can be arranged in sections, for each of which there is a grid and for which the model is to be fitted separately. Also, the rows and columns of a grid are not necessarily one observational unit wide. The spatial model is only added if the information criterion of the supplied model is decreased with the addition of the local spatial model.

One or more rows is added to the `test.summary.data.frame` of the `asrtests.object`, for each section and each spatial model, stating whether or not the new model has been swapped for a model in which the spatial model has been added to the supplied model. 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 to exhibit the differences between the supplied and any new model.

## Usage

```
## S3 method for class 'asrtests'
chooseSpatialModelOnIC(asrtests.obj, trySpatial = "all",
  sections = NULL,
  row.covar = "cRow", col.covar = "cCol",
  row.factor = NULL, col.factor = NULL,
  nsegs = NULL, nestorder = c(1,1),
  asreml.option = "mbf",
  tpps4mbf.obj = NULL,
  allow.unconverged = FALSE,
  allow.fixedcorrelation = FALSE,
  checkboundaryonly = FALSE, update = FALSE,
  IClikelihood = "full", which.IC = "AIC",
  return.asrts = "best", ...)
```

## Arguments

asrtests.obj	An <a href="#">asrtests.object</a> containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary.
trySpatial	A character string nominating the types of spatial model whose fits are to be assessed. Possible values are none, corr, TPNCSS, TPPCS, and TPP1LS. If set to none, then just the supplied nonspatial model and the information about its information criteria will be returned.
sections	A single character string that species the name of the column in the <a href="#">data.frame</a> that contains the <a href="#">factor</a> that identifies different sections of the data to which separate spatial models are to be fitted.
row.covar	A single character string nominating a <a href="#">numeric</a> column in the <a href="#">data.frame</a> that contains the values of a centred covariate indexing the rows of the grid.
col.covar	A single character string nominating a <a href="#">numeric</a> column in the <a href="#">data.frame</a> that contains the values of a centred covariate indexing the columns of the grid.
row.factor	A single character string nominating a <a href="#">factor</a> in the <a href="#">data.frame</a> that has as many levels as there are unique values in row.covar. This argument is required for spatial.model set to TPNCSS or TPPS. It is used to remove a term corresponding to the row.factor and a random row deviations term based on row.covar will be included in the model. If the argument is NULL, it is assumed that such a term is not included in the fitted model stored in asrtests.obj.
col.factor	A single character string nominating a <a href="#">factor</a> in the <a href="#">data.frame</a> that has as many levels as there are unique values in col.covar. This argument is required for spatial.model set to TPNCSS or TPPS. It is used to remove a term corresponding to the col.factor and a random column deviations term based on col.covar will be included in the model. If the argument is NULL, it is assumed that such a term is not included in the fitted model stored in asrtests.obj.
nsegs	A pair of <a href="#">numeric</a> values giving the number of segments into which the column and row ranges are to be split, respectively (each value specifies the number of internal knots + 1). If only one number is specified, that value is used in both dimensions. If not specified, then (number of unique values - 1) is used in each dimension; for a grid layout with equal spacing, this gives a knot at each data value.
nestorder	A <a href="#">character</a> of length 2. The order of nesting for column and row dimensions, respectively; default=1 (no nesting). A value of 2 generates a spline with half

	the number of segments in that dimension, etc. The number of segments in each direction must be a multiple of the order of nesting.
asreml.option	A single character string specifying whether the grp or mbf methods are to be used to supply externally formed covariate matrices to asreml. If the mbf method is to be used, then <code>makeTPPSplineMats.data.frame</code> must be used before calling <code>addSpatialModelOnIC.asrtests</code> . Compared to the mbf method, the grp method creates large asreml objects, but is faster. The grp method adds columns to the <code>data.frame</code> containing the data; the mbf method adds only fixed covariate to data and stores the random covariates externally.
tps4mbf.obj	An object made with <code>makeTPPSplineMats.data.frame</code> and which contains the spline basis information, that is extra to the <code>data.frames</code> created by <code>makeTPPSplineMats.data.frame</code> in the environment in which it is called and that is needed to fit a TPPS model using the mbf method of asreml.
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 <code>asrtests.obj</code> 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.
allow.fixedcorrelation	A logical indicating whether to accept a new model even when it contains correlations in the model whose values have been designated as fixed, bound or singular. If FALSE and the new model contains correlations whose values have not been able to be estimated, the supplied <code>asrtests.obj</code> is returned. The fit in the <code>asreml.obj</code> component of the supplied <code>asrtests.obj</code> will also be tested and a warning issued if both fixed correlations are found in it and <code>allow.fixedcorrelation</code> is FALSE.
checkboundaryonly	If TRUE then boundary and singular terms are not removed by <code>rmboundary.asrtests</code> ; a warning is issued instead.
update	If TRUE then <code>update.asreml</code> is called to fit the model to be tested. In doing this the arguments <code>R.param</code> and <code>G.param</code> are set to those in the asreml object stored in <code>asrtests.obj</code> 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 modified as specified and (ii) modifications specified via ... are made.
which.IC	A character specifying the information criterion to be used in selecting the best model. Possible values are AIC and BIC. The values of the criterion for supplied model must exceed that for changed model for the changed model to be returned.
IClikelihood	A character specifying whether Restricted Maximum Likelihood (REML) or the full likelihood (full) are to be used in calculating the information criteria.
return.asrts	A character string specifying whether the <code>asrtests.object</code> for the best fitting model (smallest AIC or BIC) is returned or the <code>asrtests.objects</code> resulting from the attempted fits of all of the models specified using <code>trySpatial</code> are returned.
...	Further arguments passed to <code>changeModelOnIC.asrtests</code> , asreml and tpsmb.

## Details

A fitted spatial model is only returned if it improves the fit over an above that achieved with the model fit supplied in the `asrtests.obj`. If `return.asrts` is all, then this applies to each spatial

model specified by `trySpatial`. The model fit supplied in the `asrtests.obj` should not include terms that will be included in any local spatial model. All spatial model terms are fitted as fixed or random. Consequently, the residual model does not have to be iid. The improvement in the fit resulting from the addition of a spatial model to the supplied model is evaluated.

For the `corr` spatial model, an exponential model (`exp`) is used for each dimension to model the spatial correlation. A series of models are tried, beginning with the addition of row correlation and followed by the addition of column correlation. Only if the model fit is improved is a correlation retained. Finally, if any correlation is retained, the improvement to the fit of a nugget term is assessed. In this model, the correlation between observations from different rows is the correlation between observations in adjacent rows raised to the power equal to the absolute value of the difference in their `row.covar` values; similarly for the correlation in the column dimension.

The tensor-product natural-cubic-smoothing-spline `TPNCSS` spatial model is as described by Verbyla et al. (2018), the tensor-product penalized-cubic-spline `TPPCS` model is as described by Rodriguez-Alvarez et al. (2018), and the tensor-product, first-difference-penalty, linear spline `TPP1LS` model that is amongst those described by Piepho, Boer and Williams (2022). The fixed terms for these models are `row.covar + col.covar + row.covar:col.covar` and the random terms `spl(row.covar) + spl(col.covar) + dev(row.covar) + dev(col.covar) + spl(row.covar):col.covar + row.covar:spl(col.covar) + spl(row.covar):spl(col.covar)`. The supplied model should not include any of these terms. However, any fixed or random main-effect term for either `row.factor` or `col.factor` will be removed from the fit.

The `TPPCS` and `TPP1LS` models are fitted using the function `tpsmmb` from the R package `TPSbits` authored by Sue Welham (2022). There are two methods for supplying the spline basis information produced by `tpsmmb` to `asreml`. The `grp` method adds the it to the `data.frame` holding the information for the analysis. The `mbf` method requires the spline basis information to be in the same environment as the function that is called to make a fit using `asreml`. To this end, and prior to invoking the calling function, `makeTPPSplineMats.data.frame` must be used produce the `data.frames`.

All models utilize the function `changeModelOnIC.asrtests` to assess the model fit, the information criteria used in assessing the fit being calculated using `infoCriteria`. Arguments from `tpsmmb` and `changeModelOnIC.asrtests` can be supplied in calls to `chooseSpatialModelOnIC.asrtests` and will be passed on to the relevant function through the ellipses argument (`...`).

The data for experiment can be divided into sections and an attempt to fit the same spatial model to each is made. The fit may differ for each of the sections, but the fit over all of the sections is assessed.

Each combination of a `row.coords` and a `col.coords` does not have to specify a single observation; for example, to fit a local spatial model to the main units of a split-unit design, each combination would correspond to a main unit and all subunits of the main unit would have the same combination.

## Value

A `list` containing four components: (i) `asrts`, (ii) `spatial.IC`, (iii) `best.spatial.mod`, and (iv) `best.spatial.IC`.

The component `asrts` itself holds a `list` of one or more `asrtests.objects`, either the best overall out of the supplied model and the spatial models, or, for each spatial model, the best out of the supplied model and that spatial model. Each `asrtests.object` contains the components: (i) `asreml.obj`, (ii) `wald.tab`, and (iii) `test.summary`.

The `spatial.IC` component holds a `data.frame` with summary of the values of the information criteria for the supplied model and those resulting from adding the spatial model to the supplied model (if the spatial model did not fit, then all values will be `NA`).



The `best.spatial` component is a character giving the name of the best spatial model, and `best.spatial.AIC` gives the value of its AIC.

### Author(s)

Chris Brien

### References

Piepho, H.-P., Boer, M. P., & Williams, E. R. (2022). Two-dimensional P-spline smoothing for spatial analysis of plant breeding trials. *Biometrical Journal*, **64**, 835-857.

Rodriguez-Alvarez, M. X., Boer, M. P., van Eeuwijk, F. A., & Eilers, P. H. C. (2018). Correcting for spatial heterogeneity in plant breeding experiments with P-splines. *Spatial Statistics*, **23**, 52-71.

Verbyla, A. P., De Faveri, J., Wilkie, J. D., & Lewis, T. (2018). Tensor Cubic Smoothing Splines in Designed Experiments Requiring Residual Modelling. *Journal of Agricultural, Biological and Environmental Statistics*, **23**(4), 478-508.

Welham, S. J. (2022) *TPSbits: Creates Structures to Enable Fitting and Examination of 2D Tensor-Product Splines using ASReml-R*. Version 1.0.0 <https://mmade.org/tpsbits/>

### See Also

`as.asrtests`, `rmboundary.asrtests`, `addSpatialModelOnIC.asrtests`, `addSpatialModel.asrtests`, `testtranfix.asrtests`, `testresidual.asrtests`, `newfit.asreml`, `reparamSigDevn.asrtests`, `chooseModel.asrtests`, `changeModelOnIC.asrtests`, `infoCriteria.asreml`

### Examples

```
## Not run:

data(Wheat.dat)

#Add row and column covariates
Wheat.dat <- within(Wheat.dat,
{
  cColumn <- dae::as.numfac(Column)
  cColumn <- cColumn - mean(unique(cColumn))
  cRow <- dae::as.numfac(Row)
  cRow <- cRow - mean(unique(cRow))
})

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

#Create an asrtests object, removing boundary terms
current.asrt <- as.asrtests(current.asr, NULL, NULL,
  label = "Random Row and Column effects")
current.asrt <- rmboundary(current.asrt)

# Choose the best of three models the local spatial variation
current.asrt <- chooseSpatialModelOnIC(current.asrt,
  row.covar = "cRow", col.covar = "cColumn",
  row.factor = "Row", col.factor = "Column",
```

```
asreml.option = "grp")

## End(Not run)
```

---

estimateV.asreml	<i>Forms the estimated variance, random or residual matrix for the observations from the variance parameter estimates.</i>
------------------	--

---

## 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 <b>G</b> , corresponding to the random formula, or "R" to produce the matrix <b>R</b> , 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 more 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 passing 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, <https://asreml.kb.vsnl.co.uk/>.

## 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)
```

---

exploreLSDs.alldiffs    *Explores the computed LSD values for pairwise differences between predictions.*

---

## Description

Given an `alldiffs.object` with an `sed` component, the LSDs are calculated for all pairwise comparisons of predictions. It then calculates (i) a table of frequencies of the LSD values, (ii) the distinct values of the LSDs after rounding, (iii) various statistics from the LSD values, (iv) a measure of the accuracy of each of the LSD statistics, (v) the numbers of false positives and false negatives for each of the LSD statistics if pairwise comparisons are based on the LSD statistic, (vi) the accuracy of each statistic in representing the LSD values for each prediction and (vii) a matrix containing the LSD values for comparing each pair of predictions. Histograms of the frequencies can also be produced.

## Usage

```
## S3 method for class 'alldiffs'
exploreLSDs(alldiffs.obj, LSDtype = "overall", LSDby = NULL,
            LSDaccuracy = "maxAbsDeviation", alpha = 0.05, digits = 3,
            retain.zeroLSDs = FALSE,
            zero.tolerance = .Machine$double.eps ^ 0.5,
            plotHistogram = FALSE, ...)
```

## Arguments

<code>alldiffs.obj</code>	An <code>alldiffs.object</code> .
<code>LSDtype</code>	A <code>character</code> string that can be <code>overall</code> or <code>factor.combinations</code> . It determines whether the LSD values that are investigated and stored are (i) the overall minimum, <code>quantile10</code> , <code>quantile25</code> , <code>mean</code> , <code>median</code> , <code>quantile75</code> , <code>quantile90</code> , and maximum of all pairwise LSDs, or (ii) the minimum, <code>quantile10</code> , <code>quantile25</code> , <code>mean</code> , <code>median</code> , <code>quantile75</code> , <code>quantile90</code> , and maximum for the pairwise LSDs for each <code>factor.combination</code> , unless there is only one prediction for a <code>factor.combination</code> , when notional LSDs are calculated. The <code>LSDtype</code> specified here does not have to match that used in the creating the <code>alldiffs.object</code> . See <code>LSD.frame</code> for further information on how the LSD statistics are calculated.
<code>LSDby</code>	A <code>character</code> (vector) of variables names, being the names of the <code>factors</code> or <code>numerics</code> in the <code>classify</code> ; for each combination of the values the of the <code>factors</code> and <code>numerics</code> , the LSD statistics and accuracy are computed, as well histograms plotted, when <code>LSDtype</code> is <code>factor.combinations</code> . The <code>LSDby</code> specified here does not have to match that used in the creating the <code>alldiffs.object</code> .
<code>LSDaccuracy</code>	A <code>character</code> nominating one of <code>maxAbsDeviation</code> , <code>maxDeviation</code> , <code>q90Deviation</code> or <code>RootMeanSqDeviation</code> as the statistic to be calculated as a measure of the accuracy of an LSD statistic when its values are used as an approximate LSD. The option <code>q90Deviation</code> produces the sample quantile corresponding to a probability of 0.90. The deviations are the differences between a set of LSDs and an LSD statistic calculated from those LSDs; the accuracy is expressed as a proportion of the value of the LSD statistic.
<code>alpha</code>	A <code>numeric</code> specifying the significance level for an LSD to compare a pair of predictions.

digits	A <b>numeric</b> specifying the number of significant digits to retain in rounding the LSDs before determining the distinct rounded LSDs.
retain.zeroLSDs	A <b>logical</b> indicating whether to retain or omit LSDs that are zero when calculating the summaries of LSDs.
zero.tolerance	A <b>numeric</b> specifying the value such that if an LSD is less than it, it will be considered to be zero.
plotHistogram	A <b>logical</b> indicating whether or not histograms of the LSD values are to be plotted. The LSDtype argument controls whether one histogram of all LSD values is plotted or histograms are plotted for each combination of the levels of the factors specified by the LSDby argument.
...	Provision for passing arguments to functions called internally - not used at present.

## Details

The false positives and negatives are computed by comparing, for each pair of predictions within each levels-combination of the LSDby variables, the significance of the pair difference determined using (i) the true LSD that is computed from the standard error of differences for the pair and (ii) the approximate LSD that is a statistic computed from the true LSDs for all pairwise difference within each levels-combination of the LSDby variables. The number of false positives is the number of pairwise differences for which a difference is declared significant using the approximate LSD, but not using the true LSD. The number of false negatives is the number of pairwise differences for which a difference is declared nonsignificant using the approximate LSD, but significant using the true LSD.

The LSD accuracy for a set of LSDs is a function of the deviations of those LSDs and an LSD statistic calculated from them; the accuracy is expressed as a proportion of the value of the LSD statistic.

## Value

A **list** with components frequencies, distinct.vals, statistics, accuracy, per.pred.accuracy and LSD:

1. frequencies is a data.frame with the frequency distribution of the LSD values;
2. distinct.vals is a list, each component of which contains the distinct values of the LSDs after rounding;
3. statistics is a data.frame with the minimum, quantile10, quantile25, mean, median, quantile75, quantile90, and maximum of the LSD values;
4. accuracy is a data.frame with the accuracies of the minimum, quantile10, quantile25, mean, median, quantile75, quantile90, and maximum of the LSD values with respect to the values from which these statistics are calculated;
5. false.pos is a data.frame with the numbers of false positives for the pairwise comparisons within each levels-combination of the LSDby variables when each of the minimum, quantile10, quantile25, mean, median, quantile75, quantile90, and maximum of the LSD values is used as an approximate LSD in determining the significance of the pairwise differences;
6. false.neg is a data.frame with the numbers of false negatives for the pairwise comparisons within each levels-combination of the LSDby variables when each of the minimum, quantile10, quantile25, mean, median, quantile75, quantile90, and maximum of the LSD values is used as an approximate LSD in determining the significance of the pairwise differences;

7. `per.pred.accuracy` is a data.frame with the accuracies of the minimum, quantile10, quantile25, mean, median, quantile75, quantile90, and maximum of the LSD values for a set of predictions when these statistics are used to represent the LSDs for the comparisons amongst the set of predictions;
8. LSD is a square matrix containing the LSD values for all pairwise comparisons of the predictions contained in the supplied `alldiffs.obj`.

In the statistics, `accuracy`, `false.pos` and `false.neg` data.frames, `c` is the number of pairwise comparisons on which the values in the same row are based. The accuracy measure is specified by the `LSDaccuracy` argument.

### Author(s)

Chris Brien

### See Also

[asremlPlus-package](#), [plotLSDs.data.frame](#), [plotLSDs.alldiffs](#),  
[plotLSDerrors.alldiffs](#), [plotLSDerrors.data.frame](#), [recalcLSD.alldiffs](#),  
[pickLSDstatistics.alldiffs](#), [redoErrorIntervals.alldiffs](#)

### 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.asrttests(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 emmeans 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
els <- as.numeric(rownames(TS.preds))
TS.vcov <- vcov(TS.emm)[els,els]
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"))
{
  ##Explore the LSD values for predictions obtained using asreml or lmerTest
  LSDstat <- exploreLSDs(TS.diffs, LSDtype = "factor.combinations",
                        LSDby = "Sources")
}

```

---

facCombine.alldiffs	<i>Combines several factors into one in the components of an alldiffs.object</i>
---------------------	--

---

## 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 and the attributes of the **alldiffs.object**. If any of the factors to be combined are in LSDby, they are removed from the LSDby, unless the factors to be combined are exactly those in the LSDby. 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 <b>alldiffs.object</b> .
factors	A <b>character</b> containing the names of <b>factors</b> 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 <b>factors</b> are to be considered as numbered when forming the levels of the combined <b>factor</b> ; 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 <b>factor</b> are to be combined from those of the <b>factors</b> 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 <b>factors</b> , 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 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 <a href="#">redoErrorIntervals.alldiffs</a> .

**Value**

A modified [alldiffs.object](#).

**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.srtests(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 emmeans 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)
}

```

---

facRecast.alldiffs	<i>Reorders and/or revises the factor levels using the order of old levels in levels.order and the new labels for the levels given in newlabels. The values in levels.order must be unique.</i>
--------------------	---

---

## Description

Reorders and revises the levels and labels of a [factor](#), in the prediction component of an [alldiffs.object](#). The values in the levels.order vector should be the same as the levels in the existing [factor](#), but the order can be changed. To revise the levels, specify the new levels in the newlabels vector and these will replace the corresponding value in the levels.order vector. The matching changes are made to the other components and attributes of the [alldiffs.object](#).

## Usage

```

## S3 method for class 'alldiffs'
facRecast(object, factor, levels.order = NULL, newlabels = NULL, ...)

```

## Arguments

object	An <a href="#">alldiffs.object</a> .
factor	A <a href="#">character</a> containing the name of a <a href="#">factor</a> in the prediction component of object whose levels and labels are to be recast.
levels.order	A <a href="#">vector</a> of length levels(factor) containing the old levels in the new order for the factor being created. If levels.order is NULL, then the current levels of levels(factor) are used.
newlabels	A <a href="#">vector</a> of length levels(factor) containing values to use in the revision.
...	Further arguments passed to the <a href="#">factor</a> call creating the new <a href="#">factor</a> .

## Value

A modified [alldiffs.object](#).

**Author(s)**

Chris Brien

**See Also**

`as.alldiffs`, `allDifferences.data.frame`, `print.alldiffs`, `sort.alldiffs`,  
`facCombine.alldiffs`, `facRename.alldiffs`, `renewClassify.alldiffs`; `fac.recode` 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 emmeans 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 <- allDifferences(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)

## Recast the Ladybird and Host factors
HCL.diffs <- facRecast(HCL.diffs, factor = "Ladybird",
                      newlabels = c("none", "present"))
HCL.diffs <- facRecast(HCL.diffs, factor = "Ladybird",
                      levels.order = c("present", "none"),
                      newlabels = c("yes", "no"))
HCL.diffs <- facRecast.alldiffs(HCL.diffs, factor = "Host",
                              levels.order = c("trefoil", "bean"))

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

```

---

facRename.alldiffs      *Renames **factors** in the prediction component of an **alldiffs.object**.*

---

## Description

Renames **factors** in the prediction component of an **alldiffs.object**. These changes are propagated to the other components and attributes of the **alldiffs.object**.

## Usage

```
## S3 method for class 'alldiffs'
facRename(object, factor.names, newnames, ...)
```

## Arguments

object	An <b>alldiffs.object</b> .
factor.names	A <b>character</b> containing the names of the <b>factors</b> in the prediction component of object that are to be renamed.
newnames	A <b>character</b> containing the new names of the <b>factors</b> in the prediction component of object.
...	Provision for passing arguments to functions called internally - not used at present.

## Value

A modified **alldiffs.object**.

## Author(s)

Chris Brien

## See Also

**as.alldiffs**, **allDifferences.data.frame**, **print.alldiffs**, **sort.alldiffs**, **facCombine.alldiffs**, **facRecast.alldiffs**, **renewClassify.alldiffs**; **fac.recode** 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 emmeans 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 <- allDifferences(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)

  ## Rename Cadavers
  HCL.diffs <- facRename(HCL.diffs, factor.names = "Cadavers", newnames = "Cadaver.nos")

  ## 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)
```

---

```
getFormulae.asreml
```

*Gets the formulae from an asreml object.*

---

### Description

Gets the **formulae** nominated in the which argument from the call stored in an asreml object.

### Usage

```
## S3 method for class 'asreml'
getFormulae(asreml.obj, which = c("fixed", "random", "residual"),
            expanded = FALSE, envir = parent.frame(), ...)
```

**Arguments**

<code>asreml.obj</code>	An <code>asreml</code> object resulting from the fitting of a model using REML.
<code>which</code>	A character listing the <a href="#">formula(e)</a> to be extracted from the call stored in <code>asreml.obj</code> . It should be some combination of fixed, random, residual, sparse and all. If all is included then all <a href="#">formula(e)</a> will be returned, those not having been specified in the call being NULL.
<code>expanded</code>	A logical indicating whether terms are to be expanded to the sum of a set of individual terms.
<code>envir</code>	The environment in which the <a href="#">formula(e)</a> are to be evaluated. May also be NULL, a list, a data.frame, a pairlist or an integer as specified to <code>sys.call</code> .
<code>...</code>	Arguments passed on to <code>update.formula</code> and ultimately to <code>terms.formula</code> .

**Value**

A list containing a component with each of the extracted [formula\(e\)](#), the name of a component being the [formula](#) that it contains.

**Author(s)**

Chris Brien

**See Also**

[printFormulae.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)
getFormulae(current.asr)

## End(Not run)
```

---

`getTestEntry.asrtests` *Gets the entry for a test recorded in the test.summary data.frame of an [asrtests.object](#)*

---

**Description**

Matches the label in the term column of the `test.summary data.frame` in the supplied [asrtests.object](#) and extracts the line for it. It only matches the last occurrence of label.

**Usage**

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

**Arguments**

asrtests.obj	An <a href="#">asrtests.object</a> containing the components (i) <code>asreml.obj</code> , (ii) <code>wald.tab</code> , and (iii) <code>test.summary</code> .
label	A character specifying the label of the test for which the entry is required. If <a href="#">testranfix.asrtests</a> was used for the test of interest, then the label will be the value of the term argument supplied to <a href="#">testranfix.asrtests</a> . For <a href="#">changeModelOnIC.asrtests</a> , the label will be the value of the label argument. Other arguments will be relevant for other test and change functions.
...	provision for passing arguments to functions called internally - not used at present.

**Value**

A one-line data.frame containing the entry.

**Author(s)**

Chris Brien

**See Also**

[getTestPvalue.asrtests](#), [as.asrtests](#),  
[testranfix.asrtests](#), [testswapran.asrtests](#), [testresidual.asrtests](#),  
[changeModelOnIC.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)
getTestEntry(current.asrt, label = "units")

## 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 test.summary data.frame in the supplied [asrtests.object](#) and extracts its p-value. It only matches the last occurrence of label.

**Usage**

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

**Arguments**

asrtests.obj	An <a href="#">asrtests.object</a> containing the components (i) <code>asreml.obj</code> , (ii) <code>wald.tab</code> , and (iii) <code>test.summary</code> .
label	A character specifying the label of the test for which the p-value is required. If <a href="#">testranfix.asrtests</a> was used for the test of interest, then the label will be the value of the term argument supplied to <a href="#">testranfix.asrtests</a> . Other arguments will be relevant for other test functions.
...	provision for passing arguments to functions called internally - not used at present.

**Value**

A 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**

[getTestEntry.asrtests](#), [as.asrtests](#),  
[testranfix.asrtests](#), [testswapan.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	<i>Computes AIC and BIC for models.</i>
--------------	---

---

## Description

Computes Akiake and Bayesian (Schwarz) Information Criteria for models. Either the Restricted Maximum likelihood (REML) or the full likelihood (full) can be used. The full likelihood is used when it is desired to compare models that differ in their fixed models.

## Usage

```
## S3 method for class 'asreml'
infoCriteria(object, DF = NULL,
             bound.exclusions = c("F","B","S","C"),
             IClkelihood = "REML", fixedDF = NULL, varDF = NULL, ...)
## S3 method for class 'list'
infoCriteria(object, bound.exclusions = c("F","B","S","C"),
             IClkelihood = "REML", fixedDF = NULL, varDF = NULL, ...)
```

## Arguments

object	An asreml object resulting from the fitting of a model using REML or a list of asreml objects. If the components of the list are named, then those names will be used as the rownames for the returned data.frame.
DF	A numeric giving the number of estimated variance parameters. If NULL then this is determined from the information in object. This argument has been replaced by varDF, but is retained for compatibility with legacy code. It is not available with the list method.
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.
IClikelihood	A character specifying whether Restricted Maximum Likelihood (REML) or the full likelihood (full) are to be used in calculating the information criteria for family set to asr_gaussian. For family set to asr_binomial or asr_poisson and with dispersion set to 1, the deviance is extracted from object and used to calculate the AIC and BIC (as suggested by Damian Collins); the setting of IClkelihood is ignored and the log-likelihood set to NA. The information criteria are not valid for other settings of family and dispersion.
fixedDF	A numeric giving the number of estimated fixed parameters. If NULL then this is determined from the information in object. For object a list only a single value that is used for all components of the list has been implemented.
varDF	A numeric giving the number of estimated variance parameters. If NULL then this is determined from the information in object. It replaces the DF argument. For object a list only a single value that is used for all components of the list has been implemented.
...	Provision for passing arguments to functions called internally - not used at present.

## Details

The variance degrees of freedom (varDF) 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 varDF is not NULL, the supplied value is used. Otherwise varDF is determined from the information in object, i.e. if object is an `asreml` object then from it, or if object is a list then from each `asreml` object in the list. Similarly, the fixed degrees of freedom (fixedDF) are the number of number of fixed parameters that have been estimated, any coefficients that have the value NA being excluded. If fixedDF is not NULL, the supplied value is used. Otherwise fixedDF is determined from the information in object.

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 calculation of the information criteria is an adaption of the code supplied in File S1 of Verbyla (2019). The log-likelihood is calculated as  $\text{loglik} = \log(\text{REML}) - \log(|\mathbf{C}|)/2$ , where  $\mathbf{C}$  is the inverse coefficient matrix; the term involving  $\mathbf{C}$  is omitted for REML. The AIC is calculated as  $-2 * \text{loglik} + 2 * (\text{varDF} + \text{fixedDF})$  and the BIC as  $-2 * \text{loglik} + (\text{fixedDF} + \text{varDF}) * \log(n - r + \text{fixedDF})$ , where  $n$  is the number of observations and  $r$  is the rank of the fixed effects design matrix. For REML,  $\text{fixedDF} = 0$ .

## Value

A `data.frame` containing the numbers of estimated fixed (fixedDF) and variance (varDF) parameters, the number of bound parameters (NBound), AIC, BIC and the value of the log-likelihood (loglik). All elements of the `data.frame` will be set to NA for the invalid combinations of family and dispersion as noted in the `IClikelihood` argument. If object is a list and its components are named, then those names will be used to set the rownames of the `data.frame`.

## Author(s)

Chris Brien

## References

Verbyla, A. P. (2019). A note on model selection using information criteria for general linear models estimated using REML. *Australian & New Zealand Journal of Statistics*, **61**, 39–50. doi:10.1111/anzs.12254.

## See Also

[REMLRT.asreml](#), [changeTerms.asrtests](#), [changeModelOnIC.asrtests](#)

## Examples

```
## Not run:
data(Wheat.dat)
## Fit several models to the wheat data and calculate their ICs
# Fit initial model
m.max <- asreml(yield ~ Rep + WithinColPairs + Variety,
               random = ~ Row + Column + units,
               residual = ~ ar1(Row):ar1(Column),
               data=Wheat.dat)
infoCriteria(m.max.asr, IClikelihood = "full")
```

```

#Drop term for within Column pairs
m1 <- asreml(yield ~ Rep + Variety,
             random = ~ Row + Column + units,
             residual = ~ ar1(Row):ar1(Column),
             data=Wheat.dat)

#Drop nugget term
m2 <- asreml(yield ~ Rep + WithinColPairs + Variety,
             random = ~ Row + Column,
             residual = ~ ar1(Row):ar1(Column),
             data=Wheat.dat)

#Drop Row autocorrelation
m3 <- asreml(yield ~ Rep + WithinColPairs + Variety,
             random = ~ Row + Column + units,
             residual = ~ Row:ar1(Column),
             data=Wheat.dat)

#Drop Col autocorrelation
m4 <- asreml(yield ~ Rep + WithinColPairs + Variety,
             random = ~ Row + Column + units,
             residual = ~ ar1(Row):Column,
             data=Wheat.dat)

mods.asr <- list(m.max, m1, m2, m3, m4)
infoCriteria(mods.asr, IClikelihood = "full")

## 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 emmeans 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](#), [validPredictionsFrame](#), [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 emmeans 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)
}

```

---

iterate.asrtests	<i>Subject the fitted asreml.obj stored in an asrtests.object to further iterations of the fitting process.</i>
------------------	---

---

## Description

In an effort to improve convergence, subject the fitted asreml.obj stored in an [asrtests.object](#) to further iterations of the fitting process; the model specification is not changed. While no change is made to the test.summary, the wald.tab is updated.

## Usage

```

## S3 method for class 'asrtests'
iterate(asrtests.obj, denDF="numeric", trace = FALSE, ...)

```

**Arguments**

<code>asrtests.obj</code>	an <a href="#">asrtests.object</a> containing the components (i) <code>asreml.obj</code> , (ii) <code>wald.tab</code> , and (iii) <code>test.summary</code> .
<code>denDF</code>	Specifies the method to use in computing approximate denominator degrees of freedom when <code>wald.asreml</code> is called. Can be <code>none</code> to suppress the computations, <code>numeric</code> for numerical methods, <code>algebraic</code> for algebraic methods or <code>default</code> , the default, to automatically 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.
<code>trace</code>	If <code>TRUE</code> then partial iteration details are displayed when <code>ASReml-R</code> functions are invoked; if <code>FALSE</code> then no output is displayed.
<code>...</code>	further arguments passed to <code>update.asreml</code> .

**Value**

An object of S3-class `asrtests`.

**Author(s)**

Chris Brien

**References**

Kenward, M. G., & Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics*, **53**, 983-997.

**See Also**

[as.asrtests](#), [asrtests.object](#), [newfit.asreml](#)

**Examples**

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

## End(Not run)
```

---

Ladybird.dat	<i>Data for an experiment to investigate whether ladybirds transfer aphids</i>
--------------	--

---

**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 of the lower and upper limits of their `error.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, accuracy.threshold = NA,
             LSDtype = "overall", LSDsupplied = NULL,
             LSDby = NULL, LSDstatistic = "mean",
```



```

LSDaccuracy = "maxAbsDeviation",
zero.tolerance = .Machine$double.eps ^ 0.5,
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 <code>alldiffs.object</code> .  |
| classify              | A <code>character</code> string giving the variables that define the margins of the multiway table corresponding to the predictions in <code>alldiffs.obj</code> . Multiway tables are specified by forming an interaction type term from the classifying variables, that is, separating the variable names with the <code>:</code> operator.  |
| term                  | A <code>character</code> string giving the variables that define the term that was fitted using <code>asreml</code> and that corresponds to <code>classify</code> . It only needs to be specified when it is different to <code>classify</code> ; it is stored as an attribute of the <code>alldiffs.object</code> . It is likely to be needed when the fitted model includes terms that involve both a <code>numeric</code> covariate and a <code>factor</code> that parallel each other; the <code>classify</code> would include the covariate and the term would include the factor.  |
| linear.transformation | <p>A <code>formula</code> or a <code>matrix</code>. If a <code>formula</code> is given then it is taken to be a submodel of a model term corresponding to the <code>classify</code>. The projection matrix that transforms the predictions so that they conform to the submodel is obtained; the submodel does not have to involve variables in the <code>classify</code>, but the variables must be columns in the predictions component of <code>alldiffs.obj</code> and the space for the submodel must be a subspace of the space for the term specified by the <code>classify</code>. For example, for <code>classify</code> set to <code>"A:B"</code>, the submodel <code>~ A + B</code> will result in the predictions for the combinations of A and B being made additive for the <code>factors</code> A and B. The submodel space corresponding to <code>A + B</code> is a subspace of the space <code>A:B</code>. In this case both the submodel and the <code>classify</code> involve only the factors A and B. To fit an intercept-only submodel, specify <code>linear.transformation</code> to be the formula <code>~1</code>.</p> <p>If a <code>matrix</code> is provided then it will be used to apply the linear transformation to the predictions. The number of rows in the <code>matrix</code> should equal the number of linear combinations of the predictions desired and the number of columns should equal the number of predictions.</p> <p>In either case, as well as the values of the linear combinations, their standard errors, pairwise differences and associated statistics are returned.</p> |
| Vmatrix               | A <code>logical</code> indicating whether the variance matrix of the predictions will be stored as a component of the <code>alldiffs.object</code> that is returned. If <code>linear.transformation</code> is set, it will be stored irrespective of the value of <code>Vmatrix</code> .   |
| error.intervals       | A <code>character</code> string indicating the type of error interval, if any, to calculate in order to indicate uncertainty in the results. Possible values are <code>"none"</code> , <code>"StandardError"</code> , <code>"Confidence"</code> and <code>"halfLeastSignificant"</code> . The default is for confidence limits to be used. The <code>"halfLeastSignificant"</code> 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 the LSD is zero, as can happen when predictions are constrained to be   |

equal, then the limits of the error intervals are set to NA. If LSDtype 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. To have it ignored, set it to NA. 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 LSDtype are calculated and used in error.intervals and plots.
2. Irrespective of the setting of LSDtype, if avsed.tolerance is not exceeded then the mean LSDs are used in error.intervals and plots.
3. If LSDtype 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 LSDtype 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 LSDtype 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.

accuracy.threshold

A [numeric](#) specifying the value of the LSD accuracy measure, which measure is specified by LSDaccuracy, as a threshold value in determining whether the halfLeastSignificant error.interval for a predicted value is a reasonable approximation; this will be the case if the LSDs across all pairwise comparisons for which the interval's LSD was computed, as specified by LSDtype and LSDby, are similar enough to the interval's LSD, as measured by LSDaccuracy. If it is NA, it will be ignored. If it is not NA, a column of [logicals](#) named LSDwarning will be added to the predictions component of the alldiffs.object. The value of LSDwarning for a predicted.value will be TRUE if the value of the LSDaccuracy measure computed from the LSDs for differences between this predicted.value and the other predicted.values as compared to its assignedLSD exceeds the value of accuracy.threshold. Otherwise, the value of LSDwarning for a predicted.value will be FALSE.

LSDtype

A [character](#) string that can be overall, factor.combinations, per.prediction or supplied. It determines whether the values stored in a row of a [LSD.frame](#) are the values calculated (i) overall from the LSD values for all pairwise comparison2, (ii) the values calculated from the pairwise LSDs for the levels of each factor.combination, unless there is only one prediction for a level of the factor.combination, when a notional LSD is calculated, (iii) per.prediction, being based, for each prediction, on all pairwise differences involving that prediction, or (iv) as supplied values of the LSD, specified with the LSDsupplied argument; these supplied values are to be placed in the assignedLSD column of the [LSD.frame](#) stored in an [alldiffs.object](#) so that they can be used in LSD calculations.

See [LSD.frame](#) for further information on the values in a row of this data.frame and how they are calculated.

LSDsupplied	A <a href="#">data.frame</a> or a named <a href="#">numeric</a> containing a set of LSD values that correspond to the observed combinations of the values of the LSDby variables in the <a href="#">predictions.frame</a> or a single LSD value that is an overall LSD. If a <a href="#">data.frame</a> , it may have (i) a column for the LSDby variable and a column of LSD values or (ii) a single column of LSD values with rownames being the combinations of the observed values of the LSDby variables. Any name can be used for the column of LSD values; assignedLSD is sensible, but not obligatory. Otherwise, a <a href="#">numeric</a> containing the LSD values, each of which is named for the observed combination of the values of the LSDby variables to which it corresponds. (Applying the function <code>dae::fac.combine</code> to the predictions component is one way of forming the required combinations for the (row) names.) The values supplied will be incorporated into assignedLSD column of the <a href="#">LSD.frame</a> stored as the LSD component of the <a href="#">alldiffs.object</a> .
LSDby	A <a href="#">character</a> (vector) of variables names, being the names of the <a href="#">factors</a> or <a href="#">numerics</a> in the <code>classify</code> ; for each combination of their levels and values, there will be or is a row in the <a href="#">LSD.frame</a> stored in the LSD component of the <a href="#">alldiffs.object</a> when LSDtype is <code>factor.combinations</code> .
LSDstatistic	A <a href="#">character</a> nominating one or more of minnum, q10, q25, mean, median, q75, q90 or maximum as the value(s) to be stored in the assignedLSD column in an <a href="#">LSD.frame</a> ; the values in the assignedLSD column are used in computing halfLeastSignificant error.intervals. Here q10, q25, q75 and q90 indicate the sample quantiles corresponding to probabilities of 0.1, 0.25, 0.75 and 0.9 for the group of LSDs from which a single LSD value is calculated. The function <a href="#">quantile</a> is used to obtain them. The mean LSD is calculated as the square root of the mean of the squares of the LSDs for the group. The median is calculated using the <a href="#">median</a> function. Multiple values are only produced for LSDtype set to <code>factor.combination</code> , in which case LSDby must not be NULL and the number of values must equal the number of observed combinations of the values of the variables specified by LSDby. If LSDstatistic is NULL, it is reset to mean.
LSDaccuracy	A <a href="#">character</a> nominating one of maxAbsDeviation, maxDeviation, q90Deviation or RootMeanSqDeviation as the statistic to be calculated as a measure of the accuracy of assignedLSD. The option q90Deviation produces the sample quantile corresponding to a probability of 0.90. The deviations are the differences between the LSDs used in calculating the LSD statistics and each assigned LSD and the accuracy is expressed as a proportion of the assigned LSD value. The calculated values are stored in the column named accuracyLSD in an <a href="#">LSD.frame</a> .
zero.tolerance	A <a href="#">numeric</a> specifying the value such that if a predicted.value, its variance-covariance, or an LSD is less than it, it will be considered to be zero.
response	A character specifying the response variable for the predictions. It is stored as an attribute to the <a href="#">alldiffs.object</a> .
response.title	A character specifying the title for the response variable for the predictions. It is stored as an attribute to the <a href="#">alldiffs.object</a> .
x.num	A <a href="#">character</a> 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 <a href="#">character</a> 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 <code>x.num</code> . The levels of <code>x.fac</code> must be in the order in which they are to be plotted - if they are dates, then they should be in the form <code>yyyymmdd</code> , which can be achieved using <code>as.Date</code> . However, the levels can be non-numeric in nature, provided that <code>x.num</code> is also set.
<code>tables</code>	A <a href="#">character</a> vector containing a combination of <code>none</code> , <code>predictions</code> , <code>vcov</code> , <code>backtransforms</code> , <code>differences</code> , <code>p.differences</code> , <code>sed</code> , <code>LSD</code> and <code>all</code> . These nominate which components of the <code>alldiffs.object</code> to print.
<code>level.length</code>	The maximum number of characters from 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.
<code>pairwise</code>	A <a href="#">logical</a> indicating whether all pairwise differences of the predictions and their standard errors and p-values are to be computed and stored. If <code>tables</code> is equal to <code>"differences"</code> or <code>"all"</code> or <code>error.intervals</code> is equal to <code>"halfLeastSignificant"</code> , they will be stored irrespective of the value of <code>pairwise</code> .
<code>alpha</code>	A <a href="#">numeric</a> giving the significance level for LSDs or one minus the confidence level for confidence intervals. It is stored as an attribute to the <code>alldiffs.object</code> .
<code>inestimable.rm</code>	A <a href="#">logical</a> indicating whether rows for predictions that are not estimable are to be removed from the components of the <code>alldiffs.object</code> .
<code>...</code>	further arguments passed to <code>redoErrorIntervals.alldiffs</code> .

## 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  $\mathbf{LV}_p\mathbf{L}^T$ . 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` component, 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`, `alpha`, `sortFactor` and the `sortOrder` will be set as attributes to the object. Also, if `error.intervals` is `"halfLeastSignificant"`, then those of `LSDtype`, `LSDby` and `LSDstatistic` that are not `NULL` will be added as attributes of the object and of the predictions frame; additionally, `LSDvalues` will be added as attribute of the predictions frame, `LSDvalues` being the LSD values used in calculating the `error.intervals`.

**Author(s)**

Chris Brien

**See Also**

linTransform, predictPlus.asreml, as.alldiffs, print.alldiffs, sort.alldiffs, subset.alldiffs, allDifferences.data.frame, redoErrorIntervals.alldiffs, recalLSD.alldiffs, pickLSDstatistics.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 emmeans 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	<i>Ensures that a specific version of asreml is loaded.</i>
-------------------	---

---

## 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 version 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 asrem13")
## End(Not run)
```

---

LSD.frame	<i>Description of an LSD frame</i>
-----------	------------------------------------

---

## Description

A data.frame that stores Least Significant differences (LSDs) for predictions for a fitted model.

## Value

A data.frame that can be a component of an [alldiffs.object](#) and that contains LSD values and statistics to be used in determining the significance of the pairwise differences. In particular, they are used in calculating halfLeastSignificant limits to be included in a predictions.frame.

Exactly what an LSD.frame contains is determined by the following arguments to functions that return an [alldiffs.object](#): LSDtype, LSDby, LSDstatistic, LSDaccuracy and LSDsupplied. The rownames of the LSD.frame indicate, for each of its rows, for what group of predictions the entries in the row were calculated, this being controlled by the LSDtype and LSDby arguments. The values for all of the LSD arguments are stored as attributes to the [alldiffs.object](#) and the predictions and, if present backtransforms, components of the [alldiffs.object](#).

An LSD.frame always has the eight columns c, minimumLSD, meanLSD, maximumLSD, assignedLSD, accuracyLSD, falsePos and falseNeg.

1. c: This gives the number of pairwise comparison of predictions for the combinations of the factor levels given by the row name. If the row name is overall then it is for all predictions.
2. minimumLSD, meanLSD, maximumLSD: These are computed for either overall, factor.combinations, per.prediction or supplied LSD values, as specified by the LSDtype argument. The meanLSD is calculated using the square root of the mean of the variances of set of pairwise differences appropriate to the specific LSDtype argument.

For overall, the mean, minimum and maximum of the LSDs for all pairwise comparisons are computed.

If factor.combinations was specified for LSDtype when the LSDs were being calculated, then the LSD.frame contains a row for each combination of the values of the [factors](#) and [numerics](#) specified by LSDby. The values in a row are calculated from the LSD values for the pairwise differences for each combination of the [factors](#) and [numerics](#) values, unless there is only one prediction for a combination, when notional LSDs are calculated that are based on the standard error of the prediction multiplied by the square root of two.

For per.prediction, the minimum, mean and maximum LSD, based, for each prediction, on the LSD values for all pairwise differences involving that prediction are computed.

For supplied, the LSD.frame is set up based on the setting of LSDby: a single row with name overall if LSDby is NULL or, if LSDby is a vector of [factor](#) and [numeric](#) names, rows for each observed combinations of the values of the named [factors](#) and [numerics](#). The LSDsupplied argument is used to provide the values to be stored in the column assignedLSD.

3. assignedLSD: The assignedLSD column contains the values that are assigned for use in calculating halfLeastSignificant error.intervals. Its contents are determined by LSDstatistic and LSDsupplied arguments. The LSDsupplied argument allows the direct specification of values to be placed in the assignedLSD column of the LSD.frame. The default is to use the values in the meanLSD column.



4. **LSDaccuracy**: The **LSDaccuracy** gives an indication of the proportion that the correct LSD for a single predicted.value might deviate from its assignedLSD value. The contents of the **accuracyLSD** column is controlled by the **LSDaccuracy** argument.
5. **falsePos** and **falseNeg**: These columns contain the number of false positives and negatives if the assignedLSD value(s) is(are) used to determine the significance of the pairwise predictions differences. Each LSD value in the assignedLSD column is used to determine the significance of pairwise differences that involve predictions for the combination of values given by the row name for the LSD value.

See [recalcLSD.alldiffs](#) for more information.

### Author(s)

Chris Brien

### See Also

[recalcLSD.alldiffs](#), [redoErrorIntervals.alldiffs](#), [predictPresent.asrem1](#),  
[predictPlus.asrem1](#)

### Examples

```
data(Oats.dat)

## Use asrem1 to get predictions and associated statistics

## Not run:
m1.asr <- asrem1(Yield ~ Nitrogen*Variety,
                 random=~Blocks/Wplots,
                 data=Oats.dat)
current.asrt <- as.asrtests(m1.asr)
Var.diffs <- predictPlus(m1.asr, classify="Nitrogen:Variety",
                        wald.tab = current.asrt$wald.tab,
                        tables = "none")

## End(Not run)

## Use lmerTest and emmeans 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)

  #Get predictions
  Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
  Var.preds <- summary(Var.emm)
  ## 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

  #Set up an alldiffs object, which includes overall LSDs
  Var.diffs <- allDifferences(predictions = Var.preds, classify = "Variety:Nitrogen",
                             sed = Var.sed, vcov = Var.vcov, tdf = 45)
```



```

}

if (exists("Var.diffs"))
{
  ## Use recalLSD to get LSDs for within Variety differences
  Var.LSD.diffs <- recalLSD(Var.diffs,
                           LSDtype = "factor.combinations", LSDby = "Variety")
  print(Var.LSD.diffs$LSD)
}

```

---

```
makeTPPSplineMats.data.frame
```

*Make the spline basis matrices and data needed to fit Tensor Product P-splines.*

---

## Description

Prepares the fixed and random sP-spline basis matrices, and associated information, that are needed for fitting of Tensor Product P-splines (TPPS) as described by Rodriguez-Alvarez et al. (2018). When `asreml.option` is set to `mbf`, `makeTPPSplineMats.data.frame` must be run prior to fitting TPPS models for local spatial variation using [addSpatialModelOnIC.asrtests](#) and [chooseSpatialModelOnIC.asrtests](#). The spline basis matrices are created in the parent environment of `makeTPPSplineMats.data.frame` when it is called. If the `grp` is to be used to supply the basis functions to `asreml-R`, then this function need not be called; the spatial spline fitting functions will set up the basis functions.

## Usage

```

## S3 method for class 'data.frame'
makeTPPSplineMats(data, sections = NULL,
                  row.covar, col.covar,
                  nsegs = NULL, nestorder = c(1,1),
                  degree = c(3,3), difforder = c(2,2),
                  asreml.option = "mbf", ...)

```

## Arguments

<code>data</code>	An <a href="#">data.frame</a> that holds the spline bases for a section. It is indexed by columns named <code>col</code> and <code>row</code> .
<code>sections</code>	A single character string that species the name of the column in the <a href="#">data.frame</a> that contains the <a href="#">factor</a> that identifies different sections of the data to which separate spatial models are to be fitted.
<code>row.covar</code>	A single <a href="#">character</a> string nominating a <a href="#">numeric</a> column in the <a href="#">data.frame</a> that contains the values of a covariate indexing the rows of the grid.
<code>col.covar</code>	A single <a href="#">character</a> string nominating a <a href="#">numeric</a> column in the <a href="#">data.frame</a> that contains the values of a covariate indexing the columns of the grid.
<code>nsegs</code>	A pair of <a href="#">numeric</a> values giving the number of segments into which the column and row ranges are to be split, respectively (each value specifies the number of internal knots + 1). If only one number is specified, that value is used in both dimensions. If not specified, then (number of unique values - 1) is used in each dimension; for a grid layout with equal spacing, this gives a knot at each data value.

nestorder	A <b>character</b> of length 2. The order of nesting for column and row dimensions, respectively; default=1 (no nesting). A value of 2 generates a spline with half the number of segments in that dimension, etc. The number of segments in each direction must be a multiple of the order of nesting.
degree	A <b>character</b> of length 2. The degree of polynomial spline to be used for column and row dimensions respectively; default=3.
difforder	A <b>character</b> of length 2. The order of differencing for column and row dimensions, respectively; default=2.
asreml.option	A single character string whose value may be mbf or grp, indicating the method is to be used to supply externally formed covariate matrices to asreml.
...	Further arguments passed to tpsmmb from package TPSbits.

### Details

The objects are formed using the function `tpsmmb` from the R package `TPSbits` authored by Sue Welham (2022).

Each combination of a `row.covar` and a `col.covar` does not have to specify a single observation; for example, to fit a local spatial variation model to the main units of a split-unit design, each combination would correspond to a main unit and all subunits of the main unit would have the same combination.

The data for experiment can be divided sections and the spline bases and associated data will be produced for each section. If there is more than one sections, then a **list** is returned that has a component for each section. The component for a section contains:

### Value

A **list** of length equal to the number of sections is produced. Each of these components is a **list** with 8 or 9 compnents. named `data.plus`, being the input `data.frame` to which has been added the columns required to fit the TPPS model (the `data.frame` stored in the `data` component holds only the covariates from `data`).

List of length 8 or 9 (according to the `asreml.option`).

1. `data` = the input data frame augmented with structures required to fit tensor product splines in `asreml-R`. This data frame can be used to fit the TPS model.

Added columns:

- `TP.col`, `TP.row` = column and row coordinates
- `TP.CxR` = combined index for use with `smooth x smooth` term
- `TP.C.n` for `n=1:diff.c` = `X` parts of column spline for use in random model (where `diff.c` is the order of column differencing)
- `TP.R.n` for `n=1:diff.r` = `X` parts of row spline for use in random model (where `diff.r` is the order of row differencing)
- `TP.CR.n` for `n=1:(diff.c*diff.r)` = interaction between the two `X` parts for use in fixed model. The first variate is a constant term which should be omitted from the model when the constant (1) is present. If all elements are included in the model then the constant term should be omitted, eg.  $y \sim -1 + TP.CR.1 + TP.CR.2 + TP.CR.3 + TP.CR.4 + \text{other terms} \dots$
- when `asreml="grp"` or `"sepgrp"`, the spline basis functions are also added into the data frame. Column numbers for each term are given in the `grp` list structure.

2. `mbflist` = list that can be used in call to `asreml` (so long as `Z` matrix data frames extracted with right names, eg `BcZ<stub>.df`)

3. BcZ.df = mbf data frame mapping onto smooth part of column spline, last column (labelled TP.col) gives column index
4. BrZ.df = mbf data frame mapping onto smooth part of row spline, last column (labelled TP.row) gives row index
5. BcrZ.df = mbf data frame mapping onto smooth x smooth term, last column (labelled TP.CxR) maps onto col x row combined index
6. dim = list structure, holding dimension values relating to the model:
  - (a) "diff.c" = order of differencing used in column dimension
  - (b) "nbc" = number of random basis functions in column dimension
  - (c) "nbcn" = number of nested random basis functions in column dimension used in smooth x smooth term
  - (d) "diff.r" = order of differencing used in row dimension
  - (e) "nbr" = number of random basis functions in row dimension
  - (f) "nbrn" = number of nested random basis functions in row dimension used in smooth x smooth term
7. trace = list of trace values for ZGZ' for the random TPSpline terms, where Z is the design matrix and G is the known diagonal variance matrix derived from eigenvalues. This can be used to rescale the spline design matrix (or equivalently variance components).
8. grp = list structure, only added for setting asrem1="grp". For asrem1="grp", provides column indexes for each of the 5 random components of the 2D splines in data.plus. Dimensions of the components can be derived from the values in the dim item.
9. data.plus = the input `data.frame` to which has been added the columns required to fit tensor product splines in asrem1-R. This `data.frame` can be used to fit the TPS model. For multiple sections, this `data.frame` will occur in the component for each section.

### Author(s)

Chris Brien

### References

Rodriguez-Alvarez, M. X., Boer, M. P., van Eeuwijk, F. A., & Eilers, P. H. C. (2018). Correcting for spatial heterogeneity in plant breeding experiments with P-splines. *Spatial Statistics*, **23**, 52-71.

Welham, S. J. (2022) TPSbits: *Creates Structures to Enable Fitting and Examination of 2D Tensor-Product Splines using ASReml-R*. Version 1.0.0 <https://mmade.org/tpsbits/>

### See Also

`addSpatialModelOnIC.asrtests`, `chooseSpatialModelOnIC.asrtests`, `tpsmmb`

### Examples

```
## Not run:
```

```
data(Wheat.dat)
```

```
#Add row and column covariates
```

```
Wheat.dat <- within(Wheat.dat,
  {
    cColumn <- dae::as.numfac(Column)
    cColumn <- cColumn - mean(unique(cColumn))
  })
```

```

        cRow <- dae::as.numfac(Row)
        cRow <- cRow - mean(unique(cRow))
    })

#Set up the matrices
tps.XZmat <- makeTPPSplineMats(wheat.dat,
                               row.covar = "cRow", col.covar = "cColumn")

## End(Not run)

```

---

newfit.asreml	<i>Refits an asreml model with modified model formula using either a call to update.asreml or a direct call to asreml.</i>
---------------	--

---

## 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, trace = FALSE,
       allow.unconverged = TRUE, allow.fixedcorrelation = TRUE,
       keep.order = TRUE, set.terms = NULL, ignore.suffices = TRUE,
       bounds = "P", initial.values = NA, ...)

```

## Arguments

<code>asreml.obj</code>	A valid <code>asreml</code> object with with a component named <code>call</code> (from a previous call to either <code>asreml</code> or <code>update.asreml</code> ).
<code>fixed.</code>	A character or formula specifying changes to the fixed formula. This is a two-sided formula where <code>"."</code> is substituted for existing components in the fixed component of <code>asreml.obj\$call</code> . If changes are specified, the fixed terms will be re-ordered so that single-variable terms come first, followed by two-variable terms and so on.
<code>random.</code>	A character or formula specifying changes to the random formula. This is a one-sided formula where <code>"."</code> is substituted for existing components in the random component of <code>asreml.obj\$call</code> .
<code>sparse.</code>	A character or formula specifying changes to the sparse formula. This is a one-sided formula where <code>"."</code> is substituted for existing components in the sparse component of <code>asreml.obj\$call</code> .
<code>residual.</code>	A character or formula specifying changes to the error formula, used when version 4 or later of <code>ASReml-R</code> is loaded. This is a one-sided formula where <code>"."</code> is substituted for existing components in the residual component of <code>asreml.obj\$call</code> .

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 <code>asreml.obj\$call</code> .
update	A logical indicated whether to use <code>update.asreml</code> or <code>asreml</code> to evaluate the modified call. If TRUE, use <code>update.asreml</code> to evaluate the modified call. In doing this the arguments <code>R.param</code> and <code>G.param</code> are set to those in the <code>asreml.obj</code> so that the values from the previous model are used as starting values. If FALSE then a call is made to <code>asreml</code> itself, in which the only changes from the previous call are those specified in the arguments to <code>newfit.asreml</code> .
trace	A <b>logical</b> 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.
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 <code>asreml.obj</code> is returned.
allow.fixedcorrelation	A logical indicating whether to accept a new model even when it contains correlations in the model whose values have been designated as fixed, bound or singular. If FALSE and the new model contains correlations whose values have not been able to be estimated, the supplied <code>asreml.obj</code> is returned. The fit in the supplied the <code>asreml.obj</code> will also be tested and a warning issued if both fixed correlations are found in it and <code>allow.fixedcorrelation</code> is FALSE.
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. The names must match those in the <code>vparameters</code> component of the new <code>asreml.obj</code> .
ignore.suffices	A logical vector specifying whether the suffices of the <code>asreml</code> -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 <code>asreml</code> -assigned names. If FALSE for an element of terms, the element must exactly match an <code>asreml</code> -assigned name for a variance term. This vector must be of length one or the same length as <code>terms</code> . If it is of length one then the same action is applied to the <code>asreml</code> -assigned suffices for all the terms in <code>terms</code> .
bounds	A <b>character</b> vector specifying the bounds to be applied to the terms specified in <code>set.terms</code> . This vector must be of length one or the same length as <code>set.terms</code> . If it is of length one then the same constraint is applied to all the terms in <code>set.terms</code> . 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 <code>terms</code> . This vector must be of length one or the same length as <code>terms</code> . If it is of length one then the same initial value is applied to all the terms in <code>terms</code> . If any of the <code>initial.values</code> 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, <https://asreml.kb.vsnl.co.uk/>.

**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 *i*th 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.

---

```
pairediffsTransform.alldiffs
```

*Calculates the differences between nominated pairs of predictions stored in an [alldiffs.object](#).*

---

## Description

Predictions of differences and their error intervals are formed for two levels of a factor, the `pairs.factor`. For each pair of a level of the `pairs.factor` in `numerator.levels` with a level in `denominator.levels`, an `alldiffs.object` is formed that contains the differences between predictions with this pair of levels for all of the combinations of the levels of the other factors in the `classify` of the `alldiffs.object`. These prediction differences are obtained using `linTransform` by forming a suitable contrast matrix to specify the linear transformation. This function has the advantage that the factors indexing the differences are included in the components of the `alldiffs.objects`.

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`.

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'
pairdiffsTransform(alldiffs.obj, pairs.factor, first.levels, second.levels,
                   Vmatrix = FALSE, error.intervals = "Confidence",
                   avsed.tolerance = 0.25, accuracy.threshold = NA,
                   LSDtype = "overall", LSDsupplied = NULL, LSDby = NULL,
                   LSDstatistic = "mean", LSDaccuracy = "maxAbsDeviation",
                   response = NULL, response.title = NULL, tables = "all",
                   pairwise = TRUE, alpha = 0.05, ...)
```

## Arguments

- |                              |  |
|------------------------------|--|
| <code>alldiffs.obj</code>    | An <code>alldiffs.object</code> .  |
| <code>pairs.factor</code>    | A <code>character</code> string giving the name of the factor for whose levels the differences are to be calculated.   |
| <code>first.levels</code>    | A <code>character</code> string containing the levels of the <code>pairs.factor</code> whose predictions are those subtracted from.  |
| <code>second.levels</code>   | A <code>character</code> string containing the levels of the <code>pairs.factor</code> whose predictions are those that are subtracted.  |
| <code>Vmatrix</code>         | A <code>logical</code> indicating whether the variance matrix of the predictions will be stored as a component of the <code>alldiffs.object</code> that is returned.   |
| <code>error.intervals</code> | A <code>character</code> 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 the LSD is zero, as can happen when predictions are constrained to be equal, then the limits of the error intervals are set to NA. If <code>LSDtype</code> is set to overall, the <code>avsed.tolerance</code> is not NA and the range of the SEDs divided by the average of the SEDs exceeds <code>avsed.tolerance</code> then the <code>error.intervals</code> 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`. To have it ignored, set it to NA. 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 `LSDtype` are calculated and used in `error.intervals` and plots.
2. Irrespective of the setting of `LSDtype`, if `avsed.tolerance` is not exceeded then the mean LSDs are used in `error.intervals` and plots.
3. If `LSDtype` 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 `LSDtype` 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 `LSDtype` 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.

accuracy.threshold

A [numeric](#) specifying the value of the LSD accuracy measure, which measure is specified by `LSDaccuracy`, as a threshold value in determining whether the `halfLeastSignificant` `error.interval` for a predicted value is a reasonable approximation; this will be the case if the LSDs across all pairwise comparisons for which the interval's LSD was computed, as specified by `LSDtype` and `LSDby`, are similar enough to the interval's LSD, as measured by `LSDaccuracy`. If it is NA, it will be ignored. If it is not NA, a column of [logicals](#) named `LSDwarning` will be added to the `predictions` component of the `alldiffs.object`. The value of `LSDwarning` for a `predicted.value` will be TRUE if the value of the `LSDaccuracy` measure computed from the LSDs for differences between this `predicted.value` and the other `predicted.values` as compared to its `assignedLSD` exceeds the value of `accuracy.threshold`. Otherwise, the value of `LSDwarning` for a `predicted.value` will be FALSE.

LSDtype

A [character](#) string that can be `overall`, `factor.combinations`, `per.prediction` or supplied. It determines whether the values stored in a row of a [LSD.frame](#) are the values calculated (i) `overall` from the LSD values for all pairwise comparison2, (ii) the values calculated from the pairwise LSDs for the levels of each `factor.combination`, unless there is only one prediction for a level of the `factor.combination`, when a notional LSD is calculated, (iii) `per.prediction`, being based, for each prediction, on all pairwise differences involving that prediction, or (iv) as supplied values of the LSD, specified with the `LSDsupplied` argument; these supplied values are to be placed in the `assignedLSD` column of the [LSD.frame](#) stored in an `alldiffs.object` so that they can be used in LSD calculations.

See [LSD.frame](#) for further information on the values in a row of this `data.frame` and how they are calculated.

LSDsupplied

A [data.frame](#) or a named [numeric](#) containing a set of LSD values that correspond to the observed combinations of the values of the `LSDby` variables in the [predictions.frame](#) or a single LSD value that is an overall LSD. If a

	<p><code>data.frame</code>, it may have (i) a column for the LSDby variable and a column of LSD values or (ii) a single column of LSD values with rownames being the combinations of the observed values of the LSDby variables. Any name can be used for the column of LSD values; assignedLSD is sensible, but not obligatory. Otherwise, a <code>numeric</code> containing the LSD values, each of which is named for the observed combination of the values of the LSDby variables to which it corresponds. (Applying the function <code>dae::fac.combine</code> to the predictions component is one way of forming the required combinations for the (row) names.) The values supplied will be incorporated into assignedLSD column of the <code>LSD.frame</code> stored as the LSD component of the <code>alldiffs.object</code>.</p>
LSDby	<p>A <code>character</code> (vector) of variables names, being the names of the <code>factors</code> or <code>numerics</code> in the <code>classify</code>; for each combination of their levels and values, there will be or is a row in the <code>LSD.frame</code> stored in the LSD component of the <code>alldiffs.object</code> when LSDtype is <code>factor.combinatons</code>.</p>
LSDstatistic	<p>A <code>character</code> nominating one or more of minmum, q10, q25, mean, median, q75, q90 or maximum as the value(s) to be stored in the assignedLSD column in an <code>LSD.frame</code>; the values in the assignedLSD column are used in computing halfLeastSignificant error.intervals. Here q10, q25, q75 and q90 indicate the sample quantiles corresponding to probabilities of 0.1, 0.25, 0.75 and 0.9 for the group of LSDs from which a single LSD value is calculated. The function <code>quantile</code> is used to obtain them. The mean LSD is calculated as the square root of the mean of the squares of the LSDs for the group. The median is calculated using the <code>median</code> function. Multiple values are only produced for LSDtype set to <code>factor.combination</code>, in which case LSDby must not be NULL and the number of values must equal the number of observed combinations of the values of the variables specified by LSDby. If LSDstatistic is NULL, it is reset to mean.</p>
LSDaccuracy	<p>A <code>character</code> nominating one of maxAbsDeviation, maxDeviation, q90Deviation or RootMeanSqDeviation as the statistic to be calculated as a measure of the accuracy of assignedLSD. The option q90Deviation produces the sample quantile corresponding to a probability of 0.90. The deviations are the differences between the LSDs used in calculating the LSD statistics and each assigned LSD and the accuracy is expressed as a proportion of the assigned LSD value. The calculated values are stored in the column named accuracyLSD in an <code>LSD.frame</code>.</p>
response	<p>A character specifying the response variable for the predictions. It is stored as an attribute to the <code>alldiffs.object</code>.</p>
response.title	<p>A character specifying the title for the response variable for the predictions. It is stored as an attribute to the <code>alldiffs.object</code>.</p>
tables	<p>A <code>character</code> vector containing a combination of none, predictions, vcov, backtransforms, differences, p.differences, sed, LSD and all. These nominate which components of the <code>alldiffs.object</code> to print.</p>
pairwise	<p>A <code>logical</code> 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.</p>
alpha	<p>A <code>numeric</code> giving the significance level for LSDs or one minus the confidence level for confidence intervals. It is stored as an attribute to the <code>alldiffs.object</code>.</p>
...	<p>further arguments passed to <code>linTransform.alldiffs</code>.</p>

## Value

A list of `alldiffs.objects` with a component for each combination of a `first.levels` with a `second.levels`. The name of a component will be a level from `first.levels` combined with a level from `second.levels`, separated by a comma. If the predictions in the supplied `alldiffs.object` are based on a response that was transformed, each `alldiffs.object` in the list will include a `backtransforms` component that contains a column labelled `backtransformed.predictions`, along with the backtransforms of the nominated `error.intervals`. The predictions and backtransforms components in an `alldiffs.object` will be indexed by the variables in the `classify` of `alldiffs.obj`, except that the `pairs.factor` is omitted. If the transformation was the logarithmic transformation, these `backtransformed.predictions` are predicted ratios of the untransformed response.

If `sortFactor` attribute is set and is not the `ratio.factor`, the predictions and, if present, their backtransforms will be sorted using the `sortOrder` attribute of the `alldiffs.object`, and both `sortFactor` and `sortOrder` will be set as attributes to the object.

## Author(s)

Chris Brien

## See Also

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

## Examples

```
##### Form the differences for log(RGR) for Salinity
load(system.file("extdata", "testDiffs.rda", package = "asremlPlus", mustWork = TRUE))
##### For the ratios for Cl per WU Temperature - use backtransforms of log-predictions
Preds.ratio.ClUp <- pairediffsTransform(diffs.ClUp,
                                         pairs.factor = "Temperature",
                                         first.levels = "Hot",
                                         second.levels = "Cool",
                                         error.intervals = "halfLeast",
                                         tables = "backtransforms") #Backtransforms are ratios

##### Form the differences for Nitrogen compared to no Nitrogen
data("Oats.dat")
## Not run:
m1.asr <- asreml(Yield ~ Nitrogen*Variety,
                 random=~Blocks/Wplots,
                 data=Oats.dat)
current.asrt <- as.asrtests(m1.asr)
wald.tab <- current.asrt$wald.tab
Var.diffs <- predictPlus(m1.asr, classify="Nitrogen:Variety", pairwise = TRUE,
                        Vmatrix = TRUE, error.intervals = "halfLeast",
                        LSDtype = "factor", LSDby = "Variety",
                        wald.tab = wald.tab)

## End(Not run)

## Use lme4 and emmeans 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)

  ## Set up a wald.tab
  int <- as.data.frame(rbind(rep(NA,4)))
  rownames(int) <- "(Intercept)"
  wald.tab <- anova(m1.lmer, ddf = "Kenward", type = 1)[,3:6]
  names(wald.tab) <- names(int) <- c("Df", "denDF", "F.inc", "Pr")
  wald.tab <- rbind(int, wald.tab)
  #Get predictions
  Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
  Var.preds <- summary(Var.emm)
  ## 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
  den.df <- wald.tab[match("Variety", rownames(wald.tab)), "denDF"]

  #Create alldiffs object
  Var.diffs <- as.alldiffs(predictions = Var.preds,
                          sed = Var.sed, vcov = Var.vcov,
                          classify = "Nitrogen:Variety", response = "Yield", tdf = den.df)
}

if (exists("Var.diffs"))
  Preds.diffs.OatsN <- pairdiffsTransform(alldiffs.obj = Var.diffs,
                                          pairs.factor = "Nitrogen",
                                          first.levels = c("0.2", "0.4", "0.6"),
                                          second.levels = "0", error.intervals = "halfLeast",
                                          tables = "none")

```

---

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)
```

---

pickLSDstatistics.alldiffs

*Pick LSDstatistics whose values minimize the number of errors in pairwise comparisons of predictions.*

---

## Description

Given an `alldiffs.object` with an `sed` component, `exploreLSDs.alldiffs` is used to calculate the LSD values for each set of prediction comparisons specified by `LSDtype` and `LSDby` using each of the statistics `minum`, `q10`, `q25`, `mean`, `median`, `q75`, `q90` and `maximum`. Then the numbers of false positives and false negatives resulting from employing each of the calculated LSDs is obtained. For each set of comparisons, the LSD value(s) with the lowest number of false positives are identified and, from these, the smallest value with the lowest number of false negatives. That is, a conservative approach is taken to picking LSD values by putting the priority on avoiding false positives. Before using the LSDstatistics that this function suggests, the number of false positives and negatives generated by them should be checked. For example, it may be that there are too many false negatives and a better balance between the numbers of false positives and negatives can be identified using `exploreLSDs.alldiffs`,

## Usage

```
## S3 method for class 'alldiffs'
pickLSDstatistics(alldiffs.obj,
  LSDtype = "overall", LSDby = NULL,
  alpha = 0.05, digits = 3,
  retain.zeroLSDs = FALSE,
  zero.tolerance = .Machine$double.eps ^ 0.5,
  ...)
```

## Arguments

- |                           |   |
|---------------------------|---|
| <code>alldiffs.obj</code> | An <code>alldiffs.object</code> .   |
| <code>LSDtype</code>      | A <code>character</code> string that can be <code>overall</code> or <code>factor.combinations</code> . It determines whether the LSD values that are investigated and stored are (i) the overall minimum, <code>quantile10</code> , <code>quantile25</code> , <code>mean</code> , <code>median</code> , <code>quantile75</code> , <code>quantile90</code> , and <code>maximum</code> of all pairwise LSDs, or (ii) the minimum, <code>quantile10</code> , <code>quantile25</code> , <code>mean</code> , <code>median</code> , <code>quantile75</code> , <code>quantile90</code> , and <code>maximum</code> for the pairwise LSDs for each combination of the values of the <code>factors</code> and <code>numerics</code> named in <code>LSDby</code> , unless there is only one prediction for a combination, when notional LSDs are calculated. The <code>LSDtype</code> specified here does not have to match that used in the creating the <code>alldiffs.object</code> .<br>See <code>LSD.frame</code> for further information on how the LSD statistics are calculated. |
| <code>LSDby</code>        | A <code>character</code> (vector) of variables names, being the names of the <code>factors</code> or <code>numerics</code> in the <code>classify</code> ; for each combination of the values the of the <code>factors</code> and <code>numerics</code> , the LSD errors are to be computed when <code>LSDtype</code> is <code>factor.combinations</code> . The <code>LSDby</code> specified here does not have to match that used in the creating the <code>alldiffs.object</code> .  |
| <code>alpha</code>        | A <code>numeric</code> specifying the significance level for an LSD to compare a pair of predictions.   |

digits	A <b>numeric</b> specifying the number of significant digits to retain in rounding the LSDs before determining the distinct rounded LSDs.
retain.zeroLSDs	A <b>logical</b> indicating whether to retain or omit LSDs that are zero when calculating the summaries of LSDs.
zero.tolerance	A <b>numeric</b> specifying the value such that if an LSD is less than it, it will be considered to be zero.
...	Provision for passing arguments to functions called internally - not used at present.

### Value

A **character** of length one for LSDby set to overall or of length equal to the number of observed combinations of the values of the **factors** and **numerics** in LSDby. Each element of the returned **character** is one of minimum, q10, q25, mean, median, q75, q90 or maximum, reflecting the value(s) of the LSD from amongst those calculated that minimizes the number of false positives; if there is more than one such value, then the element will correspond to the value of the LSD from amongst those with the minimum number of false positives that minimizes the number of false negatives.

### Author(s)

Chris Brien

### See Also

[asremlPlus-package](#), [exploreLSDs.alldiffs](#), [plotLSDs.data.frame](#), [plotLSDs.alldiffs](#), [plotLSDerrors.alldiffs](#), [plotLSDerrors.data.frame](#), [recalcLSD.alldiffs](#), [redoErrorIntervals.alldiffs](#)

### 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 emmeans 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
els <- as.numeric(rownames(TS.preds))
TS.vcov <- vcov(TS.emm)[els,els]
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"))
{
  ##Pick the LSD values for predictions obtained using asreml or lmerTest
  LSDstat <- pickLSDstatistics(TS.diffs)
  TS.diffs <- redoErrorIntervals(TS.diffs, LSDstatistic = LSDstat)
  TS.diffs$LSD
  LSDstat <- pickLSDstatistics(TS.diffs, LSDtype = "factor.combinations",
                              LSDby = "Sources")
  TS.diffs <- redoErrorIntervals(TS.diffs, LSDtype = "factor.combinations",
                              LSDby = "Sources", LSDstatistic = LSDstat)
  TS.diffs$LSD
}

```

---

plotLSDerrors.alldiffs

*Plots a map of the errors that occur in using the computed LSD values for pairwise differences between predictions.*

---

## Description

Produces a plot of the errors that occur in using the computed LSD values for pairwise differences predictions by comparing the result obtained from using the LSDs stored in the assignedLSD column of the LSD component of the `alldiffs.object` with those computed from the sed component using the t-value for the df stored in the tdf attribute of the `alldiffs.object`. The sed component 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 attribute for the `alldiffs.object`. The plots are produced using `plotLSDerrors.data.frame`. The order of plotting the levels of one of the factors indexing the predictions can be modified using `sort.alldiffs`.

## Usage

```
plotLSDerrors(object, ...)
```



```
## S3 method for class 'alldiffs'
plotLSDerrors(object, alpha = 0.05, useIntervals = FALSE,
               sections = NULL, gridspacing = 0, factors.per.grid = 0,
               triangles = "both", title = NULL,
               axis.labels = TRUE, axis.text.size = 12,
               sep=",", colours = c("white","blue","red","grey"),
               ggplotFuns = NULL, printPlot = TRUE,
               sortFactor = NULL, sortParallelToCombo = NULL,
               sortNestingFactor = NULL, sortOrder = NULL,
               decreasing = FALSE, ...)
```

### Arguments

object	An <code>alldiffs.object</code> with both LSD and sed components that are not NULL.
alpha	A <code>numeric</code> giving the significance level for the LSD.
useIntervals	A <code>logical</code> indicating whether to use the interval limits stored in the predictions component of object, instead of the LSDs stored in the LSD component, for determining whether pairs of predictions are significantly different. It allows a check of how the <code>error.intervals</code> in the predictions component will perform if they are used for all pairwise predictions comparisons, whereas the comparisons to which the LSDs apply may be restricted by the setting of the <code>LSDby</code> attribute of object. There is no restriction on the <code>error.intervals</code> that can be used. However, the limits for them must be in columns in the predictions component of object and their names must end with <code>.limits</code> and begin with <code>lower.</code> and <code>upper.</code>
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 <code>factors.per.grid</code> 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, <i>k</i> say, is given then a grid line is placed after every <i>k</i> 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 <code>gridspacing</code> will then be computed based on the numbers of combinations observed within the levels of the remaining factors in a single plot. The <code>gridspacing</code> argument to this function will be ignored if <code>factors.per.grid</code> is greater than zero. Grids are most useful when two or more factors index the rows and columns of each plot.
triangles	A character indicating whether the plot should include the lower, upper or both triangle(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 LSD values are calculated.

axis.text.size	A <a href="#">numeric</a> giving the size of the labels on the axes of the heatmap.
sep	A character giving the characters separating the levels of different factors in the row and column names of the sed component.
colours	A vector of of colours to be passed to the ggplot function <code>scale\_colour\_gradientn</code> .
ggplotFuncs	A <a href="#">list</a> , each element of which contains the results of evaluating a <a href="#">ggplot</a> function. It is created by calling the <a href="#">list</a> function with a <a href="#">ggplot</a> function call for each element. It is passed to ggplot via <code>plotLSDerrors.data.frame</code> to be applied in creating the ggplot object.
printPlot	A logical indicating whether or not the a plot is to be printed. This would be used when just the returned <code>data.frame</code> is required.
sortFactor	A <a href="#">character</a> 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 <code>classify</code> term then <code>sortFactor</code> can be <code>NULL</code> and the order is defined by the complete set of predicted values. If there is more than one variable in the <code>classify</code> term then <code>sortFactor</code> must be set. In this case the <code>sortFactor</code> is sorted in the same order within each combination of the values of the <code>sortParallelToCombo</code> variables: the <code>classify</code> variables, excluding the <code>sortFactor</code> . There should be only one predicted value for each unique value of <code>sortFactor</code> within each set defined by a combination of the values of the <code>classify</code> variables, excluding the <code>sortFactor</code> factor. The order to use is determined by either <code>sortParallelToCombo</code> or <code>sortOrder</code> .
sortParallelToCombo	A <a href="#">list</a> that specifies a combination of the values of the factors and numerics, excluding <code>sortFactor</code> , that are in <code>classify</code> . Each of the components of the supplied <a href="#">list</a> is named for a <code>classify</code> variable and specifies a single value for it. 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 <code>sortFactor</code> . Each of the other combinations of the values of the factors and numerics will be sorted in parallel. If <code>sortParallelToCombo</code> is <code>NULL</code> then the first value of each <code>classify</code> variable, except for the <code>sortFactor</code> factor, in the predictions component is used to define <code>sortParallelToCombo</code> . If there is only one variable in the <code>classify</code> then <code>sortParallelToCombo</code> is ignored.
sortNestingFactor	A <a href="#">character</a> containing the name of the factor that defines groups of the <code>sortFactor</code> within which the predicted values are to be ordered. If there is only one variable in the <code>classify</code> then <code>sortNestingFactor</code> is ignored.
sortOrder	A character vector whose length is the same as the number of levels for <code>sortFactor</code> in the predictions component of the <code>alldiffs.object</code> . It specifies the desired order of the levels in the reordered components of the <code>alldiffs.object</code> . The argument <code>sortParallelToCombo</code> is ignored.  The following creates a <code>sortOrder</code> vector <code>levs</code> for factor <code>f</code> based on the values in <code>x</code> : <code>levs &lt;- levels(f)[order(x)]</code> .
decreasing	A logical passed to <code>order</code> that determines whether the order for sorting the <code>alldiffs.object</code> components is for increasing or decreasing magnitude of the predicted values.
...	Provision for passing arguments to functions called internally - not used at present.

**Value**

A [list](#) with components named LSDresults and plots. The LSDresults component contains the data.frame with the columns Rows, Columns, LSDresults, sections1 and sections2. This data.frame is formed using the LSD and sed components of object and is used by [plotLSDerrors.data.frame](#) in producing the plots. The plots component contains a list of ggplot objects, one for each plot produced. Multiple plots are stored in the plots component if the sections argument is set and the plots are named for the levels combinations of the sections.

**Author(s)**

Chris Brien

**See Also**

[plotLSDerrors.alldiffs](#), [plotLSDerrors.data.frame](#), [plotLSDs.data.frame](#), [exploreLSDs](#), [sort.alldiffs](#), [subset.alldiffs](#), [ggplot](#)

**Examples**

```
##Subset WaterRunoff data to reduce time to execute
data(WaterRunoff.dat)
tmp <- subset(WaterRunoff.dat, Date == "05-18" & Benches != "3")

##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= tmp)
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 emmeans 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
  els <- as.numeric(rownames(TS.preds))
}
```

```

TS.vcov <- vcov(TS.emm)[els,els]
TS.diffs <- allDifferences(predictions = TS.preds, classify = "Sources:Type",
                          vcov = TS.vcov, tdf = den.df)
validAlldiffs(TS.diffs)
}

## Plot LSD values for predictions obtained using asreml or lmerTest
if (exists("TS.diffs"))
{
  plotLSDerrors(TS.diffs, gridspacing = rep(c(3,4), c(4,2)))

  plotLSDerrors(TS.diffs, sections = "Sources", axis.labels = TRUE)
}

```

---

plotLSDerrors.data.frame

*Plots a map of the supplied errors that occur in using the computed LSD values for pairwise differences between predictions.*

---

## Description

Produces a plot of the errors that have been supplied in a `data.frame`. The `data.frame` includes two factors whose levels specify, for each LSD result, which combinations of factor levels are being compared. The function `plotLSDerrors.alldiffs` produces such `data.frames`.

## Usage

```

## S3 method for class 'data.frame'
plotLSDerrors(object, LSDresults = "LSDresults", x, y,
              alpha = 0.05, triangles = "both",
              gridspacing = 0, title = NULL,
              axis.labels = NULL, axis.text.size = 12,
              colours = c("white", "blue", "red", "grey"),
              ggplotFuncs = NULL, printPlot = TRUE, ...)

```

## Arguments

<code>object</code>	A <a href="#">data.frame</a> containing the three columns specified by <code>LSDresults</code> , <code>x</code> and <code>y</code> .
<code>LSDresults</code>	A <a href="#">character</a> giving the name of the column in <code>object</code> that contains the LSDresults values to be plotted. The column should be a <a href="#">character</a> or <a href="#">factor</a> with values or levels that are a subset of Ok, FN, FP and na.
<code>x</code>	A <a href="#">character</a> giving the name of the column in <code>object</code> that contains the factor whose levels index the LSD values that are to be plotted in the same column.
<code>y</code>	A <a href="#">character</a> giving the name of the column in <code>object</code> that contains the labels of the LSD values that are to be plotted as the rows.
<code>alpha</code>	A <a href="#">numeric</a> giving the significance level for the LSD.
<code>triangles</code>	A <a href="#">character</a> indicating whether the plot should include the lower, upper or both triangle(s). Here it is only used to adjust gridlines for the omission of the diagonal.

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.
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.
axis.text.size	A <a href="#">numeric</a> giving the size of the labels on the axes of the heatmap.
colours	A vector of of colours to be passed to the ggplot function <code>scale\_colour\_gradientn</code> .
ggplotFuncs	A <a href="#">list</a> , each element of which contains the results of evaluating a <a href="#">ggplot</a> function. It is created by calling the <a href="#">list</a> function with a <a href="#">ggplot</a> function call for each element. These functions are applied in creating the ggplot object.
printPlot	A logical indicating whether or not the a plot is to be printed. This would be used when just the returned ggplot object is required.
...	Provision for passing arguments to functions called internally - not used at present.

**Value**

An object of class "[ggplot](#)", which can be plotted using `print` or otherwise manipulated.

**Author(s)**

Chris Brien

**See Also**

[plotLSDs.data.frame](#), [plotLSDs.alldiffs](#), [exploreLSDs](#), [ggplot](#)

**Examples**

```
##Subset WaterRunoff data to reduce time to execute
data(WaterRunoff.dat)
tmp <- subset(WaterRunoff.dat, Date == "05-18")

##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= tmp))
current.asrt <- as.asrttests(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
  els <- as.numeric(rownames(TS.preds))
  TS.vcov <- vcov(TS.emm)[els,els]
  TS.diffs <- allDifferences(predictions = TS.preds, classify = "Sources:Type",
                            vcov = TS.vcov, tdf = den.df)
  validAlldiffs(TS.diffs)
}

## Plot LSD values for predictions obtained using asreml or lmerTest
if (exists("TS.diffs"))
{
  LSDresults <- within(reshape2::melt(TS.diffs$p.differences),
                      {
                        Var1 <- factor(Var1, levels=dimnames(TS.diffs$p.differences)[[1]])
                        Var2 <- factor(Var2, levels=levels(Var1))
                      })
  names(LSDresults) <- c("Rows", "Columns", "LSDresults")
  plotLSDerrors(LSDresults, x = "Rows", y = "Columns", gridspacing = rep(c(3,4), c(4,2)))
}

```

---

plotLSDs.alldiffs	<i>Plots a heat map of computed LSD values for pairwise differences between predictions.</i>
-------------------	--

---

## Description

Produces a heat-map plot of the computed LSD values for pairwise differences between predictions by multiplying the values stored in the `sed` component of an `all.diffs` object by the `t`-value for the `df` stored in the `tdf` attribute of the object. This component 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` attribute for the `alldiffs` object. The plots are produced using `plotLSDs.data.frame`. The order of plotting the levels of one of the factors indexing the predictions can be modified using `sort.alldiffs`.

## Usage

```

plotLSDs(object, ...)
## S3 method for class 'alldiffs'

```

```
plotLSDs(object, alpha = 0.05,
         sections = NULL, gridspacing = 0, factors.per.grid = 0,
         triangles = "both",
         title = NULL, axis.labels = TRUE, axis.text.size = 12,
         sep=",", colours = RColorBrewer::brewer.pal(3, "Set2"),
         ggplotFuncs = NULL, printPlot = TRUE,
         sortFactor = NULL, sortParallelToCombo = NULL,
         sortNestingFactor = NULL, sortOrder = NULL,
         decreasing = FALSE, ...)
```

## Arguments

object	An <code>alldiffs.object</code> with an <code>sed</code> component that is not <code>NULL</code> .
alpha	A <code>numeric</code> giving the significance level for the LSD.
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 <code>factors.per.grid</code> 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 <code>gridspacing</code> will then be computed based on the numbers of combinations observed within the levels of the remaining factors in a single plot. The <code>gridspacing</code> argument to this function will be ignored if <code>factors.per.grid</code> is greater than zero. Grids are most useful when two or more factors index the rows and columns of each plot.
triangles	A character indicating whether the plot should include the lower, upper or both triangle(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 <code>TRUE</code> , the label is the comma-separated list of factors whose levels combinations are involved in the prediction differences for which the LSD values are calculated.
axis.text.size	A <code>numeric</code> giving the size of the labels on the axes of the heatmap.
sep	A character giving the characters separating the levels of different factors in the row and column names of the <code>sed</code> component.
colours	A vector of colours to be passed to the ggplot function <code>scale\_colour\_gradientn</code> .
ggplotFuncs	A <code>list</code> , each element of which contains the results of evaluating a <code>ggplot</code> function. It is created by calling the <code>list</code> function with a <code>ggplot</code> function call for each element. It is passed to ggplot via <code>plotLSDs.data.frame</code> to be applied in creating the ggplot object.
printPlot	A logical indicating whether or not the a plot is to be printed. This would be used when just the returned <code>data.frame</code> is required.

sortFactor	A <a href="#">character</a> 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 sortParallelToCombo 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 classify variables, excluding the sortFactor factor. The order to use is determined by either sortParallelToCombo or sortOrder.
sortParallelToCombo	A <a href="#">list</a> that specifies a combination of the values of the factors and numerics, excluding sortFactor, that are in classify. Each of the components of the supplied <a href="#">list</a> is named for a classify variable and specifies a single value for it. 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. Each of the other combinations of the values of the factors and numerics will be sorted in parallel. If sortParallelToCombo is NULL then the first value of each classify variable, except for the sortFactor factor, in the predictions component is used to define sortParallelToCombo. If there is only one variable in the classify then sortParallelToCombo is ignored.
sortNestingFactor	A <a href="#">character</a> containing the name of the factor that defines groups of the sortFactor within which the predicted values are to be ordered. If there is only one variable in the classify then sortNestingFactor is ignored.
sortOrder	A character vector whose length is the same as the number of levels for sortFactor in the predictions component of the <a href="#">alldiffs.object</a> . It specifies the desired order of the levels in the reordered components of the <a href="#">alldiffs.object</a> . The argument sortParallelToCombo is ignored.  The following creates a sortOrder vector levs for factor f based on the values in x: <code>levs &lt;- levels(f)[order(x)]</code> .
decreasing	A logical passed to order that determines whether the order for sorting the <a href="#">alldiffs.object</a> components is for increasing or decreasing magnitude of the predicted values.
...	Provision for passing arguments to functions called internally - not used at present.

## Value

A [list](#) with components named LSDs and plots. The LSDs component contains the data.frame with the columns Rows, Columns, LSDs, sections1 and sections2. This data.frame is formed using the sed component of object and is used by [plotLSDs.data.frame](#) in producing the plot. The plots component contains a list of ggplot objects, one for each plot produced. Multiple plots are stored in the plots component if the sections argument is set and the plots are named for the levels combinations of the sections.

## Author(s)

Chris Brien



**See Also**

[plotLSDs.data.frame](#), [exploreLSDs](#), [sort.alldiffs](#), [subset.alldiffs](#), [ggplot](#)

**Examples**

```
##Subset WaterRunoff data to reduce time to execute
data(WaterRunoff.dat)
tmp <- subset(WaterRunoff.dat, Date == "05-18" & Benches != "3")

##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= tmp)
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 emmeans 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
  els <- as.numeric(rownames(TS.preds))
  TS.vcov <- vcov(TS.emm)[els,els]
  TS.diffs <- allDifferences(predictions = TS.preds, classify = "Sources:Type",
                           vcov = TS.vcov, tdf = den.df)
  validAlldiffs(TS.diffs)
}

## Plot LSD values for predictions obtained using asreml or lmerTest
if (exists("TS.diffs"))
{
  plotLSDs(TS.diffs, gridspacing = rep(c(3,4), c(4,2)))

  plotLSDs(TS.diffs, sections = "Sources", axis.labels = TRUE)
}
```

---

plotLSDs.data.frame	<i>Plots a heat map of computed LSD-values for pairwise differences between predictions.</i>
---------------------	--

---

### Description

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

### Usage

```
## S3 method for class 'data.frame'
plotLSDs(object, LSD = "LSDs", x, y, alpha = 0.05,
         triangles = "both", gridspacing = 0,
         title = NULL, axis.labels = NULL, axis.text.size = 12,
         colours = RColorBrewer::brewer.pal(3, "Set2"),
         ggplotFuncs = NULL, printPlot = TRUE, ...)
```

### Arguments

<code>object</code>	A <code>data.frame</code> containing the three columns specified by <code>LSD</code> , <code>x</code> and <code>y</code> .
<code>LSD</code>	A character giving the name of the column in <code>object</code> that contains the LSD values to be plotted.
<code>x</code>	A character giving the name of the column in <code>object</code> that contains the factor whose levels index the LSD values that are to be plotted in the same column.
<code>y</code>	A character giving the name of the column in <code>object</code> that contains the labels of the LSD values that are to be plotted as the rows.
<code>alpha</code>	A <a href="#">numeric</a> giving the significance level for the LSD.
<code>triangles</code>	A character indicating whether the plot should include the lower, upper or both triangle(s). Here it is only used to adjust gridlines for the omission of the diagonal.
<code>gridspacing</code>	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, <i>k</i> say, is given then a grid line is placed after every <i>k</i> 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.
<code>title</code>	A character string giving the main title for the plot.
<code>axis.labels</code>	A character string giving the label to use for both the x- and y-axis.
<code>axis.text.size</code>	A <a href="#">numeric</a> giving the size of the labels on the axes of the heatmap.
<code>colours</code>	A vector of of colours to be passed to the <code>ggplot</code> function <code>scale\_colour\_gradientn</code> .
<code>ggplotFuncs</code>	A <a href="#">list</a> , each element of which contains the results of evaluating a <a href="#">ggplot</a> function. It is created by calling the <a href="#">list</a> function with a <a href="#">ggplot</a> function call for each element. These functions are applied in creating the <code>ggplot</code> object.
<code>printPlot</code>	A logical indicating whether or not the a plot is to be printed. This would be used when just the returned <code>ggplot</code> object is required.
<code>...</code>	Provision for passing arguments to functions called internally - not used at present.

**Value**

An object of class "[ggplot](#)", which can be plotted using `print` or otherwise manipulated.

**Author(s)**

Chris Brien

**See Also**

[plotLSDs.alldiffs](#), [plotLSDerrors.alldiffs](#), [plotLSDerrors.data.frame](#), [explorelSDs](#), [ggplot](#)

**Examples**

```
##Subset WaterRunoff data to reduce time to execute
data(WaterRunoff.dat)
tmp <- subset(WaterRunoff.dat, Date == "05-18")

##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= tmp))
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 emmeans 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
  els <- as.numeric(rownames(TS.preds))
  TS.vcov <- vcov(TS.emm)[els,els]
  TS.diffs <- allDifferences(predictions = TS.preds, classify = "Sources:Type",
                           vcov = TS.vcov, tdf = den.df)
  validAlldiffs(TS.diffs)
}
```

```
## Plot LSD values for predictions obtained using asreml or lmerTest
if (exists("TS.diffs"))
{
  LSD <- within(reshape2::melt(TS.diffs$p.differences),
    {
      Var1 <- factor(Var1, levels=dimnames(TS.diffs$p.differences)[[1]])
      Var2 <- factor(Var2, levels=levels(Var1))
    })
  names(LSD) <- c("Rows", "Columns", "LSDs")
  plotLSDs(LSD, x = "Rows", y = "Columns", gridspacing = rep(c(3,4), c(4,2)))
}
```

---

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", interval.annotate = TRUE,
  titles = NULL, y.title = NULL,
  filestem = NULL, ggplotFuncs = NULL, ...)
```

## Arguments

<code>data</code>	A <a href="#">predictions.frame</a> , or <code>data.frame</code> , 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 <code>y</code> argument, usually <code>predicted.value</code> or <code>backtransformed.predictions</code> ; each row contains a single predicted value. It should also include columns for the <code>standard.error</code> and <code>est.status</code> . The number of rows should equal the number of unique combinations of the classifying variables. While such a <code>data.frame</code> can be constructed from the beginning, the <code>pvals</code> component of the value produced by <code>predict.asreml</code> is a suitable value to supply for this argument. Note that the names <code>standard.error</code> and <code>est.status</code> have been changed to <code>std.error</code> and <code>status</code> in the <code>pvals</code> component produced by <code>asreml-R4</code> ; if the new names are in the <code>data.frame</code> supplied to <code>predictions</code> , they will be returned to the previous names.
-------------------	--

	<p>If <code>error.intervals</code> 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.</p>
<code>classify</code>	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 <code>:</code> operator. To predict the overall mean, set the <code>classify</code> to "(Intercept)".
<code>y</code>	A character string giving the name of the variable that is to be plotted on the Y axis.
<code>x.num</code>	A character string giving the name of the numeric covariate that corresponds to <code>x.fac</code> , 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 <code>x.fac</code> .
<code>x.fac</code>	A character string giving the name of the factor that corresponds to <code>x.num</code> , 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 <code>x.num</code> . The levels of <code>x.fac</code> must be in the order in which they are to be plotted - if they are dates, then they should be in the form <code>yyyymmdd</code> , which can be achieved using <code>as.Date</code> . However, the levels can be non-numeric in nature, provided that <code>x.num</code> is also set.
<code>nonx.fac.order</code>	A character vector giving the order in which factors other than <code>x.fac</code> are to be plotted in faceted 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 <code>x.num</code> or <code>x.fac</code> . 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.
<code>colour.scheme</code>	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.
<code>panels</code>	Possible values are "single" and "multiple". When line plots are to be produced, because variables involving <code>x.num</code> or <code>x.fac</code> are involved in <code>classify</code> for the predictions, <code>panels</code> determines whether or not a single panel or multiple panels in a single window are produced. The <code>panels</code> argument is ignored for bar charts.
<code>graphics.device</code>	A character specifying a graphics device for plotting. The default is <code>graphics.device = NULL</code> , 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.
<code>error.intervals</code>	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.
<code>interval.annotate</code>	A logical indicating whether the plot annotation indicating the type of <code>error.intervals</code> is to be included in the plot.

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. These functions are applied in creating the ggplot object for plotting.
...	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.asrttests(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 emmeans 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 = "emmmean",
                                   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 using `sort.alldiffs`.

## Usage

```
plotPvalues(object, ...)
## S3 method for class 'alldiffs'
plotPvalues(object, sections = NULL,
             gridspacing = 0, factors.per.grid = 0,
             show.sig = FALSE, alpha = 0.10,
             sig.size = 3, sig.colour = "black",
             sig.face = "plain", sig.family = "",
             triangles = "both",
             title = NULL, axis.labels = TRUE, axis.text.size = 12,
             sep=",", colours = RColorBrewer::brewer.pal(3, "Set2"),
             ggplotFuncs = NULL, printPlot = TRUE,
             sortFactor = NULL, sortParallelToCombo = NULL,
             sortNestingFactor = NULL, sortOrder = NULL,
             decreasing = FALSE, ...)
```

## Arguments

object	An <code>alldiffs.object</code> 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 <code>factors.per.grid</code> 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 <code>gridspacing</code> will then be computed based on the numbers of combinations observed within the levels of the remaining factors in a single plot. The <code>gridspacing</code> argument to this function will be ignored if <code>factors.per.grid</code> 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 $0.05 < p \leq 0.10$ . The last is only included for $\alpha = 0.10$ .
alpha	A numeric giving the significance level for testing pairwise differences; must be 0.05 or 0.10.
sig.size	A numeric specifying the size, in pts, of the significance asterisks.



sig.colour	A <a href="#">character</a> specifying the colour to use for the significance asterisks.
sig.face	A <a href="#">character</a> specifying the font face for the significance asterisks ("plain", "italic", "bold", "bold.italic").
sig.family	A <a href="#">character</a> specifying the font family for the significance asterisks. The font families that are available depends on the system. For font families other than the basic Postscript fonts, see the <a href="#">extrafont</a> package.
triangles	A <a href="#">character</a> indicating whether the plot should include the lower, upper or both triangle(s).
title	A <a href="#">character</a> 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 <a href="#">logical</a> 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.
axis.text.size	A <a href="#">numeric</a> giving the size of the labels on the axes of the heatmap.
sep	A <a href="#">character</a> giving the characters separating the levels of different factors in the row and column names of the p.differences component.
colours	A vector of of colours to be passed to the <a href="#">ggplot</a> function <code>scale\_colour\_gradientn</code> .
ggplotFuncs	A <a href="#">list</a> , each element of which contains the results of evaluating a <a href="#">ggplot</a> function. It is created by calling the <a href="#">list</a> function with a <a href="#">ggplot</a> function call for each element. It is passed to <a href="#">ggplot</a> via <a href="#">plotPvalues.data.frame</a> to be applied in creating the <a href="#">ggplot</a> object.
printPlot	A <a href="#">logical</a> indicating whether or not the a plot is to be printed. This would be used when just the returned <code>data.frame</code> is required.
sortFactor	A <a href="#">character</a> 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 <code>classify</code> term then <code>sortFactor</code> can be NULL and the order is defined by the complete set of predicted values. If there is more than one variable in the <code>classify</code> term then <code>sortFactor</code> must be set. In this case the <code>sortFactor</code> is sorted in the same order within each combination of the values of the <code>sortParallelToCombo</code> variables: the <code>classify</code> variables, excluding the <code>sortFactor</code> . There should be only one predicted value for each unique value of <code>sortFactor</code> within each set defined by a combination of the values of the <code>classify</code> variables, excluding the <code>sortFactor</code> factor. The order to use is determined by either <code>sortParallelToCombo</code> or <code>sortOrder</code> .
sortParallelToCombo	A <a href="#">list</a> that specifies a combination of the values of the factors and numerics, excluding <code>sortFactor</code> , that are in <code>classify</code> . Each of the components of the supplied <a href="#">list</a> is named for a <code>classify</code> variable and specifies a single value for it. 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 <code>sortFactor</code> . Each of the other combinations of the values of the factors and numerics will be sorted in parallel. If <code>sortParallelToCombo</code> is NULL then the first value of each <code>classify</code> variable, except for the <code>sortFactor</code> factor, in the predictions component is used to define <code>sortParallelToCombo</code> . If there is only one variable in the <code>classify</code> then <code>sortParallelToCombo</code> is ignored.
sortNestingFactor	A <a href="#">character</a> containing the name of the factor that defines groups of the <code>sortFactor</code> within which the predicted values are to be ordered. If there is only one variable in the <code>classify</code> then <code>sortNestingFactor</code> is ignored.

sortOrder	<p>A character vector whose length is the same as the number of levels for sortFactor in the predictions component of the <code>alldiffs.object</code>. It specifies the desired order of the levels in the reordered components of the <code>alldiffs.object</code>. The argument <code>sortParallelToCombo</code> is ignored.</p> <p>The following creates a <code>sortOrder</code> vector <code>levs</code> for factor <code>f</code> based on the values in <code>x</code>: <code>levs &lt;- levels(f)[order(x)]</code>.</p>
decreasing	A logical passed to <code>order</code> that determines whether the order for sorting the <code>alldiffs.object</code> components is for increasing or decreasing magnitude of the predicted values.
...	Provision for passing arguments to functions called internally - not used at present.

### Value

A `list` with components named `pvalues` and `plots`. The `pvalues` component contains the `data.frame` with the columns `Rows`, `Columns`, `p`, `sections1` and `sections2`. This `data.frame` is formed using the `sed` component of `object` and is used by `plotPvalues.data.frame` in producing the plot. The `plots` component contains a list of `ggplot` objects, one for each plot produced. Multiple plots are stored in the `plots` component if the `sections` argument is set and the plots are named for the levels combinations of the sections.

### Author(s)

Chris Brien

### See Also

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

### Examples

```
##Subset WaterRunoff data to reduce time to execute
data(WaterRunoff.dat)
tmp <- subset(WaterRunoff.dat, Date == "05-18" & Benches != "3")

##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= tmp)
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 emmeans 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
  els <- as.numeric(rownames(TS.preds))
  TS.vcov <- vcov(TS.emm)[els,els]
  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"))
{
  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, alpha = 0.10,
             sig.size = 3, sig.colour = "black",
             sig.face = "plain", sig.family = "",
             triangles = "both",
             title = NULL, axis.labels = NULL, axis.text.size = 12,
             colours = RColorBrewer::brewer.pal(3, "Set2"),
             ggplotFuncs = NULL, printPlot = TRUE, ...)

```

**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 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 $0.05 < p \leq 0.10$ . The last is only included for alpha = 0.10.
alpha	A numeric giving the significance level for testing pairwise differences; must be 0.05 or 0.10.
sig.size	A numeric specifying the size, in pts, of the significance asterisks.
sig.colour	A character specifying the colour to use for the significance asterisks.
sig.face	A character specifying the font face for the significance asterisks ("plain", "italic", "bold", "bold.italic").
sig.family	A character specifying the font family for the significance asterisks. The font families that are available depends on the system. For font families other than the basic Postscript fonts, see the extrafont package.
triangles	A character indicating whether the plot should include the lower, upper or both triangle(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.
axis.text.size	A numeric giving the size of the labels on the axes of the heatmap.
colours	A vector of colours to be passed to the ggplot function <code>scale\_colour\_gradientn</code> .
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. These functions are applied in creating the ggplot object.
printPlot	A logical indicating whether or not the a plot is to be printed. This would be used when just the returned ggplot object is required.
...	Provision for passing arguments to functions called internally - not used at present.

**Value**

An object of class "ggplot", which can be plotted using `print` or otherwise manipulated.

**Author(s)**

Chris Brien

**See Also**[plotPvalues.alldiffs](#), [allDifferences.data.frame](#), [ggplot](#)**Examples**

```
##Subset WaterRunoff data to reduce time to execute
data(WaterRunoff.dat)
tmp <- subset(WaterRunoff.dat, Date == "05-18")

##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= tmp))
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 emmeans 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
  els <- as.numeric(rownames(TS.preds))
  TS.vcov <- vcov(TS.emm)[els,els]
  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"))
{
  p <- within(reshape2::melt(TS.diffs$p.differences),
```

```

    {
      Var1 <- factor(Var1, levels=dimnames(TS.diffs$p.differences)[[1]])
      Var2 <- factor(Var2, levels=levels(Var1))
    })
  names(p) <- c("Rows", "Columns", "p")
  plotPvalues(p, x = "Rows", y = "Columns",
             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

<code>data</code>	A <code>data.frame</code> 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.
<code>residuals</code>	A <code>data.frame</code> , with either 2 or 3 initial columns followed by columns, each of which are the residuals from a simulated data set.
<code>restype</code>	A character describing the type of residuals that have been supplied. It will be used in the plot titles.
<code>...</code>	Other arguments that are passed down to the function <code>asreml.variogram</code> .

## 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 (Stefanova 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	<i>Performs a combination of a linear and a power transformation on a variable. The transformed variable is stored in the data.frame data.</i>
----------------	--

---

### 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

<code>var.name</code>	A character string specifying the name of the variable in the <code>data.frame</code> data that is to be transformed.
<code>power</code>	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 <code>offset</code> . If <code>power = 0</code> , 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 <code>offset</code> and/or a <code>scale</code> not equal to one is used.
<code>offset</code>	A number to be added to each value of the variable, after any scaling and before applying any power transformation.
<code>scale</code>	A number to multiply each value of the variable, before adding any <code>offset</code> and applying any power transformation.
<code>titles</code>	A character vector, each element of which is named for a variable in <code>data</code> and is a character string giving a title to use in output (e.g. tables and graphs) involving the variable. If <code>titles</code> are not supplied, the column name of the variable in <code>data</code> is used.
<code>data</code>	A <code>data.frame</code> 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	<i>Description of a predictions object</i>
-------------------	--

---

### 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 that begins with the variables classifying the predictions, in the same order as in the classify, followed by a column of predictions that is named either predicted.value or backtransformed.predictions; it also contains columns named 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.

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.

IF `accuracy.threshold` is set to a numeric value at the time the `prediction.frame` is formed, it will also include a column logical values named `LSDwarning`.

When `halfLeastSignificant` limits have been included in a `predictions.frame`, its attributes will include those that are not NULL of `LSDtype`, `LSDby`, `LSDstatistic`, `LSDaccuracy` and `LSDvalues`. `LSDvalues` are the LSD values used to calculate the `halfLeastSignificant` `error.intervals` and are an expanded version of the values stored in the assignedLSD column of the [LSD.frame](#).

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 emmeans 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	<i>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 alldiffs.</i>
--------------------	---

---

## 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 denominator 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,

```

```

inestimable.rm = TRUE, linear.transformation = NULL,
error.intervals = "Confidence", alpha = 0.05,
wald.tab = NULL, ddf.na = "residual", ddf.values = NULL,
pairwise = TRUE, Vmatrix = FALSE,
avsed.tolerance = 0.25, accuracy.threshold = NA,
LSDtype = "overall", LSDsupplied = NULL, LSDby = NULL,
LSDstatistic = "mean", LSDaccuracy = "maxAbsDeviation",
x.num = NULL, x.fac = NULL,
x.pred.values = NULL, x.plot.values = NULL,
titles = NULL, tables = "all", level.length = NA,
transform.power = 1, offset = 0, scale = 1,
transform.function = "identity",
sortFactor = NULL, sortParallelToCombo = NULL,
sortNestingFactor = NULL, sortOrder = NULL,
decreasing = FALSE, trace = FALSE, ...)

```

## Arguments

<code>asreml.obj</code>	asreml object for a fitted model.
<code>classify</code>	A <a href="#">character</a> 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 <code>:</code> operator. To predict the overall mean, set the <code>classify</code> to <code>"(Intercept)"</code> .
<code>term</code>	A <a href="#">character</a> string giving the variables that define the term that was fitted using asreml and that corresponds to <code>classify</code> . It only needs to be specified when it is different to <code>classify</code> ; it is stored as an attribute of the <code>alldiffs.object</code> . It is likely to be needed when the fitted model includes terms that involve both a <a href="#">numeric</a> covariate and a <a href="#">factor</a> that parallel each other; the <code>classify</code> would include the covariate and the term would include the factor.
<code>inestimable.rm</code>	A logical indicating whether rows for predictions that are not estimable are to be removed from the components of the <code>alldiffs.object</code> .
<code>linear.transformation</code>	<p>A <a href="#">formula</a> or a <a href="#">matrix</a>. If a <a href="#">formula</a> is given then it is taken to be a submodel of a model term corresponding to the <code>classify</code>. The projection matrix that transforms the predictions so that they conform to the submodel is obtained; the submodel does not have to involve variables in the <code>classify</code>, but the variables must be columns in the predictions component of <code>alldiffs.obj</code> and the space for the submodel must be a subspace of the space for the term specified by the <code>classify</code>. For example, for <code>classify</code> set to <code>"A:B"</code>, the submodel <code>~ A + B</code> will result in the predictions for the combinations of A and B being made additive for the <a href="#">factors</a> A and B. The submodel space corresponding to <code>A + B</code> is a subspace of the space <code>A:B</code>. In this case both the submodel and the <code>classify</code> involve only the factors A and B. To fit an intercept-only submodel, specify <code>linear.transformation</code> to be the formula <code>~1</code>.</p> <p>If a <a href="#">matrix</a> is provided then it will be used to apply the linear transformation to the predictions. It might be a contrast <a href="#">matrix</a> or a <a href="#">matrix</a> of weights for a factor used to obtain the weighted average over that factor. The number of rows in the <a href="#">matrix</a> should equal the number of linear combinations of the predictions desired and the number of columns should equal the number of predictions.</p>

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

`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 the LSD is zero, as can happen when predictions are constrained to be equal, then the limits of the error intervals are set to NA. If LSDtype 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`

A [numeric](#) giving the significance level for LSDs or one minus the confidence level for confidence intervals. It is stored as an attribute to 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 determining the degrees of freedom for calculating confidence or half-LSD `error.intervals` and p-values, the latter to be stored in the `p.differences` component of the `alldiffs.object` that is created.

`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$nedf` are used. If `dDF.na = "none"`, no substitute denominator degrees of freedom are employed; if `dDF.na = "maximum"`, the maximum of those `denDF` that are available, excluding that for the Intercept, is used; if all `denDF` are NA, `asreml.obj$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.

`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`.

`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`. To have it ignored, set it to NA. 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 `LSDtype` are calculated and used in `error.intervals` and plots.
2. Irrespective of the setting of `LSDtype`, if `avsed.tolerance` is not exceeded then the mean LSDs are used in `error.intervals` and plots.
3. If `LSDtype` 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 `LSDtype` 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 `LSDtype` 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.

#### `accuracy.threshold`

A **numeric** specifying the value of the LSD accuracy measure, which measure is specified by `LSDaccuracy`, as a threshold value in determining whether the halfLeastSignificant `error.interval` for a predicted value is a reasonable approximation; this will be the case if the LSDs across all pairwise comparisons for which the interval's LSD was computed, as specified by `LSDtype` and `LSDby`, are similar enough to the interval's LSD, as measured by `LSDaccuracy`. If it is NA, it will be ignored. If it is not NA, a column of **logicals** named `LSDwarning` will be added to the predictions component of the `alldiffs.object`. The value of `LSDwarning` for a predicted.value will be TRUE if the value of the `LSDaccuracy` measure computed from the LSDs for differences between this predicted.value and the other predicted.values as compared to its assignedLSD exceeds the value of `accuracy.threshold`. Otherwise, the value of `LSDwarning` for a predicted.value will be FALSE.

#### `LSDtype`

A **character** string that can be `overall`, `factor.combinations`, `per.prediction` or supplied. It determines whether the values stored in a row of a `LSD.frame` are the values calculated (i) `overall` from the LSD values for all pairwise comparison2, (ii) the values calculated from the pairwise LSDs for the levels of each `factor.combination`, unless there is only one prediction for a level of the `factor.combination`, when a notional LSD is calculated, (iii) `per.prediction`, being based, for each prediction, on all pairwise differences involving that prediction, or (iv) as supplied values of the LSD, specified with the `LSDsupplied` argument; these supplied values are to be placed in the assignedLSD column of the `LSD.frame` stored in an `alldiffs.object` so that they can be used in LSD calculations.

See `LSD.frame` for further information on the values in a row of this `data.frame` and how they are calculated.

#### `LSDsupplied`

A **data.frame** or a named **numeric** containing a set of LSD values that correspond to the observed combinations of the values of the `LSDby` variables in the `predictions.frame` or a single LSD value that is an overall LSD. If a **data.frame**, it may have (i) a column for the `LSDby` variable and a column of LSD values or (ii) a single column of LSD values with rownames being the combinations of the observed values of the `LSDby` variables. Any name can be used for the column of LSD values; `assignedLSD` is sensible, but not obligatory. Otherwise, a **numeric** containing the LSD values, each of which is named for the observed combination of the values of the `LSDby` variables to which it corresponds.

(Applying the function `dae::fac.combine` to the predictions component is one way of forming the required combinations for the (row) names.) The values supplied will be incorporated into assignedLSD column of the `LSD.frame` stored as the LSD component of the `alldiffs.object`.

LSDby	A <code>character</code> (vector) of variables names, being the names of the <code>factors</code> or <code>numerics</code> in the <code>classify</code> ; for each combination of their levels and values, there will be or is a row in the <code>LSD.frame</code> stored in the LSD component of the <code>alldiffs.object</code> when LSDtype is <code>factor.combinatons</code> .
LSDstatistic	A <code>character</code> nominating one or more of minnum, q10, q25, mean, median, q75, q90 or maximum as the value(s) to be stored in the assignedLSD column in an <code>LSD.frame</code> ; the values in the assignedLSD column are used in computing halfLeastSignificant error.intervals. Here q10, q25, q75 and q90 indicate the sample quantiles corresponding to probabilities of 0.1, 0.25, 0.75 and 0.9 for the group of LSDs from which a single LSD value is calculated. The function <code>quantile</code> is used to obtain them. The mean LSD is calculated as the square root of the mean of the squares of the LSDs for the group. The median is calculated using the <code>median</code> function. Multiple values are only produced for LSDtype set to <code>factor.combination</code> , in which case LSDby must not be NULL and the number of values must equal the number of observed combinations of the values of the variables specified by LSDby. If LSDstatistic is NULL, it is reset to mean.
LSDaccuracy	A <code>character</code> nominating one of <code>maxAbsDeviation</code> , <code>maxDeviation</code> , <code>q90Deviation</code> or <code>RootMeanSqDeviation</code> as the statistic to be calculated as a measure of the accuracy of assignedLSD. The option <code>q90Deviation</code> produces the sample quantile corresponding to a probability of 0.90. The deviations are the differences between the LSDs used in calculating the LSD statistics and each assigned LSD and the accuracy is expressed as a proportion of the assigned LSD value. The calculated values are stored in the column named <code>accuracyLSD</code> in an <code>LSD.frame</code> .
titles	A <code>list</code> , each component of which is named for a column in the <code>data.frame</code> for <code>asreml.obj</code> 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.
tables	A <code>character</code> vector containing a combination of <code>none</code> , <code>predictions</code> , <code>vcov</code> , <code>backtransforms</code> , <code>differences</code> , <code>p.differences</code> , <code>sed</code> , <code>LSD</code> and <code>all</code> . These nominate which components of the <code>alldiffs.object</code> to print.
x.num	A <code>character</code> string giving the name of the numeric covariate that (i) corresponds to <code>x.fac</code> , (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 <code>x.fac</code> .
x.fac	A <code>character</code> string giving the name of the factor that (i) corresponds to <code>x.num</code> , (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 <code>x.num</code> . The levels of <code>x.fac</code> must be in the order in which they are to be plotted - if they are dates, then they should be in the form <code>yyyymmdd</code> , which can be achieved using <code>as.Date</code> . However, the levels can be non-numeric in nature, provided that <code>x.num</code> is also set.
x.pred.values	The values of <code>x.num</code> for which predicted values are required. If <code>levels</code> is set for passing to <code>predict.asreml</code> , <code>x.pred.values</code> is ignored. Note that while <code>levels</code> is and alternative to <code>x.pred.values</code> , 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.
level.length	The maximum number of characters from 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 <b>numeric</b> 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 stored in the backtransforms component of the <b>alldiffs.object</b> . 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 <b>numeric</b> that has been added to each value of the response after any scaling and before applying any power transformation.
scale	A <b>numeric</b> by which each value of the response has been multiplied before adding any offset and applying any power transformation.
transform.function	A <b>character</b> giving the name of a function that specifies the scale on which the predicted values are defined. This may be the result of a transformation of the data using the function or the use of the function as a link function in the fitting of a generalized linear (mixed) model (GL(M)M). The possible transform.functions are identity, log, inverse, sqrt, logit, probit, and cloglog. The predicted.values and error.intervals, if not StandardError.intervals, will be back-transformed using the inverse function of the transform.function. The standard.error column will be set to NA, unless (i) asreml returns columns named transformed.value and approx.se, as well as those called predicted.values and standard.error (such as when a GLM is fitted) and (ii) the values in transformed.value are equal to those obtained by backtransforming the predicted.values using the inverse function of the transform.function. Then, the approx.se values will be saved in the standard.error column of the backtransforms component of the returned alldiffs.obj. Also, the transformed.value and approx.se columns are removed from both the predictions and backtransforms components of the alldiffs.obj. Note that the values that end up in the standard errors column are approximate for the backtransformed values and are not used in calculating error.intervals.
sortFactor	A <b>character</b> 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 sortParallelToCombo 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 classify variables, excluding the sortFactor factor. The order to use is determined by either sortParallelToCombo or sortOrder.
sortParallelToCombo	A <b>list</b> that specifies a combination of the values of the factors and numerics, excluding sortFactor, that are in classify. Each of the components of the supplied <b>list</b> is named for a classify variable and specifies a single value for



it. 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. Each of the other combinations of the values of the factors and numerics will be sorted in parallel. If sortParallelToCombo is NULL then the first value of each classify variable, except for the sortFactor factor, in the predictions component is used to define sortParallelToCombo. If there is only one variable in the classify then sortParallelToCombo is ignored.

sortNestingFactor	A <b>character</b> containing the name of the factor that defines groups of the sortFactor within which the predicted values are to be ordered. If there is only one variable in the classify then sortNestingFactor is ignored.
sortOrder	A character vector whose length is the same as the number of levels for sortFactor in the predictions component of the <b>alldiffs.object</b> . It specifies the desired order of the levels in the reordered components of the <b>alldiffs.object</b> . The argument sortParallelToCombo is ignored.  The following creates a sortOrder vector levs for factor f based on the values in x: <code>levs &lt;- levels(f)[order(x)]</code> .
decreasing	A logical passed to order that determines whether the order for sorting the components of the <b>alldiffs.object</b> is for increasing or decreasing magnitude of the predicted values.
trace	A <b>logical</b> 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. Also, if error.intervals is "halfLeastSignificant", then those of LSDtype, LSDby and LSDstatistic that are not NULL will be added as attributes of the object and of the predictions frame; additionally, LSDvalues will be added as attribute of the predictions frame, LSDvalues being the LSD values used in calculating the error.intervals. 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)

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### See Also

`alldiffs.object`, `as.alldiffs`, `print.alldiffs`, `linTransform.alldiffs`, `sort.alldiffs`, `subset.alldiffs`, `allDifferences.data.frame`, `redoErrorIntervals.alldiffs`, `recalcLSD.alldiffs`, `exploreLSDs.alldiffs`, `pickLSDstatistics.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, inestimable.rm = TRUE,
  linear.transformation = NULL,
  error.intervals = "Confidence", alpha = 0.05,
  wald.tab = NULL, dDF.na = "residual", dDF.values = NULL,
  pairwise = TRUE, Vmatrix = FALSE,
  avsed.tolerance = 0.25, accuracy.threshold = NA,
  LSDtype = "overall", LSDsupplied = NULL, LSDby = NULL,
  LSDstatistic = "mean", LSDaccuracy = "maxAbsDeviation",
  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, interval.annotate = TRUE,
  titles = NULL, colour.scheme = "colour", save.plots = FALSE,
  transform.power = 1, offset = 0, scale = 1,
  transform.function = "identity",
  tables = "all", level.length = NA,
  sortFactor = NULL, sortParallelToCombo = NULL,
  sortNestingFactor = 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.   |
| inestimable.rm        | A logical indicating whether rows for predictions that are not estimable are to be removed from the components of the <a href="#">alldiffs.object</a> .   |
| linear.transformation | <p>A <a href="#">formula</a> or a <a href="#">matrix</a>. If a <a href="#">formula</a> is given then it is taken to be a submodel of a model term corresponding to the <a href="#">classify</a>. The projection matrix that transforms the predictions so that they conform to the submodel is obtained; the submodel does not have to involve variables in the <a href="#">classify</a>, but the variables must be columns in the predictions component of <a href="#">alldiffs.obj</a> and the space for the submodel must be a subspace of the space for the term specified by the <a href="#">classify</a>. For example, for <a href="#">classify</a> set to "A:B", the submodel <math>\sim A + B</math> will result in the predictions for the combinations of A and B being made additive for the <a href="#">factors</a> A and B. The submodel space corresponding to <math>A + B</math> is a subspace of the space A:B. In this case both the submodel and the the <a href="#">classify</a> involve only the factors A and B. To fit an intercept-only submodel, specify <a href="#">linear.transformation</a> to be the formula <math>\sim 1</math>.</p> <p>If a <a href="#">matrix</a> is provided then it will be used to apply the linear transformation to the predictions. It might be a contrast <a href="#">matrix</a> or a <a href="#">matrix</a> of weights for a factor used to obtain the weighted average over that factor. The number of rows in the <a href="#">matrix</a> should equal the number of linear combinations of the predictions desired and the number of columns should equal the number of predictions.</p> <p>In either case, as well as the values of the linear combinations, their standard errors, pairwise differences and associated statistics are returned in the <a href="#">alldiffs.object</a>.</p> |

`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 the LSD is zero, as can happen when predictions are constrained to be equal, then the limits of the error intervals are set to NA. If `LSDtype` 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`

A [numeric](#) giving the significance level for LSDs or one minus the confidence level for confidence intervals. It is stored as an attribute to 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 determining the degrees of freedom for calculating confidence or half-LSD `error.intervals` and p-values, the latter to be stored in the `p.differences` component of the `alldiffs.object` that is created.

`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$nedf` are used. If `dDF.na` = "none", no substitute denominator degrees of freedom are employed; if `dDF.na` = "maximum", the maximum of those `denDF` that are available, excluding that for the Intercept, is used; if all `denDF` are NA, `asreml.obj$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.

`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`.

`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 `LSDtype` are calculated and used in `error.intervals` and plots.
2. Irrespective of the setting of `LSDtype`, if `avsed.tolerance` is not exceeded then the mean LSDs are used in `error.intervals` and plots.

3. If `LSDtype` 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 `LSDtype` 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 `LSDtype` 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.

#### `accuracy.threshold`

A [numeric](#) specifying the value of the LSD accuracy measure, which measure is specified by `LSDaccuracy`, as a threshold value in determining whether the halfLeastSignificant `error.interval` for a predicted value is a reasonable approximation; this will be the case if the LSDs across all pairwise comparisons for which the interval's LSD was computed, as specified by `LSDtype` and `LSDby`, are similar enough to the interval's LSD, as measured by `LSDaccuracy`. If it is NA, it will be ignored. If it is not NA, a column of [logicals](#) named `LSDwarning` will be added to the predictions component of the [alldiffs.object](#). The value of `LSDwarning` for a `predicted.value` will be TRUE if the value of the `LSDaccuracy` measure computed from the LSDs for differences between this `predicted.value` and the other `predicted.values` as compared to its `assignedLSD` exceeds the value of `accuracy.threshold`. Otherwise, the value of `LSDwarning` for a `predicted.value` will be FALSE.

#### `LSDtype`

A [character](#) string that can be `overall`, `factor.combinations`, `per.prediction` or supplied. It determines whether the values stored in a row of a [LSD.frame](#) are the values calculated (i) `overall` from the LSD values for all pairwise comparison2, (ii) the values calculated from the pairwise LSDs for the levels of each `factor.combination`, unless there is only one prediction for a level of the `factor.combination`, when a notional LSD is calculated, (iii) `per.prediction`, being based, for each prediction, on all pairwise differences involving that prediction, or (iv) as supplied values of the LSD, specified with the `LSDsupplied` argument; these supplied values are to be placed in the `assignedLSD` column of the [LSD.frame](#) stored in an [alldiffs.object](#) so that they can be used in LSD calculations.

See [LSD.frame](#) for further information on the values in a row of this `data.frame` and how they are calculated.

#### `LSDsupplied`

A [data.frame](#) or a named [numeric](#) containing a set of LSD values that correspond to the observed combinations of the values of the `LSDby` variables in the [predictions.frame](#) or a single LSD value that is an overall LSD. If a [data.frame](#), it may have (i) a column for the `LSDby` variable and a column of LSD values or (ii) a single column of LSD values with rownames being the combinations of the observed values of the `LSDby` variables. Any name can be used for the column of LSD values; `assignedLSD` is sensible, but not obligatory. Otherwise, a [numeric](#) containing the LSD values, each of which is named for the observed combination of the values of the `LSDby` variables to which it corresponds. (Applying the function `dae::fac.combine` to the predictions component is one way of forming the required combinations for the (row) names.) The values supplied will be incorporated into `assignedLSD` column of the [LSD.frame](#) stored as the LSD component of the [alldiffs.object](#).

LSDby	A <b>character</b> (vector) of variables names, being the names of the <b>factors</b> or <b>numerics</b> in the <b>classify</b> ; for each combination of their levels and values, there will be or is a row in the <b>LSD.frame</b> stored in the LSD component of the <b>alldiffs.object</b> when <b>LSDtype</b> is <b>factor.combinatons</b> .
LSDstatistic	A <b>character</b> nominating one or more of <b>minnum</b> , <b>q10</b> , <b>q25</b> , <b>mean</b> , <b>median</b> , <b>q75</b> , <b>q90</b> or <b>maximum</b> as the value(s) to be stored in the assignedLSD column in an <b>LSD.frame</b> ; the values in the assignedLSD column are used in computing <b>halfLeastSignificant error.intervals</b> . Here <b>q10</b> , <b>q25</b> , <b>q75</b> and <b>q90</b> indicate the sample quantiles corresponding to probabilities of 0.1, 0.25, 0.75 and 0.9 for the group of LSDs from which a single LSD value is calculated. The function <b>quantile</b> is used to obtain them. The mean LSD is calculated as the square root of the mean of the squares of the LSDs for the group. The median is calculated using the <b>median</b> function. Multiple values are only produced for <b>LSDtype</b> set to <b>factor.combination</b> , in which case <b>LSDby</b> must not be <b>NULL</b> and the number of values must equal the number of observed combinations of the values of the variables specified by <b>LSDby</b> . If <b>LSDstatistic</b> is <b>NULL</b> , it is reset to <b>mean</b> .
LSDaccuracy	A <b>character</b> nominating one of <b>maxAbsDeviation</b> , <b>maxDeviation</b> , <b>q90Deviation</b> or <b>RootMeanSqDeviation</b> as the statistic to be calculated as a measure of the accuracy of assignedLSD. The option <b>q90Deviation</b> produces the sample quantile corresponding to a probability of 0.90. The deviations are the differences between the LSDs used in calculating the LSD statistics and each assigned LSD and the accuracy is expressed as a proportion of the assigned LSD value. The calculated values are stored in the column named <b>accuracyLSD</b> in an <b>LSD.frame</b> .
x.num	A character string giving the name of the numeric covariate that corresponds to <b>x.fac</b> , 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 <b>x.fac</b> .
x.fac	A character string giving the name of the factor that corresponds to <b>x.num</b> , 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 <b>x.num</b> . The levels of <b>x.fac</b> must be in the order in which they are to be plotted - if they are dates, then they should be in the form <b>yyyymmdd</b> , which can be achieved using <b>as.Date</b> . However, the levels can be non-numeric in nature, provided that <b>x.num</b> is also set.
nonx.fac.order	A character vector giving the order in which factors other than <b>x.fac</b> 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 <b>x.num</b> or <b>x.fac</b> . 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 <b>x.num</b> 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 <b>x.num</b> are to be plotted or <b>x.fac</b> is to be plotted because there is no <b>x.num</b> term corresponding to the same term with <b>x.fac</b> .
plots	Possible values are <b>"none"</b> , <b>"predictions"</b> , <b>"backtransforms"</b> and <b>"both"</b> . Plots are not produced if the value is <b>"none"</b> . If data are not transformed for analysis ( <b>transform.power = 1</b> ), a plot of the predictions is produced provided <b>plots</b> is not <b>"none"</b> . If the data are transformed, the value of <b>plots</b> determines what is produced.



panels	Possible values are "single" and "multiple". When line plots are to be produced, because variables involving <code>x.num</code> or <code>x.fac</code> are involved in <code>classify</code> for the predictions, <code>panels</code> determines whether or not a single panel or multiple panels in a single window are produced. The <code>panels</code> argument is ignored for bar charts.
graphics.device	A character specifying a graphics device for plotting. The default is <code>graphics.device = NULL</code> , 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.
interval.annotate	A logical indicating whether the plot annotation indicating the type of error . interval is to be included in the plot.
titles	A list, each component of which is named for a column in the <code>data.frame</code> for <code>asrem1.obj</code> 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 <code>.back</code> if backtransformed values are being plotted, the classify term, Bar or Line and, if <code>error.intervals</code> 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 <a href="#">numeric</a> 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 stored in the <code>backtransforms</code> component of the <code>alldiffs.object</code> . The <code>plots</code> and <code>tables</code> arguments control the plotting and output of the predictions and backtransforms. The back-transformation raises the predictions to the power equal to the reciprocal of <code>transform.power</code> , unless it equals 0 in which case the exponential of the predictions is taken.
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 stored in the <code>backtransforms</code> component of the <code>alldiffs.object</code> . The <code>plots</code> and <code>tables</code> arguments control the plotting and output of the predictions and backtransforms. 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 stored in the <code>backtransforms</code> component of the <code>alldiffs.object</code> . The <code>plots</code> and <code>tables</code> arguments control the plotting and output of the predictions and backtransforms. The backtransformation will, after backtransforming for any power transformation and then subtracting the offset, divide by the scale.
transform.function	A <a href="#">character</a> giving the name of a function that specifies the scale on which the predicted values are defined. This may be the result of a transformation

of the data using the function or the use of the function as a link function in the fitting of a generalized linear (mixed) model (GL(M)M). The possible transform.functions are identity, log, inverse, sqrt, logit, probit, and cloglog. The predicted.values and error.intervals, if not StandardError intervals, will be back-transformed using the inverse function of the transform.function. The standard.error column will be set to NA, unless (i) asreml returns columns named transformed.value and approx.se, as well as those called predicted.values and standard.error (such as when a GLM is fitted) and (ii) the values in transformed.value are equal to those obtained by backtransforming the predicted.values using the inverse function of the transform.function. Then, the approx.se values will be saved in the standard.error column of the backtransforms component of the returned alldiffs.obj. Also, the transformed.value and approx.se columns are removed from both the predictions and backtransforms components of the alldiffs.obj. Note that the values that end up in the standard errors column are approximate for the backtransformed values and are not used in calculating error.intervals.

tables	A character vector containing a combination of predictions, vcov, backtransforms, differences, p.differences, sed, LSD and all. These nominate which components of the <a href="#">alldiffs.object</a> to print.
level.length	The maximum number of characters from the levels of factors to use in the row and column labels of the tables produced by <a href="#">allDifferences.data.frame</a> .
sortFactor	A <a href="#">character</a> 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 sortParallelToCombo 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 classify variables, excluding the sortFactor factor. The order to use is determined by either sortParallelToCombo or sortOrder.
sortParallelToCombo	A <a href="#">list</a> that specifies a combination of the values of the factors and numerics, excluding sortFactor, that are in classify. Each of the components of the supplied <a href="#">list</a> is named for a classify variable and specifies a single value for it. 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. Each of the other combinations of the values of the factors and numerics will be sorted in parallel. If sortParallelToCombo is NULL then the first value of each classify variable, except for the sortFactor factor, in the predictions component is used to define sortParallelToCombo. If there is only one variable in the classify then sortParallelToCombo is ignored.
sortNestingFactor	A <a href="#">character</a> containing the name of the factor that defines groups of the sortFactor within which the predicted values are to be ordered. If there is only one variable in the classify then sortNestingFactor is ignored.
sortOrder	A character vector whose length is the same as the number of levels for sortFactor in the predictions component of the <a href="#">alldiffs.object</a> . It specifies the desired order of the levels in the reordered components of the <a href="#">alldiffs.object</a> . The argument sortParallelToCombo is ignored.





```

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	<i>Prints the values in an <code>alldiffs</code> object in a nice format.</i>
----------------	---

---

## 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 significant 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 <code>alldiffs</code> 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 <code>alldiffs</code> object to print.
colourise	A <b>logical</b> which, if TRUE, results in the header text produced by <code>predict.asreml</code> being displayed in a different colour, if supported by the output terminal device. It overrides the TRUE setting of the <code>colourise</code> argument of <code>asreml::asreml.options</code> .
...	further arguments passed to <code>print.predictions.frame</code> .

## 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	<i>Prints the values in an <a href="#">asrtests.object</a></i>
----------------	--

---

## Description

Prints a summary of the asreml object, the pseudanova and the test.summary data.frame that are stored in the [asrtests.object](#).

## Usage

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

## Arguments

x	An <a href="#">asrtests.object</a> .
which	Which elements of the <a href="#">asrtests.object</a> to print. Possible values are some combination of asremlsummary, vparameterssummary, pseudoanova, wald.tab, testsummary and key or all. The option wald.tab is a synonym for pseudoanova. The options key and all are mutually exclusive; key includes vparameterssummary, but not the rest of asremlsummary, while all includes the full asremlsummary that includes the vparameterssummary.
colourise	A <a href="#">logical</a> 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.LSDdata	<i>Prints the components of a list containing data on the LSDs for all pairwise differences of predictions.</i>
---------------	---

---

**Description**

Prints the components of an LSDdata [list](#) created by [exploreLSDs](#), that contains data on the LSDs for all pairwise differences of predictions stored in an [alldiffs.object](#).

**Usage**

```
## S3 method for class 'LSDdata'
print(x, which.print = c("statistics", "false.pos", "false.neg"), ...)
```

**Arguments**

x	An object that, ideally, is of class LSDdata.
which.print	Which components of the LSDdata <a href="#">list</a> to print. Possible values are any combination of frequencies, distinct.vals, statistics, accuracy, false.pos, false.neg, per.pred.accuracy, LSD, summary and all, except that summary and all cannot occur together. For a description of the components, see <a href="#">alldiffs.object</a> . The default is to print statistics, false.pos, false.neg. The option summary results in the printing of distinct.vals, statistics, false.pos, false.neg.
...	further arguments passed to print.

**Value**

No value is returned, but components of x are printed as specified in which.print.

**Author(s)**

Chris Brien

**See Also**

[exploreLSDs.alldiffs](#), [alldiffs.object](#)

## 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"))
LSDdata <- exploreLSDs(diffs, LSDtype = "factor.combinations", LSDby = "Sources")
print(LSDdata)

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

## 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.test.summary
```

*Prints a data.frame containing a test.summary.*

---

**Description**

Prints a `test.summary` (also a `choose.summary`) with or without a title and with p-values limited to 4-digits.

**Usage**

```
## S3 method for class 'test.summary'
print(x, which.print = c("title", "table"), omit.columns = NULL, ...)
```

**Arguments**

<code>x</code>	A object that, ideally, is of class <code>test.summary</code> .
<code>which.print</code>	A character specifying the aspects of the <code>test.summary</code> to print. Possible values are some combination of <code>title</code> , <code>table</code> and <code>all</code> .
<code>omit.columns</code>	A character specifying the columns of the <code>test.summary</code> table to be omitted from the print. If <code>NULL</code> , none are omitted.
<code>...</code>	further arguments passed to <code>print</code> , but is only operational when the table is also printed.

**Value**

No value is returned, but `x` is printed, possibly with a title.

**Author(s)**

Chris Brien

**See Also**[print.wald.tab](#), [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", simplifier=TRUE)
print(current.asrt$test.summary)

## End(Not run)
```

---

print.wald.tab	<i>Prints a data.frame containing a Wald or pseudoanova table.</i>
----------------	--

---

**Description**

Prints a wald.tab with or without title and/or heading. The printing of the p-values is limited to 4 digits.

**Usage**

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

**Arguments**

x	An 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 <a href="#">logical</a> 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 x is printed as specified in which.wald.

**Author(s)**

Chris Brien

**See Also**

[print.test.summary](#), [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)
```

---

```
printFormulae.asreml  Prints the formulae from an asreml object.
```

---

## Description

Prints the [formulae](#) nominated in the which argument from the call stored in an asreml object.

## Usage

```
## S3 method for class 'asreml'
printFormulae(asreml.obj, which = c("fixed", "random", "residual"),
              expanded = FALSE, envir = parent.frame(), ...)
```

## Arguments

asreml.obj	An asreml object resulting from the fitting of a model using REML.
which	A character listing the <a href="#">formula(e)</a> to be printed from the call stored in asreml.obj. It should be some combination of fixed, random, residual, sparse and all. If all is included then all <a href="#">formula(e)</a> will be printed.
expanded	A logical indicating whether terms are to be expanded to the sum of a set of individual terms.
envir	The environment in which the <a href="#">formula(e)</a> are to be evaluated. May also be NULL, a list, a data.frame, a pairlist or an integer as specified to sys.call.
...	Arguments passed on to getFormulae.asreml and ultimately to update.formula and terms.formula.

## Value

Invisibly returns a character, each element of which contains one of the extracted [formulae](#).

## Author(s)

Chris Brien



**See Also**

[printFormulae.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)
printFormulae(current.asr)

## End(Not run)
```

---

ratioTransform.alldiffs

*Calculates the ratios of nominated pairs of predictions stored in an [alldiffs.object](#).*

---

**Description**

Ratio predictions and error intervals are formed for two levels of a factor, the `ratio.factor`. For each pair of a level of the `ratio.factor` in `numerator.levels` with a level in `denominator.levels`, the ratio predictions are formed from all combinations of the other factors as the ratio of the two predictions for each combination, along with confidence intervals for the ratio predictions computed using the Fieller (1954) method.

The printing of the components produced is controlled by the `tables` argument.

**Usage**

```
## S3 method for class 'alldiffs'
ratioTransform(alldiffs.obj, ratio.factor,
               numerator.levels, denominator.levels,
               method = "Fieller", alpha = 0.05,
               response = NULL, response.title = NULL,
               tables = "predictions", ...)
```

**Arguments**

<code>alldiffs.obj</code>	An <a href="#">alldiffs.object</a> .
<code>ratio.factor</code>	A <a href="#">character</a> string giving the name of the factor for whose levels the ratios are to be calculated.
<code>numerator.levels</code>	A <a href="#">character</a> string containing the levels of <code>ratio.factor</code> to be used as numerators of the ratio.
<code>denominator.levels</code>	A <a href="#">character</a> string containing the levels of <code>ratio.factor</code> to be used as denominators of the ratio.

method	A <a href="#">character</a> string specifying the method to use in calculating the ratios and their error.intervals. At present only Fieller is available. For the Fieller method, ratios of predictions are formed and confidence intervals formed for them using Fieller's (1954) theorem.
alpha	A <a href="#">numeric</a> giving the significance level for LSDs or one minus the confidence level for confidence intervals.
response	A character specifying the response variable for the predictions. It is stored as an attribute to the <a href="#">alldiffs.object</a> .
response.title	A character specifying the title for the response variable for the predictions. It is stored as an attribute to the <a href="#">alldiffs.object</a> .
tables	A <a href="#">character</a> vector containing either none or predictions
...	further arguments passed to <a href="#">linTransform.alldiffs</a> .

### Value

A list of [predictions.frames](#), each containing the ratio predictions and their confidence limits for a combination of the numerator.levels with the denominator.levels. It will also contain the values of the variables in the classify of [alldiffs.obj](#) that index the ratio predictions, except that the ratio.factor is omitted.

If sortFactor attribute of the [alldiffs.object](#) is set and is not the ratio.factor, the predictions and their backtransforms will be sorted using the sortOrder attribute of the [alldiffs.object](#).

### Author(s)

Chris Brien

### References

Fieller, E. C. (1954). Some Problems in Interval Estimation. *Journal of the Royal Statistical Society. Series B (Methodological)*, **16**, 175-185.

### See Also

[pairdiffsTransform](#), [linTransform](#), [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

```
#### Form the ratios and Fieller CIs for RGR Salinity
load(system.file("extdata", "testDiffs.rda", package = "asremlPlus", mustWork = TRUE))
Preds.ratio.RGR <- ratioTransform(diffs.RGR,
                                ratio.factor = "Salinity",
                                numerator.levels = "Salt",
                                denominator.levels = "Control")

#### Form the ratios and Fieller CIs for Nitrogen compared to no Nitrogen
data("Oats.dat")
## Not run:
m1.asr <- asreml(Yield ~ Nitrogen*Variety,
                 random=~Blocks/Wplots,
```

```

        data=Oats.dat)
current.asrt <- as.asrtests(m1.asr)
wald.tab <- current.asrt$wald.tab
Var.diffs <- predictPlus(m1.asr, classify="Nitrogen:Variety", pairwise = TRUE,
                        Vmatrix = TRUE, error.intervals = "halfLeast",
                        LSDtype = "factor", LSDby = "Variety",
                        wald.tab = wald.tab)

## End(Not run)

## Use lme4 and emmeans 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)

  ## Set up a wald.tab
  int <- as.data.frame(rbind(rep(NA,4)))
  rownames(int) <- "(Intercept)"
  wald.tab <- anova(m1.lmer, ddf = "Kenward", type = 1)[,3:6]
  names(wald.tab) <- names(int) <- c("Df", "denDF", "F.inc", "Pr")
  wald.tab <- rbind(int, wald.tab)
  #Get predictions
  Var.emm <- emmeans::emmeans(m1.lmer, specs = ~ Nitrogen:Variety)
  Var.preds <- summary(Var.emm)
  ## 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
  den.df <- wald.tab[match("Variety", rownames(wald.tab)), "denDF"]

  #Create alldiffs object
  Var.diffs <- as.alldiffs(predictions = Var.preds,
                          sed = Var.sed, vcov = Var.vcov,
                          classify = "Nitrogen:Variety", response = "Yield", tdf = den.df)
}

if (exists("Var.diffs"))
  Preds.ratio.OatsN <- ratioTransform(alldiffs.obj = Var.diffs,
                                     ratio.factor = "Nitrogen",
                                     numerator.levels = c("0.2", "0.4", "0.6"),
                                     denominator.levels = "0.2")

```

---

recalcLSD.alldiffs	<i>Adds or recalculates the <b>LSD.frame</b> that is a component of an <b>alldiffs.object</b>.</i>
--------------------	--

---

## Description

Given an **alldiffs.object**, adds or recalculate its **LSD.frame**. **N.B. No changes are made to the **error.intervals** — use **redoErrorIntervals.alldiffs** to modify both the **error.intervals** and the **LSD.frame**.**

## Usage

```
## S3 method for class 'alldiffs'
recalcLSD(alldiffs.obj, LSDtype = "overall", LSDsupplied = NULL,
          LSDby = NULL, LSDstatistic = "mean", LSDaccuracy = "maxAbsDeviation",
          alpha = 0.05, ...)
```

## Arguments

- |              |   |
|--------------|---|
| alldiffs.obj | An <a href="#">alldiffs.object</a> .  |
| LSDtype      | A <a href="#">character</a> string that can be overall, factor.combinations, per.prediction or supplied. It determines whether the values stored in a row of a <a href="#">LSD.frame</a> are the values calculated (i) overall from the LSD values for all pairwise comparison2, (ii) the values calculated from the pairwise LSDs for the levels of each factor.combination, unless there is only one prediction for a level of the factor.combination, when a notional LSD is calculated, (iii) per.prediction, being based, for each prediction, on all pairwise differences involving that prediction, or (iv) as supplied values of the LSD, specified with the LSDsupplied argument; these supplied values are to be placed in the assignedLSD column of the <a href="#">LSD.frame</a> stored in an <a href="#">alldiffs.object</a> so that they can be used in LSD calculations.<br><br>See <a href="#">LSD.frame</a> for further information on the values in a row of this data.frame and how they are calculated.   |
| LSDsupplied  | A <a href="#">data.frame</a> or a named <a href="#">numeric</a> containing a set of LSD values that correspond to the observed combinations of the values of the LSDby variables in the <a href="#">predictions.frame</a> or a single LSD value that is an overall LSD. If a <a href="#">data.frame</a> , it may have (i) a column for the LSDby variable and a column of LSD values or (ii) a single column of LSD values with rownames being the combinations of the observed values of the LSDby variables. Any name can be used for the column of LSD values; assignedLSD is sensible, but not obligatory. Otherwise, a <a href="#">numeric</a> containing the LSD values, each of which is named for the observed combination of the values of the LSDby variables to which it corresponds. (Applying the function <code>dae::fac.combine</code> to the predictions component is one way of forming the required combinations for the (row) names.) The values supplied will be incorporated into assignedLSD column of the <a href="#">LSD.frame</a> stored as the LSD component of the <a href="#">alldiffs.object</a> . |
| LSDby        | A <a href="#">character</a> (vector) of variables names, being the names of the <a href="#">factors</a> or <a href="#">numerics</a> in the classify; for each combination of their levels and values, there will be or is a row in the <a href="#">LSD.frame</a> stored in the LSD component of the <a href="#">alldiffs.object</a> when LSDtype is factor.combinatons.   |
| LSDstatistic | A <a href="#">character</a> nominating one or more of minnum, q10, q25, mean, median, q75, q90 or maximum as the value(s) to be stored in the assignedLSD column in an <a href="#">LSD.frame</a> ; the values in the assignedLSD column are used in computing halfLeastSignificant error.intervals. Here q10, q25, q75 and q90 indicate the sample quantiles corresponding to probabilities of 0.1, 0.25, 0.75 and 0.9 for the group of LSDs from which a single LSD value is calculated. The function <a href="#">quantile</a> is used to obtain them. The mean LSD is calculated as the square root of the mean of the squares of the LSDs for the group. The median is calculated using the <a href="#">median</a> function. Multiple values are only produced for LSDtype set to factor.combination, in which case LSDby must not be NULL and the number of values must equal the number of observed combinations of  |

	the values of the variables specified by LSDby. If LSDstatistic is NULL, it is reset to mean.
LSDaccuracy	A <a href="#">character</a> nominating one of maxAbsDeviation, maxDeviation, q90Deviation or RootMeanSqDeviation as the statistic to be calculated as a measure of the accuracy of assignedLSD. The option q90Deviation produces the sample quantile corresponding to a probability of 0.90. The deviations are the differences between the LSDs used in calculating the LSD statistics and each assigned LSD and the accuracy is expressed as a proportion of the assigned LSD value. The calculated values are stored in the column named accuracyLSD in an <a href="#">LSD.frame</a> .
alpha	The significance level for an LSD to compare a pair of predictions. It is stored as an attribute to the <a href="#">alldiffs.object</a> .
...	further arguments passed to <a href="#">allDifferences.data.frame</a> ; attributes tranform.power, offset and scale cannot be passed.

### 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](#), [exploreLSDs.alldiffs](#), [pickLSDstatistics.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.asrttests(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 emmeans 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
els <- as.numeric(rownames(TS.preds))
TS.vcov <- vcov(TS.emm)[els,els]
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, LSDtype = "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 pseudo-anova 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 automatically 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

**References**

Kenward, M. G., & Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics*, **53**, 983-997.

**See Also**

[as.asrtests](#), [testtranfix.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 retrieved 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, accuracy.threshold = NA,
  LSDtype = NULL, LSDsupplied = NULL,
  LSDby = NULL, LSDstatistic = "mean",
  LSDaccuracy = "maxAbsDeviation",
  retain.zeroLSDs = FALSE,
  zero.tolerance = .Machine$double.eps ^ 0.5, ...)
```

## 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 the LSD is zero, as can happen when predictions are constrained to be equal, then the limits of the error intervals are set to NA. If `LSDtype` 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` A `numeric` giving the significance level for LSDs or one minus the confidence level for confidence intervals. It is stored as an attribute to the `alldiffs.object`.

`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`. To have it ignored, set it to NA. 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 `LSDtype` are calculated and used in `error.intervals` and plots.



2. Irrespective of the setting of LSDtype, if avsed.tolerance is not exceeded then the mean LSDs are used in error.intervals and plots.
3. If LSDtype 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 LSDtype 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 LSDtype 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.

#### accuracy.threshold

A [numeric](#) specifying the value of the LSD accuracy measure, which measure is specified by LSDaccuracy, as a threshold value in determining whether the halfLeastSignificant error.interval for a predicted value is a reasonable approximation; this will be the case if the LSDs across all pairwise comparisons for which the interval's LSD was computed, as specified by LSDtype and LSDby, are similar enough to the interval's LSD, as measured by LSDaccuracy. If it is NA, it will be ignored. If it is not NA, a column of [logicals](#) named LSDwarning will be added to the predictions component of the [alldiffs.object](#). The value of LSDwarning for a predicted.value will be TRUE if the value of the LSDaccuracy measure computed from the LSDs for differences between this predicted.value and the other predicted.values as compared to its assignedLSD exceeds the value of accuracy.threshold. Otherwise, the value of LSDwarning for a predicted.value will be FALSE.

#### LSDtype

A [character](#) string that can be overall, factor.combinations, per.prediction or supplied. It determines whether the values stored in a row of a [LSD.frame](#) are the values calculated (i) overall from the LSD values for all pairwise comparison2, (ii) the values calculated from the pairwise LSDs for the levels of each factor.combination, unless there is only one prediction for a level of the factor.combination, when a notional LSD is calculated, (iii) per.prediction, being based, for each prediction, on all pairwise differences involving that prediction, or (iv) as supplied values of the LSD, specified with the LSDsupplied argument; these supplied values are to be placed in the assignedLSD column of the [LSD.frame](#) stored in an [alldiffs.object](#) so that they can be used in LSD calculations.

If LSDtype is NULL (the default), the LSDtype attribute of the alldiffs.obj will be used; it is also NULL, then the LSDtype will be set to overall.

See [LSD.frame](#) for further information on the values in a row of this data.frame and how they are calculated.

#### LSDsupplied

A [data.frame](#) or a named [numeric](#) containing a set of LSD values that correspond to the observed combinations of the values of the LSDby variables in the [predictions.frame](#) or a single LSD value that is an overall LSD. If a [data.frame](#), it may have (i) a column for the LSDby variable and a column of LSD values or (ii) a single column of LSD values with rownames being the combinations of the observed values of the LSDby variables. Any name can be used for the column of LSD values; assignedLSD is sensible, but not obligatory. Otherwise, a [numeric](#) containing the LSD values, each of which is named for the observed combination of the values of the LSDby variables to which it corresponds.

(Applying the function `dae::fac.combine` to the predictions component is one way of forming the required combinations for the (row) names.) The values supplied will be incorporated into assignedLSD column of the `LSD.frame` stored as the LSD component of the `alldiffs.object`.

LSDby	A <code>character</code> (vector) of variables names, being the names of the <code>factors</code> or <code>numerics</code> in the <code>classify</code> ; for each combination of their levels and values, there will be or is a row in the <code>LSD.frame</code> stored in the LSD component of the <code>alldiffs.object</code> when LSDtype is <code>factor.combinations</code> .
LSDstatistic	A <code>character</code> nominating one or more of minnum, q10, q25, mean, median, q75, q90 or maximum as the value(s) to be stored in the assignedLSD column in an <code>LSD.frame</code> ; the values in the assignedLSD column are used in computing halfLeastSignificant error.intervals. Here q10, q25, q75 and q90 indicate the sample quantiles corresponding to probabilities of 0.1, 0.25, 0.75 and 0.9 for the group of LSDs from which a single LSD value is calculated. The function <code>quantile</code> is used to obtain them. The mean LSD is calculated as the square root of the mean of the squares of the LSDs for the group. The median is calculated using the <code>median</code> function. Multiple values are only produced for LSDtype set to <code>factor.combination</code> , in which case LSDby must not be NULL and the number of values must equal the number of observed combinations of the values of the variables specified by LSDby. If LSDstatistic is NULL, it is reset to mean.
LSDaccuracy	A <code>character</code> nominating one of <code>maxAbsDeviation</code> , <code>maxDeviation</code> , <code>q90Deviation</code> or <code>RootMeanSqDeviation</code> as the statistic to be calculated as a measure of the accuracy of assignedLSD. The option <code>q90Deviation</code> produces the sample quantile corresponding to a probability of 0.90. The deviations are the differences between the LSDs used in calculating the LSD statistics and each assigned LSD and the accuracy is expressed as a proportion of the assigned LSD value. The calculated values are stored in the column named <code>accuracyLSD</code> in an <code>LSD.frame</code> .
retain.zeroLSDs	A <code>logical</code> indicating whether to retain or omit LSDs that are zero when calculating the summaries of LSDs.
zero.tolerance	A <code>numeric</code> specifying the value such that if an LSD is less than it, it will be considered to be zero.
...	further arguments passed to <code>recalcLSD.alldiffs</code> .

## 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. Also, if `error.intervals` is "halfLeastSignificant", then those of `LSDtype`, `LSDby` and `LSDstatistic` that are not NULL will be added as attributes of the object and of the `predictions` frame; additionally, `LSDvalues` will be added as attribute of the `predictions` frame, `LSDvalues` being the LSD values used in calculating the `error.intervals`.

**Author(s)**

Chris Brien

**See Also**

[recalcLSD.alldiffs](#), [exploreLSDs.alldiffs](#), [pickLSDstatistics.alldiffs](#),  
[predictPresent.asreml](#), [plotPredictions.data.frame](#), [allDifferences.data.frame](#),  
[as.alldiffs](#), [print.alldiffs](#), [sort.alldiffs](#), [subset.alldiffs](#),  
[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.asrttests(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 emmeans 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
  els <- as.numeric(rownames(TS.preds))
  TS.vcov <- vcov(TS.emm)[els,els]
  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 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

- |                                    |  |
|------------------------------------|--|
| <code>h0.asreml.obj</code>         | <code>asreml</code> object containing the fit under the model for the null hypothesis.   |
| <code>h1.asreml.obj</code>         | <code>asreml</code> object containing the fit under the model for the alternative hypothesis.  |
| <code>positive.zero</code>         | 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 <code>bound.test.parameters</code> is set.   |
| <code>bound.test.parameters</code> | 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 <code>positive.zero</code> is <code>TRUE</code> then <code>bound.test.parameters</code> is taken to be "onlybound". When <code>bound.test.parameters</code> 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. |
| <code>DF</code>                    | A numeric giving the difference between the two models in the number of variance parameters whose estimates are not of the type specified in <code>bound.exclusions</code> . If <code>NULL</code> then this is determined from the information in <code>full.asreml.obj</code> and <code>reduced.asreml.obj</code> .   |

`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 passing 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  $2(\log(EML)_1 - \log(EML)_0)$ .

This procedure is only appropriate 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; first replace Combination in the predictions component with the new set of variables and then call renewClassify.

## Usage

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

## Arguments

- |                     |  |
|---------------------|--|
| alldiffs.obj        | An <a href="#">alldiffs.object</a> .   |
| newclassify         | A <a href="#">character</a> 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 <a href="#">character</a> 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 sortParallelToCombo 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 classify variables, excluding the sortFactor factor. The order to use is determined by either sortParallelToCombo or sortOrder. |
| sortParallelToCombo | A <a href="#">list</a> that specifies a combination of the values of the factors and numerics, excluding sortFactor, that are in classify. Each of the components of the supplied <a href="#">list</a> is named for a classify variable and specifies a single value for it. 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. Each of the other combinations of the values of the factors and numerics will be sorted in parallel. If sortParallelToCombo is NULL then the first value of each classify variable, except for the sortFactor factor, in the predictions component is used to define sortParallelToCombo. If there is only one variable in the classify then sortParallelToCombo is ignored.

sortNestingFactor

A **character** containing the name of the factor that defines groups of the sortFactor within which the predicted values are to be ordered. If there is only one variable in the classify then sortNestingFactor 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 sortParallelToCombo 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 determines whether the order is for increasing or decreasing magnitude of the predicted values.

...

further arguments passed to **allDifferences.data.frame**; attributes tranform.power, offset and scale cannot be passed.

## 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, sortParallelToCombo, 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 emmeans 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
  els <- as.numeric(rownames(TS.preds))
  TS.vcov <- vcov(TS.emm)[els,els]
  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 reparameterizes 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 ensures 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, allow.fixedcorrelation = TRUE,
               checkboundaryonly = FALSE,
               denDF = "numeric", ICLikelihood = "none",
               trace = FALSE, update = TRUE,
               set.terms = NULL, ignore.suffices = TRUE,
               bounds = "P", initial.values = NA,...)
```

## Arguments

- |                        |  |
|------------------------|--|
| asrtests.obj           | an <a href="#">asrtests.object</a> containing the components (i) asreml.obj, (ii) wald.tab, and (iii) test.summary.  |
| terms                  | A character string vector giving the random 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. The name must match those in the vparameters component of the asreml.obj component in the asrtests.obj.   |
| 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 asrtests.obj is returned.  |
| allow.fixedcorrelation | A logical indicating whether to accept a new model even when it contains correlations in the model whose values have been designated as fixed, bound or singular. If FALSE and the new model contains correlations whose values have not been able to be estimated, the supplied asrtests.obj is returned. The fit in the asreml.obj component of the supplied asrtests.obj will also be tested and a warning issued if both fixed correlations are found in it and allow.fixedcorrelation is FALSE. |
| checkboundaryonly      | If TRUE then boundary and singular terms are not removed by <a href="#">rmboundary.asrtests</a> ; a warning is issued instead.   |
| 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 automatically 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.
IClikelihood	A character that controls both the occurrence and the type of likelihood for information criterion in the test.summary of the new <code>asrtests.object</code> . If none, none are included. Otherwise, if REML, then the AIC and BIC based on the Restricted Maximum Likelihood are included; if full, then the AIC and BIC based on the full likelihood are included. (See also <code>infoCriteria.asreml</code> .)
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 <code>update.asreml</code> is called in removing and adding terms to the model. In doing this the arguments <code>R.param</code> and <code>G.param</code> are set to those in the <code>asreml</code> object stored in the supplied <code>asrtests.obj</code> so that the values from the previous model are used as starting values. If FALSE then calls are made to <code>asreml</code> in which the only changes from the previous call are (i) that the models are updated and (ii) modifications specified via <code>...</code> 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 <code>asreml</code> -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 <code>asreml</code> -assigned names. If FALSE for an element of terms, the element must exactly match an <code>asreml</code> -assigned name for a variance term. This vector must be of length one or the same length as <code>terms</code> . If it is of length one then the same action is applied to the <code>asreml</code> -assigned suffices for all the terms in <code>terms</code> .
bounds	A <code>character</code> vector specifying the bounds to be applied to the terms specified in <code>set.terms</code> . This vector must be of length one or the same length as <code>set.terms</code> . If it is of length one then the same constraint is applied to all the terms in <code>set.terms</code> . 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 <code>terms</code> . This vector must be of length one or the same length as <code>terms</code> . If it is of length one then the same initial value is applied to all the terms in <code>terms</code> . If any of the <code>initial.values</code> are equal to NA then they are left unchanged for those terms.
...	further arguments passed to <code>asreml</code> via <code>changeTerms.asrtests</code> and <code>as.asrtests</code> .

**Value**

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

**Author(s)**

Chris Brien

**References**

Kenward, M. G., & Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics*, **53**, 983-997.

**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	<i>Removes any boundary or singular variance components from the fit stored in asrtests.obj and records their removal in an <a href="#">asrtests.object</a>.</i>
---------------------	--

---

## 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 re-fitted. 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,
           ICLikelihood = "none", trace = FALSE, update = TRUE,
           set.terms = NULL, ignore.suffices = TRUE,
           bounds = "P", initial.values = NA, ...)
```

## Arguments

- |                   |   |
|-------------------|---|
| asrtests.obj      | an <a href="#">asrtests.object</a> containing the components (i) <code>asreml.obj</code> , (ii) <code>wald.tab</code> , and (iii) <code>test.summary</code> .   |
| checkboundaryonly | If TRUE then boundary and singular terms are not removed by <a href="#">rmboundary.asrtests</a> ; a warning is issued instead.  |
| ICLikelihood      | A character that controls both the occurrence and the type of likelihood for information criterion in the <code>test.summary</code> of the new <a href="#">asrtests.object</a> . If none, none are included. Otherwise, if REML, then the AIC and BIC based on the Restricted Maximum Likelihood are included; if full, then the AIC and BIC based on the full likelihood are included. (See also <a href="#">infoCriteria.asreml</a> .)  |
| 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 <code>update.asreml</code> is called to fit the model with any boundary terms removed. In doing this the arguments <code>R.param</code> and <code>G.param</code> are set to those in the <code>asreml</code> object stored in <code>asrtests.obj</code> so that the values from the previous model are used as starting values. If FALSE then a call is made to <code>asreml</code> 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 <code>...</code> are made.   |
| set.terms         | A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting. The names must match those in the <code>vparameters</code> component of the <code>asreml.obj</code> component in the <a href="#">asrtests.object</a> .  |
| ignore.suffices   | A logical vector specifying whether the suffices of the <code>asreml</code> -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 <code>asreml</code> -assigned names. If FALSE for an element of terms, the element must exactly match an <code>asreml</code> -assigned name for a variance term. This vector must be of length one or the same length as <code>terms</code> . If it is of length one then the same action is applied to the <code>asreml</code> -assigned suffices for all the terms in <code>terms</code> . |
| bounds            | A <a href="#">character</a> vector specifying the bounds to be applied to the terms specified in <code>set.terms</code> . This vector must be of length one or the same length as <code>set.terms</code> . If it is of length one then the same constraint is applied to all the terms in <code>set.terms</code> . 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 <code>terms</code> . This vector must be of length one or the same length as <code>terms</code> . If it is of length one then the same initial value is applied to all the terms in <code>terms</code> . If any of the <code>initial.values</code> are equal to NA then they are left unchanged for those terms.  |
| ...               | further arguments passed to <code>asreml</code> .   |

**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**

<code>call</code>	an unevaluated call to <code>asreml</code> . One way to create such a call is to use the <code>call</code> function with its <code>name</code> argument set to <code>"asreml"</code> . Another is to obtain it from the <code>call</code> component of an <code>asreml</code> object (e.g. <code>call &lt;- asreml.obj\$call</code> ).
<code>terms</code>	A character vector specifying the terms that are to have bounds and/or initial values specified. The names must match those in the <code>vparameters</code> component of the <code>asreml.obj</code> component in the <code>asrtests.object</code> .

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, <https://asreml.kb.vsnl.co.uk/>.

## 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	<i>Produce sets of simulated data from a multivariate normal distribution and save quantites related to the simulated data</i>
-----------------	--

---

## 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.asrttests(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	<i>Sorts the components in an <a href="#">alldiffs.object</a> according to the predicted values associated with a factor.</i>
---------------	---

---

## 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`, `sortParallelToCombo` 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 [renewClassify.alldiffs](#) is called after sorting to ensure that the order of the rows and columns of the components is in standard order for the new variable order.

## Usage

```

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

```

## Arguments

x	An <a href="#">alldiffs.object</a> .
decreasing	A <a href="#">logical</a> passed to <code>order</code> that determines whether the order is for increasing or decreasing magnitude of the predicted values.
classify	A <a href="#">character</a> 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 <code>:</code> operator. If <code>NULL</code> , it will be obtained from the <code>classify</code> attribute of the <a href="#">as.alldiffs</a> object supplied through <code>x</code> .

sortFactor	A <a href="#">character</a> 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 sortParallelToCombo 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 classify variables, excluding the sortFactor factor. The order to use is determined by either sortParallelToCombo or sortOrder.
sortParallelToCombo	A <a href="#">list</a> that specifies a combination of the values of the factors and numerics, excluding sortFactor, that are in classify. Each of the components of the supplied <a href="#">list</a> is named for a classify variable and specifies a single value for it. 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. Each of the other combinations of the values of the factors and numerics will be sorted in parallel. If sortParallelToCombo is NULL then the first value of each classify variable, except for the sortFactor factor, in the predictions component is used to define sortParallelToCombo. If there is only one variable in the classify then sortParallelToCombo is ignored.
sortNestingFactor	A <a href="#">character</a> containing the name of the factor that defines groups of the sortFactor within which the predicted values are to be ordered. If there is only one variable in the classify then sortNestingFactor is ignored.
sortOrder	A <a href="#">character</a> vector whose length is the same as the number of levels for sortFactor in the predictions component of the <a href="#">alldiffs.object</a> . It specifies the desired order of the levels in the reordered components of the <a href="#">alldiffs.object</a> . The argument sortParallelToCombo is ignored. The following creates a sortOrder vector levs for factor f based on the values in x: <code>levs &lt;- levels(f)[order(x)]</code> .
...	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 sortParallelToCombo combination, 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 sortParallelToCombo 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,
sort.predictions.frame, renewClassify.alldiffs, redoErrorIntervals.alldiffs,
recalcLSD.alldiffs, predictPlus.asreml, predictPresent.asreml
```

**Examples**

```
##Halve WaterRunoff data to reduce time to execute
data(WaterRunoff.dat)
tmp <- subset(WaterRunoff.dat, Date == "05-18")

##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= tmp)
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(TS.diffs, sortFactor = "Sources",
                     sortParallelToCombo = 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= tmp)
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 emmeans 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(tmp))
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
els <- as.numeric(rownames(TS.preds))
TS.vcov <- vcov(TS.emm)[els,els]
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",
                     sortParallelToCombo = 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(tmp))
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
els <- as.numeric(rownames(TS.preds))
TS.vcov <- vcov(TS.emm)[els,els]
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)
}

```

---

sort.predictions.frame

*Sorts a [predictions.frame](#) according to the predicted values associated with a factor.*

---

## Description

Sorts the rows of a [predictions.frame](#) according to the predicted values in the predictions.frame. 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, sortParallelToCombo and sortOrder. If there is only one variable in the classify then the `predictions.frame` is sorted according to the order of the complete set of predictions.

## Usage

```
## S3 method for class 'predictions.frame'
sort(x, decreasing = FALSE, classify, sortFactor = NULL,
     sortParallelToCombo = NULL, sortNestingFactor = NULL,
     sortOrder = NULL, ...)
```

## Arguments

x	A <code>predictions.frame</code> .
decreasing	A <code>logical</code> passed to order that determines whether the order is for increasing or decreasing magnitude of the predicted values.
classify	A <code>character</code> 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 <code>:</code> operator.
sortFactor	A <code>character</code> 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 sortParallelToCombo 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 classify variables, excluding the sortFactor factor. The order to use is determined by either sortParallelToCombo or sortOrder.
sortParallelToCombo	A <code>list</code> that specifies a combination of the values of the factors and numerics, excluding sortFactor, that are in classify. Each of the components of the supplied <code>list</code> is named for a classify variable and specifies a single value for it. 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. Each of the other combinations of the values of the factors and numerics will be sorted in parallel. If sortParallelToCombo is NULL then the first value of each classify variable, except for the sortFactor factor, in the predictions component is used to define sortParallelToCombo. If there is only one variable in the classify then sortParallelToCombo is ignored.
sortNestingFactor	A <code>character</code> containing the name of the factor that defines groups of the sortFactor within which the predicted values are to be ordered. If there is only one variable in the classify then sortNestingFactor is ignored.
sortOrder	A <code>character</code> vector whose length is the same as the number of levels for sortFactor in the predictions.frame. It specifies the desired order of the levels in the reordered the <code>predictions.frame</code> . The argument sortParallelToCombo 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.frame 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 sortParallelToCombo combination, 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 sortParallelToCombo variables: the classify term, excluding the sortFactor.

## Value

The sorted `predictions.frame`. Also, the sortFactor and sortOrder attributes are set.

## Author(s)

Chris Brien

## See Also

`as.predictions.frame`, `print.predictions.frame`, `sort.alldiffs`,  
`predictPlus.asreml`, `predictPresent.asreml`

## Examples

```
##Halve WaterRunoff data to reduce time to execute
data(WaterRunoff.dat)
tmp <- subset(WaterRunoff.dat, Date == "05-18")

##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= tmp)
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.predictions.frame and save order for use with other response variables
TS.preds <- TS.diffs$predictions
TS.preds.sort <- sort(TS.preds, sortFactor = "Sources",
  sortParallelToCombo = list(Type = "Control"))
```

```

sort.order <- attr(TS.preds.sort, which = "sortOrder")

#Analyse Turbidity
m2.asr <- asreml(fixed = Turbidity ~ Benches + (Sources * (Type + Species)),
               random = ~ Benches:MainPlots,
               keep.order=TRUE, data= tmp)
current.asrt <- as.asrtests(m2.asr)
#Use pH sort.order to sort Turbidity alldiffs object
TS.diffs2 <- predictPlus(m2.asr, classify = "Sources:Type",
                       pairwise = FALSE, error.intervals = "Stand",
                       tables = "none", present = c("Type", "Species", "Sources"))
TS.preds2 <- TS.diffs2$predictions
TS.preds2.sort <- sort(TS.preds, sortFactor = "Sources", sortOrder = sort.order)

## End(Not run)

## Use lmeTest and emmeans 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(tmp))
  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"))

  #Use sort.predictions.frame and save order for use with other response variables
  TS.preds.sort <- sort(TS.preds, classify = "Sources:Type", sortFactor = "Sources",
                      sortParallelToCombo = list(Type = "Control"))
  sort.order <- attr(TS.preds.sort, which = "sortOrder")

  #Analyse Turbidity
  m2.lmer <- lmerTest::lmer(Turbidity ~ Benches + (Sources * (Type + Species)) +
                        (1|Benches:MainPlots),
                        data=na.omit(tmp))
  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"))
}

```

---

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.frame` stored in the `LSD` component, with any arguments supplied via the `...` argument passed to it.

The `select` argument of `subset` is not implemented, but can be achieved for variables in the `classify` using the `rmClassifyVars` argument.

## Usage

```
## S3 method for class 'alldiffs'
subset(x, subset = rep(TRUE, nrow(x$predictions)),
       rmClassifyVars = NULL, ...)
```

## Arguments

<code>x</code>	An <code>alldiffs.object</code> .
<code>subset</code>	A <code>logical</code> that determines rows of the predictions component of <code>x</code> to be included in the subset. By default all are included.
<code>rmClassifyVars</code>	A <code>character</code> that contains the names of the variables in the <code>classify</code> attribute of <code>x</code> that are to be removed from the predictions data.frame and the names of the dimensions of the other components of <code>x</code> . In doing this, the combinations of the remaining <code>classify</code> variables must uniquely index the predictions.
<code>...</code>	further arguments passed to <code>recalcLSD.alldiffs</code> .

## Value

An `alldiffs.object` with the following components of the supplied `alldiffs.object` subsetting, if present in the original object: `predictions`, `vcov`, `backtransforms`, `differences`, `p.differences` and `sed`. In addition, if `sed` is present, the `LSD.frame` in 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 emmeans 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
  els <- as.numeric(rownames(TS.preds))
  TS.vcov <- vcov(TS.emm)[els,els]
  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"))
}

```

subset.list

*Forms a **list** that contains a subset of the components of the supplied **list**.*

## Description

Select components of a **list** specified by a list of numbers or names, or by a logical indicating for each component of the list whether or not it is to be retained.

## Usage

```
## S3 method for class 'list'
subset(x, select = 1:length(x), ...)
```

**Arguments**

<code>x</code>	An <a href="#">list</a> object.
<code>select</code>	A <a href="#">numeric</a> or <a href="#">character</a> that lists or names the components of the <a href="#">list</a> <code>x</code> that are to be retained in the subset. It can also be a <a href="#">logical</a> that is the same length as <code>x</code> and indicates whether or not a component is to be retained.
<code>...</code>	further arguments passed to or from other methods. Not used at present.

**Value**

A [list](#) with just the subset of the components from `x`. If the components of `x` are named, then these names are retained in the subset [list](#).

**Author(s)**

Chris Brien

**See Also**

[subset.alldiffs](#)

**Examples**

```
x <- list(1:3, letters[1:3], LETTERS[1:3])
y <- subset.list(x, select = c(1,3))
y <- subset.list(x, select = c(TRUE,FALSE,TRUE))

names(x) <- LETTERS[1:3]
y <- subset.list(x, select = c(1,3))
z <- subset.list(x, select = LETTERS[c(1,3)])
x <- list(1:3, letters[1:3], LETTERS[1:3])
names(x)[c(1,3)] <- LETTERS[c(1,3)]
z <- subset.list(x, select = c(1,2))
v <- subset.list(x)
```

---

<code>testranfix.asrtests</code>	<i>Tests for a single fixed or random term in model fitted using <code>asreml</code> and records the result in an <a href="#">asrtests.object</a>.</i>
----------------------------------	--

---

**Description**

Tests for a single term, using a REML ratio test (REMLRT) 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 REMLRT 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, allow.fixedcorrelation = 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, IClikelihood = "none",
  trace = FALSE, update = TRUE,
  set.terms = NULL, ignore.suffices = TRUE,
  bounds = "P", initial.values = NA, ...)
```

## Arguments

- |                        |   |
|------------------------|---|
| asrtests.obj           | An <a href="#">asrtests.object</a> containing the components (i) <code>asreml.obj</code> , (ii) <code>wald.tab</code> , and (iii) <code>test.summary</code> .   |
| term                   | A single model term that is valid in <code>asreml</code> , stored as a character. The names of fixed terms must match those in the <code>wald.tab</code> component of the <code>asrtests.obj</code> , while the names of random terms must match those in the <code>vparameters</code> component of the <code>asreml.obj</code> component in the <code>asrtests.obj</code> .  |
| 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 <code>FALSE</code> , 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 <code>FALSE</code> and the fit of the new model has converged, but that of the old model has not, the new model will be accepted.   |
| allow.fixedcorrelation | A logical indicating whether to accept a new model even when it contains correlations in the model whose values have been designated as fixed, bound or singular. If <code>FALSE</code> and the new model contains correlations whose values have not been able to be estimated, the supplied <code>asrtests.obj</code> is returned. The fit in the <code>asreml.obj</code> component of the supplied <code>asrtests.obj</code> will also be tested and a warning issued if both fixed correlations are found in it and <code>allow.fixedcorrelation</code> is <code>FALSE</code> . |
| checkboundaryonly      | If <code>TRUE</code> then boundary and singular terms are not removed by <a href="#">rmboundary.asrtests</a> ; a warning is issued instead.   |
| drop.ran.ns            | A logical indicating whether to drop a random term from the model when it is nonsignificant. Note that multiple terms specified using a single <code>asreml::at</code> function will only be dropped as a whole. If the term was specified using an <code>asreml::at</code> function with a single level, then it can be removed and either the level itself or its <a href="#">numeric</a> position in the levels returned by the <a href="#">levels</a> function can be specified in <code>term</code> .  |
| 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 <code>bound.test.parameters</code> 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 <a href="#">REMLRT.asreml</a> . 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 <a href="#">REMLRT.asreml</a> . 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. Note that multiple terms specified using a single asreml::at function can only be dropped as a whole. If the term was specified using an asreml::at function with a single level, then it can be removed and either the level itself or its <a href="#">numeric</a> position in the levels returned by the <a href="#">levels</a> function can be specified.
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 automatically 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.
IClikelihood	A character that controls both the occurrence and the type of likelihood for information criterion in the test.summary of the new <a href="#">asrtests.object</a> . If none, none are included. Otherwise, if REML and family is set to asr_guassian (the default), then the AIC and BIC based on the Restricted Maximum Likelihood are included; if full and family is set to asr_guassian, then the AIC and BIC based on the full likelihood are included. if family is asr_binomial or

	asr_poisson, with dispersion set to 1, the deviance is extracted from object and used to calculate the AIC and BIC. (See also <a href="#">infoCriteria.asreml</a> .)
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 <code>update.asreml</code> is called to fit the model to be tested. In doing this the arguments <code>R.param</code> and <code>G.param</code> are set to those in the <code>asreml</code> object stored in <code>asrtests.obj</code> so that the values from the previous model are used as starting values. If FALSE then a call is made to <code>asreml</code> in which the only changes from the previous call are that (i) models are modified for the supplied terms and (ii) modifications specified via <code>...</code> are made.
set.terms	A character vector specifying the terms that are to have bounds and/or initial values set prior to fitting. The names must match those in the <code>vparameters</code> component of the <code>asreml.obj</code> component in the new <a href="#">asrtests.object</a> .
ignore.suffices	A logical vector specifying whether the suffices of the <code>asreml</code> -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 <code>asreml</code> -assigned names. If FALSE for an element of terms, the element must exactly match an <code>asreml</code> -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 <code>asreml</code> -assigned suffices for all the terms in terms.
bounds	A <a href="#">character</a> vector specifying the bounds to be applied to the terms specified in <code>set.terms</code> . This vector must be of length one or the same length as <code>set.terms</code> . If it is of length one then the same constraint is applied to all the terms in <code>set.terms</code> . 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 <code>initial.values</code> are equal to NA then they are left unchanged for those terms.
...	Further arguments passed to <code>asreml</code> , <code>wald.asreml</code> and <a href="#">as.asrtests</a> .

## 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

## References

Kenward, M. G., & Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics*, **53**, 983-997.

**See Also**

[asremlPlus-package](#), [as.asrtests](#), [chooseModel.asrtests](#), [REMLRT.asreml](#), [rmboundary.asrtests](#), [newfit.asreml](#), [changeModelOnIC.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 nugget term
current.asrt <- teststranfix(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`. If the two models have the same number of variance parameters, then no change is made to the residual. 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, allow.fixedcorrelation = TRUE,
             checkboundaryonly = FALSE, positive.zero = FALSE,
             bound.test.parameters = "none",
             bound.exclusions = c("F", "B", "S", "C"), REMLDF = NULL,
             denDF="numeric", IClikelihood = "none",
             update = TRUE, trace = FALSE,
             set.terms = NULL, ignore.suffices = TRUE,
             bounds = "P", initial.values = NA, ...)
```

## Arguments

<code>asrtests.obj</code>	an <a href="#">asrtests.object</a> for a fitted model that is a list containing the componets (i) <code>asreml.obj</code> , (ii) <code>wald.tab</code> (iii) <code>test.summary</code> .
<code>terms</code>	A model for the residual argument in <code>asreml-R4</code> (the <code>rcov</code> formula in older versions of <code>asreml</code> ), stored as a character. To remove the model, enter <code>"-(.)"</code> .
<code>label</code>	A character string to use as the label in <code>test.summary</code> and which indicates what is being tested.
<code>simpler</code>	A logical indicating whether the new model to be fitted is simpler than the already fitted model whose fit is stored in <code>asrtests.obj</code> .
<code>alpha</code>	The significance level for the test.
<code>allow.unconverged</code>	A logical indicating whether to accept a new model even when it does not converge. If <code>FALSE</code> and the fit of the new model does not converge, the supplied <code>asreml</code> object is returned. Also, if <code>FALSE</code> and the fit of the new model has converged, but that of the old model has not, the new model will be accepted.
<code>allow.fixedcorrelation</code>	A logical indicating whether to accept a new model even when it contains correlations in the model whose values have been designated as fixed, bound or singular. If <code>FALSE</code> and the new model contains correlations whose values have not been able to be estimated, the supplied <code>asrtests.obj</code> is returned. The fit in the <code>asreml.obj</code> component of the supplied <code>asrtests.obj</code> will also be tested and a warning issued if both fixed correlations are found in it and <code>allow.fixedcorrelation</code> is <code>FALSE</code> .
<code>checkboundaryonly</code>	If <code>TRUE</code> then boundary and singular terms are not removed by <a href="#">rmboundary.asrtests</a> ; a warning is issued instead.
<code>positive.zero</code>	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 <code>bound.test.parameters</code> is set.
<code>bound.test.parameters</code>	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 <code>"none"</code> , <code>"onlybound"</code> and <code>"one-and-one"</code> . The default is <code>"none"</code> , although if it is set to <code>"none"</code> and <code>positive.zero</code> is <code>TRUE</code> then <code>bound.test.parameters</code> is taken to be <code>"onlybound"</code> . When <code>bound.test.parameters</code> is set to <code>"one-and-one"</code> , 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.
<code>bound.exclusions</code>	A <a href="#">character</a> 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 <a href="#">REMLRT.asreml</a> . If set to <code>NULL</code> then none will be excluded.
<code>REMLDF</code>	A numeric giving the difference in the number of variance parameters whose estimates are not of the type specified in <code>bound.exclusions</code> for two models being compared in a REML ratio test using <a href="#">REMLRT.asreml</a> . If <code>NULL</code> then this is determined from the information in the <code>asreml</code> object for the two models.



denDF	Specifies the method to use in computing approximate denominator degrees of freedom when <code>wald.asreml</code> is called. Can be none to suppress the computations, numeric for numerical methods, algebraic for algebraic methods or default, the default, to automatically 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.
IClikelihood	A character that controls both the occurrence and the type of likelihood for information criterion in the <code>test.summary</code> of the new <code>asrtests.object</code> . If none, none are included. Otherwise, if REML, then the AIC and BIC based on the Restricted Maximum Likelihood are included; if full, then the AIC and BIC based on the full likelihood are included. (See also <code>infoCriteria.asreml</code> .)
update	If TRUE then <code>update.asreml</code> is called to fit the model with the residual (rcov) model supplied in terms. In doing this the arguments <code>R.param</code> and <code>G.param</code> are set to those in the <code>asreml</code> object stored in <code>asrtests.obj</code> so that the values from the previous model are used as starting values. If FALSE then a call is made to <code>asreml</code> 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 <code>character</code> vector specifying the terms that are to have bounds and/or initial values set prior to fitting. The names must match those in the <code>vparameters</code> component of the <code>asreml.obj</code> component in the new <code>asrtests.object</code> .
ignore.suffices	A <code>logical</code> vector specifying whether the suffices of the <code>asreml</code> -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 <code>asreml</code> -assigned names. If FALSE for an element of terms, the element must exactly match an <code>asreml</code> -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 <code>asreml</code> -assigned suffices for all the terms in terms.
bounds	A <code>character</code> vector specifying the bounds to be applied to the terms specified in <code>set.terms</code> . This vector must be of length one or the same length as <code>set.terms</code> . If it is of length one then the same constraint is applied to all the terms in <code>set.terms</code> . 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 <code>asreml</code> , <code>wald.asreml</code> and <code>as.asrtests</code> .

## 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

**References**

Kenward, M. G., & Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics*, **53**, 983-997.

**See Also**

[asremlPlus-package](#), [as.asrtests](#), [changeTerms.asrtests](#),  
[chooseModel.asrtests](#), [REMLRT.asreml](#), [rmboundary.asrtests](#),  
[newfit.asreml](#), [testswapran.asrtests](#), [changeModelOnIC.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	<i>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 <a href="#">asrtests.object</a>.</i>
----------------------	---

---

**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](#). If the models are not nested, then using [changeModelOnIC.asrtests](#) may be the more appropriate approach for comparing models.

## 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, allow.fixedcorrelation = TRUE,
            checkboundaryonly = FALSE,
            positive.zero = FALSE, bound.test.parameters = "none",
            bound.exclusions = c("F", "B", "S", "C"), REMLDF = NULL,
            denDF="numeric", ICllikelihood = "none",
            trace = FALSE, update = TRUE,
            set.terms = NULL, ignore.suffices = TRUE,
            bounds = "P", initial.values = NA, ...)
```

## Arguments

- |                        |   |
|------------------------|---|
| asrtests.obj           | an <a href="#">asrtests.object</a> 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. The names of the terms must match those in the vparameters component of the asreml.obj component in asrtests.obj. Note that multiple terms specified using a single asreml::at function can only be dropped as a whole. If the term was specified using an asreml::at function with a single level, then it can be removed and either the level itself or its <a href="#">numeric</a> position in the levels returned by the <a href="#">levels</a> function can be specified. |
| 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 asrtests.obj 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.  |
| allow.fixedcorrelation | A logical indicating whether to accept a new model even when it contains correlations in the model whose values have been designated as fixed, bound or singular. If FALSE and the new model contains correlations whose values have not been able to be estimated, the supplied asrtests.obj is returned. The fit in the asreml.obj component of the supplied asrtests.obj will also be tested and a warning issued if both fixed correlations are found in it and allow.fixedcorrelation is FALSE.  |
| checkboundaryonly      | If TRUE then boundary and singular terms are not removed by <a href="#">rmboundary.asrtests</a> ; 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 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 automatically 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.

#### `IClikelihood`

A character that controls both the occurrence and the type of likelihood for information criterion in the `test.summary` of the new [asrtests.object](#). If none, none are included. Otherwise, if REML, then the AIC and BIC based on the Restricted Maximum Likelihood are included; if full, then the AIC and BIC based on the full likelihood are included. (See also [infoCriteria.asreml](#).)

#### `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 modified 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. The names must match those in the `vparameters` component of the `asreml.obj` component in the [asrtests.object](#).

#### `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 <a href="#">character</a> 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 <a href="#">as.asrtests</a> .

## 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

## References

Kenward, M. G., & Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics*, **53**, 983-997.

## See Also

[as.asrtests](#), [chooseModel.asrtests](#), [REMLRT.asreml](#), [rmboundary.asrtests](#), [newfit.asreml](#), [testresidual.asrtests](#), [changeModelOnIC.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 emmeans 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	<i>Checks that an object is a valid asrtests object.</i>
---------------	--

---

### 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`, `is.predictions.frame`, `as.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 emmeans 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	<i>Plots empirical variogram faces, including envelopes, as described by Stefanova, Smith &amp; Cullis (2009).</i>
-------------------	--

---

## 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

<code>asreml.obj</code>	An <code>asreml</code> object from a call to <code>asreml</code> in which the data argument has been set.
<code>means</code>	The vector of means to be used in generating simulated data sets. If it is <code>NULL</code> , the fitted values based on object are used. It must be the same length as the response variable for object.
<code>V</code>	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 <code>V</code> is <code>NULL</code> then <code>estimateV.asreml</code> is called to obtain it from <code>asreml.obj</code>

<code>nsim</code>	The number of data sets to be simulated in obtaining the envelopes.
<code>seed</code>	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 <code>nextRNGStream</code> is used to seed each core from the original seed.
<code>extra.matrix</code>	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 <code>asreml.obj</code> . It is assumed that the sigma-parameterized values of the variance parameter estimates, such as is given in the <code>varcomp</code> component of <code>summary.asreml</code> , have been used in calculating <code>extra.matrix</code> ; the values in the <code>vparameters</code> component of <code>G.param</code> and <code>R.param</code> may be either gamma- or sigma-parameterized. The argument <code>extra.matrix</code> can be used in conjunction with <code>ignore.terms</code> as a workaround to include components of the variance matrix for variance functions that have not been implemented in <code>estimateV</code> .
<code>ignore.terms</code>	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 <code>vparameters</code> component of the <code>asreml</code> object or the <code>varcomp</code> component produced by <code>summary.asreml</code> , but only up to the first exclamation mark (!). This can be used in conjunction with <code>estimateV.asreml</code> as a workaround to include components of the variance matrix for variance functions that have not been implemented in <code>estimateV</code> .
<code>fixed.spline.terms</code>	A character vector giving one or more 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 <code>vparameters</code> component of the <code>asreml</code> object or the <code>varcomp</code> component produced by <code>summary.asreml</code> , but only up to the first exclamation mark (!).
<code>bound.exclusions</code>	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 <code>NULL</code> then none will be excluded.
<code>tolerance</code>	The value such that eigenvalues less than it are considered to be zero.
<code>units</code>	A character indicating whether the BLUPs for <code>units</code> are added to the residuals when this reserved factor is included in the random model. Possible values are <code>addtoresiduals</code> and <code>ignore</code> . If standardized conditional residuals are plotted and the BLUPs for <code>units</code> are to be added then it is the standardized BLUPs that are added.
<code>update</code>	If <code>TRUE</code> then the arguments <code>R.param</code> and <code>G.param</code> are set to those in the <code>asreml</code> object supplied in <code>object</code> so that the values from the original model are used as starting values. If <code>FALSE</code> then calls are made to <code>asreml</code> in which the only changes from the previous call are (i) the model is fitted to simulated data and (ii) modifications specified via <code>...</code> are made, except that changes cannot be made to any of the models.
<code>trace</code>	If <code>TRUE</code> then partial iteration details are displayed when <code>ASReml-R</code> functions are invoked; if <code>FALSE</code> then no output is displayed.
<code>graphics.device</code>	A character specifying a graphics device for plotting. The default is <code>graphics.device = NULL</code> , 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.
<code>ncores</code>	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 conditional 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 a 1976 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 spring 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 the Wheat vignettes [Enter `vignette(package = "asremlPlus")`] 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  $10 \times 15$  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, <https://asreml.kb.vsnr.co.uk/>.

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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