Using `asremlPlus`, in conjunction with `asreml`, to do the analysis of a wheat experiment that includes choosing a local spatial variation model using AICs

Chris Brien

24 August, 2023

This vignette shows how to use `asremlPlus` (Brien, 2023), in conjunction with `asreml` (Butler et al., 2023), to select the terms to be included in a mixed model for an experiment that involves spatial variation by comparing of information criteria . It also illustrates diagnostic checking and prediction production and presentation for this experiment. Here, `asremlPlus` and `asreml` are packages for the `R` Statistical Computing environment (R Core Team, 2023).

It is divided into the following main sections:

1. Set up the initial model for this experiment
2. Compare a series of information criteria to select a linear mixed model for the data
3. Diagnostic checking using residual plots and variofaces
4. Prediction production and presentation

1. Set up the initial model for this experiment

```
library(asreml, quietly=TRUE)
```

```
## Offline License checked out Thu Aug 24 10:11:56 2023
```

```
## Loading ASReml-R version 4.2
```

```
library(asremlPlus)
suppressMessages(library(qqplotr, quietly=TRUE))
options(width = 100)
```

Get data available in asremlPlus

The data are from a 1976 spring wheat experiment and are taken from Gilmour et al. (1995). An analysis is presented in the `asreml` manual by Butler et al. (2023, Section 7.6), although they suggest that it is a barley experiment.

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

Add row and column covariates for the spatial modelling

```
tmp.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 an initial model - Row and column random

In the following, an initial model is fitted that has the terms that would be included for a balanced lattice. In addition, a term WithinColPairs has been included to allow for extraneous variation arising between pairs of adjacent lanes.

```
current.asr <- do.call(asreml,
                       list(yield ~ Rep + WithinColPairs + Variety,
                            random = ~ Row + Column,
                            residual = ~ Row:Column,
                            data = tmp.dat))
```

Intialize a model sequence by loading the current fit into an asrtests object

In creating the `asrtests` object, `IClikelihood` is set to `full` so that the full Restricted Maximum Likelihood (full REML) of Verbyla, 2019 is incorporated into the `tests.summary` of the `asrtests` object.

```
current.asrt <- as.asrtests(current.asr, NULL, NULL, IClikelihood = "full",
                            label = "Initial model")
```

```
## Warning in (function (fixed = ~1, random = ~NULL, sparse = ~NULL, residual = ~NULL, :
## Log-likelihood not converged
```

Check for and remove any boundary terms and print a summary of the fit in the asrtests object

```
current.asrt <- rmboundary(current.asrt)
print(current.asrt)
```

```
##
##
## ####  Summary of the fitted variance parameters
##
##              component std.error  z.ratio bound %ch
## Row           5943.898  3815.514 1.557824     P 0.0
## Column       12380.527  6323.542 1.957847     P 0.3
## Row:Column!R 20477.280  2896.642 7.069316     P 0.0
##
##
## ####  Pseudo-anova table for fixed terms
##
##
## Wald tests for fixed effects.
## Response: yield
##
##                Df denDF   F.inc     Pr
## (Intercept)     1  14.9 1390.00 0.0000
## Rep             5  25.3    6.04 0.0008
## WithinColPairs  1  10.4    0.49 0.4998
## Variety        24 104.8    4.71 0.0000
##
```

```
##
## ####  Sequence of model investigations
##
## (If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)
##
##           terms DF denDF  p      AIC      BIC         action
## 1 Initial model 31     3 NA 1720.891 1823.253 Starting model
```

The `test.summary` output shows that no changes have been made to the model loaded using `as.asrtests`.
The pseudo-anova table shows that Varieties are highly significant ($p < 0.001$)

2. Compare a series of information criteria to select a linear mixed model for the data

In this section, models are compared using Akaike Information Criterion (AICs) based on the full REML.

Check the need for the term for within Column pairs (a post hoc factor)

```
current.asrt <- changeModelOnIC(current.asrt, dropFixed = "WithinColPairs",
                                label = "Try dropping withinColPairs", IClikelihood = "full")
```

```
## Warning in (function (fixed = ~1, random = ~NULL, sparse = ~NULL, residual = ~NULL, :
## Log-likelihood not converged
```

```
print(current.asrt)
```

```
##
##
## ####  Summary of the fitted variance parameters
##
##              component std.error  z.ratio bound %ch
## Row           5941.153  3813.586 1.557891     P   0
## Column       11165.335  5583.267 1.999785     P   0
## Row:Column!R 20472.402  2895.582 7.070219     P   0
##
##
## ####  Pseudo-anova table for fixed terms
##
##
## Wald tests for fixed effects.
## Response: yield
##
##             Df denDF   F.inc    Pr
## (Intercept)  1  15.3 1466.00 0e+00
## Rep          5  26.7    6.11 7e-04
## Variety     24 105.3    4.73 0e+00
##
##
## ####  Sequence of model investigations
##
## (If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)
##
##                          terms DF denDF  p         AIC        BIC         action
## 1               Initial model 31     3 NA 1720.891308 1823.25291 Starting model
```

```
## 2 Try dropping withinColPairs -1     0 NA   -2.281894   -5.29253        Swapped
```

It is clear in the call to `changeModelOnIC` that the model is being changed by dropping the `withinColPairs` term, which could also be achieved using `update.asreml`. However, an `asremlPlus` model-changing function operates on an `asrtests` object, that includes an `asreml` object, and, except for `changeTerms.asrtests`, results in an `asrtests` object that may contain the changed model or the supplied model depending on the results of hypothesis tests or comparisons of information criteria. In addition, the result of the test or comparison will be added to a `test.summary` data.frame stored in the new `asrtests` object and, if the model was changed, the `wald.tab` in the new `asrtests` object will have been updated for the new model.

In this case, as can be seen from the summary of `current.asrt` after the call, the model without `withinColPairs` had a smaller AIC and so now the model stored in `current.asrt` does not include `withinColPAirs`. The `wald.tab` has been updated for the new model.

Choose a model for local spatial variation from several potential models

This example has been analyzed using a model for the local spatial variation based on a separable a separable autocorrelation process of order one (Butler et al., 2023). The need for this model can be assessed using the function `addSpatialModelOnIC` from `asremlPlus` that uses a forward selection strategy for fitting a correlation model (see output below). For this function, the spatial model to be fitted, the centred covariates for the two dimensions of the grid, and the factors corresponding to the covariates must be specified. Also, `checkboundaryonly` is set to `TRUE` so that no terms are removed until the final model has been fitted and `IClikelihood` is set to `full` so that the likelihood will be based on the full REML. Because the model that incorporates the spatial model has a smaller AIC, it is the model returned in `spatial.ar1.asrt`.

The `print` of `spatial.ar1.asrt` shows that an `ar1` model for `Row` was tried first and was found to reduce the AIC by 11.898 and so became the current model. Next a model that incorporates an `ar1` function for `Column` was similarly tried and became the current model. Then an appraisal of the need for a nugget term was made by comparing the fits with the residual variance unfixed and fixed at one. The model with the unfixed residual variance was chosen and is the model to be returned. The nugget term represents non-spatial variance, such as measurement error.

```
spatial.ar1.asrt <- addSpatialModelOnIC(current.asrt, spatial.model = "corr",
                                        row.covar = "cRow", col.covar = "cColumn",
                                        row.factor = "Row", col.factor = "Column",
                                        checkboundaryonly = TRUE, IClikelihood = "full")
```

```
## Warning in (function (fixed = ~1, random = ~NULL, sparse = ~NULL, residual = ~NULL, :
## Log-likelihood not converged
```

```
## Warning in (function (fixed = ~1, random = ~NULL, sparse = ~NULL, residual = ~NULL, : Some
## components changed by more than 1% on the last iteration
```

```
## Warning in (function (fixed = ~1, random = ~NULL, sparse = ~NULL, residual = ~NULL, :
## Log-likelihood not converged
```

```
## Warning in (function (fixed = ~1, random = ~NULL, sparse = ~NULL, residual = ~NULL, : Some
## components changed by more than 1% on the last iteration
```

```
## Warning in infoCriteria.asreml(asreml.obj, IClikelihood = ic.lik, bound.exclusions = bound.exclusions
##  Column
```

```
## Warning in rmboundary.asrtests(as.asrtests(asreml.obj, wald.tab, test.summary, : In analysing yield,
##               but not removed because checkboundaryonly = TRUE:
## Column
```

```
## Warning in infoCriteria.asreml(new.asrtests.obj$asreml.obj, IClikelihood = ic.lik, : The following bo
##  Column
```

```
## Warning in infoCriteria.asreml(asrtests.obj$asreml.obj, IClikelihood = ic.lik, : The following bound
```

```
##  Column

## Warning in (function (fixed = ~1, random = ~NULL, sparse = ~NULL, residual = ~NULL, :
## Log-likelihood not converged

## Warning in (function (fixed = ~1, random = ~NULL, sparse = ~NULL, residual = ~NULL, : Some
## components changed by more than 1% on the last iteration

## Warning in infoCriteria.asreml(asreml.obj, IClikelihood = ic.lik, bound.exclusions = bound.exclusions
##  Column, Row:Column!R

## Warning in rmboundary.asrtests(as.asrtests(asreml.obj, wald.tab, test.summary, : In analysing yield,
##               but not removed because checkboundaryonly = TRUE:
## Column

## Warning in infoCriteria.asreml(new.asrtests.obj$asreml.obj, IClikelihood = ic.lik, : The following bo
##  Column, Row:Column!R
```

```
spatial.ar1.asrt <- rmboundary(spatial.ar1.asrt)
infoCriteria(list(nonspatial = current.asrt$asreml.obj,
                  ar1 = spatial.ar1.asrt$asreml.obj))
```

```
##            fixedDF varDF NBound      AIC      BIC    loglik
## nonspatial       0     3      0 1409.023 1417.386 -701.5117
## ar1              0     5      0 1353.762 1367.700 -671.8811
```

```
print(spatial.ar1.asrt)
```

```
##
##
## ####  Summary of the fitted variance parameters
##
##                            component    std.error   z.ratio bound %ch
## Row                     2.198199e+03 8.220214e+03 0.2674138     P 0.1
## Row:Column              5.182611e+04 3.379376e+04 1.5336001     P 0.0
## Row:Column!Row!cor      7.121385e-01 9.571021e-02 7.4405696     U 0.0
## Row:Column!Column!cor   8.599836e-01 1.104248e-01 7.7879542     U 0.0
## Row:Column!R            4.821195e+03 1.717266e+03 2.8074825     P 0.0
##
##
## ####  Pseudo-anova table for fixed terms
##
##
## Wald tests for fixed effects.
## Response: yield
##
##             Df denDF   F.inc     Pr
## (Intercept)  1   1.8 194.600 0.0076
## Rep          5  21.8   0.559 0.7303
## Variety     24  74.3  10.560 0.0000
##
##
## ####  Sequence of model investigations
##
## (If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)
##
##                         terms DF denDF  p         AIC         BIC         action
## 1               Initial model 31     3 NA 1720.891308 1823.252908 Starting model
```

```
## 2 Try dropping withinColPairs -1     0 NA   -2.281894   -5.292530        Swapped
## 3                 Try ar1(Row)  0     2 NA  -11.897888   -5.876617        Swapped
## 4              Try ar1(Column)  0     0 NA  -55.397582  -55.397582        Swapped
## 5 Try fixed residual variance  0    -1 NA    1.809461   -1.201174      Unswapped
## 6                       Column  1    NA NA          NA          NA       Boundary
```

However, the spatial models that are available in `asremlPlus` also include those based on two-dimensional tensor-product natural cubic smoothing splines (TPNCSS), as described by Verbyla et al. (2018), and on two-dimensional tensor-product P-splines (TPPS), as described by Rodriguez-Alvarez et al. (2018) and Piepho, Boer and Williams (2022). The P-splines have been implemented using functions from the `R` package `TPSbits` authored by Sue Welham (2022)

The `asremlPlus` function `chooseSpatialModelOnIC` allows one to select the best model from amongst these spatial correlation models using the AIC. The four models from which it selects are (i) a separable autocorrelation model on both row and column dimensions (`corr`), (ii) a two-dimensional tensor-product natural cubic smoothing spline (`TPNCSS`), (ii) a two-dimensional tensor-product cubic P-spline with second-difference penalties (`TPPCS`), and (iii) a tensor-product two-dimensional linear P-spline with first-difference penalties (`TPP1LS`). By default all four are fitted and compared, but the `trySpatial` argument can be used to specify a subset of them.

The call to `chooseSpatialModelOnIC`, in addition to the arguments specifying covariates and factors, has further arguments: (i) `dropRowTerm` and `dropColTerm` that are needed in fitting P-splines, if overall Row and Column terms have been fitted in the supplied model, because the code also automatically includes these terms, (ii) `rotateX` and `ngridangles` so that a grid of angles of every five degrees between 0 and 90 in both directions is explored for rotating the eigenvectors of the penalty matrix for the linear component of the P-splines (requiring $(18 + 1)^2 = 361$ re-analyses), (iii) an `asreml.option` argument to specify that the `grp` method be used in fitting the P-spline terms, this being required for `rotateX` set to `TRUE`, and (iv) `return.asrts` to specify which `asrtests` objects are to be returned. Here we specify `all` so that `asrtests` objects for the fits for all four spatial models will be returned. In this case, neither the `checkboundaryonly` nor the `IClikelihood` arguments were set because their defaults for `chooseSpatialModelOnIC` are appropriate.

```
suppressWarnings(
  spatial.asrts <- chooseSpatialModelOnIC(current.asrt,
                                          row.covar = "cRow", col.covar = "cColumn",
                                          row.factor = "Row", col.factor = "Column",
                                          dropRowterm = "Row", dropColterm = "Column",
                                          rotateX = TRUE, ngridangles = c(18,18),
                                          asreml.option = "grp", return.asrts = "all"))
```

```
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .000900 have been merged
```

```
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 0 time 3.29 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 1 time 6.68 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 2 time 9.91 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 3 time 13.3 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 4 time 16.72 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 5 time 20.08 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 6 time 23.41 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 7 time 26.77 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 8 time 30.16 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 9 time 33.41 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 10 time 36.69 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 11 time 40.13 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 12 time 43.35 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 13 time 46.63 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 14 time 49.91 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 15 time 53.4 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 16 time 56.68 seconds
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 17 time 59.94 seconds
```

```
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## sc 18 time 63.35 seconds
##
##
## #### Optimal thetas: 15, 90
##
## Notice  : Spline design points closer than .000900 have been merged
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Notice  : Spline design points closer than .000900 have been merged
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Notice  : Spline design points closer than .000900 have been merged
## Terms with zero df listed in attribute 'zerodf' of the wald table.
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .000900 have been merged
## Notice  : Spline design points closer than .000900 have been merged
```

Output the results

```
print(spatial.asrts$spatial.IC)
```

```
##            fixedDF varDF      AIC      BIC    loglik
```

```
## nonspatial      30     3 1718.609 1817.960 -826.3047
## corr            30     5 1651.314 1756.686 -790.6570
## TPNCSS          33     6 1639.489 1756.904 -780.7445
## TPPCS           32     6 1645.033 1759.437 -784.5164
## TPP1LS          30     3 1708.443 1807.794 -821.2215
```

```
print(spatial.asrts$best.spatial.mod)
```

```
## [1] "TPNCSS"
```

```
print(spatial.asrts$asrts$TPNCSS)
```

```
##
##
## ####  Summary of the fitted variance parameters
##
##                          component std.error  z.ratio bound %ch
## spl(cRow):cColumn        523.2004  372.8016 1.403429     P   0
## dev(cRow)               7664.0211 4442.0646 1.725329     P   0
## spl(cColumn)           13338.7348 9236.0511 1.444203     P   0
## spl(cColumn):cRow        366.7707  322.7484 1.136399     P   0
## spl(cRow):spl(cColumn)  3630.2187 2186.1497 1.660554     P   0
## Row:Column!R            7658.0113 1312.2026 5.835998     P   0
##
##
## ####  Pseudo-anova table for fixed terms
##
##
## Wald tests for fixed effects.
## Response: yield
##
##              Df denDF   F.inc     Pr
## (Intercept)   1   6.8 2645.00 0.0000
## Rep           5  41.3   20.45 0.0000
## Variety      24  86.5   10.15 0.0000
## cRow          1   7.0    0.07 0.7954
## cColumn       1  30.1   20.30 0.0001
## cRow:cColumn  1  64.3   22.00 0.0000
##
##
## ####  Sequence of model investigations
##
## (If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)
##
##                         terms DF denDF  p         AIC        BIC         action
## 1               Initial model 31     3 NA 1720.891308 1823.25291 Starting model
## 2 Try dropping withinColPairs -1     0 NA   -2.281894   -5.29253        Swapped
## 3      Try tensor NCS splines  3     3 NA  -79.120426  -61.05661        Swapped
## 4                dev(cColumn)  1    NA NA 1639.488959 1756.90374       Boundary
## 5                   spl(cRow)  1    NA NA 1639.489011 1756.90379       Boundary
```

```
printFormulae(spatial.asrts$asrts$TPNCSS$asreml.obj)
```

```
##
##
## #### Formulae from asreml object
```

```
##
## fixed: yield ~ Rep + Variety + cRow + cColumn + cRow:cColumn
## random: ~ spl(cColumn) + dev(cRow) + spl(cRow):cColumn + spl(cColumn):cRow + spl(cRow):spl(cColumn)
## residual: ~ Row:Column
```

The output shows that the TPNCSS model has the lowest AIC and so is selected as the best model. The model fitted for the TPNCSS model has been printed using `printFormulae.asreml`. The fitted model includes the term `dev(cRow)` that is equivalent to a random `Row` term and measures the deviations of the Row trend from a linear trend, the `spl(cRow)` term having been dropped because it was estimated to be zero. The Wald F-statistic for `Variety` is now 10.15 with 86.5 denominator degrees of freedom, as compared to 10.56 and 74.3 for the correlation model and 4.71 and 104.8 for the initial nonspatial model.

3. Diagnosting checking using residual plots and variofaces

Get current fitted asreml object and update to include standardized residuals

```
current.asr <- spatial.asrts$asrts$TPNCSS$asreml.obj
current.asr <- update(current.asr, aom=TRUE)
```

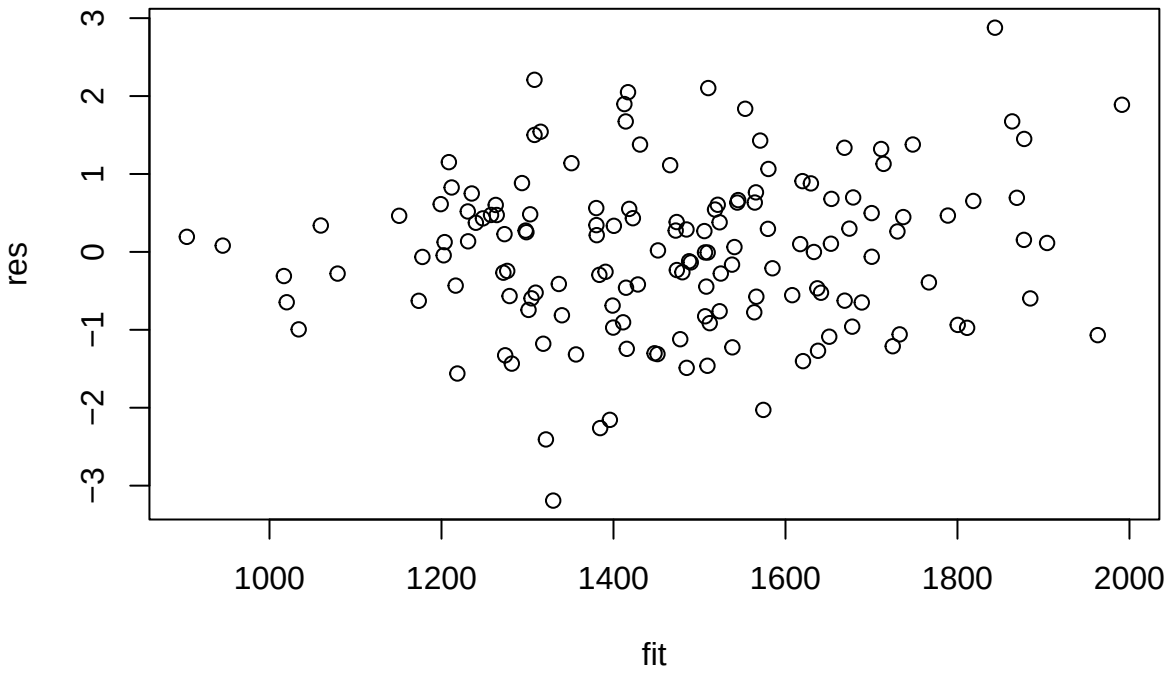
```
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
```

```
Wheat.dat$res <- residuals(current.asr, type = "stdCond")
Wheat.dat$fit <- fitted(current.asr)
```

Do diagnostic checking

Do residuals-versus-fitted values plot

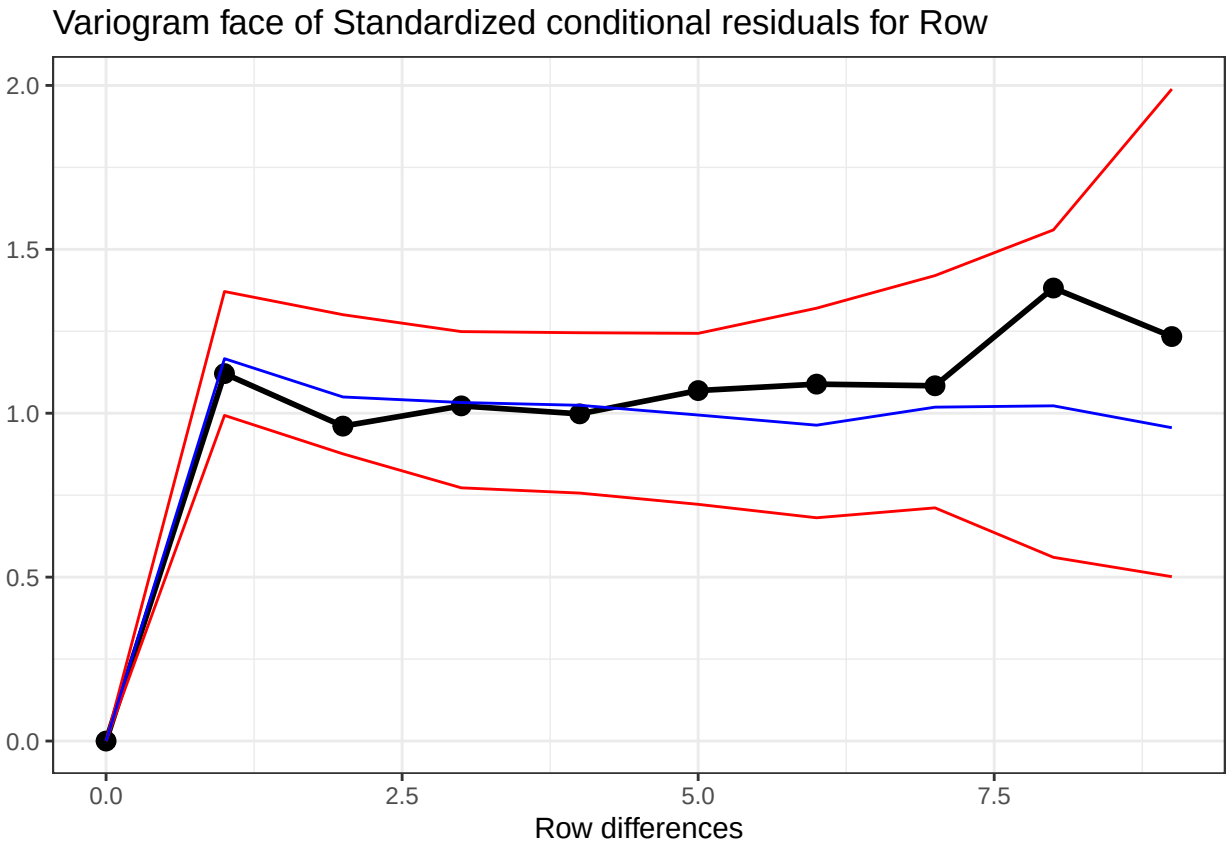
```
with(Wheat.dat, plot(fit, res))
```

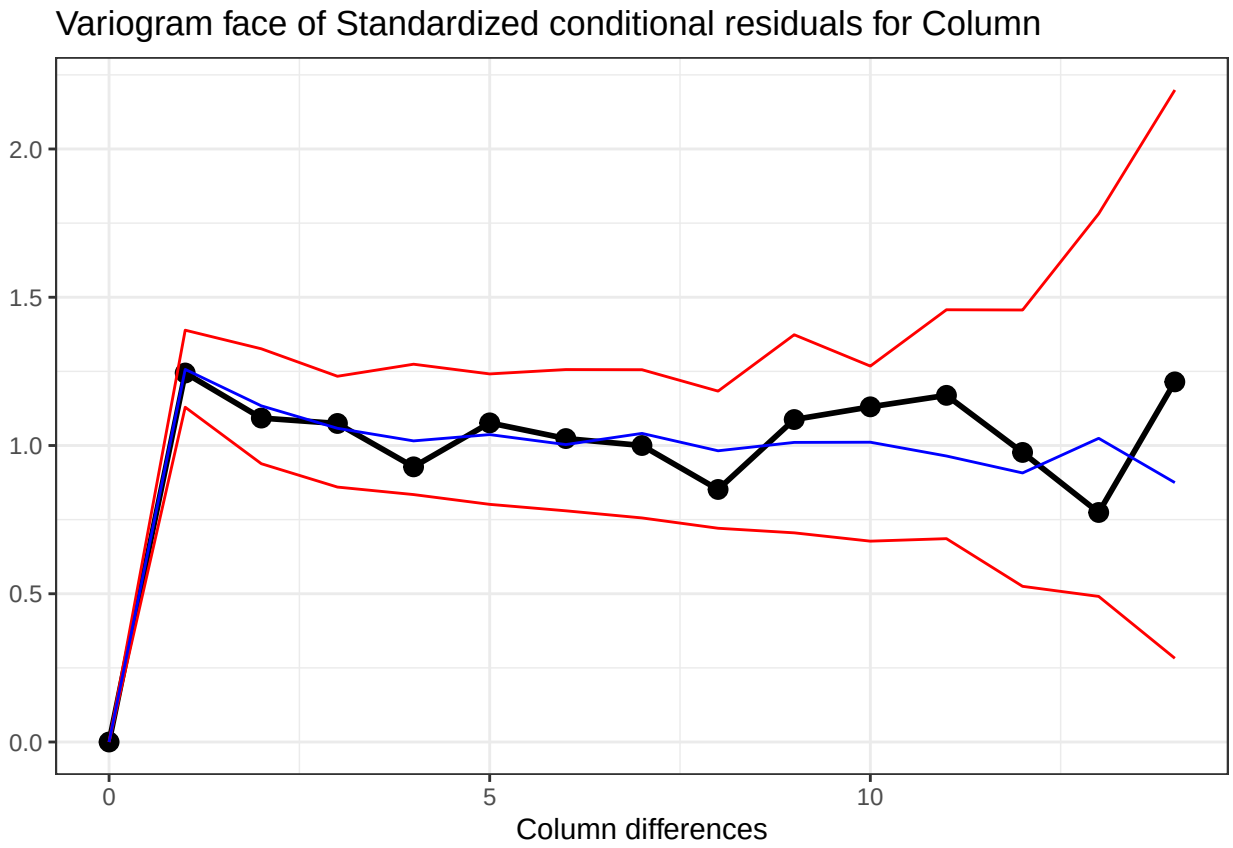


Plot variofaces

```
variofaces(current.asr, V=NULL, units="addtores",
           maxiter=50, update = FALSE)
```

```
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
```



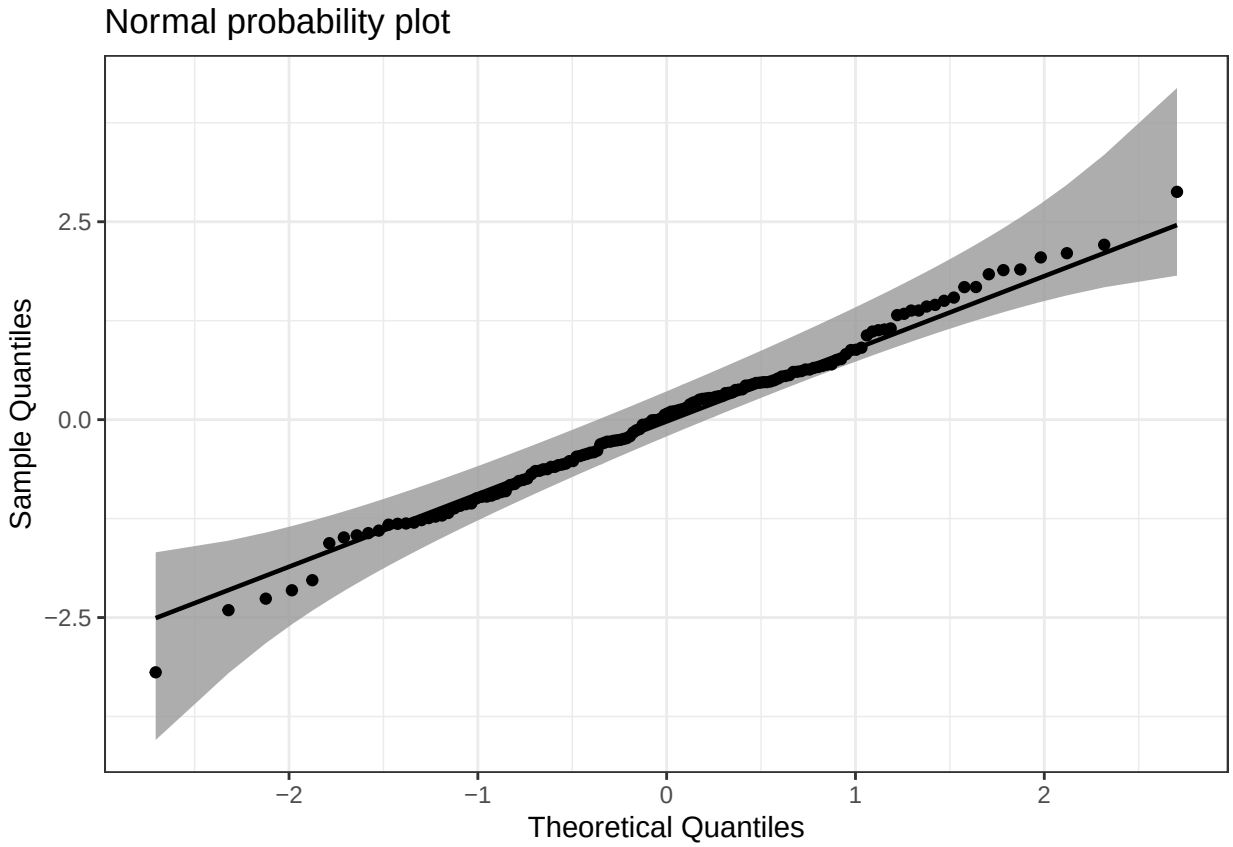


The variofaces are the lag 1 plots of the sample semivariogram with simulated confidence envelopes (Stefanova et al., 2009).

Plot normal quantile plot

The plot is obtained using the `ggplot` function with extensions available from the `qqplotr` package (Almeida et al., 2023).

```
ggplot(data = Wheat.dat, mapping = aes(sample = res)) +
  stat_qq_band(bandType = "ts") + stat_qq_line() + stat_qq_point() +
  labs(x = "Theoretical Quantiles", y = "Sample Quantiles",
       title = "Normal probability plot") +
  theme(plot.title = element_text(size = 12, face = "bold")) + theme_bw()
```



4. Prediction production and presentation

Get Variety predictions 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")
```

```
## Notice  : Spline design points closer than .001400 have been merged
## Notice  : Spline design points closer than .000900 have been merged
##
##
## #### Predictions for yield from Variety
##
##
## Notes:
## - The predictions are obtained by averaging across the hypertable
##   calculated from model terms constructed solely from factors in
##   the averaging and classify sets.
## - Use 'average' to move ignored factors into the averaging set.
## - spl(cRow) evaluated at average value of 0.00000
## - spl(cColumn) evaluated at average value of 0.00000
## - The simple averaging set: Rep
```

```
##
##    Variety predicted.value standard.error upper.halfLeastSignificant.limit
## 1       10        1196.214       64.11316                           1255.028
## 2        9        1266.442       69.62176                           1325.255
## 3       16        1268.206       74.01873                           1327.020
## 4        1        1273.794       69.30592                           1332.608
## 5       14        1310.806       70.75661                           1369.620
## 6       23        1329.114       73.70238                           1387.928
## 7       11        1340.668       75.07426                           1399.481
## 8        4        1406.408       76.83336                           1465.222
## 9        3        1408.543       71.85868                           1467.356
## 10       7        1414.471       72.23082                           1473.284
## 11      12        1423.303       71.18629                           1482.117
## 12       8        1445.533       75.37805                           1504.347
## 13       5        1480.687       70.31499                           1539.500
## 14      15        1485.249       74.28025                           1544.063
## 15      17        1495.212       71.09930                           1554.026
## 16      21        1512.767       72.53109                           1571.580
## 17       6        1520.841       72.50721                           1579.654
## 18      24        1563.649       65.33308                           1622.463
## 19      18        1568.887       71.06200                           1627.700
## 20      25        1579.929       70.52509                           1638.743
## 21       2        1585.398       74.96623                           1644.211
## 22      22        1633.080       71.38265                           1691.894
## 23      13        1637.119       66.24775                           1695.932
## 24      19        1651.533       74.93686                           1710.347
## 25      20        1657.612       68.65452                           1716.426
##    lower.halfLeastSignificant.limit est.status
## 1                          1137.400  Estimable
## 2                          1207.628  Estimable
## 3                          1209.393  Estimable
## 4                          1214.980  Estimable
## 5                          1251.993  Estimable
## 6                          1270.300  Estimable
## 7                          1281.854  Estimable
## 8                          1347.594  Estimable
## 9                          1349.729  Estimable
## 10                         1355.657  Estimable
## 11                         1364.490  Estimable
## 12                         1386.720  Estimable
## 13                         1421.873  Estimable
## 14                         1426.435  Estimable
## 15                         1436.399  Estimable
## 16                         1453.953  Estimable
## 17                         1462.027  Estimable
## 18                         1504.836  Estimable
## 19                         1510.073  Estimable
## 20                         1521.115  Estimable
## 21                         1526.584  Estimable
## 22                         1574.266  Estimable
## 23                         1578.305  Estimable
## 24                         1592.719  Estimable
## 25                         1598.798  Estimable
##
```

```
##
## LSD values
##
## minimum LSD =  109.6008
##
## mean LSD =  117.6273
##
## maximum LSD =  126.3422
##
## (sed range / mean sed =  0.142 )
```

We have set `error.intervals` to `halfLeast` so that the limits for each prediction $\pm$ (0.5 LSD) are calculated. When these are plotted overlapping error bars indicate predictions that are not significant, while those that do not overlap are significantly different (Snee, 1981).

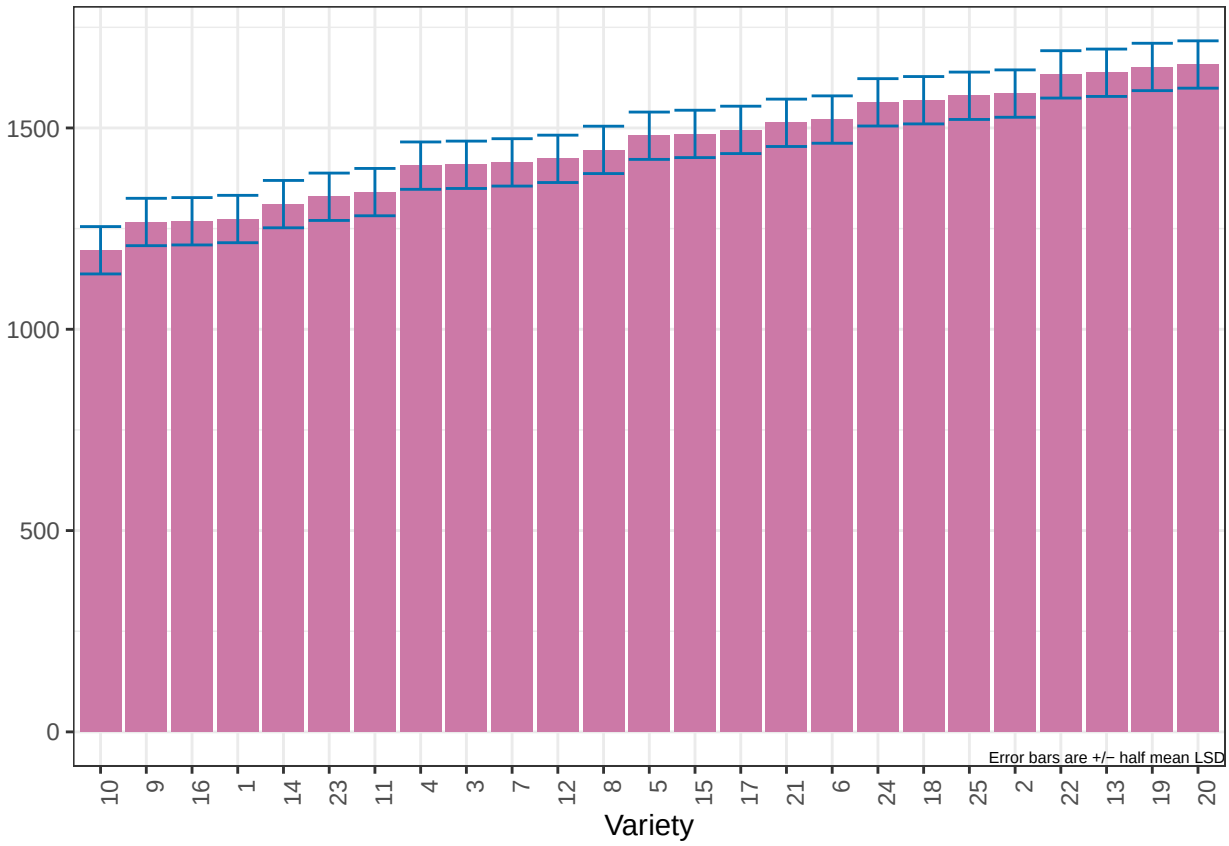
Also set was `sortFactor`, so that the results would be ordered for the values of the predictions for Variety.

The function `predictPlus` returns an `alldiffs` object, a list consisting of the following components:

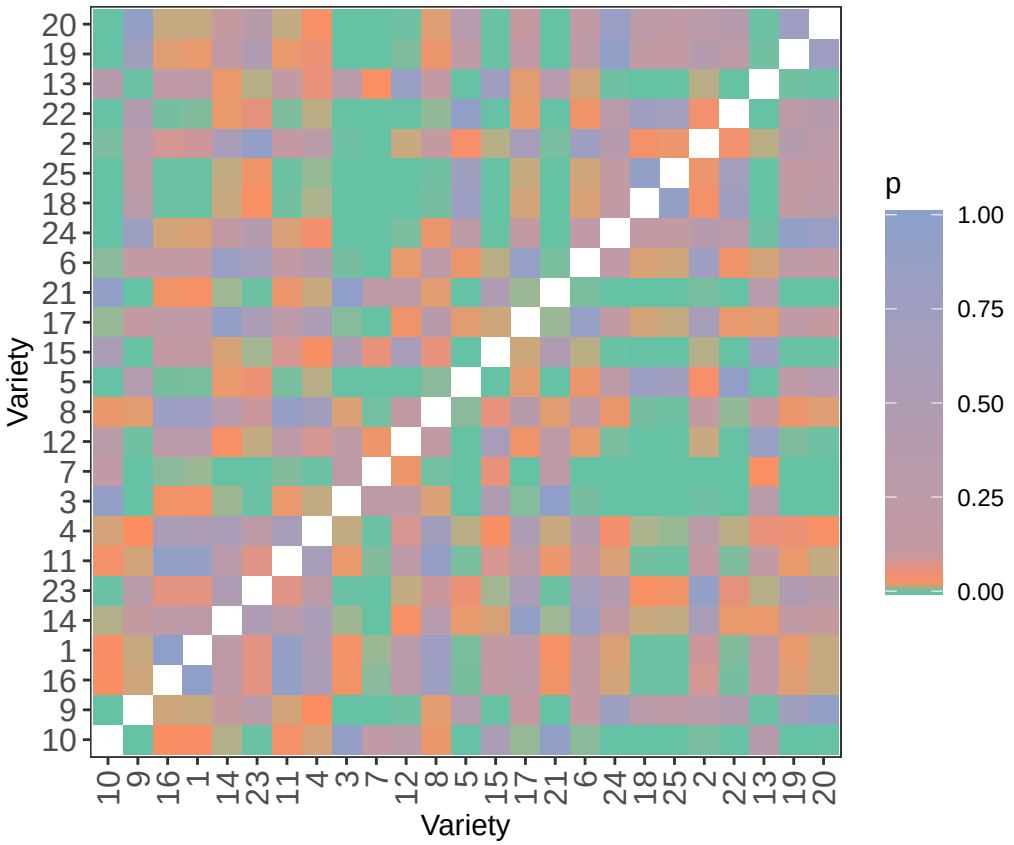
- `predictions`: the predictions, their standard errors and error intervals;
- `vcov`: the variance matrix of the predictions;
- `differences`: all pairwise differences between the predictions,
- `p.differences`: p-values for all pairwise differences between the predictions;
- `sed`: the standard errors of all pairwise differences between the predictions;
- `LSD`: the mean, minimum and maximum of the LSDs.

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)
```



References

Almeida, A., Loy, A. and Heike Hofmann, H. (2023) `qqplotr`: *Quantile-Quantile plot extensions for 'ggplot2'*, Version 0.0.6. http://cran.r-project.org/package=qqplotr/ or https://github.com/aloy/qqplotr.

Brien, C. J. (2023) `asremlPlus`: *Augments ASReml-R in fitting mixed models and packages generally in exploring prediction differences.* Version 4.4.13. http://cran.r-project.org/package=asremlPlus/ or http://chris.brien.name/rpackages/.

Butler, D. G., Cullis, B. R., Gilmour, A. R., Gogel, B. J. and Thompson, R. (2023). *ASReml-R Reference Manual Version 4.2.* VSN International Ltd, https://asreml.kb.vsni.co.uk/.

Gilmour, A. R., Thompson, R., & Cullis, B. R. (1995). Average Information REML: An Efficient Algorithm for Variance Parameter Estimation in Linear Mixed Models. *Biometrics*, **51**, 1440–1450.

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

R Core Team (2023) *R: A language and environment for statistical computing.* Vienna, Austria: R Foundation for Statistical Computing. http://www.r-project.org.

Snee, R. D. (1981). Graphical Display and Assessment of Means. *Biometrics*, **37**, 835–836.

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.

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.

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**, 478-508.

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.

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/}