

Using **asremlPlus**, in conjunction with **asreml**, to do a linear mixed model analysis of a wheat experiment using hypothesis tests

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This vignette shows how to use **asremlPlus** (Brien, 2025), in conjunction with **asreml** (Butler et al., 2020), to employ hypothesis tests to select the terms to be included in a mixed model for an experiment that involves spatial variation. 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, 2025).

It is divided into the following main sections:

1. Set up the maximal model for this experiment
2. Perform a series of hypothesis tests 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 maximal model for this experiment

```
library(knitr)
opts_chunk$set("tidy" = FALSE, comment = NA)
suppressMessages(library(asreml, quietly=TRUE))
```

```
## Offline License checked out Thu Aug 14 00:35:06 2025
```

```
packageVersion("asreml")
```

```
## [1] '4.2.0.370'
```

```
suppressMessages(library(asremlPlus))
packageVersion("asremlPlus")
```

```
## [1] '4.4.51'
```

```
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. (2020, Section 7.6), although they suggest that it is a barley experiment.

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

Fit the maximal model

In the following a 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. Also, separable `ar1` residual autocorrelation has been included. This model represents the maximal anticipated model,

```
current.asr <- asreml(yield ~ WithinColPairs + Variety,
  random = ~ Rep/(Row + Column) + units,
  residual = ~ ar1(Row):ar1(Column),
  maxit = 30, data=Wheat.dat)
```

ASReml Version 4.2 14/08/2025 00:35:07

| | LogLik | Sigma2 | DF | wall |
|---|-----------|----------|-----|--------------------------|
| 1 | -724.1213 | 23034.14 | 124 | 00:35:07 |
| 2 | -717.4149 | 9206.931 | 124 | 00:35:07 (2 restrained) |
| 3 | -694.8752 | 26492.99 | 124 | 00:35:07 (2 restrained) |
| 4 | -694.1600 | 33101.80 | 124 | 00:35:07 (1 restrained) |
| 5 | -692.0020 | 36912.26 | 124 | 00:35:07 (1 restrained) |
| 6 | -691.7892 | 46701.51 | 124 | 00:35:07 (2 restrained) |
| 7 | -691.8336 | 46208.51 | 124 | 00:35:07 (1 restrained) |
| 8 | -691.7749 | 47698.26 | 124 | 00:35:07 |
| 9 | -691.7711 | 47041.85 | 124 | 00:35:07 |

Warning in `asreml(yield ~ WithinColPairs + Variety, random = ~Rep/(Row + : Some components changed by more than 1% on the last iteration`

The warning from `asreml` is probably due to a bound term.

Initialize a testing sequence by loading the current fit into an `asrtests` object

A label and the information criteria based on the full likelihood (Verbyla, 2019) are included in the `test.summary` stored in the `asrtests` object.

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

Warning in `infoCriteria.asreml(asreml.obj, IClikelihood = ic.lik, bound.exclusions = bound.exclusions):`
Rep

Warning in `asreml(fixed = yield ~ WithinColPairs + Variety, random = ~Rep/(Row + : Log-likelihood not converged`

Check for and remove any boundary terms

```
current.asrt <- rmboundary(current.asrt, ICLikelihood = "full")
```

Warning in infoCriteria.asreml(asreml.obj, ICLikelihood = ic.lik): The following bound terms were discovered

ASReml Version 4.2 14/08/2025 00:35:07

| | LogLik | Sigma2 | DF | wall |
|---|-----------|----------|-----|----------|
| 1 | -691.7710 | 47071.42 | 124 | 00:35:07 |

Warning in asreml(fixed = yield ~ WithinColPairs + Variety, random = ~Rep/(Row + : Log-likelihood not converged

```
summary(current.asrt$asreml.obj)$varcomp
```

| | component | std.error | z.ratio | bound | %ch |
|-----------------------|--------------|--------------|------------|-------|-----|
| Rep:Row | 4.293282e+03 | 3.199458e+03 | 1.3418779 | P | 0.0 |
| Rep:Column | 1.575689e+02 | 1.480357e+03 | 0.1064398 | P | 0.7 |
| units | 5.742689e+03 | 1.652457e+03 | 3.4752438 | P | 0.0 |
| Row:Column!R | 4.706787e+04 | 2.515832e+04 | 1.8708669 | P | 0.0 |
| Row:Column!Row!cor | 7.920301e-01 | 1.014691e-01 | 7.8056280 | U | 0.0 |
| Row:Column!Column!cor | 8.799559e-01 | 7.370402e-02 | 11.9390486 | U | 0.0 |

```
print(current.asrt, which = "testsummary")
```

Sequence of model investigations for yield

(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 | Maximal model | 26 | 6 | NA | 1646.129 | 1742.47 | Starting model |
| 2 | Rep | 1 | NA | NA | 1646.129 | 1742.47 | Boundary |

Rep has been removed because it has been constrained to zero. Following the recommendation of Littell et al. (2006, p. 150), the bound on all variance components is set to unconstrained (U) using `setvariances.asreml` so as to avoid bias in the estimate of the residual variance. Alternatively, one could move Rep to the fixed model.

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")
```

ASReml Version 4.2 14/08/2025 00:35:07

| | LogLik | Sigma2 | DF | wall | |
|----|-----------|----------|-----|----------|-----------------|
| 1 | -724.1213 | 23034.14 | 124 | 00:35:07 | |
| 2 | -717.4149 | 9206.931 | 124 | 00:35:07 | (2 restrained) |
| 3 | -694.8752 | 26492.99 | 124 | 00:35:07 | (2 restrained) |
| 4 | -693.9744 | 33129.65 | 124 | 00:35:07 | (1 restrained) |
| 5 | -692.8856 | 39662.12 | 124 | 00:35:07 | |
| 6 | -691.4276 | 53103.83 | 124 | 00:35:08 | |
| 7 | -691.2387 | 48092.17 | 124 | 00:35:08 | |
| 8 | -691.1808 | 47278.94 | 124 | 00:35:08 | |
| 9 | -691.1710 | 46850.98 | 124 | 00:35:08 | |
| 10 | -691.1700 | 46690.46 | 124 | 00:35:08 | |

Warning in asreml(fixed = yield ~ WithinColPairs + Variety, random = ~Rep/(Row + : Some components changed by more than 1% on the last iteration

WARN [2025-08-14 00:35:08] Some components changed by more than 1% on the last iteration

Warning in asreml(fixed = yield ~ WithinColPairs + Variety, random = ~Rep/(Row + : Some components changed by more than 1% on the last iteration

WARN [2025-08-14 00:35:08] Some components changed by more than 1% on the last iteration

Warning in asreml(fixed = yield ~ WithinColPairs + Variety, random = ~Rep/(Row + : Some components changed by more than 1% on the last iteration

```
current.asrt <- as.asrttests(current.asr, wald.tab = NULL, test.summary = current.asrt$test.summary,
                             IClikelihood = "full", label = "Max model & Unbound components")
current.asrt <- rmboundary(current.asrt)
summary(current.asrt$asreml.obj)$varcomp
```

| | component | std.error | z.ratio | bound | %ch |
|-----------------------|---------------|--------------|-----------|-------|-----|
| Rep | -2462.3785858 | 1.191435e+03 | -2.066734 | U | 0.2 |
| Rep:Row | 5012.4021415 | 3.396848e+03 | 1.475604 | U | 0.1 |
| Rep:Column | 920.5936391 | 1.704008e+03 | 0.540252 | U | 1.1 |
| units | 5964.9099377 | 1.608792e+03 | 3.707695 | P | 0.1 |
| Row:Column!R | 46690.4620387 | 2.731906e+04 | 1.709080 | P | 0.0 |
| Row:Column!Row!cor | 0.8152180 | 9.988929e-02 | 8.161216 | U | 0.1 |
| Row:Column!Column!cor | 0.8857252 | 7.487875e-02 | 11.828793 | U | 0.0 |

```
print(current.asrt, which = "testsummary")
```

Sequence of model investigations for yield

(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 | Maximal model | 26 | 6 | NA | 1646.129 | 1742.470 | Starting model |
| 2 | Rep | 1 | NA | NA | 1646.129 | 1742.470 | Boundary |
| 3 | Max model & Unbound components | 26 | 7 | NA | 1647.200 | 1746.551 | Starting model |

```
print(current.asrt, which = "pseudoanova")
```

```
#### Pseudo-anova table for fixed terms
```

```
Wald tests for fixed effects.  
Response: yield
```

| | Df | denDF | F.inc | Pr |
|----------------|----|-------|---------|--------|
| (Intercept) | 1 | 1.7 | 153.400 | 0.0115 |
| WithinColPairs | 1 | 15.6 | 2.543 | 0.1308 |
| Variety | 24 | 76.1 | 10.110 | 0.0000 |

Now the Rep component estimate is negative.

The `test.summary` output has been extended, by supplying the previous `test.summary` to `as.asrtests`, to show that there is a new starting model. The pseudo-anova table shows that Varieties are highly significant ($p < 0.001$)

2. Perform a series of hypothesis tests to select a linear mixed model for the data

The hypothesis tests in this section are Wald tests for fixed terms, with denominator degrees of freedom calculated using the Kenward-Rogers adjustment (Kenward and Rogers (1997), and Restricted Maximum Likelihood Ratio Tests (REMLRT) for random terms.

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

The information criteria based on the full likelihood (Verbyla, 2019) is also included in the `test.summary` stored in the `asrtests` object.

```
current.asrt <- testranfix(current.asrt, term = "WithinColPairs",  
                           drop.fix.ns=TRUE, IClikelihood = "full")
```

```
WARN [2025-08-14 00:35:08] Some components changed by more than 1% on the last iteration
```

```
Warning in asreml(fixed = yield ~ Variety, random = ~Rep/(Row + Column) + : Some components changed  
by more than 1% on the last iteration
```

```
WARN [2025-08-14 00:35:08] Some components changed by more than 1% on the last iteration
```

```
Warning in asreml(fixed = yield ~ Variety, random = ~Rep/(Row + Column) + : Some components changed  
by more than 1% on the last iteration
```

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

Summary of the fitted variance parameters for yield

| | component | std.error | z.ratio | bound | %ch |
|-----------------------|---------------|--------------|------------|-------|-----|
| Rep | -2392.1616314 | 1.199592e+03 | -1.9941460 | U | 0.4 |
| Rep:Row | 5033.2850607 | 3.408523e+03 | 1.4766764 | U | 0.2 |
| Rep:Column | 760.1498938 | 1.617038e+03 | 0.4700879 | U | 2.5 |
| units | 5929.0518909 | 1.609478e+03 | 3.6838361 | P | 0.0 |
| Row:Column!R | 45940.6913910 | 2.634982e+04 | 1.7434920 | P | 0.0 |
| Row:Column!Row!cor | 0.8101561 | 9.995026e-02 | 8.1055925 | U | 0.1 |
| Row:Column!Column!cor | 0.8846454 | 7.504265e-02 | 11.7885681 | U | 0.0 |

Pseudo-anova table for fixed terms

Wald tests for fixed effects.
Response: yield

| | Df | denDF | F.inc | Pr |
|-------------|----|-------|--------|--------|
| (Intercept) | 1 | 1.7 | 159.00 | 0.0112 |
| Variety | 24 | 76.8 | 10.27 | 0.0000 |

Sequence of model investigations for yield

(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 | Maximal model | 26 | 6.0 | NA | 1646.129 | 1742.470 | Starting model |
| 2 | Rep | 1 | NA | NA | 1646.129 | 1742.470 | Boundary |
| 3 | Max model & Unbound components | 26 | 7.0 | NA | 1647.200 | 1746.551 | Starting model |
| 4 | WithinColPairs | 1 | 15.6 | 0.1308 | 1645.326 | 1741.666 | Dropped |

It is clear in the call to `testranfix` 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 *p*-value for the `withinColPairs` was greater than 0.05 and so now the model stored in `current.asrt` does not include `withinColPairs`. The `wald.tab` has been updated for the new model.

Test the nugget term

The nugget term represents non-spatial variance, such as random plot and measurement error. It is fitted using the `asreml` reserved word `units`.

```
current.asrt <- teststranfix(current.asrt, "units", positive=TRUE, IClikelihood = "full")
```

WARN [2025-08-14 00:35:09] Some components changed by more than 1% on the last iteration

Warning in asreml(fixed = yield ~ Variety, random = ~Rep + Rep:Row + Rep:Column, : Some components changed by more than 1% on the last iteration

WARN [2025-08-14 00:35:09] Some components changed by more than 1% on the last iteration

Warning in asreml(fixed = yield ~ Variety, random = ~Rep + Rep:Row + Rep:Column, : Some components changed by more than 1% on the last iteration

Test Row autocorrelation

We begin testing the autocorrelation by dropping the Row autocorrelation. Because of messages about the instability of the fit, `iterate.asrtests` is used to execute extra iterations of the fitting process.

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

WARN [2025-08-14 00:35:10] Some components changed by more than 1% on the last iteration

Warning in asreml(fixed = yield ~ Variety, random = ~Rep/(Row + Column) + : Some components changed by more than 1% on the last iteration

WARN [2025-08-14 00:35:10] Some components changed by more than 1% on the last iteration

Warning in asreml(fixed = yield ~ Variety, random = ~Rep/(Row + Column) + : Some components changed by more than 1% on the last iteration

```
current.asrt <- iterate(current.asrt)
```

WARN [2025-08-14 00:35:10] Some components changed by more than 1% on the last iteration

Warning in asreml(fixed = yield ~ Variety, random = ~Rep/(Row + Column) + : Some components changed by more than 1% on the last iteration

WARN [2025-08-14 00:35:10] Some components changed by more than 1% on the last iteration

Warning in asreml(fixed = yield ~ Variety, random = ~Rep/(Row + Column) + : Some components changed by more than 1% on the last iteration

Test Column autocorrelation (depends on whether Row autocorrelation retained)

The function `getTestPvalue` is used to get the p-value for the Row autocorrelation test. If it is significant then the Column autocorrelation is tested by dropping the Column autocorrelation, while retaining the Row autocorrelation. Otherwise the model with just Row autocorrelation, whose fit is returned via `current.asrt` after the test, is compared to one with no autocorrelation.

```
(p <- getTestPvalue(current.asrt, label = "Row autocorrelation"))
```

```
[1] 4.675632e-06
```

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

Warning in DFdiff(bound.h1, bound.h0, DF = DF, bound.exclusions = bound.exclusions): There were a total
The following bound terms occur in only one of the models compared and so were discounted:
Row:Column!Row!cor

Output the results

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

```
#### Summary of the fitted variance parameters for yield
```

| | component | std.error | z.ratio | bound | %ch |
|-----------------------|---------------|--------------|------------|-------|-----|
| Rep | -2392.1616314 | 1.199592e+03 | -1.9941460 | U | 0.4 |
| Rep:Row | 5033.2850607 | 3.408523e+03 | 1.4766764 | U | 0.2 |
| Rep:Column | 760.1498938 | 1.617038e+03 | 0.4700879 | U | 2.5 |
| units | 5929.0518909 | 1.609478e+03 | 3.6838361 | P | 0.0 |
| Row:Column!R | 45940.6913910 | 2.634982e+04 | 1.7434920 | P | 0.0 |
| Row:Column!Row!cor | 0.8101561 | 9.995026e-02 | 8.1055925 | U | 0.1 |
| Row:Column!Column!cor | 0.8846454 | 7.504265e-02 | 11.7885681 | U | 0.0 |

```
#### Pseudo-anova table for fixed terms
```

Wald tests for fixed effects.
Response: yield

| | Df | denDF | F.inc | Pr |
|-------------|----|-------|--------|--------|
| (Intercept) | 1 | 1.7 | 159.00 | 0.0112 |
| Variety | 24 | 76.8 | 10.27 | 0.0000 |

```
#### Sequence of model investigations for yield
```

(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 | Maximal model | 26 | 6.0 | NA | 1646.129 | 1742.470 | Starting model |
| 2 | Rep | 1 | NA | NA | 1646.129 | 1742.470 | Boundary |
| 3 | Max model & Unbound components | 26 | 7.0 | NA | 1647.200 | 1746.551 | Starting model |
| 4 | WithinColPairs | 1 | 15.6 | 0.1308 | 1645.326 | 1741.666 | Dropped |
| 5 | units | 1 | NA | 0.0006 | 1645.326 | 1741.666 | Retained |
| 6 | Row autocorrelation | 1 | NA | 0.0000 | 1645.326 | 1741.666 | Unswapped |
| 7 | Col autocorrelation | 2 | NA | 0.0000 | 1645.326 | 1741.666 | Unswapped |

```
printFormulae(current.asrt$asreml.obj)
```

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

```
fixed: yield ~ Variety
random: ~ Rep/(Row + Column) + units
residual: ~ ar1(Row):ar1(Column)
```

```
print(R2adj(current.asrt$asreml.obj, include.which.random = ~ .))
```

```
ASReml Version 4.2 14/08/2025 00:35:11
      LogLik      Sigma2      DF      wall
1      -694.6149      45873.83      125      00:35:11
2      -694.6149      45868.25      125      00:35:11
[1] 44.62078
attr(,"fixed")
~.
<environment: 0x000002022c97f588>
attr(,"random")
~.
```

The `test.summary` shows is that both Row and Column autocorrelation were retained in the model, as was the units term. The `asreml.obj` in `current.asrt` contains the model selected by the selection process, which has been printed using `printFormulae.asrtests`. It is clear that no changes were made to the variance terms. The adjusted R^2 value shows that the fixed and random terms in the fitted model account for 45% of the total variation in the yield.

3. Diagnostic checking using residual plots and variofaces

Get current fitted asreml object and update to include standardized residuals

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

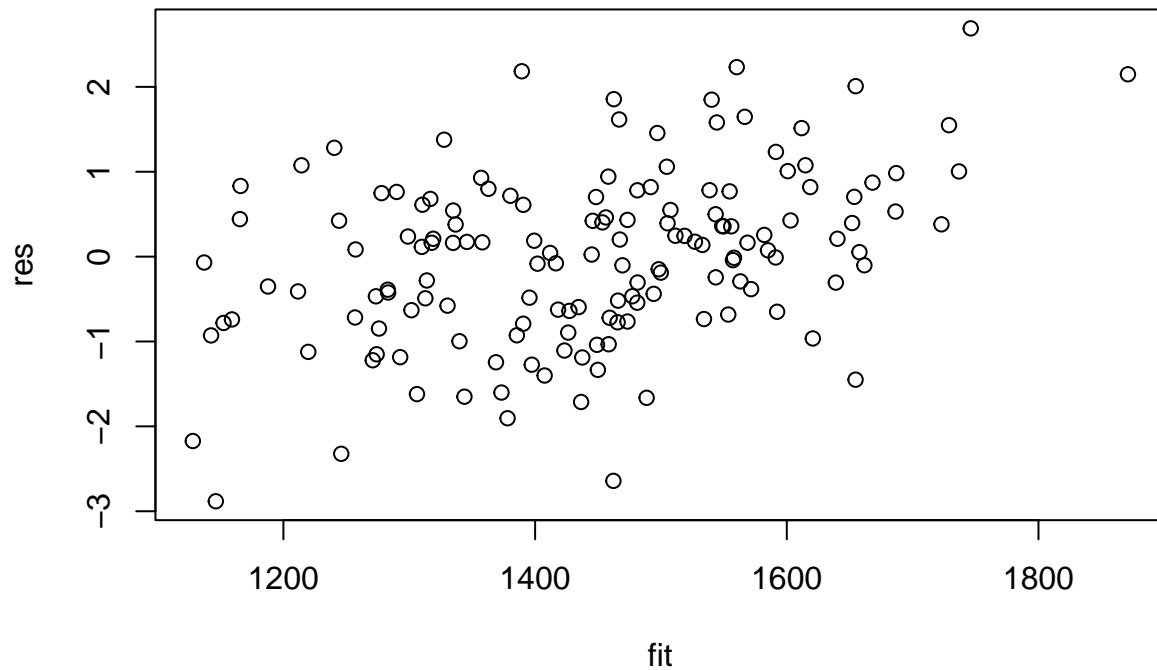
```
ASReml Version 4.2 14/08/2025 00:35:11
      LogLik      Sigma2      DF      wall
1      -694.6149      45873.83      125      00:35:11
2      -694.6149      45868.25      125      00:35:11
3      -694.6149      45854.78      125      00:35:11
```

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

Do diagnostic checking

Do residuals-versus-fitted values plot

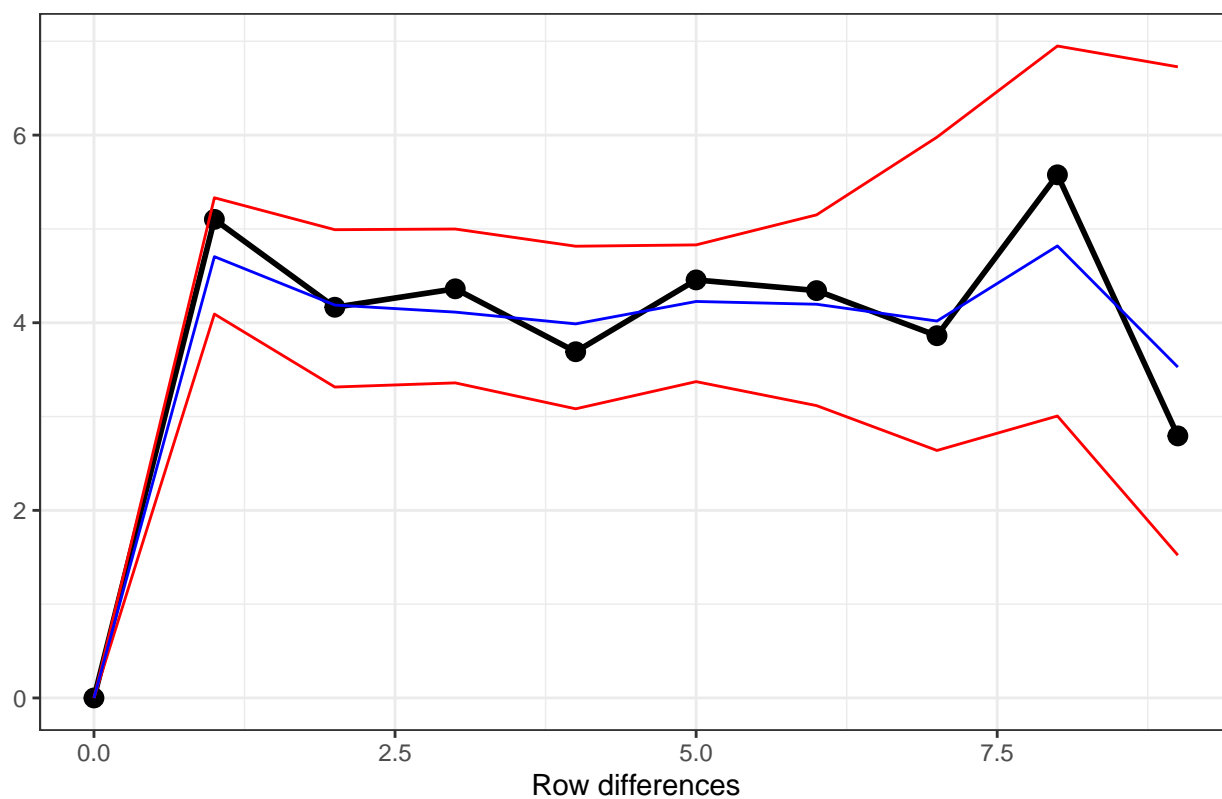
```
with(Wheat.dat, plot(fit, res))
```



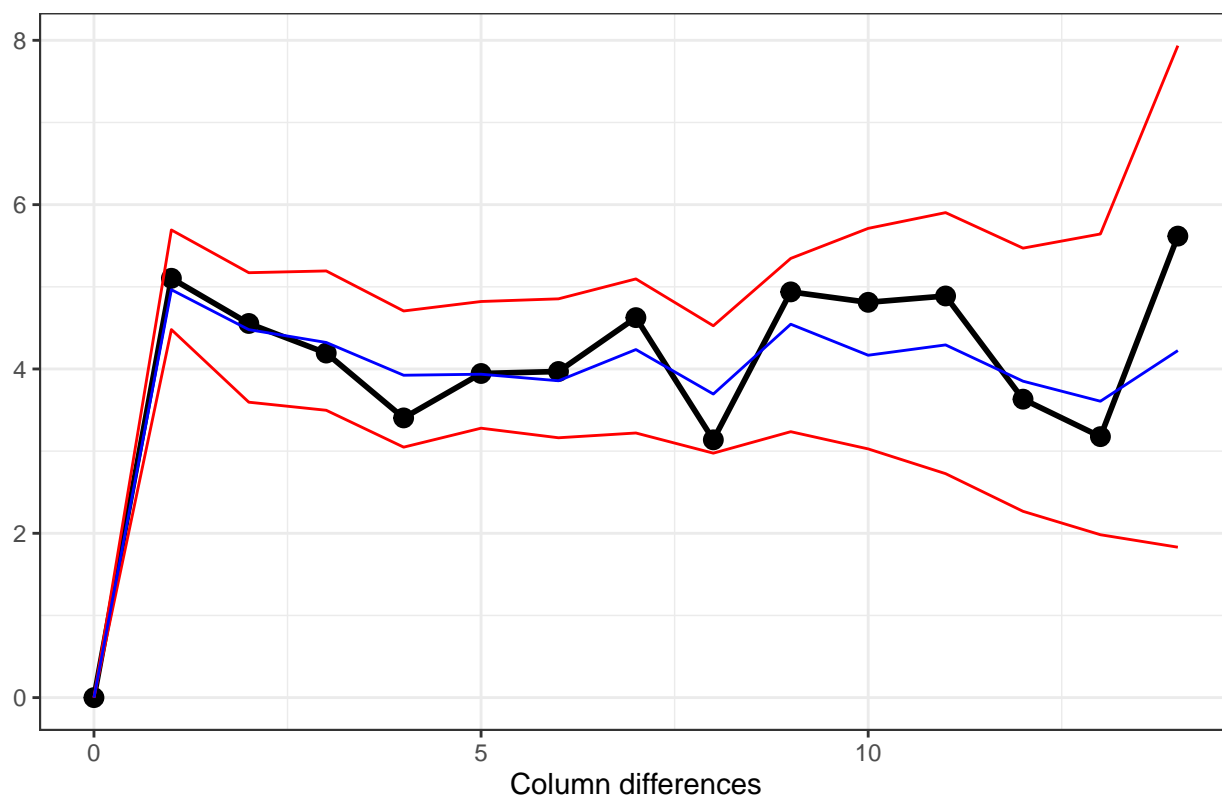
Plot varifaces

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

Variogram face of Standardized conditional residuals for Row



Variogram face of Standardized conditional residuals for Column



The variofaces are the lag 1 plots of the sample semivariogram with simulated confidence envelopes (Stefanova

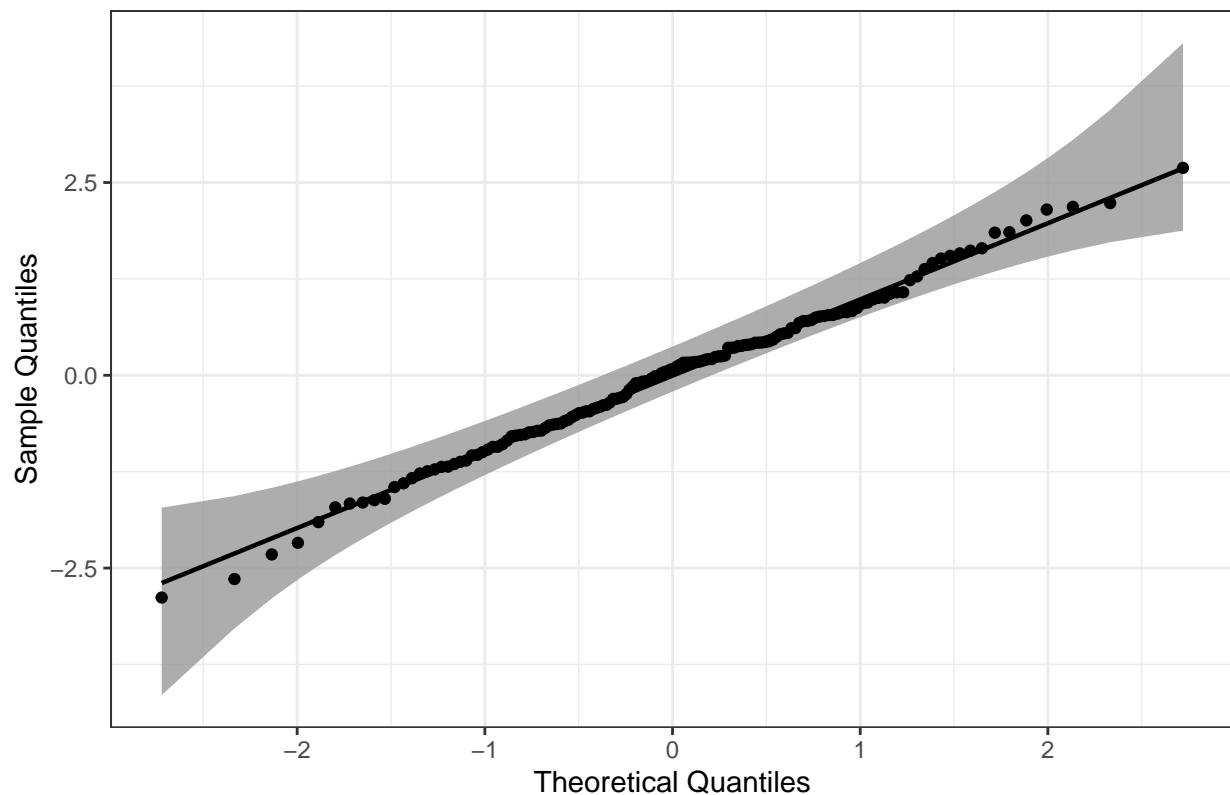
et al., 2009).

Plot normal quantile plot

The plot is obtained using the `ggplot` function with extensions available from the `qqplotr` package (Almeida, A., Loy, A. and Hofmann, H., 2023).

```
suppressWarnings(  
  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())
```

Normal probability plot



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")
```

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.
- The ignored set: Rep,Row,Column,units
- Variety is included in this prediction
- (Intercept) is included in this prediction
- units is ignored in this prediction

| | Variety | predicted.value | standard.error | upper.halfLeastSignificant.limit |
|----|---|-----------------|----------------|----------------------------------|
| 1 | 10 | 1168.989 | 120.4776 | 1228.315 |
| 2 | 1 | 1242.750 | 119.8112 | 1302.076 |
| 3 | 9 | 1257.137 | 119.9716 | 1316.463 |
| 4 | 16 | 1285.719 | 119.9407 | 1345.045 |
| 5 | 14 | 1293.527 | 119.9234 | 1352.853 |
| 6 | 23 | 1313.653 | 120.2937 | 1372.979 |
| 7 | 11 | 1322.159 | 120.1971 | 1381.485 |
| 8 | 7 | 1374.446 | 120.2415 | 1433.773 |
| 9 | 3 | 1394.070 | 120.4040 | 1453.396 |
| 10 | 4 | 1410.980 | 120.1063 | 1470.306 |
| 11 | 12 | 1444.557 | 120.6042 | 1503.883 |
| 12 | 8 | 1453.396 | 120.5948 | 1512.722 |
| 13 | 15 | 1458.383 | 120.4354 | 1517.709 |
| 14 | 5 | 1473.782 | 120.4462 | 1533.108 |
| 15 | 17 | 1487.828 | 120.2904 | 1547.154 |
| 16 | 6 | 1498.294 | 120.1196 | 1557.621 |
| 17 | 21 | 1517.121 | 120.2270 | 1576.447 |
| 18 | 2 | 1520.466 | 119.6330 | 1579.792 |
| 19 | 24 | 1533.768 | 120.3003 | 1593.095 |
| 20 | 18 | 1541.148 | 120.3671 | 1600.474 |
| 21 | 25 | 1575.795 | 120.5149 | 1635.121 |
| 22 | 22 | 1610.482 | 120.3289 | 1669.808 |
| 23 | 13 | 1610.761 | 120.4582 | 1670.088 |
| 24 | 20 | 1627.971 | 120.2336 | 1687.297 |
| 25 | 19 | 1652.992 | 120.3443 | 1712.318 |
| | lower.halfLeastSignificant.limit est.status | | | |
| 1 | | 1109.662 | Estimable | |
| 2 | | 1183.424 | Estimable | |
| 3 | | 1197.811 | Estimable | |
| 4 | | 1226.392 | Estimable | |
| 5 | | 1234.200 | Estimable | |
| 6 | | 1254.327 | Estimable | |
| 7 | | 1262.832 | Estimable | |
| 8 | | 1315.120 | Estimable | |

| | | |
|----|----------|-----------|
| 9 | 1334.743 | Estimable |
| 10 | 1351.654 | Estimable |
| 11 | 1385.231 | Estimable |
| 12 | 1394.070 | Estimable |
| 13 | 1399.057 | Estimable |
| 14 | 1414.456 | Estimable |
| 15 | 1428.501 | Estimable |
| 16 | 1438.968 | Estimable |
| 17 | 1457.795 | Estimable |
| 18 | 1461.140 | Estimable |
| 19 | 1474.442 | Estimable |
| 20 | 1481.822 | Estimable |
| 21 | 1516.468 | Estimable |
| 22 | 1551.156 | Estimable |
| 23 | 1551.435 | Estimable |
| 24 | 1568.645 | Estimable |
| 25 | 1593.666 | Estimable |

LSD values

minimum LSD = 114.0129

mean LSD = 118.6523

maximum LSD = 123.3577

(sed range / mean sed = 0.0788)

We have set `error.intervals` to `halfLeast` so that the limits for 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).

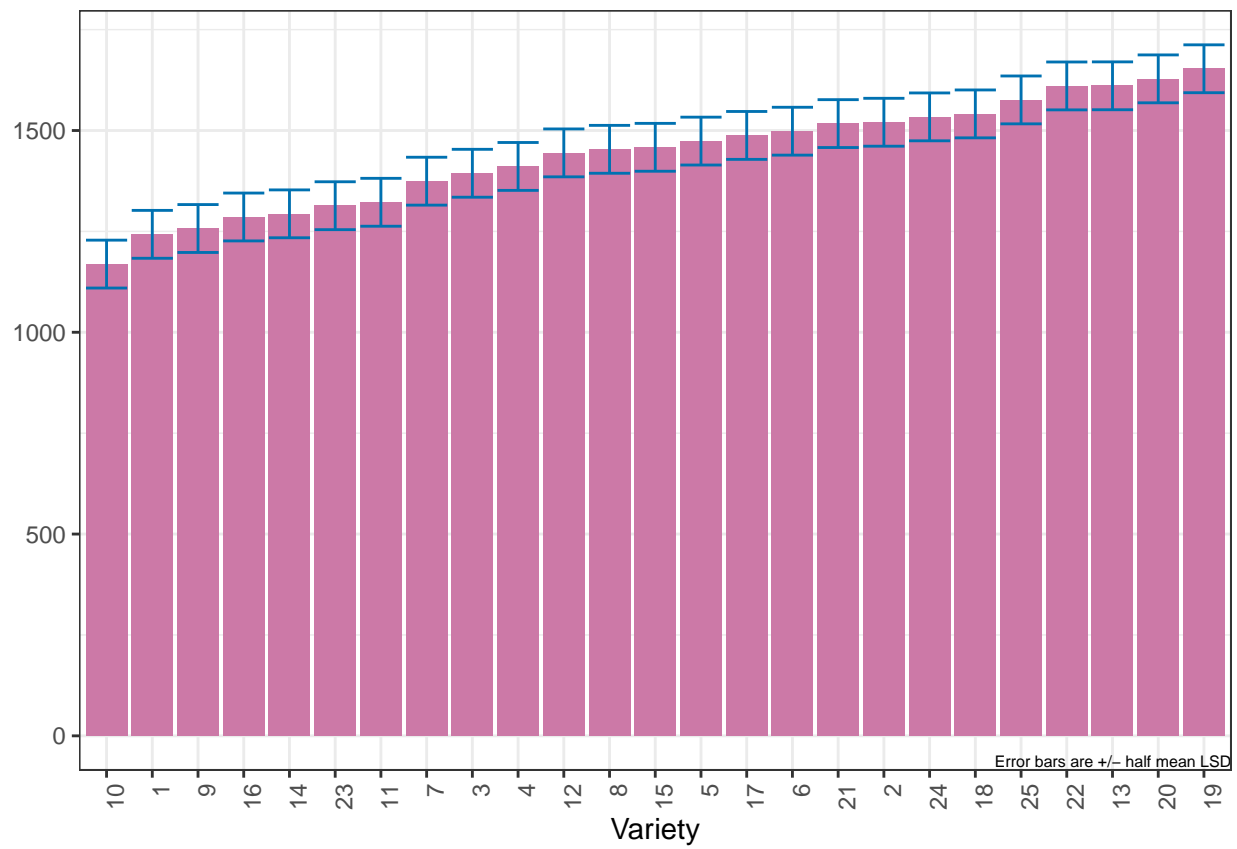
Also set was `sortFactor`, so that the results would be ordered for the values of the predictions for Variety.

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

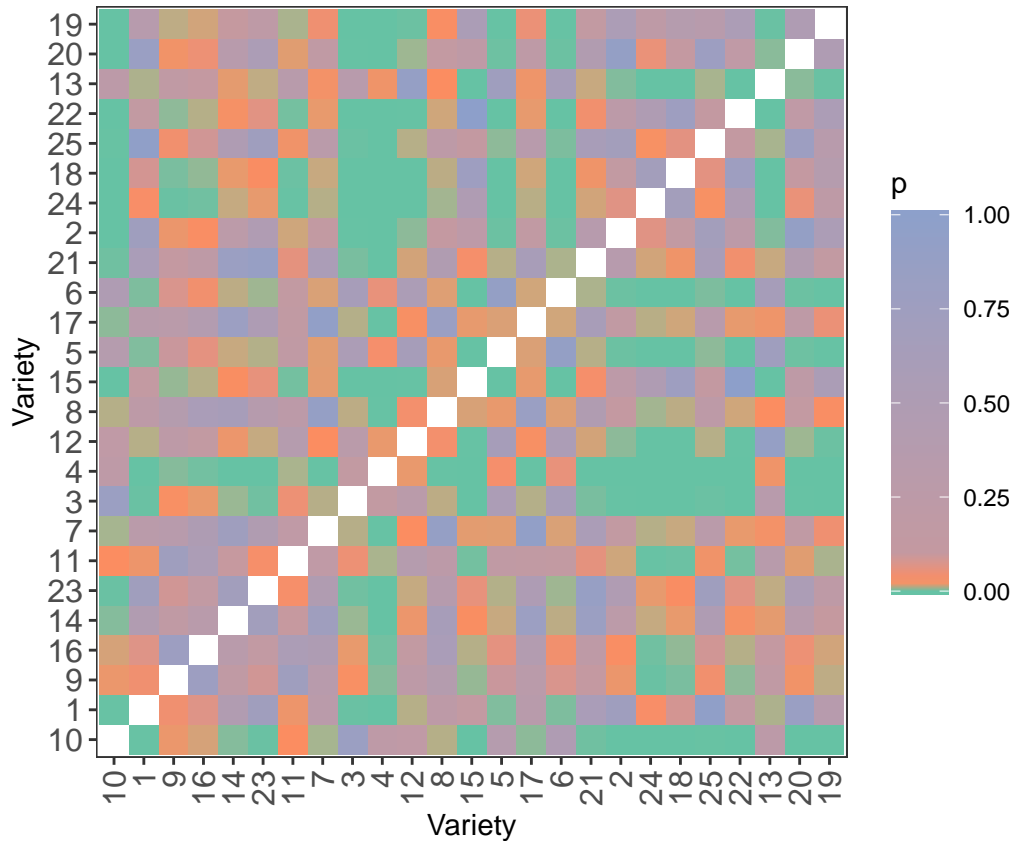
- `predictions`: the predictions, their standard errors and error intervals;
- `vcov`: the variance matrix of the predictions;
- `differences`: all pairwise differences between the predictions,
- `p.differences`: p-values for all pairwise differences between the predictions;
- `sed`: the standard errors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

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