The wheat example from section 7.6 of the asreml reference manual (Butler et al. 2018)

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

Get data available in asremlPlus

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

Fit the initial 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),
                      data=Wheat.dat)
```

```
## Model fitted using the gamma parameterization.
## ASReml 4.1.0 Sat Apr  6 15:23:15 2019
##           LogLik        Sigma2     DF     wall    cpu
##  1      -724.121      23034.14    124 15:23:15    0.0
##  2      -717.415       9206.93    124 15:23:15    0.0 (2 restrained)
##  3      -694.875      26492.99    124 15:23:15    0.0 (2 restrained)
##  4      -694.160      33101.80    124 15:23:15    0.0 (1 restrained)
##  5      -692.002      36912.26    124 15:23:15    0.0 (1 restrained)
##  6      -691.789      46701.51    124 15:23:15    0.0 (2 restrained)
##  7      -691.834      46208.51    124 15:23:15    0.0 (1 restrained)
##  8      -691.775      47698.26    124 15:23:15    0.0
##  9      -691.771      47041.85    124 15:23:15    0.0
```

```
## 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.

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

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

```
## Calculating denominator DF
```

Check for and remove any boundary terms

```
current.asrt <- rmboundary(current.asrt)
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 terms whose status in the model has been investigated
##
##   terms DF denDF  p   action
## 1   Rep  1    NA NA Boundary
```

Rep has been removed because it has been constrained to zero. Following the recommendation of Littel et al. (2006, p. 150), the bound on all variance components is set to unconstrained (U) so as to avoid bias in the estimate of the residual variance.

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")
```

```
## Model fitted using the gamma parameterization.
## ASReml 4.1.0 Sat Apr  6 15:23:16 2019
##           LogLik        Sigma2     DF     wall    cpu
##  1      -724.121      23034.14    124 15:23:16    0.0
##  2      -717.415       9206.93    124 15:23:16    0.0 (2 restrained)
##  3      -694.875      26492.99    124 15:23:16    0.0 (2 restrained)
##  4      -693.974      33129.65    124 15:23:16    0.0 (1 restrained)
##  5      -692.886      39662.12    124 15:23:16    0.0
##  6      -691.428      53103.83    124 15:23:16    0.0
##  7      -691.239      48092.17    124 15:23:16    0.0
##  8      -691.181      47278.94    124 15:23:16    0.0
##  9      -691.171      46850.98    124 15:23:16    0.0
## 10      -691.170      46690.46    124 15:23:16    0.0
```

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

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

```
## Calculating denominator DF
```

```
current.asrt <- rmboundary(current.asrt)
summary(current.asrt$asreml.obj)$varcomp
```

```
##                             component    std.error   z.ratio bound %ch
## Rep                     -2462.3785859 1.191435e+03 -2.066734     U 0.2
## Rep:Row                  5012.4021416 3.396848e+03  1.475604     U 0.1
## Rep:Column                920.5936392 1.704008e+03  0.540252     U 1.1
## units                    5964.9099379 1.608792e+03  3.707695     P 0.1
## Row:Column!R            46690.4620404 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 terms whose status in the model has been investigated
## 
## [1] terms  DF     denDF  p      action
## <0 rows> (or 0-length row.names)
```

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

Check term for within Column pairs (a post hoc covariate)

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

```
## Calculating denominator DF
```

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

```
## Calculating denominator DF
```

Generally, to determine what has been tested between two fits using `asreml` involves comparing two `asreml` calls and deciding what is different. For example what is the difference between the `asreml` call to fit the initial model and the following call?

```
current.asr <- asreml(yield ~ Variety,
                  `random = ~ Rep/(Row + Column) + units,

                  residual = ~ ar1(Row):ar1(Column),

                  data=Wheat.dat)`
```

On the other hand, it is clear from the `testranfix` call that the term `withinColPAirs` is being tested.

Test nugget term

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

```
current.asrt <- testranfix(current.asrt, "units", positive=TRUE)
```

```
## 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.

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

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

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

```
## Warning in newfit.asreml(asreml.obj, residual. = term.form, trace = trace, :
```

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 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] 4.654398e-06
```

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

```
## Warning in DFdiff(bound.h1, bound.h0, DF = DF, bound.exclusions = bound.exclusions): There were a to
##   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, which = "test")
```

```
##
##
##   Sequence of model terms whose status in the model has been investigated
##
##                  terms DF denDF      p                        action
## 1      WithinColPairs  1  15.6 0.1308                       Dropped
## 2               units  1    NA 0.0006                      Retained
## 3 Row autocorrelation  1    NA 0.0000 Unswapped - new unconverged
## 4 Col autocorrelation  2    NA 0.0000                     Unswapped
```

```
info <- infoCriteria(current.asrt$asreml.obj)
summary(current.asrt$asreml.obj)$varcomp
```

```
##                            component    std.error    z.ratio bound %ch
## Rep                    -2392.1643977 1.194200e+03 -2.0031528     U 0.4
## Rep:Row                 5035.7265976 3.405769e+03  1.4785872     U 0.3
## Rep:Column               762.1738644 1.612310e+03  0.4727218     U 1.3
## units                   5933.5126842 1.610749e+03  3.6836971     P 0.1
## Row:Column!R           45973.2573645 2.635502e+04  1.7443833     P 0.0
## Row:Column!Row!cor         0.8101706 9.994728e-02  8.1059792     U 0.1
## Row:Column!Column!cor      0.8846993 7.502816e-02 11.7915640     U 0.0
```

The `test.summary` shows is that the model with Row and without Column autocorrelation failed to converge. It is also clear that no changes were made to the variance terms.

The `asreml.obj` in `current.asrt` contains the model selected by the testing process.

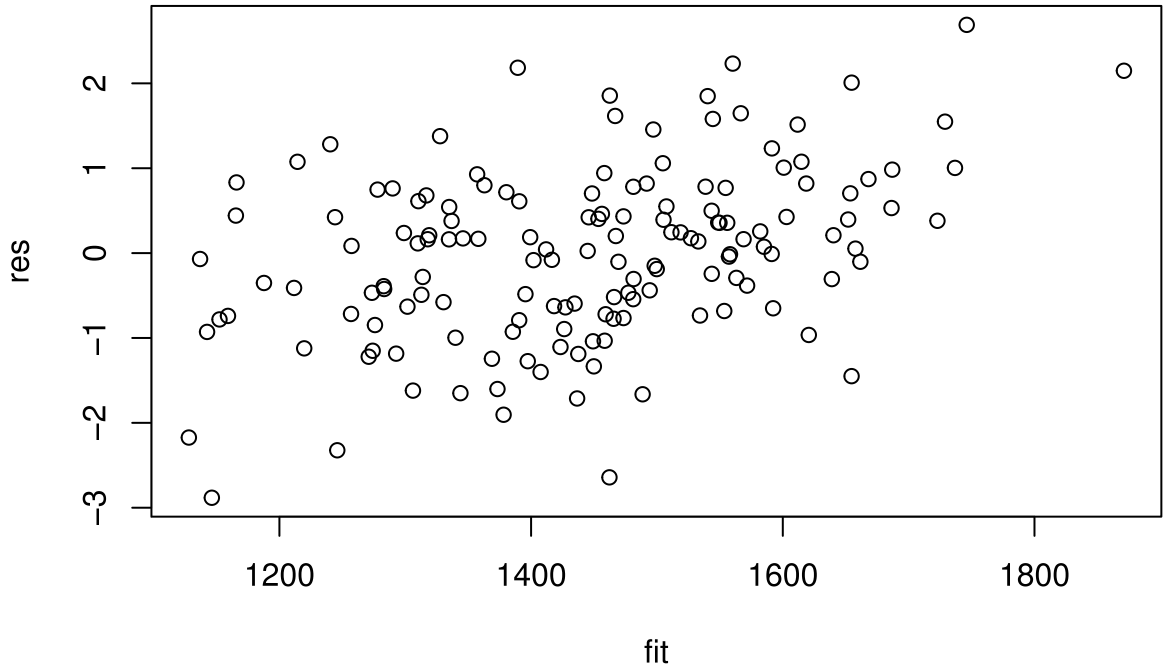
Get current fitted asreml object and update to include standardized residuals

```
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

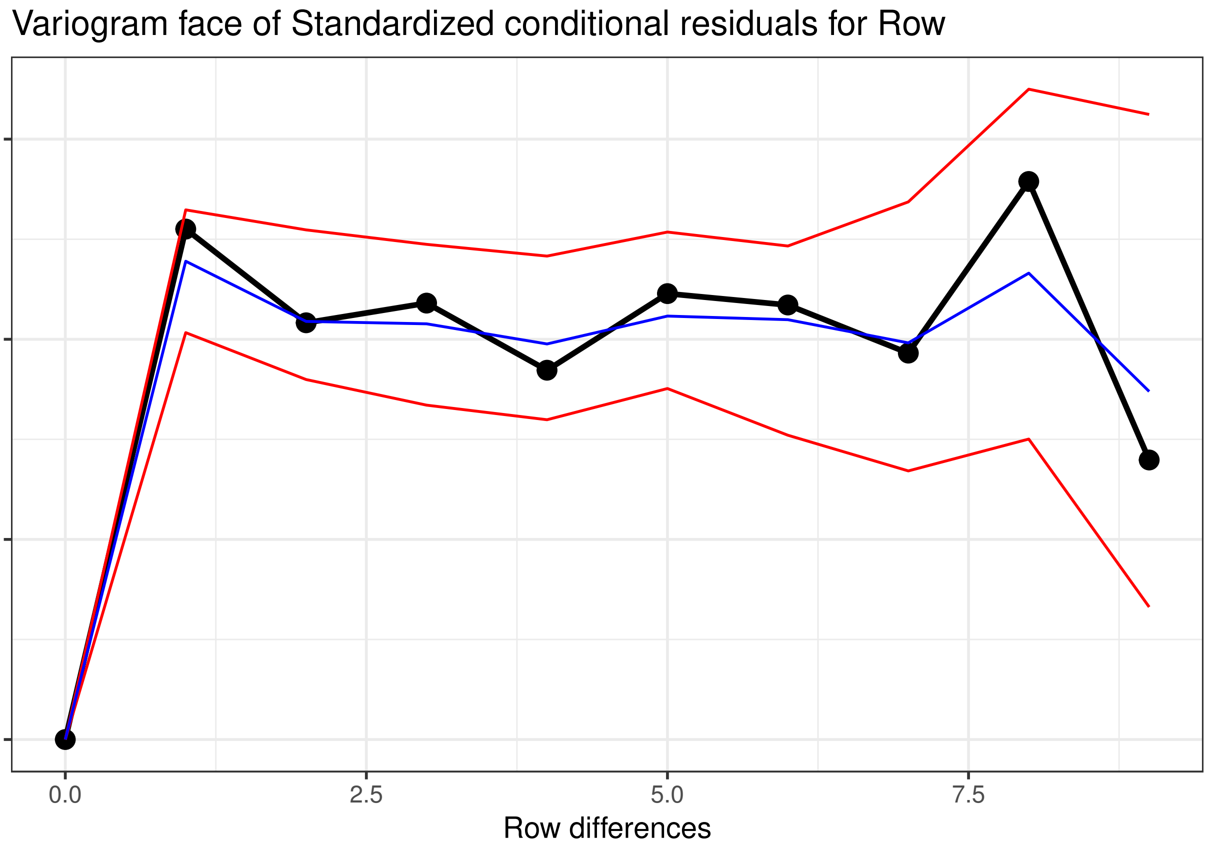
Do residuals-versus-fitted values plot

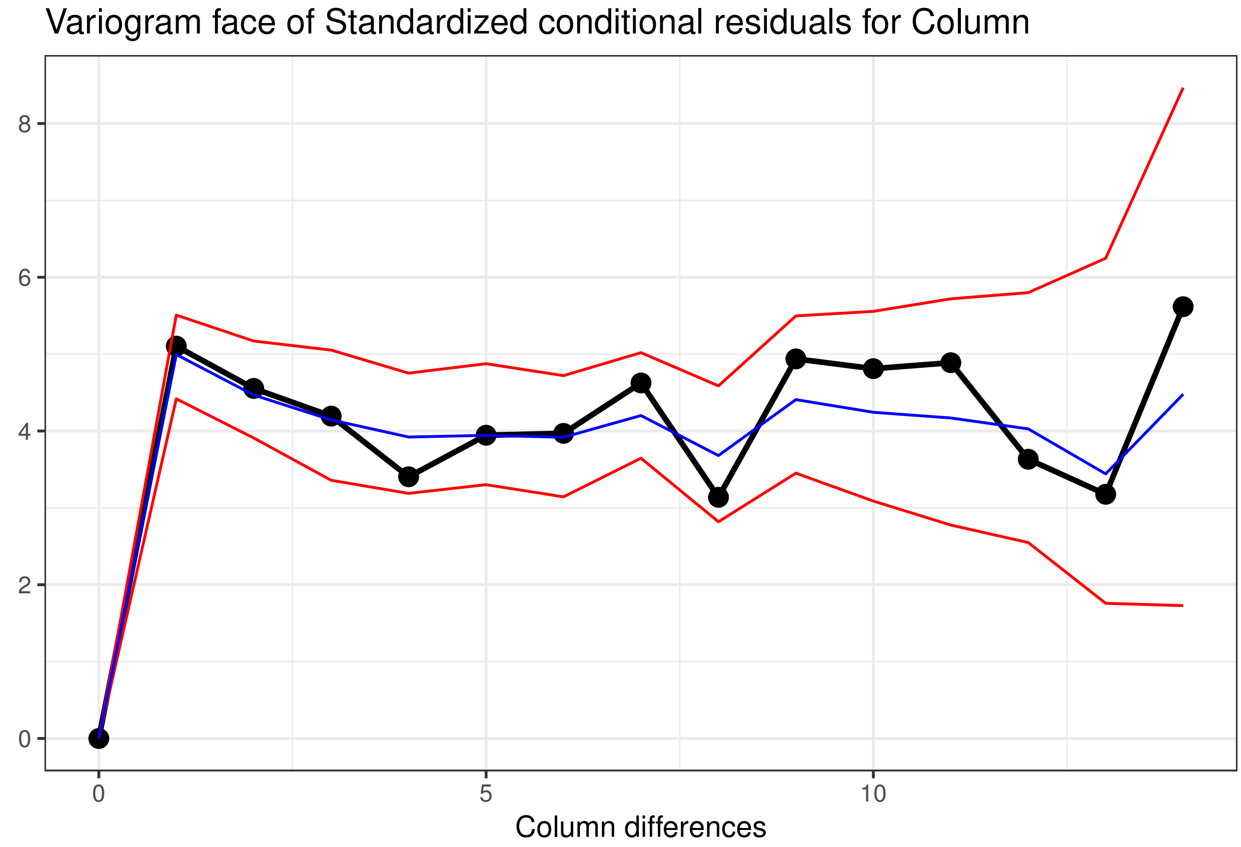
```
with(Wheat.dat, plot(fit, res))
```



Plot variofaces

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


Variogram face of Standardized conditional residuals for Row
6
4
2
0
0.0
2.5
5.0
7.5
Row differences

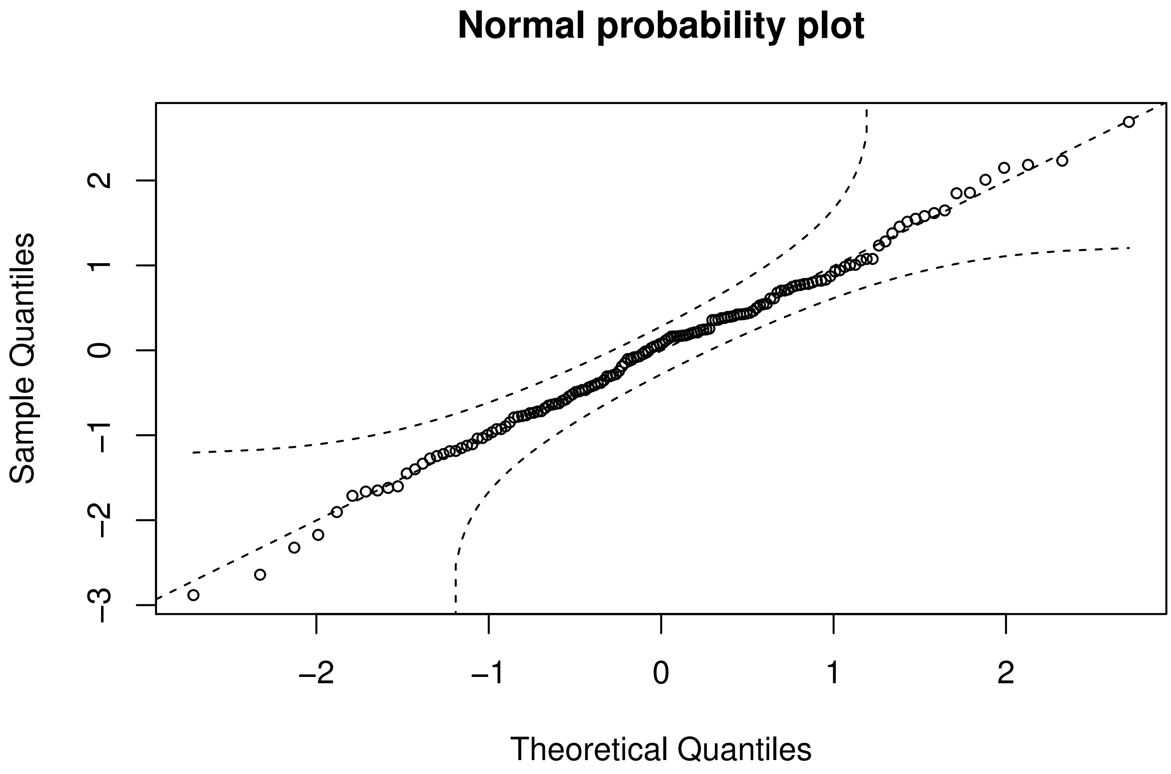


The variofaces are the lag 1 plots of the sample semivariogram with simulated confidence envelopes (Stefanova et al., 2009).

Plot normal quantile plot

The plot is obtained using the `qqPlot` function from the `QTLRel` function (Cheng, 2018).

```
with(Wheat.dat, qqPlot(y = res,
                       xlab = "Theoretical Quantiles", ylab = "Sample Quantiles",
                       main="Normal probability plot"))
```



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
## 10      10        1168.989       120.4773                         1228.315
## 1        1        1242.750       119.8109                         1302.076
## 9        9        1257.137       119.9713                         1316.463
## 16      16        1285.718       119.9405                         1345.045
## 14      14        1293.527       119.9232                         1352.853
## 23      23        1313.653       120.2934                         1372.979
## 11      11        1322.159       120.1969                         1381.485
## 7        7        1374.447       120.2412                         1433.773
## 3        3        1394.070       120.4037                         1453.396
## 4        4        1410.980       120.1060                         1470.306
## 12      12        1444.557       120.6039                         1503.883
## 8        8        1453.396       120.5945                         1512.723
## 15      15        1458.383       120.4351                         1517.709
## 5        5        1473.782       120.4460                         1533.108
## 17      17        1487.828       120.2901                         1547.154
## 6        6        1498.294       120.1194                         1557.620
## 21      21        1517.121       120.2267                         1576.448
## 2        2        1520.466       119.6327                         1579.792
## 24      24        1533.769       120.3000                         1593.095
## 18      18        1541.148       120.3669                         1600.474
## 25      25        1575.794       120.5147                         1635.121
## 22      22        1610.482       120.3286                         1669.808
## 13      13        1610.762       120.4580                         1670.088
## 20      20        1627.971       120.2333                         1687.297
## 19      19        1652.992       120.3440                         1712.318
##    lower.halfLeastSignificant.limit est.status
## 10                         1109.663  Estimable
## 1                          1183.424  Estimable
## 9                          1197.811  Estimable
## 16                         1226.392  Estimable
## 14                         1234.200  Estimable
## 23                         1254.327  Estimable
## 11                         1262.833  Estimable
## 7                          1315.120  Estimable
## 3                          1334.744  Estimable
## 4                          1351.654  Estimable
## 12                         1385.231  Estimable
## 8                          1394.070  Estimable
## 15                         1399.057  Estimable
## 5                          1414.456  Estimable
## 17                         1428.502  Estimable
## 6                          1438.968  Estimable
## 21                         1457.795  Estimable
## 2                          1461.139  Estimable
## 24                         1474.442  Estimable
## 18                         1481.821  Estimable
## 25                         1516.468  Estimable
## 22                         1551.156  Estimable
## 13                         1551.436  Estimable
## 20                         1568.645  Estimable
## 19                         1593.666  Estimable
##
##
```

```
## LSD values
##
## minimum LSD =  114.0128
##
## 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 $\pm o.5LSD$ 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).

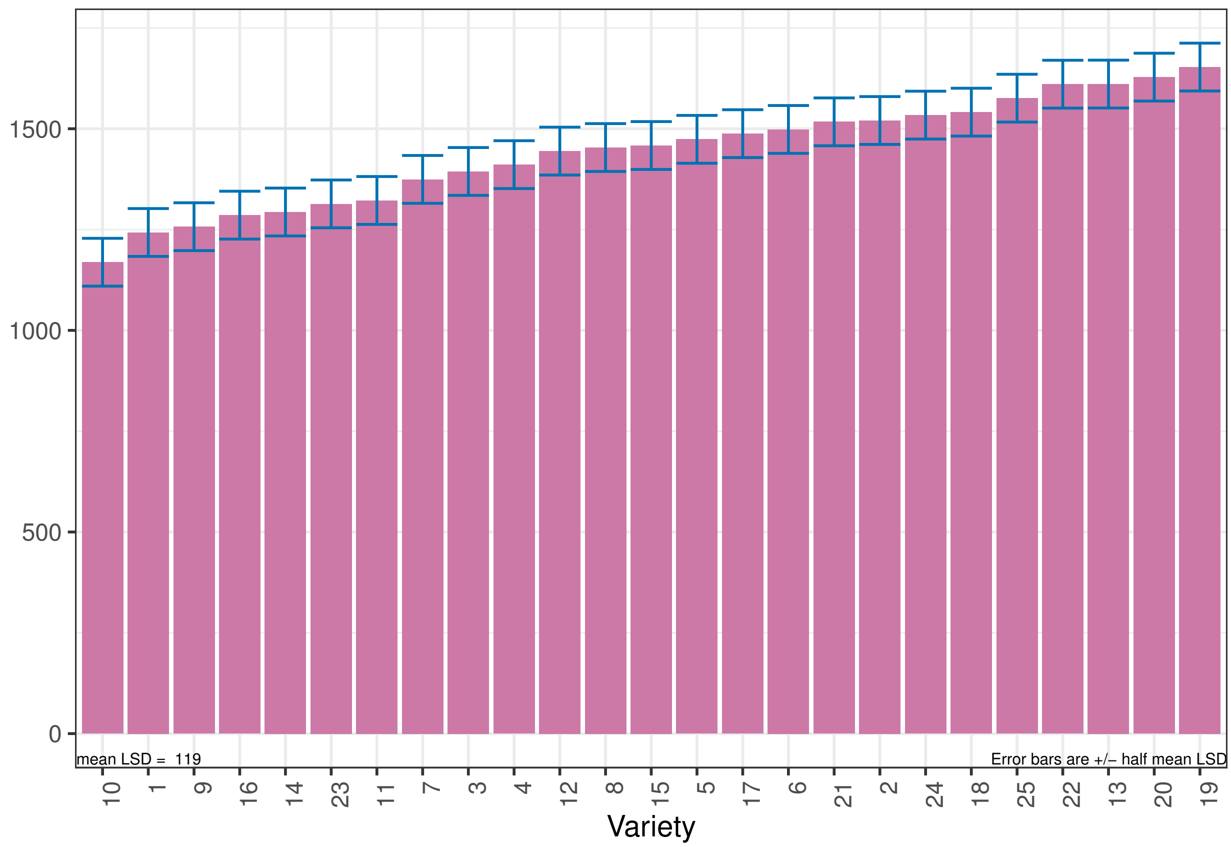
Also set was `sortFactor`, so that the results would be ordered for the values of the predictions for Variety.

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

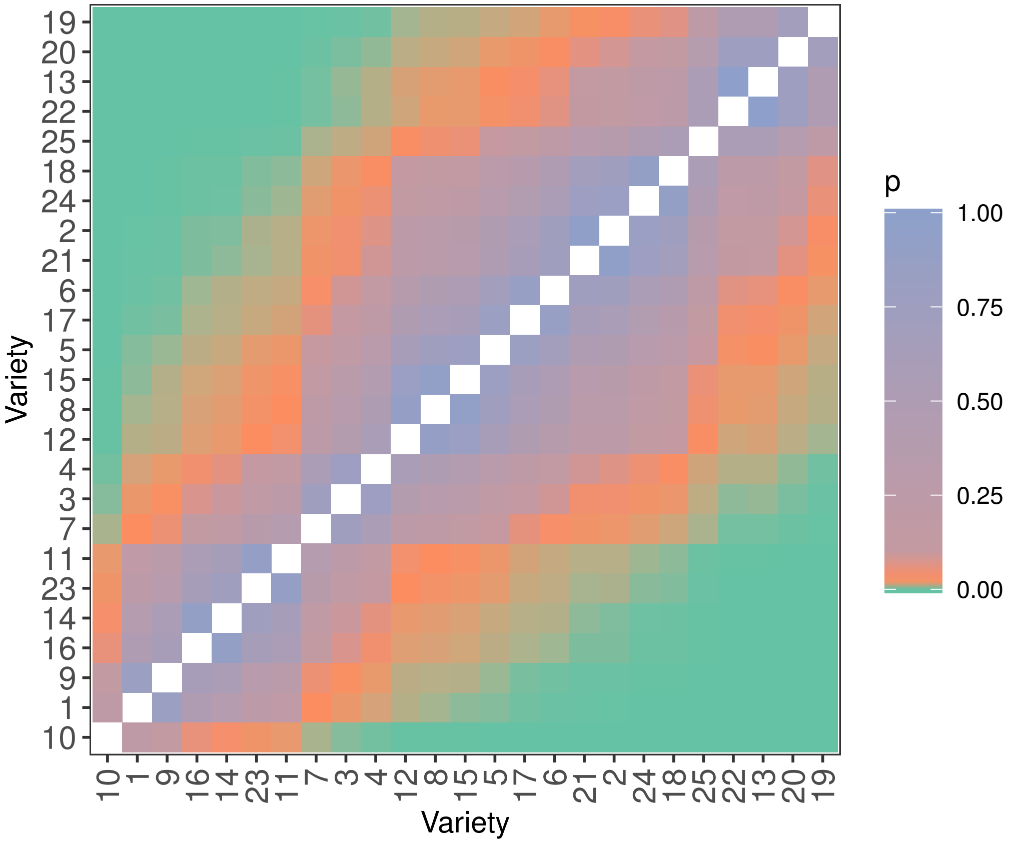
- `predictions`: the predictions, their standard errors and error intervals;
- `vcov`: the variance matrix of the predictions;
- `differences`: all pairwise differences between the predictions,
- `p.differences`: p-values for all pairwise differences between the predictions;
- `sed`: the standard errors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

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

Cheng, R. (2018) QTLRel: tools for mapping of quantitative traits of genetically related individuals and calculating identity coefficients from pedigrees. https://CRAN.R-project.org/package=QTLRel.

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.

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

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.