

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

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```
library(knitr)
#knitr::spin("WheatTalk.r")
library(dae, quietly=TRUE)
library(scales)
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 Wed Jan 30 22:58:27 2019
```

##		LogLik	Sigma2	DF	wall	cpu
##	1	-724.121	23034.14	124	22:58:27	0.0
##	2	-717.415	9206.93	124	22:58:27	0.0 (2 restrained)
##	3	-694.875	26492.99	124	22:58:27	0.0 (2 restrained)
##	4	-694.160	33101.80	124	22:58:27	0.0 (1 restrained)
##	5	-692.002	36912.26	124	22:58:27	0.0 (1 restrained)
##	6	-691.789	46701.51	124	22:58:27	0.0 (2 restrained)
##	7	-691.834	46208.51	124	22:58:27	0.0 (1 restrained)
##	8	-691.775	47698.26	124	22:58:27	0.0
##	9	-691.771	47041.85	124	22:58:27	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 dies to a bound term.

## Initialize 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 Littell 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 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 Wed Jan 30 22:58:30 2019
```

```
##      LogLik      Sigma2      DF      wall      cpu
## 1      -724.121      23034.14      124 22:58:31      0.0
## 2      -717.415       9206.93      124 22:58:31      0.0 (2 restrained)
## 3      -694.875      26492.99      124 22:58:31      0.0 (2 restrained)
## 4      -693.974      33129.65      124 22:58:31      0.0 (1 restrained)
## 5      -692.886      39662.12      124 22:58:31      0.0
## 6      -691.428      53103.83      124 22:58:31      0.0
## 7      -691.239      48092.17      124 22:58:31      0.0
## 8      -691.181      47278.94      124 22:58:31      0.0
## 9      -691.171      46850.98      124 22:58:31      0.0
## 10     -691.170      46690.46      124 22:58:31      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       46690.4620402  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")
```

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 Varieties 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",
                             simplr=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 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",
                              simplr=TRUE, update=FALSE)
else
  current.asrt <- testresidual(current.asrt, "~ Row:Column",
                              label="Col autocorrelation",
                              simplr=TRUE, update=FALSE)
}
```

```
## Warning in DFdiff(bound.h1, bound.h0, bound.exclusions = bound.exclusions): There were a total of 1
## bound terms.
```

```
## Warning in DFdiff(bound.h1, bound.h0, bound.exclusions = bound.exclusions): The following bound term
## 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

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.

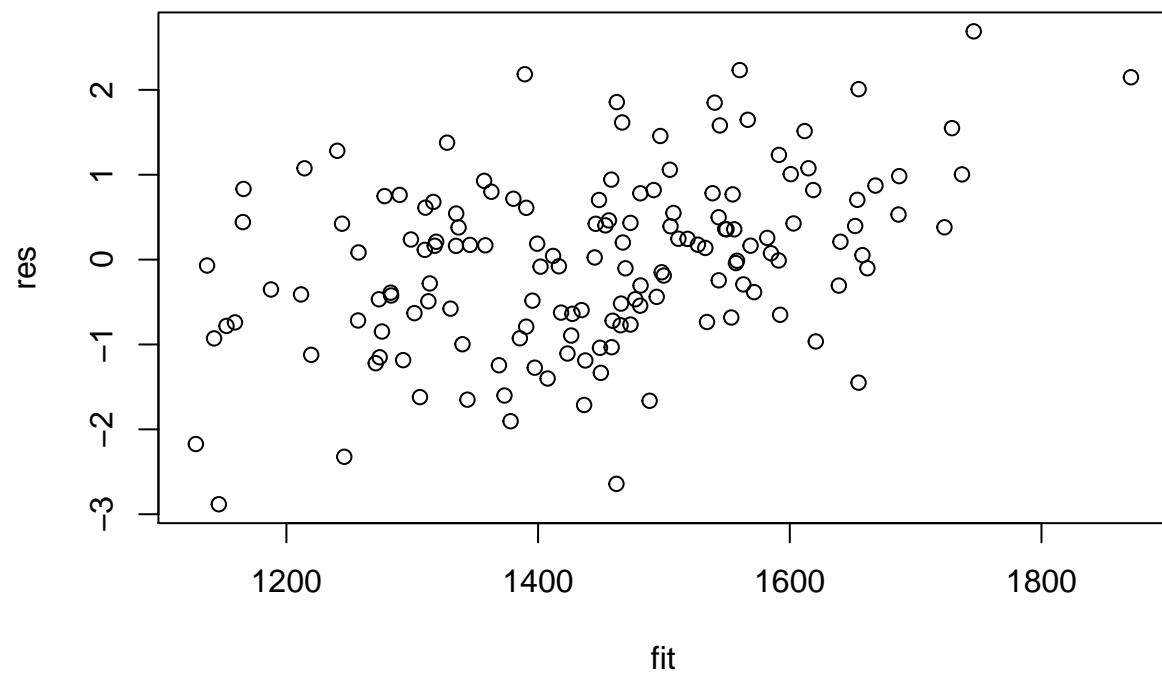
## Get current fitted asreml object an update to include standardized residuals

```
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

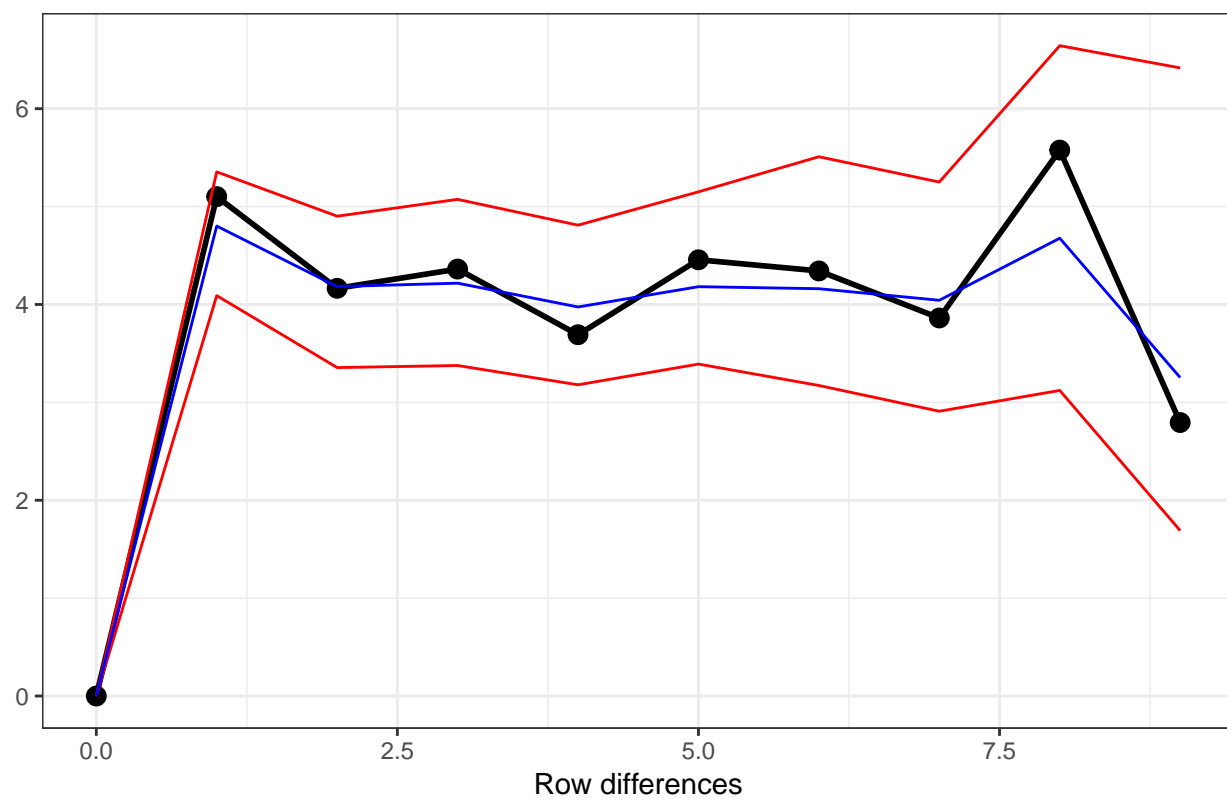
```
with(Wheat.dat, plot(fit, res))
```



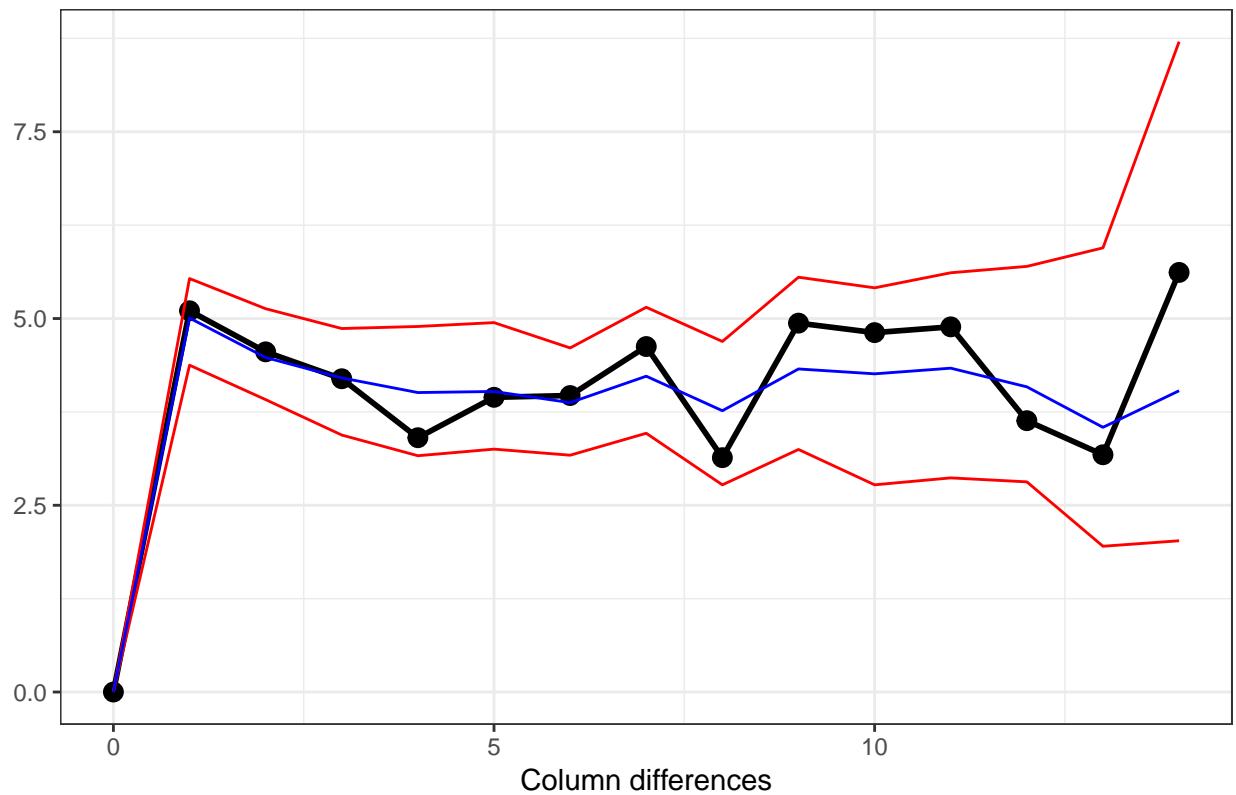
Plot variofaces

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

Variogram face of Standardized conditional residuals for Row



Variogram face of Standardized conditional residuals for Column



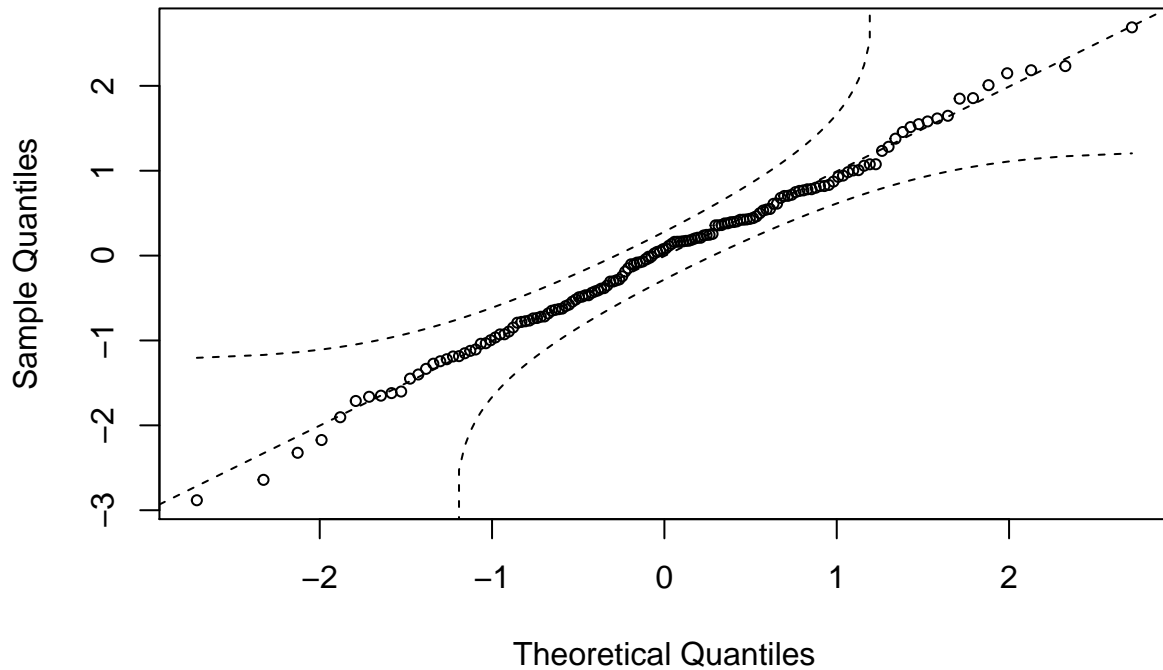
The variofaces are the lag 1 plots of the sample semivariogram with simulated confidence envelopes (Stefanova et al., 2009).

#### Plot normal quantile plot

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



## 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
##
##      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     1575.795      120.5146      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  $\pm 0.5LSD$  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).

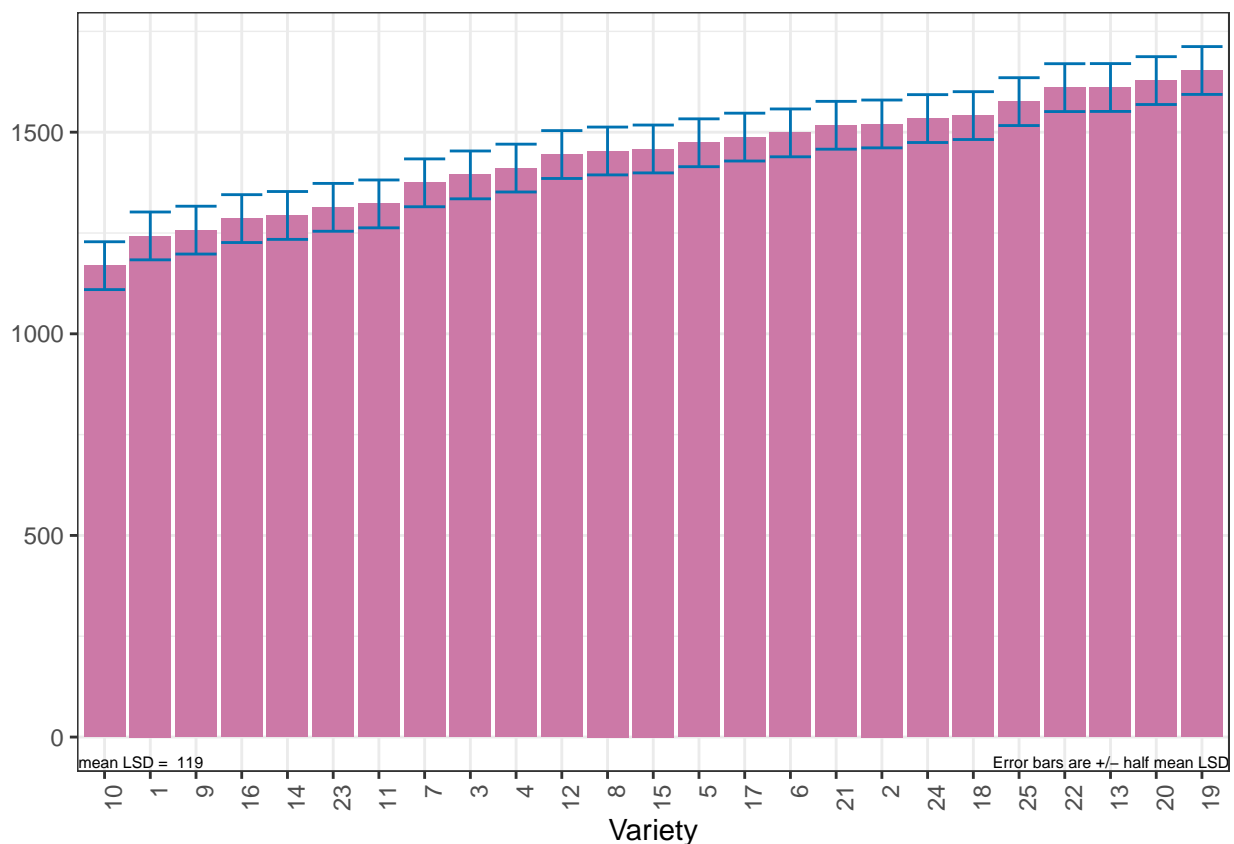
Also set was `sortFactor`, so that the results would be ordered for the values of the predictions for Variety.

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

```
plotPredictions(Var.diffs$predictions,  
  classify = "Variety", y = "predicted.value",  
  error.intervals = "half")
```



## 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.orglink>.

- 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.