

Using `asremlPlus`, in conjunction with `asreml`, to do a linear mixed model analysis of a wheat experiment

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This vignette shows how to use `asremlPlus` (Brien, 2021), 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, 2021).

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))

## Online License checked out Thu Sep 23 10:38:18 2021
packageVersion("asreml")

## [1] '4.1.0.154'

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

## [1] '4.3.21'

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),
                    data=Wheat.dat)
```

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Model fitted using the gamma parameterization.

ASReml 4.1.0 Thu Sep 23 10:38:19 2021

	LogLik	Sigma2	DF	wall	cpu
1	-724.121	23034.14	124	10:38:19	0.0
2	-717.415	9206.93	124	10:38:19	0.0 (2 restrained)
3	-694.875	26492.99	124	10:38:19	0.0 (2 restrained)
4	-694.160	33101.80	124	10:38:19	0.0 (1 restrained)
5	-692.002	36912.26	124	10:38:19	0.0 (1 restrained)
6	-691.789	46701.51	124	10:38:19	0.0 (2 restrained)
7	-691.834	46208.51	124	10:38:19	0.0 (1 restrained)
8	-691.775	47698.26	124	10:38:19	0.0
9	-691.771	47041.85	124	10:38:19	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.

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", IClkelihood = "full")
```

Warning in `infoCriteria.asreml(asreml.obj, IClkelihood = 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, IClkelihood = "full")
```

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

Model fitted using the gamma parameterization.

ASReml 4.1.0 Thu Sep 23 10:38:20 2021

	LogLik	Sigma2	DF	wall	cpu
1	-691.771	47071.42	124	10:38:20	0.0

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
```

(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	1742.469	Starting model
2	Rep	1	NA	NA	1646.129	1742.469	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) 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")
```

Model fitted using the gamma parameterization.

ASReml 4.1.0 Thu Sep 23 10:38:20 2021

	LogLik	Sigma2	DF	wall	cpu
1	-724.121	23034.14	124	10:38:20	0.0
2	-717.415	9206.93	124	10:38:20	0.0 (2 restrained)
3	-694.875	26492.99	124	10:38:20	0.0 (2 restrained)
4	-693.974	33129.65	124	10:38:20	0.0 (1 restrained)
5	-692.886	39662.12	124	10:38:20	0.0
6	-691.428	53103.83	124	10:38:20	0.0
7	-691.239	48092.17	124	10:38:20	0.0
8	-691.181	47278.94	124	10:38:20	0.0
9	-691.171	46850.98	124	10:38:20	0.0
10	-691.170	46690.46	124	10:38:20	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, 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	-2462.3785855	1.191435e+03	-2.066734	U	0.2

```

Rep:Row          5012.4021413 3.396848e+03 1.475604    U 0.1
Rep:Column       920.5936388 1.704008e+03 0.540252    U 1.1
units            5964.9099373 1.608792e+03 3.707695    P 0.1
Row:Column!R     46690.4620354 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
```

(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	NA	1646.129	1742.469	Starting model
2	Rep	1	NA NA	NA	1646.129	1742.469	Boundary
3	Max model & Unbound components	26	7 NA	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	153.500	0.0115
WithinColPairs	1	17.9	2.545	0.1281
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.asrttests`, 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 `asrttests` object.

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

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

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 the 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, IClkelihood = "full")
```

```
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",
                             simplifier=TRUE, IClkelihood = "full")
```

```
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, :
```

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

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",
                              simplifier=TRUE, IClkelihood = "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 of 7 bound terms. 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 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	Maximal model	26	6.0	NA	1646.129	1742.469	Starting model
2	Rep	1	NA	NA	1646.129	1742.469	Boundary
3	Max model & Unbound components	26	7.0	NA	1647.200	1746.551	Starting model
4	WithinColPairs	1	17.9	0.1281	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 - new unconverged
7	Col autocorrelation	2	NA	0.0000	1645.318	1741.658	Unswapped

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

Formulae from asreml object

```

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

```

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

	component	std.error	z.ratio	bound	%ch
Rep	-2385.9128545	1.211137e+03	-1.9699784	U	0.0
Rep:Row	5027.7499257	3.415346e+03	1.4721055	U	0.0
Rep:Column	753.6322682	1.609917e+03	0.4681187	U	0.6
units	5920.4104825	1.611261e+03	3.6743960	P	0.0
Row:Column!R	45870.5610760	2.623679e+04	1.7483295	P	0.0
Row:Column!Row!cor	0.8098804	1.001790e-01	8.0843355	U	0.0
Row:Column!Column!cor	0.8845772	7.510551e-02	11.7777939	U	0.0

The test.summary shows is that the model with Row and without Column autocorrelation failed to converge. 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.

3. Diagnosing 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)
```

```
Model fitted using the gamma parameterization.  
ASReML 4.1.0 Thu Sep 23 10:38:24 2021
```

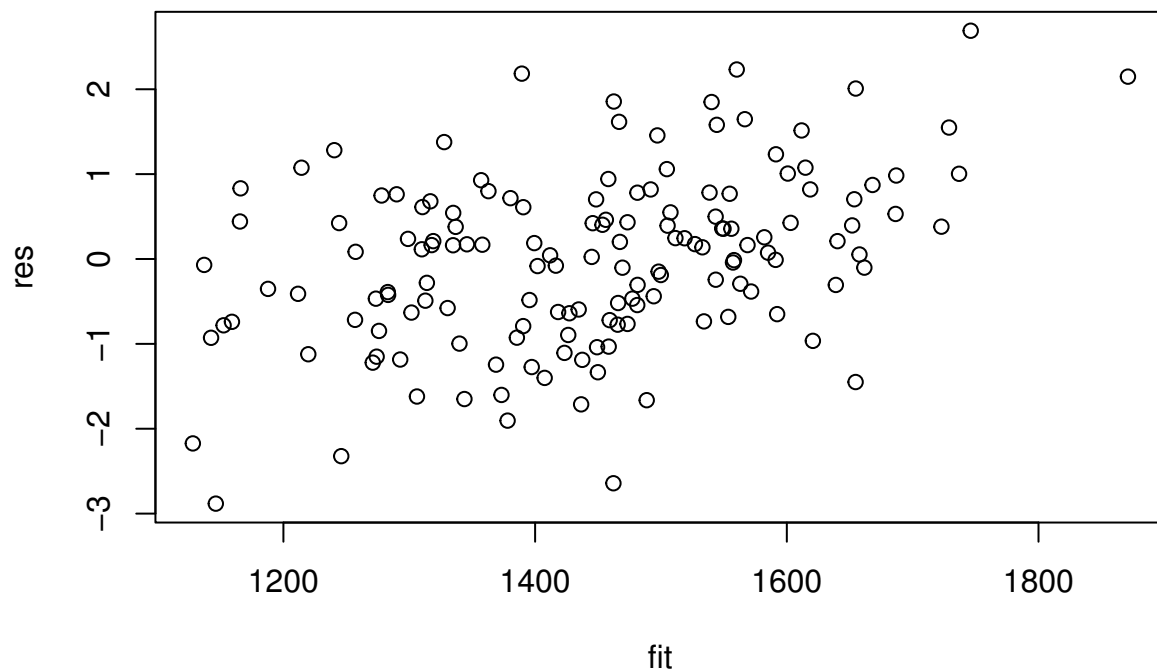
	LogLik	Sigma2	DF	wall	cpu
1	-694.615	45855.43	125	10:38:24	0.0
2	-694.615	45854.15	125	10:38:24	0.0
3	-694.615	45851.11	125	10:38:24	0.0

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

Do diagnostic checking

Do residuals-versus-fitted values plot

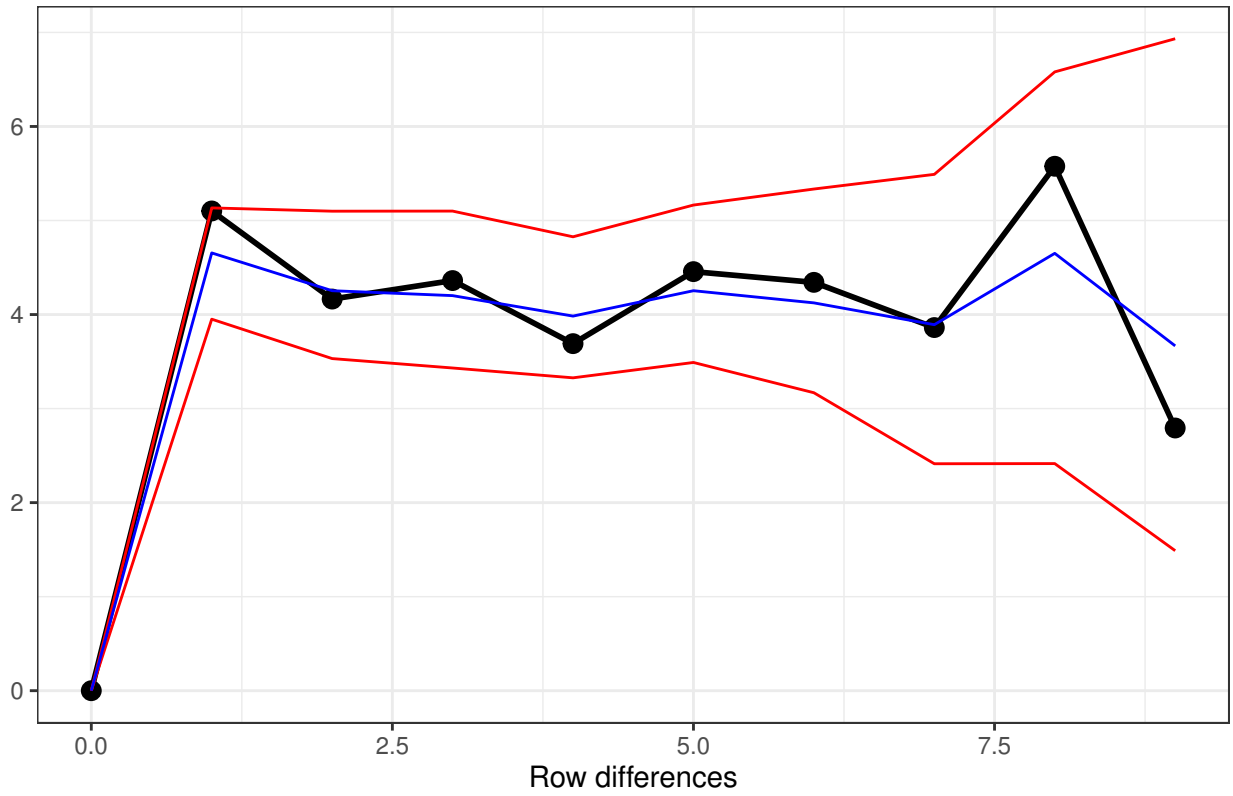
```
with(Wheat.dat, plot(fit, res))
```



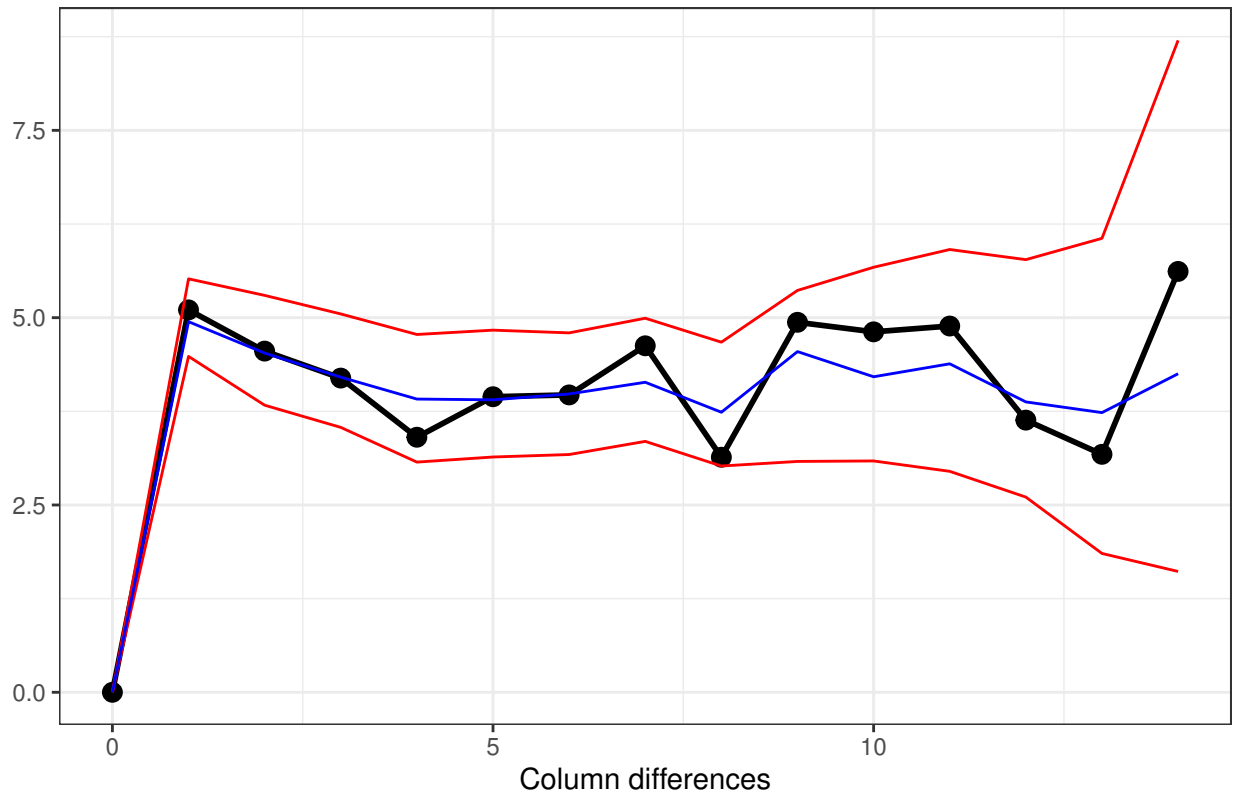
Plot variofaces

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

Variogram face of Standardized conditional residuals for Row



Variogram face of Standardized conditional residuals for Column

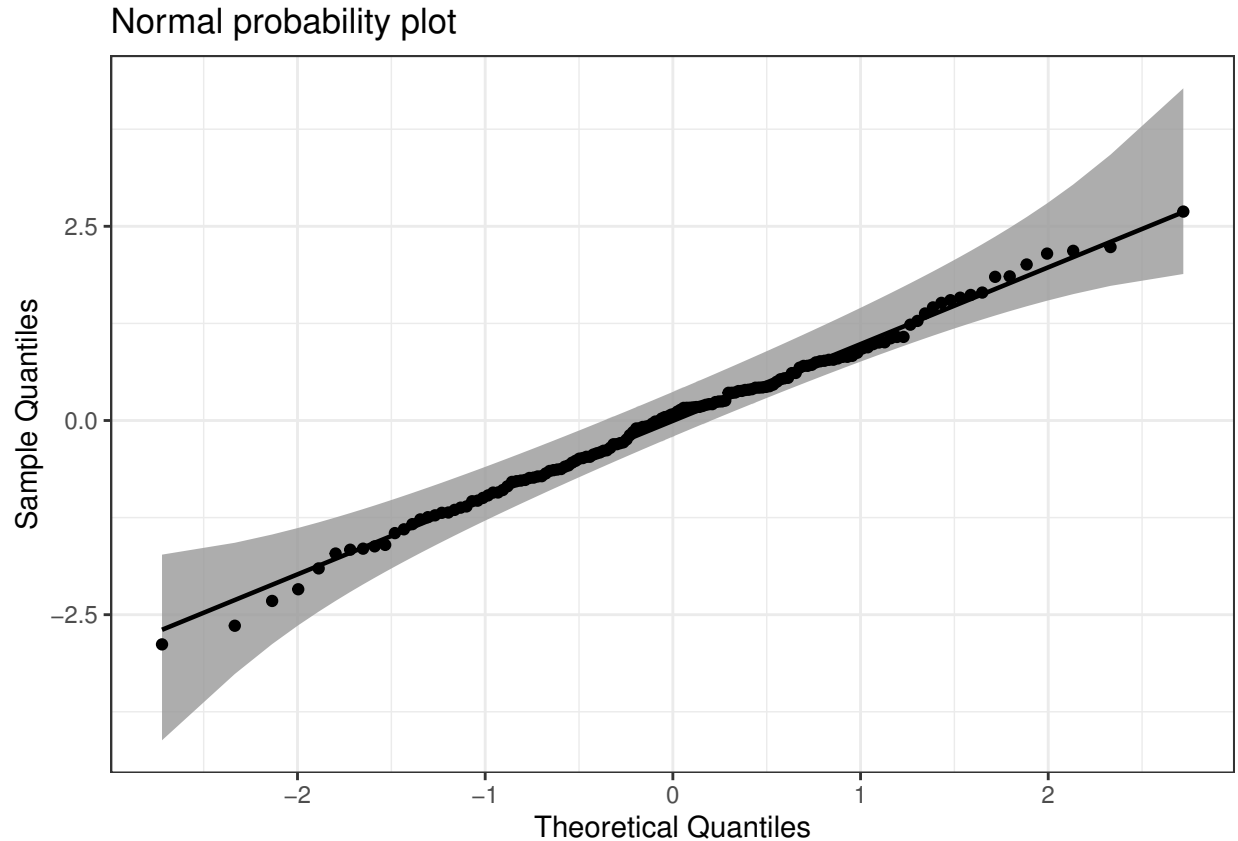


The variofaces are the lag 1 plots of the sample semivariogram with simulated confidence envelopes (Stefanova et al., 2009).

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., 2020).

```
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")
```

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	120.4768	1228.315
2	1	1242.750	119.8105	1302.076
3	9	1257.137	119.9708	1316.463
4	16	1285.718	119.9400	1345.045
5	14	1293.526	119.9227	1352.853
6	23	1313.653	120.2930	1372.979
7	11	1322.159	120.1964	1381.485
8	7	1374.447	120.2407	1433.773
9	3	1394.070	120.4032	1453.396
10	4	1410.980	120.1055	1470.306
11	12	1444.557	120.6034	1503.883
12	8	1453.396	120.5940	1512.723
13	15	1458.383	120.4346	1517.709
14	5	1473.782	120.4455	1533.108
15	17	1487.828	120.2896	1547.154
16	6	1498.294	120.1189	1557.620
17	21	1517.121	120.2262	1576.447
18	2	1520.466	119.6322	1579.792
19	24	1533.769	120.2995	1593.095
20	18	1541.148	120.3664	1600.474
21	25	1575.795	120.5142	1635.121
22	22	1610.482	120.3281	1669.808
23	13	1610.762	120.4575	1670.088
24	20	1627.971	120.2328	1687.297
25	19	1652.992	120.3435	1712.318

	lower.halfLeastSignificant.limit	est.status
1	1109.663	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	1351.653	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	1474.443	Estimable
20	1481.821	Estimable
21	1516.468	Estimable
22	1551.156	Estimable
23	1551.436	Estimable
24	1568.645	Estimable
25	1593.666	Estimable

LSD values

minimum LSD = 114.0128

mean LSD = 118.6523

maximum LSD = 123.3578

(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).

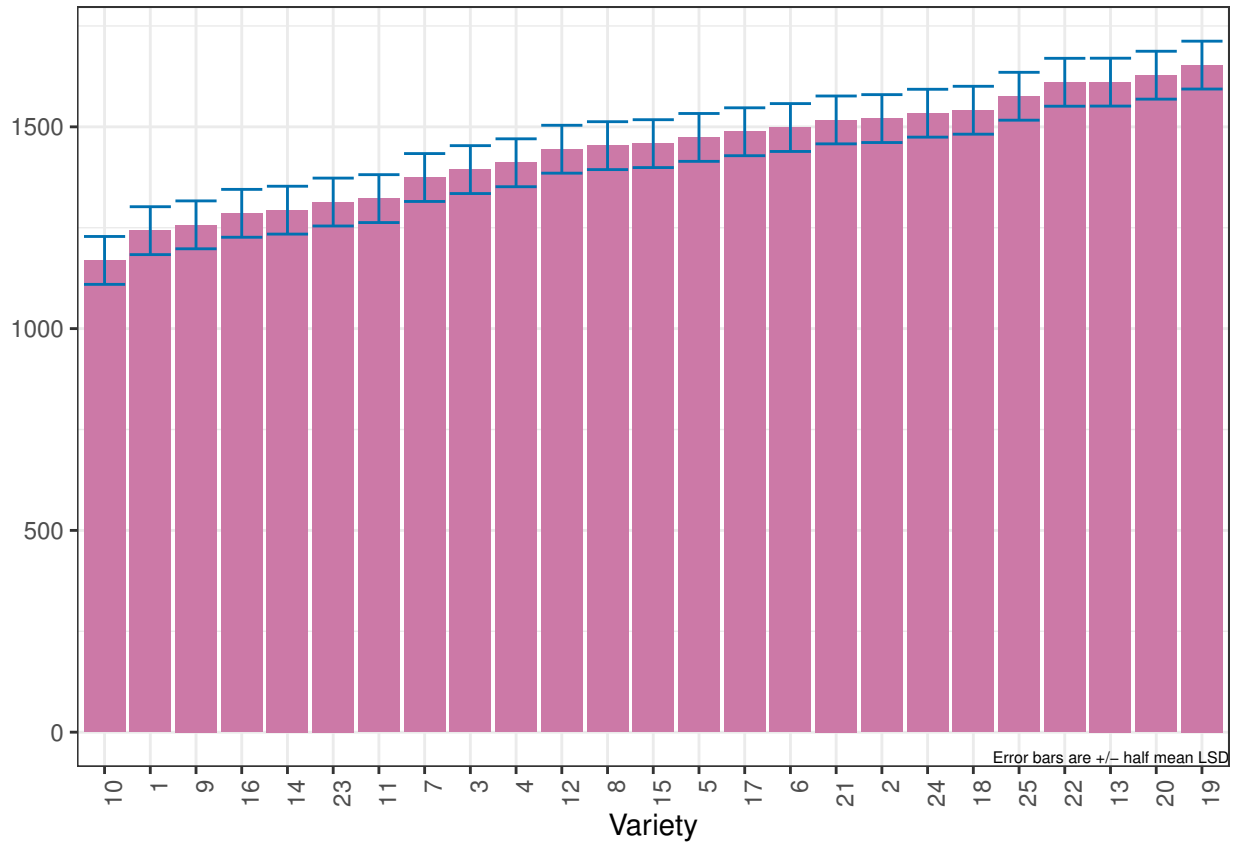
Also set was `sortFactor`, so that the results would be ordered for the values of the predictions for Variety.

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

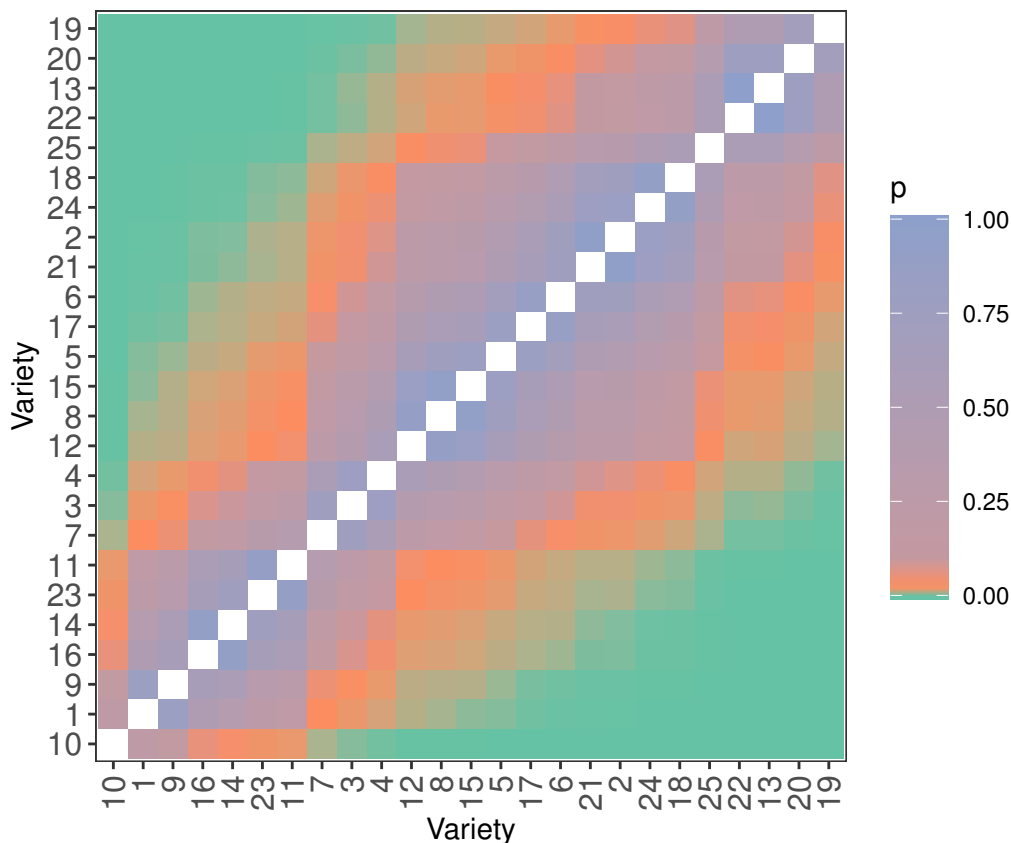
- `predictions`: the predictions, their standard errors and error intervals;
- `vcov`: the variance matrix of the predictions;
- `differences`: all pairwise differences between the predictions,
- `p.differences`: p-values for all pairwise differences between the predictions;
- `sed`: the standard errors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

Plot the Variety predictions, 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 Hofmann, H. (2020) *qqplotr: Quantile-Quantile plot extensions for 'ggplot2'*, Version 0.0.3. <https://cran.r-project.org/package=qqplotr/> or <https://github.com/aloy/qqplotr/>.
- Brien, C. J. (2021) *asremlPlus: Augments ASReML-R in fitting mixed models and packages generally in exploring prediction differences*. Version 4.3-19. <https://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. (2020). *ASReML-R Reference Manual Version 4.1.0.130*. VSN International Ltd, <https://asreml.kb.vsn.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.
- Littell, R. C., Milliken, G. A., Stroup, W. W., Wolfinger, R. D., & Schabenberger, O. (2006). *SAS for Mixed Models* (2nd ed.). Cary, N.C.: SAS Press.
- R Core Team (2021) *R: A language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing. <https://www.r-project.org/>.
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- 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. (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.<https://doi.org/10.1111/anzs.12254/>.