Employing \texttt{asremlPlus}, in conjunction with \texttt{asreml}, to calculate and use information criteria

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This vignette illustrates the facilities in \texttt{asremlPlus} (Brien, 2020), in conjunction with \texttt{asreml} (Butler et al., 2018), for calculating and using information. Here, \texttt{asremlPlus} and \texttt{asreml} are packages for the \texttt{R} Statistical Computing environment (R Core Team, 2020).

It is divided into the following main sections:

1. Set up the maximal model for this experiment
2. Obtaining information criteria for separate models
3. Obtaining information criteria for a prescribed sequence of model changes
4. Using information criteria to decide model changes

1. Set up the maximal model for this experiment

\begin{verbatim}
library(knitr)
opts_chunk$set("tidy" = FALSE, comment = NA)
suppressMessages(library(asreml, quietly=TRUE))
packageVersion("asreml")
## [1] '4.1.0.122'
suppressMessages(library(asremlPlus))
packageVersion("asremlPlus")
## [1] '4.2.17'
options(width = 100)
\end{verbatim}

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 \texttt{asreml} manual by Butler et al. (2018, Section 7.6), although they suggest that it is a barley experiment.

\texttt{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 \texttt{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,
max.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 Mon Mar 16 09:22:14 2020

<table>
<thead>
<tr>
<th></th>
<th>LogLik</th>
<th>Sigma2</th>
<th>DF</th>
<th>wall</th>
<th>cpu</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-724.121</td>
<td>23034.14</td>
<td>124</td>
<td>09:22:14</td>
<td>0.0</td>
</tr>
<tr>
<td>2</td>
<td>-717.415</td>
<td>9206.93</td>
<td>124</td>
<td>09:22:14</td>
<td>0.0</td>
</tr>
<tr>
<td>3</td>
<td>-694.875</td>
<td>26492.99</td>
<td>124</td>
<td>09:22:14</td>
<td>0.0</td>
</tr>
<tr>
<td>4</td>
<td>-694.160</td>
<td>33101.80</td>
<td>124</td>
<td>09:22:14</td>
<td>0.0</td>
</tr>
<tr>
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<td>-692.002</td>
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<td>124</td>
<td>09:22:14</td>
<td>0.0</td>
</tr>
<tr>
<td>6</td>
<td>-691.789</td>
<td>46701.51</td>
<td>124</td>
<td>09:22:14</td>
<td>0.0</td>
</tr>
<tr>
<td>7</td>
<td>-691.834</td>
<td>46208.51</td>
<td>124</td>
<td>09:22:14</td>
<td>0.0</td>
</tr>
<tr>
<td>8</td>
<td>-691.775</td>
<td>47698.26</td>
<td>124</td>
<td>09:22:14</td>
<td>0.0</td>
</tr>
<tr>
<td>9</td>
<td>-691.771</td>
<td>47041.85</td>
<td>124</td>
<td>09:22:14</td>
<td>0.0</td>
</tr>
</tbody>
</table>

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*

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

*Calculating denominator DF*

*Check for and remove any boundary terms*

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

### 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
Rep 1 NA NA 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) 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

```r
max.asr <- setvarianceterms(max.asr$call,
    terms = c("Rep", "Rep:Row", "Rep:Column"),
    bounds = "U")
```

Model fitted using the gamma parameterization.

ASReml 4.1.0 Mon Mar 16 09:22:15 2020

<table>
<thead>
<tr>
<th>LogLik</th>
<th>Sigma2</th>
<th>DF</th>
<th>wall</th>
<th>cpu</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 -724.121</td>
<td>23034.14</td>
<td>124</td>
<td>09:22:15</td>
<td>0.0</td>
</tr>
<tr>
<td>2 -717.415</td>
<td>9206.93</td>
<td>124</td>
<td>09:22:15</td>
<td>0.0 (2 restrained)</td>
</tr>
<tr>
<td>3 -694.875</td>
<td>26492.99</td>
<td>124</td>
<td>09:22:15</td>
<td>0.0 (2 restrained)</td>
</tr>
<tr>
<td>4 -693.974</td>
<td>33129.65</td>
<td>124</td>
<td>09:22:15</td>
<td>0.0 (1 restrained)</td>
</tr>
<tr>
<td>5 -692.886</td>
<td>39662.12</td>
<td>124</td>
<td>09:22:15</td>
<td>0.0</td>
</tr>
<tr>
<td>6 -691.428</td>
<td>53103.83</td>
<td>124</td>
<td>09:22:15</td>
<td>0.0</td>
</tr>
<tr>
<td>7 -691.239</td>
<td>48092.17</td>
<td>124</td>
<td>09:22:15</td>
<td>0.0</td>
</tr>
<tr>
<td>8 -691.181</td>
<td>47278.94</td>
<td>124</td>
<td>09:22:15</td>
<td>0.0</td>
</tr>
<tr>
<td>9 -691.171</td>
<td>46850.98</td>
<td>124</td>
<td>09:22:15</td>
<td>0.0</td>
</tr>
<tr>
<td>10 -691.170</td>
<td>46690.46</td>
<td>124</td>
<td>09:22:15</td>
<td>0.0</td>
</tr>
</tbody>
</table>

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

max.asrt <- as.asrtests(max.asr, NULL, NULL)

Calculating denominator DF

```r
max.asrt <- rmboundary(max.asrt)
```

```r
data.frame(component = max.asrt$asreml.obj$varcomp$component,
    std.error = max.asrt$asreml.obj$varcomp$std.error,
    z.ratio = max.asrt$asreml.obj$varcomp$z.ratio,
    bound = max.asrt$asreml.obj$varcomp$bound,
    %ch = max.asrt$asreml.obj$varcomp$%ch)
```

```r
print(max.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)

```
[1] terms DF denDF p AIC BIC action
<0 rows> (or 0-length row.names)
```

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 \((p < 0.001)\)
2. Obtaining information criteria for separate models

The method infoCriteria has two methods for calculating information criteria. One, infoCriteria.asreml, is a method for asreml objects and the other, infoCriteria.list, if for 'listobjects, the components of the list being asreml' objects.

Single models

Firstly, infoCriteria is called with the default IClikelihood, which is REML. Then it is called with IClikelihood set to full (Verbyla, 2019).

```
infoCriteria(max.asr)
```

```
fixedDF varDF NBound  AIC     BIC     loglik
1     0       7       0 1396.34 1416.082 -691.17
```

```
infoCriteria(max.asr, IClikelihood = "full")
```

Model fitted using the gamma parameterization.

```
LogLik Sigma2 DF wall cpu
1  -691.170 46641.98 124 09:22:16 0.0
```

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

```
fixedDF varDF NBound  AIC     BIC     loglik
1     26      7       0 1647.193 1746.544 -790.5967
```

A list of models

Now, a second model, from which the withinColPairs term has been omitted, is fitted; to be consistent, the variance components are unconstrained using setvariances.asreml. Then the asreml objects for this model and the maximal model are combined into a list and a data.frame produced that includes their information criteria.

```
m1.asr <- asreml(yield ~ Variety,
                 random = ~ Rep/(Row + Column) + units,
                 residual = ~ ar1(Row):ar1(Column),
                 data=Wheat.dat)
```

Model fitted using the gamma parameterization.

```
LogLik Sigma2 DF wall cpu
1  -727.774 22898.99 125 09:22:16 0.0
2  -721.097 9190.30 125 09:22:16 0.0 (2 restrained)
3  -698.313 26671.76 125 09:22:16 0.0 (2 restrained)
4  -697.517 32677.28 125 09:22:16 0.0 (1 restrained)
5  -695.419 36662.27 125 09:22:16 0.0 (1 restrained)
6  -695.208 46263.96 125 09:22:16 0.0 (2 restrained)
7  -695.198 46156.63 125 09:22:16 0.0
8  -695.191 46630.21 125 09:22:16 0.0
```

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

```
m1.asr <- setvarianceterms(m1.asr$call,
                           terms = c("Rep", "Rep:Row", "Rep:Column"),
                           bounds = "U")
```
Model fitted using the gamma parameterization.

ASReml 4.1.0 Mon Mar 16 09:22:16 2020

<table>
<thead>
<tr>
<th></th>
<th>LogLik</th>
<th>Sigma2</th>
<th>DF</th>
<th>wall</th>
<th>cpu</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-727.774</td>
<td>22898.99</td>
<td>125</td>
<td>09:22:16</td>
<td>0.0</td>
</tr>
<tr>
<td>2</td>
<td>-721.097</td>
<td>9190.30</td>
<td>125</td>
<td>09:22:16</td>
<td>0.0 (2 restrained)</td>
</tr>
<tr>
<td>3</td>
<td>-698.313</td>
<td>26671.76</td>
<td>125</td>
<td>09:22:16</td>
<td>0.0 (2 restrained)</td>
</tr>
<tr>
<td>4</td>
<td>-697.333</td>
<td>32689.33</td>
<td>125</td>
<td>09:22:16</td>
<td>0.0 (1 restrained)</td>
</tr>
<tr>
<td>5</td>
<td>-697.016</td>
<td>39975.97</td>
<td>125</td>
<td>09:22:16</td>
<td>0.0</td>
</tr>
<tr>
<td>6</td>
<td>-695.070</td>
<td>54825.30</td>
<td>125</td>
<td>09:22:16</td>
<td>0.0</td>
</tr>
<tr>
<td>7</td>
<td>-694.757</td>
<td>47637.20</td>
<td>125</td>
<td>09:22:16</td>
<td>0.0</td>
</tr>
<tr>
<td>8</td>
<td>-694.644</td>
<td>46775.41</td>
<td>125</td>
<td>09:22:16</td>
<td>0.0</td>
</tr>
<tr>
<td>9</td>
<td>-694.618</td>
<td>46175.06</td>
<td>125</td>
<td>09:22:16</td>
<td>0.0</td>
</tr>
<tr>
<td>10</td>
<td>-694.615</td>
<td>45940.69</td>
<td>125</td>
<td>09:22:16</td>
<td>0.0</td>
</tr>
</tbody>
</table>

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

```r
mods <- list(max = max.asr, m1 = m1.asr)
ic <- infoCriteria(mods, IClikelihood = "full")
print(ic)
```

<table>
<thead>
<tr>
<th>fixedDF</th>
<th>varDF</th>
<th>NBound</th>
<th>AIC</th>
<th>BIC</th>
<th>loglik</th>
</tr>
</thead>
<tbody>
<tr>
<td>max</td>
<td>26</td>
<td>7</td>
<td>1647.193</td>
<td>1746.544</td>
<td>-790.5967</td>
</tr>
<tr>
<td>m1</td>
<td>25</td>
<td>7</td>
<td>1645.326</td>
<td>1741.666</td>
<td>-790.6629</td>
</tr>
</tbody>
</table>

3. Obtaining information criteria for a prescribed sequence of model changes

The use of changeTerms.asrtests is demonstrated for a sequence of models, starting with the maximal model.

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

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

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

Calculating denominator DF

```r
current.asrt <- changeTerms(current.asrt, dropFixed = "WithinColPairs", label = "Drop withinColPairs", IClikelihood = "full")
```

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

Calculating denominator DF

```r
print(current.asrt, which = "testsummary", omit.columns = "p")
```

### Sequence of model investigations

(If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)
So the same values of the information criteria have been obtained as when infoCriteria.list was used on a list containing the asreml objects for the two models. The differences is that here there is ultimately only one fitted model, the model stored in the asreml object in the asrtests object named current.asrt: this is the model with withinColPairs omitted.

Note this use of the omit.columns argument from print.test.summary to omit the irrelevant column p from the test.summary.

**Drop nugget term**

```r
current.asrt <- changeTerms(current.asrt, dropRandom = "units",
                           label = "Drop units", IClikelihood = "full")
```

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

Calculating denominator DF

Calculating denominator DF

**Check Row autocorrelation**

```r
current.asrt <- changeTerms(current.asrt, newResidual = "Row:ar1( Column)",
                           label="Row autocorrelation", IClikelihood = "full")
```

Calculating denominator DF

Calculating denominator DF

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

#### Sequence of model investigations

(If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)

<table>
<thead>
<tr>
<th>terms</th>
<th>DF</th>
<th>denDF</th>
<th>AIC</th>
<th>BIC</th>
<th>action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maximal model</td>
<td>26</td>
<td>7</td>
<td>1647.193</td>
<td>1746.544</td>
<td>Starting model</td>
</tr>
<tr>
<td>Drop withinColPairs</td>
<td>25</td>
<td>7</td>
<td>1645.326</td>
<td>1741.666</td>
<td>Changed fixed</td>
</tr>
<tr>
<td>Drop units</td>
<td>25</td>
<td>6</td>
<td>1650.126</td>
<td>1743.456</td>
<td>Changed random</td>
</tr>
<tr>
<td>Row autocorrelation</td>
<td>25</td>
<td>5</td>
<td>1660.882</td>
<td>1751.201</td>
<td>Changed residual</td>
</tr>
</tbody>
</table>

4. **Using information criteria to decide model changes**

This sections illustrates the use of changeModelOnIC.asrtests to decide between consecutive models in a sequence of models. The default information criterion to use for this is the AIC. However, which.IC can be used to specify the use of the BIC or both. Here we use the AIC and the full likelihood.

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

As before, we start with the maximal model, in which the variance components have been unconstrained and look to decide whether of not to drop the withinColPairs term.
current.asrt <- as.asrtests(max.asrt$asreml.obj, NULL, NULL,
label = "Maximal model", IClikelihood = "full")

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

current.asrt <- iterate(current.asrt)

Calculating denominator DF

current.asrt <- changeModelOnIC(current.asrt, dropFixed = "WithinColPairs",
label = "withinColPairs", IClikelihood = "full", which.IC = "AIC",
allow.unconverged = FALSE)

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

Calculating denominator DF
Calculating denominator DF

print(current.asrt, which = "testsummary", omit.columns = "p")

#### Sequence of model investigations
(If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)

<table>
<thead>
<tr>
<th>terms</th>
<th>DF</th>
<th>denDF</th>
<th>AIC</th>
<th>BIC</th>
<th>action</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maximal model</td>
<td>26</td>
<td>7</td>
<td>1647.193455</td>
<td>1746.544420</td>
<td>Starting model</td>
</tr>
<tr>
<td>withinColPairs</td>
<td>-1</td>
<td>0</td>
<td>-1.867556</td>
<td>-4.878191</td>
<td>Swapped</td>
</tr>
</tbody>
</table>

Given the warning about a lack of convergence, we use iterate.asrtests to perform additional iterations
of the fitting process. It seems that it was successful.

It can be seen from the test.summary that the term has been swapped out and this has the effect of reducing
the number of fixed parameters by one and makes no change to the variance parameters.

Check the nugget term

current.asrt <- changeModelOnIC(current.asrt, dropRandom = "units",
label = "units", IClikelihood = "full",
allow.unconverged = FALSE)

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

Calculating denominator DF
Calculating denominator DF

Check Row autocorrelation

current.asrt <- changeModelOnIC(current.asrt, newResidual = "Row:ar1(Column)",
label="Row autocorrelation", IClikelihood = "full",
allow.unconverged = FALSE)
Warning in asreml(fixed = yield ~ Variety, random = ~Rep + units + Rep:Row + : Log-likelihood not converged

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

Warning in newfit.asreml(asreml.obj, fixed. = fix.form, random. = ran.form, :
Calculating denominator DF

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

Check Column autocorrelation (depends on whether Row autocorrelation retained)

```
{  
  last.action <- current.asrt$test.summary$action[current.asrt$test.summary$terms == "Row autocorrelation"]
  if (grepl("Unswapped", last.action, fixed = TRUE) |
      grepl("Unchanged", last.action, fixed = TRUE))
    current.asrt <- changeModelOnIC(current.asrt, newResidual = "ar1(Row):Column",
                                     label="Col autocorrelation", IClikelihood = "full",
                                     allow.unconverged = FALSE)
  else
    current.asrt <- testresidual(current.asrt, newResidual = "Row:Column",
                                 label="Col autocorrelation", IClikelihood = "full",
                                 allow.unconverged = FALSE)
}
```

Calculating denominator DF

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

Warning in rmboundary.asrtests(as.asrtests(asreml.obj, wald.tab, test.summary), :
In analysing yield, cannot remove the following boundary/singular term(s): Row:Column!Row!cor
Calculating denominator DF

Warning in infoCriteria.asreml(new.asrtests.obj$asreml.obj, IClikelihood = ic.lik, : The following bound terms were discounted: Row:Column!Row!cor

Output the results

```
print(current.asrt, which = "test", omit.columns = "p")
```

###### Sequence of model investigations

(If a row has NA for p but not denDF, DF and denDF relate to fixed and variance parameter numbers)

<table>
<thead>
<tr>
<th>terms</th>
<th>DF</th>
<th>denDF</th>
<th>AIC</th>
<th>BIC</th>
<th>action</th>
</tr>
</thead>
<tbody>
<tr>
<td>8</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
summary(current.asrt$asreml.obj)$varcomp

<table>
<thead>
<tr>
<th>component</th>
<th>std.error</th>
<th>z.ratio</th>
<th>bound</th>
<th>%ch</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rep</td>
<td>-2391.94</td>
<td>1.1945</td>
<td>-2.00</td>
<td>U</td>
</tr>
<tr>
<td>Rep:Row</td>
<td>5035.53</td>
<td>3.406</td>
<td>1.48</td>
<td>U</td>
</tr>
<tr>
<td>Rep:Column</td>
<td>761.96</td>
<td>1.6121</td>
<td>0.47</td>
<td>U</td>
</tr>
<tr>
<td>units</td>
<td>5933.21</td>
<td>1.6108</td>
<td>3.68</td>
<td>P</td>
</tr>
<tr>
<td>Row:Column!R</td>
<td>45970.83</td>
<td>2.6351</td>
<td>1.74</td>
<td>P</td>
</tr>
<tr>
<td>Row:Column!Row!cor</td>
<td>0.8101</td>
<td>9.9954</td>
<td>8.10</td>
<td>U</td>
</tr>
<tr>
<td>Row:Column!Column!cor</td>
<td>0.8846</td>
<td>7.5030</td>
<td>11.79</td>
<td>U</td>
</tr>
</tbody>
</table>

The test.summary shows us that the model without the autocorrelation failed to converge and so no change was made to the model. It, and the messages from checking the Column autocorrelation, also show us that the omission of the Column autocorrelation resulted in the Row autocorrelation becoming bound. That is, dropping the Column autocorrelation resulted in the dropping of two variance parameters.

The function printFormulae.asreml is used to display the fitted model.

### Formulae from asreml object

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

References


