Getting started with DiallelAnalysisR

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1 Abstract

DiallelAnalysisR analyses diallel crosses laid out in randomized complete blocks. This vignette takes one data set, an eight-parent diallel with reciprocals, from the plot data to the analysis of variance, the combining-ability effects with their standard errors and the plots, in a few minutes of reading. Each later vignette takes one part further.

2 The data

Each row is one plot: the female parent (`Cross1`), the male parent (`Cross2`), the replicate (`Rep`) and the yield.

```
head(GriffingData1)
```

```
  Cross1 Cross2 Rep  Yield
1      1      1   1 104.86
2      1      2   1  88.66
3      1      3   1 109.76
4      1      4   1 128.10
5      1      5   1 128.36
6      1      6   1  74.40
```

```
dim(GriffingData1)
```

```
[1] 256   4
```

```
with(data = GriffingData1, expr = table(Cross1, Cross2))[1:4, 1:4]
```

```
      Cross2
Cross1 1 2 3 4
     1 4 4 4 4
     2 4 4 4 4
     3 4 4 4 4
     4 4 4 4 4
```

The 8 parents, their 28 crosses and the 28 reciprocal crosses (64 cells) are each grown in 4 replicates.

3 One analysis

Griffing's Method 1 (parents, F_1 and reciprocals) with the fixed-effects model (Model 1):

```
fit <-
  Griffing(
      y          = Yield
    , Rep        = Rep
    , Cross1     = Cross1
    , Cross2     = Cross2
    , data       = GriffingData1
    , Method     = 1
    , Model      = 1
    , Reciprocal = c("combined", "split")[1]
    )
fit
```

```
Griffing's Method 1, Model 1 (fixed effects); 8 parents, 4 replicates

Analysis of variance
             Df Sum Sq Mean Sq F value Pr(>F)
```

```
gca           7   3805   543.5  18.887 <2e-16 ***
sca          28  22061   787.9  27.378 <2e-16 ***
reciprocals  28    366    13.1   0.454  0.992
Error       189   5439    28.8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Components
           Components
gca          32.17142
sca         759.10758
Reciprocal   -7.86142
gca/sca       0.04238

General combining ability effects (standard error 1.255)
       1        2        3        4        5        6        7        8
 0.06188  0.46800  9.02700 -3.43800 -2.32500 -1.93500  7.23800 -9.09600

All components: names(x); tests of the effects: summary(x); figures: plot(x)
```

The result is the list that `Griffing()` has always returned, with a class that gives it methods:

```
summary(fit)
```

```
Griffing's Method 1, Model 1 (fixed effects); 8 parents, 4 replicates

Analysis of variance
             Df Sum Sq Mean Sq F value Pr(>F)
gca           7   3805   543.5  18.887 <2e-16 ***
sca          28  22061   787.9  27.378 <2e-16 ***
reciprocals  28    366    13.1   0.454  0.992
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Components
           Components
gca          32.17142
sca         759.10758
Reciprocal   -7.86142
gca/sca       0.04238

General combining ability effects
   parent Estimate StdErr  t.value   p.value
1:      1  0.06188  1.255  0.04932 9.607e-01
2:      2  0.46797  1.255  0.37303 7.095e-01
```

```
3:      3  9.02672  1.255  7.19544 1.420e-11
4:      4 -3.43797  1.255 -2.74050 6.723e-03
5:      5 -2.32547  1.255 -1.85369 6.534e-02
6:      6 -1.93484  1.255 -1.54232 1.247e-01
7:      7  7.23750  1.255  5.76921 3.208e-08
8:      8 -9.09578  1.255 -7.25050 1.034e-11

Crosses with the largest specific combining ability effects
   Cross1 Cross2 Estimate StdErr t.value   p.value
1:      7      8    32.83  3.353   9.792 1.431e-18
2:      1      4    29.66  3.353   8.846 6.417e-16
3:      1      5    27.30  3.353   8.144 5.072e-14
4:      3      8    25.89  3.353   7.721 6.517e-13
5:      6      7    22.59  3.353   6.737 1.892e-10
```

4 The analysis of variance

```
knitr::kable(x = fit$ANOVA, digits = 3)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
gca	7	3804.643	543.520	18.887	0.000
sca	28	22060.789	787.885	27.378	0.000
reciprocals	28	365.537	13.055	0.454	0.992
Error	189	5438.991	28.778	NA	NA

General and specific combining ability are both highly significant; the reciprocal differences are not. The mean squares are on the scale of a cell mean, so the error line is MS_E/B, the residual mean square of the block analysis divided by the number of replicates.

5 Effects and standard errors

```
round(x = fit$GCA, digits = 3)
```

```
    1     2     3     4     5     6     7     8
0.062 0.468 9.027 -3.438 -2.325 -1.935 7.238 -9.096
```

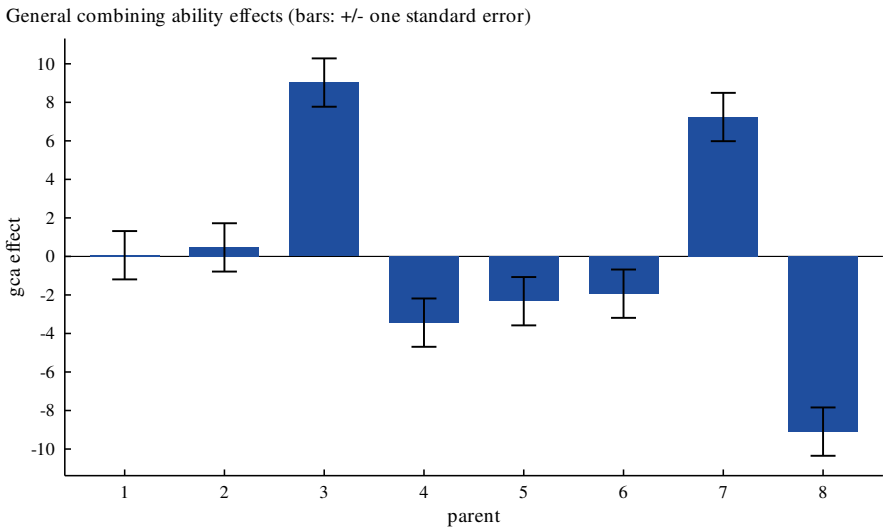
```
round(x = fit$StdErr, digits = 3)
```

```
    gi    sii    sij    rij  gi_gj sii_sjj sii_sij sii_sjk sij_sik sij_skl
 1.255  4.694  3.353  3.793  1.897  6.570  6.290  5.690  5.018  4.646
rij_rkl
 5.364
```

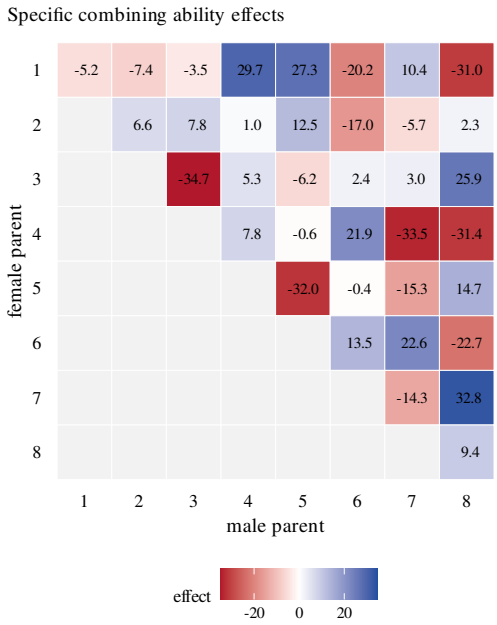
Parents 3 and 7 are the best general combiners, parent 8 the poorest. A difference between two gca effects larger than about twice `gi_gj` is significant at about the 5% level.

6 Plots

```
plot(fit)
```




```
plot(fit, which = "sca")
```



7 The usual model functions

`summary()` adds the t tests of every gca effect and the crosses with the largest sca effects; `anova()`, `coef()`, `vcov()`, `confint()`, `fitted()`, `residuals()` and `predict()` work as for other models in R.

```
summary(object = fit, top = 5)
```

```
Griffing's Method 1, Model 1 (fixed effects); 8 parents, 4 replicates

Analysis of variance
             Df Sum Sq Mean Sq F value Pr(>F)
gca           7   3805   543.5  18.887 <2e-16 ***
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General combining ability effects
   parent Estimate StdErr  t.value   p.value
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2:      2  0.46797  1.255  0.37303 7.095e-01
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4:      3      8    25.89  3.353   7.721 6.517e-13
5:      6      7    22.59  3.353   6.737 1.892e-10
```

```r
head(confint(object = fit, parm = NULL, level = 0.95), 8)
```

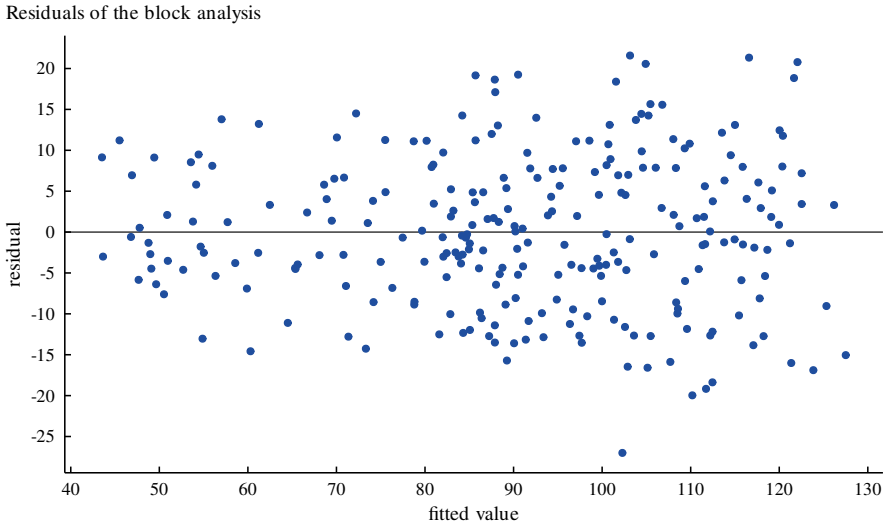
```
         2.5 %    97.5 %
g_1  -2.412755  2.536505
g_2  -2.006661  2.942599
g_3   6.552089 11.501349
g_4  -5.912599 -0.963339
g_5  -4.800099  0.149161
g_6  -4.409474  0.539786
g_7   4.762870  9.712130
g_8 -11.570411 -6.621151
```

```r
predict(
    object  = fit
  , newdata = data.frame(Cross1 = c(3, 3), Cross2 = c(7, 8))
  , type    = c("gca", "full")[1]
  )
```

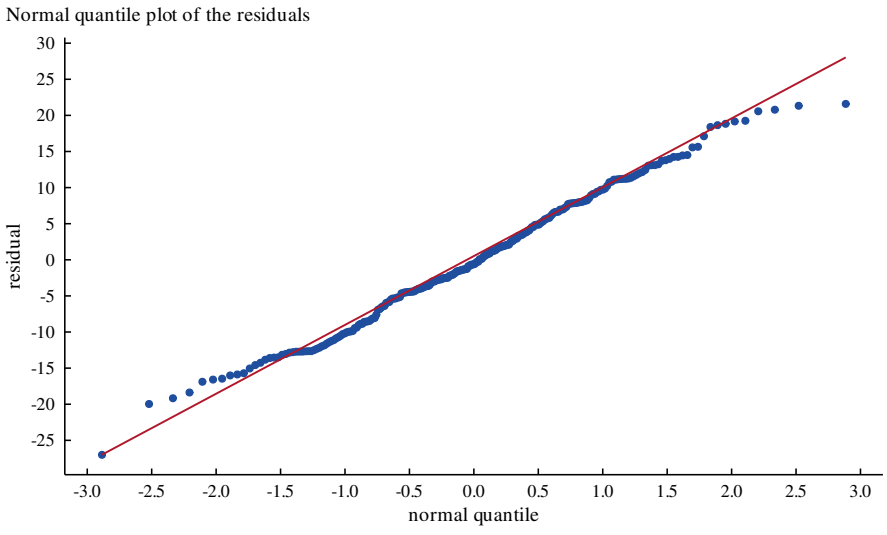
```
   Cross1 Cross2 predicted
1:      3      7 107.01281
2:      3      8  90.67953
```

The residuals of the block analysis check its assumptions:

```
plot(x = fit, which = c("gca", "sca", "residuals", "qq")[3])
```




```
plot(x = fit, which = c("gca", "sca", "residuals", "qq")[4])
```



8 Tables for a report

Any component converts to a table, with the row names in a column `term`:

```
data.table::as.data.table(fit, component = "ANOVA")
```

```
          term  Df     Sum Sq   Mean Sq    F value       Pr(>F)
1:         gca   7  3804.6427 543.52039 18.8868412 5.293328e-19
2:         sca  28 22060.7885 787.88531 27.3783005 3.518704e-52
3: reciprocals  28   365.5369  13.05489  0.4536456 9.923291e-01
4:       Error 189  5438.9907  28.77773         NA           NA
```

9 Summary

One call of `Griffing()` gives the analysis of variance, the effects with their standard errors and the variance components; `plot()` draws the effects. Vignette 02 helps choose an analysis; vignettes 04 to 07 explain Griffing's, Hayman's and the partial diallel analyses, 08 to 11 heterosis, related designs, environments and planning, and 12 the tables for papers and the interactive application. Vignettes 13 to 15 cover validation, speed and extending the package.

10 References

Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences*, 9(4), 463–493.

Singh, R. K. and Chaudhary, B. D. (2004). *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi.