Diallels over environments and the biplot

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1 Abstract

A diallel grown in several environments shows whether combining ability is stable. `GriffingEnv()` pools Griffing's analyses over environments and splits each line into its main effect and its interaction with environments. The biplot of the cross means shows the best general combiners and the best crosses on one graph.

2 A diallel over several environments

`GriffingEnv()` pools Griffing's analyses of the same diallel in several environments. Each line of the analysis is a projection of the table of cross means, so the sum over environments of a line's sum of squares splits into the line itself and its interaction with environments. The example simulates six parents of Method 2 in three environments with gca × environment effects:

```
d <-
  DiallelSim(
      Parents = 6
    , Method  = 2
    , Rep     = 3
    , Env     = 3
```

```
    , Mean    = 50
    , gca     = 4
    , sca     = 2
    , rec     = 0
    , gcaEnv  = 1.5
    , scaEnv  = 1
    , EnvSD   = 2
    , Block   = 1
    , Error   = 3
    , seed    = 1
    )
fe <-
  GriffingEnv(
      y      = y
    , Rep    = Rep
    , Cross1 = Cross1
    , Cross2 = Cross2
    , Env    = Env
    , data   = d
    , Method = 2
    , Model  = 2
    )
fe$ANOVA
```

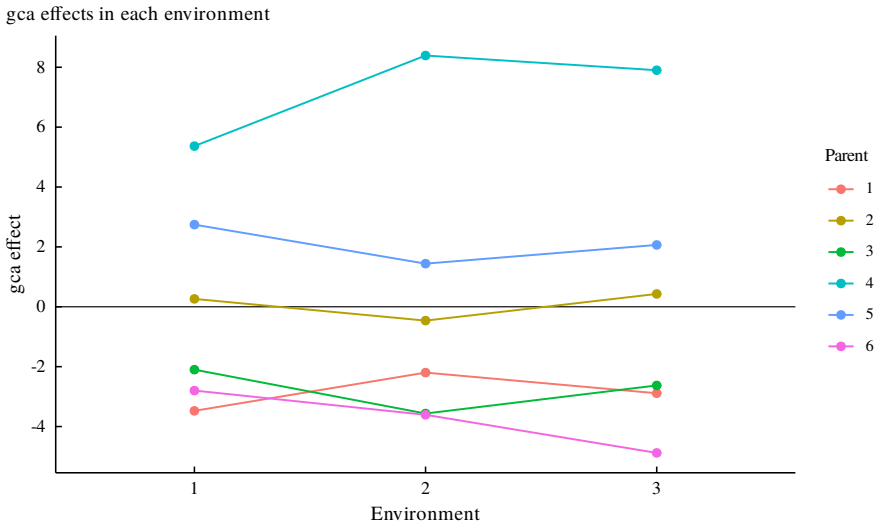
```
           Df  Sum Sq Mean Sq F value    Pr(>F)
Env         2   81.91   40.95  9.1418  0.015084 *
Rep(Env)    6   26.88    4.48  1.5694  0.161861
gca         5 2073.78  414.76 48.4875 1.088e-06 ***
sca        15  200.96   13.40  5.1141 7.288e-05 ***
gca:Env    10   85.54    8.55  2.9968  0.002076 **
sca:Env    30   78.59    2.62  0.9178  0.593124
Error     120  342.52    2.85
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
fe$Genetic.Components
```

```
         Components
gca      16.4760483
sca       3.5924821
gca:Env   0.7417799
sca:Env  -0.2347162
Error     2.8543549
gca/sca   4.5862576
```

In Model 2 gca and sca are tested against their interactions with environments. The gca effects in each environment show which parents combine well everywhere:

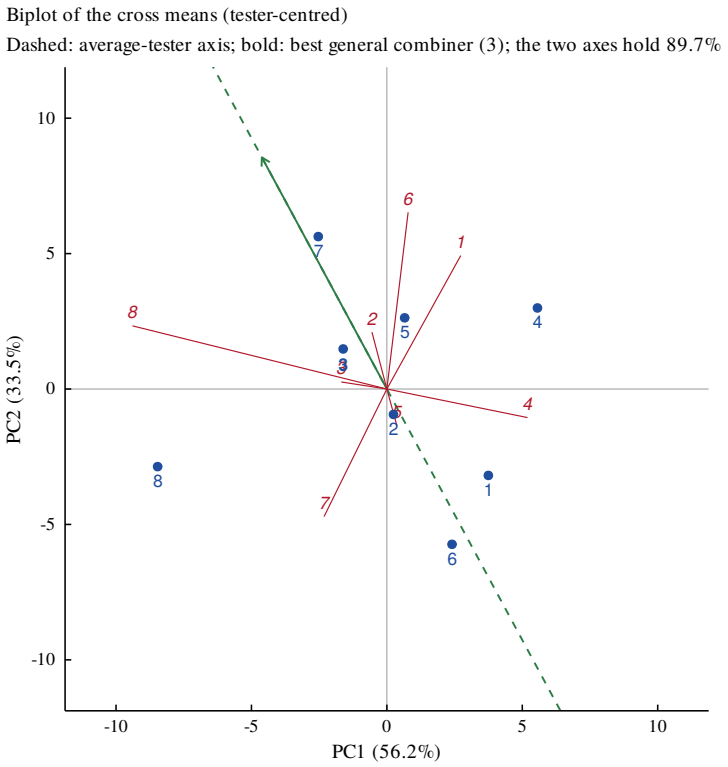
```
plot(x = fe, which = c("gca", "gcaenv", "sca", "residuals", "qq")[2])
```



3 A biplot of the crosses

`plot(fit, which = "biplot")` draws the table of cross means as a biplot (Yan and Hunt 2002): the table of a cross and its reciprocal averaged, the selfs left out and filled by a rank-two fit, centred on the tester (column) means, and its first two principal components with the singular values split between parents and testers. Parents far along the average-tester axis (dashed) combine well in general; a parent close to a tester's vector combines well with that tester.

```
g4 <-
  Griffing(
      y          = Yield
    , Rep        = Rep
    , Cross1     = Cross1
    , Cross2     = Cross2
    , data       = GriffingData4
    , Method     = 4
    , Model      = 1
    , Reciprocal = c("combined", "split")[1]
    )
plot(x = g4, which = c("gca", "sca", "biplot", "residuals", "qq")[3])
```



When specific combining ability is large the two axes show mainly the sca pattern; the parent with the largest gca effect is printed in bold.

4 Summary

The gca × environment and sca × environment lines show whether combining ability holds across environments; the biplot shows which parents and crosses stand out.

5 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.

Yan, W. and Hunt, L. A. (2002). Biplot analysis of diallel data. *Crop Science*, 42(1), 21–30.

Zhang, Y. and Kang, M. S. (1997). DIALLEL-SAS: a SAS program for Griffing's diallel analyses. *Agronomy Journal*, 89(2), 176–182.