Griffing's methods with fixed effects

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2026-11-03

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1 Abstract

Griffing's four methods with the fixed-effects model (Model 1): the analysis of variance, the gca, sca and reciprocal effects, their standard errors and how to compare parents and crosses.

2 The four methods on one data set

The data sets for Methods 2 to 4 are subsets of the complete diallel, so the methods can be compared directly.

```
fits <-
  lapply(
      X   = 1:4
```

```
    , FUN = function(m) Griffing(
          y          = Yield
        , Rep        = Rep
        , Cross1     = Cross1
        , Cross2     = Cross2
        , data       = get(paste0("GriffingData", m))
        , Method     = m
        , Model      = 1
        , Reciprocal = c("combined", "split")[1]
        )
    )
names(fits) <- paste("Method", 1:4)
do.call(
    what = rbind
  , args = lapply(X = fits, FUN = function(f) f$ANOVA[c("gca", "sca"),
↪  "Mean Sq"])
  )
```

```
             [,1]     [,2]
Method 1 543.5204 787.8853
Method 2 264.4133 447.4681
Method 3 801.7759 916.8174
Method 4 446.6969 465.2278
```

3 Method 1: parents, F_1 and reciprocals

With $a_i = Y_{i\cdot} + Y_{\cdot i}$ and $Y_{\cdot\cdot}$ the grand total,

$$SS_g = \frac{1}{2P}\sum_i a_i^2 - \frac{2}{P^2}Y_{\cdot\cdot}^2, \qquad \hat{g}_i = \frac{a_i}{2P} - \frac{Y_{\cdot\cdot}}{P^2}, \qquad \hat{R}_{ij} = \frac{Y_{ij} - Y_{ji}}{2}.$$

```
f1 <- fits[["Method 1"]]
knitr::kable(x = f1$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

```
knitr::kable(x = f1$Genetic.Components, digits = 4)
```

	Components
gca	32.1714
sca	759.1076
Reciprocal	-7.8614
gca/sca	0.0424

The table `Effects` keeps the layout of earlier versions: gca effects on the diagonal, sca effects above it and reciprocal effects below it. The full matrices are in `SCA` and `Reciprocal`:

```
round(x = f1$Effects, digits = 2)
```

```
      1     2     3     4     5      6      7      8
1  0.06 -7.43 -3.49 29.66 27.30 -20.18  10.41 -31.03
2  3.16  0.47  7.82  0.96 12.52 -17.00  -5.72   2.28
3 -5.89  3.51  9.03  5.32 -6.17   2.39   2.98  25.89
4 -2.09 -0.57 -1.02 -3.44 -0.65  21.85 -33.50 -31.42
5  4.50 -1.48  3.01  0.95 -2.33  -0.43 -15.32  14.74
6 -0.14  0.98  0.65 -1.43 -1.91  -1.93  22.59 -22.73
7 -0.81  4.91  1.55  3.40  1.59   2.97   7.24  32.83
8  1.96  1.25  1.17  0.06  0.75  -3.25   3.55  -9.10
```

```
round(x = f1$SCA[1:4, 1:4], digits = 2)
```

```
      1     2      3     4
1 -5.23 -7.43  -3.49 29.66
2 -7.43  6.58   7.82  0.96
3 -3.49  7.82 -34.73  5.32
4 29.66  0.96   5.32  7.77
```

4 Standard errors and comparisons

`StdErr` gives the standard errors of single effects and of differences between effects; for Method 1 $\mathrm{Var}(\hat{g}_i) = (P-1)\sigma_m^2/(2P^2)$ and $\mathrm{Var}(\hat{g}_i - \hat{g}_j) = \sigma_m^2/P$.

```
round(x = f1$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
```

```
t_gca <- f1$GCA / f1$StdErr[["gi"]]
round(x = t_gca, digits = 2)
```

```
   1    2    3    4    5    6    7    8
```

```
 0.05  0.37  7.20 -2.74 -1.85 -1.54  5.77 -7.25
```

A parent's gca effect is significant at the 5% level when $|t|$ exceeds the t quantile on the error degrees of freedom:

```
qt(p = 0.975, df = f1$ANOVA["Error", "Df"])
```

```
[1] 1.972595
```

5 Predicting crosses from general combining ability

Under the fixed model a cross is predicted by $\hat{\mu}+\hat{g}_i+\hat{g}_j$ from the gca effects alone (the prediction for a cross not yet made) or by adding $\hat{S}_{ij}+\hat{R}_{ij}$ (which reproduces the observed mean). The gap between the two is the specific combining ability of the cross:

```
pr_g <- predict(object = f1, newdata = NULL, type = c("gca", "full")[1])
pr_f <- predict(object = f1, newdata = NULL, type = c("gca", "full")[2])
pr <- merge(x = pr_g, y = pr_f, by = c("Cross1", "Cross2"), suffixes =
 ↪  c("_gca", "_full"))
head(pr[order(-predicted_full)], 8)
```

```
   Cross1 Cross2 predicted_gca predicted_full
1:      7      8      88.89031        125.270
2:      6      7      96.05125        121.610
3:      1      5      88.48500        120.290
4:      4      1      87.37250        119.115
5:      8      7      88.89031        118.170
6:      3      8      90.67953        117.735
7:      7      6      96.05125        115.670
8:      8      3      90.67953        115.400
```

6 Methods 2, 3 and 4

```
knitr::kable(x = fits[["Method 2"]]$ANOVA, digits = 3)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
gca	7	1850.893	264.413	9.470	0
sca	28	12529.107	447.468	16.026	0
Error	105	2931.770	27.922	NA	NA

```
knitr::kable(x = fits[["Method 3"]]$ANOVA, digits = 3)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
gca	7	5612.432	801.776	26.434	0.000
sca	20	18336.349	916.817	30.227	0.000
reciprocals	28	365.537	13.055	0.430	0.995
Error	165	5004.571	30.331	NA	NA

```
knitr::kable(x = fits[["Method 4"]]$ANOVA, digits = 3)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
gca	7	3126.878	446.697	14.323	0
sca	20	9304.556	465.228	14.917	0
Error	81	2526.151	31.187	NA	NA

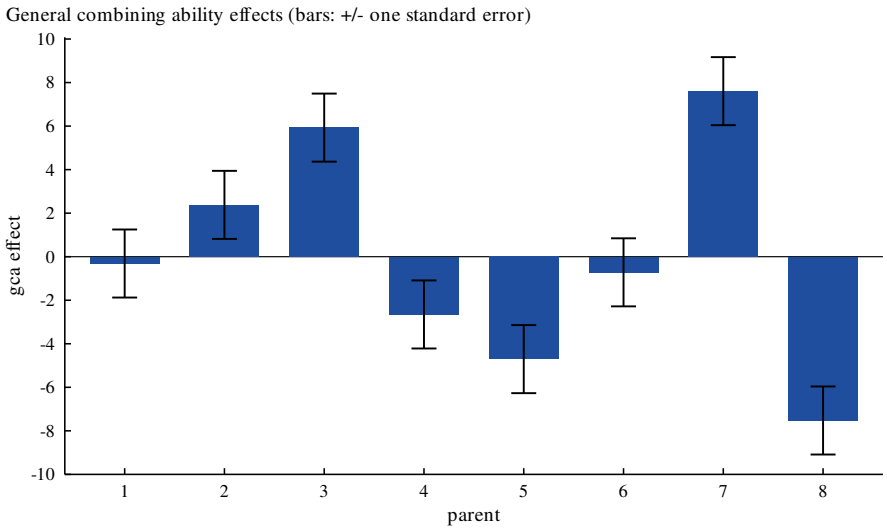
```
round(
    x      = rbind(
        Method1 = fits[[1]]$GCA
      , Method2 = fits[[2]]$GCA
      , Method3 = fits[[3]]$GCA
      , Method4 = fits[[4]]$GCA
      )
  , digits = 2
  )
```

```
            1     2     3     4     5     6     7      8
Method1  0.06  0.47  9.03 -3.44 -2.33 -1.93  7.24  -9.10
Method2 -0.31  2.38  5.93 -2.65 -4.71 -0.72  7.60  -7.52
Method3 -0.09 -1.65 13.80 -5.75  1.99 -5.21  8.60 -11.69
Method4 -0.86 -0.58 13.40 -6.76  2.33 -6.45 10.57 -11.66
```

The best general combiners (parents 3 and 7) and the poorest (parent 8) are the same in all four methods; including the parents themselves (Methods 1, 2) or the reciprocals (Methods 1, 3) changes the size of the effects and the order of the parents in between.

7 Plots

```
plot(fits[["Method 2"]])
```



8 Summary

Model 1 gives the effects of each parent and cross with their standard errors; the `Effects` table keeps the layout of earlier versions and `GCA`, `SCA`, `Reciprocal` give the effects in full.

9 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.