# Griffing's methods with random effects

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## 1 Abstract

With random effects (Model 2), Griffing's analysis estimates the variances of general and specific combining ability and, through them, the additive and dominance variances of the population the parents come from.

## 2 Variance components

```
r1 <-
  Griffing(
      y          = Yield
    , Rep        = Rep
    , Cross1     = Cross1
    , Cross2     = Cross2
    , data       = GriffingData1
    , Method     = 1
    , Model      = 2
    , Reciprocal = c("combined", "split")[1]
    )
knitr::kable(x = r1$ANOVA, digits = 3)
```

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|---|---|---|---|---|---|
| gca | 7 | 3804.643 | 543.520 | 0.690 | 0.680 |
| 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 = r1$Genetic.Components, digits = 3)
```

| | Components |
|---|---|
| gca | -14.440 |
| sca | 426.166 |
| Reciprocal | -7.861 |
| Error | 28.778 |
| Additive | -28.881 |
| Dominant | 426.166 |
| gca/sca | -0.034 |

In the random model gca is tested against sca (the mean square that contains every term of E($MS_g$) except $\sigma^2_g$), and sca and reciprocals against the error.

# 3 All four methods

```
comp <-
  sapply(
      X   = 1:4
    , FUN = function(m) {
        f <-
          Griffing(
              y          = Yield
            , Rep        = Rep
            , Cross1     = Cross1
            , Cross2     = Cross2
            , data       = get(paste0("GriffingData", m))
            , Method     = m
            , Model      = 2
            , Reciprocal = c("combined", "split")[1]
            )
        f$Genetic.Components[c("gca", "sca", "Error"), "Components"]
      }
    )
dimnames(comp) <- list(c("gca", "sca", "Error"), paste("Method", 1:4))
round(x = comp, digits = 2)
```

```
      Method 1 Method 2 Method 3 Method 4
gca      -14.44   -18.31    -9.59    -3.09
sca      426.17   419.55   443.24   434.04
Error     28.78    27.92    30.33    31.19
```

The variance of sca is far larger than that of gca in every method: in this material most of the variation among crosses is non-additive. A negative estimate (here gca) means that the true component is small; it is reported as computed so that the analysis of variance and the components stay consistent.

# 4 Additive and dominance variance

For non-inbred parents without epistasis $\sigma^2_A = 2\sigma^2_g$ and $\sigma^2_D = \sigma^2_s$; their ratio, and the ratio $\sigma^2_g/\sigma^2_s$ (also called the predictability ratio), indicate how far selection on parental performance can predict the crosses.

```
r1$Genetic.Components[c("Additive", "Dominant", "gca/sca"), , drop =
↪  FALSE]
```

```
          Components
Additive -28.8809045
Dominant 426.1656570
gca/sca   -0.0338846
```

# 5 Summary

Model 2 answers a question about a population (how much additive and dominance variance) rather than about the parents tested; its components come from the expected mean squares of vignette 03.

# 6 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.