Line by tester and North Carolina designs

Muhammad Yaseen

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1 Abstract

Not every crossing scheme is a diallel. In a line × tester experiment each of L lines is crossed with each of T testers; the North Carolina designs of Comstock and Robinson estimate additive and dominance variance from half-sib and full-sib families. Both are analysed from the plot data of a randomized complete block experiment, with the same result objects, plots and tables as the diallel analyses.

2 Line × tester analysis

`LineTester()` gives Kempthorne's analysis of L lines crossed with T testers: the split of the crosses into lines, testers and their interaction with the proportional contribution of each, the gca and sca effects with standard errors, and the genetic variances; `Inbreeding` is the inbreeding coefficient F of the parents.

```
lt <-
  LineTester(
      y          = Yield
    , Rep        = Rep
    , Line       = Line
    , Tester     = Tester
```

```
    , data       = LineTesterData
    , Inbreeding = 1
    )
lt
```

```
Line x tester analysis: 8 lines, 3 testers, 3 replicates

              Df Sum Sq Mean Sq F value   Pr(>F)
Rep            2    427   213.3  14.894 1.03e-05 ***
Crosses       23   5469   237.8  16.607 2.76e-15 ***
Lines          7   3476   496.6  34.685 2.70e-16 ***
Testers        2   1038   519.0  36.244 3.54e-10 ***
Lines:Testers 14    955    68.2   4.762 2.76e-05 ***
Error         46    659    14.3
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Proportional contributions (%)
        Lines       Testers Lines:Testers
        63.57         18.98         17.45

Genetic components
                    Components
gca_lines              47.6060
gca_testers            18.7824
gca                    35.1418
sca                    17.9554
gca/sca                 1.9572
Additive               70.2835
Dominance              17.9554
Dominance/Additive      0.2555
Degree of dominance     0.7148
```

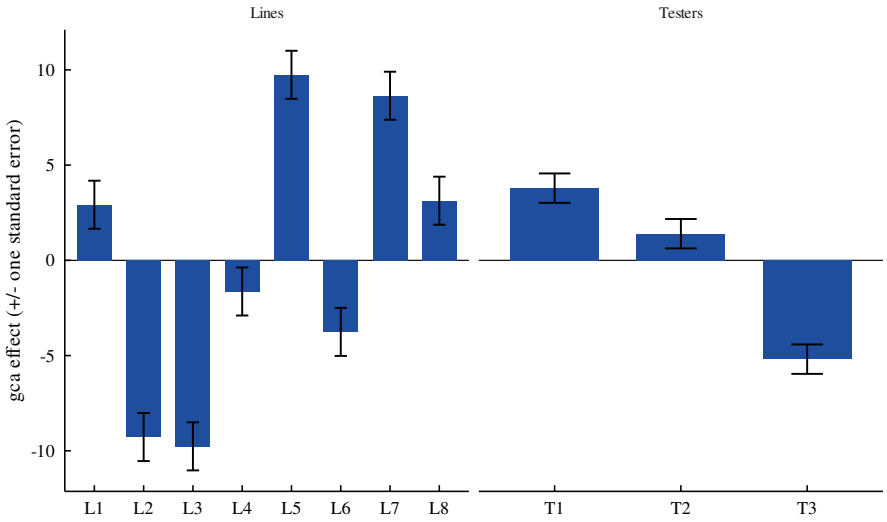
```
round(x = lt$GCA.Lines, digits = 2)
```

```
   L1    L2    L3    L4    L5    L6    L7    L8
 2.92 -9.28 -9.77 -1.63  9.74 -3.76  8.64  3.13
```

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

```
    gca_line   gca_tester          sca   gi_gj_line gi_gj_tester      sij_skl
       1.261        0.772        2.185        1.784        1.092        3.090
```

```
plot(x = lt, which = c("gca", "sca", "contribution", "biplot",
 ↪  "residuals", "qq")[1])
```



3 North Carolina designs

`NCDesign()` analyses the three designs of Comstock and Robinson: females nested in males (Design I), males crossed with females (Design II), and F_2 males backcrossed to both inbred parents (Design III). Each gives the additive and dominance variances and the average degree of dominance $\sqrt{2\sigma_D^2/\sigma_A^2}$.

```
nc <- lapply(X = 1:3, FUN = function(k) {
  NCDesign(
      y           = Yield
    , Rep         = Rep
    , Male        = Male
    , Female      = Female
    , data        = NCData[NCData$Design == k, ]
    , Design      = k
    , Inbreeding = 0
    )
})
nc[[2]]$ANOVA
```

```
              Df Sum Sq Mean Sq F value    Pr(>F)
Rep            2 280.67 140.333 13.6687 3.371e-05 ***
Males          4 250.42  62.605  2.9919  0.062947 .
Females        3 517.45 172.482  8.2428  0.003026 **
Males:Females 12 251.10  20.925  2.0382  0.047573 *
Error         38 390.13  10.267
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
round(
    x      = sapply(
        X   = nc
      , FUN = function(z) z$Genetic.Components[c("Additive", "Dominance",
 ↪  "Degree of dominance"),
                                                                          ↪  "Components"]
                                                                          ↪  ]
      )
  , digits = 3
  )
```

```
       [,1]   [,2]   [,3]
[1,] 11.867 27.154 58.248
[2,] 56.203 14.211 14.806
[3,]  3.078  1.023  0.713
```

4 Summary

`LineTester()` gives combining ability and the contribution of lines, testers and their interaction; `NCDesign()` gives the additive and dominance variances of Designs I, II and III.

5 References

Comstock, R. E. and Robinson, H. F. (1948). The components of genetic variance in populations of biparental progenies and their use in estimating the average degree of dominance. *Biometrics*, 4(4), 254–266.

Kempthorne, O. (1957). *An Introduction to Genetic Statistics*. John Wiley and Sons, New York.

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