Analyses of variance

Muhammad Yaseen

2026-11-03

Table of contents

1 Abstract **1**

2 Each environment **1**

3 Combined analysis **3**

4 Eberhart and Russell **4**

5 Summary **5**

6 References **5**

1 Abstract

The analysis of each environment, the combined analysis and Eberhart and Russell's analysis, with what each tells before the stability statistics.

2 Each environment

```
ia <-
  indiv_anova(
      .data = ge_data
    , .y    = Yield
    , .rep  = Rep
    , .gen  = Gen
    , .env  = Env
    )
ia$Summary
```

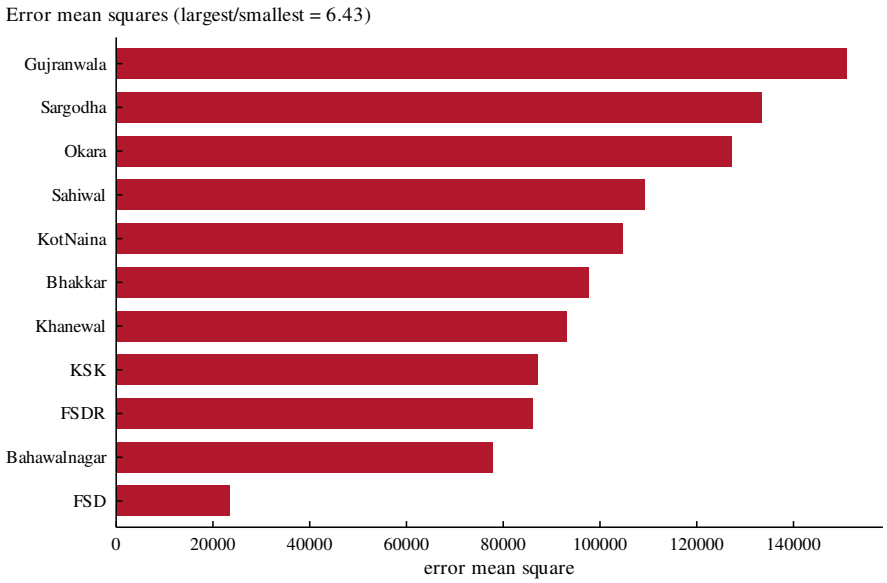
```
  Env     Mean       CV       MSE Df.error     F.Gen        p.Gen
1 FSD 4629.308 3.310148  23481.57       59 32.859696 9.777146e-30
2 FSDR 4063.192 7.219829  86057.45       59  2.761218 7.071620e-05
```

```
3         Okara 3634.433 9.816853 127296.96       59  3.568674 1.206599e-06
4      Sargodha 4605.117 7.929968 133359.54       59  4.878042 3.670660e-09
5    Gujranwala 4014.283 9.678154 150938.88       59  4.700962 7.608923e-09
6      KotNaina 3759.633 8.606654 104703.14       59  4.320895 3.845328e-08
7           KSK 3469.967 8.509432  87187.01       59  3.477938 1.870247e-06
8      Khanewal 4718.567 6.465435  93071.27       59  2.754444 7.328681e-05
9       Sahiwal 4477.833 7.381166 109241.03       59  4.051051 1.274773e-07
10      Bhakkar 3714.667 8.415070  97713.64       59  1.885585 8.069768e-03
11 Bahawalnagar 3581.325 7.787843  77789.65       59  2.117464 2.279749e-03
```

```
ia$Homogeneity
```

```
     Chisq Df     p.value    Ratio
1 53.65762 10 5.61929e-08 6.427973
```

```
plot(x = ia, which = "error")
```



The error mean squares differ more than three-fold; Bartlett's test rejects equality. The combined analysis below still pools them, which is the usual practice, but the comparison of environments should keep this in mind.

```
stab_interpret(
    x             = ia
  , higher_better = TRUE
  , top           = 5
  )
```

```
Analysis of variance in each environment
```

Genotypes differ significantly in 11 of 11 environments; error variances are too heterogeneous for pooling (largest/smallest ratio 6.43).

Findings:
- Environment means range from 3,470 (KSK) to 4,719 (Khanewal).
- Genotypes differ significantly in every environment.
- Coefficients of variation range from 3.3% to 9.8%.
- Bartlett's test of equal error variances: chi-square 53.66 on 10 df, p < 0.001.

Recommendations:
- Pool the environments with care: weight environments by the inverse of their error variance or analyse groups of similar environments.

3 Combined analysis

```
aa <-
  add_anova(
      .data = ge_data
    , .y    = Yield
    , .rep  = Rep
    , .gen  = Gen
    , .env  = Env
    )
aa$anova
```

```
Analysis of Variance Table

Response: y

            Df    Sum Sq  Mean Sq F value    Pr(>F)
Env         10 263940496 26394050 68.0551 1.995e-08 ***
Rep(Env)    11   4266167   387833
Gen         59  71662431  1214617 12.2482 < 2.2e-16 ***
Gen:Env    590 201336476   341248  3.4411 < 2.2e-16 ***
Residuals  649  64359568    99167
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
aa$Summary
```

```
      Mean       CV Genotypes Environments Replicates  Env.pct  Gen.pct
1 4060.757 7.754918        60           11          2 49.15648 13.34647
   GxE.pct
1 37.49706
```

The interaction is significant and larger than the genotype effect: genotype means alone would mislead.

4 Eberhart and Russell

```
er <-
  er_anova(
      .data = ge_data
    , .y    = Yield
    , .rep  = Rep
    , .gen  = Gen
    , .env  = Env
    )
er$er_anova[c(1:6, nrow(er$er_anova)), ]
```

```
                     Df    Sum Sq Mean Sq F value  Pr(>F)
Total               659 268469701
Gen                  59  35831215  607309  3.7773 < 2e-16 ***
Env + (Gen x Env)   600 232638486
  Env (linear)        1 131970248
  Gen x Env(linear)  59  13847665  234706  1.4598 0.01781 *
  Pooled deviation  540  86820573  160779
Pooled error        649  32179784   49584
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
head(x = er$Parameters[order(-Mean)], n = 8)
```

```
            Gen     Mean     Slope        SE       p.b1        S2d        p.S2d
1:        DN126 4480.864 1.7107903 0.2411656 0.01629193  78341.346 6.340228e-03
2:       V14170 4463.818 1.2797954 0.3002920 0.37578673 148757.234 5.435608e-05
3:        PR115 4444.273 0.8154056 0.2401408 0.46176985  77256.484 6.793988e-03
4:     12B.2511 4414.409 1.6375025 0.2843871 0.05170192 128303.522 2.261371e-04
5:       V14154 4364.727 0.6902389 0.1384097 0.05201277  -7447.194 5.703363e-01
6: FAISALABAD08 4360.591 1.5736825 0.3009176 0.08896639 149584.475 5.128356e-05
7:       V14168 4342.045 0.9672779 0.2755105 0.90806723 117372.034 4.787298e-04
8:        NR491 4319.500 1.5680940 0.2641503 0.05997351 103887.622 1.190712e-03
```

```
stab_interpret(
    x             = er
  , higher_better = TRUE
  , top           = 5
  )
```

```
Eberhart and Russell's stability analysis

2 of 60 genotypes meet Eberhart and Russell's criteria (mean above average,
```

```
slope not different from 1, no significant deviations): V14154 and PR119.

Findings:
- Genotypes differ when tested against the pooled deviation (p < 0.001).
- The linear part of the interaction (differences between slopes) is
  significant (p = 0.018): genotypes respond differently to better
  environments.
- The deviations from regression are significant overall (p < 0.001); 55
  genotype(s) have significant deviations and so an unpredictable response.
- Slopes significantly above 1 (responsive to favourable environments): DN126
  and 122557.
- Slopes significantly below 1 (better suited to poor environments):
  BARDC1016.

Recommendations:
- For wide adaptation consider V14154 and PR119.
- Genotypes with slopes above 1 suit high-input, favourable environments.
- Genotypes with slopes below 1 suit low-input or stress-prone environments.

Cautions:
- Because deviations from regression are large, the slope explains only part
  of the interaction; use AMMI or the GGE biplot as well.
- The environment index is computed from the same genotypes; with few
  environments the slopes are imprecise.
```

5 Summary

`indiv_anova()` checks precision and the pooling of errors, `add_anova()` the size of the interaction, and `er_anova()` splits it into a linear part (different slopes) and deviations (unpredictable response).

6 References

Eberhart, S. A. and Russell, W. A. (1966). Stability parameters for comparing varieties. *Crop Science*, 6(1), 36–40.

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