AMMI analysis and AMMI stability values

Muhammad Yaseen

2026-11-03

Table of contents

1 Abstract **1**

2 The model **1**

3 Biplots **3**

4 Stability values **5**

5 Summary **8**

6 References **8**

1 Abstract

The AMMI model, its biplots and the stability values built on its axes.

2 The model

```
am <-
  ammi(
      .data = ge_data
    , .y    = Yield
    , .rep  = Rep
    , .gen  = Gen
    , .env  = Env
    )
am$pc_anova
```

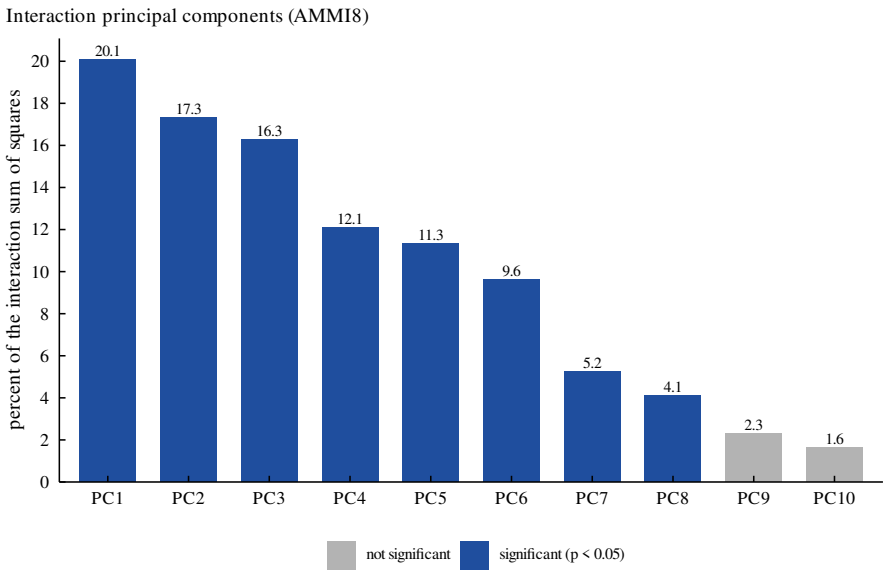
```
      PC  SingVal   Percent AccumPerc Df       SS    MeanSq    Fvalue
 1:  PC1 4496.142 20.081104  20.08110 68 40430588 594567.47 5.9956010
 2:  PC2 4174.531 17.311027  37.39213 66 34853411 528081.98 5.3251633
 3:  PC3 4046.566 16.266000  53.65813 64 32749392 511709.24 5.1600611
```

```
 4:  PC4 3489.555 12.096162  65.75429 62 24353985 392806.22 3.9610464
 5:  PC5 3380.195 11.349876  77.10417 60 22851440 380857.33 3.8405542
 6:  PC6 3113.224  9.627826  86.73199 58 19384326 334212.52 3.3701893
 7:  PC7 2297.953  5.245534  91.97753 56 10561173 188592.38 1.9017601
 8:  PC8 2030.472  4.095450  96.07298 54  8245635 152696.94 1.5397915
 9:  PC9 1521.907  2.300825  98.37380 52  4632399  89084.60 0.8983265
10: PC10 1279.478  1.626196 100.00000 50  3274127  65482.53 0.6603240
           ProbF
 1: 2.428622e-36
 2: 1.511108e-30
 3: 1.150112e-28
 4: 3.679112e-19
 5: 7.571781e-18
 6: 4.018722e-14
 7: 1.448407e-04
 8: 9.520167e-03
 9: 6.770319e-01
10: 9.659157e-01
```

```
am$ammi_model
```

```
[1] "AMMI8"
```

```
plot(x = am, which = "scree")
```




```
stab_interpret(
    x             = am
```

```
  , higher_better = TRUE
  , top           = 5
  )
```

```
AMMI analysis

AMMI8: 8 interaction axes are significant; the first two axes explain 20.1%
and 17.3% of the interaction.

Findings:
- The interaction is significant (p < 0.001).
- Genotypes with a mean above average and the smallest first-axis scores
  (stable): NIBGE GANDUM3, PR119, V14154, V14170 and TWS12464.
- Environments with the strongest interaction (largest first-axis scores):
  Gujranwala, FSD and KSK; the weakest: FSDR, Sahiwal and Khanewal.
- Genotypes and environments with first-axis scores of the same sign interact
  positively (the genotype does better there than its mean predicts).

Recommendations:
- Use AMMI8 for predictions and the stability indices (stab_asv(),
  stab_masv() with .m = 8).
- Look at the AMMI1 biplot (plot(x, which = "ammi1")) to see mean and
  interaction together.

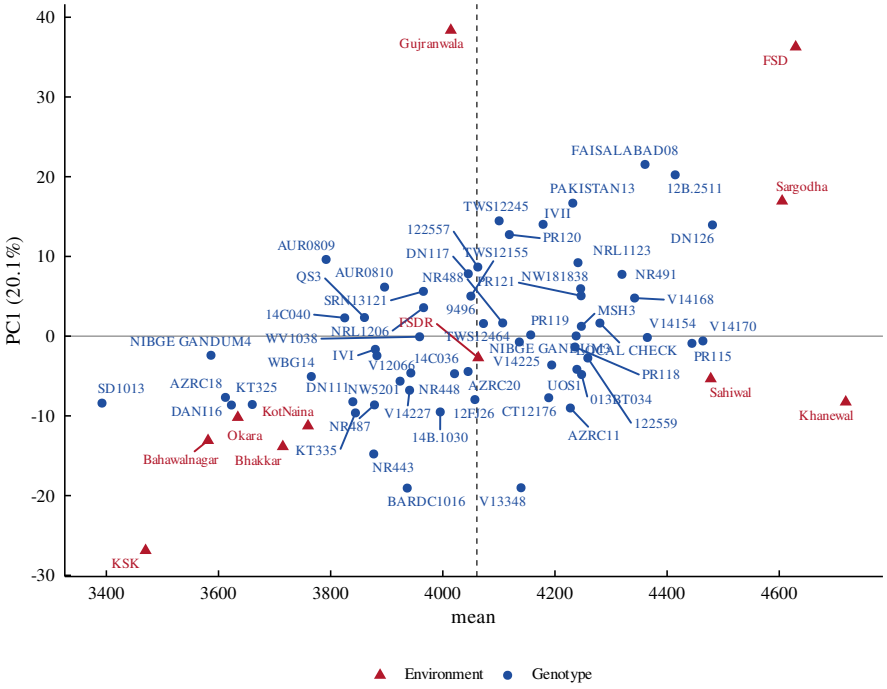
Cautions:
- The first two axes explain less than half of the interaction; biplots show
  it only partly.
```

3 Biplots

```
ab <-
  ammi_biplot(
      .data = ge_data
    , .y    = Yield
    , .rep  = Rep
    , .gen  = Gen
    , .env  = Env
    )
plot(x = ab, which = "ammi1")
```

AMMI1 biplot

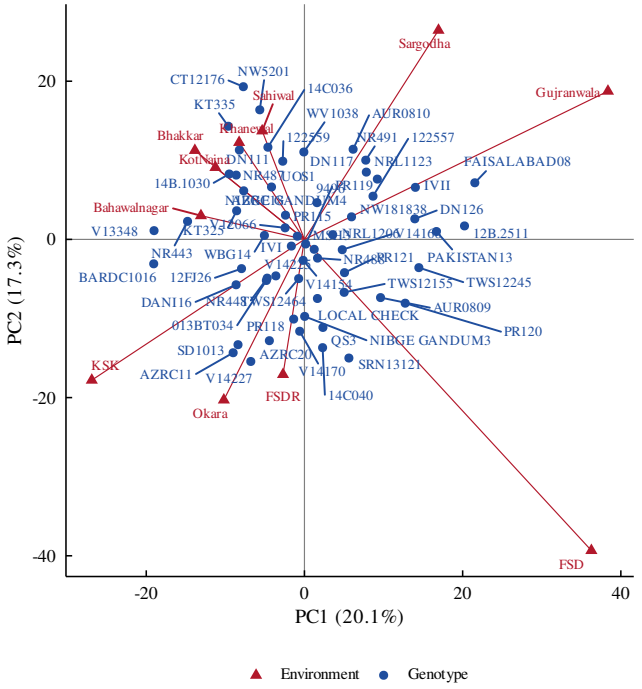
right of the dashed line: above the grand mean; near PC1 = 0: stable




```
plot(x = ab, which = "ammi2")
```

AMMI2 biplot

near the origin: small interaction (stable); long environment vectors: strong interaction



4 Stability values

```
asv <-
  stab_asv(
      .data = ge_data
    , .y    = Yield
    , .rep  = Rep
    , .gen  = Gen
    , .env  = Env
    )
head(x = asv$ASD, n = 6)
```

	Gen	Mean	ASD	rMean	rASD	YSI	PC1	PC2
1:	PR115	4444.273	1.1235033	3	2	5	-0.9031507	0.4057644
2:	V14154	4364.727	2.6556975	5	5	10	-0.1647526	-2.6488118
3:	MSH3	4247.045	1.9014683	12	3	15	1.2330175	-1.2529001
4:	V14168	4342.045	5.6958779	7	12	19	4.7800620	-1.3024826
5:	PR119	4156.727	0.6095297	24	1	25	0.1556221	-0.5821833
6:	LOCAL CHECK	4280.136	7.7084442	9	19	28	1.6384767	-7.4704480

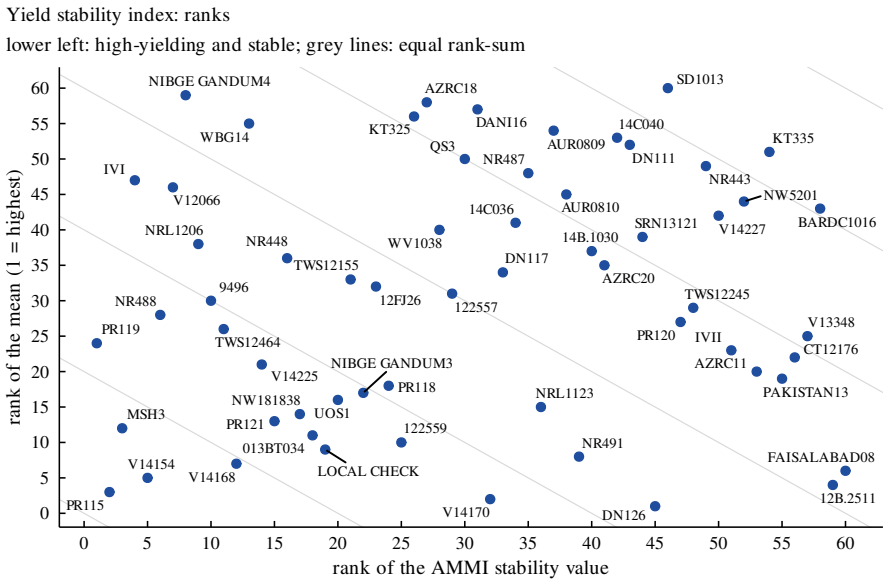
```
masv <-
  stab_masv(
      .data = ge_data
    , .y    = Yield
    , .rep  = Rep
    , .gen  = Gen
    , .env  = Env
    , .m    = 4
    )
head(x = masv$MASD, n = 6)
```

```
           Gen     Mean      MASD rMean rMASD MYSI
1:      V14154 4364.727  3.893937     5     1    6
2:       PR115 4444.273 12.339474     3    11   14
3:    013BT034 4247.500  7.787213    11     3   14
4: LOCAL CHECK 4280.136 12.868956     9    14   23
5:        UOS1 4239.091 11.462978    16     9   25
6:      V14225 4194.182  8.494185    21     5   26
```

```
dst <-
  stab_dist(
      .data = ge_data
    , .y    = Yield
    , .rep  = Rep
    , .gen  = Gen
    , .env  = Env
    , .m    = 4
    )
head(x = dst$stabDist, n = 6)
```

```
           Gen     Mean      Dist rMean rDist YSIDist
1:      V14154 4364.727  3.696609     5     1       6
2:       PR115 4444.273 11.318617     3    12      15
3:    013BT034 4247.500  7.394034    11     4      15
4: LOCAL CHECK 4280.136 12.514985     9    16      25
5:        UOS1 4239.091 11.101746    16    10      26
6:      V14225 4194.182  7.893190    21     5      26
```

```
plot(x = asv, which = "ranks")
```



`stab_masv()` is the MASV of Zali et al. (2012). The earlier versions computed it on two axes; the function now takes any number of axes `.m`, from 2 to the number of non-zero interaction axes. The ratio of the sums of squares of each axis to the next weighs the first axes heavily. `stab_dist()` is the AMMI stability distance developed by the package author: the Euclidean distance from the origin over the first `.m` axes of the AMMI scores, in which every axis enters only through its scores. Use for `.m` the number of significant axes found by `ammi()`.

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

```
Modified AMMI stability value

Best on the yield stability index (yield and stability ranks together):
V14154, PR115, 013BT034, LOCAL CHECK and UOS1.

Findings:
- Smallest modified AMMI stability value (most stable in the AMMI sense):
  V14154, NIBGE GANDUM4, 013BT034, PR119 and V14225.
- 17 genotype(s) combine a mean above average with a modified AMMI stability
  value below the median.
- The rank correlation between mean and modified AMMI stability value is
  0.03.
```

```
Recommendations:
- Consider V14154, PR115 and 013BT034; check their adaptation in the AMMI or
  GGE biplot.

Cautions:
- The index rests on the AMMI axes it uses; when more axes are significant
  (see ammi()), stab_masv() with more axes is more complete.
```

5 Summary

Many significant axes mean the interaction has several independent patterns; the first two show only part of it, and indices over more axes (`stab_masv()`) describe the stability more fully.

6 References

Gauch, H. G. (1992). *Statistical Analysis of Regional Yield Trials: AMMI Analysis of Factorial Designs*. Elsevier, Amsterdam.

Gollob, H. F. (1968). A statistical model which combines features of factor analytic and analysis of variance techniques. *Psychometrika*, 33(1), 73–115.

Purchase, J. L., Hatting, H. and van Deventer, C. S. (2000). Genotype x environment interaction of winter wheat in South Africa: II. Stability analysis of yield performance. *South African Journal of Plant and Soil*, 17(3), 101–107.

Zali, H., Farshadfar, E., Sabaghpour, S. H. and Karimizadeh, R. (2012). Evaluation of genotype x environment interaction in chickpea using measures of stability from AMMI model. *Annals of Biological Research*, 3(7), 3126–3136.