Inference on the biplot

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2026-11-04

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1 Abstract

A least-squares AMMI biplot shows point estimates only. Its Bayesian counterpart gives every genotype and environment a highest posterior density (HPD) region. A region that contains the origin marks a stable genotype or environment, regions that overlap mark a homogeneous group, and the marginal interval on the first term decides the direction of the interaction. This vignette shows how `biplots()` builds the regions and how to read them.

2 The coordinates

For draw s the point of genotype i is $\left(\lambda_1^{(s)1/2}\alpha_{i1}^{(s)}, \lambda_2^{(s)1/2}\alpha_{i2}^{(s)}\right)$. The draws of a genotype form a cloud whose shape shows the uncertainty of its interaction.

```
fit <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
```

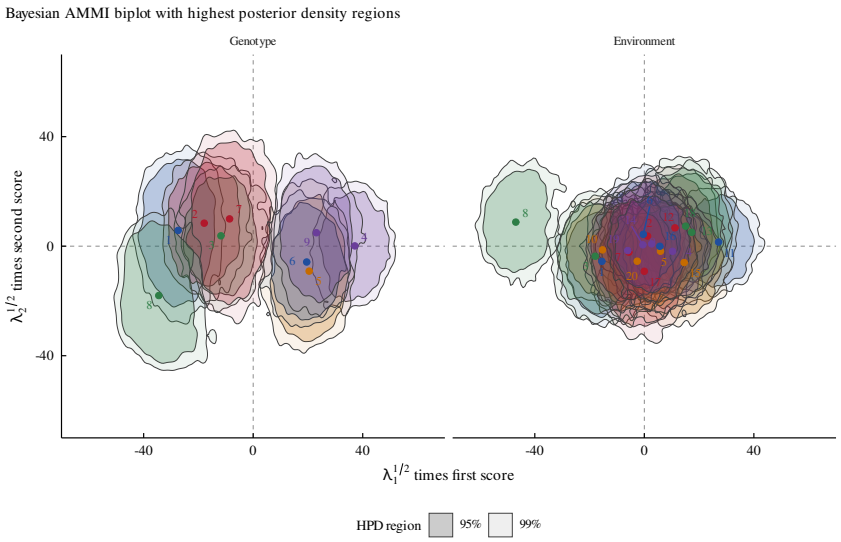
```
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 6000
    , .k      = 2
    , .burnin = 1000
    , .thin   = 1
    , .chains = 2
    , .priors = bam_priors(
          mu_mean     = 0
        , mu_var      = 1e+8
        , tau_mean    = 0
        , tau_var     = 1e+8
        , delta_mean  = 0
        , delta_var   = 1e+8
        , lambda_mean = 0
        , lambda_var  = 1e+8
        , nu          = 1
        , s2          = NULL
        )
    , .level  = 0.95
    , .seed   = 4
    , .align  = TRUE
    , .model  = "AMMI"
    , .het    = FALSE
    , .waic   = TRUE
    )
```

3 HPD regions

A bivariate kernel density $\hat{f}$ is estimated from the cloud. The $100(1-p)\%$ HPD region is the set where $\hat{f}$ exceeds the p-quantile of $\hat{f}$ at the draws, so it holds $100(1-p)\%$ of them and is the smallest such set (Hyndman 1996). It contains the origin exactly when $\hat{f}(\mathbf{0})$ reaches that quantile.

```
bp <-
  biplots(
      model         = fit
    , burnin        = 0
    , thin          = 0.5
    , pb            = c(0.05, 0.01)
    , plot_stable   = TRUE
    , plot_unstable = TRUE
    , ncolors       = 5
    , .which        = "both"
    , .grid         = 100
    )
```

```
bp$biplot
```



4 Stable genotypes and environments

```
bp$biplot_data[, list(byplot, name, x, y, stable, axis1_lower,
↪  axis1_upper, group)]
```

	byplot	name	x	y	stable	axis1_lower	axis1_upper
1:	Genotype	1	-27.39165676	5.76438212	FALSE	-38.27946935	-16.186961
2:	Genotype	2	-17.88925076	8.40300672	FALSE	-28.32124518	-6.547069
3:	Genotype	3	-11.78567779	3.78193269	TRUE	-22.73533406	-1.082809
4:	Genotype	4	37.11735449	0.09401861	FALSE	26.60001160	46.697197
5:	Genotype	5	20.43844153	-9.10673615	FALSE	9.03528012	31.512507
6:	Genotype	6	19.54334049	-5.78161457	FALSE	8.91289231	30.093179
7:	Genotype	7	-8.63141072	9.96597984	TRUE	-19.98012491	4.090398
8:	Genotype	8	-34.47493736	-18.02866280	FALSE	-45.52039819	-22.302477
9:	Genotype	9	23.07379688	4.90769355	FALSE	12.32697873	33.828219
10:	Environment	1	-15.50657921	-5.55082820	FALSE	-26.34872405	-4.743675
11:	Environment	2	1.17617282	3.68818862	TRUE	-9.69787599	12.000181
12:	Environment	3	-17.92256587	-3.66236650	FALSE	-28.83775413	-6.725737
13:	Environment	4	10.29797179	-1.87419076	TRUE	-0.05076488	21.354530
14:	Environment	5	5.90081820	-1.84457566	TRUE	-5.09290073	16.566620
15:	Environment	6	-0.37997269	4.32224532	TRUE	-10.77625345	10.981398
16:	Environment	7	-5.64668555	-2.18620563	TRUE	-16.65112969	4.768966
17:	Environment	8	-46.94161098	8.79385892	FALSE	-56.69780534	-36.925315
18:	Environment	9	2.67647433	0.83060165	TRUE	-8.35287890	13.265884

```
19: Environment   10 -15.28337774  -1.34734626  FALSE -25.39295576   -4.598291
20: Environment   11  27.11174574   1.51012117  FALSE  16.85410381   37.375407
21: Environment   12  11.17082006   6.69505350   TRUE  -0.28560818   21.643977
22: Environment   13  17.28972011   5.07043354  FALSE   5.48043438   27.665171
23: Environment   14  -0.54832049   0.49671271   TRUE -11.70112079    9.279971
24: Environment   15  14.55743946  -5.97775500  FALSE   3.28371897   25.392452
25: Environment   16   5.66452684  -0.03517786   TRUE  -4.62622081   16.839005
26: Environment   17  -0.01626159  -9.16130318   TRUE -11.30940962   10.851369
27: Environment   18  15.08382629   7.31282769  FALSE   3.72421775   25.565660
28: Environment   19  -6.06837963  -1.59997864   TRUE -17.33199141    4.525090
29: Environment   20  -2.61576189  -5.48031542   TRUE -13.60933486    7.968492
         byplot name            x            y stable  axis1_lower axis1_upper
              group
 1:        negative
 2:        negative
 3:        negative
 4:        positive
 5:        positive
 6:        positive
 7: not significant
 8:        negative
 9:        positive
10:        negative
11: not significant
12:        negative
13: not significant
14: not significant
15: not significant
16: not significant
17:        negative
18: not significant
19:        negative
20:        positive
21: not significant
22:        positive
23: not significant
24:        positive
25: not significant
26: not significant
27:        positive
28: not significant
29: not significant
              group
```

- `stable = TRUE`: the 95% region contains the origin, so the interaction of the genotype (environment) is not different from zero on the two terms

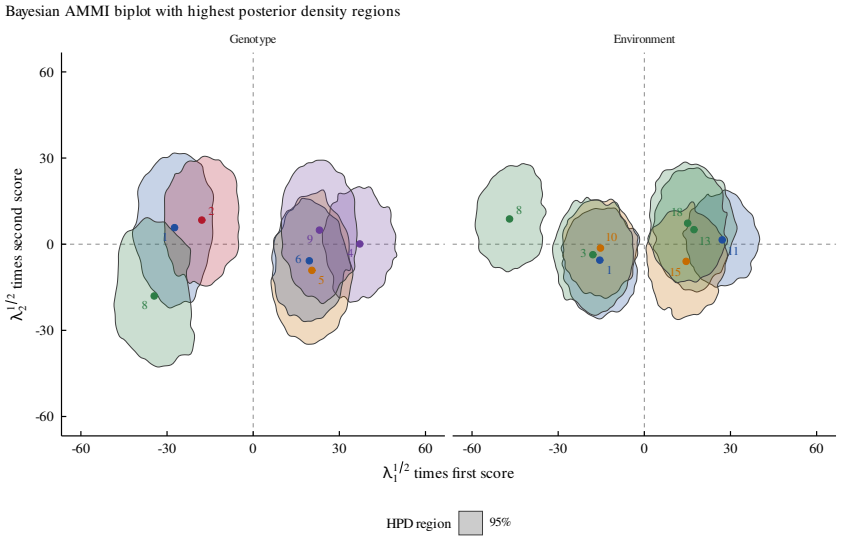
jointly.

- `group`: the marginal 95% HPD interval of the first coordinate. “positive” and “negative” groups interact in opposite directions; the paper uses this criterion.

A genotype can be stable in the joint sense and still have a first coordinate that differs from zero. This happens when the second term is so uncertain that the region stretches over the origin along the second axis.

5 Only the unstable ones

```
bp_u <-
  biplots(
      model          = fit
    , burnin         = 0
    , thin           = 0.5
    , pb             = 0.05
    , plot_stable    = FALSE
    , plot_unstable  = TRUE
    , ncolors        = 5
    , .which         = "both"
    , .grid          = 100
    )
bp_u$biplot
```



6 Reading genotype and environment together

A genotype yields more than its main effects predict in environments whose first scores have the same sign as its own, and less where the signs differ. The genotypes in the positive group are therefore adapted to the environments in the positive group.

```
bam_interpret(
    x             = bp
  , higher_better = TRUE
  , top           = 5
  )
```

```
Biplot with highest posterior density regions

7 of 9 genotypes and 8 of 20 environments have a 95% HPD region that excludes
the origin (significant interaction).

Findings:
- Genotypes whose region contains the origin (interaction not different from
  zero, stable): 3 and 7.
- Groups on the first term (marginal HPD interval excludes zero): positive 4,
  5, 6 and 9; negative 1, 2, 3 and 8.
- Environments on the first term: positive 11, 13, 15 and 18; negative 1, 3,
  8 and 10; the others do not differ from zero.
- Overlapping regions mark genotypes (environments) whose interaction
  parameters do not differ: a homogeneous group.

Recommendations:
- Genotypes 4, 5, 6 and 9 are adapted to environments 11, 13, 15 and 18 (both
  positive on the first term).
- Genotypes 1, 2, 3 and 8 are adapted to environments 1, 3, 8 and 10 (both
  negative on the first term).

Cautions:
- The regions are estimated from the draws by a kernel density; with few
  draws their outline is rough.
- The second term is usually estimated with much more uncertainty than the
  first: long regions along the second axis.

Sources:
- Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J. M., Viele, K., Liu,
  G. and Cornelius, P. L. (2011). Bayesian estimation of the additive main
  effects and multiplicative interaction model. Crop Science, 51(4),
  1458-1469. doi:10.2135/cropsci2010.06.0343
```

7 References

Crossa, J., Perez-Elizalde, S., Jarquin, D., Cotes, J. M., Viele, K., Liu, G. and Cornelius, P. L. (2011). Bayesian estimation of the additive main effects and multiplicative interaction model. *Crop Science*, 51(4), 1458–1469. doi:10.2135/cropsci2010.06.0343

Hyndman, R. J. (1996). Computing and graphing highest density regions. *The American Statistician*, 50(2), 120–126.