Reproducing Crossa et al. (2011)

Muhammad Yaseen

2026-11-04

Table of contents

1 Abstract **1**

2 The run of the paper **1**

3 Table 1 **2**
3.1 The error variance 4

4 Table B1: the first term **5**

5 Table B1: the second term **6**

6 Figure 1: traces and histograms of the singular values **8**

7 Figures 2 to 4: biplots **10**

8 References **12**

1 Abstract

Crossa et al. (2011) fitted the Bayesian AMMI model with two bilinear terms to the maize trial `Maiz`. They ran two chains of 35000 iterations, discarded a burn-in of 5000 and thinned by 2. This vignette repeats that run and compares the posterior summaries with their Tables 1 and B1. The overall mean, the error variance, the main effects, the singular values and the scores of the first term agree within Monte Carlo error. The second scores differ, for a reason the paper does not discuss: the sign of a weak term.

2 The run of the paper

```
fit <-
  bayes_ammi(
```

```
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 30000
    , .k      = 2
    , .burnin = 5000
    , .thin   = 2
    , .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   = 2011
    , .align  = TRUE
    , .model  = "AMMI"
    , .het    = FALSE
    , .waic   = TRUE
    )
fit$settings$seconds
```

```
[1] 13.451
```

3 Table 1

```
pub <- utils::read.csv(file = system.file("extdata", "crossa2011.csv",
 ↪  package = "bayesammi"))
s <- fit$summary
t1 <- merge(x = pub[pub$table == "1", ], y = s[, list(parameter, mean,
 ↪  sd, lower, upper)],
            by = "parameter", suffixes = c(".paper", ".here"), sort =
             ↪  FALSE)
t1$dev_sd <- round(x = (t1$mean.here - t1$mean.paper) / t1$sd.paper,
 ↪  digits = 3)
num <- c("mean.paper", "mean.here", "sd.paper", "sd.here", "lower.paper",
 ↪  "lower.here", "upper.paper", "upper.here")
t1[num] <- lapply(X = t1[num], FUN = signif, digits = 5)
```

```
t1[, c("parameter", "mean.paper", "mean.here", "sd.paper", "sd.here",
 ↪  "dev_sd")]
```

```
   parameter mean.paper  mean.here sd.paper   sd.here dev_sd
1         mu    4858.00   4857.600    32.71    32.539 -0.012
2     sigma2  763600.00 762820.000 43580.00 43631.000 -0.018
3     tau[1]    -241.70   -241.050    91.78    92.348  0.007
4     tau[2]    -255.00   -254.360    91.97    91.456  0.007
5     tau[3]     -34.66    -35.607    91.75    91.862 -0.010
6     tau[4]     359.20    359.270    91.68    92.234  0.001
7     tau[5]     389.70    388.110    92.32    91.983 -0.017
8     tau[6]     472.50    471.850    91.47    92.025 -0.007
9     tau[7]    -186.00   -185.970    92.19    92.082  0.000
10    tau[8]    -574.90   -574.570    91.69    91.876  0.004
11    tau[9]      70.95     72.330    91.90    91.695  0.015
12  delta[1]   -1245.00  -1244.600   141.80   142.300  0.003
13  delta[2]    -647.30   -649.780   141.50   142.460 -0.018
14  delta[3]     246.60    246.630   141.60   141.440  0.000
15  delta[4]     371.60    371.080   141.60   142.390 -0.004
16  delta[5]      96.01     97.451   141.60   141.430  0.010
17  delta[6]    1448.00   1447.300   141.60   140.490 -0.005
18  delta[7]   -1629.00  -1627.500   142.40   141.550  0.011
19  delta[8]    -830.60   -831.110   142.50   142.130 -0.004
20  delta[9]     111.70    113.250   141.80   142.240  0.011
21 delta[10]   -1921.00  -1920.500   141.80   141.840  0.003
22 delta[11]     449.20    449.080   143.00   143.990 -0.001
23 delta[12]    2659.00   2656.400   141.90   141.660 -0.018
24 delta[13]    1474.00   1473.400   142.60   141.550 -0.004
25 delta[14]    1194.00   1192.900   141.80   141.030 -0.008
26 delta[15]     189.30    189.090   141.60   141.600 -0.002
27 delta[16]     549.30    548.820   142.40   143.030 -0.003
28 delta[17]      17.62     18.970   141.70   142.970  0.010
29 delta[18]    -305.50   -306.320   142.00   142.840 -0.006
30 delta[19]   -2207.00  -2205.100   141.40   140.800  0.014
31 delta[20]     -19.72    -19.467   140.80   141.200  0.002
32 lambda[1]    5483.00   5470.700   458.40   455.830 -0.027
33 lambda[2]    1627.00   1658.100   786.80   775.400  0.040
```

```
t1[, c("parameter", "lower.paper", "lower.here", "upper.paper",
 ↪  "upper.here")]
```

```
   parameter lower.paper lower.here upper.paper upper.here
1         mu   4792.9000   4793.000   4921.0000   4920.100
2     sigma2 680570.0000 677110.000 849750.0000 847100.000
3     tau[1]   -421.8000   -419.590    -61.8490    -56.881
4     tau[2]   -433.0500   -435.610    -72.3490    -78.355
```

5	tau[3]	-213.5800	-216.420	147.9200	144.300
6	tau[4]	180.6000	175.520	541.1600	535.570
7	tau[5]	206.3700	206.740	567.9200	566.120
8	tau[6]	296.9900	295.540	655.4900	654.760
9	tau[7]	-363.9800	-369.400	-3.5244	-9.515
10	tau[8]	-758.7400	-749.270	-401.0400	-392.460
11	tau[9]	-107.7900	-107.690	247.4000	252.980
12	delta[1]	-1518.8000	-1530.600	-963.8600	-974.240
13	delta[2]	-925.3100	-925.220	-373.4200	-363.950
14	delta[3]	-28.9430	-22.012	525.8100	529.360
15	delta[4]	93.7570	89.982	647.7600	649.060
16	delta[5]	-186.8900	-180.950	365.2200	371.100
17	delta[6]	1170.0000	1178.100	1722.1000	1726.200
18	delta[7]	-1906.1000	-1893.700	-1351.2000	-1337.500
19	delta[8]	-1111.0000	-1111.500	-552.4400	-556.380
20	delta[9]	-164.9300	-166.010	391.3200	392.030
21	delta[10]	-2191.5000	-2197.800	-1637.0000	-1645.900
22	delta[11]	176.6500	168.460	738.1900	729.650
23	delta[12]	2387.1000	2385.300	2942.4000	2937.800
24	delta[13]	1188.2000	1194.900	1748.4000	1745.400
25	delta[14]	914.8800	912.030	1470.3000	1463.600
26	delta[15]	-95.9140	-89.349	457.7000	462.400
27	delta[16]	265.9100	265.810	821.7100	826.410
28	delta[17]	-265.4700	-254.970	290.3300	301.350
29	delta[18]	-588.1600	-585.660	-34.3380	-28.091
30	delta[19]	-2481.3000	-2481.600	-1928.5000	-1930.300
31	delta[20]	-289.2900	-300.400	261.1700	250.560
32	lambda[1]	4573.8000	4581.700	6366.0000	6364.600
33	lambda[2]	2.0887	13.071	2822.7000	2833.800

The column `dev_sd` is the difference of the posterior means in units of the posterior standard deviation; its largest absolute value is 0.04. Both columns are Monte Carlo estimates, so they agree up to Monte Carlo error.

3.1 The error variance

The paper reports a prior scale of $S_0 = 10^8$ with $\nu = 1$, but its posterior of σ^2 (mean 763600) is what a vague prior gives. Taken literally, with $S_0^2 = 10^8$, the prior would add $10^8/721$ to the posterior mean:

```
fit_s2 <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
```

```
    , .nIter  = 3000
    , .k      = 2
    , .burnin = 500
    , .thin   = 1
    , .chains = 1
    , .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          = 1e8
        )
    , .level  = 0.95
    , .seed   = 1
    , .align  = TRUE
    , .model  = "AMMI"
    , .het    = FALSE
    , .waic   = TRUE
    )
c(default = s[parameter == "sigma2", mean], s2_1e8 =
 ↪  fit_s2$summary[parameter == "sigma2", mean])
```

```
 default   s2_1e8
762815.3 922193.4
```

The package therefore defaults to the least-squares residual mean square as the scale, which reproduces Table 1.

4 Table B1: the first term

```
b1 <-
  merge(
      x        = pub[pub$table == "B1" & grepl(pattern = ",1\\]$", x =
       ↪  pub$parameter), ]
    , y        = s[, list(parameter, mean, sd, lower, upper)]
    , by       = "parameter"
    , suffixes = c(".paper", ".here")
    , sort     = FALSE
    )
b1$dev_sd <- round(x = (b1$mean.here - b1$mean.paper) / b1$sd.paper,
 ↪  digits = 3)
b1[c("mean.here", "sd.here")] <- lapply(X = b1[c("mean.here",
 ↪  "sd.here")], FUN = round, digits = 4)
```

```
b1[, c("parameter", "mean.paper", "mean.here", "sd.paper", "sd.here",
 ↪  "dev_sd")]
```

```
     parameter mean.paper mean.here sd.paper sd.here dev_sd
1   gamma[1,1]    -0.2110   -0.2121   0.0751  0.0751 -0.015
2   gamma[2,1]     0.0169    0.0163   0.0757  0.0755 -0.008
3   gamma[3,1]    -0.2427   -0.2426   0.0752  0.0748  0.001
4   gamma[4,1]     0.1389    0.1389   0.0734  0.0741  0.000
5   gamma[5,1]     0.0811    0.0808   0.0754  0.0751 -0.005
6   gamma[6,1]    -0.0068   -0.0055   0.0766  0.0765  0.017
7   gamma[7,1]    -0.0763   -0.0765   0.0753  0.0761 -0.003
8   gamma[8,1]    -0.6353   -0.6340   0.0613  0.0614  0.021
9   gamma[9,1]     0.0359    0.0358   0.0752  0.0751 -0.002
10 gamma[10,1]    -0.2052   -0.2056   0.0729  0.0730 -0.005
11 gamma[11,1]     0.3673    0.3676   0.0690  0.0690  0.005
12 gamma[12,1]     0.1510    0.1516   0.0754  0.0762  0.008
13 gamma[13,1]     0.2358    0.2356   0.0761  0.0764 -0.003
14 gamma[14,1]    -0.0058   -0.0066   0.0743  0.0740 -0.011
15 gamma[15,1]     0.1950    0.1960   0.0755  0.0752  0.013
16 gamma[16,1]     0.0746    0.0747   0.0739  0.0740  0.002
17 gamma[17,1]    -0.0008   -0.0004   0.0783  0.0781  0.006
18 gamma[18,1]     0.2042    0.2040   0.0769  0.0769 -0.003
19 gamma[19,1]    -0.0826   -0.0836   0.0761  0.0770 -0.013
20 gamma[20,1]    -0.0343   -0.0343   0.0760  0.0761  0.001
21  alpha[1,1]    -0.3724   -0.3703   0.0742  0.0748  0.028
22  alpha[2,1]    -0.2416   -0.2407   0.0756  0.0759  0.012
23  alpha[3,1]    -0.1603   -0.1610   0.0753  0.0754 -0.009
24  alpha[4,1]     0.5016    0.5020   0.0647  0.0645  0.006
25  alpha[5,1]     0.2756    0.2759   0.0775  0.0773  0.003
26  alpha[6,1]     0.2649    0.2639   0.0727  0.0735 -0.013
27  alpha[7,1]    -0.1152   -0.1158   0.0827  0.0820 -0.007
28  alpha[8,1]    -0.4661   -0.4676   0.0776  0.0782 -0.019
29  alpha[9,1]     0.3135    0.3136   0.0741  0.0735  0.002
```

The largest absolute deviation is 0.028 posterior standard deviations.

5 Table B1: the second term

```
b2 <-
  merge(
      x        = pub[pub$table == "B1" & grepl(pattern = ",2\\]$", x =
       ↪  pub$parameter), ]
    , y        = s[, list(parameter, mean, sd)]
    , by       = "parameter"
    , suffixes = c(".paper", ".here")
```

```
    , sort     = FALSE
    )
b2[c("mean.here", "sd.here")] <- lapply(X = b2[c("mean.here",
 ↪  "sd.here")], FUN = round, digits = 4)
b2[, c("parameter", "mean.paper", "mean.here", "sd.paper", "sd.here")]
```

```
     parameter mean.paper mean.here sd.paper sd.here
1   gamma[1,2]     0.0840   -0.1314   0.2205  0.1979
2   gamma[2,2]    -0.0562    0.0866   0.2060  0.1963
3   gamma[3,2]     0.0539   -0.0867   0.2187  0.2085
4   gamma[4,2]     0.0271   -0.0429   0.1869  0.1821
5   gamma[5,2]     0.0300   -0.0400   0.1952  0.1906
6   gamma[6,2]    -0.0621    0.0973   0.2177  0.2032
7   gamma[7,2]     0.0331   -0.0524   0.1974  0.1910
8   gamma[8,2]    -0.1302    0.2057   0.2395  0.1855
9   gamma[9,2]    -0.0173    0.0230   0.1919  0.1899
10 gamma[10,2]     0.0184   -0.0340   0.1827  0.1792
11 gamma[11,2]    -0.0189    0.0335   0.1773  0.1742
12 gamma[12,2]    -0.0967    0.1561   0.2279  0.1934
13 gamma[13,2]    -0.0762    0.1207   0.2350  0.2184
14 gamma[14,2]    -0.0074    0.0114   0.1795  0.1768
15 gamma[15,2]     0.0884   -0.1396   0.2229  0.1959
16 gamma[16,2]    -0.0014    0.0010   0.1822  0.1815
17 gamma[17,2]     0.1313   -0.2093   0.2619  0.2055
18 gamma[18,2]    -0.1026    0.1661   0.2524  0.2159
19 gamma[19,2]     0.0246   -0.0398   0.2145  0.2127
20 gamma[20,2]     0.0784   -0.1252   0.2167  0.1916
21  alpha[1,2]    -0.0841    0.1441   0.3087  0.2883
22  alpha[2,2]    -0.1145    0.2020   0.2964  0.2433
23  alpha[3,2]    -0.0568    0.0935   0.2620  0.2484
24  alpha[4,2]     0.0059   -0.0016   0.2222  0.2189
25  alpha[5,2]     0.1241   -0.2186   0.3260  0.2752
26  alpha[6,2]     0.0820   -0.1387   0.2619  0.2321
27  alpha[7,2]    -0.1333    0.2362   0.3656  0.3086
28  alpha[8,2]     0.2483   -0.4364   0.4262  0.2385
29  alpha[9,2]    -0.0716    0.1195   0.2805  0.2617
```

Here the means differ, mostly in sign, and the published means are smaller in absolute value. The second term is weak: the HPD interval of λ_2 reaches down to near zero, both in the paper (2.09) and here (13.07). A chain without sign alignment then moves between the two mirror images $(\boldsymbol{\alpha}_2, \boldsymbol{\gamma}_2)$ and $(-\boldsymbol{\alpha}_2, -\boldsymbol{\gamma}_2)$. Its posterior means are averages over both images and shrink towards zero:

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

```
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 30000
    , .k      = 2
    , .burnin = 5000
    , .thin   = 2
    , .chains = 1
    , .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   = 2011
    , .align  = FALSE
    , .model  = "AMMI"
    , .het    = FALSE
    , .waic   = TRUE
    )
d <- fit_free$draws[[1]][, "alpha[8,2]"]
c(share_positive = mean(d > 0), mean = mean(d), paper =
 ↪  pub$mean[pub$parameter == "alpha[8,2]"])
```

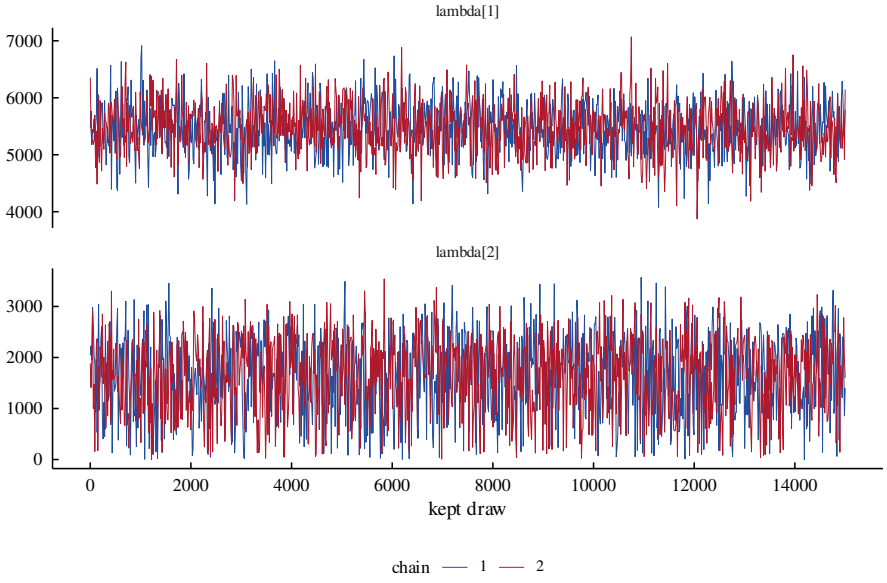
```
share_positive           mean          paper
    0.51626667     0.01630027     0.24830000
```

The published value, 0.2483, is smaller in absolute value than the aligned posterior mean, -0.436, and has the opposite sign. A chain that spends a share q of its run in the image opposite to the least-squares orientation has a mean of about $(1 - 2q)$ times the aligned one. The published value corresponds to $q \approx 0.78$: the published chain spent most of its run in the other image. The aligned summaries in this package describe one orientation of the term, and the scores of genotypes then keep their meaning relative to each other.

6 Figure 1: traces and histograms of the singular values

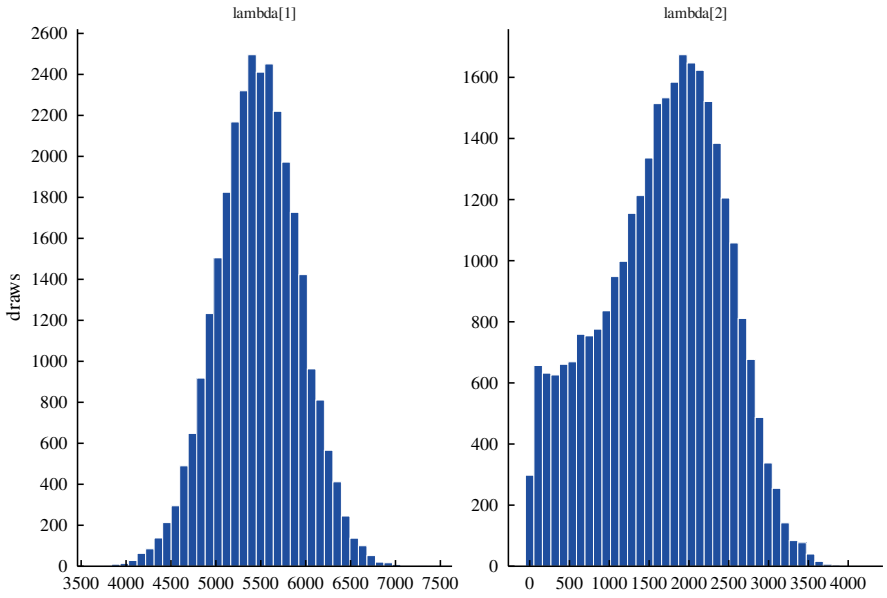
```
plot(x = fit, which = "trace", pars = c("lambda[1]", "lambda[2]"))
```

Traces of the Markov chains



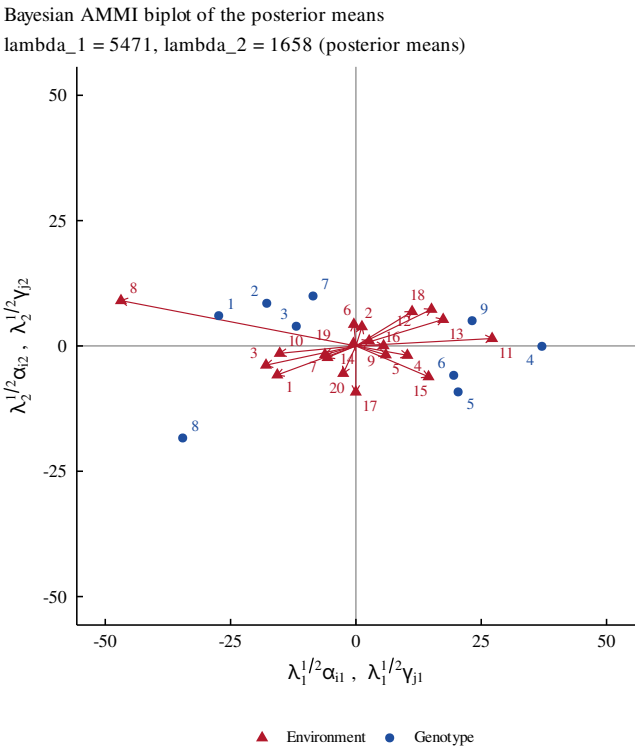

```
plot(x = fit, which = "density", pars = c("lambda[1]", "lambda[2]"))
```

Marginal posterior distributions



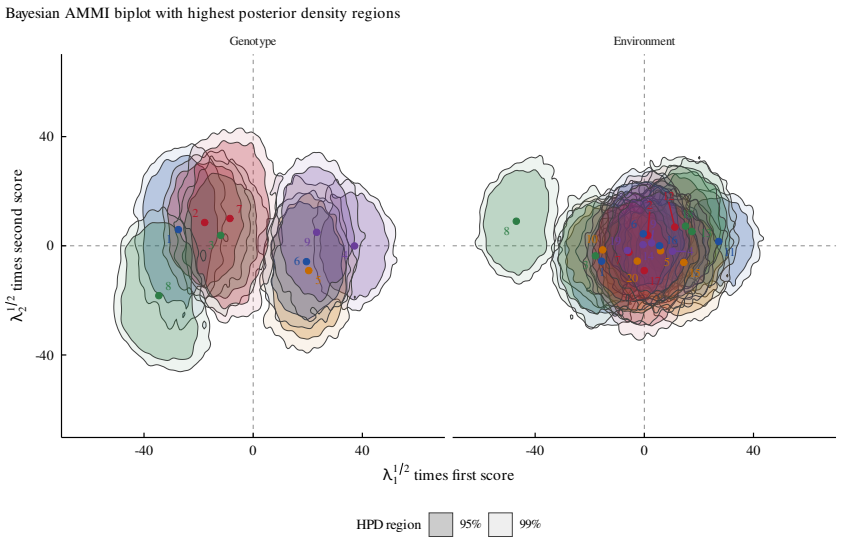
7 Figures 2 to 4: biplots

```
plot(x = fit, which = "biplot")
```



The coordinates are $\lambda_k^{1/2}\alpha_{ik}$ and $\lambda_k^{1/2}\gamma_{jk}$, as the paper defines them. The axes of its figures run from -1 to 1, so they show a rescaled version; the relative positions are the same.

```
bp <-
  biplots(
      model         = fit
    , burnin        = 0
    , thin          = 0.25
    , pb            = c(0.05, 0.01)
    , plot_stable   = TRUE
    , plot_unstable = TRUE
    , ncolors       = 5
    , .which        = "both"
    , .grid         = 100
    )
bp$biplot
```




```
bp$biplot_data[axis1_significant == TRUE, list(byplot, name, x,
 ↪  axis1_lower, axis1_upper, group)]
```

```
         byplot name         x axis1_lower axis1_upper    group
 1:    Genotype    1 -27.40119  -39.009787 -17.0056562 negative
 2:    Genotype    2 -17.78439  -28.769313  -6.9059935 negative
 3:    Genotype    3 -11.92951  -22.387334  -0.5460779 negative
 4:    Genotype    4  37.11681   26.547850  46.4285760 positive
 5:    Genotype    5  20.33477    8.388511  30.8259011 positive
 6:    Genotype    6  19.51037    9.088838  30.3996106 positive
 7:    Genotype    8 -34.57251  -46.037088 -22.9895206 negative
 8:    Genotype    9  23.26336   11.850401  33.6434950 positive
 9: Environment    1 -15.64906  -26.568920  -4.8800356 negative
10: Environment    3 -17.92078  -28.906052  -7.3859744 negative
11: Environment    8 -46.91103  -56.836455 -37.1519907 negative
12: Environment   10 -15.26108  -25.257391  -4.2795139 negative
13: Environment   11  27.22102   16.825997  37.3800310 positive
14: Environment   13  17.43228    6.882893  28.7666430 positive
15: Environment   15  14.44714    3.701040  25.1896927 positive
16: Environment   18  15.08558    3.669220  25.8574122 positive
```

On the first term, genotypes 4, 5, 6 and 9 form a positive group and genotypes 1 and 8 a negative group, as in the paper's Figure 3. Sites S8 (negative) and S11, S13 and S18 (positive) stand out, as in its Figure 4. With the intervals of Table B1, genotypes 2 and 3 and some further sites also exclude zero at 95%; the paper's figures show a subset of them.

8 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