The built-in application

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1 Abstract

`bys_app()` opens an application in the web browser that runs the analyses of the package without code: the trial, the earlier trial as prior, the Bayesian AMMI or SREG model, the biplot with HPD regions and a comparison of models. This vignette describes its pages and how it keeps its results reproducible.

2 Starting the application

```
bys_app(
    launch.browser = TRUE
  )
```

The application needs the suggested packages **shiny**, **bslib** and **DT**. **magick** with WebP support is optional: with it the plots are sent to the browser as lossless WebP images, smaller than the same PNG.

```
isTRUE(tryCatch(requireNamespace("magick", quietly = TRUE) &&
 ↪  isTRUE(magick::magick_config()$webp),
                error = function(e) FALSE))
```

```
[1] TRUE
```

`TRUE` means WebP is available; otherwise the application sends PNG images.

3 The pages

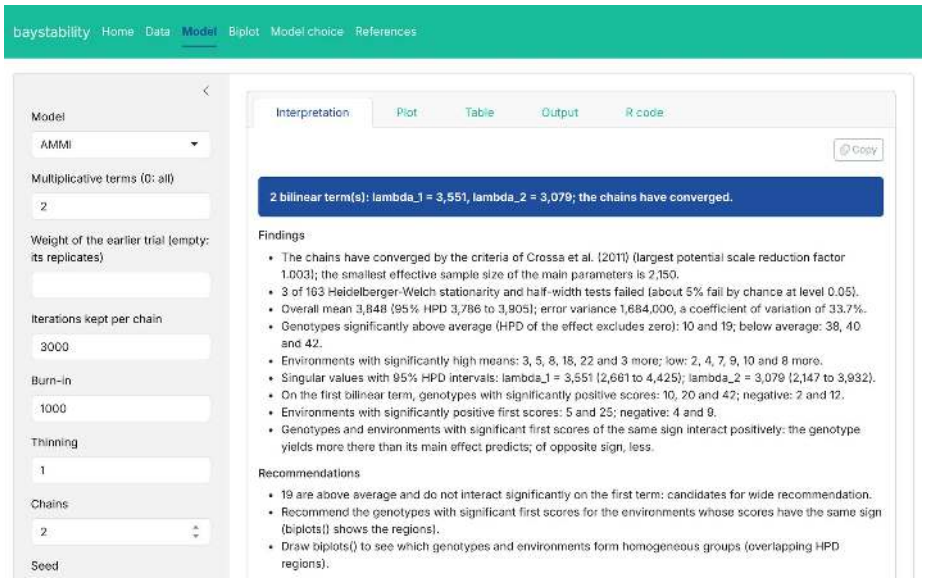
Page	What it does
Home	what the application does and the order of the pages
Data	the `cultivo2009` example or a CSV file with one row per plot; the response, genotype, environment and replicate columns; the earlier trial as prior: none, `cultivo2008` or a CSV file with the same columns
Model	AMMI or SREG, number of terms (0 for all), weight of the earlier trial, iterations, burn-in, thinning, chains, seed and vague priors; then the summary, traces, densities, the biplot of posterior means and the main effects
Biplot	the biplot with HPD regions, for genotypes, environments or both
Model choice	DIC and WAIC of models with different numbers of terms, with the earlier trial and, on request, without it
References	the articles behind the methods, as `bys_cite()` prints them

Every result page has the same tabs:

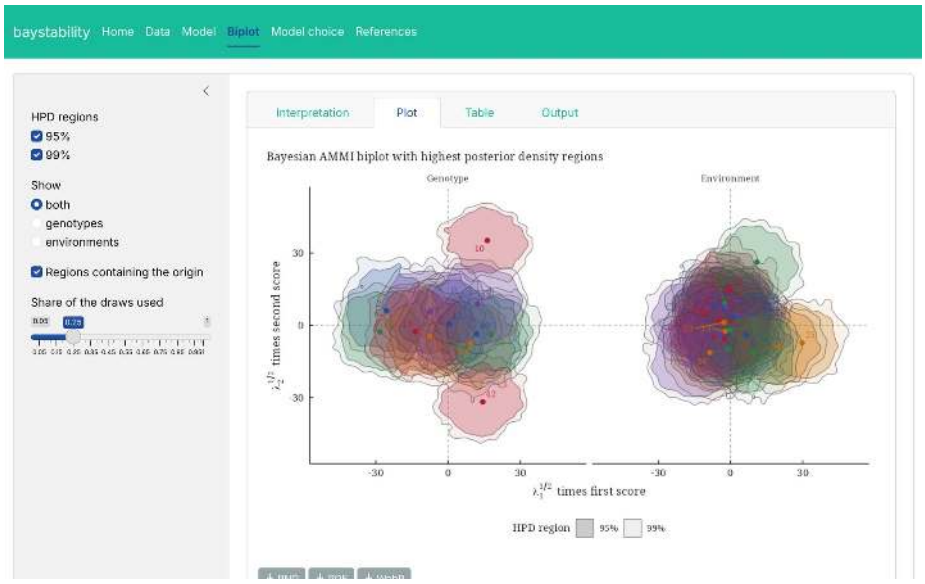
- **Interpretation** gives the plain-language reading of `bys_interpret()`, with a button that copies it.
- **Plot** shows the figure, which can be saved as PNG, PDF or WebP.
- **Table** shows the numbers, rounded, in a sortable table with buttons to copy them or save them as CSV or Excel.
- **Output** shows the printed result as text, with a button that copies it.

The model page has a further tab, **R code**, with the code that reproduces the fit outside the application.

The model page after a fit of `cultivo2009` with `cultivo2008` as prior and two terms:



The biplot page of the same fit:



4 Reproducibility

For the settings of the screenshots, the R code tab shows:

```r
settings <-
  list(
      .y      = "y"
    , .gen    = "entry"
    , .env    = "site"
    , .rep    = "rep"
    , .nIter  = 3000
    , .n0     = NULL
    , .model  = "AMMI"
    , .k      = 2
    , .burnin = 1000
    , .thin   = 1
    , .chains = 2
    , .priors = bys_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   = 1
    )
cat(baystability:::.bys_app_code(a = settings, source = "cultivo",
 ↪  prior_source = "cultivo"))
```

```r
library(baystability)
data(cultivo2009)
data(cultivo2008)
fit <-
  bayes_ammi(
      .data       = cultivo2009
    , .y          = y
    , .gen        = entry
    , .env        = site
    , .rep        = rep
    , .nIter      = 3000
    , .prior_data = cultivo2008
    , .n0         = NULL
    , .model      = "AMMI"
    , .k          = 2
    , .burnin     = 1000
    , .thin       = 1
```

```
    , .chains     = 2
    , .priors     = bys_priors(lambda_var = 1e+08, nu = 1)
    , .level      = 0.95
    , .seed       = 1
    , .align      = TRUE
    , .waic       = TRUE
    )
fit
bys_interpret(
    x             = fit
  , higher_better = TRUE
  , top           = 5
  )
```

The seed fixes the draws, so the code returns the same numbers as the application.

5 Deploying

`bys_app_object()` returns the application object without running it, for a server:

```
# app.R on a Shiny server
baystability::bys_app_object()
```

6 References

Perez-Elizalde, S., Jarquin, D. and Crossa, J. (2012). A general Bayesian estimation method of linear-bilinear models applied to plant breeding trials with genotype x environment interaction. *Journal of Agricultural, Biological, and Environmental Statistics*, 17(1), 15–37. doi:10.1007/s13253-011-0063-9