Package: baystability (via r-universe)

November 11, 2026

Type Package

Title Bayesian Stability Analysis of Genotype by Environment Interaction (GEI)

Version 1.0.0

Date 2026-11-04

Description Performs the general Bayesian estimation method of linear-bilinear models for genotype x environment interaction of Perez-Elizalde, Jarquin and Crossa (2012) <doi:10.1007/s13253-011-0063-9>: the additive main effects and multiplicative interaction (AMMI) model and the sites regression (SREG, GGE) model, with the data of an earlier trial as the prior (conjugate normal and von Mises-Fisher priors weighted by its replicates) or with vague priors; a compiled Gibbs sampler; posterior summaries with highest posterior density intervals; convergence diagnostics; biplots with highest posterior density regions; DIC and WAIC; a plain-language interpretation of every result; and a built-in 'shiny' application. For Bayesian stability analysis in general (regression and variance models, stability indices, probabilities of superior performance), see the package 'bayesstability'.

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URL https://myaseen208.com/baystability/, https://github.com/myaseen208/baystability

BugReports https://github.com/myaseen208/baystability/issues

Encoding UTF-8

Language en-US

LazyData true

Depends R (>= 4.2)

Imports coda, collapse, data.table, ggplot2, ggrepel, grDevices, MASS, Rcpp, scales, stats, utils

LinkingTo Rcpp, RcppArmadillo

Suggests bayesplot, bslib, DT, flextable, knitr, lme4, loo, magick, officer, pkgload, posterior, quarto, ragg, R.rsp, shiny, svglite, testthat (>= 3.0.0), withr

VignetteBuilder quarto, R.rsp

Config/testthat/edition 3

Config/skill/prefix bys

RoxygenNote 7.3.1

NeedsCompilation yes

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Repository https://cran.r-universe.dev

Date/Publication 2026-11-10 09:40:14 UTC

RemoteUrl https://github.com/cran/baystability

RemoteRef HEAD

RemoteSha 66070c9b0b5d7943ec00567ee6dccda219082699

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`bayes_ammi` *Bayesian estimation of linear-bilinear models: AMMI and SREG (GGE)*

Description

`bayes_ammi()` estimates the linear-bilinear models of a multi-environment trial by the general Bayesian method of Perez-Elizalde et al. (2012): the additive main effects and multiplicative interaction (AMMI) model and the sites regression (SREG, GGE) model. The data of an earlier trial with the same genotypes and environments can be the prior (`.prior_data`): its cell means, effects and singular value decomposition give conjugate priors whose weight is its number of replicates, as in the paper's analysis of two years of a maize trial. Without an earlier trial the priors are vague but proper. The sampler is compiled (C++); every parameter has a posterior distribution, and `bayes_ammi_biplot()` draws the biplot with highest posterior density (HPD) regions.

Usage

```
bayes_ammi(
  .data,
  .y,
  .gen,
  .env,
  .rep,
  .nIter = 1000L,
  .prior_data = NULL,
  .n0 = NULL,
  .model = c("AMMI", "SREG", "GGE"),
  .k = NULL,
  .burnin = 0L,
  .thin = 1L,
  .chains = 1L,
  .priors = bys_priors(),
  .level = 0.95,
  .seed = NULL,
  .align = TRUE,
  .waic = TRUE
)

## Default S3 method:
bayes_ammi(
  .data,
  .y,
  .gen,
```

```
  .env,
  .rep,
  .nIter = 1000L,
  .prior_data = NULL,
  .n0 = NULL,
  .model = c("AMMI", "SREG", "GGE"),
  .k = NULL,
  .burnin = 0L,
  .thin = 1L,
  .chains = 1L,
  .priors = bys_priors(),
  .level = 0.95,
  .seed = NULL,
  .align = TRUE,
  .waic = TRUE
)
```

Arguments

`.data`	a data frame with one row per plot.
`.y`, `.gen`, `.env`, `.rep`	the columns of the response, genotypes, environments and replicates: bare names or strings. The same names are used in `.prior_data`.
`.nIter`	number of iterations kept per chain before thinning (after the burn-in).
`.prior_data`	`NULL` (default: vague priors) or a data frame of an earlier trial with the same columns, genotypes and environments, used as prior (Perez-Elizalde et al. 2012).
`.n0`	weight of the earlier trial: the number of its observations per cell in the prior (default its number of replicates).
`.model`	`"AMMI"` (default) or `"SREG"` (sites regression, GGE; `"GGE"` is accepted).
`.k`	number of bilinear terms K (default `NULL`: all of them).
`.burnin`	number of iterations discarded at the start of every chain (default 0).
`.thin`	keep every `.thin`-th iteration (default 1).
`.chains`	number of chains (default 1).
`.priors`	the vague priors used without an earlier trial, from `bys_priors()`.
`.level`	probability of the HPD intervals (default 0.95).
`.seed`	integer seed for a reproducible run, or `NULL`; the random number state of the session is restored afterwards.
`.align`	keep the sign of every bilinear term (default `TRUE`).
`.waic`	compute WAIC during sampling (default `TRUE`).

Details

Models. For genotype i, replicate l and environment j,

$$\text{AMMI: } y_{ijl} = \mu + \tau_i + \delta_j + \sum_{k=1}^{K} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ijl}, \qquad \text{SREG: } y_{ijl} = \mu + \delta_j + \sum_{k=1}^{K} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ijl},$$

$e_{ijl} \sim N(0, \sigma^2)$, with $\sum_i \tau_i = \sum_j \delta_j = 0$, $\lambda_1 \geq \cdots \geq \lambda_K > 0$, and orthonormal score matrices $\mathbf{U} = (\boldsymbol{\alpha}_k)$ and $\mathbf{V} = (\boldsymbol{\gamma}_k)$, $\mathbf{U}^\top \mathbf{1} = \mathbf{0}$, and for AMMI also $\mathbf{V}^\top \mathbf{1} = \mathbf{0}$ (paper, eq. 1.2-1.3). By default all $\min(G, E) - 1$ terms are fitted ($\min(G-1, E)$ for SREG), as in the paper and the earlier versions; `.k` fits fewer.

An earlier trial as prior (`.prior_data`). With n_0 its number of replicates (`.n0`), $\mathbf{Y}_0$ its table of cell means and μ_0, $\boldsymbol{\tau}_0$, $\boldsymbol{\delta}_0$, $\mathbf{U}_0\mathbf{D}_0\mathbf{V}_0^\top$ its least-squares fit (paper, Section 2.2):

$$\mu \sim N\left(\mu_0, \frac{\sigma^2}{n_0 GE}\right), \quad \mathbf{K}_G\boldsymbol{\tau} \sim N\left(\mathbf{K}_G\boldsymbol{\tau}_0, \frac{\sigma^2}{n_0 E}\mathbf{I}\right), \quad \mathbf{K}_E\boldsymbol{\delta} \sim N\left(\mathbf{K}_E\boldsymbol{\delta}_0, \frac{\sigma^2}{n_0 G}\mathbf{I}\right),$$

$\lambda_k \sim N(\lambda_{0k}, \sigma^2/n_0)$ truncated to the order (eq. 2.9), von Mises-Fisher priors $p(\mathbf{U}) \propto \mathrm{etr}(n_0\mathbf{Y}_0\mathbf{V}_0\mathbf{D}_0\mathbf{U}^\top/\sigma^2)$ and $p(\mathbf{V}) \propto \mathrm{etr}(n_0\mathbf{Y}_0^\top\mathbf{U}_0\mathbf{D}_0\mathbf{V}^\top/\sigma^2)$ (eq. 2.7-2.8), and $aS_0^2/\sigma^2 \sim \chi^2_a$ with $a = n_0 - 1$ and S_0^2 the within-cell mean square of the earlier trial (eq. 2.11; the values of the earlier versions of the package).

Conditional distributions (paper, Section 2.3). With $\mathbf{Y}$ the cell means of the trial, B its replicates and $n = BGE$, the linear effects are normal with means $(n\bar{y} + n_0 GE\mu_0)/(n + n_0 GE)$ and so on; the singular values are truncated normal with mean $(B\,\boldsymbol{\alpha}_k^\top\mathbf{Y}\boldsymbol{\gamma}_k + n_0\lambda_{0k})/(B + n_0)$ and variance $\sigma^2/(B + n_0)$ (eq. 2.15); the score matrices are von Mises-Fisher (eq. 2.13-2.14), drawn one column at a time on the sphere orthogonal to $\mathbf{1}$ and the other columns (Hoff 2009) with parameters $(B\lambda_k\mathbf{Y}\boldsymbol{\gamma}_k + n_0\lambda_{0k}\mathbf{Y}_0\boldsymbol{\gamma}_{0k})/\sigma^2$ and the same for $\mathbf{V}$; and

$$\sigma^2 \sim \frac{aS_0^2 + \mathrm{SSW} + B\sum_{ij}(\bar{y}_{ij} - \hat{y}_{ij})^2}{\chi^2_{a+n}}.$$

As in the paper, the dependence of the priors on σ^2 is left out of its conditional distribution (it would involve the normalising constants of the von Mises-Fisher priors). Without an earlier trial the priors of `bys_priors()` apply, which do not depend on σ^2, and all conditionals are exact (Crossa et al. 2011).

Starting values and signs. With an earlier trial the first chain starts at its least-squares fit and every draw keeps the orientation of its score vectors (`.align`); otherwise the first chain starts at the least-squares fit of the trial. Other chains start at dispersed values. With all terms fitted and a prior trial that disagrees with the data, the posterior of the scores can have several modes; compare chains (`.chains`) and the potential scale reduction factors.

Unbalanced trials. Missing plots and cells are completed by data augmentation (see `bys_priors`); an earlier trial with empty cells is completed by the EM algorithm before its fit.

Changes from version 0.2.0. The function no longer reads the earlier trial from objects in the workspace (`n0`, `mu0`, `tau0`, ...; it stopped with "object 'n0' not found" without them): the earlier trial is the argument `.prior_data`. The singular values were computed once and never sampled; `tau1` held a precision drawn from a residual matrix that was never updated; the scores were drawn without their constraints and orthogonalised afterwards; the columns of `delta1` were named for the genotypes. `tau1` now holds the draws of the error variance σ^2.

Value

An object of class `c("bys_bayes_ammi", "bys_result", "list")`; the components of version 0.2.0 come first, the draws of all chains one after the other:

`mu1` `data.table`, column `mu`: draws of the overall mean.

`tau1` `data.table`, column `tau`: draws of the error variance σ^2.

`tao1` `data.table`, columns `tao1`, ..., `taoG`: draws of the genotype effects (no columns for SREG).

`delta1` `data.table`, columns `delta1`, ..., `deltaE`: draws of the environment effects.

`lambdas1` `data.table`, columns `lambdas1`, ...: draws of the singular values.

`alphas1`, `gammas1` `data.tables`, one row per draw, columns `alphas1`, ..., `alphas<GK>` (genotype scores, genotypes within terms) and `gammas1`, ... (environment scores).

`Mean_Alphas`, `Mean_Gammas` `data.tables`, columns `V1`, ..., `VK`: posterior means of the score matrices.

`summary` `data.table`: posterior mean, standard deviation, Monte Carlo standard error, HPD interval, effective sample size and potential scale reduction factor of every parameter.

`scores` `data.table`: posterior means of the biplot coordinates.

`draws` `coda::mcmc.list` of all parameters.

`diagnostics` Gelman-Rubin, Raftery-Lewis and Heidelberger-Welch diagnostics.

`ls` least-squares fit of the trial; `prior`: the fit of the earlier trial used as prior.

`fit` DIC and WAIC.

`settings` iterations, burn-in, thinning, chains, terms, model, priors, level, seed, time used.

Methods: `print()`, `summary()`, `plot()`, `bayes_ammi_biplot()`, `bys_interpret()`, `bys_compare()`, `bys_cite()`.

Author(s)

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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/s1325301100639

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

Hoff, P. D. (2009). Simulation of the matrix Bingham-von Mises-Fisher distribution, with applications to multivariate and relational data. *Journal of Computational and Graphical Statistics*, **18**(2), 438–456. doi:10.1198/jcgs.2009.07177

Wood, A. T. A. (1994). Simulation of the von Mises Fisher distribution. *Communications in Statistics - Simulation and Computation*, **23**(1), 157–164.

See Also

`bayes_ammi_biplot`, `bys_priors`, `bys_interpret`, `bys_ls_ammi`

Examples

```
data(cultivo2008)
data(cultivo2009)
fm3 <-
  bayes_ammi(
      .data       = cultivo2009
    , .y          = y
    , .gen        = entry
    , .env        = site
    , .rep        = rep
    , .nIter      = 300
    , .prior_data = cultivo2008
    , .n0         = NULL
    , .model      = "AMMI"
    , .k          = NULL
    , .burnin     = 100
    , .thin       = 1
    , .chains     = 1
    , .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
    , .align      = TRUE
    , .waic       = TRUE
    )
fm3
fm3$Mean_Alphas
plot(x = fm3, which = "biplot")
```

---

bayes_ammi_biplot *AMMI and GGE biplots with highest posterior density regions*

Description

`bayes_ammi_biplot()` and `bayes_gge_biplot()` draw the Bayesian AMMI or GGE (SREG) biplot of the first two bilinear terms with a highest posterior density (HPD) region around every genotype and environment (Crossa et al. 2011, Fig. 3 and 4). A region that contains the origin marks a genotype or environment whose interaction is not different from zero (stable); regions that overlap mark genotypes or environments that cannot be told apart, a homogeneous group.

Usage

```
bayes_ammi_biplot(
  fit,
  burnin = 0,
  thin = 0.5,
  pb = 0.05,
  plot_stable = TRUE,
  plot_unstable = TRUE,
  ncolors = 5,
  .which = c("both", "genotype", "environment"),
  .grid = 100L
)

## Default S3 method:
bayes_ammi_biplot(
  fit,
  burnin = 0,
  thin = 0.5,
  pb = 0.05,
  plot_stable = TRUE,
  plot_unstable = TRUE,
  ncolors = 5,
  .which = c("both", "genotype", "environment"),
  .grid = 100L
)

bayes_gge_biplot(
  fit,
  burnin = 0,
  thin = 0.5,
  pb = 0.05,
  plot_stable = TRUE,
  plot_unstable = TRUE,
  ncolors = 5,
  .which = c("both", "genotype", "environment"),
  .grid = 100L
)

## Default S3 method:
bayes_gge_biplot(
  fit,
  burnin = 0,
  thin = 0.5,
  pb = 0.05,
  plot_stable = TRUE,
  plot_unstable = TRUE,
  ncolors = 5,
  .which = c("both", "genotype", "environment"),
```

```
  .grid = 100L
)
```

Arguments

`fit`	a result of `bayes_ammi()` with at least two terms: an AMMI fit for `bayes_ammi_biplot()`, a SREG (GGE) fit for `bayes_gge_biplot()` (`bayes_gge()`).
`burnin`	proportion of the stored draws of every chain discarded at its start (default 0).
`thin`	proportion of the remaining draws used (default 0.5: every second draw).
`pb`	one or more probabilities p: the regions hold $100(1-p)\%$ of the posterior (default 0.05, the 95% region; `c(0.05, 0.01)` draws the 95% and 99% regions of the paper). The classification uses the first value.
`plot_stable`, `plot_unstable`	draw the regions that contain the origin, and those that do not (default both).
`ncolors`	number of colours used for the regions (default 5).
`.which`	`"both"` (default), `"genotype"` or `"environment"`.
`.grid`	number of grid points per axis of the density estimate (default 100).

Details

The points are the biplot coordinates of the paper,

$$\left(\lambda_1^{1/2}\alpha_{i1}, \lambda_2^{1/2}\alpha_{i2}\right), \qquad \left(\lambda_1^{1/2}\gamma_{j1}, \lambda_2^{1/2}\gamma_{j2}\right),$$

computed draw by draw. For each genotype and environment a bivariate kernel density $\hat{f}$ is estimated from the draws (normal kernels, normal reference bandwidths); the $100(1-p)\%$ HPD region is $\{\mathbf{x} : \hat{f}(\mathbf{x}) \geq c_p\}$ with c_p the p-quantile of $\hat{f}$ at the draws, so that the region holds $100(1-p)\%$ of them. The region contains the origin when $\hat{f}(\mathbf{0}) \geq c_p$ (`stable`). The criterion of the paper, the marginal HPD interval of the first coordinate excluding zero, is given as `axis1_significant`.

Changes from the earlier versions. The regions were drawn for the singular vectors without the factor $\lambda_k^{1/2}$, with a fixed bandwidth of 0.2 whatever the scale; a genotype counted as stable when the bounding box of its contour covered the origin.

Value

An object of class `c("bys_biplots", "bys_result", "list")`, with the components of the earlier version:

`contorns` `data.table` of the region boundaries: `byplot` (Genotype, Environment), `ID` (number), `name`, `prob` (the region, for instance "95%"), `piece` (a region can have several pieces), `x`, `y`, `stable`.

`biplot_data` `data.table`, one row per genotype and environment: `byplot`, `ID`, `name`, `x`, `y` (posterior means of the coordinates), `stable` (region contains the origin), `axis1_lower`, `axis1_upper` (marginal HPD interval of the first coordinate), `axis1_significant` (it excludes zero), `group` (sign of the first coordinate when significant: positive, negative, or not significant).

`biplot` the `ggplot`.

Methods: `print()`, `plot()`, `bys_interpret()`.

Author(s)

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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.

See Also

bayes_ammi, bys_interpret

Examples

```
data(cultivo2009)
fm1 <-
  bayes_ammi(
      .data       = cultivo2009
    , .y          = y
    , .gen        = entry
    , .env        = site
    , .rep        = rep
    , .nIter      = 1000
    , .prior_data = NULL
    , .n0         = NULL
    , .model      = "AMMI"
    , .k          = 2
    , .burnin     = 200
    , .thin       = 1
    , .chains     = 1
    , .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
    , .align      = TRUE
    , .waic       = TRUE
    )
```

```
bp <-
  bayes_ammi_biplot(
      fit           = fm1
    , burnin        = 0
    , thin          = 1
    , pb            = c(0.05, 0.01)
    , plot_stable   = TRUE
    , plot_unstable = TRUE
    , ncolors       = 5
    , .which        = "both"
    , .grid         = 100
    )
bp$biplot
bp$biplot_data
```

---

bayes_gge *Bayesian GGE (sites regression) model*

Description

`bayes_gge()` fits the sites regression (SREG) model behind the GGE biplot by the method of Perez-Elizalde et al. (2012): it is `bayes_ammi(.model = "SREG")`, under the name used by the package **bayesstability**. The genotype main effect is part of the multiplicative terms; an earlier trial enters as prior through `.prior_data`.

Usage

```
bayes_gge(
  .data,
  .y,
  .gen,
  .env,
  .rep,
  .nIter = 1000L,
  .prior_data = NULL,
  .n0 = NULL,
  .k = NULL,
  .burnin = 0L,
  .thin = 1L,
  .chains = 1L,
  .priors = bys_priors(),
  .level = 0.95,
  .seed = NULL,
  .align = TRUE,
  .waic = TRUE
)

## Default S3 method:
```

```
bayes_gge(
  .data,
  .y,
  .gen,
  .env,
  .rep,
  .nIter = 1000L,
  .prior_data = NULL,
  .n0 = NULL,
  .k = NULL,
  .burnin = 0L,
  .thin = 1L,
  .chains = 1L,
  .priors = bys_priors(),
  .level = 0.95,
  .seed = NULL,
  .align = TRUE,
  .waic = TRUE
)
```

Arguments

`.data`	a data frame with one row per plot.
`.y`, `.gen`, `.env`, `.rep`	the columns of the response, genotypes, environments and replicates: bare names or strings. The same names are used in `.prior_data`.
`.nIter`	number of iterations kept per chain before thinning (after the burn-in).
`.prior_data`	`NULL` (default: vague priors) or a data frame of an earlier trial with the same columns, genotypes and environments, used as prior (Perez-Elizalde et al. 2012).
`.n0`	weight of the earlier trial: the number of its observations per cell in the prior (default its number of replicates).
`.k`	number of bilinear terms K (default `NULL`: all of them).
`.burnin`	number of iterations discarded at the start of every chain (default 0).
`.thin`	keep every `.thin`-th iteration (default 1).
`.chains`	number of chains (default 1).
`.priors`	the vague priors used without an earlier trial, from `bys_priors()`.
`.level`	probability of the HPD intervals (default 0.95).
`.seed`	integer seed for a reproducible run, or `NULL`; the random number state of the session is restored afterwards.
`.align`	keep the sign of every bilinear term (default `TRUE`).
`.waic`	compute WAIC during sampling (default `TRUE`).

Value

An object of class `c("bys_bayes_ammi", "bys_result", "list")`; see `bayes_ammi()`.

Author(s)

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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/s1325301100639

See Also

bayes_ammi, bayes_gge_biplot

Examples

```
data(cultivo2008)
data(cultivo2009)
fg <-
  bayes_gge(
      .data       = cultivo2009
    , .y          = y
    , .gen        = entry
    , .env        = site
    , .rep        = rep
    , .nIter      = 400
    , .prior_data = cultivo2008
    , .n0         = NULL
    , .k          = 2
    , .burnin     = 100
    , .thin       = 1
    , .chains     = 1
    , .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
    , .align      = TRUE
    , .waic       = TRUE
    )
fg
bp <-
  bayes_gge_biplot(
```

```
      fit           = fg
    , burnin        = 0
    , thin          = 1
    , pb            = 0.05
    , plot_stable   = TRUE
    , plot_unstable = TRUE
    , ncolors       = 5
    , .which        = "both"
    , .grid         = 100
    )
bp$biplot
```

---

bys-draws *The draws of a fit for posterior, bayesplot and coda*

Description

The draws of `bayes_ammi()` are a `coda::mcmc.list` (component `draws`). These methods hand them to the packages **posterior** and **coda**; every plot of **bayesplot** (`mcmc_trace()`, `mcmc_areas()`, `mcmc_rank_overlay()`, ...) then works on them, as does `posterior::summarise_draws()` (rank-normalised $\hat{R}$, bulk and tail effective sample sizes).

Usage

```
## S3 method for class 'bys_bayes_ammi'
as_draws_df(x, ...)

## S3 method for class 'bys_bayes_ammi'
as_draws(x, ...)

## S3 method for class 'bys_bayes_ammi'
as.mcmc.list(x, ...)
```

Arguments

`x`	a result of `bayes_ammi()`.
`...`	unused.

Value

`as_draws_df()`: a `posterior::draws_df`; `as_draws()`: a `posterior::draws_list`; `as.mcmc.list()`: the `coda::mcmc.list`.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

Gabry, J., Simpson, D., Vehtari, A., Betancourt, M. and Gelman, A. (2019). Visualization in Bayesian workflow. *Journal of the Royal Statistical Society A*, **182**(2), 389–402. doi:10.1111/rssa.12378

Vehtari, A., Gelman, A., Simpson, D., Carpenter, B. and Burkner, P.-C. (2021). Rank-normalization, folding, and localization: an improved R-hat for assessing convergence of MCMC. *Bayesian Analysis*, **16**(2), 667–718. doi:10.1214/20BA1221

Examples

```
data(cultivo2009)
fit <-
  bayes_ammi(
      .data       = cultivo2009
    , .y          = y
    , .gen        = entry
    , .env        = site
    , .rep        = rep
    , .nIter      = 500
    , .prior_data = NULL
    , .n0         = NULL
    , .model      = "AMMI"
    , .k          = 2
    , .burnin     = 100
    , .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
    , .align      = TRUE
    , .waic       = TRUE
    )
if (requireNamespace("posterior", quietly = TRUE)) {
  dr <- posterior::as_draws_df(x = fit)
  posterior::summarise_draws(
      .x = posterior::subset_draws(
          x        = dr
        , variable = c("mu", "lambda[1]", "lambda[2]")
        )
    )
```

```
}
if (requireNamespace("bayesplot", quietly = TRUE)) {
  bayesplot::mcmc_trace(x = fit$draws, pars = c("lambda[1]", "lambda[2]"))
}
```

---

bys-methods *Methods for baystability results*

Description

The analysis functions of **baystability** return the named list they have always returned, now with the class `c("bys_<analysis>", "bys_result", "list")`. Components are read as before (`x$ANOVA`, `x[["Means"]]`); the methods below print, summarise and plot the result and turn any component into a `data.table`.

Usage

```
## S3 method for class 'bys_result'
print(x, digits = 4L, ...)

## S3 method for class 'bys_result'
summary(object, ...)

## S3 method for class 'summary.bys_result'
print(x, ...)

## S3 method for class 'bys_result'
format(x, ...)

## S3 method for class 'bys_result'
as.data.table(x, keep.rownames = FALSE, ..., component = 1L)

## S3 method for class 'bys_result'
as.data.frame(x, row.names = NULL, optional = FALSE, ..., component = 1L)

## S3 method for class 'bys_result'
plot(x, ...)
```

Arguments

`x`, `object`	a baystability result.
`digits`	significant digits of printed numbers (default 4).
`...`	passed on (to `print()` of the components, or to the plotting function for `plot()`).
`keep.rownames`, `row.names`, `optional`	as in `data.table::as.data.table()` and `as.data.frame()`; row names of a matrix or data frame component are always kept, in a first column `term`.
`component`	name or number of the component to convert (default: the first one).

Value

`print()` returns `x` invisibly; `summary()` an object of class `summary.bys_result`; `format()` a character string; `as.data.table()` and `as.data.frame()` the chosen component as a table; `plot()` a `ggplot` object.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

`bys_app` *Bayesian AMMI and SREG analysis in a web browser*

Description

`bys_app()` starts the application of **baystability**: load a trial (the example `cultivo2009` or a CSV file with one row per plot) and, optionally, an earlier trial of the same genotypes and environments as the prior (the example `cultivo2008` or a CSV file), fit the Bayesian AMMI or SREG (GGE) model of Perez-Elizalde et al. (2012), check convergence, draw the biplot with HPD regions and compare models of different numbers of terms, with and without the earlier trial. Every page shows an interpretation computed from the results (`bys_interpret()`), the output as R prints it, formatted tables, plots and the R code that repeats the analysis, each with a Copy button.

Usage

```
bys_app(launch.browser = interactive(), ...)

bys_app_object()
```

Arguments

`launch.browser`	passed to `shiny::runApp()`: `TRUE` (default in an interactive session) opens the application in the web browser.
`...`	further arguments to `shiny::runApp()`, such as `port`.

Details

The application needs the suggested packages **shiny**, **bslib** and **DT**. Plots are sent to the browser as WebP images when **magick** is installed (smaller than PNG; PNG otherwise) and can be downloaded as PNG, PDF or WebP. Text is set in IBM Plex Sans and output in IBM Plex Mono when the browser can reach Google Fonts, in the system fonts otherwise.

Value

`bys_app()` is called for its side effect and returns the value of `shiny::runApp()` when the application is closed; `bys_app_object()` returns the application object (for `shiny::runApp()`, `shiny::testServer()` or deployment on a server).

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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/s1325301100639)

See Also

bayes_ammi, bayes_ammi_biplot, bys_compare, bys_interpret

Examples

```
if (interactive()) {
  bys_app(
      launch.browser = TRUE
    )
}
```

---

bys_cite *References of a result or of the package*

Description

bys_cite() gives the references of the methods behind a result of the package, or the references of every method in the package, as text or BibTeX. citation("baystability") cites the package and its main methods.

Usage

```
bys_cite(x = NULL, style = c("text", "bibtex"))

## Default S3 method:
bys_cite(x = NULL, style = c("text", "bibtex"))
```

Arguments

x	a result of a function of the package, or NULL (default) for every reference of the package.
style	"text" (default) or "bibtex".

Value

An object of class bibentry (printed in the chosen style).

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

Examples

```
bys_cite(
    x     = NULL
  , style = "text"
  )
data(cultivo2009)
g <-
  bys_ls_ammi(
      .data = cultivo2009
    , .y    = y
    , .gen  = entry
    , .env  = site
    , .rep  = rep
    )
bys_cite(
    x     = g
  , style = "bibtex"
  )
```

`bys_compare` *Compare Bayesian AMMI and GGE models*

Description

`bys_compare()` compares fits of `bayes_ammi()` that differ in the number of multiplicative terms, the model (AMMI or GGE), the error variances or the priors, by the deviance information criterion (DIC) and the widely applicable information criterion (WAIC). Smaller values predict new data better.

Usage

```
bys_compare(...)

## Default S3 method:
bys_compare(...)
```

Arguments

`...`	fits of `bayes_ammi()` to the same data, named or not (names label the rows).

Details

With $D(\boldsymbol{\theta}) = -2 \log p(\mathbf{y} \mid \boldsymbol{\theta})$ over the observed plots,

$$\mathrm{DIC} = D(\bar{\boldsymbol{\theta}}) + 2p_D, \qquad p_D = \overline{D(\boldsymbol{\theta})} - D(\bar{\boldsymbol{\theta}})$$

(Spiegelhalter et al. 2002), the deviance evaluated at the posterior means of the cell means and variances; and

$$\mathrm{WAIC} = -2 \left(\sum_o \log \frac{1}{S} \sum_s p(y_o \mid \boldsymbol{\theta}^{(s)}) - \sum_o \mathrm{Var}_s \log p(y_o \mid \boldsymbol{\theta}^{(s)}) \right)$$

(Watanabe 2010; Gelman et al. 2014), accumulated over all draws during sampling. All fits must use the same data.

The standard error of a difference in WAIC comes from the plot-by-plot differences of the contributions w_o to WAIC: $\mathrm{se} = \sqrt{n \, \mathrm{Var}_o(w_o^{(m)} - w_o^{(\mathrm{best})})}$ (Vehtari et al. 2017). Because the models are fitted to the same plots, it is smaller than the standard error of either WAIC. A difference of less than about two of its standard errors does not separate two models.

Value

An object of class `c("bys_compare", "bys_result", "list")` with `table` (`data.table` sorted by WAIC: `model`, `terms`, `variances`, `DIC`, `pD`, `WAIC`, `p_waic`, `se` (standard error of WAIC), `lambda_last_lower` (lower HPD limit of the last singular value), `lambda_last_mean`, `dWAIC` (difference from the best) and `dWAIC_se` (its standard error)). Methods: `print()`, `plot()`, `bys_interpret()`.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

Spiegelhalter, D. J., Best, N. G., Carlin, B. P. and van der Linde, A. (2002). Bayesian measures of model complexity and fit. *Journal of the Royal Statistical Society B*, **64**(4), 583–639. doi:10.1111/14679868.00353

Watanabe, S. (2010). Asymptotic equivalence of Bayes cross validation and widely applicable information criterion in singular learning theory. *Journal of Machine Learning Research*, **11**, 3571–3594.

Gelman, A., Hwang, J. and Vehtari, A. (2014). Understanding predictive information criteria for Bayesian models. *Statistics and Computing*, **24**(6), 997–1016. doi:10.1007/s1122201394162

Vehtari, A., Gelman, A. and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*, **27**(5), 1413–1432. doi:10.1007/s1122201696964

Examples

```
data(cultivo2009)
fits <-
  lapply(
```

```
  X   = 1:2
, FUN = function(K) {
    bayes_ammi(
        .data       = cultivo2009
      , .y          = y
      , .gen        = entry
      , .env        = site
      , .rep        = rep
      , .nIter      = 600
      , .prior_data = NULL
      , .n0         = NULL
      , .model      = "AMMI"
      , .k          = K
      , .burnin     = 100
      , .thin       = 1
      , .chains     = 1
      , .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
      , .align      = TRUE
      , .waic       = TRUE
      )
  }
)
bys_compare(
    AMMI1 = fits[[1]]
  , AMMI2 = fits[[2]]
  )
```

`bys_contrasts` *Orthonormal contrast matrix*

Description

`bys_contrasts()` returns the $(n-1) \times n$ matrix $\mathbf{K}_n$ whose rows are orthonormal and orthogonal to $\mathbf{1}_n$ (Helmert contrasts). `bayes_ammi()` writes the main effects as $\boldsymbol{\tau} = \mathbf{K}_G^\top \mathbf{t}$, which keeps them summing to zero.

Usage

```
bys_contrasts(n)

## Default S3 method:
bys_contrasts(n)
```

Arguments

n	number of columns (at least 2).

Details

Row r ($r = 1, \ldots, n-1$) has 0 in its first $r-1$ positions, $(n-r)/c_r$ in position r and $-1/c_r$ after it, with $c_r = \sqrt{(n-r)(n-r+1)}$, so that

$$\mathbf{K}_n \mathbf{K}_n^\top = \mathbf{I}_{n-1}, \qquad \mathbf{K}_n \mathbf{1}_n = \mathbf{0}, \qquad \mathbf{K}_n^\top \mathbf{K}_n = \mathbf{I}_n - \frac{1}{n}\mathbf{J}_n.$$

Value

The $(n-1) \times n$ matrix $\mathbf{K}_n$.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

See Also

bys_orthonormal

Examples

```
K <-
  bys_contrasts(
    n = 4
  )
K
round(x = K %*% t(K), digits = 10)
```

bys_interpret *Interpretation of a Bayesian AMMI analysis*

Description

bys_interpret() turns a result of bayes_ammi(), bayes_ammi_biplot() or bys_ls_ammi() into a plain-language interpretation: whether the chains have converged, which genotypes and environments differ from the average (main effects whose HPD interval excludes zero), how strong the bilinear terms are, which genotypes and environments interact significantly and in which direction, which are stable, and what to check before acting on the results. Every statement is computed from the numbers of the result.

Usage

```
bys_interpret(x, higher_better = TRUE, top = 5L, ...)

## Default S3 method:
bys_interpret(x, higher_better = TRUE, top = 5L, ...)

## S3 method for class 'bys_interpretation'
print(x, ...)

## S3 method for class 'bys_interpretation'
format(x, style = c("text", "markdown"), width = getOption("width", 80L), ...)
```

Arguments

x	a result of bayes_ammi(), bayes_ammi_biplot() or bys_ls_ammi().
higher_better	TRUE (default) when larger values of the trait are better.
top	number of genotypes or environments named in lists (default 5).
...	unused.
style	"text" (default) or "markdown".
width	line width of the text (default getOption("width")).

Details

The rules:

- convergence: potential scale reduction factor below 1.1 (two or more chains), effective sample size of at least 400, Raftery-Lewis dependence factor below 5 and the Heidelberger-Welch tests passed (Crossa et al. 2011);
- main effects: a genotype or environment differs from the average when the HPD interval of its effect excludes zero;
- bilinear terms: a term whose HPD interval of λ_k reaches down to near zero (lower limit below a tenth of the posterior mean) is weakly supported;

- interaction: a genotype (environment) interacts significantly on the first term when the HPD interval of its first score excludes zero; genotypes and environments with significant scores of the same sign interact positively (the genotype does better there than its main effect predicts), of opposite sign negatively;
- stability (`bayes_ammi_biplot()`): a genotype is stable when its HPD region contains the origin.

Value

An object of class `"bys_interpretation"`: a list with `analysis`, `title`, `headline`, `findings`, `recommendations` and `cautions` (sentences), `facts` (the numbers and lists behind the sentences), `guide` (how the method is read) and `sources` (the full references of the method; `bys_cite()` gives them as BibTeX). `print()` shows the text; `format(x, style = "markdown")` returns it as Markdown.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

See Also

`bayes_ammi`, `bayes_ammi_biplot`

Examples

```
data(cultivo2009)
fm1 <-
  bayes_ammi(
      .data       = cultivo2009
    , .y          = y
    , .gen        = entry
    , .env        = site
    , .rep        = rep
    , .nIter      = 500
    , .prior_data = NULL
    , .n0         = NULL
    , .model      = c("AMMI", "GGE")
    , .k          = 2
    , .burnin     = 100
    , .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
      , .align      = TRUE
      , .waic       = TRUE
      )
txt <-
  bys_interpret(
       x             = fm1
      , higher_better = TRUE
      , top           = 5
      )
txt
cat(format(x = txt, style = "markdown"))
```

`bys_ls_ammi` *Least-squares AMMI model*

Description

`bys_ls_ammi()` computes the least-squares estimates of the AMMI model with all interaction axes: grand mean, genotype and environment effects, singular values and vectors of the interaction, and the error variance. They are the starting values of `bayes_ammi()` and the classical estimates it is compared with.

Usage

```
bys_ls_ammi(.data, .y, .gen, .env, .rep)

## Default S3 method:
bys_ls_ammi(.data, .y, .gen, .env, .rep)
```

Arguments

`.data`	a data frame with one row per plot.
`.y`, `.gen`, `.env`, `.rep`	the columns of the response, genotypes, environments and replicates: bare names, strings or vectors.

Details

With the cell means $\bar{y}_{ij}$ of B replicates, $\hat{\mu} = \bar{y}$, $\hat{\tau}_i = \bar{y}_{i\cdot} - \bar{y}$, $\hat{\delta}_j = \bar{y}_{\cdot j} - \bar{y}$ and the singular value decomposition of the interaction effects (`bys_ls_ge_effects()`), $K = \min(G, E) - 1$ axes. The error variance is the residual variance of the model with random replicates within environments (`bys_ls_model()`), in closed form for balanced data:

$$\hat{\sigma}^2 = \frac{\mathrm{SSW} - \mathrm{SS}_{B(E)}}{E(B-1)(G-1)}$$

when the replicate mean square is not smaller, otherwise (the replicate variance component estimated as zero) $\mathrm{SSW}/(GE(B-1))$; SSW is the within-cell and $\mathrm{SS}_{B(E)}$ the replicate-within-environment sum of squares.

Change from the earlier versions. The error variance came from `lme4::lmer()`; the closed form gives the same value for balanced data without needing **lme4**.

Value

A list (class `c("bys_ge_ammi", "bys_result", "list")`) with the components of the earlier versions:

`g`, `e`, `Rep`, `k` numbers of genotypes, environments, replicates and axes.

`ge_means` the result of `bys_ls_means()`.

`mu`, `sigma2`, `tau` grand mean, error variance and its reciprocal (precision).

`tao`, `delta` genotype and environment effects (`bys_ls_gen_effects()`, `bys_ls_env_effects()`).

`lambdas`, `alphas`, `gammas` singular values and genotype and environment singular vectors of the interaction.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

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

See Also

`bayes_ammi`, `bys_ls_ge_effects`

Examples

```
data(cultivo2009)
fit <-
  bys_ls_ammi(
      .data = cultivo2009
    , .y    = y
    , .gen  = entry
    , .env  = site
    , .rep  = rep
    )
fit$lambdas
fit$sigma2
```

---

bys_ls_env_effects *Environment effects*

Description

`bys_ls_env_effects()` computes the environment main effects, the deviations of the environment means from the grand mean.

Usage

```
bys_ls_env_effects(.data, .y, .gen, .env)

## Default S3 method:
bys_ls_env_effects(.data, .y, .gen, .env)
```

Arguments

`.data`	a data frame with one row per plot.
`.y`, `.gen`, `.env`	the columns of the response, genotypes and environments: bare names, strings or vectors.

Details

$$\hat{\delta}_j = \bar{y}_{\cdot j} - \bar{y}, \qquad \bar{y}_{\cdot j} = \frac{1}{G}\sum_i \bar{y}_{ij}.$$

Value

An $E \times 1$ matrix with column `EEffs` (row names: environments).

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

See Also

bys_ls_gen_effects, bys_ls_ge_effects

Examples

```
data(cultivo2009)
bys_ls_env_effects(
    .data = cultivo2009
  , .y    = y
  , .gen  = entry
  , .env  = site
  )
```

---

bys_ls_ge_effects *Genotype-by-environment interaction effects*

Description

`bys_ls_ge_effects()` computes the interaction effects (the cell means centred on genotype and environment means) and their singular value decomposition, the least-squares estimate of the multiplicative part of the AMMI model.

Usage

```
bys_ls_ge_effects(.data, .y, .gen, .env)

## Default S3 method:
bys_ls_ge_effects(.data, .y, .gen, .env)
```

Arguments

`.data`	a data frame with one row per plot.
`.y`, `.gen`, `.env`	the columns of the response, genotypes and environments: bare names, strings or vectors.

Details

$$\mathbf{Z} = (z_{ij}), \quad z_{ij} = \bar{y}_{ij} - \bar{y}_{i\cdot} - \bar{y}_{\cdot j} + \bar{y}, \qquad \mathbf{Z} = \sum_k \lambda_k \boldsymbol{\alpha}_k \boldsymbol{\gamma}_k^\top,$$

with singular values $\lambda_1 \geq \lambda_2 \geq \cdots$ and orthonormal singular vectors orthogonal to $\mathbf{1}$.

Value

A list (class `c("bys_ge_eff", "bys_result", "list")`) with `ge_effects` (the $G \times E$ matrix $\mathbf{Z}$) and `ge_svd` (`svd()` of it: `d`, `u`, `v`).

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

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

See Also

`bys_ls_ammi`

Examples

```
data(cultivo2009)
fit <-
  bys_ls_ge_effects(
      .data = cultivo2009
    , .y    = y
    , .gen  = entry
    , .env  = site
    )
fit$ge_svd$d
```

`bys_ls_gen_effects` *Genotype effects*

Description

`bys_ls_gen_effects()` computes the genotype main effects, the deviations of the genotype means from the grand mean.

Usage

```
bys_ls_gen_effects(.data, .y, .gen, .env)

## Default S3 method:
bys_ls_gen_effects(.data, .y, .gen, .env)
```

Arguments

`.data`	a data frame with one row per plot.
`.y, .gen, .env`	the columns of the response, genotypes and environments: bare names, strings or vectors.

Details

$$\hat{\tau}_i = \bar{y}_{i\cdot} - \bar{y}, \qquad \bar{y}_{i\cdot} = \frac{1}{E}\sum_j \bar{y}_{ij},$$

the least-squares estimates of the AMMI model (equal to the deviations of the plot means when the data are balanced).

Value

A $G \times 1$ matrix with column `GEffs` (row names: genotypes).

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

See Also

`bys_ls_env_effects`, `bys_ls_ge_effects`

Examples

```
data(cultivo2009)
bys_ls_gen_effects(
    .data = cultivo2009
  , .y    = y
  , .gen  = entry
  , .env  = site
  )
```

bys_ls_means *Genotype-by-environment means*

Description

`bys_ls_means()` computes the table of genotype-by-environment cell means and the grand mean, the data of the AMMI model.

Usage

```
bys_ls_means(.data, .y, .gen, .env)

## Default S3 method:
bys_ls_means(.data, .y, .gen, .env)
```

Arguments

`.data`	a data frame with one row per plot.
`.y`, `.gen`, `.env`	the columns of the response, genotypes and environments: bare names, strings or vectors.

Details

With y_{ijl} the response of genotype i in replicate l of environment j and n_{ij} the number of replicates of the cell,

$$\bar{y}_{ij} = \frac{1}{n_{ij}} \sum_{l} y_{ijl}, \qquad \bar{y} = \frac{1}{GE} \sum_{ij} \bar{y}_{ij}.$$

Genotypes and environments are in the order of their factor levels (sorted values when the columns are not factors).

Value

A list (class `c("bys_ge_mean", "bys_result", "list")`) with `ge_means`, the $G \times E$ matrix of means (row and column names: genotypes and environments), and `grand_mean`.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

See Also

`bys_ls_var`, `bys_ls_ge_effects`, `bys_ls_ammi`

Examples

```
data(cultivo2009)
bys_ls_means(
    .data = cultivo2009
  , .y    = y
  , .gen  = entry
  , .env  = site
  )
```

`bys_ls_model` *Linear mixed model of a multi-environment trial*

Description

`bys_ls_model()` fits the two-way model with interaction and random replicates within environments by restricted maximum likelihood (`lme4::lmer()`). Its residual variance is the error variance of the least-squares AMMI fit (`bys_ls_ammi()`, which computes it in closed form).

Usage

```
bys_ls_model(.data, .y, .gen, .env, .rep)

## Default S3 method:
bys_ls_model(.data, .y, .gen, .env, .rep)
```

Arguments

`.data`	a data frame with one row per plot.
`.y`, `.gen`, `.env`, `.rep`	the columns of the response, genotypes, environments and replicates: bare names, strings or vectors.

Details

$$y_{ijl} = \mu + \delta_j + \tau_i + (\tau\delta)_{ij} + b_{l(j)} + e_{ijl}, \qquad b_{l(j)} \sim N(0, \sigma_b^2), \quad e_{ijl} \sim N(0, \sigma^2).$$

The package **lme4** is needed (it is suggested, not required, since version 1.0.0).

Value

The `lmerMod` object of `lme4::lmer(Y ~ Env + Gen + Env:Gen + (1 | Env:Rep))`.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

Bates, D., Maechler, M., Bolker, B. and Walker, S. (2015). Fitting linear mixed-effects models using lme4. *Journal of Statistical Software*, **67**(1), 1–48. doi:10.18637/jss.v067.i01

See Also

bys_ls_ammi

Examples

```
data(cultivo2009)
if (requireNamespace("lme4", quietly = TRUE)) {
  fm <-
    bys_ls_model(
        .data = cultivo2009
      , .y    = y
      , .gen  = entry
      , .env  = site
      , .rep  = rep
      )
  stats::sigma(fm)^2
}
```

---

bys_ls_var *Genotype-by-environment variances*

Description

`bys_ls_var()` computes the variance of the replicates of every genotype-by-environment cell.

Usage

```
bys_ls_var(.data, .y, .gen, .env)

## Default S3 method:
bys_ls_var(.data, .y, .gen, .env)
```

Arguments

`.data`	a data frame with one row per plot.
`.y, .gen, .env`	the columns of the response, genotypes and environments: bare names, strings or vectors.

Details

$$s_{ij}^2 = \frac{1}{n_{ij} - 1} \sum_l (y_{ijl} - \bar{y}_{ij})^2,$$

`NA` for a cell with one replicate. The within-cell sum of squares of the Bayesian AMMI model is $\sum_{ij}(n_{ij} - 1)s_{ij}^2$.

Change from the earlier versions. `bayes_ammi()` used the sum of these variances in place of the within-cell sum of squares.

Value

A list (class `c("bys_ge_var", "bys_result", "list")`) with `ge_variances`, the $G \times E$ matrix of variances.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

See Also

`bys_ls_means`

Examples

```
data(cultivo2009)
bys_ls_var(
    .data = cultivo2009
  , .y    = y
  , .gen  = entry
  , .env  = site
  )
```

`bys_notation` *Notation of baystability*

Description

The symbols used in the help pages and vignettes of **baystability**, with their meaning and the argument or result component that holds them. The notation follows one rule throughout: scalars are upper-case letters in normal face (P, R), indices lower-case italic (i, j), vectors lower-case bold ($\mathbf{y}$, $\boldsymbol{\beta}$) and matrices upper-case bold ($\mathbf{X}$, $\boldsymbol{\Sigma}$).

Usage

```
bys_notation(format = c("table", "path", "tex"))
```

Arguments

format	"table" (default: a data.table with columns symbol (LaTeX), text (plain text), kind (scalar, index, vector, matrix, set, function, operator), meaning and argument), "path" (the path of notation.csv) or "tex" (the path of Notations.tex, the notation appendix used in the articles).

Value

See format.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

See Also

Other baystability utilities: bys_reference(), bys_save(), bys_theme()

Examples

```
bys_notation(
    format = c("table", "path", "tex")[1]
  )
```

---

bys_orthonormal *Gram-Schmidt orthonormalisation*

Description

bys_orthonormal() orthogonalises the columns of a matrix by the Gram-Schmidt process, optionally completes them to a basis of the whole space and scales them to unit length.

Usage

```
bys_orthonormal(u = NULL, basis = TRUE, norm = TRUE)

## Default S3 method:
bys_orthonormal(u = NULL, basis = TRUE, norm = TRUE)
```

Arguments

u	a matrix (or vector) whose columns are orthogonalised.
basis	complete the columns to a basis of the whole space (default TRUE).
norm	scale the columns to unit length (default TRUE).

Details

For columns $\mathbf{u}_1, \ldots, \mathbf{u}_m$,

$$\mathbf{v}_1 = \mathbf{u}_1, \qquad \mathbf{v}_i = \mathbf{u}_i - \sum_{h<i} \frac{\mathbf{u}_i^\top \mathbf{v}_h}{\mathbf{v}_h^\top \mathbf{v}_h} \mathbf{v}_h,$$

each divided by its length when `norm = TRUE`. With `basis = TRUE` and fewer columns than rows, unit vectors are added (those least explained by the given columns) to complete a basis.

Value

The matrix of orthogonal (orthonormal with `norm = TRUE`) columns; `NULL` for `u = NULL`.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

See Also

`bys_contrasts`

Examples

```
V <-
  bys_orthonormal(
      u     = cbind(1, 1:4)
    , basis = TRUE
    , norm  = TRUE
    )
round(x = crossprod(V), digits = 10)
```

`bys_priors` *Prior distributions of the Bayesian AMMI model*

Description

`bys_priors()` sets the hyperparameters of the prior distributions of `bayes_ammi()`. The defaults are the vague but proper priors of Crossa et al. (2011): normal priors with mean zero and variance 10^8 for the overall mean, the main effects and the singular values, and a scaled inverse chi-square prior with one degree of freedom for the error variance.

Usage

```
bys_priors(
  mu_mean = 0,
  mu_var = 1e+08,
  tau_mean = 0,
  tau_var = 1e+08,
  delta_mean = 0,
  delta_var = 1e+08,
  lambda_mean = 0,
  lambda_var = 1e+08,
  nu = 1,
  s2 = NULL
)

## S3 method for class 'bys_priors'
print(x, ...)
```

Arguments

`mu_mean`, `mu_var`	prior mean and variance of the overall mean μ.
`tau_mean`, `tau_var`	prior mean (a scalar or a vector of length G) and variance of the genotype effects τ_i.
`delta_mean`, `delta_var`	prior mean (scalar or length E) and variance of the environment effects δ_j.
`lambda_mean`, `lambda_var`	prior mean and variance of the singular values λ_k.
`nu`, `s2`	degrees of freedom ν and scale S_0^2 of the prior of the error variance (`s2 = NULL`: the least-squares residual mean square).
`x`	a `"bys_priors"` object.
`...`	unused.

Details

With G genotypes, E environments and K bilinear terms,

$$\mu \sim N(\mu_0, \sigma_\mu^2), \quad \boldsymbol{\tau} \sim N(\mathbf{m}_\tau, \sigma_\tau^2 \mathbf{I}_G), \quad \boldsymbol{\delta} \sim N(\mathbf{m}_\delta, \sigma_\delta^2 \mathbf{I}_E),$$

each main effect restricted to sum zero,

$$\lambda_k \sim N^+(\lambda_0, \sigma_\lambda^2), \quad \lambda_1 \geq \lambda_2 \geq \cdots \geq \lambda_K > 0, \qquad \sigma^2 \sim \text{Inv-}\chi^2(\nu, S_0^2),$$

and spherical uniform priors for the singular vectors on the subspaces orthogonal to $\mathbf{1}$ and to the other vectors. S_0^2 = `NULL` (default) takes the residual mean square of the least-squares AMMI fit, so that the prior is equally vague whatever the unit of the trait; with $\nu = 1$ it carries the information of a single observation. Crossa et al. (2011) report $S_0 = 10^8$; their published posterior of σ^2 is reproduced with the vague default (see the vignette on validation).

Value

A list of class "bys_priors" with these elements.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

Hobert, J. P. and Casella, G. (1996). The effect of improper priors on Gibbs sampling in hierarchical linear mixed models. *Journal of the American Statistical Association*, **91**(436), 1461–1473.

See Also

bayes_ammi

Examples

```
bys_priors(
    mu_mean     = 0
  , mu_var      = 1e8
  , tau_mean    = 0
  , tau_var     = 1e8
  , delta_mean  = 0
  , delta_var   = 1e8
  , lambda_mean = 0
  , lambda_var  = 1e8
  , nu          = 1
  , s2          = NULL
  )
```

---

bys_reference *Published values used by the tests and vignettes*

Description

Reads inst/extdata/reference.csv: one row per published number, with its source, the R call that recomputes it with this package (call), the expression that extracts the number from the result (extract, in terms of x), the printed value and the digits to compare. The same file drives the test of published values and the vignette that reproduces the published examples. Each distinct call is evaluated once.

Usage

```
bys_reference(source = NULL, evaluate = FALSE, level = 1)
```

Arguments

source	optional regular expression; keep rows whose source matches.
evaluate	logical; evaluate the rows and add columns computed and agrees (default FALSE).
level	largest level evaluated (1 = fast rows, 2 = slow rows; default 1); rows above it get NA.

Value

A data.table with columns id, source, quantity, call, extract, value, digits, level, note (and computed, agrees).

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

See Also

Other baystability utilities: bys_notation(), bys_save(), bys_theme()

Examples

```
ref <-
  bys_reference(
      source   = NULL
    , evaluate = FALSE
    , level    = 1
    )
ref

bys_reference(
    source   = "."
  , evaluate = TRUE
  , level    = 1
  )
```

---

bys_save *Save a figure (vector PDF by default)*

Description

A wrapper of ggsave with the defaults of the package: a vector PDF through cairo_pdf (embedded fonts, correct glyphs), A4 landscape (11.69 x 8.27 inches) and 600 dpi for raster formats. The device follows the file extension for other formats (.png, .svg, .tiff, ...).

Usage

```
bys_save(
  plot = ggplot2::last_plot(),
  filename,
  path = NULL,
  width = 11.69,
  height = 8.27,
  units = c("in", "cm", "mm"),
  dpi = 600,
  scale = 1,
  device = NULL,
  limitsize = TRUE,
  ...
)

## Default S3 method:
bys_save(
  plot = ggplot2::last_plot(),
  filename,
  path = NULL,
  width = 11.69,
  height = 8.27,
  units = c("in", "cm", "mm"),
  dpi = 600,
  scale = 1,
  device = NULL,
  limitsize = TRUE,
  ...
)
```

Arguments

plot	a ggplot object, for example the result of plot() on a baystability result (default: the last plot).
filename	file name; its extension chooses the format.
path	directory to save in (default NULL: the working directory or the path in filename).
width, height	size (default 11.69 x 8.27, A4 landscape, in units).
units	"in" (default), "cm" or "mm".
dpi	resolution for raster formats (default 600).
scale	multiplicative scaling factor (default 1).
device	NULL (default: cairo_pdf for .pdf, otherwise chosen from the extension) or a device function or name, passed to ggsave(). A file name ending in .webp gives a WebP image (drawn as PNG, then converted without loss by the suggested package **magick**; about half the size of the PNG).
limitsize	logical; refuse images larger than 50 x 50 inches (default TRUE).
...	passed to ggsave.

Value

The file name, invisibly.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

See Also

Other baystability utilities: bys_notation(), bys_reference(), bys_theme()

Examples

```
library(ggplot2)
p <-
  ggplot(data = data.frame(x = 1:10, y = (1:10)^2), mapping = aes(x = x, y = y)) +
  geom_line() +
  bys_theme(
      base_size       = 11
    , base_family     = "serif"
    , ticks_inward    = TRUE
    , legend_position = "bottom"
    )
f <- tempfile(fileext = ".pdf")
bys_save(
    plot      = p
  , filename  = f
  , path      = NULL
  , width     = 11.69
  , height    = 8.27
  , units     = c("in", "cm", "mm")[1]
  , dpi       = 600
  , scale     = 1
  , device    = NULL
  , limitsize = TRUE
  )
bys_save(
    plot      = p
  , filename  = basename(f)
  , path      = tempdir()
  , width     = 11.69
  , height    = 8.27
  , units     = c("in", "cm", "mm")[1]
  , dpi       = 600
  , scale     = 1
  , device    = grDevices::cairo_pdf
  , limitsize = TRUE
  )
bys_save(
    plot      = p
  , filename  = tempfile(fileext = ".png")
  , path      = NULL
```

```
  , width     = 6
  , height    = 4
  , units     = c("in", "cm", "mm")[1]
  , dpi       = 300
  , scale     = 1
  , device    = NULL
  , limitsize = TRUE
  )
```

---

bys_theme *ggplot2 theme of baystability*

Description

The theme used by every `plot()` method of **baystability** (identical in all packages of the author): `theme_classic` with a serif font, black axis lines, ticks pointing inwards and no grid, close to the look of TikZ/pgfplots figures in LaTeX documents. The `plot()` methods also use `scales::pretty_breaks(n = 10)` on every continuous axis. Save figures with `bys_save`.

Usage

```
bys_theme(
  base_size = 11,
  base_family = "serif",
  ticks_inward = TRUE,
  legend_position = "bottom"
)
```

Arguments

`base_size`	base font size in points (default 11).
`base_family`	font family (default `"serif"`; for example `"Latin Modern Roman"` when installed, to match LaTeX documents).
`ticks_inward`	logical; ticks point into the panel, as in pgfplots (default `TRUE`).
`legend_position`	position of the legend (default `"bottom"`).

Value

A `ggplot2` theme.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

See Also

Other baystability utilities: `bys_notation()`, `bys_reference()`, `bys_save()`

Examples

```
library(ggplot2)
p <-
  ggplot(data = data.frame(x = 1:20, y = cumsum(sin(1:20))), mapping = aes(x = x, y = y)) +
  geom_line()
p +
  bys_theme(
      base_size       = 11
    , base_family     = "serif"
    , ticks_inward    = TRUE
    , legend_position = "bottom"
    )
p +
  bys_theme(
      base_size       = 12
    , base_family     = "serif"
    , ticks_inward    = FALSE
    , legend_position = "right"
    ) +
  scale_x_continuous(breaks = scales::pretty_breaks(n = 10))
```

---

cultivo2008 *Maize trials of 2008 and 2009*

Description

Grain yield of 12 maize hybrids in 25 environments in two consecutive years, the multi-environment trial of Perez-Elizalde et al. (2012), Section 3.2: `cultivo2008` (the first year, used as the prior) and `cultivo2009` (the second year). Randomized complete blocks with 3 replicates in every environment.

Format

Data frames with 900 rows (12 genotypes x 25 environments x 3 replicates) and 4 columns:

`site` environment, 1 to 25 (the same environments in both years).

`rep` replicate, 1 to 3.

`entry` genotype, 1 to 12.

`y` grain yield (kg/ha).

Details

The paper describes two replicates; the data have three. The posterior means of its Table B.1 are, to within a posterior standard deviation of a hundredth, the averages of the least-squares estimates of the two years, as the method gives with equal weights for both years (see the vignette on the published analysis). The help page of version 0.2.0 described another data set.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

Source

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/s1325301100639

Examples

```
data(cultivo2008)
data(cultivo2009)
str(cultivo2009)
bys_ls_means(
    .data = cultivo2009
  , .y    = y
  , .gen  = entry
  , .env  = site
  )$grand_mean
```

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