Package 'bayesammi'

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Type Package

Title Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model

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Description Bayesian estimation of the additive main effects and multiplicative interaction (AMMI) model of multi-environment trials by the Gibbs sampler of Crossa, Perez-Elizalde, Jarquin, Cotes, Viele, Liu and Cornelius (2011) <doi:10.2135/cropsci2010.06.0343>: posterior distributions of the overall mean, genotype and environment effects, singular values, genotype and environment scores (von Mises-Fisher conditionals on the constrained spheres) and error variance; several chains with burn-in and thinning; posterior summaries with highest posterior density intervals; the convergence diagnostics of Raftery-Lewis, Heidelberger-Welch and Gelman-Rubin; the AMMI biplot with highest posterior density regions for inference on genotypes and environments; least-squares AMMI; and a plain-language interpretation of every result, computed from its numbers. Beyond the article: unbalanced trials with missing plots and cells (data augmentation), environment-specific error variances, the Bayesian GGE (sites regression) model of Perez-Elizalde, Jarquin and Crossa (2012) <doi:10.1007/s13253-011-0063-9>, probabilities of superior performance and stability (Dias et al. 2022 <doi:10.1007/s00122-022-04041-y>), posterior ranks, Bayesian stability measures, predictions and the winner of every environment, model choice by DIC and WAIC with posterior predictive checks, draws for the 'posterior', 'bayesplot' and 'coda' packages, a compiled sampler, and a built-in 'shiny' application. Bayesian stability analysis: the Finlay-Wilkinson, Eberhart-Russell and Shukla models by Gibbs sampling, and the posterior distributions of classical stability indices (Wricke, Shukla, Lin-Binns, Annicchiarico, Eskridge's safety-first) and of AMMI-based indices (ASV, SIPC, EV, Za, WAAS, WAASY). Every result prints the references of its method.

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

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

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`bam-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 'bam_bayes_ammi'
as_draws_df(x, ...)

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

## S3 method for class 'bam_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(Maiz)
fit <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 500
    , .k      = 2
    , .burnin = 100
    , .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   = 1
    , .align  = TRUE
    , .model  = "AMMI"
    , .het    = FALSE
    , .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]"))
}
```

`bam-methods` *Methods for bayesammi results*

Description

The analysis functions of **bayesammi** return the named list they have always returned, now with the class `c("bam_<analysis>", "bam_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 'bam_result'
print(x, digits = 4L, ...)

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

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

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

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

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

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

Arguments

x, object	a bayesammi 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.bam_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>)

---

bam_ammi_indices *Posterior distributions of AMMI-based stability indices*

Description

bam_ammi_indices() computes the AMMI stability value and the other stability indices built from the singular values and genotype scores of an AMMI or GGE fit on every posterior draw: ASV (Purchase et al. 2000), SIPC (Sneller et al. 1997), EV (Zobel 1994), Za (Zali et al. 2012), WAAS and the mean-stability index WAASY (Olivoto et al. 2019).

Usage

```
bam_ammi_indices(fit, higher_better = TRUE, .weight_y = 50)
```

Arguments

fit	a result of bayes_ammi().
higher_better	TRUE (default) when larger values of the trait are better (for WAASY).
.weight_y	weight θ_Y (0-100) of the mean in WAASY (default 50, equal weights).

Details

With K multiplicative terms, singular values λ_k, genotype scores α_{ik}, coordinates $\mathrm{PC}_{ik} = \lambda_k^{1/2}\alpha_{ik}$ and the share of term k in the fitted interaction $\theta_k = \lambda_k^2 / \sum_m \lambda_m^2$, on every draw:

`ASV` $\sqrt{(\lambda_1^2/\lambda_2^2\,\mathrm{PC}_{i1})^2 + \mathrm{PC}_{i2}^2}$, with the ratio of the posterior means of the singular values (as in `bam_stability()`; a ratio of draws explodes when λ_2 comes near zero); needs $K \geq 2$.

`SIPC` $\sum_k |\mathrm{PC}_{ik}|$.

`EV` $\sum_k \alpha_{ik}^2 / K$.

`Za` $\sum_k \theta_k |\alpha_{ik}|$.

`WAAS` $\sum_k \theta_k |\mathrm{PC}_{ik}|$ (the weights sum to one).

`WAASY` $(\theta_Y R_i^Y + (100 - \theta_Y) R_i^W)/100$, where R_i^Y rescales the genotype means to 0-100 (100 for the best) and R_i^W rescales WAAS to 0-100 (100 for the most stable); larger is better.

All but WAASY are smaller for more stable genotypes. The shares θ_k are those of the K fitted terms; Zali et al. (2012) and Olivoto et al. (2019) use the shares of the significant terms in the whole interaction, which differ by a constant factor for Za and not at all for WAAS.

Value

An object of class `c("bam_ammi_indices", "bam_result", "list")` with `indices` and `means`, as in `bam_indices()`. Methods: `print()`, `plot()`, `bam_interpret()`, `bam_cite()`.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

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

Sneller, C. H., Kilgore-Norquest, L. and Dombek, D. (1997). Repeatability of yield stability statistics in soybean. *Crop Science*, **37**(2), 383–390.

Zobel, R. W. (1994). Stress resistance and root systems. In *Proceedings of the Workshop on Adaptation of Plants to Soil Stress*, INTSORMIL Publication 94-2, 80–99. University of Nebraska-Lincoln.

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

Olivoto, T., Lucio, A. D. C., da Silva, J. A. G., Marchioro, V. S., de Souza, V. Q. and Jost, E. (2019). Mean performance and stability in multi-environment trials I: combining features of AMMI and BLUP techniques. *Agronomy Journal*, **111**(6), 2949–2960. doi:10.2134/agronj2019.03.0220

See Also

`bam_indices`, `bam_stability`

Other stability: `bam_indices()`, `bam_stab_priors()`, `bayes_stability()`

Examples

```
data(Maiz)
fit <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 600
    , .k      = 2
    , .burnin = 100
    , .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          = NULL
        )
    , .level  = 0.95
    , .seed   = 1
    , .align  = TRUE
    , .model  = "AMMI"
    , .het    = FALSE
    , .waic   = TRUE
    )
ai <-
  bam_ammi_indices(
      fit           = fit
    , higher_better = TRUE
    , .weight_y     = 50
    )
ai$means
plot(x = ai)
```

---

bam_app *Bayesian AMMI and GGE analysis in a web browser*

Description

`bam_app()` starts the application of **bayesammi**: load a trial (the example `Maiz` or a CSV file with one row per plot), fit the Bayesian AMMI or GGE model, check convergence, draw the biplot with HPD regions, and turn the posterior into decisions (which genotype wins where, probabilities of

superior performance and stability, ranks, Bayesian stability, predictions of missing cells), and compare models. Every page shows an interpretation computed from the results (bam_interpret()), the output as R prints it, formatted tables, plots and the R code that repeats the analysis, each with a Copy button.

Usage

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

bam_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

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

Author(s)

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See Also

bayes_ammi, bam_interpret

Examples

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

bam_cite *References of a result or of the package*

Description

bam_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("bayesammi") cites the package and its main methods.

Usage

```
bam_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

```
bam_cite(
    x     = NULL
  , style = "text"
  )
data(Maiz)
g <-
  ge_ammi(
      .data = Maiz
    , .y    = y
    , .gen  = entry
    , .env  = site
    , .rep  = rep
    )
bam_cite(
    x     = g
  , style = "bibtex"
  )
```

`bam_compare` *Compare Bayesian AMMI and GGE models*

Description

`bam_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

```
bam_compare(...)
```

Arguments

`...`	fits of `bayes_ammi()` or `bayes_stability()` 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("bam_compare", "bam_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()`, `bam_interpret()`.

Author(s)

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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

See Also

bam_ppc

Other model choice: bam_ppc()

Examples

```
data(Maiz)
fits <-
  lapply(
      X   = 1:2
    , FUN = function(K) {
        bayes_ammi(
            .data   = Maiz
          , .y      = y
          , .gen    = entry
          , .env    = site
          , .rep    = rep
          , .nIter  = 600
          , .k      = K
          , .burnin = 100
          , .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          = NULL
              )
          , .level  = 0.95
          , .seed   = 1
```

```
          , .align  = TRUE
          , .model  = "AMMI"
          , .het    = FALSE
          , .waic   = TRUE
          )
      }
    )
bam_compare(
    AMMI1 = fits[[1]]
  , AMMI2 = fits[[2]]
  )
```

`bam_indices` *Posterior distributions of classical stability indices*

Description

`bam_indices()` computes five classical stability and superiority indices on every posterior draw of the cell means of a fit, so that each index has a posterior mean, an HPD interval and, for every genotype, a probability of being the best. The indices are those of Wricke (1962), Shukla (1972), Lin and Binns (1988), Annicchiarico (1992) and Eskridge (1990).

Usage

```
bam_indices(fit, higher_better = TRUE, .prob = 0.25, .alpha = 0.05)
```

Arguments

`fit`	a result of `bayes_ammi()` or `bayes_stability()`.
`higher_better`	`TRUE` (default) when larger values of the trait are better.
`.prob`	error probability p of Annicchiarico's index (default 0.25).
`.alpha`	probability α of the safety-first index (default 0.05).

Details

With η_{ij} the cell mean of genotype i in environment j (one posterior draw), $\bar{\eta}_{i\cdot}$, $\bar{\eta}_{\cdot j}$ and $\bar{\eta}_{\cdot\cdot}$ the genotype, environment and overall means, and the interaction $\epsilon_{ij} = \eta_{ij} - \bar{\eta}_{i\cdot} - \bar{\eta}_{\cdot j} + \bar{\eta}_{\cdot\cdot}$:

`wricke` ecovalence $W_i = \sum_j \epsilon_{ij}^2$; smaller is more stable.

`shukla` stability variance $\sigma_i^2 = \frac{G}{(G-2)(E-1)} W_i - \frac{\sum_k W_k}{(G-1)(G-2)(E-1)}$; smaller is more stable.

`lin_binns` superiority $P_i = \sum_j (\eta_{ij} - M_j)^2/(2E)$, M_j the best cell mean of environment j; smaller is better.

`annicchiarico` reliability $I_i = \bar{Z}_i - z_{1-p} s_{Z_i}$ with $Z_{ij} = 100\,\eta_{ij}/\bar{\eta}_{\cdot j}$; larger is better (with `higher_better = FALSE`: $\bar{Z}_i + z_{1-p} s_{Z_i}$, smaller better).

`safety_first` Eskridge's index with the variance across environments, $\bar{\eta}_{i\cdot} - z_{1-\alpha} s_i$; larger is better (with `higher_better = FALSE`: $\bar{\eta}_{i\cdot} + z_{1-\alpha} s_i$, smaller better). `bayes_stability()` gives the model-based versions of the regression and Shukla models.

Because the indices are computed from the posterior of the cell means, they measure the stability of the expected performance, free of the plot error; the HPD intervals show how well the trial determines them.

Value

An object of class `c("bam_indices", "bam_result", "list")` with

`indices` `data.table` in long form: `index`, `Gen`, `mean`, `lower`, `upper` (HPD interval), `prob_best` (posterior probability that the genotype is the best on this index) and `rank_mean` (expected rank, 1 = best).

`means` `data.table`: one row per genotype with the posterior means of the indices and the mean of their expected ranks (`rank_overall`), sorted by it.

Methods: `print()`, `plot()`, `bam_interpret()`, `bam_cite()`.

Author(s)

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References

Wricke, G. (1962). Uber eine Methode zur Erfassung der okologischen Streubreite in Feldversuchen. *Zeitschrift fur Pflanzenzuchtung*, **47**, 92–96.

Shukla, G. K. (1972). Some statistical aspects of partitioning genotype-environmental components of variability. *Heredity*, **29**(2), 237–245. doi:10.1038/hdy.1972.87

Lin, C. S. and Binns, M. R. (1988). A superiority measure of cultivar performance for cultivar x location data. *Canadian Journal of Plant Science*, **68**(1), 193–198. doi:10.4141/cjps88018

Annicchiarico, P. (1992). Cultivar adaptation and recommendation from alfalfa trials in Northern Italy. *Journal of Genetics and Breeding*, **46**, 269–278.

Eskridge, K. M. (1990). Selection of stable cultivars using a safety-first rule. *Crop Science*, **30**, 369–374.

See Also

`bam_ammi_indices`, `bayes_stability`, `bam_superiority`

Other stability: `bam_ammi_indices()`, `bam_stab_priors()`, `bayes_stability()`

Examples

```
data(Maiz)
fit <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 600
```

```
    , .k      = 2
    , .burnin = 100
    , .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          = NULL
        )
    , .level  = 0.95
    , .seed   = 1
    , .align  = TRUE
    , .model  = "AMMI"
    , .het    = FALSE
    , .waic   = TRUE
    )
ind <-
  bam_indices(
      fit           = fit
    , higher_better = TRUE
    , .prob         = 0.25
    , .alpha        = 0.05
    )
ind$means
plot(x = ind)
```

`bam_interpret` *Interpretation of a Bayesian AMMI analysis*

Description

`bam_interpret()` turns a result of `bayes_ammi()`, `biplots()` or `ge_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

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

## S3 method for class 'bam_interpretation'
```

```
print(x, ...)

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

Arguments

x	a result of bayes_ammi(), biplots() or ge_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 (biplots()): a genotype is stable when its HPD region contains the origin.

Value

An object of class "bam_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; bam_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, biplots

Examples

```
data(Maiz)
fm1 <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 500
    , .k      = 2
    , .burnin = 100
    , .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   = 1
    , .align  = TRUE
    , .model  = c("AMMI", "GGE")
    , .het    = FALSE
    , .waic   = TRUE
    )
txt <-
  bam_interpret(
      x             = fm1
    , higher_better = TRUE
    , top           = 5
    )
txt
cat(format(x = txt, style = "markdown"))
```

---

bam_notation *Notation of bayesammi*

Description

The symbols used in the help pages and vignettes of **bayesammi**, 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

```
bam_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 bayesammi utilities: `bam_reference()`, `bam_save()`, `bam_theme()`

Examples

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

---

bam_ppc *Posterior predictive checks*

Description

`bam_ppc()` compares statistics of the observed trial with their distribution in trials replicated from the posterior predictive distribution (Gelman et al. 1996). A posterior predictive p-value near 0 or 1 shows a feature of the data that the model does not reproduce, for instance unequal error variances or a missing interaction term.

Usage

```
bam_ppc(fit, .draws = 1000L, .seed = NULL)
```

Arguments

fit	a result of bayes_ammi() or bayes_stability().
.draws	number of posterior draws used (default 1000).
.seed	seed for the replicated trials (the random number state of the session is restored).

Details

For a subset of .draws posterior draws, a trial $\mathbf{y}^{\text{rep}}$ with the observed plots is simulated from $N(\eta_{ij}, \sigma_j^2)$, and for each statistic T $p = \Pr(T(\mathbf{y}^{\text{rep}}) \geq T(\mathbf{y}) \mid \mathbf{y})$. The statistics: variance of the cell means, largest and smallest cell mean, variance of the genotype means, first singular value of the interaction effects of the cell means, pooled within-cell variance, and the ratio of the largest to the smallest within-environment variance.

Value

An object of class c("bam_ppc", "bam_result", "list") with checks (data.table: statistic, observed, mean_rep, p_value) and replicated (data.table of the replicated statistics). Methods: print(), plot(), bam_interpret().

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

Gelman, A., Meng, X.-L. and Stern, H. (1996). Posterior predictive assessment of model fitness via realized discrepancies. *Statistica Sinica*, **6**(4), 733–807.

See Also

bam_compare

Other model choice: bam_compare()

Examples

```
data(Maiz)
fit <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 600
    , .k      = 2
    , .burnin = 100
    , .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          = NULL
          )
      , .level  = 0.95
      , .seed   = 1
      , .align  = TRUE
      , .model  = "AMMI"
      , .het    = FALSE
      , .waic   = TRUE
      )
pc <-
  bam_ppc(
      fit    = fit
    , .draws = 300
    , .seed  = 1
    )
pc$checks
plot(x = pc)
```

`bam_predict` *Predictions of every genotype-environment cell*

Description

`bam_predict()` gives the posterior distribution of the expected response of every genotype in every environment, including the cells that were not observed, and of the genotype means over the environments.

Usage

```
bam_predict(fit, .level = NULL)
```

Arguments

`fit`	a result of `bayes_ammi()` or `bayes_stability()` (`bam_stability()` needs `bayes_ammi()`).
`.level`	probability of the HPD intervals (default: that of the fit).

Details

For draw s,

$$\eta_{ij}^{(s)} = \mu^{(s)} + \tau_i^{(s)} + \delta_j^{(s)} + \sum_{k=1}^{K} \lambda_k^{(s)} \alpha_{ik}^{(s)} \gamma_{jk}^{(s)}$$

(without τ_i in the GGE model); the genotype mean over the environments is $\bar{\eta}_{i\cdot} = E^{-1} \sum_j \eta_{ij}$. A missing cell is predicted from the main effects and from the interaction pattern its genotype and environment show in the other cells; the data augmentation of `bayes_ammi()` has already propagated its uncertainty into all parameters.

Value

An object of class `c("bam_predict", "bam_result", "list")`:

`cells` `data.table`: `Gen`, `Env`, `n` (plots observed), `observed` (their mean, `NA` when missing), `mean`, `sd`, `lower`, `upper`.

`genotypes` `data.table`: posterior mean, sd and HPD interval of every genotype mean.

Methods: `print()`, `plot()` (`which = c("cells", "genotypes")`), `bam_interpret()`.

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

`bam_winners`, `bam_superiority`

Other decisions: `bam_ranks()`, `bam_stability()`, `bam_superiority()`, `bam_winners()`

Examples

```
data(Maiz)
d <- Maiz[!(Maiz$entry == 8 & Maiz$site == 8), ]
fit <-
  bayes_ammi(
      .data   = d
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 1000
    , .k      = 2
    , .burnin = 200
    , .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          = NULL
        )
    , .level  = 0.95
    , .seed   = 1
    , .align  = TRUE
    , .model  = "AMMI"
    , .het    = FALSE
    , .waic   = TRUE
    )
pr <-
  bam_predict(
      fit    = fit
    , .level = 0.95
    )
pr$cells[n == 0]
```

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

Description

`bam_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

```
bam_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 'bam_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 "bam_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 "bam_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

```
bam_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
  )
```

---

bam_ranks *Posterior distribution of the ranks of the genotypes*

Description

bam_ranks() gives the posterior probability that each genotype takes each rank, by its mean over the environments (the marginal value) or within one environment, with the expected rank and its HPD interval.

Usage

```
bam_ranks(fit, higher_better = TRUE, .env = NULL)
```

Arguments

fit	a result of bayes_ammi() or bayes_stability() (bam_stability() needs bayes_ammi()).
higher_better	TRUE (default) when larger values of the trait are better.
.env	NULL (default: marginal values) or the label of an environment.

Details

In draw s the genotypes are ranked by $\bar{\eta}_{i\cdot}^{(s)}$ (1 = best); the probability of rank r is the share of draws in which genotype i takes it. Ranks summarise the uncertainty of a selection decision better than intervals of the means, since they account for all the genotypes jointly.

Value

An object of class `c("bam_ranks", "bam_result", "list")`: `probabilities` (matrix genotypes x ranks) and `summary` (`data.table`: `Gen`, `mean_rank`, `median_rank`, `lower`, `upper` of the HPD interval of the rank, `prob_first`). Methods: `print()`, `plot()`, `bam_interpret()`.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

Dias, K. O. G., dos Santos, J. P. R., Krause, M. D., Piepho, H.-P., Guimaraes, L. J. M., Pastina, M. M. and Garcia, A. A. F. (2022). Leveraging probability concepts for cultivar recommendation in multi-environment trials. *Theoretical and Applied Genetics*. doi:10.1007/s0012202204041y

See Also

`bam_superiority`

Other decisions: `bam_predict()`, `bam_stability()`, `bam_superiority()`, `bam_winners()`

Examples

```
data(Maiz)
fit <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 1000
    , .k      = 2
    , .burnin = 200
    , .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          = NULL
         )
    , .level  = 0.95
    , .seed   = 1
    , .align  = TRUE
    , .model  = "AMMI"
    , .het    = FALSE
    , .waic   = TRUE
    )
rk <-
  bam_ranks(
      fit           = fit
    , higher_better = TRUE
    , .env          = NULL
    )
rk$summary
plot(x = rk)
```

---

bam_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

```
bam_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 bayesammi utilities: bam_notation(), bam_save(), bam_theme()

Examples

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

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

---

bam_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

```
bam_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 bayesammi 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 bayesammi utilities: bam_notation(), bam_reference(), bam_theme()

Examples

```
library(ggplot2)
p <-
  ggplot(data = data.frame(x = 1:10, y = (1:10)^2), mapping = aes(x = x, y = y)) +
  geom_line() +
  bam_theme(
      base_size       = 11
    , base_family     = "serif"
    , ticks_inward    = TRUE
    , legend_position = "bottom"
    )
f <- tempfile(fileext = ".pdf")
bam_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
  )
bam_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
  )
bam_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
  )
```

`bam_stability` *Bayesian stability of the genotypes*

Description

`bam_stability()` gives the posterior distributions of two stability measures of every genotype: the AMMI stability value (ASV) of Purchase et al. (2000) computed draw by draw, and the variance of the interaction effects over the environments (Shukla's stability variance of the model), with posterior means, HPD intervals, the probability of being the most stable genotype and the posterior expected ranks, combined with the mean into a Bayesian yield stability index.

Usage

```
bam_stability(fit, higher_better = TRUE)
```

Arguments

`fit`	a result of `bayes_ammi()` or `bayes_stability()` (`bam_stability()` needs `bayes_ammi()`).
`higher_better`	`TRUE` (default) when larger values of the trait are better.

Details

With the biplot scores $u_{ik} = \lambda_k^{1/2}\alpha_{ik}$ and the sums of squares of the terms proportional to λ_k^2,

$$\mathrm{ASV}_i = \sqrt{\left(\frac{\bar{\lambda}_1^2}{\bar{\lambda}_2^2}u_{i1}\right)^2 + u_{i2}^2}, \qquad V_i = \frac{1}{E-1}\sum_j ge_{ij}^2,$$

($\mathrm{ASV}_i = |u_{i1}|$ with one term), evaluated in every draw. The weight of the first axis uses the posterior means $\bar{\lambda}_k$ of the singular values: the ratio of the draws themselves has no finite mean when the posterior of λ_2 reaches zero. The Bayesian yield stability index is the sum of the posterior expected ranks of the mean and of the ASV.

Value

An object of class `c("bam_stability", "bam_result", "list")` with `stability` (`data.table` sorted by the index: `Gen`, `mean`, `ASV`, `ASV_lower`, `ASV_upper`, `variance`, `prob_most_stable` (smallest ASV), `rank_mean`, `rank_ASV`, `YSI`). Methods: `print()`, `plot()`, `bam_interpret()`.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

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

Shukla, G. K. (1972). Some statistical aspects of partitioning genotype-environmental components of variability. *Heredity*, **29**(2), 237–245. doi:10.1038/hdy.1972.87

See Also

`bam_superiority`

Other decisions: `bam_predict()`, `bam_ranks()`, `bam_superiority()`, `bam_winners()`

Examples

```
data(Maiz)
fit <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 1000
    , .k      = 2
    , .burnin = 200
    , .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          = NULL
        )
    , .level  = 0.95
    , .seed   = 1
    , .align  = TRUE
    , .model  = "AMMI"
    , .het    = FALSE
    , .waic   = TRUE
    )
st <-
  bam_stability(
      fit           = fit
    , higher_better = TRUE
    )
st$stability
```

`bam_stab_priors` *Priors of the Bayesian stability models*

Description

`bam_stab_priors()` sets the prior distributions of `bayes_stability()`: normal priors for the overall mean and the contrasts of the genotype effects, environment effects (the environmental index) and slope deviations, and scaled inverse chi-squared priors for the error variance and the deviation variances.

Usage

```
bam_stab_priors(
  mu_var = NULL,
  g_var = NULL,
  h_var = NULL,
  b_var = 100,
  nu = 1,
  s2 = NULL,
  nu_d = 1,
  s2_d = NULL
)
```

Arguments

`mu_var`, `g_var`, `h_var`
: prior variances of the overall mean and of the contrasts of the genotype and environment effects (`NULL`: 10^4 times the variance of the response).

`b_var`
: prior variance of the contrasts of the slope deviations b_i (default 100; the slopes are $1 + b_i$, without unit).

`nu`, `s2`
: degrees of freedom and scale of the prior of the error variance (`s2 = NULL`: the within-cell mean square).

`nu_d`, `s2_d`
: degrees of freedom and scale of the prior of the deviation variances (`s2_d = NULL`: the pooled least-squares deviation variance).

Details

$$\mu \sim N(0, \sigma_\mu^2), \quad \mathbf{K}_G\mathbf{g} \sim N(\mathbf{0}, \sigma_g^2\mathbf{I}), \quad \mathbf{K}_E\mathbf{h} \sim N(\mathbf{0}, \sigma_h^2\mathbf{I}), \quad \mathbf{K}_G\mathbf{b} \sim N(\mathbf{0}, \sigma_b^2\mathbf{I}),$$
$$\sigma^2 \sim \text{Inv-}\chi^2(\nu, S_0^2), \qquad \sigma_{d,i}^2 \sim \text{Inv-}\chi^2(\nu_d, S_d^2),$$

where $\mathbf{K}_n$ are the orthonormal contrasts of `matrix_k()`, so that the effects and the slope deviations sum to zero. Variances left `NULL` are set from the data: 10^4 times the variance of the response for the effects, and the least-squares estimates for S_0^2 and S_d^2, so that the priors carry the information of ν and ν_d observations whatever the unit of the trait.

Value

An object of class `c("bam_stab_priors", "list")`.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

Lian, L. and de los Campos, G. (2016). FW: an R package for Finlay-Wilkinson regression that incorporates genomic/pedigree information and covariance structures between environments. *G3: Genes, Genomes, Genetics*, **6**(3), 589–597. doi:10.1534/g3.115.026328

See Also

`bayes_stability`

Other stability: `bam_ammi_indices()`, `bam_indices()`, `bayes_stability()`

Examples

```
bam_stab_priors(
    mu_var = NULL
  , g_var  = NULL
  , h_var  = NULL
  , b_var  = 100
  , nu     = 1
```

```
, s2     = NULL
, nu_d   = 1
, s2_d   = NULL
)
```

`bam_superiority` *Probabilities of superior performance and stability*

Description

`bam_superiority()` computes the probabilities of Dias et al. (2022) for recommending cultivars: the probability that a genotype is among the best selected fraction across environments and within each environment, the probability that it is among the most stable, their joint probability, and pairwise probabilities that one genotype outperforms or is more stable than another.

Usage

```
bam_superiority(fit, .s = 0.2, higher_better = TRUE)
```

Arguments

`fit`	a result of `bayes_ammi()` or `bayes_stability()` (`bam_stability()` needs `bayes_ammi()`).
`.s`	selection intensity: the proportion of genotypes selected (default 0.2).
`higher_better`	`TRUE` (default) when larger values of the trait are better.

Details

With $\Omega^{(s)}$ the $\lceil sG \rceil$ genotypes with the best marginal values $\bar{\eta}_{i\cdot}^{(s)}$ in draw s (selection intensity s = `.s`),

$$P_i^{\text{perf}} = \Pr(i \in \Omega \mid \mathbf{y}), \qquad P_{ij}^{\text{perf}} = \Pr(i \in \Omega_j \mid \mathbf{y}),$$

where Ω_j selects on η_{ij} within environment j. Stability is the variance over environments of the interaction effects $ge_{ij} = \eta_{ij} - \bar{\eta}_{i\cdot} - \bar{\eta}_{\cdot j} + \bar{\eta}_{\cdot\cdot}$ (Shukla 1972): P_i^{stab} is the probability that genotype i is among the $\lceil sG \rceil$ genotypes with the smallest variance, and the joint probability is $P_i^{\text{perf}} P_i^{\text{stab}}$, as in Dias et al. (2022). Pairwise, $\Pr(\bar{\eta}_{i\cdot} > \bar{\eta}_{i'\cdot} \mid \mathbf{y})$ and $\Pr(\text{var}_i < \text{var}_{i'} \mid \mathbf{y})$.

Value

An object of class `c("bam_superiority", "bam_result", "list")`:

`marginal` `data.table` sorted by the joint probability: `Gen`, `mean` (posterior mean of the marginal value), `prob_performance`, `prob_stability`, `prob_joint`.

`conditional` matrix $G \times E$: probability of superior performance in every environment.

`pairwise_performance`, `pairwise_stability` matrices $G \times G$: entry (i, i') is the probability that row genotype i is better (more stable) than i'.

Methods: `print()`, `plot()` (`which` = `c("marginal", "conditional", "pairwise")`), `bam_interpret()`.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

Dias, K. O. G., dos Santos, J. P. R., Krause, M. D., Piepho, H.-P., Guimaraes, L. J. M., Pastina, M. M. and Garcia, A. A. F. (2022). Leveraging probability concepts for cultivar recommendation in multi-environment trials. *Theoretical and Applied Genetics*. doi:10.1007/s0012202204041y

Shukla, G. K. (1972). Some statistical aspects of partitioning genotype-environmental components of variability. *Heredity*, **29**(2), 237–245. doi:10.1038/hdy.1972.87

See Also

bam_winners, bam_ranks, bam_stability

Other decisions: bam_predict(), bam_ranks(), bam_stability(), bam_winners()

Examples

```
data(Maiz)
fit <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 1000
    , .k      = 2
    , .burnin = 200
    , .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          = NULL
        )
    , .level  = 0.95
    , .seed   = 1
    , .align  = TRUE
    , .model  = "AMMI"
    , .het    = FALSE
    , .waic   = TRUE
    )
sp <-
```

```
  bam_superiority(
      fit           = fit
    , .s            = 0.2
    , higher_better = TRUE
    )
sp$marginal
plot(x = sp, which = "marginal")
```

---

bam_theme *ggplot2 theme of bayesammi*

Description

The theme used by every `plot()` method of **bayesammi** (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 `bam_save`.

Usage

```
bam_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 bayesammi utilities: `bam_notation()`, `bam_reference()`, `bam_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 +
  bam_theme(
      base_size       = 11
    , base_family     = "serif"
    , ticks_inward    = TRUE
    , legend_position = "bottom"
    )
p +
  bam_theme(
      base_size       = 12
    , base_family     = "serif"
    , ticks_inward    = FALSE
    , legend_position = "right"
    ) +
  scale_x_continuous(breaks = scales::pretty_breaks(n = 10))
```

---

bam_winners *Which genotype wins where: posterior probabilities*

Description

`bam_winners()` gives, for every environment, the posterior probability that each genotype has the best expected response, the most probable winner, and the groups of environments with the same most probable winner (candidate mega-environments). This is the Bayesian counterpart of the which-won-where view of the GGE biplot, with a probability attached to every statement.

Usage

```
bam_winners(fit, higher_better = TRUE)
```

Arguments

`fit`	a result of `bayes_ammi()` or `bayes_stability()` (`bam_stability()` needs `bayes_ammi()`).
`higher_better`	`TRUE` (default) when larger values of the trait are better.

Details

$$P_{ij} = \Pr\left(\eta_{ij} = \max_{i'} \eta_{i'j} \mid \mathbf{y}\right) \approx \frac{1}{S}\sum_{s=1}^{S} I\left(\eta_{ij}^{(s)} = \max_{i'} \eta_{i'j}^{(s)}\right),$$

with the minimum instead of the maximum when `higher_better = FALSE`.

Value

An object of class `c("bam_winners", "bam_result", "list")`:

`probabilities` matrix $G \times E$ of the probabilities P_{ij}.

`winners` `data.table`: `Env`, `Winner` (most probable), `Probability`, `Second` and `Probability2` (the runner-up).

`mega` `data.table`: groups of environments with the same most probable winner.

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

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

Yan, W., Hunt, L. A., Sheng, Q. and Szlavnics, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science*, **40**(3), 597–605. doi:10.2135/cropsci2000.403597x

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**, 15–37. doi:10.1007/s13253-01100639

See Also

`bam_superiority`, `biplots`

Other decisions: `bam_predict()`, `bam_ranks()`, `bam_stability()`, `bam_superiority()`

Examples

```
data(Maiz)
fit <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 1000
    , .k      = 2
    , .burnin = 200
    , .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          = NULL
        )
    , .level  = 0.95
    , .seed   = 1
    , .align  = TRUE
    , .model  = "GGE"
    , .het    = FALSE
    , .waic   = TRUE
    )
w <-
  bam_winners(
      fit           = fit
    , higher_better = TRUE
    )
w$winners
plot(x = w)
```

---

bayes_ammi *Bayesian estimation of the AMMI and GGE models*

Description

bayes_ammi() estimates the additive main effects and multiplicative interaction (AMMI) model of a multi-environment trial by the Gibbs sampler of Crossa et al. (2011), or the GGE (sites regression, SREG) model of Perez-Elizalde et al. (2012), for balanced or unbalanced trials, with one error variance or one for every environment. The sampler is compiled (C++). Every parameter (overall mean, genotype and environment effects, singular values, genotype and environment scores of the bilinear terms, error variance) has a posterior distribution, so that the biplot carries statistical inference: highest posterior density (HPD) regions around the scores show which genotypes and environments interact significantly and which form homogeneous groups (biplots).

Usage

```
bayes_ammi(
  .data,
  .y,
  .gen,
  .env,
  .rep,
  .nIter = 1000L,
  .k = 2L,
  .burnin = 0L,
  .thin = 1L,
  .chains = 1L,
  .priors = bam_priors(),
```

```
  .level = 0.95,
  .seed = NULL,
  .align = TRUE,
  .model = c("AMMI", "GGE"),
  .het = FALSE,
  .waic = TRUE
)

## Default S3 method:
bayes_ammi(
  .data,
  .y,
  .gen,
  .env,
  .rep,
  .nIter = 1000L,
  .k = 2L,
  .burnin = 0L,
  .thin = 1L,
  .chains = 1L,
  .priors = bam_priors(),
  .level = 0.95,
  .seed = NULL,
  .align = TRUE,
  .model = c("AMMI", "GGE"),
  .het = FALSE,
  .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, strings or vectors.
`.nIter`	number of iterations kept per chain before thinning (after the burn-in).
`.k`	number of bilinear terms K (default 2, as in Crossa et al. 2011).
`.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; two or more give the Gelman-Rubin diagnostic).
`.priors`	the priors, from `bam_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 (see Signs; default `TRUE`).
`.model`	`"AMMI"` (default) or `"GGE"` (sites regression).

`.het`	`FALSE` (default): one error variance; `TRUE`: one for every environment.
`.waic`	compute WAIC during sampling (default `TRUE`; costs one pass over the plots per kept draw).

Details

Model. The response of genotype i in replicate l of environment j is

$$y_{ijl} = \mu + \tau_i + \delta_j + \sum_{k=1}^{K} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ijl}, \qquad e_{ijl} \sim N(0, \sigma^2),$$

with $\sum_i \tau_i = \sum_j \delta_j = 0$, $\lambda_1 \geq \cdots \geq \lambda_K > 0$, and genotype and environment score vectors $\boldsymbol{\alpha}_k, \boldsymbol{\gamma}_k$ of unit length, orthogonal to $\mathbf{1}$ and to each other (K = `.k`). The priors are those of `bam_priors()`.

Conditional distributions. With $\mathbf{Y}$ the $G \times E$ table of cell means, B replicates, $n = BGE$ observations, the orthonormal contrasts $\mathbf{K}_G$ of `matrix_k()` ($\boldsymbol{\tau} = \mathbf{K}_G^\top \mathbf{t}$) and $c_x = \sigma^2/\sigma_x^2$, each iteration draws

$$\mu \sim N\left(\frac{n\bar{y} + c_\mu \mu_0}{n + c_\mu}, \frac{\sigma^2}{n + c_\mu}\right), \qquad \mathbf{t} \sim N\left(\frac{BE\,\mathbf{K}_G \bar{\mathbf{y}}_G + c_\tau \mathbf{K}_G \mathbf{m}_\tau}{BE + c_\tau}, \frac{\sigma^2}{BE + c_\tau}\mathbf{I}\right),$$

the same for $\boldsymbol{\delta}$ with BG, and for $k = 1, \ldots, K$

$$\lambda_k \sim N\left(\frac{B\,\boldsymbol{\alpha}_k^\top \mathbf{Y} \boldsymbol{\gamma}_k + c_\lambda \lambda_0}{B + c_\lambda}, \frac{\sigma^2}{B + c_\lambda}\right) \text{ on } (\lambda_{k+1}, \lambda_{k-1}),$$

$$p(\boldsymbol{\alpha}_k \mid \cdot) \propto \exp\left(\frac{B\lambda_k}{\sigma^2} \boldsymbol{\alpha}_k^\top \mathbf{Y} \boldsymbol{\gamma}_k\right), \qquad p(\boldsymbol{\gamma}_k \mid \cdot) \propto \exp\left(\frac{B\lambda_k}{\sigma^2} \boldsymbol{\gamma}_k^\top \mathbf{Y}^\top \boldsymbol{\alpha}_k\right),$$

von Mises-Fisher distributions on the unit sphere of the subspace orthogonal to $\mathbf{1}$ and to the other score vectors (Crossa et al. 2011, eq. 8-9), and finally

$$\sigma^2 \sim \frac{\nu S_0^2 + \mathrm{SSW} + B \sum_{ij} (\bar{y}_{ij} - \hat{y}_{ij})^2}{\chi^2_{\nu + n}},$$

with SSW the within-cell sum of squares. The chains start at the least-squares AMMI fit (the first chain) or at dispersed values (the others).

A variance for every environment (`.het = TRUE`): $e_{ijl} \sim N(0, \sigma_j^2)$ with independent priors Inv-$\chi^2(\nu, S_{0j}^2)$. With weights $w_j = 1/\sigma_j^2$ the genotype effects keep a closed normal conditional (precision $B \sum_j w_j$); the overall mean and the environment effects are drawn jointly; λ_k has precision $B \sum_j w_j \gamma_{jk}^2$; the genotype scores stay von Mises-Fisher; the environment scores have the Bingham-von Mises-Fisher conditional

$$p(\boldsymbol{\gamma}_k \mid \cdot) \propto \exp\left(B\lambda_k \sum_j w_j \gamma_{jk} r_{\cdot jk} - \frac{B\lambda_k^2}{2} \sum_j w_j \gamma_{jk}^2\right),$$

($r_{\cdot jk} = \sum_i \alpha_{ik} r_{ijk}$ with r_{ijk} the cell residual without term k), drawn by a Gibbs sweep in the eigenbasis of its quadratic term (Hoff 2009); every σ_j^2 is a scaled inverse chi-square with $\nu + BG$ degrees of freedom.

GGE model (`.model = "GGE"`): $y_{ijl} = \mu + \delta_j + \sum_k \lambda_k \alpha_{ik} \gamma_{jk} + e_{ijl}$: the genotype main effect is part of the multiplicative terms, the genotype scores are orthogonal to $\mathbf{1}$, the environment scores only to

each other (Perez-Elizalde et al. 2012). The conditional distributions are those above without $\boldsymbol{\tau}$ and without the constraint $\boldsymbol{\gamma}_k \perp \mathbf{1}$.

Unbalanced trials. Missing plots and whole missing genotype-environment cells are completed by data augmentation: with B the largest number of replicates of a cell, every iteration first draws the missing plots from $N(\eta_{ij}, \sigma^2_j)$, then the conditional distributions of the balanced design apply exactly (the plots are assumed missing at random). Every genotype and every environment needs some data.

Model choice. With `.waic = TRUE` the sampler accumulates the pointwise log-likelihood of the observed plots, giving WAIC; the deviance of every kept draw gives DIC (component `fit`; `bam_compare()`).

Signs. The pair $(\boldsymbol{\alpha}_k, \boldsymbol{\gamma}_k)$ and its negative give the same model. With `.align = TRUE` (default) every draw takes the sign that agrees with the least-squares vectors, so that posterior means and HPD regions refer to one orientation of each axis; with `.align = FALSE` a weak axis can switch sign during the run and its posterior means shrink towards zero.

Changes from the earlier versions. The singular values were computed once and never sampled; the error variance was not returned (`tau1` held the constant precision of the least-squares fit); the residuals for σ^2 were computed against the wrong environments; the within-cell sum of squares was a sum of variances; the covariance matrices of the main effects were square roots of variances; the scores were not drawn from their constrained conditional distributions; all $\min(G, E) - 1$ axes were fitted. `tau1` now holds the draws of the error variance σ^2.

Value

An object of class `c("bam_bayes_ammi", "bam_result", "list")`; the components of the earlier versions 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 (columns `tau1`, ..., `tauE` with a variance for every environment).

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

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

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

`alphas1`, `gammas1` matrices with columns `.nIter` (draw), `Gen` or `Env` (number) and `alphas1`, ... or `gammas1`, ...: draws of the genotype and environment scores.

`alphas0`, `gammas0` `data.tables`: least-squares scores (the starting values).

`summary` `data.table`: posterior mean, standard deviation, Monte Carlo standard error, HPD interval, effective sample size and potential scale reduction factor of every parameter (Tables 1 and B1 of Crossa et al. 2011).

`scores` `data.table`: posterior means of the biplot coordinates $\lambda_k^{1/2}\alpha_{ik}$ and $\lambda_k^{1/2}\gamma_{jk}$, with the mean of every genotype and environment.

`draws` `coda::mcmc.list` of all parameters, one element per chain.

`diagnostics` list: `gelman` (potential scale reduction factors, two or more chains), `raftery` (Raftery-Lewis dependence factors), `heidel` (Heidelberger-Welch stationarity and half-width tests), for the overall mean, the error variance, the main effects and the singular values.

`ls` list: the least-squares AMMI estimates (`mu`, `tau`, `delta`, `lambda`, `alpha`, `gamma`, `sigma2`).

`fit` list: `deviance` of every kept draw, `Dbar`, `Dhat`, `pD`, `DIC`, and with `.waic = TRUE` `lppd`, `p_waic`, `WAIC`, `waic_se` and `waic_i` (the contribution of every observed plot to WAIC, in the order of the data).

`settings` list: iterations, burn-in, thinning, chains, number of terms, model, variances, priors (with the scale of the error variance filled in), level, seed, alignment, time used.

Methods: `print()`, `summary()`, `plot()` (`which = c("trace", "density", "biplot", "effects")`), `biplots()`, `bam_interpret()`, the decision tools (`bam_predict()`, `bam_winners()`, `bam_superiority()`, `bam_ranks()`, `bam_stability()`), `bam_compare()`, `bam_ppc()` and `posterior::as_draws_df()` (`bam-draws`).

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

Viele, K. and Srinivasan, C. (2000). Parsimonious estimation of multiplicative interaction in analysis of variance using Kullback-Leibler information. *Journal of Statistical Planning and Inference*, **84**(1–2), 201–219.

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**, 15–37. doi:10.1007/s13253-01100639

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

`biplots`, `bam_priors`, `bam_interpret`, `ge_ammi`

Examples

```
data(Maiz)
fm1 <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
```

```
    , .env    = site
    , .rep    = rep
    , .nIter  = 200
    , .k      = 2
    , .burnin = 50
    , .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          = NULL
        )
    , .level  = 0.95
    , .seed   = 1
    , .align  = TRUE
    , .model  = "AMMI"
    , .het    = FALSE
    , .waic   = TRUE
    )
fm1
head(fm1$summary)
fm1$fit$WAIC
plot(x = fm1, which = "trace")
plot(x = fm1, which = "biplot")
```

`bayes_stability` *Bayesian stability analysis: Finlay-Wilkinson, Eberhart-Russell and Shukla models*

Description

`bayes_stability()` fits by Gibbs sampling the joint regression models of Finlay and Wilkinson (1963) and Eberhart and Russell (1966), and the heterogeneous interaction variance model of Shukla (1972), to the plots of a multi-environment trial. Every stability parameter (slope, deviation variance, stability variance, safety-first index) then has a posterior distribution, so genotypes can be compared by probabilities rather than by significance tests. The data may be unbalanced: plots or whole genotype-environment cells may be missing.

Usage

```
bayes_stability(
  .data,
  .y,
```

```
  .gen,
  .env,
  .rep,
  .model = c("ER", "FW", "Shukla"),
  .nIter = 1000L,
  .burnin = 0L,
  .thin = 1L,
  .chains = 1L,
  .priors = bam_stab_priors(),
  .level = 0.95,
  .alpha = 0.05,
  .seed = NULL,
  .waic = TRUE
)
```

Arguments

`.data`	data frame with one row per plot.
`.y`, `.gen`, `.env`, `.rep`	columns of the response, genotype, environment and replicate (bare names or strings).
`.model`	`"ER"` (default), `"FW"` or `"Shukla"`; see Details.
`.nIter`	number of iterations kept per chain before thinning (default 1000).
`.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); the first starts at the least-squares estimates, the others at dispersed values.
`.priors`	priors from `bam_stab_priors()`.
`.level`	probability of the highest posterior density intervals (default 0.95).
`.alpha`	probability of the safety-first index (default 0.05, as in Eskridge 1990).
`.seed`	seed of the random numbers (the random number state of the session is restored afterwards).
`.waic`	compute WAIC during sampling (default `TRUE`).

Details

For genotype i, environment j and plot l,

$$y_{ijl} = \mu + g_i + (1 + b_i)h_j + d_{ij} + e_{ijl}, \qquad d_{ij} \sim N(0, \sigma^2_{d,i}), \quad e_{ijl} \sim N(0, \sigma^2),$$

with $\sum_i g_i = \sum_j h_j = \sum_i b_i = 0$. The environment effects h_j are the environmental index, estimated jointly with the other parameters as in the Bayesian Finlay-Wilkinson regression of Lian and de los Campos (2016) instead of being fixed at the environment means; the slope of genotype i is $1 + b_i$, with average 1.

`"ER"` Eberhart-Russell: slopes and a deviation variance $\sigma^2_{d,i}$ for every genotype (the Bayesian version of Oliveira et al. 2018). A stable genotype has a slope near 1 and a small deviation variance.

`"FW"` Finlay-Wilkinson: slopes and one deviation variance for all genotypes.

`"Shukla"` no slopes ($b_i = 0$) and an interaction variance $\sigma^2_{d,i}$ for every genotype: Shukla's stability variance, as in the Bayesian heterogeneous variance model of Edwards and Jannink (2006).

The sampler draws the overall mean, the genotype effects, the environmental index and the slopes from their normal conditional distributions with the deviations d_{ij} integrated out (each observed cell mean then has variance $\sigma^2_{d,i} + \sigma^2/n_{ij}$); then the deviations; then the variances from their scaled inverse chi-squared conditionals. This partially collapsed Gibbs sampler mixes well even when the deviations are large. Empty cells contribute no data; their deviations are drawn from the prior, and `bam_predict()` predicts them.

`stability` reports, for every genotype, the posterior mean and HPD interval of its mean $\mu + g_i$, slope, deviation variance and the share of its variance across environments explained by the regression, $R^2_i = (1+b_i)^2 s^2_h / ((1+b_i)^2 s^2_h + \sigma^2_{d,i})$ with s^2_h the variance of the environmental index; the posterior probability that the slope exceeds 1; and the safety-first index of Eskridge (1990), $\mu + g_i - z_{1-\alpha}\sqrt{V_i}$, with $V_i = b_i^2 s^2_h (1 - 1/E) + \sigma^2_{d,i}$ (Eberhart-Russell), $b_i^2 s^2_h (1 - 1/E)$ (Finlay-Wilkinson) or $s^2_h + \sigma^2_{d,i}$ (Shukla). When smaller values are better (`higher_better = FALSE` in `bam_interpret()` and the decision functions), the index is read the other way: $\mu + g_i + z_{1-\alpha}\sqrt{V_i}$, smaller better.

The result works with `bam_predict()`, `bam_winners()`, `bam_superiority()`, `bam_ranks()`, `bam_indices()`, `bam_compare()` and `bam_ppc()`, which use the draws of the cell means $\mu + g_i + (1 + b_i)h_j + d_{ij}$.

Value

An object of class `c("bam_bayes_stability", "bam_result", "list")`:

`stability` `data.table`, one row per genotype: `Gen`; `mean`, `mean_lower`, `mean_upper`; `slope`, `slope_lower`, `slope_upper`, `prob_slope_above_1`; `dev_var`, `dev_var_lower`, `dev_var_upper`; `R2`; `safety_first`, `safety_first_lower`, `safety_first_upper`, `prob_best_safety`.

`environments` `data.table`: `Env`, posterior mean and HPD interval of the environmental index h_j, and the observed environment mean.

`summary` `data.table` of every parameter (`mu`, `sigma2`, `g[i]`, `h[j]`, `slope[i]`, `sigma2_d[i]`): posterior mean, sd, Monte Carlo error, HPD interval, effective sample size, potential scale reduction factor.

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

`deviations` array (draws x genotypes x environments) of the deviations d_{ij}.

`diagnostics` Gelman-Rubin, Raftery-Lewis and Heidelberger-Welch diagnostics of the overall mean, error variance, slopes and deviation variances.

`fit` DIC and WAIC, as in `bayes_ammi()`.

`ls` least-squares estimates (the start of the first chain).

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

Methods: `print()`, `plot(x, which = c("slopes", "lines", "deviations", "trace", "density"))`, `bam_interpret()`, `bam_cite()`.

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>)

References

Finlay, K. W. and Wilkinson, G. N. (1963). The analysis of adaptation in a plant-breeding programme. *Australian Journal of Agricultural Research*, **14**(6), 742–754. doi:10.1071/AR9630742

Eberhart, S. A. and Russell, W. A. (1966). Stability parameters for comparing varieties. *Crop Science*, **6**(1), 36–40. doi:10.2135/cropsci1966.0011183X000600010011x

Shukla, G. K. (1972). Some statistical aspects of partitioning genotype-environmental components of variability. *Heredity*, **29**(2), 237–245. doi:10.1038/hdy.1972.87

Eskridge, K. M. (1990). Selection of stable cultivars using a safety-first rule. *Crop Science*, **30**, 369–374.

Edwards, J. W. and Jannink, J.-L. (2006). Bayesian modeling of heterogeneous error and genotype x environment interaction variances. *Crop Science*, **46**(2), 820. doi:10.2135/cropsci2005.0164

Lian, L. and de los Campos, G. (2016). FW: an R package for Finlay-Wilkinson regression that incorporates genomic/pedigree information and covariance structures between environments. *G3: Genes, Genomes, Genetics*, **6**(3), 589–597. doi:10.1534/g3.115.026328

Oliveira, T. R. A., Carvalho, H. W. L., Nascimento, M., Costa, E. F. N., Amaral Junior, A. T., Gravina, G. A. and Carvalho Filho, J. L. S. (2018). The Eberhart and Russell's Bayesian method used as an instrument to select maize hybrids. *Euphytica*, **214**, 64. doi:10.1007/s106810182146y

See Also

bam_stab_priors, bam_indices, bayes_ammi

Other stability: bam_ammi_indices(), bam_indices(), bam_stab_priors()

Examples

```
data(Maiz)
fs <-
  bayes_stability(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .model  = "ER"
    , .nIter  = 1000
    , .burnin = 200
    , .thin   = 1
    , .chains = 1
    , .priors = bam_stab_priors(
          mu_var = NULL
        , g_var  = NULL
        , h_var  = NULL
        , b_var  = 100
        , nu     = 1
        , s2     = NULL
        , nu_d   = 1
        , s2_d   = NULL
        )
```

```
    , .level  = 0.95
    , .alpha  = 0.05
    , .seed   = 1
    , .waic   = TRUE
    )
fs
plot(x = fs, which = "slopes")
```

---

biplots *Biplots with highest posterior density regions*

Description

biplots() draws the Bayesian AMMI 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

```
biplots(
  model,
  burnin = 0.3,
  thin = 0.2,
  pb = 0.05,
  plot_stable = TRUE,
  plot_unstable = TRUE,
  ncolors = 5,
  .which = c("both", "genotype", "environment"),
  .grid = 100L
)

## Default S3 method:
biplots(
  model,
  burnin = 0.3,
  thin = 0.2,
  pb = 0.05,
  plot_stable = TRUE,
  plot_unstable = TRUE,
  ncolors = 5,
  .which = c("both", "genotype", "environment"),
  .grid = 100L
)
```

Arguments

model	the result of bayes_ammi() (with .k >= 2).
burnin	proportion of the stored draws of every chain discarded at its start (default 0.3).
thin	proportion of the remaining draws used (default 0.2: every fifth 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("bam_biplots", "bam_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(), bam_interpret().

Author(s)

Julian Garcia Abadillo Velasco (<garciaabadillo.j@ufl.edu>), Diego Jarquin (<diego.jarquin@gmail.com>), 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

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

See Also

bayes_ammi, bam_interpret

Examples

```
data(Maiz)
fm1 <-
  bayes_ammi(
      .data   = Maiz
    , .y      = y
    , .gen    = entry
    , .env    = site
    , .rep    = rep
    , .nIter  = 1000
    , .k      = 2
    , .burnin = 200
    , .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          = NULL
        )
    , .level  = 0.95
    , .seed   = 1
    , .align  = TRUE
    , .model  = c("AMMI", "GGE")
    , .het    = FALSE
    , .waic   = TRUE
    )
bp <-
```

```
  biplots(
      model         = 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
```

`e_eff` *Environment effects*

Description

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

Usage

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

## Default S3 method:
e_eff(.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

`g_eff`, `ge_eff`

Examples

```
data(Maiz)
e_eff(
    .data = Maiz
  , .y    = y
  , .gen  = entry
  , .env  = site
  )
```

`ge_ammi` *Least-squares AMMI model*

Description

`ge_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

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

## Default S3 method:
ge_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 (`ge_eff()`), $K = \min(G, E) - 1$ axes. The error variance is the residual variance of the model with random replicates within environments (`ge_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("bam_ge_ammi", "bam_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 `ge_mean()`.

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

`tao`, `delta` genotype and environment effects (`g_eff()`, `e_eff()`).

`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`, `ge_eff`

Examples

```
data(Maiz)
fit <-
  ge_ammi(
      .data = Maiz
    , .y    = y
```

```
    , .gen  = entry
    , .env  = site
    , .rep  = rep
    )
fit$lambdas
fit$sigma2
```

---

ge_eff *Genotype-by-environment interaction effects*

Description

ge_eff() 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

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

## Default S3 method:
ge_eff(.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("bam_ge_eff", "bam_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

ge_ammi

Examples

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

---

ge_mean *Genotype-by-environment means*

Description

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

Usage

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

## Default S3 method:
ge_mean(.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("bam_ge_mean", "bam_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

`ge_var`, `ge_eff`, `ge_ammi`

Examples

```
data(Maiz)
ge_mean(
    .data = Maiz
  , .y    = y
  , .gen  = entry
  , .env  = site
  )
```

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

Description

`ge_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 (`ge_ammi()`, which computes it in closed form).

Usage

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

## Default S3 method:
ge_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

ge_ammi

Examples

```
data(Maiz)
if (requireNamespace("lme4", quietly = TRUE)) {
  fm <-
    ge_model(
        .data = Maiz
      , .y    = y
      , .gen  = entry
      , .env  = site
```

```
      , .rep  = rep
      )
  stats::sigma(fm)^2
}
```

---

ge_var *Genotype-by-environment variances*

Description

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

Usage

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

## Default S3 method:
ge_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("bam_ge_var", "bam_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

ge_mean

Examples

```
data(Maiz)
ge_var(
    .data = Maiz
  , .y    = y
  , .gen  = entry
  , .env  = site
  )
```

---

g_eff *Genotype effects*

Description

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

Usage

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

## Default S3 method:
g_eff(.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

`e_eff`, `ge_eff`

Examples

```
data(Maiz)
g_eff(
    .data = Maiz
  , .y    = y
  , .gen  = entry
  , .env  = site
  )
```

`Maiz` *Maize multi-environment trial*

Description

Grain yield of 9 maize (*Zea mays* L.) genotypes in 20 sites, a randomized complete block design with 4 replicates in every site: the example of Crossa et al. (2011), also used by Burgueno et al. (2008).

Usage

```
Maiz
```

Format

A `data.frame` with 720 rows and 7 columns:

`site` site (environment), 1 to 20.

`entry` genotype, 1 to 9.

`fold10`, `fold5`, `fold3` fold numbers of 10-, 5- and 3-fold cross-validation (by genotype).

`rep` replicate within the site, 1 to 4.

`y` grain yield (kg/ha).

Details

The grand mean is 4858 kg/ha; the least-squares singular values of the interaction are 5923 and 3070 for the first two terms (Crossa et al. 2011).

Change from the earlier versions. The help page described another data set (1320 rows; columns Gen, Institute, Rep, Block, Env, Yield).

Author(s)

Muhammad Yaseen (<myaseen208@gmail.com>), Jose Crossa (<j.crossa@cgiar.org>)

Source

International Maize and Wheat Improvement Center (CIMMYT).

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

Burgueno, J., Crossa, J., Cornelius, P. L. and Yang, R.-C. (2008). Using factor analytic models for joining environments and genotypes without crossover genotype x environment interaction. *Crop Science*, **48**(4), 1291–1305.

Examples

```
data(Maiz)
str(Maiz)
ge_mean(
    .data = Maiz
  , .y    = y
  , .gen  = entry
  , .env  = site
  )$grand_mean
```

---

matrix_k *Orthonormal contrast matrix*

Description

`matrix_k()` 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

```
matrix_k(n)

## Default S3 method:
matrix_k(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)

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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

See Also

orthnorm

Examples

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

---

orthnorm *Gram-Schmidt orthonormalisation*

Description

`orthnorm()` 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

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

## Default S3 method:
orthnorm(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

matrix_k

Examples

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

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