Package 'aridagri'

November 11, 2026

Type Package

Title Comprehensive Statistical Tools for Agricultural Research

Version 2.1.0

Description Analysis of variance for the experimental designs used in agricultural research, with the correct error term for every stratum, standard error of mean (SEm), standard error of difference (SEd), critical difference (CD), coefficient of variation (CV) and letter groupings: completely randomized design (CRD), randomized complete block design (RCBD) with missing plots, Latin square, two- and three-factor factorials, split-plot designs (including factorial main or sub-plots), split-split-plot and strip-plot designs, and combined analysis over environments. Also covers the augmented randomized complete block design with adjusted means and genetic parameters (Federer, 1961 <doi:10.2307/2527837>), alpha lattice designs with intra-block or residual maximum likelihood (REML) analysis (Patterson and Williams, 1976 <doi:10.1093/biomet/63.1.83>) and repeated measures with Greenhouse-Geisser and Huynh-Feldt corrections and covariance structure models. Mean comparisons (least significant difference, Duncan, Tukey, Student-Newman-Keuls, Scheffe, Bonferroni and Dunnett) follow Gomez and Gomez (1984, ISBN:0471870927), with letters assigned by the algorithm of Piepho (2004) <doi:10.1198/1061860043515>. Stability analysis includes Eberhart and Russell (1966) <doi:10.2135/cropsci1966.0011183X000600010011x> regression, additive main effects and multiplicative interaction (AMMI), Finlay-Wilkinson, Shukla, Wricke, coefficient of variation and Lin-Binns methods, and genotype plus genotype-by-environment (GGE) biplots (Yan et al., 2000 <doi:10.2135/cropsci2000.403597x>). Further tools compute growing degree days, helio-thermal and photo-thermal units, crop growth rate, relative growth rate, net assimilation rate, leaf area index and leaf area duration, harvest index, yield gaps with the technology index, nutrient use efficiency, quadratic, plateau and Mitscherlich response curves with the economic optimum dose, benefit-cost ratio, correlation, principal component, path and structural equation analysis, publication tables for many traits and figures.

License GPL-3

Encoding UTF-8

LazyData true

Depends R (>= 4.0.0)

Imports grDevices, graphics, nlme, stats, utils

Suggests agricolae, corrplot, emmeans, factoextra, ggplot2 (>= 3.4.0), knitr, lavaan, multcomp, rmarkdown, semPlot, testthat (>= 3.0.0), tibble, writexl

VignetteBuilder knitr

URL https://github.com/lalitrolaniya/aridagri, https://lalitrolaniya.github.io/aridagri/

BugReports https://github.com/lalitrolaniya/aridagri/issues

Config/testthat/edition 3

NeedsCompilation no

Config/roxygen2/version 8.1.1

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Repository CRAN

Date/Publication 2026-11-10 23:00:02 UTC

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`aridagri-package` *aridagri: Statistical Tools for Agricultural Research*

Description

Analysis of variance for the common field designs with correct error terms, standard errors, critical differences and letter groupings, plus stability analysis, repeated measures, thermal indices, crop growth analysis, nutrient use efficiency, response curves and economics.

Experimental designs

- `anova_crd`, `anova_rbd`, `anova_latin`: single-factor designs (missing plots and unequal replication handled exactly)
- `anova_factorial`, `anova_factorial_3way`: factorial experiments
- `anova_spd`, `anova_spd_ab_main`, `anova_spd_c_main_ab_sub`, `anova_spd_ab_cd`, `anova_sspd`, `anova_strip`: split-plot family with SE and CD for every comparison
- `anova_rbd_pooled`, `anova_spd_pooled`, `anova_sspd_pooled`: combined analysis over environments
- `anova_augmented`, `anova_alpha_lattice`: designs for germplasm and breeding trials
- `anova_repeated`: repeated measures with sphericity corrections and covariance-structure models
- `anova_traits`: publication table for many traits

Mean comparisons and diagnostics

`perform_posthoc`, `compare_means`, `check_assumptions`.

Genotype x environment analysis

`stability_analysis` (Eberhart-Russell, AMMI, Finlay-Wilkinson, Shukla, Wricke, CV, Lin-Binns) and `gge_biplot`.

Agronomic indices

`thermal_indices`, `day_length`, `crop_growth_analysis`, `harvest_index`, `yield_gap_analysis`, `economic_indices`, `economic_analysis`, `nue_calculate`, `nutrient_response`.

Multivariate methods

`correlation_analysis`, `pca_analysis`, `path_analysis`, `sem_analysis`.

Figures and export

`plot_means`, `plot_interaction`, `plot_stability`, `plot_response`, `plot()` methods, `theme_aridagri` (**ggplot2**); `arid_plot` (base graphics); `export_results`.

Author(s)

Lalit Kumar Rolaniya (maintainer), Ram Lal Jat, Monika Punia (deceased), Raja Ram Choudhary and Hemant Poonia (deceased)

See Also

Useful links:

- https://github.com/lalitrolaniya/aridagri
- https://lalitrolaniya.github.io/aridagri/
- Report bugs at https://github.com/lalitrolaniya/aridagri/issues

---

`anova_alpha_lattice` *Alpha Lattice Design ANOVA*

Description

Analysis of an alpha lattice (resolvable incomplete block) design. Gives the intra-block ANOVA, genotype means adjusted for incomplete blocks with exact standard errors and letter groupings, and the efficiency of the design relative to a randomized complete block design. By default replications and blocks are treated as random (REML), so that inter-block information is recovered (Patterson and Williams, 1976); `analysis = "intra"` gives the classical intra-block estimates.

Usage

```
anova_alpha_lattice(
  data,
  response,
  genotype,
  replication,
  block,
  verbose = TRUE,
  analysis = c("reml", "intra"),
  posthoc = "lsd",
  alpha = 0.05
)
```

Arguments

`data`	Data frame containing the data.
`response`	Name of the response variable.
`genotype`	Name of the genotype column.
`replication`	Name of the replication column.
`block`	Name of the incomplete block column (nested within replication; labels may repeat across replications).
`verbose`	Logical. If TRUE (default), prints the report.
`analysis`	`"reml"` (default; replications and incomplete blocks random, fitted with **nlme**, so that inter-block information is recovered) or `"intra"` (blocks fixed; the classical intra-block analysis). If the REML fit fails, the intra-block analysis is used with a message.
`posthoc`	Method for the letters (default `"lsd"`).
`alpha`	Significance level. Default 0.05.

Details

The intra-block ANOVA is the sequential analysis of the model replication + block(replication) + genotype: genotypes are tested after blocks. Blocks within replications are also shown adjusted for genotypes. Adjusted means are least-squares means. The efficiency relative to an RCBD is the average variance of a difference under the RCBD analysis ($2MSE_{RCBD}/r$) divided by the average variance of a difference of adjusted means. With REML, letters and CD use the intra-block error degrees of freedom, an approximation.

Value

An object of class `aridagri_alpha` with `anova_table`, `genotype_means` (adjusted means with SE and letters, highest first), `avg_sed`, `cd` (from the average SEd), `efficiency` (percent, relative to RCBD), `cv`, `grand_mean`, `posthoc`, `variance_components` (REML) and `model`.

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

References

Patterson, H.D. and Williams, E.R. (1976). A new class of resolvable incomplete block designs. *Biometrika*, 63(1), 83-92. doi:10.1093/biomet/63.1.83

Examples

```
data(cowpea_alpha)
res <- anova_alpha_lattice(cowpea_alpha, response = "grain_yield",
                           genotype = "genotype", replication = "rep",
                           block = "block")
head(res$genotype_means)
```

anova_augmented *Augmented Randomized Complete Block Design*

Description

Analysis of an augmented randomized complete block design (Federer, 1956), where a few check varieties are replicated in every block and the new (test) entries appear once. Gives the ANOVA with the treatment sum of squares split into checks, tests and checks vs tests, adjusted means of all entries, the four standard errors of difference, a comparison of every test entry with the checks, and genetic parameters of the test entries.

Usage

```
anova_augmented(
  data,
  response,
  genotype,
  block,
  check_names,
  verbose = TRUE,
  alpha = 0.05,
  k = 2.063
)
```

Arguments

`data`	Data frame containing the data.
`response`	Name of the response variable.
`genotype`	Name of the entry (genotype) column.
`block`	Name of the block column.
`check_names`	Character vector with the names of the check entries.
`verbose`	Logical. If TRUE (default), prints the report.
`alpha`	Significance level for CD. Default 0.05.
`k`	Standardized selection differential for genetic advance. Default 2.063 (5% selection intensity).

Details

Block effects are estimated from the checks and removed from the test entries: adjusted value = observed value - (mean of checks in its block - overall check mean). This equals the least-squares mean from the model `response ~ block + genotype`, which is used here, so the standard errors are exact. With b blocks and c checks the four standard errors of difference are: two check means $\sqrt{2MSE/b}$; two test entries in the same block $\sqrt{2MSE}$; two test entries in different blocks $\sqrt{2MSE(1+1/c)}$; a test entry and a check mean $\sqrt{MSE(1+1/b+1/c-1/(bc))}$.

Two ANOVA tables are given. In the first, treatments are fitted after blocks and their sum of squares is split into tests vs checks, checks and tests, each adjusted for blocks. In the second, blocks are fitted after treatments and the treatment sum of squares (ignoring blocks) is split into checks, tests and checks vs tests (Federer, 1961).

Genetic parameters of the test entries use the block-adjusted mean square among tests from the first table: phenotypic variance σ_p^2 = MS(tests), error variance σ_e^2 = MSE, genotypic variance $\sigma_g^2 = \sigma_p^2 - \sigma_e^2$, broad-sense heritability $h^2 = \sigma_g^2/\sigma_p^2$, GCV and PCV in percent of the mean of the adjusted test values, and genetic advance $GA = kh^2\sigma_p$.

Value

An object of class `aridagri_augmented` with `anova_adjusted` (treatments after blocks), `anova_partitioned` (blocks after treatments, treatments split), `adjusted_means` (all entries with type, raw and adjusted mean, SE and block), `se_diff` and `cd` (the four comparisons), `test_vs_checks` (difference of each test entry from the check mean and the best check, with significance), `block_effects`, `genetic_parameters`, `mse`, `df_error`, `anova_checks` and `model`.

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

References

Federer, W.T. (1956). Augmented (or hoonuiaku) designs. *Hawaiian Planters' Record*, 55, 191-208.

Federer, W.T. (1961). Augmented designs with one-way elimination of heterogeneity. *Biometrics*, 17(3), 447-473. doi:10.2307/2527837

Examples

```
data(chickpea_augmented)
res <- anova_augmented(chickpea_augmented, response = "seed_yield",
                       genotype = "entry", block = "block",
                       check_names = c("C1", "C2", "C3", "C4"))
head(res$test_vs_checks)
res$genetic_parameters
```

`anova_crd` *Completely Randomized Design (CRD) ANOVA*

Description

Analysis of variance for a completely randomized design with standard errors, critical difference, coefficient of variation, post-hoc letter groupings and assumption checks. Unequal replication is handled exactly.

Usage

```
anova_crd(
  data,
  response,
  treatment,
  posthoc = "lsd",
  alpha = 0.05,
  verbose = TRUE,
  control = NULL
)
```

Arguments

data	Data frame containing the experimental data.
response	Name of the response variable (character).
treatment	Name of the treatment column.
posthoc	Post-hoc test(s): "lsd", "duncan", "tukey", "snk", "scheffe", "bonferroni", "dunnett", a vector of these, "all" or "none". The first method supplies the letters in the means table.
alpha	Significance level for the CD and the post-hoc tests (default 0.05).
verbose	Logical. If TRUE (default), prints the report.
control	Control level for Dunnett's test (default: first level).

Details

SEm = sqrt(MSE / r), SEd = sqrt(2 MSE / r) and CD = t(alpha/2, error df) x SEd, where r is the number of replications (the harmonic mean when replication is unequal; the letters then use the exact SE of each pair). CV = 100 sqrt(MSE) / grand mean. Rows with a missing response are dropped with a message.

Value

An object of class aridagri_anova with anova_table, model, grand_mean, cv, ms_error, df_error, se_mean (SEm), se_diff (SEd), cd (at alpha), cd_5, cd_1, treatment_means (mean, SD, N, SE and letters), posthoc, diagnostics, significance and balanced.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

References

Gomez, K.A. and Gomez, A.A. (1984). *Statistical Procedures for Agricultural Research*, 2nd ed. John Wiley and Sons, New York.

Examples

```
data <- data.frame(
  treatment = rep(c("T1", "T2", "T3", "T4"), each = 5),
  yield = c(1210, 1185, 1242, 1198, 1225, 1340, 1362, 1318, 1375, 1350,
            1105, 1090, 1122, 1131, 1098, 1445, 1462, 1430, 1471, 1452)
)
res <- anova_crd(data, response = "yield", treatment = "treatment",
                 posthoc = "duncan")
res$treatment_means
```

---

anova_factorial *Two-Factor Factorial ANOVA*

Description

Analysis of variance for a two-factor factorial experiment in a randomized complete block design (when `replication` is given) or a completely randomized design, with SEm, SEd and CD for both main effects and the interaction, and letter groupings for factor means and treatment combinations.

Usage

```
anova_factorial(
  data,
  response,
  factor1,
  factor2,
  replication = NULL,
  posthoc = "lsd",
  alpha = 0.05,
  verbose = TRUE
)
```

Arguments

`data`	Data frame containing the data.
`response`	Name of the response variable.
`factor1`	Name of the first factor (A).
`factor2`	Name of the second factor (B).
`replication`	Name of the replication (block) column, or `NULL` for a completely randomized layout.
`posthoc`	Post-hoc method for the letters (see `perform_posthoc`). Default `"lsd"`.
`alpha`	Significance level for CD and letters. Default 0.05.
`verbose`	Logical. If TRUE (default), prints the report.

Value

An object of class `aridagri_factorial` with `anova_table`, `model`, `grand_mean`, `cv`, `ms_error`, `df_error`, `comparisons` (SEm, SEd and CD for A, B and A x B), `se_a`, `cd_a`, `se_b`, `cd_b`, `se_ab`, `cd_ab`, `mean_a`, `mean_b` (with letters), `interaction_means` (all combinations with letters), `mean_ab` (two-way table) and `posthoc`.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

Examples

```
data <- expand.grid(rep = 1:4, nitrogen = c("N0", "N40", "N80"),
                    phosphorus = c("P0", "P30"))
set.seed(1)
data$yield <- 900 + 3 * as.numeric(sub("N", "", data$nitrogen)) +
  2 * as.numeric(sub("P", "", data$phosphorus)) + rnorm(nrow(data), 0, 40)
res <- anova_factorial(data, response = "yield", factor1 = "nitrogen",
                       factor2 = "phosphorus", replication = "rep")
res$interaction_means
```

---

anova_factorial_3way *Three-Factor Factorial ANOVA*

Description

Analysis of variance for a three-factor factorial experiment in a randomized complete block design (when `replication` is given) or a completely randomized design, with SEm, SEd and CD for every main effect and interaction and letter groupings for main-effect means and treatment combinations.

Usage

```
anova_factorial_3way(
  data,
  response,
  factor1,
  factor2,
  factor3,
  replication = NULL,
  alpha = 0.05,
  verbose = TRUE,
  posthoc = "lsd"
)
```

Arguments

data	Data frame containing the data.
response	Name of the response variable.
factor1	Name of the first factor (A).
factor2	Name of the second factor (B).
factor3	Name of the third factor (C).
replication	Name of the replication (block) column, or NULL for a completely randomized layout.
alpha	Significance level for CD and letters. Default 0.05.
verbose	Logical. If TRUE (default), prints the report.
posthoc	Post-hoc method for the letters (see perform_posthoc). Default "lsd".

Value

An object of class aridagri_factorial3 with anova_table, model, grand_mean, cv, ms_error, df_error, comparisons (SEm, SEd and CD for all seven effects), means (a list of tables for A, B, C, A x B, A x C, B x C and A x B x C, with letters) and posthoc.

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

Examples

```
data <- expand.grid(rep = 1:3, A = c("A1", "A2"), B = c("B1", "B2"),
                    C = c("C1", "C2", "C3"))
set.seed(2)
data$yield <- rnorm(nrow(data), 1200, 60)
res <- anova_factorial_3way(data, "yield", "A", "B", "C", "rep")
res$comparisons
```

---

anova_latin *Latin Square Design ANOVA*

Description

Analysis of variance for a Latin square design with row and column blocking, SEm, SEd, CD, CV, the efficiency of the Latin square relative to a CRD and to an RCBD, and post-hoc letter groupings.

Usage

```
anova_latin(
  data,
  response,
  treatment,
  row,
  column,
  posthoc = "lsd",
  alpha = 0.05,
  verbose = TRUE,
  control = NULL
)
```

Arguments

`data`	Data frame containing the data.
`response`	Name of the response variable.
`treatment`	Name of the treatment column.
`row`	Name of the row column.
`column`	Name of the column column.
`posthoc`	Post-hoc method(s); see `perform_posthoc`.
`alpha`	Significance level. Default 0.05.
`verbose`	Logical. If TRUE (default), prints the report.
`control`	Control level for Dunnett's test.

Details

Relative efficiencies (Cochran and Cox, 1957; Gomez and Gomez, 1984) use the row (E_r), column (E_c) and error (E_e) mean squares: versus a CRD, $[E_r + E_c + (t-1)E_e]/[(t+1)E_e]$; versus an RCBD with rows as blocks, $[E_c + (t-1)E_e]/(tE_e)$; versus an RCBD with columns as blocks, $[E_r + (t-1)E_e]/(tE_e)$, each multiplied by the precision adjustment factor when the error degrees of freedom are below 20.

Value

An object of class `aridagri_anova` with the components of `anova_crd` and `relative_efficiency` (a named vector, percent).

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

Examples

```
data <- data.frame(
  row = rep(1:5, each = 5),
  col = rep(1:5, 5),
  treatment = c("A","B","C","D","E", "B","C","D","E","A",
                "C","D","E","A","B", "D","E","A","B","C",
                "E","A","B","C","D"),
  yield = c(1180, 1265, 1342, 1410, 1238, 1270, 1335, 1402, 1251, 1176,
            1340, 1415, 1245, 1190, 1258, 1405, 1232, 1178, 1262, 1339,
            1236, 1183, 1271, 1348, 1398)
)
anova_latin(data, response = "yield", treatment = "treatment",
            row = "row", column = "col")
```

---

anova_rbd *Randomized Complete Block Design (RCBD) ANOVA*

Description

Analysis of variance for a randomized complete block design with standard errors, critical difference, CV, relative efficiency over a CRD, post-hoc letter groupings and assumption checks. Missing plots are handled by least squares: treatments are tested after blocks, means are least-squares (adjusted) means and every pair is compared with its own standard error.

Usage

```
anova_rbd(
  data,
  response,
  treatment,
  block,
  posthoc = "lsd",
  alpha = 0.05,
  verbose = TRUE,
  control = NULL
)
```

Arguments

data	Data frame containing the experimental data.
response	Name of the response variable (character).
treatment	Name of the treatment column.
block	Name of the block (replication) column.
posthoc	Post-hoc test(s): "lsd", "duncan", "tukey", "snk", "scheffe", "bonferroni", "dunnett", a vector of these, "all" or "none". The first method supplies the letters in the means table.

alpha	Significance level for the CD and the post-hoc tests (default 0.05).
verbose	Logical. If TRUE (default), prints the report.
control	Control level for Dunnett's test (default: first level).

Details

Relative efficiency of the RCBD over a CRD follows Gomez and Gomez (1984):

$$RE = \frac{(r-1)E_b + r(t-1)E_e}{(rt-1)E_e}$$

where E_b and E_e are the block and error mean squares, multiplied by the precision adjustment factor $k = \frac{[(r-1)(t-1)+1][t(r-1)+3]}{[(r-1)(t-1)+3][t(r-1)+1]}$ when the error degrees of freedom are below 20. Values above 100% mean that blocking reduced the error.

Value

An object of class `aridagri_anova`. In addition to the components described in `anova_crd` it contains `relative_efficiency` (percent, adjusted), `relative_efficiency_unadjusted` and `missing_plots`.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

References

Gomez, K.A. and Gomez, A.A. (1984). *Statistical Procedures for Agricultural Research*, 2nd ed. John Wiley and Sons, New York.

Examples

```
data(mothbean_rbd)
res <- anova_rbd(mothbean_rbd, response = "seed_yield",
                 treatment = "treatment", block = "block",
                 posthoc = "duncan")
res$treatment_means
res$relative_efficiency
```

---

anova_rbd_pooled *Combined (Pooled) Analysis of RCBD Experiments over Environments*

Description

Combined analysis of variance for the same set of treatments tested in a randomized complete block design in several environments (years, seasons or locations). Gives the analysis of each environment, Bartlett's test of homogeneity of error variances, the combined ANOVA with the correct error term for every source, SE and CD for treatment, environment and interaction means, and letter groupings for the treatment means.

Usage

```
anova_rbd_pooled(
  data,
  response,
  treatment,
  environment,
  block,
  posthoc = "lsd",
  alpha = 0.05,
  verbose = TRUE,
  env_effect = c("fixed", "random"),
  control = NULL
)
```

Arguments

data	Data frame containing the experimental data.
response	Name of the response variable (character).
treatment	Name of the treatment column.
environment	Name of the environment (year, season or location) column.
block	Name of the block column (blocks are nested within environments; labels may repeat across environments).
posthoc	Post-hoc test(s): "lsd", "duncan", "tukey", "snk", "scheffe", "bonferroni", "dunnett", a vector of these, "all" or "none". The first method supplies the letters in the means table.
alpha	Significance level for the CD and the post-hoc tests (default 0.05).
verbose	Logical. If TRUE (default), prints the report.
env_effect	Either "fixed" (default; years or seasons of interest) or "random" (locations or years treated as a sample).
control	Control level for Dunnett's test (default: first level).

Details

Sources and their F-tests (McIntosh, 1983; Gomez and Gomez, 1984): environment is tested against blocks within environments; the treatment x environment interaction against the pooled error; the treatment effect against the pooled error when environments are fixed and against the treatment x environment mean square when they are random. With random environments the usual restricted mixed model is assumed, so environment is still tested against blocks within environments. The SE and CD of treatment means use the same denominator as the treatment F-test. Bartlett's chi-square tests whether the error variances of the environments can be pooled; when it is significant, interpret the combined analysis with care.

Value

An object of class aridagri_pooled with pooled_anova (combined ANOVA with correct F-tests), individual_anovas, environment_summary (mean, MSE, CV, F, p and CD of each environment), bartlett_test, treatment_means (with letters), interaction_means, se_treatment,

`cd_treatment`, `se_environment`, `cd_environment`, `se_interaction`, `cd_interaction`, `posthoc`, `cv`, `grand_mean`, `mse_values` and `model`.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

References

McIntosh, M.S. (1983). Analysis of combined experiments. *Agronomy Journal*, 75(1), 153-155. doi:10.2134/agronj1983.00021962007500010041x

Gomez, K.A. and Gomez, A.A. (1984). *Statistical Procedures for Agricultural Research*, 2nd ed. John Wiley and Sons, New York.

Examples

```
data(pearlmillet_met)
res <- anova_rbd_pooled(pearlmillet_met, response = "grain_yield",
                        treatment = "genotype", environment = "environment",
                        block = "rep", verbose = FALSE)
res$pooled_anova
res$bartlett_test
```

---

anova_repeated *Repeated Measures ANOVA (Split-Plot in Time)*

Description

Analysis of experiments in which the same experimental units (plots, animals, trees) are measured on several occasions: plant height or LAI at successive dates, soil moisture through the season, or body weight, heart rate or blood metabolites over time. Gives the univariate split-plot-in-time ANOVA, Mauchly's test of sphericity with Greenhouse-Geisser and Huynh-Feldt corrected p-values, a comparison of covariance structures by mixed models (compound symmetry, first-order autoregressive and unstructured), SE and CD for every comparison, letter groupings, and a separate analysis at each time.

Usage

```
anova_repeated(
  data,
  response,
  treatment,
  time,
  subject = NULL,
  block = NULL,
  posthoc = "lsd",
  alpha = 0.05,
```

```
  covariance = TRUE,
  verbose = TRUE
)
```

Arguments

`data`	Data frame in long format (one row per unit per time).
`response`	Name of the response variable.
`treatment`	Name of the treatment column.
`time`	Name of the time (occasion) column. Times are taken in the order of their levels (numeric times are sorted).
`subject`	Name of the column identifying the experimental unit that is measured repeatedly. If `NULL` and `block` is given, each block x treatment combination is one unit.
`block`	Name of the block column for units laid out in randomized complete blocks, or `NULL` (completely randomized units).
`posthoc`	Method for the letters (default `"lsd"`).
`alpha`	Significance level. Default 0.05.
`covariance`	Logical. If TRUE (default), fits mixed models with different covariance structures using **nlme**.
`verbose`	Logical. If TRUE (default), prints the report.

Details

Univariate analysis. Treatment (and block) are tested against the between-unit error, Error(a). Time and the treatment x time interaction are tested against the within-unit error, Error(b). With blocks, the block x time interaction is fitted as a separate within-unit term, as in the univariate tests of SAS PROC GLM with a REPEATED statement, so that the sphericity corrections apply to the same error term. This is valid when the covariance of the repeated measurements is spherical. Mauchly's test checks this, and the Greenhouse-Geisser (1959) and Huynh-Feldt (1976) epsilons, the latter with the correction of Lecoutre (1991) as in `anova.mlm()`, scale the degrees of freedom of the within-unit tests when it fails. A common rule is to use the Greenhouse-Geisser p-value when epsilon is below 0.75 and the Huynh-Feldt p-value otherwise.

Mixed models. Generalized least squares models with the same fixed effects are fitted by REML with compound symmetry (CS), first-order autoregressive (AR1, on the time order) and unstructured (UN, with separate variances per time) covariance, and compared by AIC and BIC. The marginal F-tests of the best structure are reported (with the residual degrees of freedom used by **nlme**, so tests of between-unit effects are approximate; the univariate test of treatment is exact for balanced data). Structures that fail to converge are skipped.

Comparisons. With r units per treatment, a treatments and t times, the SEd are as in a split-plot design with treatments in main plots and times in sub-plots: treatment means $\sqrt{2E_a/(rt)}$, time means $\sqrt{2E_b/(ra)}$, times within a treatment $\sqrt{2E_b/r}$, and treatments at the same time $\sqrt{2[(t-1)E_b + E_a]/(rt)}$ with the weighted t.

Value

An object of class `aridagri_repeated` with `anova_table` (univariate), `sphericity` (Mauchly's W and p, GG and HF epsilons), `corrected` (within-unit tests with GG and HF p-values), `covariance_models` (AIC/BIC table), `best_structure`, `mixed_anova`, `se_cd`, `means` (treatment x time table), `treatment_means`, `time_means`, `letters`, `by_time` (ANOVA at each time) and `models`.

References

Greenhouse, S.W. and Geisser, S. (1959). On methods in the analysis of profile data. *Psychometrika*, 24(2), 95-112. doi:10.1007/BF02289823

Lecoutre, B. (1991). A correction for the epsilon approximate test in repeated measures designs with two or more independent groups. *Journal of Educational Statistics*, 16(4), 371-372. doi:10.3102/10769986016004371

Huynh, H. and Feldt, L.S. (1976). Estimation of the Box correction for degrees of freedom from sample data in randomized block and split-plot designs. *Journal of Educational Statistics*, 1(1), 69-82. doi:10.3102/10769986001001069

Littell, R.C., Henry, P.R. and Ammerman, C.B. (1998). Statistical analysis of repeated measures data using SAS procedures. *Journal of Animal Science*, 76(4), 1216-1231. doi:10.2527/1998.7641216x

Examples

```
data(mungbean_repeated)
rm <- anova_repeated(mungbean_repeated, response = "spad",
                     treatment = "treatment", time = "das", block = "block")
rm$sphericity
rm$covariance_models
```

`anova_spd` *Split-Plot Design ANOVA*

Description

Analysis of variance for a split-plot design in randomized complete blocks, with the main-plot factor tested against Error(a) and the sub-plot factor and interaction against Error(b). Gives CV(a), CV(b), SEm, SEd and CD for all four standard comparisons and letter groupings for main-plot means, sub-plot means and each factor within the levels of the other.

Usage

```
anova_spd(
  data,
  response,
  main_plot,
  sub_plot,
```

```
  replication,
  posthoc = "lsd",
  alpha = 0.05,
  verbose = TRUE
)
```

Arguments

data	Data frame containing the experimental data.
response	Name of the response variable.
main_plot	Name of the main-plot factor (A).
sub_plot	Name of the sub-plot factor (B).
replication	Name of the replication (block) column.
posthoc	Method for the letters (see perform_posthoc), or "none". Default "lsd".
alpha	Significance level for CD and letters. Default 0.05.
verbose	Logical. If TRUE (default), prints the report.

Details

Standard errors of difference (Gomez and Gomez, 1984, table 3.10): main-plot means $\sqrt{2E_a/(rb)}$, sub-plot means $\sqrt{2E_b/(ra)}$, sub-plot means at the same main-plot level $\sqrt{2E_b/r}$, and main-plot means at the same or different sub-plot level $\sqrt{2[(b-1)E_b + E_a]/(rb)}$. For the last comparison the CD uses the weighted t value $t' = [(b-1)E_b t_b + E_a t_a]/[(b-1)E_b + E_a]$. The data must be complete (every combination once in each replication).

Value

An object of class aridagri_spd with the corrected anova_table, cv_a, cv_b, error mean squares and df, se_main, cd_main, se_sub, cd_sub, se_sub_same, cd_sub_same, se_main_same_sub, cd_main_same_sub, se_cd (all comparisons), main_means and sub_means (with letters), interaction_means, letters (each factor within the levels of the other) and model.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

References

Gomez, K.A. and Gomez, A.A. (1984). *Statistical Procedures for Agricultural Research*, 2nd ed. John Wiley and Sons, New York.

Examples

```
data(clusterbean_spd)
res <- anova_spd(clusterbean_spd, response = "seed_yield",
                 main_plot = "irrigation", sub_plot = "nitrogen",
                 replication = "rep")
res$se_cd
```

anova_spd_ab_cd *Split-Plot Design with Factorial Main and Sub-Plots*

Description

Split-plot design where the main plots carry A x B and the sub-plots carry C x D. Main-plot sources are tested against Error(a), all other sources against Error(b).

Usage

```
anova_spd_ab_cd(
  data,
  response,
  main_factor1,
  main_factor2,
  sub_factor1,
  sub_factor2,
  replication,
  verbose = TRUE,
  posthoc = "lsd",
  alpha = 0.05
)
```

Arguments

data	Data frame containing the experimental data.
response	Name of the response variable.
main_factor1	First main-plot factor (A).
main_factor2	Second main-plot factor (B).
sub_factor1	First sub-plot factor (C).
sub_factor2	Second sub-plot factor (D).
replication	Name of the replication column.
verbose	Logical. If TRUE (default), prints the report.
posthoc	Method for the letters (default "lsd").
alpha	Significance level. Default 0.05.

Value

An object of class aridagri_spd_abcd; see anova_spd_ab_main for the components.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

Examples

```
data <- expand.grid(rep = 1:3, irrigation = c("I1", "I2"),
                    tillage = c("CT", "ZT"), variety = c("V1", "V2"),
                    nitrogen = c("N1", "N2", "N3"))
set.seed(5)
data$yield <- rnorm(nrow(data), 1200, 80)
res <- anova_spd_ab_cd(data, response = "yield",
                       main_factor1 = "irrigation", main_factor2 = "tillage",
                       sub_factor1 = "variety", sub_factor2 = "nitrogen",
                       replication = "rep", verbose = FALSE)
res$anova_table
```

---

anova_spd_ab_main *Split-Plot Design with Two Factors in the Main Plot*

Description

Split-plot design where the main plots carry the factorial combination of two factors (A x B) and the sub-plots carry factor C. A, B and A x B are tested against Error(a); C and every interaction with C against Error(b).

Usage

```
anova_spd_ab_main(
  data,
  response,
  main_factor1,
  main_factor2,
  sub_plot,
  replication,
  posthoc = "lsd",
  alpha = 0.05,
  verbose = TRUE
)
```

Arguments

data	Data frame containing the experimental data.
response	Name of the response variable.
main_factor1	First main-plot factor (A).
main_factor2	Second main-plot factor (B).
sub_plot	Sub-plot factor (C).
replication	Name of the replication column.
posthoc	Method for the letters (default "lsd").
alpha	Significance level. Default 0.05.
verbose	Logical. If TRUE (default), prints the report.

Value

An object of class `aridagri_spd_ab` with the corrected `anova_table`, `cv`, error mean squares and df, `se_cd` (SEm, SEd and CD for every main effect and interaction comparison), `factor_means` (with letters), `letters`, `interaction_means` and `model`.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

Examples

```
data <- expand.grid(rep = 1:3, irrigation = c("I1", "I2"),
                    variety = c("V1", "V2", "V3"),
                    nitrogen = c("N0", "N1", "N2", "N3"))
set.seed(3)
data$yield <- rnorm(nrow(data), 1200, 80)
res <- anova_spd_ab_main(data, response = "yield",
                         main_factor1 = "irrigation",
                         main_factor2 = "variety",
                         sub_plot = "nitrogen", replication = "rep",
                         verbose = FALSE)
res$anova_table
```

---

anova_spd_c_main_ab_sub

Split-Plot Design with Two Factors in the Sub-Plot

Description

Split-plot design where the main plots carry factor C and the sub-plots carry the factorial combination of two factors (A x B). C is tested against Error(a); A, B, A x B and every interaction with C against Error(b).

Usage

```
anova_spd_c_main_ab_sub(
  data,
  response,
  main_plot,
  sub_factor1,
  sub_factor2,
  replication,
  posthoc = "lsd",
  alpha = 0.05,
  verbose = TRUE
)
```

Arguments

data	Data frame containing the experimental data.
response	Name of the response variable.
main_plot	Main-plot factor (C).
sub_factor1	First sub-plot factor (A).
sub_factor2	Second sub-plot factor (B).
replication	Name of the replication column.
posthoc	Method for the letters (default "lsd").
alpha	Significance level. Default 0.05.
verbose	Logical. If TRUE (default), prints the report.

Value

An object of class aridagri_spd_cab; see anova_spd_ab_main for the components.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

Examples

```
data <- expand.grid(rep = 1:3, irrigation = c("I1", "I2", "I3"),
                    variety = c("V1", "V2"),
                    nitrogen = c("N1", "N2", "N3", "N4"))
set.seed(4)
data$yield <- rnorm(nrow(data), 1200, 80)
res <- anova_spd_c_main_ab_sub(data, response = "yield",
                               main_plot = "irrigation",
                               sub_factor1 = "variety",
                               sub_factor2 = "nitrogen",
                               replication = "rep", verbose = FALSE)
res$anova_table
```

---

anova_spd_pooled *Combined Split-Plot Analysis over Environments*

Description

Combined (pooled) analysis of a split-plot experiment repeated in several environments (years, seasons or locations). Environments are fixed and replications random within environments: the environment effect is tested against replications within environments, main-plot sources against the pooled Error(a) and sub-plot sources against the pooled Error(b). SEm, SEd and CD are given for every comparison.

Usage

```
anova_spd_pooled(
  data,
  response,
  main_plot,
  sub_plot,
  environment,
  replication,
  verbose = TRUE,
  posthoc = "lsd",
  alpha = 0.05
)
```

Arguments

data	Data frame containing the combined data.
response	Name of the response variable.
main_plot	Name of the main-plot factor.
sub_plot	Name of the sub-plot factor.
environment	Name of the environment column.
replication	Name of the replication column (nested within environment; labels may repeat across environments).
verbose	Logical. If TRUE (default), prints the report.
posthoc	Method for the letters (default "lsd").
alpha	Significance level. Default 0.05.

Value

An object of class aridagri_spd_pooled with anova_table, cv (by stratum), se_cd, factor_means (with letters), main_means, sub_means, env_means and model.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

Examples

```
data <- expand.grid(year = c("Y1", "Y2", "Y3"), rep = 1:3,
                    irrigation = c("I1", "I2", "I3"),
                    variety = c("V1", "V2", "V3", "V4"))
set.seed(7)
data$yield <- rnorm(nrow(data), 1200, 90)
res <- anova_spd_pooled(data, response = "yield", main_plot = "irrigation",
                        sub_plot = "variety", environment = "year",
                        replication = "rep", verbose = FALSE)
res$anova_table
```

anova_sspd *Split-Split-Plot Design ANOVA*

Description

Analysis of variance for a split-split-plot design with main-plot sources tested against Error(a), sub-plot sources against Error(b) and sub-sub-plot sources against Error(c). Gives CVs for the three strata, SEm, SEd and CD for every type of comparison (including those that mix error terms) and letter groupings.

Usage

```
anova_sspd(
  data,
  response,
  main_plot,
  sub_plot,
  sub_sub_plot,
  replication,
  verbose = TRUE,
  posthoc = "lsd",
  alpha = 0.05
)
```

Arguments

`data`	Data frame containing the experimental data.
`response`	Name of the response variable.
`main_plot`	Name of the main-plot factor (A).
`sub_plot`	Name of the sub-plot factor (B).
`sub_sub_plot`	Name of the sub-sub-plot factor (C).
`replication`	Name of the replication column.
`verbose`	Logical. If TRUE (default), prints the report.
`posthoc`	Method for the letters (default `"lsd"`).
`alpha`	Significance level. Default 0.05.

Value

An object of class `aridagri_sspd` with the corrected `anova_table`, `cv`, `ms_error_a/b/c`, `df_error_a/b/c`, `se_cd`, `factor_means`, `letters`, `interaction_means` and `model`.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

References

Gomez, K.A. and Gomez, A.A. (1984). *Statistical Procedures for Agricultural Research*, 2nd ed. John Wiley and Sons, New York.

Examples

```
data <- expand.grid(rep = 1:3, A = c("A1", "A2"), B = c("B1", "B2"),
                    C = c("C1", "C2", "C3"))
set.seed(6)
data$yield <- rnorm(nrow(data), 1200, 80)
res <- anova_sspd(data, response = "yield", main_plot = "A",
                  sub_plot = "B", sub_sub_plot = "C", replication = "rep")
```

---

anova_sspd_pooled *Combined Split-Split-Plot Analysis over Environments*

Description

Combined (pooled) analysis of a split-split-plot experiment repeated in several environments, with environments fixed and replications random within environments. See anova_spd_pooled.

Usage

```
anova_sspd_pooled(
  data,
  response,
  main_plot,
  sub_plot,
  sub_sub_plot,
  environment,
  replication,
  verbose = TRUE,
  posthoc = "lsd",
  alpha = 0.05
)
```

Arguments

data	Data frame containing the combined data.
response	Name of the response variable.
main_plot	Name of the main-plot factor.
sub_plot	Name of the sub-plot factor.
sub_sub_plot	Name of the sub-sub-plot factor.
environment	Name of the environment column.
replication	Name of the replication column.

verbose	Logical. If TRUE (default), prints the report.
posthoc	Method for the letters (default "lsd").
alpha	Significance level. Default 0.05.

Value

An object of class aridagri_sspd_pooled; see anova_spd_pooled. Also contains subsub_means.

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

Examples

```
data <- expand.grid(env = c("E1", "E2"), rep = 1:3, A = c("A1", "A2"),
                    B = c("B1", "B2"), C = c("C1", "C2"))
set.seed(8)
data$yield <- rnorm(nrow(data), 1200, 90)
res <- anova_sspd_pooled(data, "yield", "A", "B", "C", "env", "rep",
                         verbose = FALSE)
res$anova_table
```

---

anova_strip *Strip-Plot (Strip-Block) Design ANOVA*

Description

Analysis of variance for a strip-plot design, where factor A is applied to horizontal strips and factor B to vertical strips in each replication. A is tested against Error(a) = Rep x A, B against Error(b) = Rep x B, and A x B against Error(c). Gives CV(a), CV(b), CV(c), SEm, SEd and CD for the four standard comparisons, and letter groupings.

Usage

```
anova_strip(
  data,
  response,
  horizontal_factor,
  vertical_factor,
  replication,
  alpha = 0.05,
  verbose = TRUE,
  posthoc = "lsd"
)
```

Arguments

`data`	Data frame containing the experimental data.
`response`	Name of the response variable.
`horizontal_factor`	Factor applied in horizontal strips (A).
`vertical_factor`	Factor applied in vertical strips (B).
`replication`	Name of the replication column.
`alpha`	Significance level. Default 0.05.
`verbose`	Logical. If TRUE (default), prints the report.
`posthoc`	Method for the letters (default `"lsd"`).

Details

Standard errors of difference (Gomez and Gomez, 1984, table 3.15), with a and b levels of A and B and r replications: A means $\sqrt{2E_a/(rb)}$; B means $\sqrt{2E_b/(ra)}$; A means at the same level of B $\sqrt{2[(b-1)E_c + E_a]/(rb)}$; B means at the same level of A $\sqrt{2[(a-1)E_c + E_b]/(ra)}$. The last two use the weighted t of Cochran and Cox.

Value

An object of class `aridagri_strip` with the corrected `anova_table`, `cv` (a, b, c), error mean squares and df, `se_cd`, `horizontal_means` and `vertical_means` (with letters), `interaction_means`, `letters` and `model`.

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

References

Gomez, K.A. and Gomez, A.A. (1984). *Statistical Procedures for Agricultural Research*, 2nd ed. John Wiley and Sons, New York.

Examples

```
data <- expand.grid(rep = 1:4, irrigation = c("I1", "I2", "I3"),
                    tillage = c("CT", "MT", "ZT"))
set.seed(9)
data$yield <- rnorm(nrow(data), 1200, 70)
anova_strip(data, response = "yield", horizontal_factor = "irrigation",
            vertical_factor = "tillage", replication = "rep")
```

anova_traits *Publication Table of Treatment Means for Many Traits*

Description

Runs the analysis of variance for several traits at once and assembles the table that agronomy journals and theses expect: treatment means followed by letters, then SEm, CD and CV for each trait (with "NS" when the F-test is not significant). Works for completely randomized, randomized block, two-factor factorial and split-plot designs.

Usage

```
anova_traits(
  data,
  traits,
  design = c("rbd", "crd", "factorial", "spd"),
  treatment = NULL,
  block = NULL,
  factor1 = NULL,
  factor2 = NULL,
  main_plot = NULL,
  sub_plot = NULL,
  posthoc = "lsd",
  alpha = 0.05,
  digits = 2,
  letters_if_ns = FALSE,
  verbose = TRUE
)
```

Arguments

data	Data frame with one row per plot.
traits	Character vector of response columns.
design	One of "rbd" (default), "crd", "factorial" or "spd".
treatment	Treatment column (CRD and RBD).
block	Block (replication) column (RBD, factorial in blocks and split-plot).
factor1, factor2	The two factors of a factorial design.
main_plot, sub_plot	Main-plot and sub-plot factors of a split-plot design.
posthoc	Method for the letters: "lsd" (default), "duncan", "tukey", "snk", "scheffe" or "bonferroni".
alpha	Significance level. Default 0.05.
digits	Decimal places for means, SEm and CD. A single number, or one per trait. Default 2.

letters_if_ns	Logical. If FALSE (default), letters are omitted when the F-test of that factor is not significant.
verbose	Logical. If TRUE (default), prints the table.

Value

An object of class aridagri_traits with table (character data frame ready to export), stats (F, p, SEm, SEd, CD and CV for each trait and factor) and results (the full analysis for each trait). Export with export_results.

Examples

```
data(mothbean_rbd)
tab <- anova_traits(mothbean_rbd,
                    traits = c("plant_height", "pods_per_plant",
                               "seed_yield", "harvest_index"),
                    design = "rbd", treatment = "treatment",
                    block = "block", posthoc = "duncan")
tab$table

data(clusterbean_spd)
anova_traits(clusterbean_spd, traits = c("seed_yield", "wue"),
             design = "spd", main_plot = "irrigation",
             sub_plot = "nitrogen", block = "rep")
```

---

arid_plot *Base-Graphics Plots for aridagri Results*

Description

Quick plots with base graphics (no extra packages): bar charts of treatment or factor means with their letters for ANOVA results, a heatmap for correlation results and the integrated ranking for stability results. For publication figures with **ggplot2** see plot_means and the plot() methods.

Usage

```
arid_plot(x, type = "bar", ...)
```

Arguments

x	An object from an aridagri analysis function.
type	Kept for compatibility; bar charts are drawn.
...	Unused.

Value

No return value; called for its side effect of drawing a plot.

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

Examples

```
data(mothbean_rbd)
res <- anova_rbd(mothbean_rbd, "seed_yield", "treatment", "block",
                 verbose = FALSE)
arid_plot(res)
```

---

check_assumptions *Check ANOVA Assumptions*

Description

Checks the assumptions behind an analysis of variance: normality of residuals (Shapiro-Wilk), homogeneity of variances across treatments (Bartlett and Levene/Brown-Forsythe), additivity of block and treatment effects (Tukey's one-degree-of-freedom test, for two-way models), serial independence (Durbin-Watson, in data order) and outliers (studentized residuals).

Usage

```
check_assumptions(model, verbose = TRUE, factor = NULL, plot = FALSE)
```

Arguments

model	A fitted aov or lm model.
verbose	Logical. If TRUE (default), prints the results.
factor	Name(s) of the factor(s) defining the groups for the variance tests. Default NULL uses the last main-effect factor in the model (the treatment in y ~ block + treatment). Give several names to use their combinations.
plot	Logical. If TRUE, draws the four standard residual plots with base graphics. Default FALSE.

Details

The variance tests use the model residuals, so block effects do not inflate the group variances. Levene's test is the Brown-Forsythe form (absolute deviations from the group median). Tukey's test for non-additivity adds the squared fitted values as a one-degree-of-freedom covariate to a model with two additive factors; a significant result suggests a transformation (Gomez and Gomez, 1984, ch. 7). The Durbin-Watson statistic is only meaningful when the rows are in field or time order.

Value

A list with shapiro, bartlett, levene, nonadditivity (where applicable), durbin_watson, outliers (row indices with |studentized residual| > 3) and groups_factor.

References

Tukey, J.W. (1949). One degree of freedom for non-additivity. *Biometrics*, 5(3), 232-242. doi:10.2307/3001938

Brown, M.B. and Forsythe, A.B. (1974). Robust tests for the equality of variances. *Journal of the American Statistical Association*, 69(346), 364-367. doi:10.1080/01621459.1974.10482955

Examples

```
data(mothbean_rbd)
fit <- aov(seed_yield ~ block + treatment, data = mothbean_rbd)
check_assumptions(fit)
```

---

chickpea_augmented *Chickpea Germplasm Evaluation (Augmented RCBD, Simulated)*

Description

Simulated augmented randomized complete block design with 48 chickpea accessions (tested once) and four checks replicated in each of six blocks.

Usage

```
chickpea_augmented
```

Format

A data frame with 72 rows and 4 variables:

block Factor, block (B1-B6).

entry Factor, checks C1-C4 and accessions IC-001 to IC-048.

seed_yield Seed yield (kg/ha).

plant_height Plant height (cm).

Source

Simulated with `data-raw/make_datasets.R` (seed 2026). Not real experimental data.

Examples

```
data(chickpea_augmented)
anova_augmented(chickpea_augmented, "seed_yield", "entry", "block",
                check_names = c("C1", "C2", "C3", "C4"))
```

clusterbean_spd *Cluster Bean Irrigation x Nitrogen Trial (Split Plot, Simulated)*

Description

Simulated split-plot experiment on cluster bean (*Cyamopsis tetragonoloba*) with three irrigation levels in main plots and four nitrogen levels in sub-plots, in three replications.

Usage

```
clusterbean_spd
```

Format

A data frame with 36 rows and 7 variables:

rep Factor, replication (R1-R3).

irrigation Factor, main-plot irrigation level.

nitrogen Factor, sub-plot nitrogen level (kg N/ha; foliar = additional 2% urea spray).

seed_yield Seed yield (kg/ha).

water_use Seasonal water use (mm).

wue Water use efficiency (kg/ha per mm).

stover_yield Stover yield (kg/ha).

Source

Simulated with `data-raw/make_datasets.R` (seed 2026). Not real experimental data.

Examples

```
data(clusterbean_spd)
anova_spd(clusterbean_spd, "seed_yield", "irrigation", "nitrogen", "rep")
```

compare_means *Mean Separation from Summary Statistics*

Description

Assigns significance letters to treatment means when only the means, the error mean square and its degrees of freedom are available (for example from a published table or from another program). Uses the same tests as `perform_posthoc`.

Usage

```
compare_means(
  means,
  mse,
  df_error,
  reps,
  method = "lsd",
  alpha = 0.05,
  verbose = TRUE
)
```

Arguments

means	Named numeric vector of treatment means.
mse	Error mean square from the ANOVA.
df_error	Error degrees of freedom.
reps	Number of replications per mean: a single number or a vector with one value per mean.
method	One of "lsd", "duncan", "tukey", "snk", "scheffe" or "bonferroni".
alpha	Significance level. Default 0.05.
verbose	Logical. If TRUE (default), prints the table.

Value

The comparison object described in perform_posthoc: groups, table, comparisons, critical_range and statistics.

Examples

```
m <- c(T1 = 1180, T2 = 1265, T3 = 1342, T4 = 1410, T5 = 1238)
compare_means(m, mse = 3600, df_error = 12, reps = 4, method = "duncan")
```

---

correlation_analysis *Correlation Analysis with Significance*

Description

Computes correlation matrix with significance levels and generates publication-ready correlation table and plot.

Usage

```
correlation_analysis(
  data,
  method = "pearson",
  plot = TRUE,
  digits = 3,
  verbose = TRUE
)
```

Arguments

data	Data frame with numeric variables
method	Correlation method: "pearson", "spearman", or "kendall"
plot	Logical, whether to generate correlation plot
digits	Number of decimal places
verbose	Logical. If TRUE (default), prints formatted output to console.

Value

List with correlation matrix and significance matrix

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

Examples

```
data <- data.frame(
  yield = c(1200, 1350, 1100, 1450, 1280),
  wue = c(4.2, 4.8, 3.9, 5.1, 4.5),
  protein = c(22.1, 23.5, 21.8, 24.2, 22.9)
)
correlation_analysis(data)
```

---

cowpea_alpha *Cowpea Genotype Trial (Alpha Lattice, Simulated)*

Description

Simulated alpha lattice trial of 24 cowpea genotypes in three replications, each with six incomplete blocks of four plots. The layout was generated with `agricolae::design.alpha()`.

Usage

```
cowpea_alpha
```

Format

A data frame with 72 rows and 5 variables:

rep Factor, replication (1-3).

block Factor, incomplete block within replication (1-6).

plot Plot number.

genotype Factor, genotype code (CP-01 to CP-24).

grain_yield Grain yield (kg/ha).

Source

Simulated with `data-raw/make_datasets.R` (seed 2026). Not real experimental data.

Examples

```
data(cowpea_alpha)
anova_alpha_lattice(cowpea_alpha, "grain_yield", "genotype", "rep",
                    "block")
```

`crop_growth_analysis` *Crop Growth Analysis (CGR, RGR, NAR, LAI, LAD)*

Description

Classical growth analysis from sequential harvests: crop growth rate, relative growth rate, net assimilation rate, leaf area index and leaf area duration for each interval between samplings.

Usage

```
crop_growth_analysis(
  dry_weight,
  leaf_area = NULL,
  days,
  verbose = TRUE,
  ground_area = NULL
)
```

Arguments

`dry_weight`	Dry matter at each sampling (g per sample).
`leaf_area`	Leaf area at each sampling (cm2 per sample), or `NULL` to compute only CGR and RGR.
`days`	Days after sowing at each sampling (strictly increasing).
`verbose`	Logical. If TRUE (default), prints the table.
`ground_area`	Land area occupied by each sample (m2). When given, CGR is expressed in g m-2 day-1 and LAI = leaf area / ground area. When `NULL` (default), CGR is in g per sample per day and LAI is leaf area / 10000 (that is, leaf area in cm2 per m2 of ground).

Details

For two samplings at t_1 and t_2 (Watson, 1952; Radford, 1967):

- CGR = $(W_2 - W_1)/[P(t_2 - t_1)]$, P = ground area
- RGR = $(\ln W_2 - \ln W_1)/(t_2 - t_1)$ (g g-1 day-1)
- NAR = $\frac{W_2 - W_1}{t_2 - t_1} \times \frac{\ln L_2 - \ln L_1}{L_2 - L_1}$, reported in g m-2 (leaf) day-1
- LAD = $(LAI_1 + LAI_2)(t_2 - t_1)/2$ (days)

Value

A data frame of class `aridagri_growth` with one row per interval: `Period`, `CGR`, `RGR` and, with leaf area, `NAR`, `LAI_start`, `LAI_end` and `LAD`.

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

References

Radford, P.J. (1967). Growth analysis formulae: their use and abuse. *Crop Science*, 7(3), 171-175. doi:10.2135/cropsci1967.0011183X000700030001x

Watson, D.J. (1952). The physiological basis of variation in yield. *Advances in Agronomy*, 4, 101-145. doi:10.1016/S00652113(08)603077

Examples

```
dry_weight <- c(0.5, 2.1, 8.5, 25, 45, 62, 75)
leaf_area <- c(15, 85, 350, 800, 950, 850, 600)
days <- c(15, 30, 45, 60, 75, 90, 105)
crop_growth_analysis(dry_weight, leaf_area, days, ground_area = 0.09)
```

---

day_length *Day Length from Latitude and Date*

Description

Maximum possible daylight hours (astronomical day length) from latitude and day of year, following FAO Irrigation and Drainage Paper 56 (equations 24, 25 and 34). Useful for photo-thermal units when measured day length is not available.

Usage

```
day_length(latitude, date)
```

Arguments

latitude	Latitude in decimal degrees (north positive).
date	A Date vector, or day of year (1-366) as numbers.

Value

Numeric vector of day length in hours.

References

Allen, R.G., Pereira, L.S., Raes, D. and Smith, M. (1998). *Crop Evapotranspiration: Guidelines for Computing Crop Water Requirements*. FAO Irrigation and Drainage Paper 56. FAO, Rome.

Examples

```
# Bikaner (28.0 N) on 15 March and 15 June
day_length(28.0, as.Date(c("2026-03-15", "2026-06-15")))
```

---

economic_analysis *Economic Analysis of a Crop*

Description

Cost of cultivation, gross and net returns, benefit-cost ratio and cost of production. Arguments may be vectors (one value per treatment).

Usage

```
economic_analysis(
  yield,
  price,
  cost_fixed,
  cost_variable,
  byproduct_yield = 0,
  byproduct_price = 0,
  verbose = TRUE
)
```

Arguments

yield	Crop yield (kg/ha).
price	Market price (Rs/kg).
cost_fixed	Fixed costs (Rs/ha).
cost_variable	Variable costs (Rs/ha).

byproduct_yield
: By-product yield (kg/ha), default 0.

byproduct_price
: By-product price (Rs/kg), default 0.

verbose
: Logical. If TRUE (default), prints the table.

Value

A data frame of class `aridagri_economics`.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

Examples

```
economic_analysis(yield = 1200, price = 65, cost_fixed = 15000,
                  cost_variable = 12000)
economic_analysis(yield = c(1050, 1200, 1340), price = 65,
                  cost_fixed = 15000, cost_variable = c(11000, 12000, 13500),
                  byproduct_yield = c(1600, 1800, 1950), byproduct_price = 5)
```

---

economic_indices *Economic Efficiency Indices (B:C Ratio)*

Description

Net return, benefit-cost ratio and return per rupee invested from gross return and total cost.

Usage

```
economic_indices(gross_return, total_cost, verbose = TRUE)
```

Arguments

gross_return
: Gross return (Rs/ha).

total_cost
: Total cost of cultivation (Rs/ha).

verbose
: Logical. If TRUE (default), prints the table.

Value

A data frame of class `aridagri_economics` with `Net_Return`, `BC_Ratio` (gross return / cost) and `Return_per_Rupee` (net return / cost).

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

Examples

```
economic_indices(gross_return = c(75000, 82000), total_cost = c(35000, 38000))
```

`export_results` *Export Results to Excel or CSV*

Description

Writes the main tables of an aridagri result to an Excel workbook (one sheet per table) or a CSV file. Multi-trait tables from `anova_traits` are written as they appear in the report.

Usage

```
export_results(x, file, format = "xlsx", digits = 3, verbose = TRUE)
```

Arguments

`x`	An aridagri result object or a data frame.
`file`	Output file path.
`format`	`"xlsx"` (default; needs **writexl**) or `"csv"` (the first table only).
`digits`	Number of decimal places for numeric columns.
`verbose`	Logical. If TRUE (default), prints the file name.

Value

Invisibly returns the file path.

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

Examples

```
data(mothbean_rbd)
res <- anova_rbd(mothbean_rbd, "seed_yield", "treatment", "block",
                 verbose = FALSE)
export_results(res, tempfile(fileext = ".csv"), format = "csv")
```

gge_biplot *GGE Biplot Analysis (Which-Won-Where and Mean vs Stability)*

Description

Genotype plus genotype-by-environment (GGE) biplot analysis of a multi-environment trial (Yan et al., 2000). Gives the genotype and environment scores on the first two principal components, the winning genotype in each environment and the resulting mega-environments (which-won-where), and the average-environment coordination (AEC) ranking of genotypes for mean performance and stability.

Usage

```
gge_biplot(
  data,
  genotype,
  environment,
  trait,
  scaling = c("none", "sd"),
  svp = c("symmetric", "genotype", "environment"),
  verbose = TRUE
)
```

Arguments

data	Data frame with genotype, environment and trait columns (plot data or genotype x environment means).
genotype	Name of the genotype column.
environment	Name of the environment column.
trait	Name of the trait column.
scaling	"none" (default) or "sd" (each environment divided by its standard deviation, giving environments equal weight).
svp	Singular value partitioning: "symmetric" (default, suited to which-won-where), "genotype" (genotype-focused, suited to comparing genotypes and the mean vs stability view) or "environment" (environment-focused).
verbose	Logical. If TRUE (default), prints a summary.

Details

The genotype x environment table of means is centred on the environment means (and optionally scaled) and decomposed by singular value decomposition. With singular values d_k, genotype scores are $u_{ik}d_k^f$ and environment scores $v_{jk}d_k^{1-f}$, with $f = 0.5, 1, 0$ for symmetric, genotype- and environment-focused partitioning. The winner in an environment is the genotype with the highest value predicted by the two-component biplot; environments with the same winner form a mega-environment. On the AEC view the abscissa (projection on the average-environment axis) ranks mean performance and the ordinate (distance from that axis) measures instability.

Value

An object of class `aridagri_gge` with `genotype_scores`, `environment_scores`, `variance_percent`, `which_won_where` (environment and winner), `mega_environments`, `aec` (genotype AEC abscissa, ordinate and ranks) and the settings used. Plot it with `plot()`.

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

Yan, W. and Kang, M.S. (2003). *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists*. CRC Press, Boca Raton.

Examples

```
data(pearlmillet_met)
gg <- gge_biplot(pearlmillet_met, "genotype", "environment", "grain_yield")
gg$which_won_where
if (requireNamespace("ggplot2", quietly = TRUE)) {
  plot(gg, type = "which_won_where")
}
```

---

harvest_index *Harvest Index*

Description

Harvest index and grain-to-straw ratio.

Usage

```
harvest_index(grain_yield, straw_yield, verbose = TRUE)
```

Arguments

`grain_yield`	Grain (economic) yield.
`straw_yield`	Straw (stover) yield, in the same unit.
`verbose`	Logical. If TRUE (default), prints the table.

Value

A data frame of class `aridagri_hi` with grain, straw and total biomass, `HI_percent` and `Grain_Straw_Ratio`.

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

Examples

```
harvest_index(grain_yield = c(1200, 1350, 1100),
              straw_yield = c(2400, 2500, 2300))
```

`mothbean_rbd` *Moth Bean Nutrient Management Trial (RCBD, Simulated)*

Description

Simulated randomized complete block experiment on moth bean (*Vigna aconitifolia*) with eight nutrient management treatments in four blocks and eight traits.

Usage

```
mothbean_rbd
```

Format

A data frame with 32 rows and 10 variables:

block Factor, block (R1-R4).

treatment Factor, eight treatments (control, recommended dose of fertilizer (RDF), and RDF with biofertilizers, FYM, sulphur or zinc).

seed_yield Seed yield (kg/ha).

plant_height Plant height at harvest (cm).

branches_per_plant Branches per plant.

pods_per_plant Pods per plant.

seeds_per_pod Seeds per pod.

test_weight 1000-seed weight (g).

stover_yield Stover yield (kg/ha).

harvest_index Harvest index (%).

Source

Simulated with `data-raw/make_datasets.R` (seed 2026). Not real experimental data.

Examples

```
data(mothbean_rbd)
anova_rbd(mothbean_rbd, "seed_yield", "treatment", "block")
```

mungbean_repeated *Mung Bean Chlorophyll over Time (Repeated Measures, Simulated)*

Description

Simulated repeated measurements of leaf chlorophyll (SPAD) on the same plots at 25, 35, 45 and 55 days after sowing, for four foliar spray treatments in four randomized complete blocks. Errors within a plot follow a first-order autoregressive process.

Usage

```
mungbean_repeated
```

Format

A data frame with 64 rows and 5 variables:

block Factor, block (R1-R4).

treatment Factor, foliar spray treatment.

das Days after sowing (25, 35, 45, 55).

plot Factor, plot identifier (block-treatment).

spad SPAD chlorophyll meter reading.

Source

Simulated with `data-raw/make_datasets.R` (seed 2026). Not real experimental data.

Examples

```
data(mungbean_repeated)
anova_repeated(mungbean_repeated, "spad", "treatment", "das",
               block = "block")
```

nue_calculate *Nutrient Use Efficiency Indices*

Description

Agronomic efficiency (AE), partial factor productivity (PFP), apparent recovery efficiency (ARE), physiological efficiency (PE), internal utilization efficiency (IE) and, when biomass is given, the biomass-based physiological efficiency and utilization efficiency of Fageria and Baligar (2005). All arguments may be vectors (one value per treatment).

Usage

```
nue_calculate(
  yield_fertilized,
  yield_control,
  nutrient_applied,
  nutrient_uptake_fert = NULL,
  nutrient_uptake_ctrl = NULL,
  biomass_fert = NULL,
  biomass_ctrl = NULL,
  verbose = TRUE
)
```

Arguments

`yield_fertilized`	Grain yield with the nutrient (kg/ha).
`yield_control`	Grain yield of the control without the nutrient (kg/ha).
`nutrient_applied`	Nutrient applied (kg/ha), greater than 0.
`nutrient_uptake_fert`	Total nutrient uptake with the nutrient (kg/ha), optional.
`nutrient_uptake_ctrl`	Total nutrient uptake of the control (kg/ha), optional.
`biomass_fert`	Total biomass with the nutrient (kg/ha), optional.
`biomass_ctrl`	Total biomass of the control (kg/ha), optional.
`verbose`	Logical. If TRUE (default), prints the table.

Details

- AE = (Yf - Yc) / N (kg grain per kg nutrient)
- PFP = Yf / N
- ARE = 100 (Uf - Uc) / N (percent)
- PE = (Yf - Yc) / (Uf - Uc) (kg grain per kg nutrient taken up; called agro-physiological efficiency by Fageria and Baligar)
- IE = Yf / Uf
- PE_biomass = (Bf - Bc) / (Uf - Uc) and UE = PE_biomass x ARE / 100 (Fageria and Baligar, 2005)

AE = PE x ARE / 100 holds by definition. PE is not computed when the uptake difference is zero or negative.

Value

A data frame of class `aridagri_nue`.

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

References

Dobermann, A. (2005). Nitrogen use efficiency - state of the art. IFA International Workshop on Enhanced-Efficiency Fertilizers, Frankfurt.

Fageria, N.K. and Baligar, V.C. (2005). Enhancing nitrogen use efficiency in crop plants. *Advances in Agronomy*, 88, 97-185. doi:10.1016/S00652113(05)880046

Examples

```
nue_calculate(yield_fertilized = 1850, yield_control = 1200,
              nutrient_applied = 40)
# Several N doses with uptake and biomass
nue_calculate(yield_fertilized = c(1450, 1720, 1850),
              yield_control = 1200, nutrient_applied = c(20, 40, 60),
              nutrient_uptake_fert = c(48, 61, 68),
              nutrient_uptake_ctrl = 35,
              biomass_fert = c(4300, 4950, 5300), biomass_ctrl = 3600)
```

---

nutrient_response *Nutrient Response Curves and Economic Optimum Dose*

Description

Fits nutrient response models and finds the dose for maximum yield and the economic optimum dose, where the marginal return equals the price ratio. Quadratic, linear-plateau, quadratic-plateau and Mitscherlich models are available; `model = "all"` fits all four and compares them.

Usage

```
nutrient_response(
  dose,
  yield,
  model = "quadratic",
  price_output = 50,
  price_nutrient = 15,
  verbose = TRUE
)
```

Arguments

`dose`	Numeric vector of nutrient doses (kg/ha).
`yield`	Numeric vector of yields (kg/ha), one per dose (replicated doses are allowed).

`model`	`"quadratic"` (default), `"linear_plateau"`, `"quadratic_plateau"`, `"mitscherlich"` or `"all"`.
`price_output`	Price of the produce (Rs/kg).
`price_nutrient`	Price of the nutrient (Rs/kg of nutrient).
`verbose`	Logical. If TRUE (default), prints the results.

Details

- Quadratic: $Y = a + bX + cX^2$; maximum at $-b/(2c)$; economic optimum $(P_n/P_y - b)/(2c)$.
- Linear-plateau: $Y = a + b\min(X, X_0)$; economic optimum at the join point X_0 when $b > P_n/P_y$.
- Quadratic-plateau: quadratic up to its vertex X_0, then flat.
- Mitscherlich: $Y = A - Be^{-cX}$; economic optimum $\ln(BcP_y/P_n)/c$; also the dose giving 95% of the asymptote.

Plateau models are fitted by profile least squares over the join point; the Mitscherlich model by `nls` with a self-starting model. All four models have three parameters (the join point counts as one), so they are compared by R-squared, adjusted R-squared, RMSE and AIC on an equal footing (AIC differences equal those of `stats::AIC()`). An optimum beyond the highest dose tested is flagged as an extrapolation.

Value

For a single model, an object of class `aridagri_response` with `model`, `coefficients`, `r_squared`, `adj_r_squared`, `rmse`, `aic`, `dose_max_yield`, `max_yield`, `dose_economic`, `yield_economic` and `fit`. For `model = "all"`, a list with `comparison` (one row per model), `models` and `best` (lowest AIC).

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

References

Cerrato, M.E. and Blackmer, A.M. (1990). Comparison of models for describing corn yield response to nitrogen fertilizer. *Agronomy Journal*, 82(1), 138-143. doi:10.2134/agronj1990.00021962008200010030x

Examples

```
dose <- c(0, 20, 40, 60, 80, 100)
yield <- c(1100, 1350, 1520, 1610, 1650, 1660)
nutrient_response(dose, yield, model = "quadratic",
                  price_output = 60, price_nutrient = 15)
nutrient_response(dose, yield, model = "all", price_output = 60,
                  price_nutrient = 15)
```

path_analysis *Path Coefficient Analysis*

Description

Performs path analysis to determine direct and indirect effects of independent variables on a dependent variable. Essential for understanding yield contributing factors.

Usage

```
path_analysis(data, dependent, independent, digits = 4, verbose = TRUE)
```

Arguments

data	Data frame with numeric variables
dependent	Name of dependent variable (e.g., "yield")
independent	Character vector of independent variable names
digits	Number of decimal places
verbose	Logical. If TRUE (default), prints formatted output to console.

Value

List with direct effects, indirect effects, and correlation breakdown

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

Examples

```
data <- data.frame(
  yield = c(1200, 1350, 1100, 1450, 1280, 1380, 1220, 1400),
  pods = c(45, 52, 42, 58, 48, 54, 46, 56),
  seeds = c(8.2, 9.1, 7.8, 9.5, 8.5, 9.0, 8.3, 9.3),
  weight = c(32, 35, 30, 38, 33, 36, 31, 37)
)
path_analysis(data, dependent = "yield",
              independent = c("pods", "seeds", "weight"))
```

pca_analysis *Principal Component Analysis*

Description

Performs PCA with visualization suitable for agricultural research data. Includes scree plot, biplot, and variable contributions.

Usage

```
pca_analysis(data, scale = TRUE, ncp = 5, plot = TRUE, verbose = TRUE)
```

Arguments

data	Data frame with numeric variables
scale	Logical, whether to scale variables (default TRUE)
ncp	Number of components to retain (default 5)
plot	Logical, whether to generate plots
verbose	Logical. If TRUE (default), prints formatted output to console.

Value

PCA results with eigenvalues, loadings, and scores

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

Examples

```
data <- data.frame(
  yield = rnorm(30, 1200, 200),
  wue = rnorm(30, 4.5, 0.5),
  protein = rnorm(30, 22, 2),
  biomass = rnorm(30, 3500, 500)
)
pca_analysis(data)
```

pearlmillet_met *Pearl Millet Multi-Environment Trial (Simulated)*

Description

Simulated trial of ten pearl millet genotypes in six environments (three locations x two years) with three replications, for stability and GGE biplot analysis.

Usage

```
pearlmillet_met
```

Format

A data frame with 180 rows and 5 variables:

environment Factor, location-year (BKN = Bikaner, JDH = Jodhpur, JSM = Jaisalmer).

rep Factor, replication within environment.

genotype Factor, genotype code (PM-01 to PM-10).

grain_yield Grain yield (kg/ha).

days_to_maturity Days to maturity.

Source

Simulated with `data-raw/make_datasets.R` (seed 2026). Not real experimental data.

Examples

```
data(pearlmillet_met)
stability_analysis(pearlmillet_met, "genotype", "environment", "rep",
                   "grain_yield", method = "eberhart")
```

perform_posthoc *Post-Hoc Mean Comparisons After ANOVA*

Description

Compares treatment means after an analysis of variance and returns compact letter displays (means sharing a letter do not differ). Fisher's LSD, Duncan's multiple range test (DMRT), Tukey's HSD, Student-Newman-Keuls, Scheffe and Bonferroni are computed inside the package, so no extra package is needed. Dunnett's test against a control uses **multcomp** when it is installed.

Usage

```
perform_posthoc(
  model,
  data,
  response,
  treatment,
  mse = NULL,
  df_error = NULL,
  posthoc = "lsd",
  alpha = 0.05,
  control = NULL,
  verbose = TRUE
)
```

Arguments

model	A fitted aov or lm model containing the treatment factor.
data	Data frame used to fit the model. Kept for compatibility; the model frame is used for the calculations.
response	Name of the response variable (used to label output).
treatment	Name of the treatment factor in the model.
mse	Error mean square. Default NULL takes it from the model. Supply it to compare means against a different error term (for example the main-plot error of a split-plot design).
df_error	Error degrees of freedom matching mse. Default NULL takes it from the model.
posthoc	Method(s): "lsd", "duncan", "tukey", "snk", "scheffe", "bonferroni", "dunnett", a vector of these, or "all".
alpha	Significance level. Default 0.05.
control	Control level for Dunnett's test. Default NULL uses the first level of the treatment factor.
verbose	Logical. If TRUE (default), prints the results.

Details

Means are least-squares means of the treatment factor averaged over the other factors in the model. With complete, balanced data they equal the arithmetic means. With missing plots or unequal replication every pair is tested with its own standard error of difference, so the letters stay exact (Tukey-Kramer form for the range tests).

Duncan's and the Student-Newman-Keuls tests use the studentized range for the number of means spanned by each pair, with the protection level $1 - (1 - \alpha)^{p-1}$ for Duncan's test, and apply the closure rule: two means are declared different only if every range of means containing them is also significant (Duncan, 1955). The p-value reported for a pair is the largest p-value of the ranges containing it, so it agrees with the letters.

Least-squares means that cannot be estimated (for example a level whose cells are all empty in a model with interactions) are left out with a warning. Dunnett's test averages differences over interacting factors and uses mse and df_error when they are supplied.

Letters are assigned with the insert-and-absorb algorithm of Piepho (2004), which gives a valid display for any pattern of significant pairs. The group containing the highest mean gets the letter "a".

Value

A list with one element per method. Each element contains `groups` (means and letters, ordered from highest to lowest, with treatments as row names), `table` (level, mean, SE, letter, replications), `comparisons` (all pairwise differences with their SE, p-value and significance), `critical_range` and `statistics`. The Dunnett element is a data frame of comparisons with the control.

References

Duncan, D.B. (1955). Multiple range and multiple F tests. *Biometrics*, 11(1), 1-42. doi:10.2307/3001478

Piepho, H.-P. (2004). An algorithm for a letter-based representation of all-pairwise comparisons. *Journal of Computational and Graphical Statistics*, 13(2), 456-466. doi:10.1198/1061860043515

Kramer, C.Y. (1956). Extension of multiple range tests to group means with unequal numbers of replications. *Biometrics*, 12(3), 307-310. doi:10.2307/3001469

See Also

`compare_means` for summary statistics, `anova_rbd`.

Examples

```
data(mothbean_rbd)
fit <- aov(seed_yield ~ block + treatment, data = mothbean_rbd)
ph <- perform_posthoc(fit, mothbean_rbd, response = "seed_yield",
                      treatment = "treatment", posthoc = c("lsd", "duncan"))
ph$duncan$groups
```

---

plot.aridagri *Plot Methods for aridagri Results*

Description

`plot()` methods that draw the standard publication figure for each kind of result with **ggplot2**: a bar chart of means with letters (CRD, RCBD, Latin square, pooled RCBD, alpha lattice, augmented), an interaction plot or bar chart (factorial and split-plot designs), a time course (repeated measures) or a stability plot. For base graphics without **ggplot2**, use `arid_plot`.

Usage

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

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

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

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

## S3 method for class 'aridagri_factorial'
plot(x, type = c("interaction", "means"), ...)

## S3 method for class 'aridagri_split'
plot(x, type = c("interaction", "means"), ...)

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

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

## S3 method for class 'aridagri_stability'
plot(x, type = c("eberhart", "ammi1", "ammi2"), ...)
```

Arguments

x	A result object.
...	Passed to plot_means, plot_interaction or plot_stability.
type	For factorial and split-plot results: "interaction" (default) or "means". For stability results: "eberhart" (default), "ammi1" or "ammi2".

Value

A ggplot2 object.

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE)) {
  data(mothbean_rbd)
  res <- anova_rbd(mothbean_rbd, "seed_yield", "treatment", "block",
                   verbose = FALSE)
  plot(res)
}
```

plot.aridagri_gge *Plot Method for GGE Biplot Results*

Description

Plot Method for GGE Biplot Results

Usage

```
## S3 method for class 'aridagri_gge'
plot(
  x,
  type = c("which_won_where", "mean_stability", "basic"),
  title = NULL,
  ...
)
```

Arguments

x	An object of class aridagri_gge.
type	"which_won_where" (default), "mean_stability" or "basic".
title	Plot title.
...	Unused.

Value

A ggplot2 object.

plot_interaction *Interaction Plot of Two Factors*

Description

Line chart of the means of every combination of two factors, with the first factor on the x-axis and one line per level of the second factor. Works with anova_factorial, anova_spd and the other split-plot functions (first two factors, or the two named in factors), anova_strip and anova_repeated (time course).

Usage

```
plot_interaction(x, factors = NULL, title = NULL, ylab = NULL)
```

Arguments

x	A result object.
factors	Optional character vector of two factor names (split-plot results with more than two factors).
title	Plot title.
ylab	Y-axis label.

Value

A ggplot2 object.

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE)) {
  data(clusterbean_spd)
  res <- anova_spd(clusterbean_spd, "seed_yield", "irrigation",
                   "nitrogen", "rep", verbose = FALSE)
  plot_interaction(res, ylab = "Seed yield (kg/ha)")
}
```

---

plot_means *Bar Chart of Treatment Means with Letters*

Description

Publication-ready bar chart of treatment means with standard-error bars and the letter groupings from an **aridagri** analysis. Works with the results of anova_crd, anova_rbd, anova_latin, anova_rbd_pooled, anova_factorial (one factor or the combinations), anova_spd and the other split-plot functions (one factor), anova_alpha_lattice and anova_augmented (adjusted means).

Usage

```
plot_means(
  x,
  which = NULL,
  sort = TRUE,
  top = 20,
  title = NULL,
  ylab = NULL,
  horizontal = NULL
)
```

Arguments

x	A result object from one of the functions above.
which	For factorial and split-plot results, the factor to plot (name), or "interaction" for the treatment combinations of a two-factor factorial. Default: the first factor.
sort	Logical. Order bars from highest to lowest mean. Default TRUE.
top	For alpha lattice and augmented results, the number of entries to show. Default 20.
title	Plot title. Default: the response name.
ylab	Y-axis label. Default: the response name.
horizontal	Logical. Draw horizontal bars. Default NULL chooses horizontal bars when labels are long or there are more than 12 bars.

Value

A ggplot2 object.

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE)) {
  data(mothbean_rbd)
  res <- anova_rbd(mothbean_rbd, "seed_yield", "treatment", "block",
                   posthoc = "duncan", verbose = FALSE)
  plot_means(res, ylab = "Seed yield (kg/ha)")
}
```

---

plot_response *Plot a Nutrient Response Curve*

Description

Observed yields and the fitted response curve(s) from nutrient_response, with the economic optimum dose marked.

Usage

```
plot_response(x, dose, yield, title = NULL)
```

Arguments

x	An object of class aridagri_response or aridagri_response_set.
dose, yield	The data used to fit the model.
title	Plot title.

Value

A ggplot2 object.

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE)) {
  dose <- c(0, 20, 40, 60, 80, 100)
  yield <- c(1100, 1350, 1520, 1610, 1650, 1660)
  nr <- nutrient_response(dose, yield, model = "all", verbose = FALSE)
  plot_response(nr, dose, yield)
}
```

---

plot_stability *Stability Plots for Multi-Environment Trials*

Description

Figures for `stability_analysis` results:

- `"eberhart"`: genotype mean against the regression coefficient b_i, with reference lines at the grand mean and $b_i = 1$.
- `"ammi1"`: AMMI1 biplot of mean against IPCA1 scores for genotypes and environments.
- `"ammi2"`: AMMI2 biplot of IPCA1 against IPCA2, with environments as vectors.

Usage

```
plot_stability(x, type = c("eberhart", "ammi1", "ammi2"), title = NULL)
```

Arguments

`x`	An object of class `aridagri_stability`.
`type`	`"eberhart"` (default), `"ammi1"` or `"ammi2"`.
`title`	Plot title.

Value

A ggplot2 object.

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE)) {
  data(pearlmillet_met)
  st <- stability_analysis(pearlmillet_met, "genotype", "environment",
                           "rep", "grain_yield", verbose = FALSE)
  plot_stability(st, "eberhart")
  plot_stability(st, "ammi2")
}
```

print.aridagri_alpha *Print Method for Alpha Lattice Results*

Description

Print Method for Alpha Lattice Results

Usage

```
## S3 method for class 'aridagri_alpha'
print(x, digits = 2, n = 15, ...)
```

Arguments

x	An object of class aridagri_alpha.
digits	Number of decimal places for means. Default 2.
n	Number of genotypes to show. Default 15.
...	Unused.

Value

Invisibly returns x.

print.aridagri_anova *Print Method for CRD and RCBD Results*

Description

Print Method for CRD and RCBD Results

Usage

```
## S3 method for class 'aridagri_anova'
print(x, digits = 2, ...)

## S3 method for class 'aridagri_latin'
print(x, digits = 2, ...)
```

Arguments

x	An object of class aridagri_anova.
digits	Number of decimal places for means. Default 2.
...	Unused.

Value

Invisibly returns x. Called for its side effect of printing the ANOVA report.

print.aridagri_augmented

Print Method for Augmented Design Results

Description

Print Method for Augmented Design Results

Usage

```
## S3 method for class 'aridagri_augmented'
print(x, digits = 2, n = 10, ...)
```

Arguments

x	An object of class aridagri_augmented.
digits	Number of decimal places for means. Default 2.
n	Number of top test entries to show. Default 10.
...	Unused.

Value

Invisibly returns x.

print.aridagri_factorial

Print Methods for Factorial Results

Description

Print Methods for Factorial Results

Usage

```
## S3 method for class 'aridagri_factorial'
print(x, digits = 2, ...)

## S3 method for class 'aridagri_factorial3'
print(x, digits = 2, ...)
```

Arguments

x	An object of class aridagri_factorial or aridagri_factorial3.
digits	Number of decimal places for means. Default 2.
...	Unused.

Value

Invisibly returns `x`.

`print.aridagri_gge` *Print Method for GGE Biplot Results*

Description

Print Method for GGE Biplot Results

Usage

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

Arguments

`x`	An object of class `aridagri_gge`.
`...`	Unused.

Value

Invisibly returns `x`.

`print.aridagri_pca` *Print Method for PCA Results*

Description

Prints the number of components retained and the variance they explain.

Usage

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

Arguments

`x`	An object of class `aridagri_pca` from `pca_analysis`.
`...`	Additional arguments (unused).

Value

The input object, invisibly.

print.aridagri_pooled *Print Method for Combined RCBD Analysis*

Description

Print Method for Combined RCBD Analysis

Usage

```
## S3 method for class 'aridagri_pooled'
print(x, digits = 2, ...)
```

Arguments

x	An object of class aridagri_pooled.
digits	Number of decimal places for means. Default 2.
...	Unused.

Value

Invisibly returns x.

print.aridagri_repeated *Print Method for Repeated Measures Results*

Description

Print Method for Repeated Measures Results

Usage

```
## S3 method for class 'aridagri_repeated'
print(x, digits = 2, ...)
```

Arguments

x	An object of class aridagri_repeated.
digits	Number of decimal places for means. Default 2.
...	Unused.

Value

Invisibly returns x.

`print.aridagri_response` *Print Methods for Nutrient Response Results*

Description

Print Methods for Nutrient Response Results

Usage

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

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

Arguments

`x`	An object of class `aridagri_response` or `aridagri_response_set`.
`...`	Unused.

Value

Invisibly returns `x`.

`print.aridagri_stability` *Print Method for Stability Analysis*

Description

Print Method for Stability Analysis

Usage

```
## S3 method for class 'aridagri_stability'
print(x, digits = 3, ...)
```

Arguments

`x`	An object of class `aridagri_stability`.
`digits`	Number of decimal places. Default 3.
`...`	Unused.

Value

Invisibly returns `x`.

print.aridagri_strip *Print Method for Split-Plot Family Results*

Description

Print Method for Split-Plot Family Results

Usage

```
## S3 method for class 'aridagri_strip'
print(x, digits = 2, ...)

## S3 method for class 'aridagri_split'
print(x, digits = 2, ...)

## S3 method for class 'aridagri_split_pooled'
print(x, digits = 2, ...)
```

Arguments

x	A result from anova_spd or a related split-plot function.
digits	Number of decimal places for means. Default 2.
...	Unused.

Value

Invisibly returns x.

print.aridagri_traits *Print Method for Multi-Trait Tables*

Description

Print Method for Multi-Trait Tables

Usage

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

Arguments

x	An object of class aridagri_traits.
...	Unused.

Value

Invisibly returns `x`.

`sem_analysis` *Structural Equation Modeling for Field Experiments*

Description

Performs SEM analysis for agricultural field experiments. Allows testing of hypothesized causal relationships among variables.

Usage

```
sem_analysis(data, model, plot = TRUE, verbose = TRUE)
```

Arguments

`data`	Data frame with variables
`model`	Model specification in lavaan syntax
`plot`	Logical, whether to generate path diagram
`verbose`	Logical. If TRUE (default), prints formatted output to console.

Value

SEM results including fit indices and parameter estimates

Author(s)

Lalit Kumar Rolaniya, ICAR-IIPR, Bikaner

Examples

```
if (requireNamespace("lavaan", quietly = TRUE)) {
  set.seed(42)
  n <- 100
  nitrogen <- rnorm(n, 60, 10)
  phosphorus <- rnorm(n, 30, 5)
  yield <- 0.5 * nitrogen + 0.3 * phosphorus + rnorm(n, 0, 5)
  df <- data.frame(yield = yield, nitrogen = nitrogen, phosphorus = phosphorus)
  model <- 'yield ~ nitrogen + phosphorus'
  result <- sem_analysis(df, model, plot = FALSE)
}
```

`stability_analysis` *Stability Analysis for Multi-Environment Trials (Seven Methods)*

Description

Stability analysis of genotypes (or treatments) tested in several environments, with the combined ANOVA and seven established methods:

- Eberhart and Russell (1966) joint regression: b_i, S^2_{di}, tests of $b_i = 1$ and $S^2_{di} = 0$, and the Eberhart-Russell ANOVA
- AMMI: ANOVA with Gollob's degrees of freedom for each IPCA, IPCA scores, AMMI stability value (ASV) and yield stability index
- Finlay and Wilkinson (1963) regression on the environment mean
- Shukla (1972) stability variance with its F-test
- Wricke (1962) ecovalence
- Coefficient of variation (Francis and Kannenberg, 1978)
- Cultivar superiority index (Lin and Binns, 1988)

An integrated ranking averages the stability ranks of the seven methods.

Usage

```
stability_analysis(
  data,
  genotype,
  environment,
  replication,
  trait,
  method = "all",
  verbose = TRUE,
  alpha = 0.05,
  fw_log = FALSE
)
```

Arguments

`data`	Data frame with genotype, environment, replication and trait columns (one row per plot). Genotype x environment means (one row per combination) can be used with `replication = NULL`; tests that need the pooled error are then omitted.
`genotype`	Name of the genotype (or treatment) column.
`environment`	Name of the environment (location, year or season) column.
`replication`	Name of the replication column, or `NULL`.
`trait`	Name of the trait (response) column.
`method`	`"all"` (default) or one or more of `"eberhart"`, `"ammi"`, `"finlay"`, `"shukla"`, `"wricke"`, `"cv"`, `"superiority"`.

`verbose`	Logical. If TRUE (default), prints the report.
`alpha`	Significance level for the tests. Default 0.05.
`fw_log`	Logical. If TRUE, the Finlay-Wilkinson regression uses log10-transformed means as in the original paper. Default FALSE (on the original scale, where the slope equals the Eberhart-Russell b_i).

Details

Calculations use the genotype x environment table of means (g genotypes, e environments, r replications). The environmental index is $I_j = \bar{y}_{.j} - \bar{y}_{..}$.

Eberhart-Russell. $b_i = \sum_j y_{ij} I_j / \sum_j I_j^2$; $S^2_{di} = \sum_j \delta^2_{ij}/(e-2) - MSE/r$, where δ_{ij} are deviations from the regression and MSE is the pooled error. $b_i = 1$ is tested with $t = (b_i - 1)/SE(b_i)$ on $e-2$ df, and $S^2_{di} = 0$ with $F = [\sum_j \delta^2_{ij}/(e-2)]/(MSE/r)$.

Shukla. $\sigma^2_i = [g(g-1)W_i - \sum W]/[(e-1)(g-1)(g-2)]$, where W_i is Wricke's ecovalence $\sum_j (\bar{y}_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..})^2$; tested with $F = \sigma^2_i/(MSE/r)$ on $e-1$ and the error df. Values are on the scale of the means.

AMMI. The interaction matrix is decomposed by singular value decomposition. IPCA k has sum of squares $r\lambda_k^2$ and $g+e-1-2k$ df (Gollob, 1968). Scores are $u_{ik}\sqrt{\lambda_k}$. ASV = $\sqrt{[(SS_1/SS_2)IPCA1]^2 + IPCA2^2}$ (Purchase et al., 2000) and the yield stability index is the sum of the ranks of mean (high = 1) and ASV.

Lin-Binns. $P_i = \sum_j (y_{ij} - M_j)^2/(2e)$, with M_j the highest mean in environment j.

Value

An object of class `aridagri_stability` containing `anova` (combined ANOVA, when replications are given), `genotype_means`, `environment_means`, `ge_matrix` and, depending on `method`, `eberhart` (with `eberhart_anova`), `ammi` (`anova`, `components`, `stability`, `genotype_scores`, `environment_scores`), `finlay`, `shukla`, `wricke`, `cv_stability`, `superiority`, `integrated` and `concordance` (Kendall's W among the seven stability rankings).

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

References

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

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

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

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

Gollob, H.F. (1968). A statistical model which combines features of factor analytic and analysis of variance techniques. *Psychometrika*, 33(1), 73-115. doi:10.1007/BF02289676

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. doi:10.1080/02571862.2000.10634878

Francis, T.R. and Kannenberg, L.W. (1978). Yield stability studies in short-season maize. I. A descriptive method for grouping genotypes. *Canadian Journal of Plant Science*, 58(4), 1029-1034. doi:10.4141/cjps78157

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

Examples

```
data(pearlmillet_met)
st <- stability_analysis(pearlmillet_met, genotype = "genotype",
                         environment = "environment", replication = "rep",
                         trait = "grain_yield")
st$eberhart
st$ammi$anova
```

---

theme_aridagri *A Clean ggplot2 Theme for Agricultural Figures*

Description

The theme used by the plotting functions of **aridagri**: white background, light grid, dark text and a bold left-aligned title. Add it to any ggplot2 figure.

Usage

```
theme_aridagri(base_size = 11)
```

Arguments

base_size	Base font size in points. Default 11.

Value

A ggplot2 theme object.

Examples

```
if (requireNamespace("ggplot2", quietly = TRUE)) {
  ggplot2::ggplot(mtcars, ggplot2::aes(wt, mpg)) +
    ggplot2::geom_point() + theme_aridagri()
}
```

`thermal_indices` *Growing Degree Days and Thermal Indices*

Description

Growing degree days (GDD), helio-thermal units (HTU), photo-thermal units (PTU), heat use efficiency (HUE) and helio-thermal use efficiency from daily temperatures.

Usage

```
thermal_indices(
  tmax,
  tmin,
  base_temp = 10,
  sunshine_hours = NULL,
  day_length = NULL,
  crop_yield = NULL,
  biomass = NULL,
  verbose = TRUE,
  upper_temp = NULL,
  method = c("average", "modified")
)
```

Arguments

`tmax`	Daily maximum temperature (degrees C).
`tmin`	Daily minimum temperature (degrees C).
`base_temp`	Base temperature (degrees C). Default 10.
`sunshine_hours`	Daily bright sunshine hours (optional, for HTU).
`day_length`	Daily day length in hours (optional, for PTU); see `day_length`.
`crop_yield`	Economic yield (kg/ha) for HUE (optional).
`biomass`	Total biomass (kg/ha) for HUE (optional).
`verbose`	Logical. If TRUE (default), prints the results.
`upper_temp`	Optional upper threshold temperature (degrees C) above which development does not increase.
`method`	`"average"` (default): GDD = max(0, (Tmax + Tmin)/2 - Tbase), with the mean capped at `upper_temp`. `"modified"`: Tmax and Tmin are each limited to the range from `base_temp` to `upper_temp` before averaging (McMaster and Wilhelm, 1997, method 2).

Details

HTU = sum of GDD x bright sunshine hours; PTU = sum of GDD x day length (Rajput, 1980). HUE = yield / GDD (kg/ha per degree-day); HTUE = yield / HTU.

Value

An object of class `aridagri_thermal`: a list with `summary` (index, value, unit), `gdd_total` and `daily` (daily and cumulative GDD, HTU and PTU).

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

References

McMaster, G.S. and Wilhelm, W.W. (1997). Growing degree-days: one equation, two interpretations. *Agricultural and Forest Meteorology*, 87(4), 291-300. doi:10.1016/S01681923(97)000270

Rajput, R.P. (1980). Response of soybean crop to climatic and soil environments. PhD thesis, IARI, New Delhi.

Examples

```
tmax <- c(31, 33, 35, 36, 38, 40, 41, 39, 37, 36)
tmin <- c(16, 17, 19, 20, 22, 24, 25, 24, 22, 21)
thermal_indices(tmax, tmin, base_temp = 10, upper_temp = 40,
                sunshine_hours = rep(9.5, 10),
                day_length = day_length(28, 70:79), crop_yield = 1250)
```

---

yield_gap_analysis *Yield Gap and Front-Line Demonstration Indices*

Description

Yield gap between actual and potential yields. When an attainable yield (for example the yield of an improved-practice or front-line demonstration plot) is supplied, the gap is split into a technology gap and an extension gap and the technology index is given.

Usage

```
yield_gap_analysis(
  actual_yield,
  potential_yield,
  attainable_yield = NULL,
  verbose = TRUE
)
```

Arguments

actual_yield	Actual (farmers' practice) yield.
potential_yield	Potential yield of the crop or variety.
attainable_yield	Attainable or demonstration yield (optional).
verbose	Logical. If TRUE (default), prints the table.

Details

Total gap = potential - actual; yield efficiency = 100 x actual / potential. With attainable yield (Samui et al., 2000): technology gap = potential - attainable; extension gap = attainable - actual; technology index = 100 x technology gap / potential; yield increase over farmers' practice = 100 x (attainable - actual) / actual.

Value

A data frame of class `aridagri_yield_gap`.

Author(s)

Lalit Kumar Rolaniya, Ram Lal Jat, Monika Punia, Raja Ram Choudhary, Hemant Poonia

References

Samui, S.K., Maitra, S., Roy, D.K., Mondal, A.K. and Saha, D. (2000). Evaluation of front line demonstration on groundnut (Arachis hypogaea L.). *Journal of the Indian Society of Coastal Agricultural Research*, 18(2), 180-183.

Examples

```
yield_gap_analysis(actual_yield = c(800, 950, 720), potential_yield = 1500)
# Front-line demonstrations: farmers' practice vs demonstration plots
yield_gap_analysis(actual_yield = c(820, 760, 905),
                   potential_yield = 1500,
                   attainable_yield = c(1080, 1010, 1150))
```

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