

Package ‘agriutilities’

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Type Package

Title Utilities for Data Analysis in Agriculture

Version 1.1.0

Description Utilities designed to make the analysis of field trials easier and more accessible for everyone working in plant breeding. It provides a simple and intuitive interface for conducting single and multi-environmental trial analysis, with minimal coding required. Whether you're a beginner or an experienced user, 'agriutilities' will help you quickly and easily carry out complex analyses with confidence. With built-in functions for fitting Linear Mixed Models, 'agriutilities' is the ideal choice for anyone who wants to save time and focus on interpreting their results. Some of the functions require the R package 'asreml' for the 'ASReml' software, this can be obtained upon purchase from 'VSN' international (<<https://vsni.co.uk/software/asreml-r>>).

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check_connectivity	<i>Check connectivity between trials</i>
--------------------	--

Description

Check connectivity between trials

Usage

```
check_connectivity(
  data = NULL,
  genotype = "line",
  trial = "Experiment",
  response = NULL,
  all = FALSE,
  return_matrix = FALSE
)
```

Arguments

data	A data.frame in a wide format.
genotype	A character string indicating the column in data that contains genotypes.
trial	A character string indicating the column in data that contains trials.
response	A character string specifying the trait.
all	Whether or not print all the table.
return_matrix	A logical value indicating if the user wants to return a (n_trial x n_trial) matrix with the amount of genotypes shared between each pair of trial. (FALSE by default)

Value

A data.frame with the genotype connectivity. If return_matrix is TRUE, it will return a n_trial x n_trial matrix with the amount of genotypes shared between each pair of trial.

Examples

```
library(agridat)
library(agriutilities)
data(besag.met)
dat <- besag.met
head(
  check_connectivity(
    data = dat,
    genotype = "gen",
    trial = "county",
    response = "yield",
    all = TRUE,
    return_matrix = FALSE
  )
)
```

Description

This function helps to identify the experimental design of each trial, filters the data and then provide a summary for the traits and the experimental design. This works as a quality check before we fit any model. Returns an object of class checkAgri.

Usage

```

check_design_met(
  data = NULL,
  genotype = NULL,
  trial = NULL,
  traits = NULL,
  rep = NULL,
  block = NULL,
  row = NULL,
  col = NULL
)

```

Arguments

data	A data.frame in a wide format.
genotype	A character string indicating the column in data that contains genotypes.
trial	A character string indicating the column in data that contains trials.
traits	A character vector specifying the traits for which the models should be fitted.
rep	A character string indicating the column in data that contains replicates.
block	A character string indicating the column in data that contains sub blocks.
row	A character string indicating the column in data that contains the row coordinates.
col	A character string indicating the column in data that contains the column coordinates.

Value

An object of class `checkAgri`, with a list of:

summ_traits	A data.frame containing a summary of the traits.
exp_design_resum	A data.frame containing a summary of the experimental design.
filter	A list by trait containing the filtered trials.
exp_design_list	A data.frame containing the experimental design of each trial.
check_connectivity	A data.frame with the genotype connectivity.
connectivity_matrix	A matrix with the amount of genotypes shared between each pair of trial.
data_design	A data frame containing the data used with two additional columns, one related to the experimental design and a sequential number (id)
inputs	A list containing the character string that indicates the column in data that contains the genotype, trial, traits, rep, block, row and col.

Examples

```
library(agridat)
library(agriutilities)
data(besag.met)
dat <- besag.met
results <- check_design_met(
  data = dat,
  genotype = "gen",
  trial = "county",
  traits = c("yield"),
  rep = "rep",
  block = "block",
  col = "col",
  row = "row"
)
print(results)
plot(results, type = "connectivity")
plot(results, type = "missing")
```

covcor_heat

Correlation Covariance Heatmap

Description

Correlation Covariance Heatmap

Usage

```
covcor_heat(matrix, corr = TRUE, size = 4, digits = 3, legend = c(0.6, 0.7))
```

Arguments

matrix	A numeric matrix.
corr	A logical value indicating if the matrix is in a scaled form (TRUE by default, correlation matrix)
size	A numeric value to define the letter size.
digits	A numeric integer to define the number of digits to plot.
legend	the position of legends ("none", "left", "right", "bottom", "top", or two-element numeric vector)

Value

A ggplot object showing the upper triangular elements of the matrix.

Examples

```
library(agriutilities)
data(iris)
M <- cor(iris[, -5])
covcor_heat(matrix = M, corr = TRUE)
```

 extract_vcov

Extract Variance-Covariance from ASReml-R

Description

Extract Variance-Covariance from ASReml-R

Usage

```
extract_vcov(model = NULL, gen = "genotype", env = "trial", vc_model = "corv")
```

Arguments

model	ASReml object
gen	A character string indicating the column in data that contains genotypes.
env	A character string indicating the column in data that contains environments or trials.
vc_model	A character string indicating the variance-covariance fitted. Can be 'diag', 'corv', 'corh', 'corgv', 'fa1', 'fa2', 'fa3', 'fa4', 'corgh', 'us' or 'rr2'.

Value

An object with a list of:

VCOV	A matrix of the estimated variance-covariance between trials.
CORR	A $n_{\text{trial}} \times n_{\text{trial}}$ matrix with the correlation between trials.
vc_model	A character string indicating the variance-covariance fitted.

Examples

```
## Not run:
library(agridat)
library(agriutilities)

data(besag.met)
dat <- besag.met
results <- check_design_met(
  data = dat,
  genotype = "gen",
  trial = "county",
  traits = c("yield"),
```

```

    rep = "rep",
    block = "block",
    col = "col",
    row = "row"
  )
  out <- single_trial_analysis(results, progress = FALSE)
  met_results <- met_analysis(out, progress = FALSE)
  extract_vcov(
    model = met_results$met_models$yield,
    vc_model = "us"
  )

  ## End(Not run)

```

fa_summary

Factor Analytic Summary

Description

Factor Analytic Summary

Usage

```

fa_summary(
  model = NULL,
  trial = "trial",
  genotype = "genotype",
  BLUEs_trial = NULL,
  mult_fa1 = -1,
  mult_fa2 = 1,
  filter_score = 1.5,
  k_biplot = 1,
  size_label_var = 2,
  alpha_label_var = 0.2,
  size_label_ind = 2,
  alpha_label_ind = 0.8,
  size_arrow = 0.2,
  alpha_arrow = 0.2,
  base_size = 12
)

```

Arguments

model	Factor Analytic Model (ASReml object)
trial	A character string indicating the column in data that contains trials.
genotype	A character string indicating the column in data that contains genotypes.
BLUEs_trial	A data.frame containing BLUEs for each trial.

mult_fa1	A constant to multiply the first loading. Must be 1 or -1. (-1 by default)
mult_fa2	A constant to multiply the second loading. Must be 1 or -1. (1 by default)
filter_score	A numeric value to filter genotypes by the distance from the origin.
k_biplot	A numeric value to multiply the scores in the biplot.
size_label_var	A numeric value to define the label size for the variables.
alpha_label_var	A numeric value between (0,1) to define the label for the variables.
size_label_ind	A numeric value to define the label size for the individuals.
alpha_label_ind	A numeric value between (0,1) to define the label for the individuals.
size_arrow	A numeric value to define the arrow size.
alpha_arrow	A numeric value between (0,1) to define the arrow.
base_size	A numeric value to define the base size.

Value

An object with a list of:

loadings	A data.frame containing the first and second loading for each trial.
loading_star	A data.frame containing the first and second loading rotated for each trial.
Gvar	A matrix of the estimated variance-covariance between trials.
Cmat	A matrix of the correlation between trials.
summary_loading	A data.frame containing a summary of the loadings.
paf_site	A data.frame containing the percentage of variance explained for each component and for each trial.
var_tot	A numeric value of the total variance.
scores	A data.frame containing the scores for each genotype.
plots	A list with different plots. Includes a plot for the loadings, biplot, biplot_scaled and loadings_c.

Examples

```
## Not run:
library(agridat)
library(agriutilities)
data(besag.met)
dat <- besag.met
results <- check_design_met(
  data = dat,
  genotype = "gen",
  trial = "county",
  traits = c("yield"),
  rep = "rep",
  block = "block",
```



```

    col = "col",
    row = "row"
  )
  out <- single_trial_analysis(results, progress = FALSE)
  met_results <- met_analysis(out, vcov = "fa2", progress = FALSE)

  pp <- met_results$trial_effects
  model <- met_results$met_models$yield
  fa_summary(
    model = model,
    trial = "trial",
    genotype = "genotype",
    BLUEs_trial = pp,
    mult_fa1 = -1,
    mult_fa2 = -1,
    filter_score = 1,
    k_biplot = 10,
    size_label_var = 3,
    alpha_label_var = 0.5,
    size_label_ind = 3,
    alpha_label_ind = 0.8,
    size_arrow = 0.2,
    alpha_arrow = 0.1
  )

  ## End(Not run)

```

 gg_cor

Triangular Correlation Plot

Description

Return a ggplot object to plot a triangular correlation figure between 2 or more variables.

Usage

```

gg_cor(
  data,
  colours = c("#db4437", "white", "#4285f4"),
  blackLabs = c(-0.7, 0.7),
  showSignif = TRUE,
  pBreaks = c(0, 0.001, 0.01, 0.05, Inf),
  pLabels = c("***", "**", "*", "ns"),
  showDiagonal = FALSE,
  Diag = NULL,
  returnTable = FALSE,
  returnN = FALSE,
  adjusted = TRUE,
  label_size = 3
)

```

Arguments

<code>data</code>	A data.frame with numerical columns for each variable to be compared.
<code>colours</code>	A vector of size three with the colors to be used for values -1, 0 and 1.
<code>blackLabs</code>	A numeric vector of size two, with min and max correlation coefficient.
<code>showSignif</code>	Logical scalar. Display significance values ?
<code>pBreaks</code>	Passed to function 'cut'. Either a numeric vector of two or more unique cut points or a single number (greater than or equal to 2) giving the number of intervals into which x is to be cut.
<code>pLabels</code>	Passed to function 'cut'. labels for the levels of the resulting category. By default, labels are constructed using "(a,b]" interval notation. If <code>pLabels = FALSE</code> , simple integer codes are returned instead of a factor.
<code>showDiagonal</code>	Logical scalar. Display main diagonal values ?
<code>Diag</code>	A named vector of labels to display in the main diagonal. The names are used to place each value in the corresponding coordinates of the diagonal. Hence, these names must be the same as the colnames of data.
<code>returnTable</code>	Return the table to display instead of a ggplot object.
<code>returnN</code>	Return plot with shared information.
<code>adjusted</code>	Use the adjusted p values for multiple testing instead of raw coeffs. TRUE by default.
<code>label_size</code>	Numeric value indicating the label size. 3 by default.

Value

A ggplot object containing a triangular correlation figure with all numeric variables in data. If `returnTable` is TRUE, the table used to produce the figure is returned instead.

Author(s)

Daniel Ariza, Johan Aparicio.

Examples

```
library(agriutilities)
data(iris)
gg_cor(
  data = iris,
  colours = c("#db4437", "white", "#4285f4"),
  label_size = 6
)
```

Description

Heritability for Factor Analytic Models in ASReml-R

Usage

```
heritability_fa(  
  model_fa = NULL,  
  genotype = "line",  
  env = "loc",  
  vc_model = c("fa2"),  
  diag = FALSE  
)
```

Arguments

model_fa	Factor Analytic ASReml model
genotype	A character string indicating the column in data that contains genotypes.
env	A character string indicating the column in data that contains environments or trials.
vc_model	A character string indicating the variance-covariance structure. Can be "fa1", "fa2", "fa3", "fa4" or "us".
diag	TRUE or FALSE depending on the user if they want to take the elements on the diagonal of the variance-covariance matrix or the elements out of the diagonal to estimate the heritability. FALSE by default.

Value

An object with a list of:

h2_cullis	A numerical value of the Cullis heritability estimate.
h2_se	A numerical value of the Cullis heritability estimate based on the standard error.

Examples

```
## Not run:  
library(agridat)  
library(agriutilities)  
data(besag.met)  
dat <- besag.met  
results <- check_design_met(  
  data = dat,  
  genotype = "gen",  
  trial = "county",
```

```
traits = c("yield"),
rep = "rep",
block = "block",
col = "col",
row = "row"
)
out <- single_trial_analysis(results, progress = FALSE)
met_results <- met_analysis(out, progress = FALSE)
model <- met_results$met_models$yield
heritability_fa(
  model_fa = model,
  genotype = "genotype",
  env = "trial",
  vc_model = "us"
)

## End(Not run)
```

h_cullis

Cullis heritability for lme4 models

Description

Cullis heritability for lme4 models

Usage

```
h_cullis(model, genotype, re_MME = FALSE)
```

Arguments

model	Object of class lmer.
genotype	A character string indicating the column in data that contains genotypes.
re_MME	A logical value to ask if we want to reconstruct the mixed models equations to estimate the Cullis heritability. (FALSE by default)

Value

A numerical value of the Cullis heritability estimate. If re_MME is TRUE, a list with matrices of the mixed models equations is returned.

Author(s)

Paul Schmidt, Johan Aparicio.

Examples

```
library(lme4)
library(agridat)
library(agriutilities)
dat <- john.alpha
g.ran <- lmer(
  formula = yield ~ rep + (1 | gen) + (1 | rep:block),
  data = dat
)
h_cullis(model = g.ran, genotype = "gen")
```

met_analysis

Multi-Environmental Trial Analysis

Description

The results of the `single_trial_analysis()` function are used in `met_analysis()` to fit multi-environmental trial models. Returns an object of class `metAgri`, with a list of trial effects, BLUPs, heritability, variance components, stability and the models fitted.

Usage

```
met_analysis(
  sma_output = NULL,
  h2_filter = 0.2,
  workspace = "1gb",
  vcov = NULL,
  filter_traits = NULL,
  remove_trials = NULL,
  progress = TRUE
)
```

Arguments

<code>sma_output</code>	Object of class <code>smaAgri</code> resulting of executing <code>single_trial_analysis()</code> function.
<code>h2_filter</code>	Numeric value to filter trials with poor heritability. 0.2 by default.
<code>workspace</code>	Sets the workspace for the core REML routines in the form of a number optionally followed directly by a valid measurement unit. "128mb" by default.
<code>vcov</code>	A character string specifying the Variance-Covariance structure to be fitted. Can be "fa2", "fa1", "us", "corh" or "corv". If NULL the function will try to fit an "us" Variance-Covariance and if it fails, it will try with "fa2" and then with "fa1".
<code>filter_traits</code>	A character vector with traits to filter. NULL by default.
<code>remove_trials</code>	A character vector with trials to remove. NULL by default.
<code>progress</code>	Should the progress of the modeling be printed. If TRUE, for every trait a line is output indicating that the model is being fitted.

Value

An object of class metAgri, with a list of:

trial_effects	A data.frame containing Trial BLUEs.
overall_BLUPs	A data.frame containing Genotypic BLUPs across trials, by trait.
BLUPs_GxE	A data.frame containing Genotypic BLUPs by trial/trait.
VCOV	A list by trait containing the variance-covariance fitted.
stability	A data.frame containing several Stability coefficients resulting of executing the function stability().
heritability	A data.frame containing overall heritabilities by trait.
met_models	A list by trait containing the fitted models.

Examples

```
## Not run:
library(agridat)
library(agriutilities)
data(besag.met)
dat <- besag.met
results <- check_design_met(
  data = dat,
  genotype = "gen",
  trial = "county",
  traits = c("yield"),
  rep = "rep",
  block = "block",
  col = "col",
  row = "row"
)
out <- single_trial_analysis(results, progress = FALSE)
met_results <- met_analysis(out, progress = FALSE)
print(met_results)
covcor_heat(matrix = met_results$VCOV$yield$CORR)

## End(Not run)
```

parameters_gg

Genetic Gain Parameters

Description

Genetic Gain Parameters

Usage

```
parameters_gg(model, trait = "trait")
```

Arguments

model Linear regression model (lm object)
 trait A character string indicating the column in data that contains trials.

Value

A data.frame with some parameters from the linear regression (Slope, se_Slope, Intercept, r2, Pr(>F)) and the percentage of Genetic Gain.

Examples

```
library(ggplot2)
library(agridat)
library(magrittr)
library(agriutilities)

data(baker.barley.uniformity)
dat <- baker.barley.uniformity
head(dat)

model <- lm(yield ~ year, dat)

dat %>%
  na.omit() %>%
  ggplot(
    aes(x = year, y = yield)
  ) +
  geom_point() +
  geom_smooth(method = "lm") +
  theme_bw()

parameters_gg(model = model, trait = "yield")
```

plot.checkAgri *Plot an object of class checkAgri*

Description

Create several plots for an object of class checkAgri

Usage

```
## S3 method for class 'checkAgri'
plot(
  x,
  type = c("connectivity", "missing", "boxplot"),
```

```
axis_size = 15,  
text_size = 5,  
...  
)
```

Arguments

x	An object inheriting from class <code>checkAgri</code> resulting of executing the function <code>check_design_met()</code>
type	A character string specifying the type of plot. "connectivity", "missing" or "boxplot".
axis_size	Numeric input to define the axis size.
text_size	Numeric input to define the text size.
...	Further graphical parameters. For future improvements.

Value

A ggplot object.

Author(s)

Johan Aparicio [aut]

Examples

```
library(agridat)  
library(agriutilities)  
data(besag.met)  
dat <- besag.met  
results <- check_design_met(  
  data = dat,  
  genotype = "gen",  
  trial = "county",  
  traits = c("yield"),  
  rep = "rep",  
  block = "block",  
  col = "col",  
  row = "row"  
)  
plot(results, type = "missing")  
plot(results, type = "boxplot")
```

plot.metAgri	<i>Plot an object of class metAgri</i>
--------------	--

Description

Create several plots for an object of class metAgri

Usage

```
## S3 method for class 'metAgri'
plot(
  x,
  type = c("correlation", "covariance", "multi_traits"),
  filter_traits = NULL,
  text_size = 4,
  ...
)
```

Arguments

x	An object inheriting from class metAgri resulting of executing the function met_analysis()
type	A character string specifying the type of plot. "correlation", "covariance" or "multi_traits"
filter_traits	An optional character vector to filter traits.
text_size	Numeric input to define the text size.
...	Further graphical parameters passed to covcor_heat().

Value

A ggplot object.

Author(s)

Johan Aparicio [aut]

Examples

```
## Not run:
library(agridat)
library(agriutilities)
data(besag.met)
dat <- besag.met
results <- check_design_met(
  data = dat,
  genotype = "gen",
  trial = "county",
```

```

traits = c("yield"),
rep = "rep",
block = "block",
col = "col",
row = "row"
)
out <- single_trial_analysis(results, progress = FALSE)
met_results <- met_analysis(out, progress = FALSE)
print(met_results)
plot(met_results, type = "correlation")
plot(met_results, type = "covariance")

## End(Not run)

```

plot.smaAgri

Plot an object of class smaAgri

Description

Create several plots for an object of class `smaAgri`

Usage

```

## S3 method for class 'smaAgri'
plot(
  x,
  type = c("summary", "correlation", "spatial"),
  filter_traits = NULL,
  nudge_y_cv = 3,
  nudge_y_h2 = 0.07,
  horizontal = FALSE,
  theme_size = 15,
  axis_size = 8,
  text_size = 4,
  ...
)

```

Arguments

<code>x</code>	An object inheriting from class <code>smaAgri</code> resulting of executing the function <code>single_trial_analysis()</code>
<code>type</code>	A character string specifying the type of plot. "summary", "correlation" or "spatial".
<code>filter_traits</code>	An optional character vector to filter traits.
<code>nudge_y_cv</code>	Vertical adjustment to nudge labels by when plotting CV bars. Only works if the argument type is "summary". 3 by default.

nudge_y_h2	Vertical adjustment to nudge labels by when plotting h2 bars. Only works if the argument type is "summary". 0.07 by default.
horizontal	If FALSE, the default, the labels are plotted vertically. If TRUE, the labels are plotted horizontally.
theme_size	Base font size, given in pts. 15 by default.
axis_size	Numeric input to define the axis size.
text_size	Numeric input to define the text size.
...	Further graphical parameters. For future improvements.

Value

A ggplot object.

Author(s)

Johan Aparicio [aut]

Examples

```
library(agridat)
library(agriutilities)
data(besag.met)
dat <- besag.met
results <- check_design_met(
  data = dat,
  genotype = "gen",
  trial = "county",
  traits = c("yield"),
  rep = "rep",
  block = "block",
  col = "col",
  row = "row"
)
out <- single_trial_analysis(results, progress = FALSE)
print(out)
plot(out, type = "summary", horizontal = TRUE)
plot(out, type = "correlation")
plot(out, type = "spatial")
```

print.checkAgri *Print an object of class checkAgri*

Description

Prints information about check_design_met() function.

Usage

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

Arguments

x An object fitted with the function `check_design_met()`.

... Options used by the tibble package to format the output. See `'tibble::print()'` for more details.

Value

an object inheriting from class `checkAgri`.

Author(s)

Johan Aparicio [aut]

Examples

```
library(agridat)  
library(agriutilities)  
data(besag.met)  
dat <- besag.met  
results <- check_design_met(  
  data = dat,  
  genotype = "gen",  
  trial = "county",  
  traits = c("yield"),  
  rep = "rep",  
  block = "block",  
  col = "col",  
  row = "row"  
)  
print(results)
```

print.metAgri *Print an object of class metAgri*

Description

Prints information about `met_analysis()` function.

Usage

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

Arguments

x An object fitted with the function `met_analysis()`.
... Options used by the tibble package to format the output. See `'tibble::print()'` for more details.

Value

an object inheriting from class `metAgri`.

Author(s)

Johan Aparicio [aut]

Examples

```
## Not run:
library(agridat)
library(agriutilities)
data(besag.met)
dat <- besag.met
results <- check_design_met(
  data = dat,
  genotype = "gen",
  trial = "county",
  traits = c("yield"),
  rep = "rep",
  block = "block",
  col = "col",
  row = "row"
)
out <- single_trial_analysis(results, progress = FALSE)
met_results <- met_analysis(out, progress = FALSE)
print(met_results)

## End(Not run)
```

print.smaAgri *Print an object of class smaAgri*

Description

Prints information about `single_trial_analysis` function.

Usage

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

Arguments

- x An object fitted with the function `single_trial_analysis()`.
- ... Options used by the tibble package to format the output. See `'tibble::print()'` for more details.

Value

an object inheriting from class `smaAgri`.

Author(s)

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Examples

```
library(agridat)
library(agriutilities)
data(besag.met)
dat <- besag.met
results <- check_design_met(
  data = dat,
  genotype = "gen",
  trial = "county",
  traits = c("yield"),
  rep = "rep",
  block = "block",
  col = "col",
  row = "row"
)
out <- single_trial_analysis(results, progress = FALSE)
print(out)
```

`single_trial_analysis` *Single Trial Analysis*

Description

The results of the `check_design_met()` function are used in `single_trial_analysis()` to fit single trial models. This function can fit, Completely Randomized Designs (CRD), Randomized Complete Block Designs (RCBD), Resolvable Incomplete Block Designs (res-IBD), Non-Resolvable Row-Column Designs (Row-Col) and Resolvable Row-Column Designs (res-Row-Col).

Returns an object of class `smaAgri`, with a list of trial summary, BLUEs, BLUPs, heritability, variance components, potential extreme observations, residuals, the models fitted and the data used. This function will generate the required output to be used in the two-stage analysis.

Usage

```
single_trial_analysis(
  results = NULL,
  progress = TRUE,
  engine = "asreml",
  remove_outliers = TRUE
)
```

Arguments

results	Object of class <code>checkAgri</code> resulting of executing <code>check_design_met()</code> function.
progress	Should the progress of the modeling be printed. If TRUE, for every trial a line is output indicating the traits fitted for the particular trial.
engine	A character string specifying the name of the mixed modeling engine to use, either <code>lme4</code> or <code>asreml</code> . For spatial designs, <code>SpATS</code> is always used, for other designs <code>asreml</code> as a default.
remove_outliers	Should outliers be removed? TRUE by default.

Value

An object of class `smaAgri`, with a list of:

fitted_models	A list containing the fitted models. (Both models, the one with Genotype as Random and the one with Genotype as Fixed)
resum_fitted_model	A data.frame containing a summary of the fitted models.
outliers	A data.frame containing extreme observations. If <code>remove_outliers</code> is TRUE, this data.frame will contain the observations removed.
blues_blups	A data.frame containing BLUPs/BLUEs for all the genotypes in each trial.
std_residuals	A data.frame containing the standardized residuals for the model with genotype as random component.
data	A data.frame containing the data used. If <code>remove_outliers</code> is TRUE, data will have missing values for the outliers detected.

Examples

```
library(agridat)
library(agriutilities)
data(besag.met)
dat <- besag.met
results <- check_design_met(
  data = dat,
  genotype = "gen",
  trial = "county",
```

```

traits = c("yield"),
rep = "rep",
block = "block",
col = "col",
row = "row"
)
out <- single_trial_analysis(results, progress = FALSE)
print(out)

```

stability

Stability Coefficients

Description

Stability Coefficients

Usage

```

stability(
  predictions = NULL,
  genotype = NULL,
  trial = NULL,
  response = NULL,
  best = "max"
)

```

Arguments

predictions	A data.frame with one value per GxE combination.
genotype	A character string indicating the column in predictions that contains genotypes.
trial	A character string indicating the column in predictions that contains trials.
response	A character string specifying the response variable.
best	A character string specifying how to define the best genotype by numeric value ("min", "max"). "max" by default.

Value

A data.frame with several stability measures. "superiority" (cultivar-superiority measure), "static" (Shukla's stability variance) and "wricke" (Wricke's ecovalence).

Examples

```
## Not run:
library(agridat)
library(agriutilities)

data(besag.met)
dat <- besag.met
results <- check_design_met(
  data = dat,
  genotype = "gen",
  trial = "county",
  traits = c("yield"),
  rep = "rep",
  block = "block",
  col = "col",
  row = "row"
)
out <- single_trial_analysis(results, progress = FALSE)
met_results <- met_analysis(out, progress = FALSE)

head(
  stability(
    predictions = met_results$BLUPs_GxE,
    genotype = "genotype",
    trial = "trial",
    response = "predicted.value"
  )
)

## End(Not run)
```

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