Package 'augmentedRCBD'

February 15, 2021

Title Analysis of Augmented Randomised Complete Block Designs

Version 0.1.4

Description Functions for analysis of data generated from experiments in
augmented randomised complete block design according to Federer, W.T. (1961)
¡doi:10.2307/2527837¿. Computes analysis of variance, adjusted means,
descriptive statistics, genetic variability statistics etc. Further includes
data visualization and report generation functions.

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Encoding UTF-8

LazyData true

Depends R (¿= 3.0.1)

VignetteBuilder knitr

RoxygenNote 7.1.1

URL https://github.com/aravind-j/augmentedRCBD

https://CRAN.R-project.org/package=augmentedRCBD

https://aravind-j.github.io/augmentedRCBD/

https://doi.org/10.5281/zenodo.1310011

BugReports https://github.com/aravind-j/augmentedRCBD/issues

Imports emmeans,
dplyr,
flextable,
ggplot2,
grDevices,
methods,
moments,
multcomp,
multcompView,
Rdpack,
stats,
stringi,

        officer,
        reshape2,
        utils

Suggests knitr,
        rmarkdown,
        pander,
        testthat,
        agricolae

RdMacros Rdpack

R topics documented:

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augmentedRCBD   *Analysis of Augmented Randomised Complete Block Design*

Description

augmentedRCBD is a function for analysis of variance of an augmented randomised block design (Federer, 1956; Federer, 1961) and the generation as well as comparison of the adjusted means of the treatments/genotypes.

Usage

```
augmentedRCBD(
  block,
  treatment,
  y,
  checks = NULL,
  method.comp = c("lsd", "tukey", "none"),
  alpha = 0.05,
  group = TRUE,
  console = TRUE,
  simplify = FALSE,
  truncate.means = TRUE
)
```

Arguments

`block`	Vector of blocks (as a factor).
`treatment`	Vector of treatments/genotypes (as a factor).
`y`	Numeric vector of response variable (Trait).
`checks`	Character vector of the checks present in `treatment` levels. If not specified, checks are inferred from the data on the basis of number of replications of treatments/genotypes.
`method.comp`	Method for comparison of treatments (`"lsd"` for least significant difference or `"tukey"` for Tukey's honest significant difference). If `"none"`, no comparisons will be made, the ANOVA output will be given as a data frame and the adjusted means will be computed directly from treatment and block effects instead of using `emmeans`.
`alpha`	Type I error probability (Significance level) to be used for multiple comparisons.
`group`	If `TRUE`, genotypes will be grouped according to `"method.comp"`. Default is `TRUE`.
`console`	If `TRUE`, output will be printed to console. Default is `TRUE`. Default is `TRUE`.
`simplify`	If `TRUE`, ANOVA output will be given as a data frame instead of a `summary.aov` object. Default is `TRUE`.
`truncate.means`	If `TRUE`, the negative adjusted means will be truncated to zero. Default is `TRUE`.

Details

This function borrows code from `DAU.test` function of `agricolae` package (de Mendiburu et al., 2016) as well as from Appendix VIII of Mathur et al., (2008).

Value

A list of class `augmentedRCBD` containing the following components:

`Details`	Details of the augmented design used.
`Means`	A data frame with the "Means", "Block", "SE", "Mix", "Max" and "Adjusted Means" for each "Treatment".
`ANOVA, Treatment Adjusted`	An object of class `summary.aov` for ANOVA table with treatments adjusted.
`ANOVA, Block Adjusted`	An object of class `summary.aov` for ANOVA table with block adjusted.
`Block effects`	A vector of block effects.
`Treatment effects`	A vector of treatment effects.
`Std. Errors`	A data frame of standard error of difference between various combinations along with critical difference and tukey's honest significant difference (when `method.comp = "tukey"`) at `alpha`.

Overall adjusted mean	
	Overall adjusted mean.
CV	Coefficient of variation.
Comparisons	A data frame of pairwise comparisons of treatments. This is computed only if argument group is TRUE
Groups	A data frame with compact letter display of pairwise comparisons of treatments. Means with at least one letter common are not significantly different statistically. This is computed only if argument group is TRUE

Note

- Data should preferably be balanced i.e. all the check genotypes should be present in all the blocks. If not, a warning is issued.

- There should not be any missing values.

- The number of test genotypes can vary within a block.

In case the large number of treatments or genotypes, it is advisable to avoid comparisons with the group = FALSE argument as it will be memory and processor intensive. Further it is advised to simplify output with simplify = TRUE in order to reduce output object size.

References

Federer WT (1956). "Augmented (or Hoonuiaku) designs." *The Hawaiian Planters' Record*, **LV(2)**, 191–208.

Federer WT (1956). "Augmented (or Hoonuiaku) Designs." Technical Report BU-74-M, Cornell University, New York.

Federer WT (1961). "Augmented designs with one-way elimination of heterogeneity." *Biometrics*, **17**(3), 447–473.

Mathur PN, Muralidharan K, Parthasarathy VA, Batugal P, Bonnot F (2008). *Data Analysis Manual for Coconut Researchers-Bioversity Technical Bulletin No. 14*. Bioversity International. ISBN 978-92-9043-736-9.

de Mendiburu F (2015). *agricolae: Statistical Procedures for Agricultural Research*. R package version 1.2-8.

See Also

DAU.test, ea1, emmeans, cld.emmGrid, aug.rcb

Examples

```
# Example data
blk <- c(rep(1,7),rep(2,6),rep(3,7))
trt <- c(1, 2, 3, 4, 7, 11, 12, 1, 2, 3, 4, 5, 9, 1, 2, 3, 4, 8, 6, 10)
y1 <- c(92, 79, 87, 81, 96, 89, 82, 79, 81, 81, 91, 79, 78, 83, 77, 78, 78,
        70, 75, 74)
y2 <- c(258, 224, 238, 278, 347, 300, 289, 260, 220, 237, 227, 281, 311, 250,
        240, 268, 287, 226, 395, 450)
data <- data.frame(blk, trt, y1, y2)
```

```
# Convert block and treatment to factors
data$blk <- as.factor(data$blk)
data$trt <- as.factor(data$trt)
# Results for variable y1 (checks inferred)
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
# Results for variable y2 (checks inferred)
out2 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)


# Results for variable y1 (checks specified)
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE,
                      checks = c("1", "2", "3", "4"))
# Results for variable y2 (checks specified)
out2 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE,
                      checks = c("1", "2", "3", "4"))


## Not run:
# Error in case checks not replicated across all blocks
# Check 1 and 4 not replicated in all 3 blocks
trt <- c(1, 2, 3, 14, 7, 11, 12, 1, 2, 3, 4, 5, 9, 13, 2, 3, 4, 8, 6, 10)
data$trt <- as.factor(trt)
table(data$trt, data$blk)
# Results for variable y1 (checks specified)
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE,
                      checks = c("1", "2", "3", "4"))


## End(Not run)


# Warning in case test treatments are replicated
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE,
                      checks = c("2", "3"))
```

---

augmentedRCBD.bulk	*Analysis of Augmented Randomised Complete Block Design for Multiple Traits/Characters*

Description

augmentedRCBD.bulk is a wrapper around the functions augmentedRCBD, describe.augmentedRCBD, freqdist.augmentedRCBD and gva.augmentedRCBD. It will carry out these analyses for multiple traits/characters from the input data as a data frame object.

Usage

```
augmentedRCBD.bulk(
  data,
  block,
  treatment,
  traits,
  checks = NULL,
  alpha = 0.05,
  describe = TRUE,
  freqdist = TRUE,
  gva = TRUE,
  check.col = "red",
  console = TRUE
)
```

Arguments

`data`	The data as a data frame object. The data frame should possess columns specifying the block, treatment and multiple traits/characters.
`block`	Name of column specifying the blocks in the design as a character string.
`treatment`	Name of column specifying the treatments as a character string.
`traits`	Name of columns specifying the multiple traits/characters as a character vector.
`checks`	Character vector of the checks present in `treatment` levels. If not specified, checks are inferred from the data on the basis of number of replications of treatments/genotypes.
`alpha`	Type I error probability (Significance level) to be used for multiple comparisons.
`describe`	If `TRUE`, descriptive statistics will be computed. Default is `TRUE`.
`freqdist`	If `TRUE`, frequency distributions be plotted. Default is `TRUE`.
`gva`	If `TRUE`, genetic variability analysis will be done. Default is `TRUE`.
`check.col`	The colour(s) to be used to highlight check values in the plot as a character vector. Must be valid colour values in R (named colours, hexadecimal representation, index of colours [1:8] in default R 'palette()' etc.).
`console`	If `TRUE`, output will be printed to console. Default is `TRUE`.

Value

A list of class `augmentedRCBD.bulk` containing the following components:

`Details`	Details of the augmented design used and the traits/characters.
`ANOVA, Treatment Adjusted`	
	A data frame of mean sum of squares of the specified traits from treatment adjusted ANOVA.

ANOVA, Block Adjusted

> A data frame of mean sum of squares of the specified traits from block adjusted ANOVA

Means

> A data frame of the adjusted means of the treatments for the specified traits.

Check statistics

> A list of data frames with check statistics such as number of replications, standard error, minimum and maximum value

alpha   Type I error probability (Significance level) used.

Std. Errors   A data frame of standard error of difference between various combinations for the specified traits.

CD   A data frame of critical difference (at the specified alpha) between various combinations for the specified traits.

Overall adjusted mean

> A data frame of the overall adjusted mean for the specified traits.

CV   A data frame of the coefficient of variance for the specified traits.

Descriptive statistics

> A data frame of descriptive statistics for the specified traits.

Frequency distribution

> A list of ggplot2 plot grobs of the frequency distribution plots.

Genetic variability analysis

> A data frame of genetic variability statistics for the specified traits.

GVA plots   A list of three ggplot2 objects with the plots for (a) Phenotypic and Genotypic CV, (b) Broad sense heritability and (c) Genetic advance over mean

warnings   A list of warning messages (if any) captured during model fitting and frequency distribution plotting.

Note

In this case treatment comparisons/grouping by least significant difference or Tukey's honest significant difference method is not computed. Also the output object size is reduced using the simplify = TRUE argument in the augmentedRCBD function.

See Also

augmentedRCBD, describe.augmentedRCBD, freqdist.augmentedRCBD, gva.augmentedRCBD

Examples

```
# Example data
blk <- c(rep(1,7),rep(2,6),rep(3,7))
trt <- c(1, 2, 3, 4, 7, 11, 12, 1, 2, 3, 4, 5, 9, 1, 2, 3, 4, 8, 6, 10)

y1 <- c(92, 79, 87, 81, 96, 89, 82, 79, 81, 81, 91, 79, 78, 83, 77, 78, 78,
        70, 75, 74)
y2 <- c(258, 224, 238, 278, 347, 300, 289, 260, 220, 237, 227, 281, 311, 250,
```

```
         240, 268, 287, 226, 395, 450)
dataf <- data.frame(blk, trt, y1, y2)

bout <- augmentedRCBD.bulk(data = dataf, block = "blk",
                              treatment = "trt", traits = c("y1", "y2"),
                              checks = NULL, alpha = 0.05, describe = TRUE,
                              freqdist = TRUE, gva = TRUE,
                              check.col = c("brown", "darkcyan",
                                            "forestgreen", "purple"),
                              console = TRUE)

# Frequency distribution plots
lapply(bout$`Frequency distribution`, plot)

# GVA plots
bout$`GVA plots`
```

---

describe.augmentedRCBD

Compute Descriptive Statistics from augmentedRCBD *Output*

Description

describe.augmentedRCBD computes descriptive statistics from the adjusted means in an
object of class augmentedRCBD.

Usage

```
describe.augmentedRCBD(aug)
```

Arguments

aug   An object of class augmentedRCBD.

Details

describe.augmentedRCBD computes the following descriptive statistics from the adjusted
means in an object of class augmentedRCBD.

- Count
- Mean
- Standard deviation
- Standard error
- Minimum
- Maximum
- Skewness statistic along with p-value from D'Agostino test of skewness (D'Agostino,
  1970).
- Kurtosis statistic along with p-value from Anscombe-Glynn test of kurtosis (Anscombe
  and Glynn, 1983).

Value

A list with the following descriptive statistics:

`Count`	The number of treatments/genotypes.
`Mean`	The mean value.
`Std.Error`	The standard error.
`Std.Deviation`	The standard deviation.
`Min`	The minimum value
`Max`	The maximum value

`Skewness(statistic)`

The skewness estimator.

`Skewness(p.value)`

The p-value from D'Agostino test of skewness.

`Kurtosis(statistic)`

The kurtosis estimator.

`Kurtosis(p.value)`

The p-value from Anscombe-Glynn test of kurtosis.

References

D'Agostino RB (1970). "Transformation to normality of the null distribution of g_1." *Biometrika*, **57**(3), 679–681.

Anscombe FJ, Glynn WJ (1983). "Distribution of the kurtosis statistic b_2 for normal samples." *Biometrika*, **70**(1), 227–234.

See Also

augmentedRCBD

Examples

```
# Example data
blk <- c(rep(1,7),rep(2,6),rep(3,7))
trt <- c(1, 2, 3, 4, 7, 11, 12, 1, 2, 3, 4, 5, 9, 1, 2, 3, 4, 8, 6, 10)
y1 <- c(92, 79, 87, 81, 96, 89, 82, 79, 81, 81, 91, 79, 78, 83, 77, 78, 78,
        70, 75, 74)
y2 <- c(258, 224, 238, 278, 347, 300, 289, 260, 220, 237, 227, 281, 311, 250,
        240, 268, 287, 226, 395, 450)
data <- data.frame(blk, trt, y1, y2)
# Convert block and treatment to factors
data$blk <- as.factor(data$blk)
data$trt <- as.factor(data$trt)
# Results for variable y1
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
# Results for variable y2
out2 <- augmentedRCBD(data$blk, data$trt, data$y2, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
```

```
# Descriptive statistics
describe.augmentedRCBD(out1)
describe.augmentedRCBD(out2)
```

---

freqdist.augmentedRCBD

Plot Frequency Distribution from augmentedRCBD *Output*

Description

freqdist.augmentedRCBD plots frequency distribution from an object of class augmentedRCBD along with the corresponding normal curve and check means with standard errors (if specified by argument highlight.check).

Usage

```
freqdist.augmentedRCBD(aug, xlab, highlight.check = TRUE, check.col = "red")
```

Arguments

aug	An object of class augmentedRCBD.
xlab	The text for x axis label as a character string.
highlight.check	
	If TRUE, the check means and standard errors are also plotted. Default is TRUE.
check.col	The colour(s) to be used to highlight check values in the plot as a character vector. Must be valid colour values in R (named colours, hexadecimal representation, index of colours [1:8] in default R palette() etc.).

Value

The frequency distribution plot as a ggplot2 plot grob.

See Also

augmentedRCBD

Examples

```
# Example data
blk <- c(rep(1,7),rep(2,6),rep(3,7))
trt <- c(1, 2, 3, 4, 7, 11, 12, 1, 2, 3, 4, 5, 9, 1, 2, 3, 4, 8, 6, 10)
y1 <- c(92, 79, 87, 81, 96, 89, 82, 79, 81, 81, 91, 79, 78, 83, 77, 78, 78,
        70, 75, 74)
y2 <- c(258, 224, 238, 278, 347, 300, 289, 260, 220, 237, 227, 281, 311, 250,
        240, 268, 287, 226, 395, 450)
data <- data.frame(blk, trt, y1, y2)
```

```
# Convert block and treatment to factors
data$blk <- as.factor(data$blk)
data$trt <- as.factor(data$trt)
# Results for variable y1
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                        alpha = 0.05, group = TRUE, console = TRUE)
# Results for variable y2
out2 <- augmentedRCBD(data$blk, data$trt, data$y2, method.comp = "lsd",
                        alpha = 0.05, group = TRUE, console = TRUE)

# Frequency distribution plots
freq1 <- freqdist.augmentedRCBD(out1, xlab = "Trait 1")
class(freq1)
plot(freq1)
freq2 <- freqdist.augmentedRCBD(out2, xlab = "Trait 2")
plot(freq2)

# Change check colours
colset <- c("red3", "green4", "purple3", "darkorange3")
freq1 <- freqdist.augmentedRCBD(out1, xlab = "Trait 1", check.col = colset)
plot(freq1)
freq2 <- freqdist.augmentedRCBD(out2, xlab = "Trait 2", check.col = colset)
plot(freq2)

# Without checks highlighted
freq1 <- freqdist.augmentedRCBD(out1, xlab = "Trait 1",
                                    highlight.check = FALSE)
plot(freq1)
freq2 <- freqdist.augmentedRCBD(out2, xlab = "Trait 2",
                                    highlight.check = FALSE)
plot(freq2)
```

---

gva.augmentedRCBD   *Perform Genetic Variability Analysis on* augmentedRCBD *Output*

Description

gva.augmentedRCBD performs genetic variability analysis on an object of class augmentedRCBD.

Usage

```
gva.augmentedRCBD(aug, k = 2.063)
```

Arguments

aug	An object of class augmentedRCBD.
k	The standardized selection differential or selection intensity. Default is 2.063 for 5% selection proportion (see **Details**).

Details

`gva.augmentedRCBD` performs genetic variability analysis from the ANOVA results in an object of class `augmentedRCBD` and computes several variability estimates.

The phenotypic, genotypic and environmental variance (σ_p^2, σ_g^2 and σ_e^2) are obtained from the ANOVA tables according to the expected value of mean square described by Federer and Searle (1976) as follows:

$$\sigma_p^2 = \text{Mean sum of squares of test treatments}$$

$$\sigma_e^2 = \text{Mean sum of squares of residuals}$$

$$\sigma_g^2 = \sigma_p^2 - \sigma_e^2$$

Phenotypic and genotypic coefficients of variation (PCV and GCV) are estimated according to Burton (1951, 1952) as follows:

$$PCV = \frac{\sigma_p^2}{\sqrt{\overline{x}}} \times 100$$

$$GCV = \frac{\sigma_g^2}{\sqrt{\overline{x}}} \times 100$$

Where $\overline{x}$ is the mean.

The estimates of PCV and GCV are categorised according to Sivasubramanian and Madhavamenon (1978) as follows:

CV (%)	Category
x < 10	Low
$10 \leq$ x < 20	Medium
≥ 20	High

The broad-sense heritability (H^2) is calculated according to method of Lush (1940) as follows:

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

The estimates of broad-sense heritability (H^2) are categorised according to Robinson (1966) as follows:

H^2	Category
x < 30	Low
$30 \leq$ x < 60	Medium
≥ 60	High

Genetic advance (GA) is estimated and categorised according to Johnson et al., (1955) as follows:

$$GA = k \times \sigma_g \times \frac{H^2}{100}$$

Where the constant k is the standardized selection differential or selection intensity. The value of k at 5% proportion selected is 2.063. Values of k at other selected proportions are available in Appendix Table A of Falconer and Mackay (1996).

Selection intensity (k) can also be computed in R as below:

If `p` is the proportion of selected individuals, then deviation of truncation point from mean (`x`) and selection intensity (`k`) are as follows:

```
x = qnorm(1-p)
```

```
k = dnorm(qnorm(1 -p))/p
```

Using the same the Appendix Table A of Falconer and Mackay (1996) can be recreated as follows.

```
TableA <- data.frame(p = c(seq(0.01, 0.10, 0.01), NA,
                           seq(0.10, 0.50, 0.02), NA,
                           seq(1, 5, 0.2), NA,
                           seq(5, 10, 0.5), NA,
                           seq(10, 50, 1)))
TableA$x <- qnorm(1-(TableA$p/100))
TableA$i <- dnorm(qnorm(1 - (TableA$p/100)))/(TableA$p/100)
```

Appendix Table A (Falconer and Mackay, 1996)

p%	x	i
0.01	3.71901649	3.9584797
0.02	3.54008380	3.7892117
0.03	3.43161440	3.6869547
0.04	3.35279478	3.6128288
0.05	3.29052673	3.5543807
0.06	3.23888012	3.5059803
0.07	3.19465105	3.4645890
0.08	3.15590676	3.4283756
0.09	3.12138915	3.3961490
0.10	3.09023231	3.3670901
¿¿	¿¿	¿¿
0.10	3.09023231	3.3670901
0.12	3.03567237	3.3162739
0.14	2.98888227	3.2727673
0.16	2.94784255	3.2346647
0.18	2.91123773	3.2007256
0.20	2.87816174	3.1700966
0.22	2.84796329	3.1421647
0.24	2.82015806	3.1164741
0.26	2.79437587	3.0926770

0.28	2.77032723	3.0705013
0.30	2.74778139	3.0497304
0.32	2.72655132	3.0301887
0.34	2.70648331	3.0117321
0.36	2.68744945	2.9942406
0.38	2.66934209	2.9776133
0.40	2.65206981	2.9617646
0.42	2.63555424	2.9466212
0.44	2.61972771	2.9321196
0.46	2.60453136	2.9182048
0.48	2.58991368	2.9048286
0.50	2.57582930	2.8919486
¿¿	¿¿	¿¿
1.00	2.32634787	2.6652142
1.20	2.25712924	2.6028159
1.40	2.19728638	2.5490627
1.60	2.14441062	2.5017227
1.80	2.09692743	2.4593391
2.00	2.05374891	2.4209068
2.20	2.01409081	2.3857019
2.40	1.97736843	2.3531856
2.60	1.94313375	2.3229451
2.80	1.91103565	2.2946575
3.00	1.88079361	2.2680650
3.20	1.85217986	2.2429584
3.40	1.82500682	2.2191656
3.60	1.79911811	2.1965431
3.80	1.77438191	2.1749703
4.00	1.75068607	2.1543444
4.20	1.72793432	2.1345772
4.40	1.70604340	2.1155928
4.60	1.68494077	2.0973249
4.80	1.66456286	2.0797152
5.00	1.64485363	2.0627128
¿¿	¿¿	¿¿
5.00	1.64485363	2.0627128
5.50	1.59819314	2.0225779
6.00	1.55477359	1.9853828
6.50	1.51410189	1.9506784
7.00	1.47579103	1.9181131
7.50	1.43953147	1.8874056
8.00	1.40507156	1.8583278
8.50	1.37220381	1.8306916
9.00	1.34075503	1.8043403
9.50	1.31057911	1.7791417
10.00	1.28155157	1.7549833
¿¿	¿¿	¿¿
10.00	1.28155157	1.7549833

11.00	1.22652812	1.7094142
12.00	1.17498679	1.6670040
13.00	1.12639113	1.6272701
14.00	1.08031934	1.5898336
15.00	1.03643339	1.5543918
16.00	0.99445788	1.5206984
17.00	0.95416525	1.4885502
18.00	0.91536509	1.4577779
19.00	0.87789630	1.4282383
20.00	0.84162123	1.3998096
21.00	0.80642125	1.3723871
22.00	0.77219321	1.3458799
23.00	0.73884685	1.3202091
24.00	0.70630256	1.2953050
25.00	0.67448975	1.2711063
26.00	0.64334541	1.2475585
27.00	0.61281299	1.2246130
28.00	0.58284151	1.2022262
29.00	0.55338472	1.1803588
30.00	0.52440051	1.1589754
31.00	0.49585035	1.1380436
32.00	0.46769880	1.1175342
33.00	0.43991317	1.0974204
34.00	0.41246313	1.0776774
35.00	0.38532047	1.0582829
36.00	0.35845879	1.0392158
37.00	0.33185335	1.0204568
38.00	0.30548079	1.0019882
39.00	0.27931903	0.9837932
40.00	0.25334710	0.9658563
41.00	0.22754498	0.9481631
42.00	0.20189348	0.9306998
43.00	0.17637416	0.9134539
44.00	0.15096922	0.8964132
45.00	0.12566135	0.8795664
46.00	0.10043372	0.8629028
47.00	0.07526986	0.8464123
48.00	0.05015358	0.8300851
49.00	0.02506891	0.8139121
50.00	0.00000000	0.7978846

Where **p%** is the selected percentage of individuals from a population, **x** is the deviation of the point of truncation of selected individuals from population mean and **i** is the selection intensity.

Genetic advance as per cent of mean (GAM) are estimated and categorised according to Johnson et al., (1955) as follows:

$$GAM = \frac{GA}{\overline{x}} \times 100$$

GAM	Category
x < 10	Low
$10 \leq x < 20$	Medium
≥ 20	High

Value

A list with the following descriptive statistics:

Mean	The mean value.
PV	Phenotyic variance.
GV	Genotyipc variance.
EV	Environmental variance.
GCV	Genotypic coefficient of variation
GCV category	The GCV category according to Sivasubramaniam and Madhavamenon (1973).
PCV	Phenotypic coefficient of variation
PCV category	The PCV category according to Sivasubramaniam and Madhavamenon (1973).
ECV	Environmental coefficient of variation
hBS	The broad-sense heritability (H^2) (Lush 1940).
hBS category	The H^2 category according to Robinson (1966).
GA	Genetic advance (Johnson et al. 1955).
GAM	Genetic advance as per cent of mean (Johnson et al. 1955).
GAM category	The GAM category according to Johnson et al. (1955).

Note

Genetic variability analysis needs to be performed only if the sum of squares of "Treatment: Test" are significant.

Negative estimates of variance components if computed are not abnormal. For information on how to deal with these, refer Dudley and Moll (1969).

References

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Robinson HF (1966). "Quantitative genetics in relation to breeding on centennial of Mendelism." *Indian Journal of Genetics and Plant Breeding*, 171.

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Federer WT, Searle SR (1976). "Model Considerations and Variance Component Estimation in Augmented Completely Randomized and Randomized Complete Blocks Designs-Preliminary Version." Technical Report BU-592-M, Cornell University, New York.

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See Also

augmentedRCBD

Examples

```
# Example data
blk <- c(rep(1,7),rep(2,6),rep(3,7))
trt <- c(1, 2, 3, 4, 7, 11, 12, 1, 2, 3, 4, 5, 9, 1, 2, 3, 4, 8, 6, 10)
y1 <- c(92, 79, 87, 81, 96, 89, 82, 79, 81, 81, 91, 79, 78, 83, 77, 78, 78,
        70, 75, 74)
y2 <- c(258, 224, 238, 278, 347, 300, 289, 260, 220, 237, 227, 281, 311, 250,
        240, 268, 287, 226, 395, 450)
data <- data.frame(blk, trt, y1, y2)
# Convert block and treatment to factors
data$blk <- as.factor(data$blk)
data$trt <- as.factor(data$trt)
# Results for variable y1
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
# Results for variable y2
out2 <- augmentedRCBD(data$blk, data$trt, data$y2, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)

# Genetic variability analysis
gva.augmentedRCBD(out1)
gva.augmentedRCBD(out2)
```

---

print.augmentedRCBD   *Prints summary of* augmentedRCBD *object*

Description

print.augmentedRCBD prints to console the summary of an object of class augmentedRCBD including the augmented design details, ANOVA (Treatment adjusted), ANOVA (Block adjusted), treatment means, coefficient of variation, overall adjusted mean, critical differences

and standard errors. The treatment/genotype groups along with the grouping method are
also printed if they were computed.

Usage

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

Arguments

x   An object of class augmentedRCBD.

...   Unused

See Also

augmentedRCBD

---

print.augmentedRCBD.bulk

Prints summary of augmentedRCBD.bulk *object*

Description

print.augmentedRCBD.bulk prints to console the summary of an object of class augmentedRCBD.bulk
including the augmented design details, trait-wise mean sum of squares from ANOVA
(Treatment adjusted) and ANOVA (Block adjusted), adjusted means, coefficient of vari-
ation, overall adjusted means critical differences, standard errors, descriptive statistics,
frequency distribution plots, genetic variability statistics and plots of genetic variability
parameters.

Usage

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

Arguments

x   An object of class augmentedRCBD.bulk.

...   Unused

See Also

augmentedRCBD.bulk

---

report.augmentedRCBD   *Generate MS Word Report from* augmentedRCBD *Output*

Description

report.augmentedRCBD generates a tidy report from an object of class augmentedRCBD as docx MS word file using the officer package.

Usage

```
report.augmentedRCBD(aug, target)
```

Arguments

aug	An object of class augmentedRCBD.
target	The path to the docx file to be created.

See Also

officer, flextable

Examples

```
# Example data
blk <- c(rep(1,7),rep(2,6),rep(3,7))
trt <- c(1, 2, 3, 4, 7, 11, 12, 1, 2, 3, 4, 5, 9, 1, 2, 3, 4, 8, 6, 10)
y1 <- c(92, 79, 87, 81, 96, 89, 82, 79, 81, 81, 91, 79, 78, 83, 77, 78, 78,
        70, 75, 74)
y2 <- c(258, 224, 238, 278, 347, 300, 289, 260, 220, 237, 227, 281, 311, 250,
        240, 268, 287, 226, 395, 450)
data <- data.frame(blk, trt, y1, y2)
# Convert block and treatment to factors
data$blk <- as.factor(data$blk)
data$trt <- as.factor(data$trt)
# Results for variable y1 (checks inferred)
out <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                     alpha = 0.05, group = TRUE, console = FALSE)


report.augmentedRCBD(out, file.path(tempdir(), "augmentedRCBD output.docx"))
```

report.augmentedRCBD.bulk

Generate MS Word Report from augmentedRCBD.bulk *Output*

Description

report.augmentedRCBD.bulk generates a tidy report from an object of class augmentedRCBD.bulk as docx MS word file using the officer package.

Usage

```
report.augmentedRCBD.bulk(aug.bulk, target)
```

Arguments

aug.bulk   An object of class augmentedRCBD.bulk.

target   The path to the docx file to be created.

See Also

officer, flextable

augmentedRCBD.bulk

Examples

```
# Example data
blk <- c(rep(1,7),rep(2,6),rep(3,7))
trt <- c(1, 2, 3, 4, 7, 11, 12, 1, 2, 3, 4, 5, 9, 1, 2, 3, 4, 8, 6, 10)

y1 <- c(92, 79, 87, 81, 96, 89, 82, 79, 81, 81, 91, 79, 78, 83, 77, 78, 78,
        70, 75, 74)
y2 <- c(258, 224, 238, 278, 347, 300, 289, 260, 220, 237, 227, 281, 311, 250,
        240, 268, 287, 226, 395, 450)
dataf <- data.frame(blk, trt, y1, y2)

bout <- augmentedRCBD.bulk(data = dataf, block = "blk",
                           treatment = "trt", traits = c("y1", "y2"),
                           checks = NULL, alpha = 0.05, describe = TRUE,
                           freqdist = TRUE, gva = TRUE,
                           check.col = c("brown", "darkcyan",
                                         "forestgreen", "purple"),
                           console = FALSE)


report.augmentedRCBD.bulk(bout, file.path(tempdir(),
                          "augmentedRCBD bulk output.docx"))
```

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