Package 'augmentedRCBD'

June 19, 2018

Title Analysis of Augmented Randomised Complete Block Designs

Version 0.0.0.9000

Description Functions for analysis of data generated from experiments in augmented randomised complete block design. 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)

RoxygenNote 6.0.1

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

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

Imports dplyr,
flextable,
ggplot2,
grDevices,
methods,
moments,
Rdpack,
stats,
stringi,
officer,
reshape2

RdMacros Rdpack

R topics documented:

`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)
```

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"`.
`console`	If `TRUE`, output will be printed to console. Default is `TRUE`.
`simplify`	If `TRUE`, ANOVA output will be given as a data frame instead of a `summary.aov` object

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

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

de Mendiburu F (2015). *agricolae: Statistical Procedures for Agricultural Research*. R package version 1.2-8. https://CRAN.R-project.org/package=agricolae.

See Also

`DAU.test`, `ea1`, `emmeans`, `cld`, `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 treatments 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.
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.

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 as follows:

$$\sigma_p^2 = \text{Sum of squares of test treatments(genotypes)}$$

$$\sigma_e^2 = \text{Sum of squares of residuals(error)}$$

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

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
$\geq$ 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
$\geq$ 60	High

Genetic advance (GA) and genetic advance as per cent of mean (GAM) are 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).

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

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

Value

A list with the following descriptive statistics:

`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.

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

Lush JL (1940). "Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics." *Proceedings of the American Society of Animal Nutrition*, **1940**(1), 293–301.

Burton GW (1951). "Quantitative Inheritance in pearl millet (*Pennisetum glaucum*)." *Agronomy Journal*, **43**(9), 409–417.

Burton GW (1952). "Qualitative inheritance in grasses. Vol. 1." In *Proceedings of the 6th International Grassland Congress, Pennsylvania State College*, 17–23.

Johnson HW, Robinson H, Comstock R (1955). "Estimates of genetic and environmental variability in soybeans." *Agronomy journal*, **47**(7), 314–318.

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

Dudley JW, Moll RH (1969). "Interpretation and Use of Estimates of Heritability and Genetic Variances in Plant Breeding." *Crop Science*, **9**(3), 257–262.

Sivasubramanian S, Madhavamenon P (1973). "Genotypic and phenotypic variability in rice." *The Madras Agricultural Journal*, **60**(9-13), 1093–1096.

Falconer DS, Mackay TFC (1996). *Introduction to quantitative genetics*. Pearson/Prenctice Hall, New York, NY.

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 variation, 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)

## Not run:
report.augmentedRCBD.bulk(bout, "augmentedRCBD output.docx")

## End(Not run)
```

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)

## Not run:
report.augmentedRCBD.bulk(bout, "augmentedRCBD bulk output.docx")

## End(Not run)
```

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