Package ‘augmentedRCBD’

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Title Analysis of Augmented Randomised Complete Block Designs

Version 0.1.1


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Encoding UTF-8

LazyData true

Depends R (>= 3.0.1)

VignetteBuilder knitr

RoxygenNote 6.1.1

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

RdMacros Rdpack

NeedsCompilation no

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R topics documented:

- augmentedRCBD
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**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**

```r
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.
augmentedRCBD

- **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


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)
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)

1https://www.rdocumentation.org/packages/easyanova/versions/5.0/topics/eal
2https://rdrr.io/rforge/plantbreeding/man/aug.rcb.html
```r
# 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)
```
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.

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

```r
# 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**


**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, 79, 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 representa-
    tion, 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**

```r
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 (\( \sigma^2_p \), \( \sigma^2_g \) and \( \sigma^2_e \)) are obtained from the ANOVA tables as follows:

\[
\sigma^2_p = \text{Sum of squares of test treatments (genotypes)}
\]

\[
\sigma^2_e = \text{Sum of squares of residuals (error)}
\]

\[
\sigma^2_g = \sigma^2_p - \sigma^2_e
\]

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

\[
PCV = \frac{\sigma_p^2}{\sqrt{\bar{x}}} \times 100
\]

\[
GCV = \frac{\sigma_g^2}{\sqrt{\bar{x}}} \times 100
\]

Where \( \bar{x} \) is the mean.

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

<table>
<thead>
<tr>
<th>CV (%)</th>
<th>Category</th>
</tr>
</thead>
<tbody>
<tr>
<td>( x &lt; 10 )</td>
<td>Low</td>
</tr>
<tr>
<td>( 10 \leq x &lt; 20 )</td>
<td>Medium</td>
</tr>
<tr>
<td>( \geq 20 )</td>
<td>High</td>
</tr>
</tbody>
</table>
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:

<table>
<thead>
<tr>
<th>$H^2$ Category</th>
<th>x</th>
<th>Category</th>
</tr>
</thead>
<tbody>
<tr>
<td>Low</td>
<td>&lt;30</td>
<td></td>
</tr>
<tr>
<td>Medium</td>
<td>30</td>
<td>≤x&lt;60</td>
</tr>
<tr>
<td>High</td>
<td>≥60</td>
<td></td>
</tr>
</tbody>
</table>

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).

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

<table>
<thead>
<tr>
<th>GAM Category</th>
<th>x</th>
<th>Category</th>
</tr>
</thead>
<tbody>
<tr>
<td>Low</td>
<td>&lt;10</td>
<td></td>
</tr>
<tr>
<td>Medium</td>
<td>10</td>
<td>≤x&lt;20</td>
</tr>
<tr>
<td>High</td>
<td>≥20</td>
<td></td>
</tr>
</tbody>
</table>

Value

A list with the following descriptive statistics:

| Mean | The mean value. |
| PV   | Phenotypic variance. |
| GV   | Genotypic 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


See Also

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

---

**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**

```r
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

```r
# 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)
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"))
```