Package ‘augmentedRCBD’

June 11, 2021

Title Analysis of Augmented Randomised Complete Block Designs

Version 0.1.5


Copyright 2015-2021, ICAR-NBPGR

License GPL-2 | GPL-3

Encoding UTF-8

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,
    mathjaxr,
    methods,
    moments,
    multcomp,
    multcompView,
    Rdpack,
    stats,
    stringi,
    officer,
    reshape2,
    utils
**augmentedRCBD**

Suggests knitr, rmarkdown, pander, testthat, agricolae

RdMacros Rdpack, mathjaxr

**R topics documented:**

<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>augmentedRCBD</td>
<td>2</td>
</tr>
<tr>
<td>augmentedRCBD.bulk</td>
<td>5</td>
</tr>
<tr>
<td>describe.augmentedRCBD</td>
<td>7</td>
</tr>
<tr>
<td>freqdist.augmentedRCBD</td>
<td>9</td>
</tr>
<tr>
<td>gva.augmentedRCBD</td>
<td>10</td>
</tr>
<tr>
<td>print.augmentedRCBD</td>
<td>16</td>
</tr>
<tr>
<td>print.augmentedRCBD.bulk</td>
<td>17</td>
</tr>
<tr>
<td>report.augmentedRCBD</td>
<td>17</td>
</tr>
<tr>
<td>report.augmentedRCBD.bulk</td>
<td>18</td>
</tr>
</tbody>
</table>

Index 20

<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>augmentedRCBD</td>
<td></td>
</tr>
</tbody>
</table>

**Description**

*augmentedRCBD* is a function for analysis of variance of an augmented randomised block design (Federer, 1956; Federer, 1961; Searle, 1965) 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 = TRUE,
  truncate.means = TRUE
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>block</td>
<td>Vector of blocks (as a factor).</td>
</tr>
<tr>
<td>treatment</td>
<td>Vector of treatments/genotypes (as a factor).</td>
</tr>
<tr>
<td>y</td>
<td>Numeric vector of response variable (Trait).</td>
</tr>
</tbody>
</table>
augmentedRCBD

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


See Also

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

Examples

```r
# Example data
data <- data.frame(blk, trt, y1, y2)
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)
```

## 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

```r
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.
describe.augmentedRCBD

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, 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 = TRUE)

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

# GVA plots
bout$s$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, 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.
gva.augmentedRCBD

Perform Genetic Variability Analysis on augmentedRCBD Output

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 according to the expected value of mean square described by Federer and Searle (1976) as follows:

$$\sigma^2_g = \sigma^2_p - \sigma^2_e$$

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

$$GCV = \frac{\sigma^2_g}{\sqrt{\bar{x}}} \times 100$$

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:

$$H^2 = \frac{\sigma^2_g}{\sigma^2_p}$$

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

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

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:

$$x = \text{qnorm}(1-p)$$
$$k = \frac{\text{dnorm(\text{qnorm}(1-p)))}{p}$$

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

```r
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$x <- \text{qnorm}(1-(TableA$p/100))
TableA$i <- \frac{\text{dnorm(\text{qnorm}(1 - (TableA$p/100))))}{(TableA$p/100)}
```

### Appendix Table A (Falconer and Mackay, 1996)

<table>
<thead>
<tr>
<th>p%</th>
<th>x</th>
<th>i</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.01</td>
<td>3.71901649</td>
<td>3.9584797</td>
</tr>
<tr>
<td>0.02</td>
<td>3.54008380</td>
<td>3.7892117</td>
</tr>
<tr>
<td>0.03</td>
<td>3.43161440</td>
<td>3.6869547</td>
</tr>
<tr>
<td>0.04</td>
<td>3.35279478</td>
<td>3.6128288</td>
</tr>
<tr>
<td>0.05</td>
<td>3.29052673</td>
<td>3.5543807</td>
</tr>
<tr>
<td>0.06</td>
<td>3.23888012</td>
<td>3.5059803</td>
</tr>
<tr>
<td>0.07</td>
<td>3.19465105</td>
<td>3.4645890</td>
</tr>
<tr>
<td>0.08</td>
<td>3.15590676</td>
<td>3.4283756</td>
</tr>
<tr>
<td>0.09</td>
<td>3.12138915</td>
<td>3.3961490</td>
</tr>
<tr>
<td>0.10</td>
<td>3.09023231</td>
<td>3.3670901</td>
</tr>
<tr>
<td>0.12</td>
<td>3.03567237</td>
<td>3.3162739</td>
</tr>
<tr>
<td>0.14</td>
<td>2.98888227</td>
<td>3.2727673</td>
</tr>
<tr>
<td>0.16</td>
<td>2.94784255</td>
<td>3.2346647</td>
</tr>
<tr>
<td>0.18</td>
<td>2.91123773</td>
<td>3.2007256</td>
</tr>
<tr>
<td>0.20</td>
<td>2.87816174</td>
<td>3.1700966</td>
</tr>
<tr>
<td>0.22</td>
<td>2.84796329</td>
<td>3.1421647</td>
</tr>
<tr>
<td>0.24</td>
<td>2.82015806</td>
<td>3.1164741</td>
</tr>
<tr>
<td>0.26</td>
<td>2.79437587</td>
<td>3.0926770</td>
</tr>
<tr>
<td>0.28</td>
<td>2.77032723</td>
<td>3.0705013</td>
</tr>
<tr>
<td>0.30</td>
<td>2.74778139</td>
<td>3.0497304</td>
</tr>
<tr>
<td>0.32</td>
<td>2.72655132</td>
<td>3.0301887</td>
</tr>
<tr>
<td>0.34</td>
<td>2.70648331</td>
<td>3.0117321</td>
</tr>
<tr>
<td>0.36</td>
<td>2.68744945</td>
<td>2.9942406</td>
</tr>
<tr>
<td>0.38</td>
<td>2.66934209</td>
<td>2.9776133</td>
</tr>
<tr>
<td>0.40</td>
<td>2.65206981</td>
<td>2.9617646</td>
</tr>
<tr>
<td>0.42</td>
<td>2.63555424</td>
<td>2.9466212</td>
</tr>
<tr>
<td>0.44</td>
<td>2.61972771</td>
<td>2.9321196</td>
</tr>
<tr>
<td>0.46</td>
<td>2.60453136</td>
<td>2.9182048</td>
</tr>
<tr>
<td>0.48</td>
<td>2.58991368</td>
<td>2.9048286</td>
</tr>
<tr>
<td>Time (s)</td>
<td>h (m)</td>
<td>f1 (Hz)</td>
</tr>
<tr>
<td>---------</td>
<td>---------</td>
<td>-------------</td>
</tr>
<tr>
<td>0.50</td>
<td>2.57582930</td>
<td>2.8919486</td>
</tr>
<tr>
<td>1.00</td>
<td>2.32634787</td>
<td>2.6652142</td>
</tr>
<tr>
<td>1.20</td>
<td>2.25712924</td>
<td>2.6028159</td>
</tr>
<tr>
<td>1.40</td>
<td>2.19728638</td>
<td>2.5490627</td>
</tr>
<tr>
<td>1.60</td>
<td>2.14441062</td>
<td>2.5017227</td>
</tr>
<tr>
<td>1.80</td>
<td>2.09692743</td>
<td>2.4593391</td>
</tr>
<tr>
<td>2.00</td>
<td>2.05374891</td>
<td>2.4209068</td>
</tr>
<tr>
<td>2.20</td>
<td>2.01409081</td>
<td>2.3857019</td>
</tr>
<tr>
<td>2.40</td>
<td>1.97736843</td>
<td>2.3531856</td>
</tr>
<tr>
<td>2.60</td>
<td>1.94313375</td>
<td>2.3229451</td>
</tr>
<tr>
<td>2.80</td>
<td>1.91103565</td>
<td>2.2946575</td>
</tr>
<tr>
<td>3.00</td>
<td>1.88079361</td>
<td>2.2680650</td>
</tr>
<tr>
<td>3.20</td>
<td>1.85217986</td>
<td>2.2429584</td>
</tr>
<tr>
<td>3.40</td>
<td>1.82500682</td>
<td>2.2191656</td>
</tr>
<tr>
<td>3.60</td>
<td>1.79911811</td>
<td>2.1965431</td>
</tr>
<tr>
<td>3.80</td>
<td>1.77438191</td>
<td>2.1749703</td>
</tr>
<tr>
<td>4.00</td>
<td>1.75068607</td>
<td>2.1543444</td>
</tr>
<tr>
<td>4.20</td>
<td>1.72793432</td>
<td>2.1345772</td>
</tr>
<tr>
<td>4.40</td>
<td>1.70604340</td>
<td>2.1155928</td>
</tr>
<tr>
<td>4.60</td>
<td>1.68494077</td>
<td>2.0973249</td>
</tr>
<tr>
<td>4.80</td>
<td>1.66456286</td>
<td>2.0797152</td>
</tr>
<tr>
<td>5.00</td>
<td>1.64485363</td>
<td>2.0627128</td>
</tr>
<tr>
<td>5.50</td>
<td>1.59819314</td>
<td>2.0225779</td>
</tr>
<tr>
<td>6.00</td>
<td>1.55477359</td>
<td>1.9853828</td>
</tr>
<tr>
<td>6.50</td>
<td>1.51410189</td>
<td>1.9506784</td>
</tr>
<tr>
<td>7.00</td>
<td>1.47579103</td>
<td>1.9181131</td>
</tr>
<tr>
<td>7.50</td>
<td>1.43953147</td>
<td>1.8874056</td>
</tr>
<tr>
<td>8.00</td>
<td>1.40507156</td>
<td>1.8583278</td>
</tr>
<tr>
<td>8.50</td>
<td>1.37220381</td>
<td>1.8306916</td>
</tr>
<tr>
<td>9.00</td>
<td>1.34075503</td>
<td>1.8043403</td>
</tr>
<tr>
<td>9.50</td>
<td>1.31057911</td>
<td>1.7791417</td>
</tr>
<tr>
<td>10.00</td>
<td>1.28155157</td>
<td>1.7549833</td>
</tr>
<tr>
<td>10.00</td>
<td>1.28155157</td>
<td>1.7549833</td>
</tr>
<tr>
<td>11.00</td>
<td>1.22652812</td>
<td>1.7094142</td>
</tr>
<tr>
<td>12.00</td>
<td>1.17498679</td>
<td>1.6670040</td>
</tr>
<tr>
<td>13.00</td>
<td>1.12639113</td>
<td>1.6272701</td>
</tr>
<tr>
<td>14.00</td>
<td>1.08031934</td>
<td>1.5898336</td>
</tr>
<tr>
<td>15.00</td>
<td>1.03643339</td>
<td>1.5543918</td>
</tr>
<tr>
<td>16.00</td>
<td>0.99445788</td>
<td>1.5206984</td>
</tr>
<tr>
<td>17.00</td>
<td>0.95416525</td>
<td>1.4885502</td>
</tr>
<tr>
<td>18.00</td>
<td>0.91536509</td>
<td>1.4577779</td>
</tr>
<tr>
<td>19.00</td>
<td>0.87789630</td>
<td>1.4282383</td>
</tr>
<tr>
<td>20.00</td>
<td>0.84162123</td>
<td>1.3998096</td>
</tr>
<tr>
<td>21.00</td>
<td>0.80642125</td>
<td>1.3723871</td>
</tr>
<tr>
<td>22.00</td>
<td>0.77219321</td>
<td>1.3458799</td>
</tr>
<tr>
<td>23.00</td>
<td>0.73884685</td>
<td>1.3202091</td>
</tr>
<tr>
<td>24.00</td>
<td>0.70630256</td>
<td>1.2953050</td>
</tr>
<tr>
<td>25.00</td>
<td>0.67448975</td>
<td>1.2711063</td>
</tr>
</tbody>
</table>
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:

\[
GAM = \frac{GA}{x} \times 100
\]

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

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 Robinson (1955) and Dudley and Moll (1969).

References


See Also

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, 92, 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
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

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

augmentedRCBD, 2, 7, 8, 10, 15, 16
augmentedRCBD.bulk, 5, 17, 18

cld.emmGrid, 4

DAU.test, 4
describe.augmentedRCBD, 7, 7

dependent.augmentedRCBD, 7, 10

emmeans, 3, 4

flextable, 17, 18
freqdist.augmentedRCBD, 7, 9

gva.augmentedRCBD, 7, 10

office, 17, 18

print.augmentedRCBD, 16
print.augmentedRCBD.bulk, 17

report.augmentedRCBD, 17
report.augmentedRCBD.bulk, 18