

# Data Analysis with **augmentedRCBD**

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## Contents

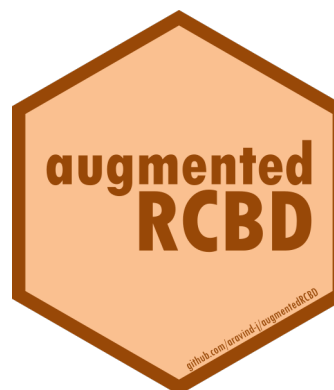
|   |           |
|---|-----------|
| <b>1 Overview</b>                             | <b>2</b>  |
| <b>2 R software</b>                           | <b>2</b>  |
| <b>3 Getting Started</b>                      | <b>3</b>  |
| 3.1 Installing R                              | 3         |
| 3.2 Installing RStudio                        | 3         |
| 3.3 The RStudio Interface                     | 4         |
| 3.3.1 Console                                 | 5         |
| 3.3.2 Source                                  | 5         |
| 3.3.3 Environment History Connections         | 5         |
| 3.3.4 Files Plots Packages Help Viewer        | 6         |
| <b>4 Some Basics</b>                          | <b>6</b>  |
| 4.1 Working Directory                         | 6         |
| 4.2 Expression and Assignment                 | 6         |
| 4.3 Objects and Functions                     | 7         |
| 4.3.1 Vector                                  | 7         |
| 4.3.2 Factor                                  | 8         |
| 4.3.3 Matrix                                  | 10        |
| 4.3.4 List                                    | 10        |
| 4.3.5 Data Frame                              | 11        |
| 4.3.6 Functions                               | 11        |
| 4.4 Special Elements                          | 12        |
| 4.5 Indexing                                  | 13        |
| 4.6 Help Documentation                        | 15        |
| 4.7 Packages                                  | 15        |
| 4.8 Importing and Exporting Tabular Data      | 16        |
| 4.9 Additional Resources                      | 17        |
| <b>5 Installation of <b>augmentedRCBD</b></b> | <b>17</b> |

|  |           |
|--|-----------|
| <b>6 Data Format</b>                                   | <b>18</b> |
| <b>7 Data Analysis for a Single Trait</b>              | <b>20</b> |
| 7.1 <code>augmentedRCBD()</code> . . . . .             | 21        |
| 7.2 <code>print.augmentedRCBD()</code> . . . . .       | 32        |
| 7.3 <code>describe.augmentedRCBD()</code> . . . . .    | 36        |
| 7.4 <code>freqdist.augmentedRCBD()</code> . . . . .    | 37        |
| 7.5 <code>gva.augmentedRCBD()</code> . . . . .         | 43        |
| 7.5 <code>report.augmentedRCBD()</code> . . . . .      | 45        |
| <b>8 Data Analysis for a Multiple Traits</b>           | <b>46</b> |
| 8.1 <code>augmentedRCBD.bulk()</code> . . . . .        | 47        |
| 8.2 <code>print.augmentedRCBD.bulk()</code> . . . . .  | 50        |
| 8.3 <code>report.augmentedRCBD.bulk()</code> . . . . . | 52        |
| <b>9 Citing <code>augmentedRCBD</code></b>             | <b>53</b> |
| <b>10 Session Info</b>                                 | <b>53</b> |
| <b>References</b>                                      | <b>54</b> |

## 1 Overview

The software `augmentedRCBD` is built on the **R statistical programming language** as an add-on (or ‘package’ in the *R lingua franca*). It performs the analysis of data generated from experiments in augmented randomised complete block design according to Federer, W.T. (1956a, 1956b, 1961; 1976). It also computes analysis of variance, adjusted means, descriptive statistics, genetic variability statistics etc. and includes options for data visualization and report generation.

This tutorial aims to educate the users in utilising this package for performing such analysis. Utilising `augmentedRCBD` for data analysis requires a basic knowledge of R programming language. However, as many of the intended end-users may not be familiar with R, [sections 2 to 4](#) give a ‘gentle’ introduction to R, especially those aspects which are necessary to get `augmentedRCBD` up and running for performing data analysis in a Windows environment. Users already familiar with R can feel free to skip to [section 5](#).



## 2 R software

It is a free software environment for statistical computing and graphics. It is free and open source, platform independent (works on Linux, Windows or MacOS), very flexible, comprehensive with robust interfaces for all the popular programming languages as well as databases. It is strengthened by its diverse library of add-on packages extending its ability as well as the incredible community support. It is one of the most popular tools being used in academia today (Tippmann, 2015).



## 3 Getting Started

This section details the steps required to set up the R programming environment under a third-party interface called RStudio in Windows.

### 3.1 Installing R

Download and install R for Windows from <http://cran.r-project.org/bin/windows/base/>.

**R-3.5.1 for Windows (32/64 bit)**

[Download R 3.5.1 for Windows](#) (62 megabytes, 32/64 bit)

[Installation and other instructions](#)

[New features in this version](#)

If you want to double-check that the package you have downloaded matches the package distributed by CRAN, you can compare the [md5sum](#) of the .exe to the [fingerprint](#) on the master server. You will need a version of md5sum for windows: both [graphical](#) and [command line versions](#) are available.

**Frequently asked questions**

- [Does R run under my version of Windows?](#)
- [How do I update packages in my previous version of R?](#)
- [Should I run 32-bit or 64-bit R?](#)

Please see the [R FAQ](#) for general information about R and the [R Windows FAQ](#) for Windows-specific information.

**Other builds**

- Patches to this release are incorporated in the [r-patched snapshot build](#).
- A build of the development version (which will eventually become the next major release of R) is available in the [r-devel snapshot build](#).
- [Previous releases](#)

Note to webmasters: A stable link which will redirect to the current Windows binary release is [CRAN.MIRROR>/bin/windows/base/release.htm](http://CRAN.MIRROR>/bin/windows/base/release.htm).

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Last change: 2018-07-02

**Fig. 1:** The R download location.

### 3.2 Installing RStudio

The basic [command line interface](#) in native R is rather limiting. There are several interfaces which enhance it's functionality and ease of use, [RStudio](#) being one of the most popular among R programmers.

Download and install RStudio for Windows from <https://www.rstudio.com/products/rstudio/download/#download>

**Installers for Supported Platforms**

| Installers   | Size    | Date       | MD5                              |
|--|---------|------------|----------------------------------|
| RStudio 1.1.456 - Windows Vista/7/8/10                         | 85.8 MB | 2018-07-19 | 24ca3fe0dad8187aabd4bfb9dc2b5ad  |
| RStudio 1.1.456 - Mac OS X 10.6+ (64-bit)                      | 74.5 MB | 2018-07-19 | 4fc4f4f70845b142bf96dc1a5b1dc556 |
| RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (32-bit)         | 89.3 MB | 2018-07-19 | 3493f9d5839e3a3d697f40b7bb1ce961 |
| RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (64-bit)         | 97.4 MB | 2018-07-19 | 863ae806120358fa0146e4d14cd75be4 |
| RStudio 1.1.456 - Ubuntu 16.04+/Debian 9+ (64-bit)             | 64.9 MB | 2018-07-19 | d96e63548c2add890bac633bdb883f32 |
| RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit) | 88.1 MB | 2018-07-19 | 1df56c7cd80e2634f8a9fdd11ca1fb2d |
| RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit) | 90.6 MB | 2018-07-19 | 5e77094a88fdbdddb0d35708752462   |

**Zip/Tarballs**

| Zip/tar archives   | Size     | Date       | MD5                              |
|--|----------|------------|----------------------------------|
| RStudio 1.1.456 - Windows Vista/7/8/10                         | 122.9 MB | 2018-07-19 | 659d6bfe716d8c97acbe501270d89fa3 |
| RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (32-bit)         | 90 MB    | 2018-07-19 | 63117c159deca4d01221a8069bd45373 |
| RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (64-bit)         | 98.3 MB  | 2018-07-19 | c53c32a71a400c6571e36c573f83dfde |
| RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit) | 88.8 MB  | 2018-07-19 | f4ba2509fb00e30c91414c6821f1c85f |
| RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit) | 91.4 MB  | 2018-07-19 | c60db6467421aa86c772227da0945a13 |

**Source Code**

A tarball containing source code for RStudio v1.1.456 can be downloaded from [here](#)

**Fig. 2:** The RStudio download location.

**3.3 The RStudio Interface**

On opening RStudio, the default interface with four panes/windows is visible as follows. Few panes have different tabs.



Fig. 3: The default RStudio interface with the four panes.

### 3.3.1 Console

This is where the action happens. Here any authentic R code typed after the '>' prompt will be executed after pressing 'Enter' to generate the output.

For example, type `1+1` in the console and press 'Enter'.

```
1+1
```

```
[1] 2
```

### 3.3.2 Source

This is where R Scripts (collection of code) can be created and edited. R scripts are text files with a `.R` extension. R Code for analysis can be typed and saved in such R scripts. New scripts can be opened by clicking 'File|New File' and selecting 'R Script'. Code can be selected from R Scripts and sent to console for evaluation by clicking 'Run' on the 'Source' pane or by pressing 'Ctrl + Enter'.

### 3.3.3 Environment|History|Connections

The 'Environment' tab shows the list of all the 'objects' (see [section 4.3](#)) defined in the current R session. It has also some buttons up top to open, save and clear the environment as well as few options for import of data under **Import Dataset**.

The 'History' tab shows a history of all the code that was previously evaluated. This is useful, if you want to go back to some code.

The ‘Connections’ tab helps to establish and manage connections with different databases and data sources.

### 3.3.4 Files|Plots|Packages|Help|Viewer

The ‘Files’ tab shows a sleek file browser to access the file directory in the computer with options to manage the working directory (see [section 4.1](#)) under the More button.

The ‘Plots’ tab shows all the plots generated in R with buttons to delete unnecessary ones and export useful ones as a pdf file or as an image file.

The ‘Packages’ tab shows a list of all the R add-on packages installed. The check box on the left shows whether they are loaded or not. There are also buttons to install and update R packages.

The ‘Viewer’ tab shows any web content output generated by an R code.

## 4 Some Basics

This section describes some basics to enable the users to have a working knowledge in R in order to use `augmentedRCBD`.

### 4.1 Working Directory

It is a file path to a folder on the computer which is recognised by R as the default location to read files from or write files to. The code `getwd()` shows the current working directory, while `setwd()` can be used to change the existing working directory.

```
# Print current working directory  
getwd()
```

```
[1] "C:/Users/Computer/Documents"
```

```
# Set new working directory  
setwd("C:/Data Analysis/")  
getwd()
```

```
[1] "C:/Data Analysis/"
```

One key detail is that file paths in R uses forward slashes (/) as in MacOS or Linux, unlike backward slashes (\) in Windows. This needs to be considered while copying paths from default Windows file explorer.

### 4.2 Expression and Assignment

Expressions are instructions in the form of code to be entered after the > prompt in the console. Expressions can be a constant, an arithmetic or a condition. A more advanced and most useful expression is a function call (see [section 4.3](#)).

```
# Constant  
123
```

```
[1] 123
```

```
# Arithmetic (add two numbers)  
1 + 2
```

```
[1] 3
```

```
# Condition
```

```
34 > 25
```

```
[1] TRUE
```

```
1 == 2
```

```
[1] FALSE
```

```
# Function call (mean of a series of numbers)
```

```
mean(c(25,56,89,35))
```

```
[1] 51.25
```

Information from an expression can be stored as an ‘object’ (see [section 4.3](#)) by assigning a name using the operator ‘<-’.

```
# Assign the result of the expression 1 + 2 to an object 'a'
```

```
a <- 1 + 2
```

```
a
```

```
[1] 3
```

It is recommended to add comments to explain the code by using the ‘#’ sign. Any code after the ‘#’ sign will be ignored by R.

## 4.3 Objects and Functions

R is an object-oriented programming language (OOP). Any kind or construct created in R is an ‘object’. Each object has a ‘class’ (shown using the `class()` function) and different ‘attributes’ which defines what operations can be done on that object. There are different types of data structure objects in R such as vectors, matrices, factors, data frames, and lists. A ‘function’ is also an object, which defines a procedure or a sequence of expressions.

### 4.3.1 Vector

A vector is a collection of elements of a single type (or ‘mode’). The common vector modes are ‘numeric’, ‘integer’, ‘character’ and ‘logical’. The `c()` function is used to create vectors. The functions `class()`, `str()` and `length()` show the attributes of vectors.

Vector modes ‘numeric’ stores real numbers, while ‘integer’ stores integers, which can be enforced by suffixing elements with ‘L’.

```
# A numeric vector
```

```
a <- c(1, 2, 3.3)
```

```
class(a)
```

```
[1] "numeric"
```

```
str(a)
```

```
num [1:3] 1 2 3.3
```

```
length(a)
```

```
[1] 3
```

```
# An integer vector
```

```
b <- c(1L, 2L, 3L)
```

```
class(b)
```

```
[1] "integer"
```

```
str(b)
```

```
int [1:3] 1 2 3
```

```
length(b)
```

```
[1] 3
```

The vector mode 'character' store text.

```
# A character vector
```

```
c <- c("one", "two", "three")
```

```
class(c)
```

```
[1] "character"
```

```
str(c)
```

```
chr [1:3] "one" "two" "three"
```

```
length(c)
```

```
[1] 3
```

The vector mode 'logical' stores 'TRUE' OR 'FALSE' logical data.

```
#logical vector
```

```
d <- c(TRUE, TRUE, TRUE, FALSE, TRUE, FALSE)
```

```
class(d)
```

```
[1] "logical"
```

```
str(d)
```

```
logi [1:6] TRUE TRUE TRUE FALSE TRUE FALSE
```

```
length(d)
```

```
[1] 6
```

#### 4.3.2 Factor

A 'factor' in R stores data from categorical data in variables as different levels.

```
catg <- c("male", "female", "female", "male", "male")
```

```
catg
```

```
[1] "male" "female" "female" "male" "male"
```

```
is.factor(catg)
```

```
[1] FALSE
```

```
# Apply the factor function
```

```
factor_catg <- factor(catg)
```

```
factor_catg
```



```
[1] male   female female male   male
Levels: female male
```

```
is.factor(factor_catg)
```

```
[1] TRUE
```

```
class(factor_catg)
```

```
[1] "factor"
```

```
str(factor_catg)
```

```
Factor w/ 2 levels "female","male": 2 1 1 2 2
```

A character, numeric or integer vector can be transformed to a factor by using the `as.factor()` function.

```
# Conversion of numeric to factor
```

```
a <- c(1, 2, 3.3)
```

```
class(a)
```

```
[1] "numeric"
```

```
str(a)
```

```
num [1:3] 1 2 3.3
```

```
fac_a <- as.factor(a)
```

```
class(fac_a)
```

```
[1] "factor"
```

```
str(fac_a)
```

```
Factor w/ 3 levels "1","2","3.3": 1 2 3
```

```
# Conversion of integer to factor
```

```
b <- c(1L, 2L, 3L)
```

```
class(b)
```

```
[1] "integer"
```

```
str(b)
```

```
int [1:3] 1 2 3
```

```
fac_b <- as.factor(b)
```

```
class(fac_b)
```

```
[1] "factor"
```

```
str(fac_b)
```

```
Factor w/ 3 levels "1","2","3": 1 2 3
```

```
# Conversion of character to factor
```

```
c <- c("one", "two", "three")
```

```
class(c)
```

```
[1] "character"
```

```
str(c)

chr [1:3] "one" "two" "three"
fac_c <- as.factor(c)
class(fac_c)

[1] "factor"
str(fac_c)

Factor w/ 3 levels "one","three",...: 1 3 2
```

### 4.3.3 Matrix

A ‘matrix’ in R is a vector with the attributes ‘nrow’ and ‘ncol’.

```
# Generate 5 * 4 numeric matrix
m <- matrix(1:20, nrow = 5, ncol = 4)
m
```

```
      [,1] [,2] [,3] [,4]
[1,]    1    6   11   16
[2,]    2    7   12   17
[3,]    3    8   13   18
[4,]    4    9   14   19
[5,]    5   10   15   20
```

```
class(m)
```

```
[1] "matrix"
```

```
typeof(m)
```

```
[1] "integer"
```

```
# Dimensions of m
```

```
dim(m)
```

```
[1] 5 4
```

### 4.3.4 List

A ‘list’ is a container containing different objects. The contents of list need not be of the same type or mode. A list can encompass a mixture of data types such as vectors, matrices, data frames, other lists or any other data structure.

```
w <- list(a, m, d, list(b, c))
class(w)
```

```
[1] "list"
```

```
str(w)
```

```
List of 4
 $ : num [1:3] 1 2 3.3
 $ : int [1:5, 1:4] 1 2 3 4 5 6 7 8 9 10 ...
 $ : logi [1:6] TRUE TRUE TRUE FALSE TRUE FALSE
 $ :List of 2
```

```
..$ : int [1:3] 1 2 3
..$ : chr [1:3] "one" "two" "three"
```

#### 4.3.5 Data Frame

A ‘data frame’ in R is a special kind of list with every element having equal length. It is very important for handling tabular data in R. It is a array like structure with rows and columns. Each column needs to be of a single data type, however data type can vary between columns.

```
L <- LETTERS[1:4]
y <- 1:4
z <- c("This", "is", "a", "data frame")
df <- data.frame(L, x = 1, y, z)
df
```

```
  L x y      z
1 A 1 1    This
2 B 1 2      is
3 C 1 3       a
4 D 1 4 data frame
```

```
str(df)
```

```
'data.frame':  4 obs. of  4 variables:
 $ L: Factor w/ 4 levels "A","B","C","D": 1 2 3 4
 $ x: num  1 1 1 1
 $ y: int  1 2 3 4
 $ z: Factor w/ 4 levels "a","data frame",...: 4 3 1 2
```

```
attributes(df)
```

```
$names
[1] "L" "x" "y" "z"
```

```
$class
[1] "data.frame"
```

```
$row.names
[1] 1 2 3 4
```

```
rownames(df)
```

```
[1] "1" "2" "3" "4"
```

```
colnames(df)
```

```
[1] "L" "x" "y" "z"
```

#### 4.3.6 Functions

All of the work in R is done by functions. It is an object defining a procedure which takes one or more objects as input (or ‘arguments’), performs some action on them and finally gives a new object as output (or ‘return’). `class()`, `mean()`, `getwd()`, `+`, etc. are all functions.

For example the function `mean()` takes a numeric vector as argument and returns the mean as a numeric vector.

```
a <- c(1, 2, 3.3)
mean(a)
```

```
[1] 2.1
```

The user can also create custom functions. For example the function `foo` adds two numbers and gives the result.

```
foo <- function(n1, n2) {
  out <- n1 + n2
  return(out)
}
foo(2,3)
```

```
[1] 5
```

## 4.4 Special Elements

In addition to numbers and text, there are some special elements which can be included in different data objects.

NA (not available) indicates missing data.

```
x <- c(2.5, NA, 8.6)
y <- c(TRUE, FALSE, NA)
z <- c("k", NA, "m", "n", "o")
is.na(x)
```

```
[1] FALSE TRUE FALSE
```

```
is.na(z)
```

```
[1] FALSE TRUE FALSE FALSE FALSE
```

```
anyNA(x)
```

```
[1] TRUE
```

```
a
```

```
[1] 1.0 2.0 3.3
```

```
is.na(a)
```

```
[1] FALSE FALSE FALSE
```

Inf indicates infinity.

```
1/0
```

```
[1] Inf
```

NaN (Not a Number) indicates any undefined value.

```
0/0
```

```
[1] NaN
```

## 4.5 Indexing

The `[]` function is used to extract elements of an object by indexing (numeric or logical). Named elements in lists and data frames can be extracted by using the `$` operator.

Consider a vector `a`.

```
a <- c(1, 2, 3.3, 2.8, 6.7)
# Numeric indexing
# Extract first element
a[1]
```

```
[1] 1
```

```
# Extract elements 2:3
a[2:3]
```

```
[1] 2.0 3.3
```

```
# Logical indexing
a[a > 3]
```

```
[1] 3.3 6.7
```

Consider a matrix `m`.

```
m <- matrix(1:9, nrow = 3, ncol = 3, byrow = TRUE)
colnames(m) <- c('a', 'b', 'c')
m
```

```
      a b c
[1,] 1 2 3
[2,] 4 5 6
[3,] 7 8 9
```

```
# Extract elements
m[,2] # 2nd column of matrix
```

```
[1] 2 5 8
```

```
m[3,] # 3rd row of matrix
```

```
a b c
7 8 9
```

```
m[2:3, 1:3] # rows 2,3 of columns 1,2,3
```

```
      a b c
[1,] 4 5 6
[2,] 7 8 9
```

```
m[2,2] # Element in 2nd column of 2nd row
```

```
b
5
```

```
m[, 'b'] # Column 'b'
```

```
[1] 2 5 8
```

```
m[, c('a', 'c')] # Column 'a' and 'c'
```

```
      a c
[1,] 1 3
[2,] 4 6
[3,] 7 9
```

Consider a list w.

```
w <- list(vec = a, mat = m, data = df, alist = list(b, c))
```

```
# Indexing by number
w[2] # As list structure
```

```
$mat
      a b c
[1,] 1 2 3
[2,] 4 5 6
[3,] 7 8 9
```

```
w[[2]] # Without list structure
```

```
      a b c
[1,] 1 2 3
[2,] 4 5 6
[3,] 7 8 9
```

```
# Indexing by name
w$vec
```

```
[1] 1.0 2.0 3.3 2.8 6.7
```

```
w$data
```

```
  L x y      z
1 A 1 1    This
2 B 1 2      is
3 C 1 3       a
4 D 1 4 data frame
```

Consider a data frame df.

```
df
```

```
  L x y      z
1 A 1 1    This
2 B 1 2      is
3 C 1 3       a
4 D 1 4 data frame
```

```
# Indexing by number
df[,2] # 2nd column of data frame
```

```
[1] 1 1 1 1
```

```
df[2] # 2nd column of data frame
```

```
  x
1 1
```

```
2 1
3 1
4 1
```

```
df[3,] # 3rd row of data frame
```

```
  L x y z
3 C 1 3 a
```

```
df[2:3, 1:3] # rows 2,3 of columns 1,2,3
```

```
  L x y
2 B 1 2
3 C 1 3
```

```
df[2,2] # Element in 2nd column of 2nd row
```

```
[1] 1
```

```
# Indexing by name
```

```
df$L
```

```
[1] A B C D
Levels: A B C D
```

```
df$z
```

```
[1] This      is      a      data frame
Levels: a data frame is This
```

## 4.6 Help Documentation

The help documentation regarding any function can be viewed using the `?` or `help()` function. The help documentation shows the default usage of the function including, the arguments that are taken by the function and the type of output object returned ('Value').

```
?ls
help(ls)

?mean

?setwd
```

## 4.7 Packages

Packages in R are collections of R functions, data, and compiled code in a well-defined format. They are add-ons which extend the functionality of R and at present, there are **15327** packages available for deployment and use at the official repository, the Comprehensive R Archive Network (CRAN).

Valid packages from CRAN can be installed by using the `install.packages()` command.

```
# Install the package 'readxl' for importing data from excel
install.packages(readxl)
```

Installed packages can be loaded using the function `library()`.

```
# Install the package 'readxl' for importing data from excel
library(readxl)
```

## 4.8 Importing and Exporting Tabular Data

Tabular data from a spreadsheet can be imported into R in different ways. Consider some data such as in Table 1. Copy this data in to a spreadsheet editor such as MS Excel and save it as `augdata.csv`, a comma-separated-value file and `augdata.xlsx`, an Excel file in the working directory (`getwd()`).

**Table 1:** Example data from an experiment in augmented RCBD design.

| blk | trt | y1 | y2  |
|-----|-----|----|-----|
| I   | 1   | 92 | 258 |
| I   | 2   | 79 | 224 |
| I   | 3   | 87 | 238 |
| I   | 4   | 81 | 278 |
| I   | 7   | 96 | 347 |
| I   | 11  | 89 | 300 |
| I   | 12  | 82 | 289 |
| II  | 1   | 79 | 260 |
| II  | 2   | 81 | 220 |
| II  | 3   | 81 | 237 |
| II  | 4   | 91 | 227 |
| II  | 5   | 79 | 281 |
| II  | 9   | 78 | 311 |
| III | 1   | 83 | 250 |
| III | 2   | 77 | 240 |
| III | 3   | 78 | 268 |
| III | 4   | 78 | 287 |
| III | 8   | 70 | 226 |
| III | 6   | 75 | 395 |
| III | 10  | 74 | 450 |

The `augdata.csv` file can be imported into R using the `read.csv()` function or the `read_csv()` function in the `readr` package.

```
data <- read.csv(file = "augdata.csv")
str(data)
```

```
'data.frame': 20 obs. of 4 variables:
 $ blk: Factor w/ 3 levels "I","II","III": 1 1 1 1 1 1 1 2 2 2 ...
 $ trt: num 1 2 3 4 7 11 12 1 2 3 ...
 $ y1 : num 92 79 87 81 96 89 82 79 81 81 ...
 $ y2 : num 258 224 238 278 347 300 289 260 220 237 ...
```

The argument `stringsAsFactors = FALSE` reads the text columns as of type `character` instead of the default `factor`.

```
data <- read.csv(file = "augdata.csv", stringsAsFactors = FALSE)
str(data)
```

```
'data.frame': 20 obs. of 4 variables:
 $ blk: chr "I" "I" "I" "I" ...
 $ trt: num 1 2 3 4 7 11 12 1 2 3 ...
 $ y1 : num 92 79 87 81 96 89 82 79 81 81 ...
 $ y2 : num 258 224 238 278 347 300 289 260 220 237 ...
```



The `augdata.xlsx` file can be imported into R using the `read_excel()` function in the `readxl` package.

```
library(readxl)
data <- read_excel(path = "augdata.xlsx")

'data.frame':  20 obs. of  4 variables:
 $ blk: chr  "I" "I" "I" "I" ...
 $ trt: num  1 2 3 4 7 11 12 1 2 3 ...
 $ y1 : num  92 79 87 81 96 89 82 79 81 81 ...
 $ y2 : num  258 224 238 278 347 300 289 260 220 237 ...
```

The tabular data can be exported from R to a `.csv` (comma-separated-value) file by the `write.csv()` function.

```
write.csv(x = data, file = "augdata.csv")
```

## 4.9 Additional Resources

To learn more about R, there are umpteen number of online tutorials as well as free courses available. Queries about various aspects can be put to the active and vibrant ‘R community online.

- Online tutorials
  - <http://www.cran.r-project.org/other-docs.html>
  - <https://bookdown.org/ndphillips/YaRrr/>
- Free online courses
  - <http://tryr.codeschool.com/>
  - <https://www.datacamp.com/courses/free-introduction-to-r>
- R community support
  - <http://stackoverflow.com/>
  - R help mailing lists : <http://www.r-project.org/mail.html>

## 5 Installation of `augmentedRCBD`

The package `augmentedRCBD` can be installed using the following functions.

```
# Install from CRAN
install.packages('augmentedRCBD', dependencies=TRUE)

# Install development version from Github
if (!require('devtools')) install.packages('devtools')
library(devtools)
install_github("aravind-j/augmentedRCBD")
```

The stable release is hosted in [CRAN](#) (see [section 4.7](#)), while the under-development version is hosted as a [Github](#) repository. To install from github, you need to use the `install_github()` function from ‘`devtools`’ package.

Then the package can be loaded using the function

```
library(augmentedRCBD)
```

The current version of the package is 0.1.1. The previous versions are as follows.

**Table 2.** Version history of `augmentedRCBD` R package.

| Version | Date       |
|---------|------------|
| 0.1.0   | 2018-07-10 |

To know detailed history of changes use `news(package='augmentedRCBD')`.

## 6 Data Format

Certain details need to be considered for arranging experimental data for analysis using the `augmentedRCBD` package.

The data should be in long/vertical form, where each row has the data from one genotype per block. For example, consider the following data (Table 3) recorded for a trait from an experiment laid out in an augmented block design with 3 blocks and 12 genotypes(or treatment) with 6 to 7 genotypes/block. 8 genotypes (Test, G 5 to G 12) are not replicated, while 4 genotypes (Check, G 1 to G 4) are replicated.

**Table 3:** Data from an experiment in augmented RCBD design.

| <b>Block I</b>   | G12       | <b>G4</b> | G11       | <b>G2</b> | <b>G1</b> | G7        | <b>G3</b> |
|------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
|                  | 82        | 81        | 89        | 79        | 92        | 96        | 87        |
| <b>Block II</b>  | G5        | G9        | –         | <b>G3</b> | <b>G1</b> | <b>G2</b> | <b>G4</b> |
|                  | 79        | 78        | –         | 81        | 79        | 81        | 91        |
| <b>Block III</b> | <b>G4</b> | <b>G2</b> | <b>G1</b> | G6        | G10       | <b>G3</b> | G8        |
|                  | 78        | 77        | 83        | 75        | 74        | 78        | 70        |

This data needs to be arranged with columns showing block, genotype (or treatment) and the data of the trait for each genotype per block (Table 4).

**Table 4:** Data from an experiment in augmented RCBD design arranged in long-form.

| Block     | Treatment | Trait |
|-----------|-----------|-------|
| Block I   | G 1       | 92    |
| Block I   | G 2       | 79    |
| Block I   | G 3       | 87    |
| Block I   | G 4       | 81    |
| Block I   | G 7       | 96    |
| Block I   | G 11      | 89    |
| Block I   | G 12      | 82    |
| Block II  | G 1       | 79    |
| Block II  | G 2       | 81    |
| Block II  | G 3       | 81    |
| Block II  | G 4       | 91    |
| Block II  | G 5       | 79    |
| Block II  | G 9       | 78    |
| Block III | G 1       | 83    |
| Block III | G 2       | 77    |
| Block III | G 3       | 78    |
| Block III | G 4       | 78    |
| Block III | G 8       | 70    |
| Block III | G 6       | 75    |

| Block     | Treatment | Trait |
|-----------|-----------|-------|
| Block III | G 10      | 74    |

The data for block and genotype (or treatment) can also be depicted as numbers (Table 5).

**Table 5:** Data from an experiment in augmented RCBD design arranged in long-form (Block and Treatment as numbers).

| Block | Treatment | Trait |
|-------|-----------|-------|
| 1     | 1         | 92    |
| 1     | 2         | 79    |
| 1     | 3         | 87    |
| 1     | 4         | 81    |
| 1     | 7         | 96    |
| 1     | 11        | 89    |
| 1     | 12        | 82    |
| 2     | 1         | 79    |
| 2     | 2         | 81    |
| 2     | 3         | 81    |
| 2     | 4         | 91    |
| 2     | 5         | 79    |
| 2     | 9         | 78    |
| 3     | 1         | 83    |
| 3     | 2         | 77    |
| 3     | 3         | 78    |
| 3     | 4         | 78    |
| 3     | 8         | 70    |
| 3     | 6         | 75    |
| 3     | 10        | 74    |

Multiple traits can be added as additional columns (Table 6).

**Table 6:** Data from an experiment in augmented RCBD design arranged in long-form (Multiple traits).

| Block     | Treatment | Trait1 | Trait2 |
|-----------|-----------|--------|--------|
| Block I   | G 1       | 92     | 258    |
| Block I   | G 2       | 79     | 224    |
| Block I   | G 3       | 87     | 238    |
| Block I   | G 4       | 81     | 278    |
| Block I   | G 7       | 96     | 347    |
| Block I   | G 11      | 89     | 300    |
| Block I   | G 12      | 82     | 289    |
| Block II  | G 1       | 79     | 260    |
| Block II  | G 2       | 81     | 220    |
| Block II  | G 3       | 81     | 237    |
| Block II  | G 4       | 91     | 227    |
| Block II  | G 5       | 79     | 281    |
| Block II  | G 9       | 78     | 311    |
| Block III | G 1       | 83     | 250    |

| Block     | Treatment | Trait1 | Trait2 |
|-----------|-----------|--------|--------|
| Block III | G 2       | 77     | 240    |
| Block III | G 3       | 78     | 268    |
| Block III | G 4       | 78     | 287    |
| Block III | G 8       | 70     | 226    |
| Block III | G 6       | 75     | 395    |
| Block III | G 10      | 74     | 450    |

Data should preferably be balanced i.e. all the check genotypes should be present in all the blocks. If not, a warning is issued. The number of test genotypes can vary within a block. There should not be any missing values. Rows of genotypes with missing values for one or more traits should be removed.

Such a tabular data should be imported ([see section 7.8](#)) into R as a data frame object ([see section 4.3.5](#)). The columns with the block and treatment categorical data should be of the type factor ([see section 4.3.2](#)), while the column(s) with the trait data should be of the type integer or numeric ([see section 4.3.1](#)).

## 7 Data Analysis for a Single Trait

Analysis of data for a single trait can be performed by using **augmentedRCBD** function. It generates an object of class **augmentedRCBD**. Such an object can then be taken as input by the several functions to print the results to console (**print.augmentedRCBD**), generate descriptive statistics from adjusted means (**describe.augmentedRCBD**), plot frequency distribution (**freqdist.augmentedRCBD**) and computed genetic variability statistics (**gva.augmentedRCBD**). All these outputs can also be exported as a MS Word report using the **report.augmentedRCBD** function.

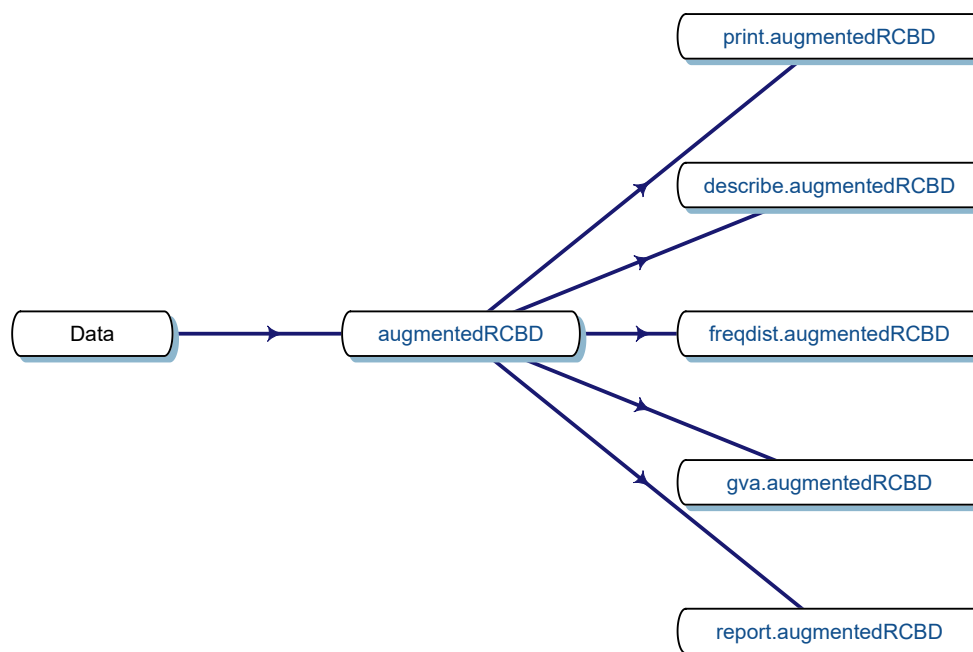


Fig. 4. Workflow for analysis of single traits with `augmentedRCBD`.

## 7.1 `augmentedRCBD()`

Consider the data in Table 1. The data can be imported into R as `vectors` as follows.

```

blk <- c(1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2, 3, 3, 3, 3, 3, 3, 3)
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)
  
```

The `blk` and `trt` vectors with the block and treatment data need to be converted into factors as follows before analysis.

```

# Convert block and treatment to factors
blk <- as.factor(blk)
trt <- as.factor(trt)
  
```

With the data in appropriate format, the analysis can be performed as follows for the trait `y1` as follows.

```

out1 <- augmentedRCBD(blk, trt, y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
  
```

```

Augmented Design Details
=====
  
```

```

Number of blocks      "3"
Number of treatments  "12"
Number of check treatments "4"
Number of test treatments "8"
Check treatments      "1, 2, 3, 4"

```

## ANOVA, Treatment Adjusted

=====

|                                    | Df | Sum Sq | Mean Sq | F value | Pr(>F)   |
|------------------------------------|----|--------|---------|---------|----------|
| Block (ignoring Treatments)        | 2  | 360.1  | 180.04  | 6.675   | 0.0298 * |
| Treatment (eliminating Blocks)     | 11 | 285.1  | 25.92   | 0.961   | 0.5499   |
| Treatment: Check                   | 3  | 52.9   | 17.64   | 0.654   | 0.6092   |
| Treatment: Test and Test vs. Check | 8  | 232.2  | 29.02   | 1.076   | 0.4779   |
| Residuals                          | 6  | 161.8  | 26.97   |         |          |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## ANOVA, Block Adjusted

=====

|                                | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|--------------------------------|----|--------|---------|---------|--------|
| Treatment (ignoring Blocks)    | 11 | 575.7  | 52.33   | 1.940   | 0.215  |
| Treatment: Check               | 3  | 52.9   | 17.64   | 0.654   | 0.609  |
| Treatment: Test                | 7  | 505.9  | 72.27   | 2.679   | 0.125  |
| Treatment: Test vs. Check      | 1  | 16.9   | 16.87   | 0.626   | 0.459  |
| Block (eliminating Treatments) | 2  | 69.5   | 34.75   | 1.288   | 0.342  |
| Residuals                      | 6  | 161.8  | 26.97   |         |        |

## Treatment Means

=====

|    | Treatment | Block | Means    | SE       | r | Min | Max | Adjusted Means |
|----|-----------|-------|----------|----------|---|-----|-----|----------------|
| 1  | 1         |       | 84.66667 | 3.844188 | 3 | 79  | 92  | 84.66667       |
| 2  | 10        | 3     | 74.00000 | NA       | 1 | 74  | 74  | 77.25000       |
| 3  | 11        | 1     | 89.00000 | NA       | 1 | 89  | 89  | 86.50000       |
| 4  | 12        | 1     | 82.00000 | NA       | 1 | 82  | 82  | 79.50000       |
| 5  | 2         |       | 79.00000 | 1.154701 | 3 | 77  | 81  | 79.00000       |
| 6  | 3         |       | 82.00000 | 2.645751 | 3 | 78  | 87  | 82.00000       |
| 7  | 4         |       | 83.33333 | 3.929942 | 3 | 78  | 91  | 83.33333       |
| 8  | 5         | 2     | 79.00000 | NA       | 1 | 79  | 79  | 78.25000       |
| 9  | 6         | 3     | 75.00000 | NA       | 1 | 75  | 75  | 78.25000       |
| 10 | 7         | 1     | 96.00000 | NA       | 1 | 96  | 96  | 93.50000       |
| 11 | 8         | 3     | 70.00000 | NA       | 1 | 70  | 70  | 73.25000       |
| 12 | 9         | 2     | 78.00000 | NA       | 1 | 78  | 78  | 77.25000       |

## Coefficient of Variation

=====

6.372367

## Overall Adjusted Mean

=====

81.0625

## Standard Errors

=====

|  |  |  | Std. Error of Diff. | CD (5%)  |
|--|--|--|---------------------|----------|
| Control Treatment Means                  |  |  | 4.240458            | 10.37603 |
| Two Test Treatments (Same Block)         |  |  | 7.344688            | 17.97180 |
| Two Test Treatments (Different Blocks)   |  |  | 8.211611            | 20.09309 |
| A Test Treatment and a Control Treatment |  |  | 6.704752            | 16.40594 |

## Treatment Groups

=====

Method : lsd

|    | Treatment | Adjusted Means | SE       | df | lower.CL | upper.CL  | Group |
|----|-----------|----------------|----------|----|----------|-----------|-------|
| 8  | 8         | 73.25000       | 5.609598 | 6  | 59.52381 | 86.97619  | 1     |
| 9  | 9         | 77.25000       | 5.609598 | 6  | 63.52381 | 90.97619  | 12    |
| 10 | 10        | 77.25000       | 5.609598 | 6  | 63.52381 | 90.97619  | 12    |
| 5  | 5         | 78.25000       | 5.609598 | 6  | 64.52381 | 91.97619  | 12    |
| 6  | 6         | 78.25000       | 5.609598 | 6  | 64.52381 | 91.97619  | 12    |
| 2  | 2         | 79.00000       | 2.998456 | 6  | 71.66304 | 86.33696  | 12    |
| 12 | 12        | 79.50000       | 5.609598 | 6  | 65.77381 | 93.22619  | 12    |
| 3  | 3         | 82.00000       | 2.998456 | 6  | 74.66304 | 89.33696  | 12    |
| 4  | 4         | 83.33333       | 2.998456 | 6  | 75.99637 | 90.67029  | 12    |
| 1  | 1         | 84.66667       | 2.998456 | 6  | 77.32971 | 92.00363  | 12    |
| 11 | 11        | 86.50000       | 5.609598 | 6  | 72.77381 | 100.22619 | 12    |
| 7  | 7         | 93.50000       | 5.609598 | 6  | 79.77381 | 107.22619 | 2     |

class(out1)

[1] "augmentedRCBD"

Similarly the analysis for the trait y2 can be computed as follows.

```
out2 <- augmentedRCBD(blk, trt, y2, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
```

## Augmented Design Details

=====

```
Number of blocks      "3"
Number of treatments  "12"
Number of check treatments "4"
Number of test treatments "8"
Check treatments      "1, 2, 3, 4"
```

## ANOVA, Treatment Adjusted

=====

|                                    | Df | Sum Sq | Mean Sq | F value | Pr(>F)       |
|------------------------------------|----|--------|---------|---------|--------------|
| Block (ignoring Treatments)        | 2  | 7019   | 3510    | 12.261  | 0.007597 **  |
| Treatment (eliminating Blocks)     | 11 | 58965  | 5360    | 18.727  | 0.000920 *** |
| Treatment: Check                   | 3  | 2150   | 717     | 2.504   | 0.156116     |
| Treatment: Test and Test vs. Check | 8  | 56815  | 7102    | 24.810  | 0.000473 *** |
| Residuals                          | 6  | 1717   | 286     |         |              |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

ANOVA, Block Adjusted

=====

|                                | Df | Sum Sq | Mean Sq | F value | Pr(>F)       |
|--------------------------------|----|--------|---------|---------|--------------|
| Treatment (ignoring Blocks)    | 11 | 64708  | 5883    | 20.550  | 0.000707 *** |
| Treatment: Check               | 3  | 2150   | 717     | 2.504   | 0.156116     |
| Treatment: Test                | 7  | 34863  | 4980    | 17.399  | 0.001366 **  |
| Treatment: Test vs. Check      | 1  | 27694  | 27694   | 96.749  | 6.36e-05 *** |
| Block (eliminating Treatments) | 2  | 1277   | 639     | 2.231   | 0.188645     |
| Residuals                      | 6  | 1718   | 286     |         |              |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Treatment Means

=====

|    | Treatment | Block | Means    | SE        | r | Min | Max | Adjusted Means |
|----|-----------|-------|----------|-----------|---|-----|-----|----------------|
| 1  | 1         |       | 256.0000 | 3.055050  | 3 | 250 | 260 | 256.0000       |
| 2  | 10        | 3     | 450.0000 | NA        | 1 | 450 | 450 | 437.6667       |
| 3  | 11        | 1     | 300.0000 | NA        | 1 | 300 | 300 | 299.4167       |
| 4  | 12        | 1     | 289.0000 | NA        | 1 | 289 | 289 | 288.4167       |
| 5  | 2         |       | 228.0000 | 6.110101  | 3 | 220 | 240 | 228.0000       |
| 6  | 3         |       | 247.6667 | 10.170764 | 3 | 237 | 268 | 247.6667       |
| 7  | 4         |       | 264.0000 | 18.681542 | 3 | 227 | 287 | 264.0000       |
| 8  | 5         | 2     | 281.0000 | NA        | 1 | 281 | 281 | 293.9167       |
| 9  | 6         | 3     | 395.0000 | NA        | 1 | 395 | 395 | 382.6667       |
| 10 | 7         | 1     | 347.0000 | NA        | 1 | 347 | 347 | 346.4167       |
| 11 | 8         | 3     | 226.0000 | NA        | 1 | 226 | 226 | 213.6667       |
| 12 | 9         | 2     | 311.0000 | NA        | 1 | 311 | 311 | 323.9167       |

Coefficient of Variation

=====

6.057617

Overall Adjusted Mean

=====

298.4792

Standard Errors

=====

|  | Std. Error of Diff. | CD (5%)  |
|--|---------------------|----------|
| Control Treatment Means                  | 13.81424            | 33.80224 |
| Two Test Treatments (Same Block)         | 23.92697            | 58.54719 |
| Two Test Treatments (Different Blocks)   | 26.75117            | 65.45775 |
| A Test Treatment and a Control Treatment | 21.84224            | 53.44603 |

Treatment Groups

=====

Method : lsd



|    | Treatment | Adjusted Means | SE        | df | lower.CL | upper.CL | Group |
|----|-----------|----------------|-----------|----|----------|----------|-------|
| 8  | 8         | 213.6667       | 18.274527 | 6  | 168.9505 | 258.3828 | 12    |
| 2  | 2         | 228.0000       | 9.768146  | 6  | 204.0982 | 251.9018 | 1     |
| 3  | 3         | 247.6667       | 9.768146  | 6  | 223.7649 | 271.5685 | 123   |
| 1  | 1         | 256.0000       | 9.768146  | 6  | 232.0982 | 279.9018 | 1234  |
| 4  | 4         | 264.0000       | 9.768146  | 6  | 240.0982 | 287.9018 | 234   |
| 12 | 12        | 288.4167       | 18.274527 | 6  | 243.7005 | 333.1328 | 345   |
| 5  | 5         | 293.9167       | 18.274527 | 6  | 249.2005 | 338.6328 | 345   |
| 11 | 11        | 299.4167       | 18.274527 | 6  | 254.7005 | 344.1328 | 45    |
| 9  | 9         | 323.9167       | 18.274527 | 6  | 279.2005 | 368.6328 | 56    |
| 7  | 7         | 346.4167       | 18.274527 | 6  | 301.7005 | 391.1328 | 56    |
| 6  | 6         | 382.6667       | 18.274527 | 6  | 337.9505 | 427.3828 | 67    |
| 10 | 10        | 437.6667       | 18.274527 | 6  | 392.9505 | 482.3828 | 7     |

```
class(out2)
```

```
[1] "augmentedRCBD"
```

The data can also be imported as a [data frame](#) and then used for analysis. Consider the data frame data imported from [Table 1](#) according to the instructions in [section 4.8](#).

```
str(data)
```

```
'data.frame':  20 obs. of  4 variables:
 $ blk: Factor w/ 3 levels "1","2","3": 1 1 1 1 1 1 2 2 2 ...
 $ trt: Factor w/ 12 levels "1","2","3","4",...: 1 2 3 4 7 11 12 1 2 3 ...
 $ y1 : num  92 79 87 81 96 89 82 79 81 81 ...
 $ y2 : num  258 224 238 278 347 300 289 260 220 237 ...
```

```
# 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)
```

```
Augmented Design Details
```

```
=====
```

```
Number of blocks      "3"
Number of treatments  "12"
Number of check treatments "4"
Number of test treatments "8"
Check treatments      "1, 2, 3, 4"
```

```
ANOVA, Treatment Adjusted
```

```
=====
```

|                                    | Df | Sum Sq | Mean Sq | F value | Pr(>F)   |
|------------------------------------|----|--------|---------|---------|----------|
| Block (ignoring Treatments)        | 2  | 360.1  | 180.04  | 6.675   | 0.0298 * |
| Treatment (eliminating Blocks)     | 11 | 285.1  | 25.92   | 0.961   | 0.5499   |
| Treatment: Check                   | 3  | 52.9   | 17.64   | 0.654   | 0.6092   |
| Treatment: Test and Test vs. Check | 8  | 232.2  | 29.02   | 1.076   | 0.4779   |
| Residuals                          | 6  | 161.8  | 26.97   |         |          |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

ANOVA, Block Adjusted

=====

|                                | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|--------------------------------|----|--------|---------|---------|--------|
| Treatment (ignoring Blocks)    | 11 | 575.7  | 52.33   | 1.940   | 0.215  |
| Treatment: Check               | 3  | 52.9   | 17.64   | 0.654   | 0.609  |
| Treatment: Test                | 7  | 505.9  | 72.27   | 2.679   | 0.125  |
| Treatment: Test vs. Check      | 1  | 16.9   | 16.87   | 0.626   | 0.459  |
| Block (eliminating Treatments) | 2  | 69.5   | 34.75   | 1.288   | 0.342  |
| Residuals                      | 6  | 161.8  | 26.97   |         |        |

Treatment Means

=====

|    | Treatment | Block | Means    | SE       | r | Min | Max | Adjusted Means |
|----|-----------|-------|----------|----------|---|-----|-----|----------------|
| 1  | 1         |       | 84.66667 | 3.844188 | 3 | 79  | 92  | 84.66667       |
| 2  | 10        | 3     | 74.00000 | NA       | 1 | 74  | 74  | 77.25000       |
| 3  | 11        | 1     | 89.00000 | NA       | 1 | 89  | 89  | 86.50000       |
| 4  | 12        | 1     | 82.00000 | NA       | 1 | 82  | 82  | 79.50000       |
| 5  | 2         |       | 79.00000 | 1.154701 | 3 | 77  | 81  | 79.00000       |
| 6  | 3         |       | 82.00000 | 2.645751 | 3 | 78  | 87  | 82.00000       |
| 7  | 4         |       | 83.33333 | 3.929942 | 3 | 78  | 91  | 83.33333       |
| 8  | 5         | 2     | 79.00000 | NA       | 1 | 79  | 79  | 78.25000       |
| 9  | 6         | 3     | 75.00000 | NA       | 1 | 75  | 75  | 78.25000       |
| 10 | 7         | 1     | 96.00000 | NA       | 1 | 96  | 96  | 93.50000       |
| 11 | 8         | 3     | 70.00000 | NA       | 1 | 70  | 70  | 73.25000       |
| 12 | 9         | 2     | 78.00000 | NA       | 1 | 78  | 78  | 77.25000       |

Coefficient of Variation

=====

6.372367

Overall Adjusted Mean

=====

81.0625

Standard Errors

=====

|  | Std. Error | of Diff. | CD (5%)  |
|--|------------|----------|----------|
| Control Treatment Means                  | 4.240458   |          | 10.37603 |
| Two Test Treatments (Same Block)         | 7.344688   |          | 17.97180 |
| Two Test Treatments (Different Blocks)   | 8.211611   |          | 20.09309 |
| A Test Treatment and a Control Treatment | 6.704752   |          | 16.40594 |

Treatment Groups

=====

Method : lsd

|   | Treatment | Adjusted Means | SE       | df | lower.CL | upper.CL | Group |
|---|-----------|----------------|----------|----|----------|----------|-------|
| 8 | 8         | 73.25000       | 5.609598 | 6  | 59.52381 | 86.97619 | 1     |

```

9          9          77.25000 5.609598 6 63.52381 90.97619 12
10         10         77.25000 5.609598 6 63.52381 90.97619 12
5          5          78.25000 5.609598 6 64.52381 91.97619 12
6          6          78.25000 5.609598 6 64.52381 91.97619 12
2          2          79.00000 2.998456 6 71.66304 86.33696 12
12         12         79.50000 5.609598 6 65.77381 93.22619 12
3          3          82.00000 2.998456 6 74.66304 89.33696 12
4          4          83.33333 2.998456 6 75.99637 90.67029 12
1          1          84.66667 2.998456 6 77.32971 92.00363 12
11         11         86.50000 5.609598 6 72.77381 100.22619 12
7          7          93.50000 5.609598 6 79.77381 107.22619 2

```

```
class(out1)
```

```
[1] "augmentedRCBD"
```

```
# Results for variable y2
```

```
out2 <- augmentedRCBD(data$blk, data$trt, data$y2, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
```

Augmented Design Details

=====

```

Number of blocks          "3"
Number of treatments      "12"
Number of check treatments "4"
Number of test treatments "8"
Check treatments          "1, 2, 3, 4"

```

ANOVA, Treatment Adjusted

=====

|                                    | Df | Sum Sq | Mean Sq | F value | Pr(>F)       |
|------------------------------------|----|--------|---------|---------|--------------|
| Block (ignoring Treatments)        | 2  | 7019   | 3510    | 12.261  | 0.007597 **  |
| Treatment (eliminating Blocks)     | 11 | 58965  | 5360    | 18.727  | 0.000920 *** |
| Treatment: Check                   | 3  | 2150   | 717     | 2.504   | 0.156116     |
| Treatment: Test and Test vs. Check | 8  | 56815  | 7102    | 24.810  | 0.000473 *** |
| Residuals                          | 6  | 1717   | 286     |         |              |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

ANOVA, Block Adjusted

=====

|                                | Df | Sum Sq | Mean Sq | F value | Pr(>F)       |
|--------------------------------|----|--------|---------|---------|--------------|
| Treatment (ignoring Blocks)    | 11 | 64708  | 5883    | 20.550  | 0.000707 *** |
| Treatment: Check               | 3  | 2150   | 717     | 2.504   | 0.156116     |
| Treatment: Test                | 7  | 34863  | 4980    | 17.399  | 0.001366 **  |
| Treatment: Test vs. Check      | 1  | 27694  | 27694   | 96.749  | 6.36e-05 *** |
| Block (eliminating Treatments) | 2  | 1277   | 639     | 2.231   | 0.188645     |
| Residuals                      | 6  | 1718   | 286     |         |              |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Treatment Means

=====

|    | Treatment | Block | Means    | SE        | r | Min | Max | Adjusted Means |
|----|-----------|-------|----------|-----------|---|-----|-----|----------------|
| 1  | 1         |       | 256.0000 | 3.055050  | 3 | 250 | 260 | 256.0000       |
| 2  | 10        | 3     | 450.0000 | NA        | 1 | 450 | 450 | 437.6667       |
| 3  | 11        | 1     | 300.0000 | NA        | 1 | 300 | 300 | 299.4167       |
| 4  | 12        | 1     | 289.0000 | NA        | 1 | 289 | 289 | 288.4167       |
| 5  | 2         |       | 228.0000 | 6.110101  | 3 | 220 | 240 | 228.0000       |
| 6  | 3         |       | 247.6667 | 10.170764 | 3 | 237 | 268 | 247.6667       |
| 7  | 4         |       | 264.0000 | 18.681542 | 3 | 227 | 287 | 264.0000       |
| 8  | 5         | 2     | 281.0000 | NA        | 1 | 281 | 281 | 293.9167       |
| 9  | 6         | 3     | 395.0000 | NA        | 1 | 395 | 395 | 382.6667       |
| 10 | 7         | 1     | 347.0000 | NA        | 1 | 347 | 347 | 346.4167       |
| 11 | 8         | 3     | 226.0000 | NA        | 1 | 226 | 226 | 213.6667       |
| 12 | 9         | 2     | 311.0000 | NA        | 1 | 311 | 311 | 323.9167       |

## Coefficient of Variation

=====

6.057617

## Overall Adjusted Mean

=====

298.4792

## Standard Errors

=====

|  | Std. Error of Diff. | CD (5%)  |
|--|---------------------|----------|
| Control Treatment Means                  | 13.81424            | 33.80224 |
| Two Test Treatments (Same Block)         | 23.92697            | 58.54719 |
| Two Test Treatments (Different Blocks)   | 26.75117            | 65.45775 |
| A Test Treatment and a Control Treatment | 21.84224            | 53.44603 |

## Treatment Groups

=====

Method : lsd

|    | Treatment | Adjusted Means | SE        | df | lower.CL | upper.CL | Group |
|----|-----------|----------------|-----------|----|----------|----------|-------|
| 8  | 8         | 213.6667       | 18.274527 | 6  | 168.9505 | 258.3828 | 12    |
| 2  | 2         | 228.0000       | 9.768146  | 6  | 204.0982 | 251.9018 | 1     |
| 3  | 3         | 247.6667       | 9.768146  | 6  | 223.7649 | 271.5685 | 123   |
| 1  | 1         | 256.0000       | 9.768146  | 6  | 232.0982 | 279.9018 | 1234  |
| 4  | 4         | 264.0000       | 9.768146  | 6  | 240.0982 | 287.9018 | 234   |
| 12 | 12        | 288.4167       | 18.274527 | 6  | 243.7005 | 333.1328 | 345   |
| 5  | 5         | 293.9167       | 18.274527 | 6  | 249.2005 | 338.6328 | 345   |
| 11 | 11        | 299.4167       | 18.274527 | 6  | 254.7005 | 344.1328 | 45    |
| 9  | 9         | 323.9167       | 18.274527 | 6  | 279.2005 | 368.6328 | 56    |
| 7  | 7         | 346.4167       | 18.274527 | 6  | 301.7005 | 391.1328 | 56    |
| 6  | 6         | 382.6667       | 18.274527 | 6  | 337.9505 | 427.3828 | 67    |
| 10 | 10        | 437.6667       | 18.274527 | 6  | 392.9505 | 482.3828 | 7     |

```
class(out2)
```

```
[1] "augmentedRCBD"
```

Check genotypes are inferred by default on the basis of number of replications. However, if some test genotypes are also replicated, they may also be falsely detected as checks. To avoid this, the checks can be specified by the `checks` argument.

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

#### Augmented Design Details

```
=====
```

```
Number of blocks      "3"
Number of treatments  "12"
Number of check treatments "4"
Number of test treatments "8"
Check treatments      "1, 2, 3, 4"
```

#### ANOVA, Treatment Adjusted

```
=====
```

|                                    | Df | Sum Sq | Mean Sq | F value | Pr(>F)   |
|------------------------------------|----|--------|---------|---------|----------|
| Block (ignoring Treatments)        | 2  | 360.1  | 180.04  | 6.675   | 0.0298 * |
| Treatment (eliminating Blocks)     | 11 | 285.1  | 25.92   | 0.961   | 0.5499   |
| Treatment: Check                   | 3  | 52.9   | 17.64   | 0.654   | 0.6092   |
| Treatment: Test and Test vs. Check | 8  | 232.2  | 29.02   | 1.076   | 0.4779   |
| Residuals                          | 6  | 161.8  | 26.97   |         |          |

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#### ANOVA, Block Adjusted

```
=====
```

|                                | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|--------------------------------|----|--------|---------|---------|--------|
| Treatment (ignoring Blocks)    | 11 | 575.7  | 52.33   | 1.940   | 0.215  |
| Treatment: Check               | 3  | 52.9   | 17.64   | 0.654   | 0.609  |
| Treatment: Test                | 7  | 505.9  | 72.27   | 2.679   | 0.125  |
| Treatment: Test vs. Check      | 1  | 16.9   | 16.87   | 0.626   | 0.459  |
| Block (eliminating Treatments) | 2  | 69.5   | 34.75   | 1.288   | 0.342  |
| Residuals                      | 6  | 161.8  | 26.97   |         |        |

#### Treatment Means

```
=====
```

|   | Treatment | Block | Means    | SE       | r | Min | Max | Adjusted Means |
|---|-----------|-------|----------|----------|---|-----|-----|----------------|
| 1 | 1         |       | 84.66667 | 3.844188 | 3 | 79  | 92  | 84.66667       |
| 2 | 10        | 3     | 74.00000 | NA       | 1 | 74  | 74  | 77.25000       |
| 3 | 11        | 1     | 89.00000 | NA       | 1 | 89  | 89  | 86.50000       |
| 4 | 12        | 1     | 82.00000 | NA       | 1 | 82  | 82  | 79.50000       |
| 5 | 2         |       | 79.00000 | 1.154701 | 3 | 77  | 81  | 79.00000       |
| 6 | 3         |       | 82.00000 | 2.645751 | 3 | 78  | 87  | 82.00000       |

|    |   |            |          |   |    |    |          |
|----|---|------------|----------|---|----|----|----------|
| 7  | 4 | 83.33333   | 3.929942 | 3 | 78 | 91 | 83.33333 |
| 8  | 5 | 2 79.00000 | NA       | 1 | 79 | 79 | 78.25000 |
| 9  | 6 | 3 75.00000 | NA       | 1 | 75 | 75 | 78.25000 |
| 10 | 7 | 1 96.00000 | NA       | 1 | 96 | 96 | 93.50000 |
| 11 | 8 | 3 70.00000 | NA       | 1 | 70 | 70 | 73.25000 |
| 12 | 9 | 2 78.00000 | NA       | 1 | 78 | 78 | 77.25000 |

Coefficient of Variation

=====

6.372367

Overall Adjusted Mean

=====

81.0625

Standard Errors

=====

Std. Error of Diff. CD (5%)

|  |          |          |
|--|----------|----------|
| Control Treatment Means                  | 4.240458 | 10.37603 |
| Two Test Treatments (Same Block)         | 7.344688 | 17.97180 |
| Two Test Treatments (Different Blocks)   | 8.211611 | 20.09309 |
| A Test Treatment and a Control Treatment | 6.704752 | 16.40594 |

Treatment Groups

=====

Method : lsd

|    | Treatment | Adjusted Means | SE       | df | lower.CL | upper.CL  | Group |
|----|-----------|----------------|----------|----|----------|-----------|-------|
| 8  | 8         | 73.25000       | 5.609598 | 6  | 59.52381 | 86.97619  | 1     |
| 9  | 9         | 77.25000       | 5.609598 | 6  | 63.52381 | 90.97619  | 12    |
| 10 | 10        | 77.25000       | 5.609598 | 6  | 63.52381 | 90.97619  | 12    |
| 5  | 5         | 78.25000       | 5.609598 | 6  | 64.52381 | 91.97619  | 12    |
| 6  | 6         | 78.25000       | 5.609598 | 6  | 64.52381 | 91.97619  | 12    |
| 2  | 2         | 79.00000       | 2.998456 | 6  | 71.66304 | 86.33696  | 12    |
| 12 | 12        | 79.50000       | 5.609598 | 6  | 65.77381 | 93.22619  | 12    |
| 3  | 3         | 82.00000       | 2.998456 | 6  | 74.66304 | 89.33696  | 12    |
| 4  | 4         | 83.33333       | 2.998456 | 6  | 75.99637 | 90.67029  | 12    |
| 1  | 1         | 84.66667       | 2.998456 | 6  | 77.32971 | 92.00363  | 12    |
| 11 | 11        | 86.50000       | 5.609598 | 6  | 72.77381 | 100.22619 | 12    |
| 7  | 7         | 93.50000       | 5.609598 | 6  | 79.77381 | 107.22619 | 2     |

# Results for variable y2 (checks specified)

```
out2 <- augmentedRCBD(data$blk, data$trt, data$y2, method.comp = "lsd",
  alpha = 0.05, group = TRUE, console = TRUE,
  checks = c("1", "2", "3", "4"))
```

Augmented Design Details

=====

Number of blocks "3"

Number of treatments "12"  
 Number of check treatments "4"  
 Number of test treatments "8"  
 Check treatments "1, 2, 3, 4"

## ANOVA, Treatment Adjusted

=====

|                                    | Df | Sum Sq | Mean Sq | F value | Pr(>F)       |
|------------------------------------|----|--------|---------|---------|--------------|
| Block (ignoring Treatments)        | 2  | 7019   | 3510    | 12.261  | 0.007597 **  |
| Treatment (eliminating Blocks)     | 11 | 58965  | 5360    | 18.727  | 0.000920 *** |
| Treatment: Check                   | 3  | 2150   | 717     | 2.504   | 0.156116     |
| Treatment: Test and Test vs. Check | 8  | 56815  | 7102    | 24.810  | 0.000473 *** |
| Residuals                          | 6  | 1717   | 286     |         |              |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## ANOVA, Block Adjusted

=====

|                                | Df | Sum Sq | Mean Sq | F value | Pr(>F)       |
|--------------------------------|----|--------|---------|---------|--------------|
| Treatment (ignoring Blocks)    | 11 | 64708  | 5883    | 20.550  | 0.000707 *** |
| Treatment: Check               | 3  | 2150   | 717     | 2.504   | 0.156116     |
| Treatment: Test                | 7  | 34863  | 4980    | 17.399  | 0.001366 **  |
| Treatment: Test vs. Check      | 1  | 27694  | 27694   | 96.749  | 6.36e-05 *** |
| Block (eliminating Treatments) | 2  | 1277   | 639     | 2.231   | 0.188645     |
| Residuals                      | 6  | 1718   | 286     |         |              |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Treatment Means

=====

|    | Treatment | Block | Means    | SE        | r | Min | Max | Adjusted Means |
|----|-----------|-------|----------|-----------|---|-----|-----|----------------|
| 1  | 1         |       | 256.0000 | 3.055050  | 3 | 250 | 260 | 256.0000       |
| 2  | 10        | 3     | 450.0000 | NA        | 1 | 450 | 450 | 437.6667       |
| 3  | 11        | 1     | 300.0000 | NA        | 1 | 300 | 300 | 299.4167       |
| 4  | 12        | 1     | 289.0000 | NA        | 1 | 289 | 289 | 288.4167       |
| 5  | 2         |       | 228.0000 | 6.110101  | 3 | 220 | 240 | 228.0000       |
| 6  | 3         |       | 247.6667 | 10.170764 | 3 | 237 | 268 | 247.6667       |
| 7  | 4         |       | 264.0000 | 18.681542 | 3 | 227 | 287 | 264.0000       |
| 8  | 5         | 2     | 281.0000 | NA        | 1 | 281 | 281 | 293.9167       |
| 9  | 6         | 3     | 395.0000 | NA        | 1 | 395 | 395 | 382.6667       |
| 10 | 7         | 1     | 347.0000 | NA        | 1 | 347 | 347 | 346.4167       |
| 11 | 8         | 3     | 226.0000 | NA        | 1 | 226 | 226 | 213.6667       |
| 12 | 9         | 2     | 311.0000 | NA        | 1 | 311 | 311 | 323.9167       |

## Coefficient of Variation

=====

6.057617

## Overall Adjusted Mean

=====

298.4792

## Standard Errors

=====

|  |  | Std. Error of Diff. | CD (5%)  |
|--|--|---------------------|----------|
| Control Treatment Means                  |  | 13.81424            | 33.80224 |
| Two Test Treatments (Same Block)         |  | 23.92697            | 58.54719 |
| Two Test Treatments (Different Blocks)   |  | 26.75117            | 65.45775 |
| A Test Treatment and a Control Treatment |  | 21.84224            | 53.44603 |

## Treatment Groups

=====

Method : lsd

|    | Treatment | Adjusted Means | SE        | df | lower.CL | upper.CL | Group |
|----|-----------|----------------|-----------|----|----------|----------|-------|
| 8  | 8         | 213.6667       | 18.274527 | 6  | 168.9505 | 258.3828 | 12    |
| 2  | 2         | 228.0000       | 9.768146  | 6  | 204.0982 | 251.9018 | 1     |
| 3  | 3         | 247.6667       | 9.768146  | 6  | 223.7649 | 271.5685 | 123   |
| 1  | 1         | 256.0000       | 9.768146  | 6  | 232.0982 | 279.9018 | 1234  |
| 4  | 4         | 264.0000       | 9.768146  | 6  | 240.0982 | 287.9018 | 234   |
| 12 | 12        | 288.4167       | 18.274527 | 6  | 243.7005 | 333.1328 | 345   |
| 5  | 5         | 293.9167       | 18.274527 | 6  | 249.2005 | 338.6328 | 345   |
| 11 | 11        | 299.4167       | 18.274527 | 6  | 254.7005 | 344.1328 | 45    |
| 9  | 9         | 323.9167       | 18.274527 | 6  | 279.2005 | 368.6328 | 56    |
| 7  | 7         | 346.4167       | 18.274527 | 6  | 301.7005 | 391.1328 | 56    |
| 6  | 6         | 382.6667       | 18.274527 | 6  | 337.9505 | 427.3828 | 67    |
| 10 | 10        | 437.6667       | 18.274527 | 6  | 392.9505 | 482.3828 | 7     |

In case the large number of treatments or genotypes, it is advisable to avoid treatment 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.

7.2 `print.augmentedRCBD()`

The results of analysis in an object of class `augmentedRCBD` can be printed to the console as follows.

```
# Print results for variable y1
print(out1)
```

## Augmented Design Details

=====

```
Number of blocks      "3"
Number of treatments  "12"
Number of check treatments "4"
Number of test treatments "8"
Check treatments      "1, 2, 3, 4"
```

## ANOVA, Treatment Adjusted

=====

|                                | Df | Sum Sq | Mean Sq | F value | Pr(>F)   |
|--------------------------------|----|--------|---------|---------|----------|
| Block (ignoring Treatments)    | 2  | 360.1  | 180.04  | 6.675   | 0.0298 * |
| Treatment (eliminating Blocks) | 11 | 285.1  | 25.92   | 0.961   | 0.5499   |



```

Treatment: Check          3   52.9   17.64   0.654 0.6092
Treatment: Test and Test vs. Check  8  232.2   29.02   1.076 0.4779
Residuals                 6  161.8   26.97

```

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ANOVA, Block Adjusted
```

```
=====
```

|                                | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|--------------------------------|----|--------|---------|---------|--------|
| Treatment (ignoring Blocks)    | 11 | 575.7  | 52.33   | 1.940   | 0.215  |
| Treatment: Check               | 3  | 52.9   | 17.64   | 0.654   | 0.609  |
| Treatment: Test                | 7  | 505.9  | 72.27   | 2.679   | 0.125  |
| Treatment: Test vs. Check      | 1  | 16.9   | 16.87   | 0.626   | 0.459  |
| Block (eliminating Treatments) | 2  | 69.5   | 34.75   | 1.288   | 0.342  |
| Residuals                      | 6  | 161.8  | 26.97   |         |        |

```
Treatment Means
```

```
=====
```

|    | Treatment | Block | Means    | SE       | r | Min | Max | Adjusted Means |
|----|-----------|-------|----------|----------|---|-----|-----|----------------|
| 1  | 1         |       | 84.66667 | 3.844188 | 3 | 79  | 92  | 84.66667       |
| 2  | 10        | 3     | 74.00000 | NA       | 1 | 74  | 74  | 77.25000       |
| 3  | 11        | 1     | 89.00000 | NA       | 1 | 89  | 89  | 86.50000       |
| 4  | 12        | 1     | 82.00000 | NA       | 1 | 82  | 82  | 79.50000       |
| 5  | 2         |       | 79.00000 | 1.154701 | 3 | 77  | 81  | 79.00000       |
| 6  | 3         |       | 82.00000 | 2.645751 | 3 | 78  | 87  | 82.00000       |
| 7  | 4         |       | 83.33333 | 3.929942 | 3 | 78  | 91  | 83.33333       |
| 8  | 5         | 2     | 79.00000 | NA       | 1 | 79  | 79  | 78.25000       |
| 9  | 6         | 3     | 75.00000 | NA       | 1 | 75  | 75  | 78.25000       |
| 10 | 7         | 1     | 96.00000 | NA       | 1 | 96  | 96  | 93.50000       |
| 11 | 8         | 3     | 70.00000 | NA       | 1 | 70  | 70  | 73.25000       |
| 12 | 9         | 2     | 78.00000 | NA       | 1 | 78  | 78  | 77.25000       |

```
Coefficient of Variation
```

```
=====
```

```
6.372367
```

```
Overall Adjusted Mean
```

```
=====
```

```
81.0625
```

```
Standard Errors
```

```
=====
```

|  | Std. Error | of Diff. | CD (5%)  |
|--|------------|----------|----------|
| Control Treatment Means                  | 4.240458   |          | 10.37603 |
| Two Test Treatments (Same Block)         | 7.344688   |          | 17.97180 |
| Two Test Treatments (Different Blocks)   | 8.211611   |          | 20.09309 |
| A Test Treatment and a Control Treatment | 6.704752   |          | 16.40594 |

```
Treatment Groups
```

```
=====
```

```
Method : lsd
```

|    | Treatment | Adjusted Means | SE       | df | lower.CL | upper.CL  | Group |
|----|-----------|----------------|----------|----|----------|-----------|-------|
| 8  | 8         | 73.25000       | 5.609598 | 6  | 59.52381 | 86.97619  | 1     |
| 9  | 9         | 77.25000       | 5.609598 | 6  | 63.52381 | 90.97619  | 12    |
| 10 | 10        | 77.25000       | 5.609598 | 6  | 63.52381 | 90.97619  | 12    |
| 5  | 5         | 78.25000       | 5.609598 | 6  | 64.52381 | 91.97619  | 12    |
| 6  | 6         | 78.25000       | 5.609598 | 6  | 64.52381 | 91.97619  | 12    |
| 2  | 2         | 79.00000       | 2.998456 | 6  | 71.66304 | 86.33696  | 12    |
| 12 | 12        | 79.50000       | 5.609598 | 6  | 65.77381 | 93.22619  | 12    |
| 3  | 3         | 82.00000       | 2.998456 | 6  | 74.66304 | 89.33696  | 12    |
| 4  | 4         | 83.33333       | 2.998456 | 6  | 75.99637 | 90.67029  | 12    |
| 1  | 1         | 84.66667       | 2.998456 | 6  | 77.32971 | 92.00363  | 12    |
| 11 | 11        | 86.50000       | 5.609598 | 6  | 72.77381 | 100.22619 | 12    |
| 7  | 7         | 93.50000       | 5.609598 | 6  | 79.77381 | 107.22619 | 2     |

```
# Print results for variable y2
print(out2)
```

#### Augmented Design Details

```
=====
```

```
Number of blocks      "3"
Number of treatments  "12"
Number of check treatments "4"
Number of test treatments "8"
Check treatments      "1, 2, 3, 4"
```

#### ANOVA, Treatment Adjusted

```
=====
```

|                                    | Df | Sum Sq | Mean Sq | F value | Pr(>F)       |
|------------------------------------|----|--------|---------|---------|--------------|
| Block (ignoring Treatments)        | 2  | 7019   | 3510    | 12.261  | 0.007597 **  |
| Treatment (eliminating Blocks)     | 11 | 58965  | 5360    | 18.727  | 0.000920 *** |
| Treatment: Check                   | 3  | 2150   | 717     | 2.504   | 0.156116     |
| Treatment: Test and Test vs. Check | 8  | 56815  | 7102    | 24.810  | 0.000473 *** |
| Residuals                          | 6  | 1717   | 286     |         |              |

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#### ANOVA, Block Adjusted

```
=====
```

|                                | Df | Sum Sq | Mean Sq | F value | Pr(>F)       |
|--------------------------------|----|--------|---------|---------|--------------|
| Treatment (ignoring Blocks)    | 11 | 64708  | 5883    | 20.550  | 0.000707 *** |
| Treatment: Check               | 3  | 2150   | 717     | 2.504   | 0.156116     |
| Treatment: Test                | 7  | 34863  | 4980    | 17.399  | 0.001366 **  |
| Treatment: Test vs. Check      | 1  | 27694  | 27694   | 96.749  | 6.36e-05 *** |
| Block (eliminating Treatments) | 2  | 1277   | 639     | 2.231   | 0.188645     |
| Residuals                      | 6  | 1718   | 286     |         |              |

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#### Treatment Means

```
=====
```

|    | Treatment | Block | Means    | SE        | r | Min | Max | Adjusted Means |
|----|-----------|-------|----------|-----------|---|-----|-----|----------------|
| 1  | 1         |       | 256.0000 | 3.055050  | 3 | 250 | 260 | 256.0000       |
| 2  | 10        | 3     | 450.0000 | NA        | 1 | 450 | 450 | 437.6667       |
| 3  | 11        | 1     | 300.0000 | NA        | 1 | 300 | 300 | 299.4167       |
| 4  | 12        | 1     | 289.0000 | NA        | 1 | 289 | 289 | 288.4167       |
| 5  | 2         |       | 228.0000 | 6.110101  | 3 | 220 | 240 | 228.0000       |
| 6  | 3         |       | 247.6667 | 10.170764 | 3 | 237 | 268 | 247.6667       |
| 7  | 4         |       | 264.0000 | 18.681542 | 3 | 227 | 287 | 264.0000       |
| 8  | 5         | 2     | 281.0000 | NA        | 1 | 281 | 281 | 293.9167       |
| 9  | 6         | 3     | 395.0000 | NA        | 1 | 395 | 395 | 382.6667       |
| 10 | 7         | 1     | 347.0000 | NA        | 1 | 347 | 347 | 346.4167       |
| 11 | 8         | 3     | 226.0000 | NA        | 1 | 226 | 226 | 213.6667       |
| 12 | 9         | 2     | 311.0000 | NA        | 1 | 311 | 311 | 323.9167       |

Coefficient of Variation

=====

6.057617

Overall Adjusted Mean

=====

298.4792

Standard Errors

=====

Std. Error of Diff. CD (5%)

|  |          |          |
|--|----------|----------|
| Control Treatment Means                  | 13.81424 | 33.80224 |
| Two Test Treatments (Same Block)         | 23.92697 | 58.54719 |
| Two Test Treatments (Different Blocks)   | 26.75117 | 65.45775 |
| A Test Treatment and a Control Treatment | 21.84224 | 53.44603 |

Treatment Groups

=====

Method : lsd

|    | Treatment | Adjusted Means | SE        | df | lower.CL | upper.CL | Group |
|----|-----------|----------------|-----------|----|----------|----------|-------|
| 8  | 8         | 213.6667       | 18.274527 | 6  | 168.9505 | 258.3828 | 12    |
| 2  | 2         | 228.0000       | 9.768146  | 6  | 204.0982 | 251.9018 | 1     |
| 3  | 3         | 247.6667       | 9.768146  | 6  | 223.7649 | 271.5685 | 123   |
| 1  | 1         | 256.0000       | 9.768146  | 6  | 232.0982 | 279.9018 | 1234  |
| 4  | 4         | 264.0000       | 9.768146  | 6  | 240.0982 | 287.9018 | 234   |
| 12 | 12        | 288.4167       | 18.274527 | 6  | 243.7005 | 333.1328 | 345   |
| 5  | 5         | 293.9167       | 18.274527 | 6  | 249.2005 | 338.6328 | 345   |
| 11 | 11        | 299.4167       | 18.274527 | 6  | 254.7005 | 344.1328 | 45    |
| 9  | 9         | 323.9167       | 18.274527 | 6  | 279.2005 | 368.6328 | 56    |
| 7  | 7         | 346.4167       | 18.274527 | 6  | 301.7005 | 391.1328 | 56    |
| 6  | 6         | 382.6667       | 18.274527 | 6  | 337.9505 | 427.3828 | 67    |
| 10 | 10        | 437.6667       | 18.274527 | 6  | 392.9505 | 482.3828 | 7     |

### 7.3 `describe.augmentedRCBD()`

The descriptive statistics such as count, mean, standard error, minimum, maximum, skewness (with p-value from D'Agostino test of skewness (D'Agostino (1970))) and kurtosis (with p-value from Anscombe-Glynn test of kurtosis (Anscombe and Glynn (1983))) for the adjusted means from the results in an object of class `augmentedRCBD` can be computed as follows.

```
# Descriptive statistics for variable y1  
describe.augmentedRCBD(out1)
```

```
$Count
```

```
[1] 12
```

```
$Mean
```

```
[1] 81.0625
```

```
$Std.Error
```

```
[1] 1.547002
```

```
$Std.Deviation
```

```
[1] 5.358973
```

```
$Min
```

```
[1] 73.25
```

```
$Max
```

```
[1] 93.5
```

```
$`Skewness(statistic)`
```

```
      skew      z
```

```
0.9250344 1.6745760
```

```
$`Skewness(p.value)`
```

```
[1] 0.09401746
```

```
$`Kurtosis(statistic)`
```

```
      kurt      z
```

```
3.522807 1.282305
```

```
$`Kurtosis(p.value)`
```

```
[1] 0.1997357
```

```
# Descriptive statistics for variable y2  
describe.augmentedRCBD(out2)
```

```
$Count
```

```
[1] 12
```

```
$Mean
```

```
[1] 298.4792
```

```
$Std.Error
```

```
[1] 18.92257
```

```
$Std.Deviation
[1] 65.5497

$Min
[1] 213.6667

$Max
[1] 437.6667

$`Skewness(statistic)`
      skew      z
0.7449405 1.3680211

$`Skewness(p.value)`
[1] 0.1713055

$`Kurtosis(statistic)`
      kurt      z
2.787997 0.536812

$`Kurtosis(p.value)`
[1] 0.5913975
```

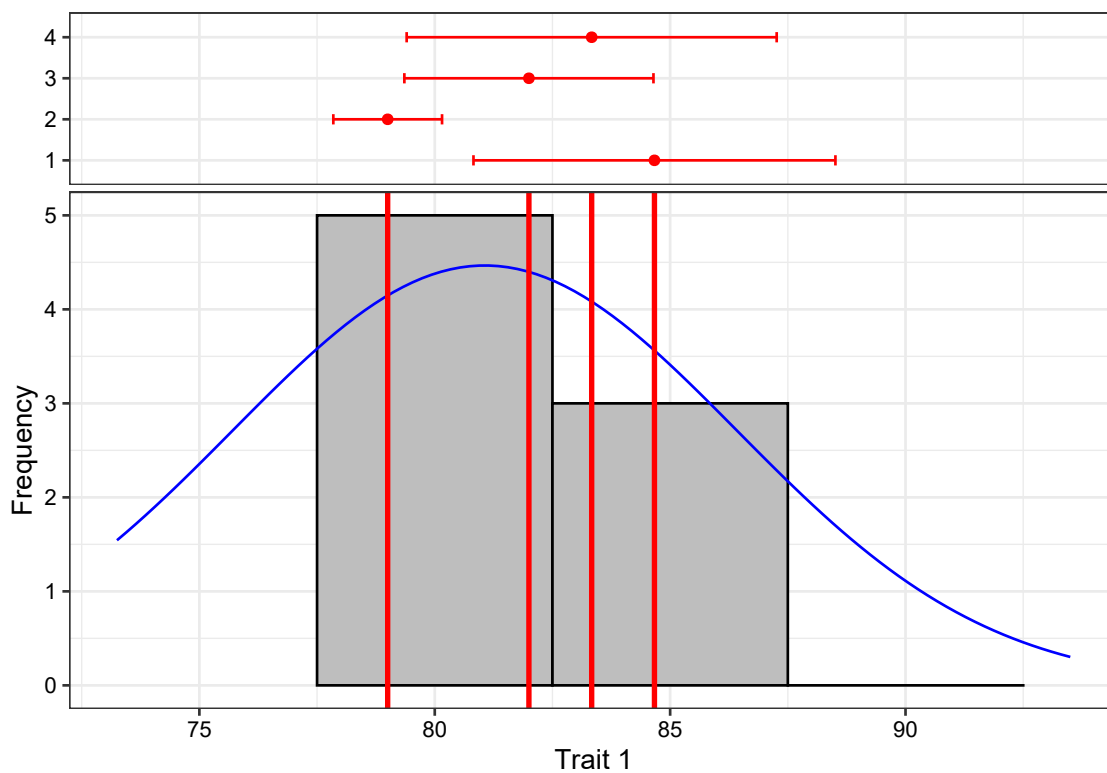
#### 7.4 `freqdist.augmentedRCBD()`

The frequency distribution of the adjusted means from the results in an object of class `augmentedRCBD` can be plotted as follows.

```
# Frequency distribution for variable y1
freq1 <- freqdist.augmentedRCBD(out1, xlab = "Trait 1")
```

Warning: Removed 2 rows containing missing values (geom\_bar).

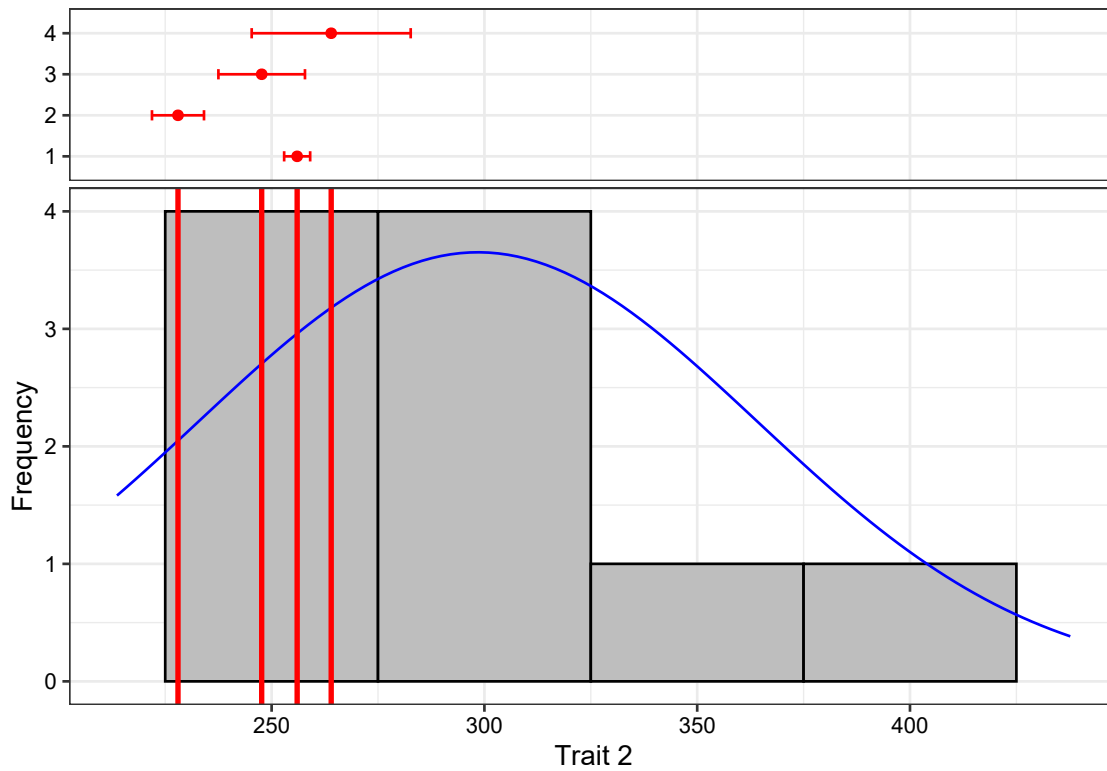
```
plot(freq1)
```



```
# Frequency distribution for variable y2
freq2 <- freqdist.augmentedRCBD(out2, xlab = "Trait 2")
```

Warning: Removed 2 rows containing missing values (geom\_bar).

```
plot(freq2)
```



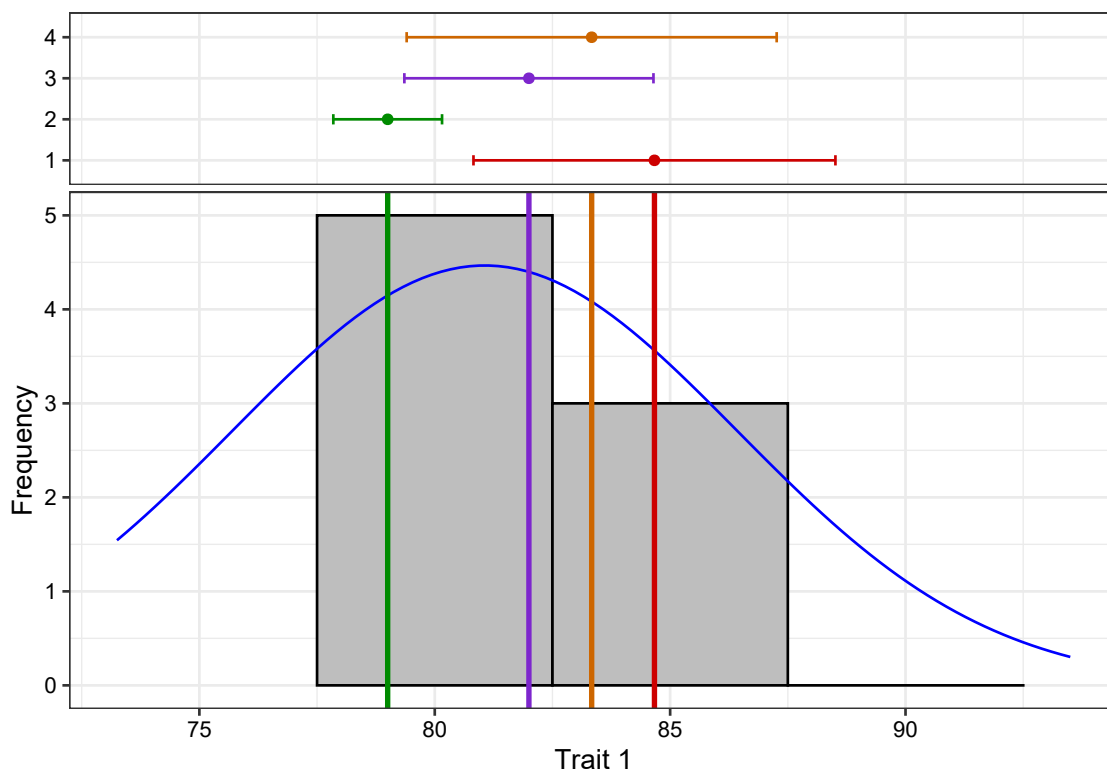
The colours for the check values may be specified using the argument `check.col`.

```
colset <- c("red3", "green4", "purple3", "darkorange3")

# Frequency distribution for variable y1
freq1 <- freqdist.augmentedRCBD(out1, xlab = "Trait 1", check.col = colset)
```

Warning: Removed 2 rows containing missing values (geom\_bar).

```
plot(freq1)
```

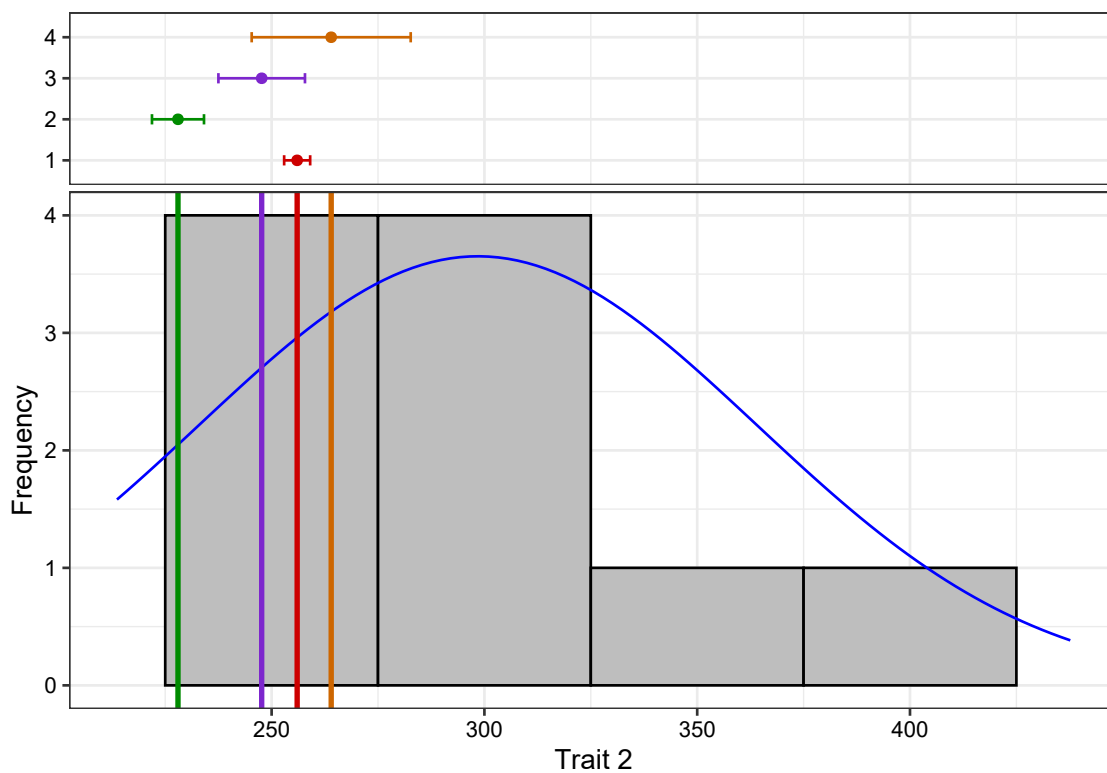


```
# Frequency distribution for variable y2
freq2 <- freqdist.augmentedRCBD(out2, xlab = "Trait 2", check.col = colset)
```

Warning: Removed 2 rows containing missing values (geom\_bar).

```
plot(freq2)
```



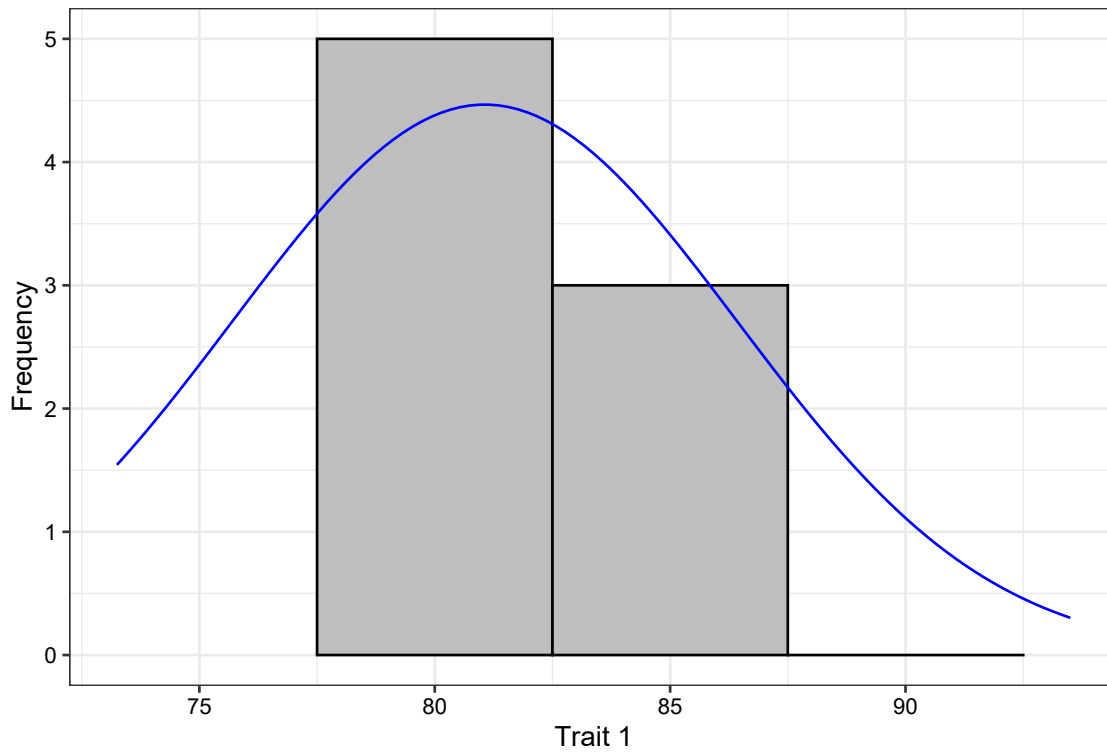


The default the check highlighting can be avoided using the argument `highlight.check = FALSE`.

```
# Frequency distribution for variable y1
freq1 <- freqdist.augmentedRCBD(out1, xlab = "Trait 1",
                                highlight.check = FALSE)
```

Warning: Removed 2 rows containing missing values (geom\_bar).

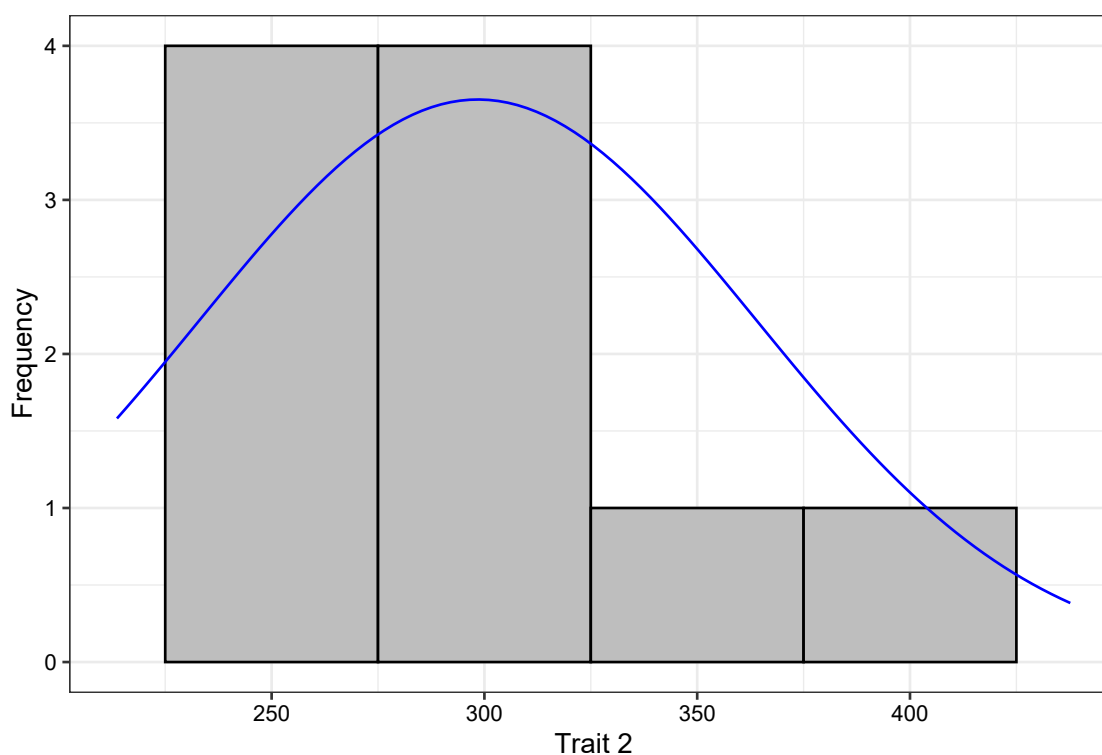
```
plot(freq1)
```



```
# Frequency distribution for variable y2
freq2 <- freqdist.augmentedRCBD(out2, xlab = "Trait 2",
                                highlight.check = FALSE)
```

Warning: Removed 2 rows containing missing values (geom\_bar).

```
plot(freq2)
```



### 7.5 `gva.augmentedRCBD()`

The genetic variability statistics such as mean, phenotypic, genotypic and environmental variation (Federer and Searle (1976)), phenotypic, genotypic and environmental coefficient of variation (Burton (1951), Burton (1952)), category of phenotypic and genotypic coefficient of variation according to Sivasubramaniam and Madhavamenon (1973), broad-sense heritability ( $H^2$ ) (Lush (1940)),  $H^2$  category according to Robinson (1966), Genetic advance (GA), genetic advance as per cent of mean (GAM) and GAM category according to Johnson et al. (1955) are computed from an object of class `augmentedRCBD` as follows.

```
# Genetic variability statistics for variable y1
gva.augmentedRCBD(out1)
```

```
$Mean
```

```
[1] 81.0625
```

```
$PV
```

```
[1] 72.26786
```

```
$GV
```

```
[1] 45.29563
```

```
$EV
```

```
[1] 26.97222
```

```
$GCV
```

```
[1] 8.302487

$`GCV category`
[1] "Low"

$PCV
[1] 10.48703

$`PCV category`
[1] "Medium"

$ECV
[1] 6.406759

$hBS
[1] 62.67743

$hBS category`
[1] "High"

$GA
[1] 10.99216

$GAM
[1] 13.5601

$`GAM category`
[1] "Medium"

# Genetic variability statistics for variable y2
gva.augmentedRCBD(out2)

$Mean
[1] 298.4792

$PV
[1] 4980.411

$GV
[1] 4694.161

$EV
[1] 286.25

$GCV
[1] 22.95435

$`GCV category`
[1] "High"

$PCV
[1] 23.64387
```

```
$`PCV` category`  
[1] "High"
```

```
$ECV  
[1] 5.668377
```

```
$hBS  
[1] 94.25248
```

```
$`hBS` category`  
[1] "High"
```

```
$GA  
[1] 137.2223
```

```
$GAM  
[1] 45.97382
```

```
$`GAM` category`  
[1] "High"
```

## 7.5 `report.augmentedRCBD()`

The results generated by the analysis can be exported to a MS Word file as follows.

```
# MS word report for variable y1  
report.augmentedRCBD(aug = out1,  
                      target = file.path(tempdir(), "augmentedRCBD output - y1.docx"))  
  
# MS word report for variable y2  
report.augmentedRCBD(aug = out1,  
                      target = file.path(tempdir(), "augmentedRCBD output - y2.docx"))
```

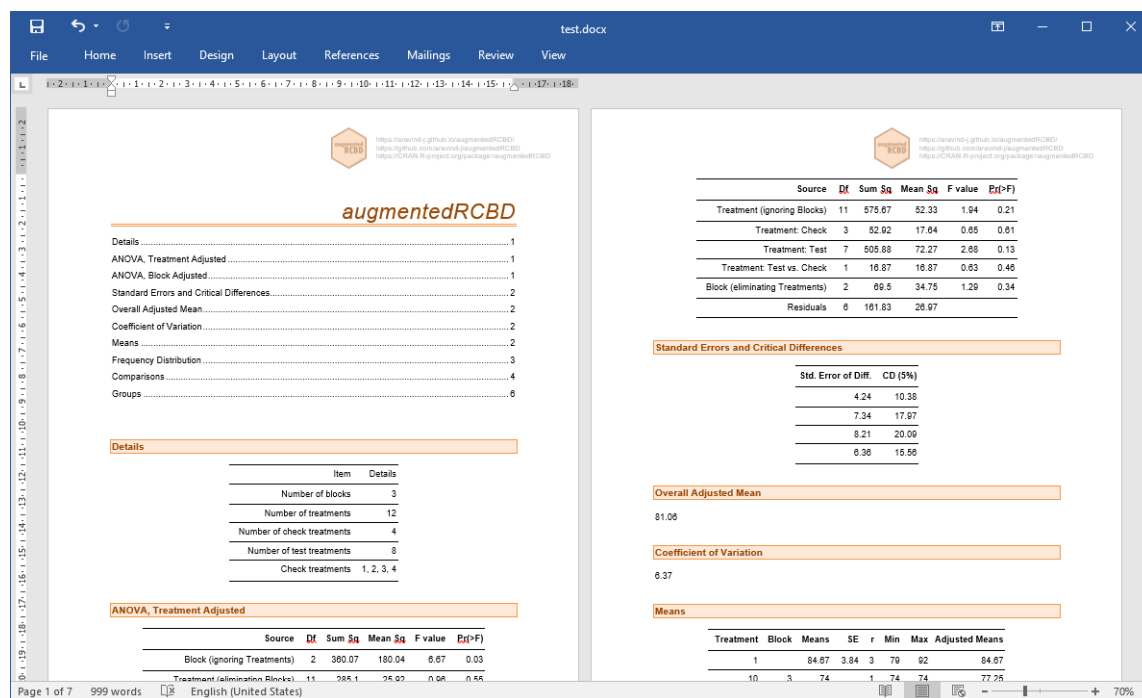


Fig. 6: MS Word report generated with `report.augmentedRCBD` function.

## 8 Data Analysis for a Multiple Traits

Analysis of data for a multiple traits simultaneously can be performed by using `augmentedRCBD.bulk` function. It generates an object of class `augmentedRCBD.bulk`. Such an object can then be taken as input by `print.augmentedRCBD.bulk` to print the results to console. The results can also be exported as a MS Word report using the `report.augmentedRCBD.bulk` function.

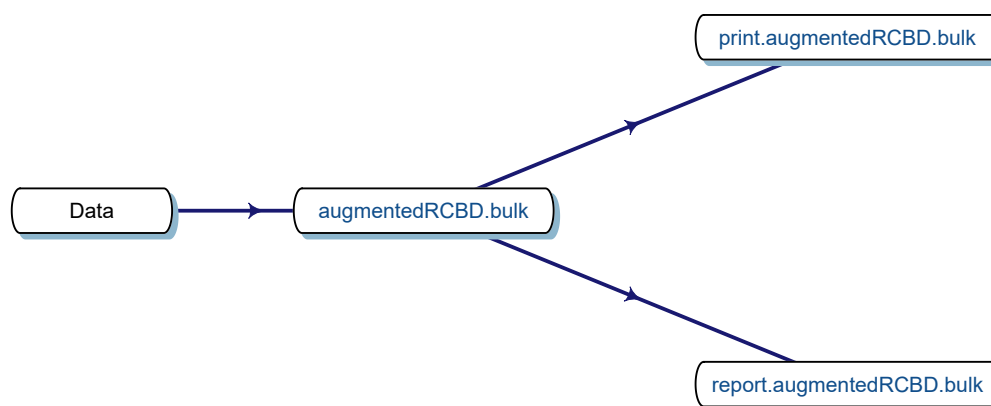


Fig. 7. Workflow for analysis of multiple traits with `augmentedRCBD`.

### 8.1 `augmentedRCBD.bulk()`

Consider the data frame `data` imported from [Table 1](#) according to the instructions in [section 4.8](#).

```
str(data)
```

```
'data.frame':  20 obs. of  4 variables:
 $ blk: Factor w/ 3 levels "1","2","3": 1 1 1 1 1 1 1 2 2 2 ...
 $ trt: Factor w/ 12 levels "1","2","3","4",...: 1 2 3 4 7 11 12 1 2 3 ...
 $ y1 : num  92 79 87 81 96 89 82 79 81 81 ...
 $ y2 : num  258 224 238 278 347 300 289 260 220 237 ...
```

```
# Convert block and treatment to factors
data$blk <- as.factor(data$blk)
data$trt <- as.factor(data$trt)
```

Rather than performing the analysis individually for each variable/trait separately using `augmentedRCBD`, the analysis can be performed simultaneously for both the traits using `augmentedRCBD.bulk` function. It is a wrapper around the `augmentedRCBD` core function and its associated helper functions.

However 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.

The logical arguments `describe`, `freqdist` and `gva` can be used to specify whether to generate the descriptive statistics, frequency distribution plots and genetic variability statistics respectively. If `gva =`

TRUE, then plots to compare phenotypic and genotypic coefficient of variation, broad sense heritability and genetic advance over mean between traits are also generated.

```
bout <- augmentedRCBD.bulk(data = data, 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)
```

ANOVA for y1 computed (1/2)

ANOVA for y2 computed (2/2)

Augmented Design Details

=====

|                            |              |
|----------------------------|--------------|
| Number of blocks           | "3"          |
| Number of treatments       | "12"         |
| Number of check treatments | "4"          |
| Number of test treatments  | "8"          |
| Check treatments           | "1, 2, 3, 4" |
| Number of traits           | "2"          |
| Traits                     | "y1, y2"     |

ANOVA, Treatment Adjusted

=====

|   | Source                             | Df |          | y1         | y2 |
|---|------------------------------------|----|----------|------------|----|
| 1 | Block (ignoring Treatments)        | 2  | 180.04 * | 3509.67 ** |    |
| 2 | Treatment (eliminating Blocks)     | 11 | 25.92 ns | 5360.49 ** |    |
| 3 | Treatment: Check                   | 3  | 17.64 ns | 716.75 ns  |    |
| 4 | Treatment: Test and Test vs. Check | 8  | 29.02 ns | 7101.89 ** |    |
| 5 | Residuals                          | 6  | 26.97    | 286.25     |    |

ANOVA, Block Adjusted

=====

|   | Source                         | Df |          | y1          | y2 |
|---|--------------------------------|----|----------|-------------|----|
| 1 | Treatment (ignoring Blocks)    | 11 | 52.33 ns | 5882.5 **   |    |
| 2 | Treatment: Check               | 3  | 17.64 ns | 716.75 ns   |    |
| 3 | Treatment: Test vs. Check      | 1  | 16.87 ns | 27694.41 ** |    |
| 4 | Treatment: Test                | 7  | 72.27 ns | 4980.41 **  |    |
| 5 | Block (eliminating Treatments) | 2  | 34.75 ns | 638.58 ns   |    |
| 6 | Residuals                      | 6  | 26.97    | 286.25      |    |

Coefficient of Variation

=====

|   | Trait | CV   |
|---|-------|------|
| 1 | y1    | 6.37 |
| 2 | y2    | 6.06 |



## Overall Adjusted Mean

=====

|   | Trait | Overall.adjusted.mean |
|---|-------|-----------------------|
| 1 | y1    | 81.06                 |
| 2 | y2    | 298.48                |

## Standard Errors

=====

|   |  | Comparison | y1   | y2    |
|---|--|------------|------|-------|
| 1 | A Test Treatment and a Control Treatment |            | 6.7  | 21.84 |
| 2 | Control Treatment Means                  |            | 4.24 | 13.81 |
| 3 | Two Test Treatments (Different Blocks)   |            | 8.21 | 26.75 |
| 4 | Two Test Treatments (Same Block)         |            | 7.34 | 23.93 |

## Critical Difference

=====

|   |  | Comparison | y1    | y2    |
|---|--|------------|-------|-------|
| 1 | A Test Treatment and a Control Treatment |            | 16.41 | 53.45 |
| 2 | Control Treatment Means                  |            | 10.38 | 33.8  |
| 3 | Two Test Treatments (Different Blocks)   |            | 20.09 | 65.46 |
| 4 | Two Test Treatments (Same Block)         |            | 17.97 | 58.55 |

## Descriptive Statistics

=====

|   | Trait | Count | Mean   | Std.Error | Std.Deviation | Min    | Max    | Skewness | Kurtosis |
|---|-------|-------|--------|-----------|---------------|--------|--------|----------|----------|
| 1 | y1    | 12    | 81.06  | 1.55      | 5.36          | 73.25  | 93.5   | 0.93 ns  | 3.52 ns  |
| 2 | y2    | 12    | 298.48 | 18.92     | 65.55         | 213.67 | 437.67 | 0.74 ns  | 2.79 ns  |

## Genetic Variability Analysis

=====

|   | Trait        | Mean   | PV      | GV           | EV     | GCV   | GCV.category | PCV   | PCV.category | ECV  | hBS   |
|---|--------------|--------|---------|--------------|--------|-------|--------------|-------|--------------|------|-------|
| 1 | y1           | 81.06  | 72.27   | 45.3         | 26.97  | 8.3   | Low          | 10.49 | Medium       | 6.41 | 62.68 |
| 2 | y2           | 298.48 | 4980.41 | 4694.16      | 286.25 | 22.95 | High         | 23.64 | High         | 5.67 | 94.25 |
|   | hBS.category | GA     | GAM     | GAM.category |        |       |              |       |              |      |       |
| 1 | High         | 10.99  | 13.56   | Medium       |        |       |              |       |              |      |       |
| 2 | High         | 137.22 | 45.97   | High         |        |       |              |       |              |      |       |

## Warning Messages

=====

y1  
Removed 2 rows containing missing values (geom\_bar).  
y2  
Removed 2 rows containing missing values (geom\_bar).

## Treatment Means

=====

| Treatment | y1 | y2 |
|-----------|----|----|
|-----------|----|----|

```

1      1 84.67 256
2     10 77.25 437.67
3     11 86.5 299.42
4     12 79.5 288.42
5      2 79 228
6      3 82 247.67
7      4 83.33 264
8      5 78.25 293.92
9      6 78.25 382.67
10     7 93.5 346.42
11     8 73.25 213.67
12     9 77.25 323.92

```

## 8.2 `print.augmentedRCBD.bulk()`

The results of analysis in an object of class `augmentedRCBD.bulk` can be printed to the console as follows.

```

# Print results
print(bout)

```

### Augmented Design Details

```
=====
```

```

Number of blocks      "3"
Number of treatments  "12"
Number of check treatments "4"
Number of test treatments "8"
Check treatments      "1, 2, 3, 4"
Number of traits      "2"
Traits                "y1, y2"

```

### ANOVA, Treatment Adjusted

```
=====
```

|   |                                    | Source | Df     |    | y1      |    | y2 |
|---|------------------------------------|--------|--------|----|---------|----|----|
| 1 | Block (ignoring Treatments)        | 2      | 180.04 | *  | 3509.67 | ** |    |
| 2 | Treatment (eliminating Blocks)     | 11     | 25.92  | ns | 5360.49 | ** |    |
| 3 | Treatment: Check                   | 3      | 17.64  | ns | 716.75  | ns |    |
| 4 | Treatment: Test and Test vs. Check | 8      | 29.02  | ns | 7101.89 | ** |    |
| 5 | Residuals                          | 6      | 26.97  |    | 286.25  |    |    |

### ANOVA, Block Adjusted

```
=====
```

|   |                                | Source | Df    |    | y1       |    | y2 |
|---|--------------------------------|--------|-------|----|----------|----|----|
| 1 | Treatment (ignoring Blocks)    | 11     | 52.33 | ns | 5882.5   | ** |    |
| 2 | Treatment: Check               | 3      | 17.64 | ns | 716.75   | ns |    |
| 3 | Treatment: Test vs. Check      | 1      | 16.87 | ns | 27694.41 | ** |    |
| 4 | Treatment: Test                | 7      | 72.27 | ns | 4980.41  | ** |    |
| 5 | Block (eliminating Treatments) | 2      | 34.75 | ns | 638.58   | ns |    |
| 6 | Residuals                      | 6      | 26.97 |    | 286.25   |    |    |

### Coefficient of Variation

=====

|   | Trait | CV   |
|---|-------|------|
| 1 | y1    | 6.37 |
| 2 | y2    | 6.06 |

Overall Adjusted Mean

=====

|   | Trait | Overall.adjusted.mean |
|---|-------|-----------------------|
| 1 | y1    | 81.06                 |
| 2 | y2    | 298.48                |

Standard Errors

=====

|   |  | Comparison | y1   | y2    |
|---|--|------------|------|-------|
| 1 | A Test Treatment and a Control Treatment |            | 6.7  | 21.84 |
| 2 | Control Treatment Means                  |            | 4.24 | 13.81 |
| 3 | Two Test Treatments (Different Blocks)   |            | 8.21 | 26.75 |
| 4 | Two Test Treatments (Same Block)         |            | 7.34 | 23.93 |

Critical Difference

=====

|   |  | Comparison | y1    | y2    |
|---|--|------------|-------|-------|
| 1 | A Test Treatment and a Control Treatment |            | 16.41 | 53.45 |
| 2 | Control Treatment Means                  |            | 10.38 | 33.8  |
| 3 | Two Test Treatments (Different Blocks)   |            | 20.09 | 65.46 |
| 4 | Two Test Treatments (Same Block)         |            | 17.97 | 58.55 |

Descriptive Statistics

=====

|   | Trait | Count | Mean   | Std.Error | Std.Deviation | Min    | Max    | Skewness | Kurtosis |
|---|-------|-------|--------|-----------|---------------|--------|--------|----------|----------|
| 1 | y1    | 12    | 81.06  | 1.55      | 5.36          | 73.25  | 93.5   | 0.93 ns  | 3.52 ns  |
| 2 | y2    | 12    | 298.48 | 18.92     | 65.55         | 213.67 | 437.67 | 0.74 ns  | 2.79 ns  |

Genetic Variability Analysis

=====

|   | Trait        | Mean   | PV      | GV           | EV     | GCV   | GCV.category | PCV   | PCV.category | ECV  | hBS   |
|---|--------------|--------|---------|--------------|--------|-------|--------------|-------|--------------|------|-------|
| 1 | y1           | 81.06  | 72.27   | 45.3         | 26.97  | 8.3   | Low          | 10.49 | Medium       | 6.41 | 62.68 |
| 2 | y2           | 298.48 | 4980.41 | 4694.16      | 286.25 | 22.95 | High         | 23.64 | High         | 5.67 | 94.25 |
|   | hBS.category | GA     | GAM     | GAM.category |        |       |              |       |              |      |       |
| 1 | High         | 10.99  | 13.56   | Medium       |        |       |              |       |              |      |       |
| 2 | High         | 137.22 | 45.97   | High         |        |       |              |       |              |      |       |

Warning Messages

=====

y1  
Removed 2 rows containing missing values (geom\_bar).

y2

Removed 2 rows containing missing values (geom\_bar).

## Treatment Means

=====

|    | Treatment | y1    | y2     |
|----|-----------|-------|--------|
| 1  | 1         | 84.67 | 256    |
| 2  | 10        | 77.25 | 437.67 |
| 3  | 11        | 86.5  | 299.42 |
| 4  | 12        | 79.5  | 288.42 |
| 5  | 2         | 79    | 228    |
| 6  | 3         | 82    | 247.67 |
| 7  | 4         | 83.33 | 264    |
| 8  | 5         | 78.25 | 293.92 |
| 9  | 6         | 78.25 | 382.67 |
| 10 | 7         | 93.5  | 346.42 |
| 11 | 8         | 73.25 | 213.67 |
| 12 | 9         | 77.25 | 323.92 |

## 8.3 report.augmentedRCBD.bulk()

The results generated by the analysis can be exported to a MS Word file as follows.

# MS word report

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

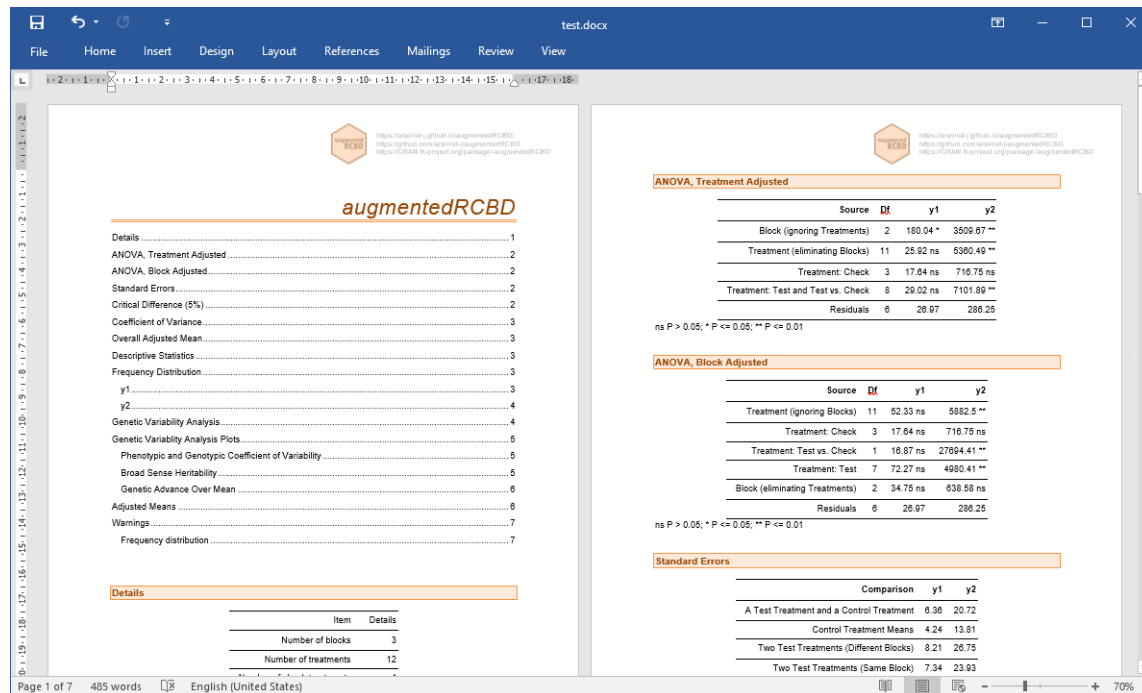


Fig. 8: MS Word report generated with report.augmentedRCBD.bulk function.

## 9 Citing augmentedRCBD

To cite the R package 'augmentedRCBD' in publications use:

```
Aravind, J., Mukesh Sankar, S., Wankhede, D. P., and Kaur, V. (2020).  
augmentedRCBD: Analysis of Augmented Randomised Complete Block Designs. R package  
version 0.1.1.9000,  
https://aravind-j.github.io/augmentedRCBD/https://cran.r-project.org/package=augmentedRCBD.
```

A BibTeX entry for LaTeX users is

```
@Manual{,  
  title = {augmentedRCBD: Analysis of Augmented Randomised Complete Block Designs},  
  author = {J. Aravind and S. {Mukesh Sankar} and Dhammaprakash Pandhari Wankhede and Vikender Kaur},  
  year = {2020},  
  note = {R package version 0.1.1.9000},  
  note = {https://aravind-j.github.io/augmentedRCBD/},  
  note = {https://cran.r-project.org/package=augmentedRCBD},  
}
```

This free and open-source software implements academic research by the authors and co-workers. If you use it, please support the project by citing the package.

## 10 Session Info

```
sessionInfo()
```

```
R Under development (unstable) (2019-11-08 r77393)  
Platform: x86_64-w64-mingw32/x64 (64-bit)  
Running under: Windows 10 x64 (build 18362)
```

```
Matrix products: default
```

```
locale:  
[1] LC_COLLATE=English_India.1252  LC_CTYPE=English_India.1252    LC_MONETARY=English_India.1252  
[4] LC_NUMERIC=C                  LC_TIME=English_India.1252
```

```
attached base packages:  
[1] stats      graphics  grDevices  utils      datasets  methods   base
```

```
other attached packages:  
[1] diagram_1.6.4          shape_1.4.4            augmentedRCBD_0.1.1.9000
```

```
loaded via a namespace (and not attached):  
[1] bitops_1.0-6           fs_1.3.1               usethis_1.5.1          devtools_2.2.1  
[5] httr_1.4.1             rprojroot_1.3-2        tools_4.0.0            backports_1.1.5  
[9] R6_2.4.1              lazyeval_0.2.2         colorspace_1.4-1       withr_2.1.2  
[13] tidyselect_0.2.5       prettyunits_1.1.1      processx_3.4.1         emmeans_1.4.3.01  
[17] moments_0.14          curl_4.3               compiler_4.0.0         cli_2.0.1  
[21] flextable_0.5.6       xml2_1.2.2             desc_1.2.0             officer_0.3.6
```

|                       |                    |                   |                   |
|-----------------------|--------------------|-------------------|-------------------|
| [25] sandwich_2.5-1   | labeling_0.3       | scales_1.1.0      | mvtnorm_1.0-12    |
| [29] callr_3.4.1      | multcompView_0.1-8 | commonmark_1.7    | systemfonts_0.1.1 |
| [33] stringr_1.4.0    | digest_0.6.23      | rmarkdown_2.1     | base64enc_0.1-3   |
| [37] pkgconfig_2.0.3  | htmltools_0.4.0    | bibtex_0.4.2.2    | sessioninfo_1.1.1 |
| [41] highr_0.8        | rlang_0.4.3        | rstudioapi_0.10   | farver_2.0.3      |
| [45] zoo_1.8-7        | dplyr_0.8.3        | zip_2.0.4         | RCurl_1.95-4.12   |
| [49] magrittr_1.5     | Matrix_1.2-18      | Rcpp_1.0.3        | munsell_0.5.0     |
| [53] fansi_0.4.1      | gdtools_0.2.1      | lifecycle_0.1.0   | stringi_1.4.5     |
| [57] multcomp_1.4-12  | yaml_2.2.0         | gbRd_0.4-11       | MASS_7.3-51.5     |
| [61] pkgbuild_1.0.6   | plyr_1.8.5         | grid_4.0.0        | crayon_1.3.4      |
| [65] lattice_0.20-38  | splines_4.0.0      | knitr_1.28        | ps_1.3.0          |
| [69] pillar_1.4.3     | uuid_0.1-2         | estimability_1.3  | reshape2_1.4.3    |
| [73] codetools_0.2-16 | pkgload_1.0.2      | XML_3.99-0.3      | glue_1.3.1        |
| [77] packrat_0.5.0    | evaluate_0.14      | data.table_1.12.8 | remotes_2.1.0     |
| [81] Rdpack_0.11-1    | testthat_2.3.1     | gtable_0.3.0      | purrr_0.3.3       |
| [85] assertthat_0.2.1 | ggplot2_3.2.1      | xfun_0.12         | xtable_1.8-4      |
| [89] coda_0.19-3      | roxygen2_7.0.2     | survival_3.1-8    | tibble_2.1.3      |
| [93] tinytex_0.19.2   | memoise_1.1.0      | TH.data_1.0-10    | ellipsis_0.3.0    |

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