Data Analysis with `augmentedRCBD`

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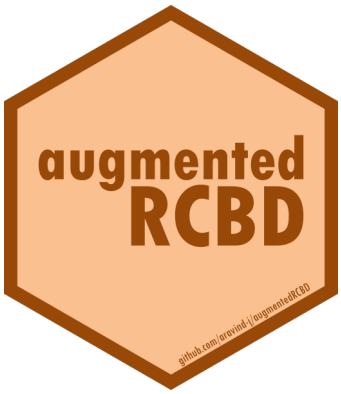
1 Overview



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

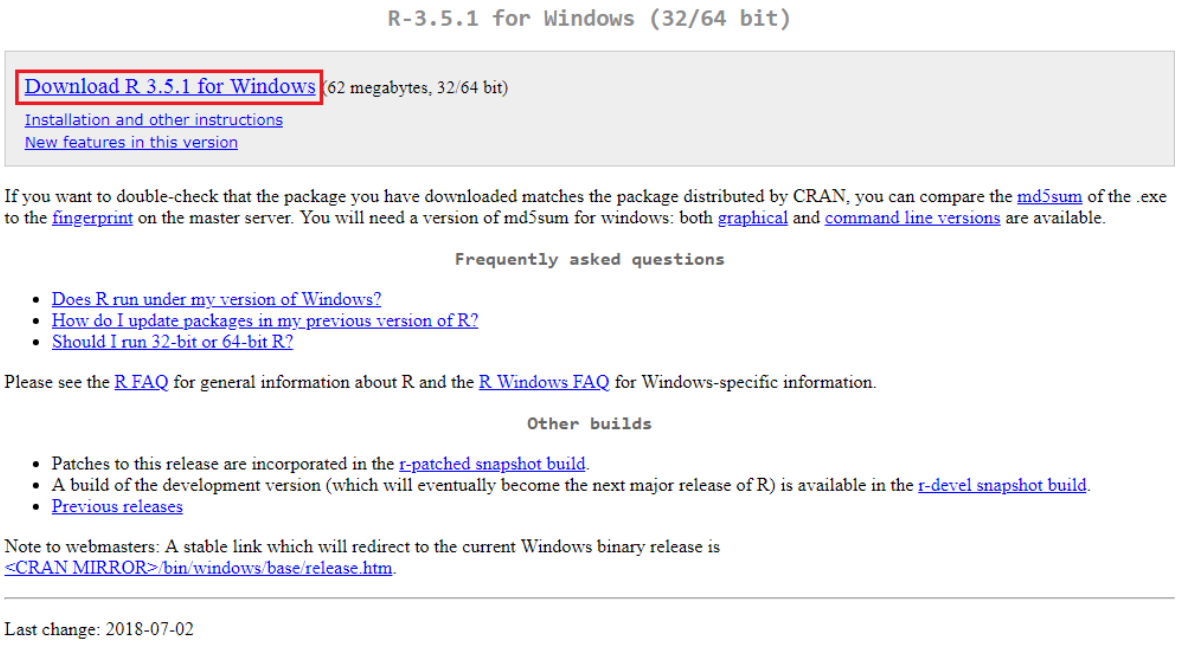
diverse library of add-on packages extending its ability as well as the incredible community support. It is one of the most popular tools being used in academia today (Tippmann, 2015).

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.

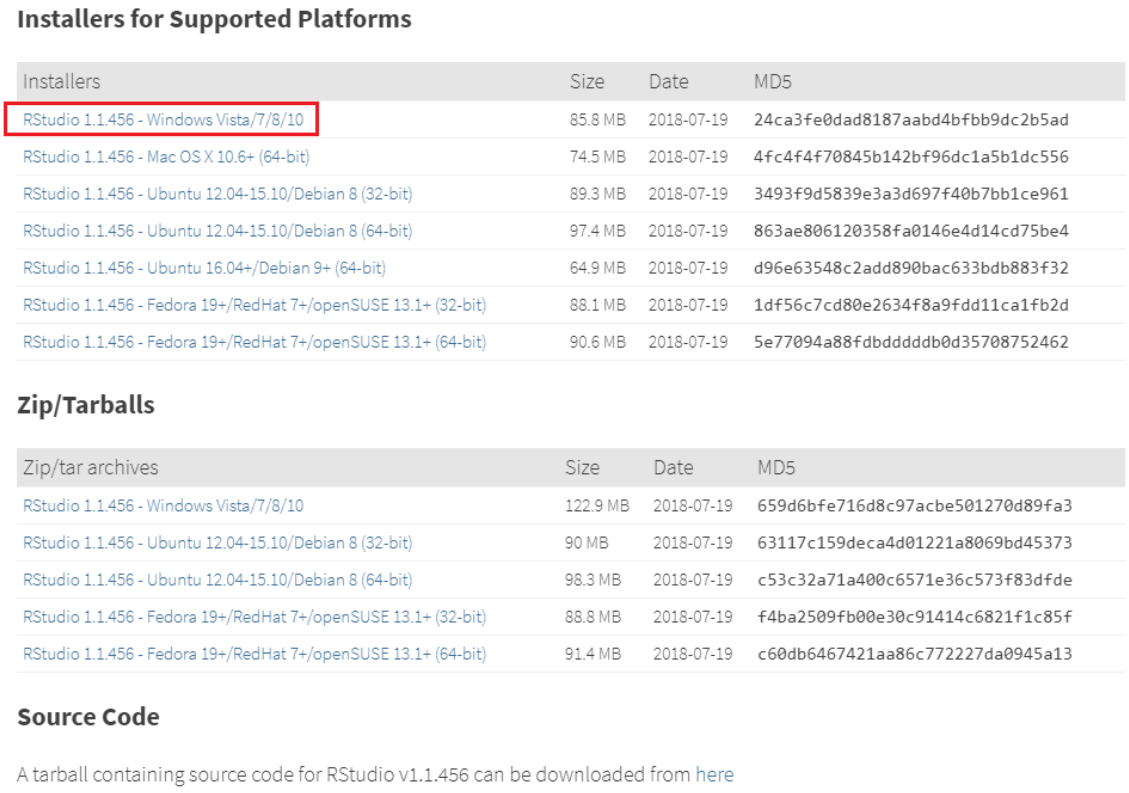
Last change: 2018-07-02

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	24ca3fe0dad8187aabd4bfbb9dc2b5ad
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	5e77094a88fdbdddddb0d35708752462

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.

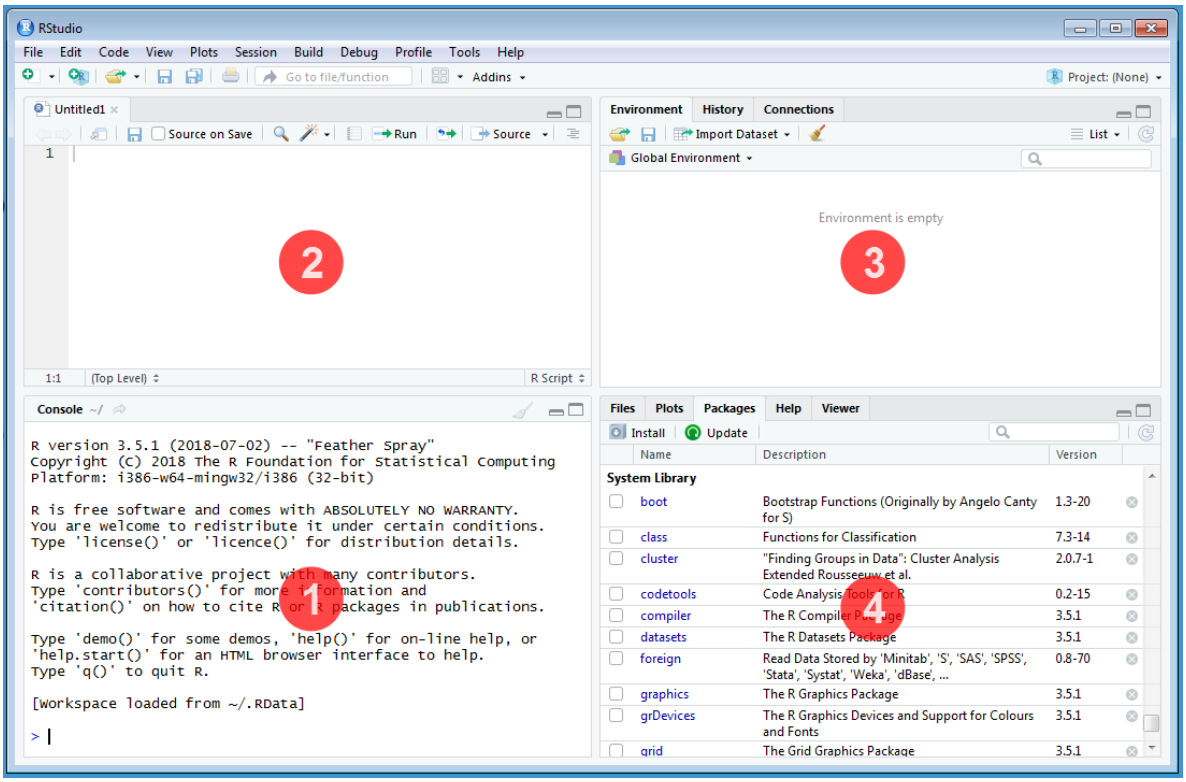


Fig. 3: The default **RStudio** interface with the four panes.

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 but-

tons 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" "array"
```

```
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: chr  "A" "B" "C" "D"
 $ x: num  1 1 1 1
 $ y: int  1 2 3 4
 $ z: chr  "This" "is" "a" "data frame"
```

```
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"
```

```
df$z
```

```
[1] "This"       "is"         "a"          "data frame"
```

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 19118 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

blk	trt	y1	y2
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 0.1.5. The previous versions are as follows.

Table 2. Version history of augmentedRCBD R package.

Version	Date
0.1.0	2018-07-10
0.1.1	2019-07-21
0.1.2	2020-03-19
0.1.3	2020-07-27
0.1.4	2021-02-17

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.

Block I	G12	**G4**	G11	**G2**	**G1**	G7	**G3**
	82	81	89	79	92	96	87
Block II	G5	G9	–	**G3**	**G1**	**G2**	**G4**
	79	78	–	81	79	81	91
Block III	**G4**	**G2**	**G1**	G6	G10	**G3**	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 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 III	G 2	77	240
Block III	G 3	78	268

Block	Treatment	Trait1	Trait2
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 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.

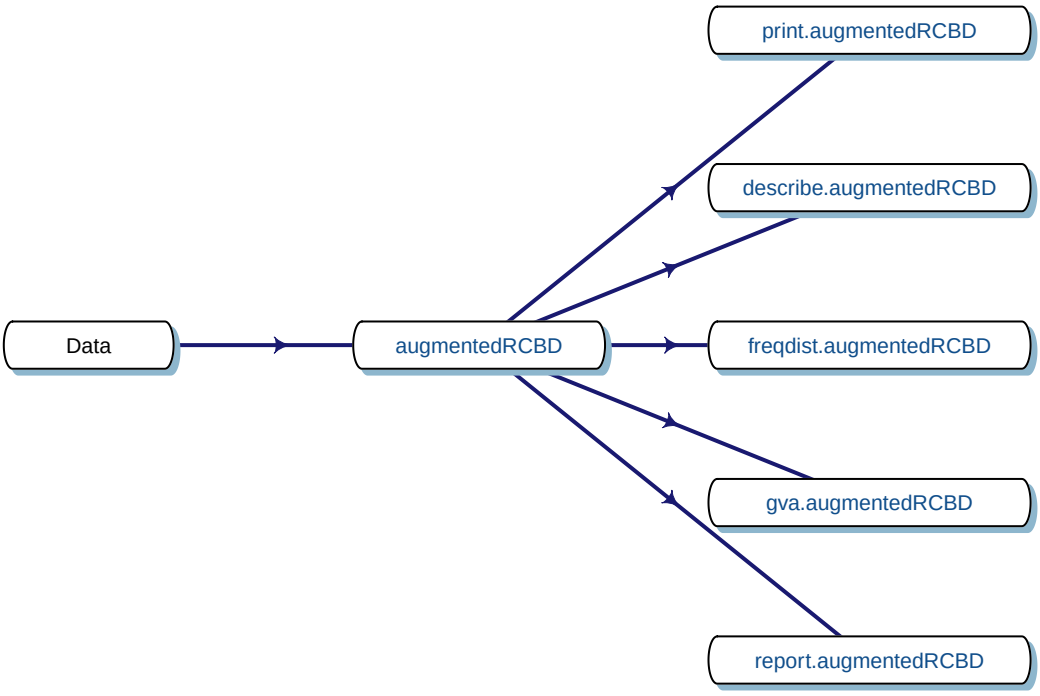


Fig. 4. Workflow for analysis of single traits with **augmentedRCBD**.

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

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 Means
===============
   Treatment Block Means   SE r   Min   Max Adjusted Means
1          1       84.67 3.84 3 79.00 92.00          84.67
2         10     3 74.00 <NA> 1 74.00 74.00          77.25
3         11     1 89.00 <NA> 1 89.00 89.00          86.50
4         12     1 82.00 <NA> 1 82.00 82.00          79.50
5          2       79.00 1.15 3 77.00 81.00          79.00
6          3       82.00 2.65 3 78.00 87.00          82.00
7          4       83.33 3.93 3 78.00 91.00          83.33
```

```
8          5     2 79.00 <NA> 1 79.00 79.00          78.25
9          6     3 75.00 <NA> 1 75.00 75.00          78.25
10         7     1 96.00 <NA> 1 96.00 96.00          93.50
11         8     3 70.00 <NA> 1 70.00 70.00          73.25
12         9     2 78.00 <NA> 1 78.00 78.00          77.25

Comparisons
===================

Method : lsd

                    contrast estimate   SE df t.ratio p.value sig
1    treatment1 - treatment2     5.67 4.24  6   1.336   0.230
2    treatment1 - treatment3     2.67 4.24  6   0.629   0.553
3    treatment1 - treatment4     1.33 4.24  6   0.314   0.764
4    treatment1 - treatment5     6.42 6.36  6   1.009   0.352
5    treatment1 - treatment6     6.42 6.36  6   1.009   0.352
6    treatment1 - treatment7    -8.83 6.36  6  -1.389   0.214
7    treatment1 - treatment8    11.42 6.36  6   1.795   0.123
8    treatment1 - treatment9     7.42 6.36  6   1.166   0.288
9   treatment1 - treatment10     7.42 6.36  6   1.166   0.288
10  treatment1 - treatment11    -1.83 6.36  6  -0.288   0.783
11  treatment1 - treatment12     5.17 6.36  6   0.812   0.448
12   treatment2 - treatment3    -3.00 4.24  6  -0.707   0.506
13   treatment2 - treatment4    -4.33 4.24  6  -1.022   0.346
14   treatment2 - treatment5     0.75 6.36  6   0.118   0.910
15   treatment2 - treatment6     0.75 6.36  6   0.118   0.910
16   treatment2 - treatment7   -14.50 6.36  6  -2.280   0.063
17   treatment2 - treatment8     5.75 6.36  6   0.904   0.401
18   treatment2 - treatment9     1.75 6.36  6   0.275   0.792
19  treatment2 - treatment10     1.75 6.36  6   0.275   0.792
20  treatment2 - treatment11    -7.50 6.36  6  -1.179   0.283
21  treatment2 - treatment12    -0.50 6.36  6  -0.079   0.940
22   treatment3 - treatment4    -1.33 4.24  6  -0.314   0.764
23   treatment3 - treatment5     3.75 6.36  6   0.590   0.577
24   treatment3 - treatment6     3.75 6.36  6   0.590   0.577
25   treatment3 - treatment7   -11.50 6.36  6  -1.808   0.121
26   treatment3 - treatment8     8.75 6.36  6   1.376   0.218
27   treatment3 - treatment9     4.75 6.36  6   0.747   0.483
28  treatment3 - treatment10     4.75 6.36  6   0.747   0.483
29  treatment3 - treatment11    -4.50 6.36  6  -0.707   0.506
30  treatment3 - treatment12     2.50 6.36  6   0.393   0.708
31   treatment4 - treatment5     5.08 6.36  6   0.799   0.455
32   treatment4 - treatment6     5.08 6.36  6   0.799   0.455
33   treatment4 - treatment7   -10.17 6.36  6  -1.598   0.161
34   treatment4 - treatment8    10.08 6.36  6   1.585   0.164
35   treatment4 - treatment9     6.08 6.36  6   0.956   0.376
36  treatment4 - treatment10     6.08 6.36  6   0.956   0.376
37  treatment4 - treatment11    -3.17 6.36  6  -0.498   0.636
38  treatment4 - treatment12     3.83 6.36  6   0.603   0.569
39   treatment5 - treatment6     0.00 8.21  6   0.000   1.000
40   treatment5 - treatment7   -15.25 8.21  6  -1.857   0.113
```

```
41   treatment5 - treatment8     5.00 8.21  6   0.609   0.565
42   treatment5 - treatment9     1.00 7.34  6   0.136   0.896
43  treatment5 - treatment10     1.00 8.21  6   0.122   0.907
44  treatment5 - treatment11    -8.25 8.21  6  -1.005   0.354
45  treatment5 - treatment12    -1.25 8.21  6  -0.152   0.884
46   treatment6 - treatment7   -15.25 8.21  6  -1.857   0.113
47   treatment6 - treatment8     5.00 7.34  6   0.681   0.521
48   treatment6 - treatment9     1.00 8.21  6   0.122   0.907
49  treatment6 - treatment10     1.00 7.34  6   0.136   0.896
50  treatment6 - treatment11    -8.25 8.21  6  -1.005   0.354
51  treatment6 - treatment12    -1.25 8.21  6  -0.152   0.884
52   treatment7 - treatment8    20.25 8.21  6   2.466   0.049   *
53   treatment7 - treatment9    16.25 8.21  6   1.979   0.095
54  treatment7 - treatment10    16.25 8.21  6   1.979   0.095
55  treatment7 - treatment11     7.00 7.34  6   0.953   0.377
56  treatment7 - treatment12    14.00 7.34  6   1.906   0.105
57   treatment8 - treatment9    -4.00 8.21  6  -0.487   0.643
58  treatment8 - treatment10    -4.00 7.34  6  -0.545   0.606
59  treatment8 - treatment11   -13.25 8.21  6  -1.614   0.158
60  treatment8 - treatment12    -6.25 8.21  6  -0.761   0.475
61  treatment9 - treatment10     0.00 8.21  6   0.000   1.000
62  treatment9 - treatment11    -9.25 8.21  6  -1.126   0.303
63  treatment9 - treatment12    -2.25 8.21  6  -0.274   0.793
64 treatment10 - treatment11    -9.25 8.21  6  -1.126   0.303
65 treatment10 - treatment12    -2.25 8.21  6  -0.274   0.793
66 treatment11 - treatment12     7.00 7.34  6   0.953   0.377

Treatment Groups
==================

Method : lsd

   Treatment Adjusted Means   SE df lower.CL upper.CL Group
8           8           73.25 5.61  6    59.52    86.98     1
9           9           77.25 5.61  6    63.52    90.98    12
10         10           77.25 5.61  6    63.52    90.98    12
5           5           78.25 5.61  6    64.52    91.98    12
6           6           78.25 5.61  6    64.52    91.98    12
2           2           79.00 3.00  6    71.66    86.34    12
12         12           79.50 5.61  6    65.77    93.23    12
3           3           82.00 3.00  6    74.66    89.34    12
4           4           83.33 3.00  6    76.00    90.67    12
1           1           84.67 3.00  6    77.33    92.00    12
11         11           86.50 5.61  6    72.77   100.23    12
7           7           93.50 5.61  6    79.77   107.23     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   1718     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 0.0000636 ***
Block (eliminating Treatments) 2   1277     639   2.231  0.188645
Residuals                      6   1717     286
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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 Means
===============
   Treatment Block  Means    SE r    Min    Max Adjusted Means
1          1       256.00  3.06 3 250.00 260.00          256.00
2         10     3 450.00  <NA> 1 450.00 450.00          437.67
3         11     1 300.00  <NA> 1 300.00 300.00          299.42
4         12     1 289.00  <NA> 1 289.00 289.00          288.42
5          2       228.00  6.11 3 220.00 240.00          228.00
6          3       247.67 10.17 3 237.00 268.00          247.67
7          4       264.00 18.68 3 227.00 287.00          264.00
8          5     2 281.00  <NA> 1 281.00 281.00          293.92
9          6     3 395.00  <NA> 1 395.00 395.00          382.67
10         7     1 347.00  <NA> 1 347.00 347.00          346.42
11         8     3 226.00  <NA> 1 226.00 226.00          213.67
12         9     2 311.00  <NA> 1 311.00 311.00          323.92

Comparisons
===================

Method : lsd

                   contrast estimate    SE df t.ratio p.value sig
1    treatment1 - treatment2    28.00 13.81  6   2.027   0.089
2    treatment1 - treatment3     8.33 13.81  6   0.603   0.568
3    treatment1 - treatment4    -8.00 13.81  6  -0.579   0.584
4    treatment1 - treatment5   -37.92 20.72  6  -1.830   0.117
5    treatment1 - treatment6  -126.67 20.72  6  -6.113   0.001 ***
6    treatment1 - treatment7   -90.42 20.72  6  -4.363   0.005  **
7    treatment1 - treatment8    42.33 20.72  6   2.043   0.087
8    treatment1 - treatment9   -67.92 20.72  6  -3.278   0.017   *
9   treatment1 - treatment10  -181.67 20.72  6  -8.767   0.000 ***
10  treatment1 - treatment11   -43.42 20.72  6  -2.095   0.081
11  treatment1 - treatment12   -32.42 20.72  6  -1.564   0.169
12   treatment2 - treatment3   -19.67 13.81  6  -1.424   0.204
13   treatment2 - treatment4   -36.00 13.81  6  -2.606   0.040   *
14   treatment2 - treatment5   -65.92 20.72  6  -3.181   0.019   *
15   treatment2 - treatment6  -154.67 20.72  6  -7.464   0.000 ***
16   treatment2 - treatment7  -118.42 20.72  6  -5.715   0.001  **
17   treatment2 - treatment8    14.33 20.72  6   0.692   0.515
18   treatment2 - treatment9   -95.92 20.72  6  -4.629   0.004  **
19  treatment2 - treatment10  -209.67 20.72  6 -10.118   0.000 ***
20  treatment2 - treatment11   -71.42 20.72  6  -3.447   0.014   *
21  treatment2 - treatment12   -60.42 20.72  6  -2.916   0.027   *
22   treatment3 - treatment4   -16.33 13.81  6  -1.182   0.282
23   treatment3 - treatment5   -46.25 20.72  6  -2.232   0.067
24   treatment3 - treatment6  -135.00 20.72  6  -6.515   0.001 ***
25   treatment3 - treatment7   -98.75 20.72  6  -4.766   0.003  **
26   treatment3 - treatment8    34.00 20.72  6   1.641   0.152
27   treatment3 - treatment9   -76.25 20.72  6  -3.680   0.010   *
28  treatment3 - treatment10  -190.00 20.72  6  -9.169   0.000 ***
29  treatment3 - treatment11   -51.75 20.72  6  -2.497   0.047   *
30  treatment3 - treatment12   -40.75 20.72  6  -1.967   0.097
```

```
31   treatment4 - treatment5   -29.92 20.72  6  -1.444   0.199
32   treatment4 - treatment6  -118.67 20.72  6  -5.727   0.001  **
33   treatment4 - treatment7   -82.42 20.72  6  -3.977   0.007  **
34   treatment4 - treatment8    50.33 20.72  6   2.429   0.051
35   treatment4 - treatment9   -59.92 20.72  6  -2.892   0.028   *
36  treatment4 - treatment10  -173.67 20.72  6  -8.381   0.000 ***
37  treatment4 - treatment11   -35.42 20.72  6  -1.709   0.138
38  treatment4 - treatment12   -24.42 20.72  6  -1.178   0.283
39   treatment5 - treatment6   -88.75 26.75  6  -3.318   0.016   *
40   treatment5 - treatment7   -52.50 26.75  6  -1.963   0.097
41   treatment5 - treatment8    80.25 26.75  6   3.000   0.024   *
42   treatment5 - treatment9   -30.00 23.93  6  -1.254   0.257
43  treatment5 - treatment10  -143.75 26.75  6  -5.374   0.002  **
44  treatment5 - treatment11    -5.50 26.75  6  -0.206   0.844
45  treatment5 - treatment12     5.50 26.75  6   0.206   0.844
46   treatment6 - treatment7    36.25 26.75  6   1.355   0.224
47   treatment6 - treatment8   169.00 23.93  6   7.063   0.000 ***
48   treatment6 - treatment9    58.75 26.75  6   2.196   0.070
49  treatment6 - treatment10   -55.00 23.93  6  -2.299   0.061
50  treatment6 - treatment11    83.25 26.75  6   3.112   0.021   *
51  treatment6 - treatment12    94.25 26.75  6   3.523   0.012   *
52   treatment7 - treatment8   132.75 26.75  6   4.962   0.003  **
53   treatment7 - treatment9    22.50 26.75  6   0.841   0.433
54  treatment7 - treatment10   -91.25 26.75  6  -3.411   0.014   *
55  treatment7 - treatment11    47.00 23.93  6   1.964   0.097
56  treatment7 - treatment12    58.00 23.93  6   2.424   0.052
57   treatment8 - treatment9  -110.25 26.75  6  -4.121   0.006  **
58  treatment8 - treatment10  -224.00 23.93  6  -9.362   0.000 ***
59  treatment8 - treatment11   -85.75 26.75  6  -3.205   0.018   *
60  treatment8 - treatment12   -74.75 26.75  6  -2.794   0.031   *
61  treatment9 - treatment10  -113.75 26.75  6  -4.252   0.005  **
62  treatment9 - treatment11    24.50 26.75  6   0.916   0.395
63  treatment9 - treatment12    35.50 26.75  6   1.327   0.233
64 treatment10 - treatment11   138.25 26.75  6   5.168   0.002  **
65 treatment10 - treatment12   149.25 26.75  6   5.579   0.001  **
66 treatment11 - treatment12    11.00 23.93  6   0.460   0.662

Treatment Groups
==================

Method : lsd

   Treatment Adjusted Means    SE df lower.CL upper.CL    Group
8          8         213.67 18.27  6   168.95   258.38  12
2          2         228.00  9.77  6   204.10   251.90  1
3          3         247.67  9.77  6   223.76   271.57  123
1          1         256.00  9.77  6   232.10   279.90  1234
4          4         264.00  9.77  6   240.10   287.90   234
12        12         288.42 18.27  6   243.70   333.13    345
5          5         293.92 18.27  6   249.20   338.63    345
11        11         299.42 18.27  6   254.70   344.13     45
9          9         323.92 18.27  6   279.20   368.63      56
```

```
7          7         346.42 18.27  6   301.70   391.13      56
6          6         382.67 18.27  6   337.95   427.38      67
10        10         437.67 18.27  6   392.95   482.38       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 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

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 Means
===============
   Treatment Block Means   SE r   Min   Max Adjusted Means
1          1       84.67 3.84 3 79.00 92.00          84.67
2         10     3 74.00 <NA> 1 74.00 74.00          77.25
3         11     1 89.00 <NA> 1 89.00 89.00          86.50
4         12     1 82.00 <NA> 1 82.00 82.00          79.50
5          2       79.00 1.15 3 77.00 81.00          79.00
6          3       82.00 2.65 3 78.00 87.00          82.00
7          4       83.33 3.93 3 78.00 91.00          83.33
8          5     2 79.00 <NA> 1 79.00 79.00          78.25
9          6     3 75.00 <NA> 1 75.00 75.00          78.25
10         7     1 96.00 <NA> 1 96.00 96.00          93.50
11         8     3 70.00 <NA> 1 70.00 70.00          73.25
12         9     2 78.00 <NA> 1 78.00 78.00          77.25

Comparisons
===================

Method : lsd

                    contrast estimate   SE df t.ratio p.value sig
1    treatment1 - treatment2     5.67 4.24  6   1.336   0.230
2    treatment1 - treatment3     2.67 4.24  6   0.629   0.553
3    treatment1 - treatment4     1.33 4.24  6   0.314   0.764
4    treatment1 - treatment5     6.42 6.36  6   1.009   0.352
5    treatment1 - treatment6     6.42 6.36  6   1.009   0.352
6    treatment1 - treatment7    -8.83 6.36  6  -1.389   0.214
7    treatment1 - treatment8    11.42 6.36  6   1.795   0.123
8    treatment1 - treatment9     7.42 6.36  6   1.166   0.288
9   treatment1 - treatment10     7.42 6.36  6   1.166   0.288
10  treatment1 - treatment11    -1.83 6.36  6  -0.288   0.783
```

```
11  treatment1 - treatment12     5.17 6.36  6   0.812   0.448
12   treatment2 - treatment3    -3.00 4.24  6  -0.707   0.506
13   treatment2 - treatment4    -4.33 4.24  6  -1.022   0.346
14   treatment2 - treatment5     0.75 6.36  6   0.118   0.910
15   treatment2 - treatment6     0.75 6.36  6   0.118   0.910
16   treatment2 - treatment7   -14.50 6.36  6  -2.280   0.063
17   treatment2 - treatment8     5.75 6.36  6   0.904   0.401
18   treatment2 - treatment9     1.75 6.36  6   0.275   0.792
19  treatment2 - treatment10     1.75 6.36  6   0.275   0.792
20  treatment2 - treatment11    -7.50 6.36  6  -1.179   0.283
21  treatment2 - treatment12    -0.50 6.36  6  -0.079   0.940
22   treatment3 - treatment4    -1.33 4.24  6  -0.314   0.764
23   treatment3 - treatment5     3.75 6.36  6   0.590   0.577
24   treatment3 - treatment6     3.75 6.36  6   0.590   0.577
25   treatment3 - treatment7   -11.50 6.36  6  -1.808   0.121
26   treatment3 - treatment8     8.75 6.36  6   1.376   0.218
27   treatment3 - treatment9     4.75 6.36  6   0.747   0.483
28  treatment3 - treatment10     4.75 6.36  6   0.747   0.483
29  treatment3 - treatment11    -4.50 6.36  6  -0.707   0.506
30  treatment3 - treatment12     2.50 6.36  6   0.393   0.708
31   treatment4 - treatment5     5.08 6.36  6   0.799   0.455
32   treatment4 - treatment6     5.08 6.36  6   0.799   0.455
33   treatment4 - treatment7   -10.17 6.36  6  -1.598   0.161
34   treatment4 - treatment8    10.08 6.36  6   1.585   0.164
35   treatment4 - treatment9     6.08 6.36  6   0.956   0.376
36  treatment4 - treatment10     6.08 6.36  6   0.956   0.376
37  treatment4 - treatment11    -3.17 6.36  6  -0.498   0.636
38  treatment4 - treatment12     3.83 6.36  6   0.603   0.569
39   treatment5 - treatment6     0.00 8.21  6   0.000   1.000
40   treatment5 - treatment7   -15.25 8.21  6  -1.857   0.113
41   treatment5 - treatment8     5.00 8.21  6   0.609   0.565
42   treatment5 - treatment9     1.00 7.34  6   0.136   0.896
43  treatment5 - treatment10     1.00 8.21  6   0.122   0.907
44  treatment5 - treatment11    -8.25 8.21  6  -1.005   0.354
45  treatment5 - treatment12    -1.25 8.21  6  -0.152   0.884
46   treatment6 - treatment7   -15.25 8.21  6  -1.857   0.113
47   treatment6 - treatment8     5.00 7.34  6   0.681   0.521
48   treatment6 - treatment9     1.00 8.21  6   0.122   0.907
49  treatment6 - treatment10     1.00 7.34  6   0.136   0.896
50  treatment6 - treatment11    -8.25 8.21  6  -1.005   0.354
51  treatment6 - treatment12    -1.25 8.21  6  -0.152   0.884
52   treatment7 - treatment8    20.25 8.21  6   2.466   0.049   *
53   treatment7 - treatment9    16.25 8.21  6   1.979   0.095
54  treatment7 - treatment10    16.25 8.21  6   1.979   0.095
55  treatment7 - treatment11     7.00 7.34  6   0.953   0.377
56  treatment7 - treatment12    14.00 7.34  6   1.906   0.105
57   treatment8 - treatment9    -4.00 8.21  6  -0.487   0.643
58  treatment8 - treatment10    -4.00 7.34  6  -0.545   0.606
59  treatment8 - treatment11   -13.25 8.21  6  -1.614   0.158
60  treatment8 - treatment12    -6.25 8.21  6  -0.761   0.475
61  treatment9 - treatment10     0.00 8.21  6   0.000   1.000
62  treatment9 - treatment11    -9.25 8.21  6  -1.126   0.303
```

```
63  treatment9 - treatment12    -2.25 8.21  6  -0.274   0.793
64 treatment10 - treatment11    -9.25 8.21  6  -1.126   0.303
65 treatment10 - treatment12    -2.25 8.21  6  -0.274   0.793
66 treatment11 - treatment12     7.00 7.34  6   0.953   0.377

Treatment Groups
==================

Method : lsd

   Treatment Adjusted Means   SE df lower.CL upper.CL Group
8           8          73.25 5.61  6    59.52    86.98     1
9           9          77.25 5.61  6    63.52    90.98    12
10         10          77.25 5.61  6    63.52    90.98    12
5           5          78.25 5.61  6    64.52    91.98    12
6           6          78.25 5.61  6    64.52    91.98    12
2           2          79.00 3.00  6    71.66    86.34    12
12         12          79.50 5.61  6    65.77    93.23    12
3           3          82.00 3.00  6    74.66    89.34    12
4           4          83.33 3.00  6    76.00    90.67    12
1           1          84.67 3.00  6    77.33    92.00    12
11         11          86.50 5.61  6    72.77   100.23    12
7           7          93.50 5.61  6    79.77   107.23     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   1718     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 0.0000636 ***
Block (eliminating Treatments)  2   1277     639   2.231  0.188645
Residuals                       6   1717     286
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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 Means
===============
   Treatment Block  Means    SE r    Min    Max Adjusted Means
1          1       256.00  3.06 3 250.00 260.00         256.00
2         10     3 450.00  <NA> 1 450.00 450.00         437.67
3         11     1 300.00  <NA> 1 300.00 300.00         299.42
4         12     1 289.00  <NA> 1 289.00 289.00         288.42
5          2       228.00  6.11 3 220.00 240.00         228.00
6          3       247.67 10.17 3 237.00 268.00         247.67
7          4       264.00 18.68 3 227.00 287.00         264.00
8          5     2 281.00  <NA> 1 281.00 281.00         293.92
9          6     3 395.00  <NA> 1 395.00 395.00         382.67
10         7     1 347.00  <NA> 1 347.00 347.00         346.42
11         8     3 226.00  <NA> 1 226.00 226.00         213.67
12         9     2 311.00  <NA> 1 311.00 311.00         323.92

Comparisons
===================

Method : lsd

                    contrast estimate    SE df t.ratio p.value sig
1    treatment1 - treatment2    28.00 13.81  6   2.027   0.089
2    treatment1 - treatment3     8.33 13.81  6   0.603   0.568
```

```
3    treatment1 - treatment4    -8.00 13.81  6  -0.579   0.584
4    treatment1 - treatment5   -37.92 20.72  6  -1.830   0.117
5    treatment1 - treatment6  -126.67 20.72  6  -6.113   0.001 ***
6    treatment1 - treatment7   -90.42 20.72  6  -4.363   0.005  **
7    treatment1 - treatment8    42.33 20.72  6   2.043   0.087
8    treatment1 - treatment9   -67.92 20.72  6  -3.278   0.017   *
9   treatment1 - treatment10  -181.67 20.72  6  -8.767   0.000 ***
10  treatment1 - treatment11   -43.42 20.72  6  -2.095   0.081
11  treatment1 - treatment12   -32.42 20.72  6  -1.564   0.169
12   treatment2 - treatment3   -19.67 13.81  6  -1.424   0.204
13   treatment2 - treatment4   -36.00 13.81  6  -2.606   0.040   *
14   treatment2 - treatment5   -65.92 20.72  6  -3.181   0.019   *
15   treatment2 - treatment6  -154.67 20.72  6  -7.464   0.000 ***
16   treatment2 - treatment7  -118.42 20.72  6  -5.715   0.001  **
17   treatment2 - treatment8    14.33 20.72  6   0.692   0.515
18   treatment2 - treatment9   -95.92 20.72  6  -4.629   0.004  **
19  treatment2 - treatment10  -209.67 20.72  6 -10.118   0.000 ***
20  treatment2 - treatment11   -71.42 20.72  6  -3.447   0.014   *
21  treatment2 - treatment12   -60.42 20.72  6  -2.916   0.027   *
22   treatment3 - treatment4   -16.33 13.81  6  -1.182   0.282
23   treatment3 - treatment5   -46.25 20.72  6  -2.232   0.067
24   treatment3 - treatment6  -135.00 20.72  6  -6.515   0.001 ***
25   treatment3 - treatment7   -98.75 20.72  6  -4.766   0.003  **
26   treatment3 - treatment8    34.00 20.72  6   1.641   0.152
27   treatment3 - treatment9   -76.25 20.72  6  -3.680   0.010   *
28  treatment3 - treatment10  -190.00 20.72  6  -9.169   0.000 ***
29  treatment3 - treatment11   -51.75 20.72  6  -2.497   0.047   *
30  treatment3 - treatment12   -40.75 20.72  6  -1.967   0.097
31   treatment4 - treatment5   -29.92 20.72  6  -1.444   0.199
32   treatment4 - treatment6  -118.67 20.72  6  -5.727   0.001  **
33   treatment4 - treatment7   -82.42 20.72  6  -3.977   0.007  **
34   treatment4 - treatment8    50.33 20.72  6   2.429   0.051
35   treatment4 - treatment9   -59.92 20.72  6  -2.892   0.028   *
36  treatment4 - treatment10  -173.67 20.72  6  -8.381   0.000 ***
37  treatment4 - treatment11   -35.42 20.72  6  -1.709   0.138
38  treatment4 - treatment12   -24.42 20.72  6  -1.178   0.283
39   treatment5 - treatment6   -88.75 26.75  6  -3.318   0.016   *
40   treatment5 - treatment7   -52.50 26.75  6  -1.963   0.097
41   treatment5 - treatment8    80.25 26.75  6   3.000   0.024   *
42   treatment5 - treatment9   -30.00 23.93  6  -1.254   0.257
43  treatment5 - treatment10  -143.75 26.75  6  -5.374   0.002  **
44  treatment5 - treatment11    -5.50 26.75  6  -0.206   0.844
45  treatment5 - treatment12     5.50 26.75  6   0.206   0.844
46   treatment6 - treatment7    36.25 26.75  6   1.355   0.224
47   treatment6 - treatment8   169.00 23.93  6   7.063   0.000 ***
48   treatment6 - treatment9    58.75 26.75  6   2.196   0.070
49  treatment6 - treatment10   -55.00 23.93  6  -2.299   0.061
50  treatment6 - treatment11    83.25 26.75  6   3.112   0.021   *
51  treatment6 - treatment12    94.25 26.75  6   3.523   0.012   *
52   treatment7 - treatment8   132.75 26.75  6   4.962   0.003  **
53   treatment7 - treatment9    22.50 26.75  6   0.841   0.433
54  treatment7 - treatment10   -91.25 26.75  6  -3.411   0.014   *
```

```
55  treatment7 - treatment11    47.00 23.93  6   1.964   0.097
56  treatment7 - treatment12    58.00 23.93  6   2.424   0.052
57   treatment8 - treatment9  -110.25 26.75  6  -4.121   0.006  **
58  treatment8 - treatment10  -224.00 23.93  6  -9.362   0.000 ***
59  treatment8 - treatment11   -85.75 26.75  6  -3.205   0.018   *
60  treatment8 - treatment12   -74.75 26.75  6  -2.794   0.031   *
61  treatment9 - treatment10  -113.75 26.75  6  -4.252   0.005  **
62  treatment9 - treatment11    24.50 26.75  6   0.916   0.395
63  treatment9 - treatment12    35.50 26.75  6   1.327   0.233
64 treatment10 - treatment11   138.25 26.75  6   5.168   0.002  **
65 treatment10 - treatment12   149.25 26.75  6   5.579   0.001  **
66 treatment11 - treatment12    11.00 23.93  6   0.460   0.662

Treatment Groups
==================

Method : lsd

   Treatment Adjusted Means    SE df lower.CL upper.CL    Group
8           8          213.67 18.27  6   168.95   258.38  12
2           2          228.00  9.77  6   204.10   251.90  1
3           3          247.67  9.77  6   223.76   271.57  123
1           1          256.00  9.77  6   232.10   279.90  1234
4           4          264.00  9.77  6   240.10   287.90   234
12         12          288.42 18.27  6   243.70   333.13    345
5           5          293.92 18.27  6   249.20   338.63    345
11         11          299.42 18.27  6   254.70   344.13     45
9           9          323.92 18.27  6   279.20   368.63      56
7           7          346.42 18.27  6   301.70   391.13      56
6           6          382.67 18.27  6   337.95   427.38       67
10         10          437.67 18.27  6   392.95   482.38        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$blk, data$trt, 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

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 Means
===============
   Treatment Block Means   SE r   Min   Max Adjusted Means
1          1       84.67 3.84 3 79.00 92.00          84.67
2         10     3 74.00 <NA> 1 74.00 74.00          77.25
3         11     1 89.00 <NA> 1 89.00 89.00          86.50
4         12     1 82.00 <NA> 1 82.00 82.00          79.50
5          2       79.00 1.15 3 77.00 81.00          79.00
6          3       82.00 2.65 3 78.00 87.00          82.00
7          4       83.33 3.93 3 78.00 91.00          83.33
8          5     2 79.00 <NA> 1 79.00 79.00          78.25
9          6     3 75.00 <NA> 1 75.00 75.00          78.25
10         7     1 96.00 <NA> 1 96.00 96.00          93.50
```

```
11         8     3 70.00 <NA> 1 70.00 70.00          73.25
12         9     2 78.00 <NA> 1 78.00 78.00          77.25

Comparisons
==================

Method : lsd

                    contrast estimate   SE df t.ratio p.value sig
1    treatment1 - treatment2     5.67 4.24  6   1.336   0.230
2    treatment1 - treatment3     2.67 4.24  6   0.629   0.553
3    treatment1 - treatment4     1.33 4.24  6   0.314   0.764
4    treatment1 - treatment5     6.42 6.36  6   1.009   0.352
5    treatment1 - treatment6     6.42 6.36  6   1.009   0.352
6    treatment1 - treatment7    -8.83 6.36  6  -1.389   0.214
7    treatment1 - treatment8    11.42 6.36  6   1.795   0.123
8    treatment1 - treatment9     7.42 6.36  6   1.166   0.288
9   treatment1 - treatment10     7.42 6.36  6   1.166   0.288
10  treatment1 - treatment11    -1.83 6.36  6  -0.288   0.783
11  treatment1 - treatment12     5.17 6.36  6   0.812   0.448
12   treatment2 - treatment3    -3.00 4.24  6  -0.707   0.506
13   treatment2 - treatment4    -4.33 4.24  6  -1.022   0.346
14   treatment2 - treatment5     0.75 6.36  6   0.118   0.910
15   treatment2 - treatment6     0.75 6.36  6   0.118   0.910
16   treatment2 - treatment7   -14.50 6.36  6  -2.280   0.063
17   treatment2 - treatment8     5.75 6.36  6   0.904   0.401
18   treatment2 - treatment9     1.75 6.36  6   0.275   0.792
19  treatment2 - treatment10     1.75 6.36  6   0.275   0.792
20  treatment2 - treatment11    -7.50 6.36  6  -1.179   0.283
21  treatment2 - treatment12    -0.50 6.36  6  -0.079   0.940
22   treatment3 - treatment4    -1.33 4.24  6  -0.314   0.764
23   treatment3 - treatment5     3.75 6.36  6   0.590   0.577
24   treatment3 - treatment6     3.75 6.36  6   0.590   0.577
25   treatment3 - treatment7   -11.50 6.36  6  -1.808   0.121
26   treatment3 - treatment8     8.75 6.36  6   1.376   0.218
27   treatment3 - treatment9     4.75 6.36  6   0.747   0.483
28  treatment3 - treatment10     4.75 6.36  6   0.747   0.483
29  treatment3 - treatment11    -4.50 6.36  6  -0.707   0.506
30  treatment3 - treatment12     2.50 6.36  6   0.393   0.708
31   treatment4 - treatment5     5.08 6.36  6   0.799   0.455
32   treatment4 - treatment6     5.08 6.36  6   0.799   0.455
33   treatment4 - treatment7   -10.17 6.36  6  -1.598   0.161
34   treatment4 - treatment8    10.08 6.36  6   1.585   0.164
35   treatment4 - treatment9     6.08 6.36  6   0.956   0.376
36  treatment4 - treatment10     6.08 6.36  6   0.956   0.376
37  treatment4 - treatment11    -3.17 6.36  6  -0.498   0.636
38  treatment4 - treatment12     3.83 6.36  6   0.603   0.569
39   treatment5 - treatment6     0.00 8.21  6   0.000   1.000
40   treatment5 - treatment7   -15.25 8.21  6  -1.857   0.113
41   treatment5 - treatment8     5.00 8.21  6   0.609   0.565
42   treatment5 - treatment9     1.00 7.34  6   0.136   0.896
43  treatment5 - treatment10     1.00 8.21  6   0.122   0.907
```

```
44  treatment5 - treatment11    -8.25 8.21  6  -1.005   0.354
45  treatment5 - treatment12    -1.25 8.21  6  -0.152   0.884
46   treatment6 - treatment7   -15.25 8.21  6  -1.857   0.113
47   treatment6 - treatment8     5.00 7.34  6   0.681   0.521
48   treatment6 - treatment9     1.00 8.21  6   0.122   0.907
49  treatment6 - treatment10     1.00 7.34  6   0.136   0.896
50  treatment6 - treatment11    -8.25 8.21  6  -1.005   0.354
51  treatment6 - treatment12    -1.25 8.21  6  -0.152   0.884
52   treatment7 - treatment8    20.25 8.21  6   2.466   0.049   *
53   treatment7 - treatment9    16.25 8.21  6   1.979   0.095
54  treatment7 - treatment10    16.25 8.21  6   1.979   0.095
55  treatment7 - treatment11     7.00 7.34  6   0.953   0.377
56  treatment7 - treatment12    14.00 7.34  6   1.906   0.105
57   treatment8 - treatment9    -4.00 8.21  6  -0.487   0.643
58  treatment8 - treatment10    -4.00 7.34  6  -0.545   0.606
59  treatment8 - treatment11   -13.25 8.21  6  -1.614   0.158
60  treatment8 - treatment12    -6.25 8.21  6  -0.761   0.475
61  treatment9 - treatment10     0.00 8.21  6   0.000   1.000
62  treatment9 - treatment11    -9.25 8.21  6  -1.126   0.303
63  treatment9 - treatment12    -2.25 8.21  6  -0.274   0.793
64 treatment10 - treatment11    -9.25 8.21  6  -1.126   0.303
65 treatment10 - treatment12    -2.25 8.21  6  -0.274   0.793
66 treatment11 - treatment12     7.00 7.34  6   0.953   0.377

Treatment Groups
==================

Method : lsd

   Treatment Adjusted Means   SE df lower.CL upper.CL Group
8           8          73.25 5.61  6    59.52    86.98     1
9           9          77.25 5.61  6    63.52    90.98    12
10         10          77.25 5.61  6    63.52    90.98    12
5           5          78.25 5.61  6    64.52    91.98    12
6           6          78.25 5.61  6    64.52    91.98    12
2           2          79.00 3.00  6    71.66    86.34    12
12         12          79.50 5.61  6    65.77    93.23    12
3           3          82.00 3.00  6    74.66    89.34    12
4           4          83.33 3.00  6    76.00    90.67    12
1           1          84.67 3.00  6    77.33    92.00    12
11         11          86.50 5.61  6    72.77   100.23    12
7           7          93.50 5.61  6    79.77   107.23     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   1718     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 0.0000636 ***
Block (eliminating Treatments) 2   1277     639   2.231  0.188645
Residuals                     6   1717     286
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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 Means
===============
   Treatment Block  Means    SE r    Min    Max Adjusted Means
1          1       256.00  3.06 3 250.00 260.00         256.00
2         10     3 450.00  <NA> 1 450.00 450.00         437.67
3         11     1 300.00  <NA> 1 300.00 300.00         299.42
4         12     1 289.00  <NA> 1 289.00 289.00         288.42
5          2       228.00  6.11 3 220.00 240.00         228.00
```

```
6          3       247.67 10.17 3 237.00 268.00         247.67
7          4       264.00 18.68 3 227.00 287.00         264.00
8          5     2 281.00  <NA> 1 281.00 281.00         293.92
9          6     3 395.00  <NA> 1 395.00 395.00         382.67
10         7     1 347.00  <NA> 1 347.00 347.00         346.42
11         8     3 226.00  <NA> 1 226.00 226.00         213.67
12         9     2 311.00  <NA> 1 311.00 311.00         323.92

Comparisons
==================

Method : lsd

                    contrast estimate    SE df t.ratio p.value sig
1    treatment1 - treatment2    28.00 13.81  6   2.027   0.089
2    treatment1 - treatment3     8.33 13.81  6   0.603   0.568
3    treatment1 - treatment4    -8.00 13.81  6  -0.579   0.584
4    treatment1 - treatment5   -37.92 20.72  6  -1.830   0.117
5    treatment1 - treatment6  -126.67 20.72  6  -6.113   0.001 ***
6    treatment1 - treatment7   -90.42 20.72  6  -4.363   0.005  **
7    treatment1 - treatment8    42.33 20.72  6   2.043   0.087
8    treatment1 - treatment9   -67.92 20.72  6  -3.278   0.017   *
9   treatment1 - treatment10  -181.67 20.72  6  -8.767   0.000 ***
10  treatment1 - treatment11   -43.42 20.72  6  -2.095   0.081
11  treatment1 - treatment12   -32.42 20.72  6  -1.564   0.169
12   treatment2 - treatment3   -19.67 13.81  6  -1.424   0.204
13   treatment2 - treatment4   -36.00 13.81  6  -2.606   0.040   *
14   treatment2 - treatment5   -65.92 20.72  6  -3.181   0.019   *
15   treatment2 - treatment6  -154.67 20.72  6  -7.464   0.000 ***
16   treatment2 - treatment7  -118.42 20.72  6  -5.715   0.001  **
17   treatment2 - treatment8    14.33 20.72  6   0.692   0.515
18   treatment2 - treatment9   -95.92 20.72  6  -4.629   0.004  **
19  treatment2 - treatment10  -209.67 20.72  6 -10.118   0.000 ***
20  treatment2 - treatment11   -71.42 20.72  6  -3.447   0.014   *
21  treatment2 - treatment12   -60.42 20.72  6  -2.916   0.027   *
22   treatment3 - treatment4   -16.33 13.81  6  -1.182   0.282
23   treatment3 - treatment5   -46.25 20.72  6  -2.232   0.067
24   treatment3 - treatment6  -135.00 20.72  6  -6.515   0.001 ***
25   treatment3 - treatment7   -98.75 20.72  6  -4.766   0.003  **
26   treatment3 - treatment8    34.00 20.72  6   1.641   0.152
27   treatment3 - treatment9   -76.25 20.72  6  -3.680   0.010   *
28  treatment3 - treatment10  -190.00 20.72  6  -9.169   0.000 ***
29  treatment3 - treatment11   -51.75 20.72  6  -2.497   0.047   *
30  treatment3 - treatment12   -40.75 20.72  6  -1.967   0.097
31   treatment4 - treatment5   -29.92 20.72  6  -1.444   0.199
32   treatment4 - treatment6  -118.67 20.72  6  -5.727   0.001  **
33   treatment4 - treatment7   -82.42 20.72  6  -3.977   0.007  **
34   treatment4 - treatment8    50.33 20.72  6   2.429   0.051
35   treatment4 - treatment9   -59.92 20.72  6  -2.892   0.028   *
36  treatment4 - treatment10  -173.67 20.72  6  -8.381   0.000 ***
37  treatment4 - treatment11   -35.42 20.72  6  -1.709   0.138
38  treatment4 - treatment12   -24.42 20.72  6  -1.178   0.283
```

```
39   treatment5 - treatment6   -88.75 26.75  6  -3.318   0.016   *
40   treatment5 - treatment7   -52.50 26.75  6  -1.963   0.097
41   treatment5 - treatment8    80.25 26.75  6   3.000   0.024   *
42   treatment5 - treatment9   -30.00 23.93  6  -1.254   0.257
43  treatment5 - treatment10  -143.75 26.75  6  -5.374   0.002  **
44  treatment5 - treatment11    -5.50 26.75  6  -0.206   0.844
45  treatment5 - treatment12     5.50 26.75  6   0.206   0.844
46   treatment6 - treatment7    36.25 26.75  6   1.355   0.224
47   treatment6 - treatment8   169.00 23.93  6   7.063   0.000 ***
48   treatment6 - treatment9    58.75 26.75  6   2.196   0.070
49  treatment6 - treatment10   -55.00 23.93  6  -2.299   0.061
50  treatment6 - treatment11    83.25 26.75  6   3.112   0.021   *
51  treatment6 - treatment12    94.25 26.75  6   3.523   0.012   *
52   treatment7 - treatment8   132.75 26.75  6   4.962   0.003  **
53   treatment7 - treatment9    22.50 26.75  6   0.841   0.433
54  treatment7 - treatment10   -91.25 26.75  6  -3.411   0.014   *
55  treatment7 - treatment11    47.00 23.93  6   1.964   0.097
56  treatment7 - treatment12    58.00 23.93  6   2.424   0.052
57   treatment8 - treatment9  -110.25 26.75  6  -4.121   0.006  **
58  treatment8 - treatment10  -224.00 23.93  6  -9.362   0.000 ***
59  treatment8 - treatment11   -85.75 26.75  6  -3.205   0.018   *
60  treatment8 - treatment12   -74.75 26.75  6  -2.794   0.031   *
61  treatment9 - treatment10  -113.75 26.75  6  -4.252   0.005  **
62  treatment9 - treatment11    24.50 26.75  6   0.916   0.395
63  treatment9 - treatment12    35.50 26.75  6   1.327   0.233
64 treatment10 - treatment11   138.25 26.75  6   5.168   0.002  **
65 treatment10 - treatment12   149.25 26.75  6   5.579   0.001  **
66 treatment11 - treatment12    11.00 23.93  6   0.460   0.662

Treatment Groups
==================

Method : lsd

   Treatment Adjusted Means    SE df lower.CL upper.CL    Group
8          8         213.67 18.27  6   168.95   258.38  12
2          2         228.00  9.77  6   204.10   251.90  1
3          3         247.67  9.77  6   223.76   271.57  123
1          1         256.00  9.77  6   232.10   279.90  1234
4          4         264.00  9.77  6   240.10   287.90   234
12        12         288.42 18.27  6   243.70   333.13    345
5          5         293.92 18.27  6   249.20   338.63    345
11        11         299.42 18.27  6   254.70   344.13     45
9          9         323.92 18.27  6   279.20   368.63      56
7          7         346.42 18.27  6   301.70   391.13      56
6          6         382.67 18.27  6   337.95   427.38       67
10        10         437.67 18.27  6   392.95   482.38        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.

If `truncate.means = TRUE`, then any negative adjusted means will be truncated to zero with a warning.

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

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 Means
===============
   Treatment Block Means   SE r   Min   Max Adjusted Means
1          1       84.67 3.84 3 79.00 92.00          84.67
2         10     3 74.00 <NA> 1 74.00 74.00          77.25
3         11     1 89.00 <NA> 1 89.00 89.00          86.50
4         12     1 82.00 <NA> 1 82.00 82.00          79.50
5          2       79.00 1.15 3 77.00 81.00          79.00
6          3       82.00 2.65 3 78.00 87.00          82.00
7          4       83.33 3.93 3 78.00 91.00          83.33
8          5     2 79.00 <NA> 1 79.00 79.00          78.25
9          6     3 75.00 <NA> 1 75.00 75.00          78.25
10         7     1 96.00 <NA> 1 96.00 96.00          93.50
11         8     3 70.00 <NA> 1 70.00 70.00          73.25
12         9     2 78.00 <NA> 1 78.00 78.00          77.25

Comparisons
===================

Method : lsd

                    contrast estimate   SE df t.ratio p.value sig
1    treatment1 - treatment2     5.67 4.24  6   1.336   0.230
2    treatment1 - treatment3     2.67 4.24  6   0.629   0.553
3    treatment1 - treatment4     1.33 4.24  6   0.314   0.764
4    treatment1 - treatment5     6.42 6.36  6   1.009   0.352
5    treatment1 - treatment6     6.42 6.36  6   1.009   0.352
6    treatment1 - treatment7    -8.83 6.36  6  -1.389   0.214
7    treatment1 - treatment8    11.42 6.36  6   1.795   0.123
8    treatment1 - treatment9     7.42 6.36  6   1.166   0.288
9   treatment1 - treatment10     7.42 6.36  6   1.166   0.288
10  treatment1 - treatment11    -1.83 6.36  6  -0.288   0.783
11  treatment1 - treatment12     5.17 6.36  6   0.812   0.448
12   treatment2 - treatment3    -3.00 4.24  6  -0.707   0.506
13   treatment2 - treatment4    -4.33 4.24  6  -1.022   0.346
14   treatment2 - treatment5     0.75 6.36  6   0.118   0.910
15   treatment2 - treatment6     0.75 6.36  6   0.118   0.910
16   treatment2 - treatment7   -14.50 6.36  6  -2.280   0.063
17   treatment2 - treatment8     5.75 6.36  6   0.904   0.401
18   treatment2 - treatment9     1.75 6.36  6   0.275   0.792
19  treatment2 - treatment10     1.75 6.36  6   0.275   0.792
20  treatment2 - treatment11    -7.50 6.36  6  -1.179   0.283
21  treatment2 - treatment12    -0.50 6.36  6  -0.079   0.940
22   treatment3 - treatment4    -1.33 4.24  6  -0.314   0.764
23   treatment3 - treatment5     3.75 6.36  6   0.590   0.577
```

```
24   treatment3 - treatment6     3.75 6.36  6   0.590   0.577
25   treatment3 - treatment7   -11.50 6.36  6  -1.808   0.121
26   treatment3 - treatment8     8.75 6.36  6   1.376   0.218
27   treatment3 - treatment9     4.75 6.36  6   0.747   0.483
28  treatment3 - treatment10     4.75 6.36  6   0.747   0.483
29  treatment3 - treatment11    -4.50 6.36  6  -0.707   0.506
30  treatment3 - treatment12     2.50 6.36  6   0.393   0.708
31   treatment4 - treatment5     5.08 6.36  6   0.799   0.455
32   treatment4 - treatment6     5.08 6.36  6   0.799   0.455
33   treatment4 - treatment7   -10.17 6.36  6  -1.598   0.161
34   treatment4 - treatment8    10.08 6.36  6   1.585   0.164
35   treatment4 - treatment9     6.08 6.36  6   0.956   0.376
36  treatment4 - treatment10     6.08 6.36  6   0.956   0.376
37  treatment4 - treatment11    -3.17 6.36  6  -0.498   0.636
38  treatment4 - treatment12     3.83 6.36  6   0.603   0.569
39   treatment5 - treatment6     0.00 8.21  6   0.000   1.000
40   treatment5 - treatment7   -15.25 8.21  6  -1.857   0.113
41   treatment5 - treatment8     5.00 8.21  6   0.609   0.565
42   treatment5 - treatment9     1.00 7.34  6   0.136   0.896
43  treatment5 - treatment10     1.00 8.21  6   0.122   0.907
44  treatment5 - treatment11    -8.25 8.21  6  -1.005   0.354
45  treatment5 - treatment12    -1.25 8.21  6  -0.152   0.884
46   treatment6 - treatment7   -15.25 8.21  6  -1.857   0.113
47   treatment6 - treatment8     5.00 7.34  6   0.681   0.521
48   treatment6 - treatment9     1.00 8.21  6   0.122   0.907
49  treatment6 - treatment10     1.00 7.34  6   0.136   0.896
50  treatment6 - treatment11    -8.25 8.21  6  -1.005   0.354
51  treatment6 - treatment12    -1.25 8.21  6  -0.152   0.884
52   treatment7 - treatment8    20.25 8.21  6   2.466   0.049   *
53   treatment7 - treatment9    16.25 8.21  6   1.979   0.095
54  treatment7 - treatment10    16.25 8.21  6   1.979   0.095
55  treatment7 - treatment11     7.00 7.34  6   0.953   0.377
56  treatment7 - treatment12    14.00 7.34  6   1.906   0.105
57   treatment8 - treatment9    -4.00 8.21  6  -0.487   0.643
58  treatment8 - treatment10    -4.00 7.34  6  -0.545   0.606
59  treatment8 - treatment11   -13.25 8.21  6  -1.614   0.158
60  treatment8 - treatment12    -6.25 8.21  6  -0.761   0.475
61  treatment9 - treatment10     0.00 8.21  6   0.000   1.000
62  treatment9 - treatment11    -9.25 8.21  6  -1.126   0.303
63  treatment9 - treatment12    -2.25 8.21  6  -0.274   0.793
64 treatment10 - treatment11    -9.25 8.21  6  -1.126   0.303
65 treatment10 - treatment12    -2.25 8.21  6  -0.274   0.793
66 treatment11 - treatment12     7.00 7.34  6   0.953   0.377

Treatment Groups
==================

Method : lsd

   Treatment Adjusted Means   SE df lower.CL upper.CL Group
8          8           73.25 5.61  6    59.52    86.98     1
9          9           77.25 5.61  6    63.52    90.98    12
```

```
10        10          77.25 5.61  6    63.52    90.98    12
5          5          78.25 5.61  6    64.52    91.98    12
6          6          78.25 5.61  6    64.52    91.98    12
2          2          79.00 3.00  6    71.66    86.34    12
12        12          79.50 5.61  6    65.77    93.23    12
3          3          82.00 3.00  6    74.66    89.34    12
4          4          83.33 3.00  6    76.00    90.67    12
1          1          84.67 3.00  6    77.33    92.00    12
11        11          86.50 5.61  6    72.77   100.23    12
7          7          93.50 5.61  6    79.77   107.23     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   1718     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 0.0000636 ***
Block (eliminating Treatments) 2   1277     639   2.231  0.188645
Residuals                      6   1717     286
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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 Means
===============
   Treatment Block  Means    SE r    Min    Max Adjusted Means
1          1       256.00  3.06 3 250.00 260.00         256.00
2         10     3 450.00  <NA> 1 450.00 450.00         437.67
3         11     1 300.00  <NA> 1 300.00 300.00         299.42
4         12     1 289.00  <NA> 1 289.00 289.00         288.42
5          2       228.00  6.11 3 220.00 240.00         228.00
6          3       247.67 10.17 3 237.00 268.00         247.67
7          4       264.00 18.68 3 227.00 287.00         264.00
8          5     2 281.00  <NA> 1 281.00 281.00         293.92
9          6     3 395.00  <NA> 1 395.00 395.00         382.67
10         7     1 347.00  <NA> 1 347.00 347.00         346.42
11         8     3 226.00  <NA> 1 226.00 226.00         213.67
12         9     2 311.00  <NA> 1 311.00 311.00         323.92

Comparisons
===================

Method : lsd

                    contrast estimate    SE df t.ratio p.value sig
1    treatment1 - treatment2    28.00 13.81  6   2.027   0.089
2    treatment1 - treatment3     8.33 13.81  6   0.603   0.568
3    treatment1 - treatment4    -8.00 13.81  6  -0.579   0.584
4    treatment1 - treatment5   -37.92 20.72  6  -1.830   0.117
5    treatment1 - treatment6  -126.67 20.72  6  -6.113   0.001 ***
6    treatment1 - treatment7   -90.42 20.72  6  -4.363   0.005  **
7    treatment1 - treatment8    42.33 20.72  6   2.043   0.087
8    treatment1 - treatment9   -67.92 20.72  6  -3.278   0.017   *
9   treatment1 - treatment10  -181.67 20.72  6  -8.767   0.000 ***
10  treatment1 - treatment11   -43.42 20.72  6  -2.095   0.081
11  treatment1 - treatment12   -32.42 20.72  6  -1.564   0.169
12   treatment2 - treatment3   -19.67 13.81  6  -1.424   0.204
13   treatment2 - treatment4   -36.00 13.81  6  -2.606   0.040   *
14   treatment2 - treatment5   -65.92 20.72  6  -3.181   0.019   *
15   treatment2 - treatment6  -154.67 20.72  6  -7.464   0.000 ***
16   treatment2 - treatment7  -118.42 20.72  6  -5.715   0.001  **
17   treatment2 - treatment8    14.33 20.72  6   0.692   0.515
18   treatment2 - treatment9   -95.92 20.72  6  -4.629   0.004  **
19  treatment2 - treatment10  -209.67 20.72  6 -10.118   0.000 ***
20  treatment2 - treatment11   -71.42 20.72  6  -3.447   0.014   *
```

```
21  treatment2 - treatment12   -60.42 20.72  6  -2.916   0.027   *
22   treatment3 - treatment4   -16.33 13.81  6  -1.182   0.282
23   treatment3 - treatment5   -46.25 20.72  6  -2.232   0.067
24   treatment3 - treatment6  -135.00 20.72  6  -6.515   0.001 ***
25   treatment3 - treatment7   -98.75 20.72  6  -4.766   0.003  **
26   treatment3 - treatment8    34.00 20.72  6   1.641   0.152
27   treatment3 - treatment9   -76.25 20.72  6  -3.680   0.010   *
28  treatment3 - treatment10  -190.00 20.72  6  -9.169   0.000 ***
29  treatment3 - treatment11   -51.75 20.72  6  -2.497   0.047   *
30  treatment3 - treatment12   -40.75 20.72  6  -1.967   0.097
31   treatment4 - treatment5   -29.92 20.72  6  -1.444   0.199
32   treatment4 - treatment6  -118.67 20.72  6  -5.727   0.001  **
33   treatment4 - treatment7   -82.42 20.72  6  -3.977   0.007  **
34   treatment4 - treatment8    50.33 20.72  6   2.429   0.051
35   treatment4 - treatment9   -59.92 20.72  6  -2.892   0.028   *
36  treatment4 - treatment10  -173.67 20.72  6  -8.381   0.000 ***
37  treatment4 - treatment11   -35.42 20.72  6  -1.709   0.138
38  treatment4 - treatment12   -24.42 20.72  6  -1.178   0.283
39   treatment5 - treatment6   -88.75 26.75  6  -3.318   0.016   *
40   treatment5 - treatment7   -52.50 26.75  6  -1.963   0.097
41   treatment5 - treatment8    80.25 26.75  6   3.000   0.024   *
42   treatment5 - treatment9   -30.00 23.93  6  -1.254   0.257
43  treatment5 - treatment10  -143.75 26.75  6  -5.374   0.002  **
44  treatment5 - treatment11    -5.50 26.75  6  -0.206   0.844
45  treatment5 - treatment12     5.50 26.75  6   0.206   0.844
46   treatment6 - treatment7    36.25 26.75  6   1.355   0.224
47   treatment6 - treatment8   169.00 23.93  6   7.063   0.000 ***
48   treatment6 - treatment9    58.75 26.75  6   2.196   0.070
49  treatment6 - treatment10   -55.00 23.93  6  -2.299   0.061
50  treatment6 - treatment11    83.25 26.75  6   3.112   0.021   *
51  treatment6 - treatment12    94.25 26.75  6   3.523   0.012   *
52   treatment7 - treatment8   132.75 26.75  6   4.962   0.003  **
53   treatment7 - treatment9    22.50 26.75  6   0.841   0.433
54  treatment7 - treatment10   -91.25 26.75  6  -3.411   0.014   *
55  treatment7 - treatment11    47.00 23.93  6   1.964   0.097
56  treatment7 - treatment12    58.00 23.93  6   2.424   0.052
57   treatment8 - treatment9  -110.25 26.75  6  -4.121   0.006  **
58  treatment8 - treatment10  -224.00 23.93  6  -9.362   0.000 ***
59  treatment8 - treatment11   -85.75 26.75  6  -3.205   0.018   *
60  treatment8 - treatment12   -74.75 26.75  6  -2.794   0.031   *
61  treatment9 - treatment10  -113.75 26.75  6  -4.252   0.005  **
62  treatment9 - treatment11    24.50 26.75  6   0.916   0.395
63  treatment9 - treatment12    35.50 26.75  6   1.327   0.233
64 treatment10 - treatment11   138.25 26.75  6   5.168   0.002  **
65 treatment10 - treatment12   149.25 26.75  6   5.579   0.001  **
66 treatment11 - treatment12    11.00 23.93  6   0.460   0.662

Treatment Groups
==================

Method : lsd
```

```
   Treatment Adjusted Means    SE df lower.CL upper.CL    Group
8          8         213.67 18.27  6   168.95   258.38  12
2          2         228.00  9.77  6   204.10   251.90  1
3          3         247.67  9.77  6   223.76   271.57  123
1          1         256.00  9.77  6   232.10   279.90  1234
4          4         264.00  9.77  6   240.10   287.90   234
12        12         288.42 18.27  6   243.70   333.13    345
5          5         293.92 18.27  6   249.20   338.63    345
11        11         299.42 18.27  6   254.70   344.13     45
9          9         323.92 18.27  6   279.20   368.63      56
7          7         346.42 18.27  6   301.70   391.13      56
6          6         382.67 18.27  6   337.95   427.38       67
10        10         437.67 18.27  6   392.95   482.38        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
```

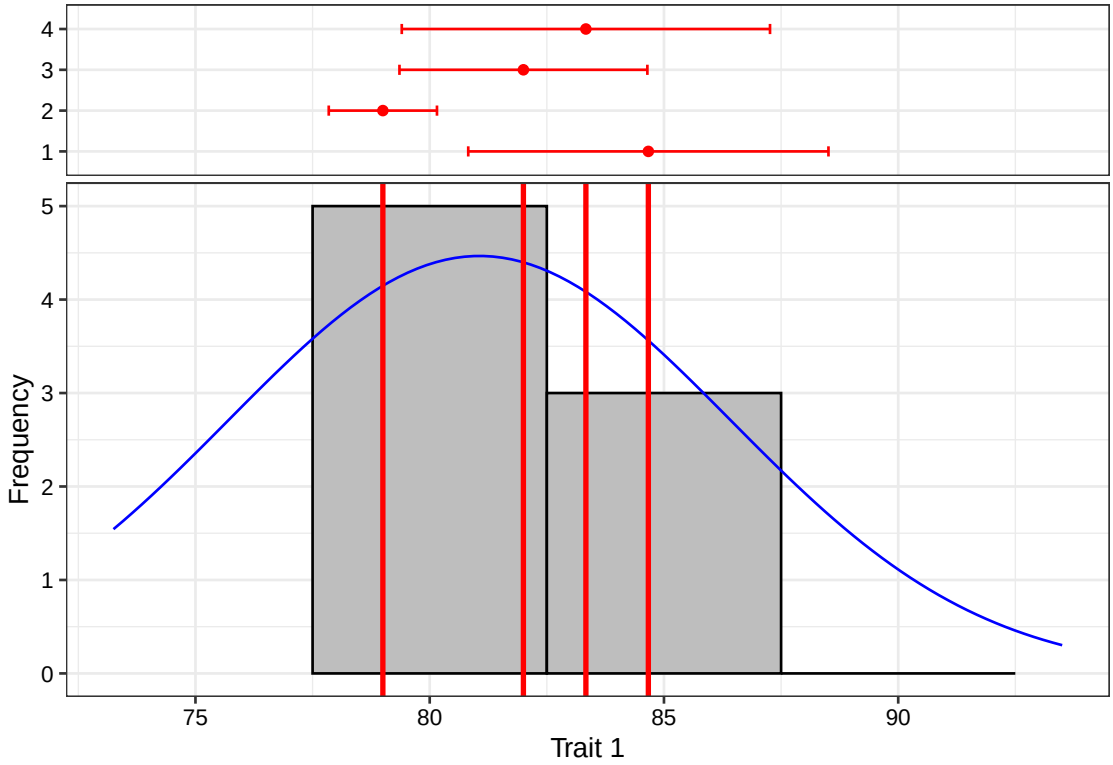
7.4 freqdist.augmentedRCBD()

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()`).
```

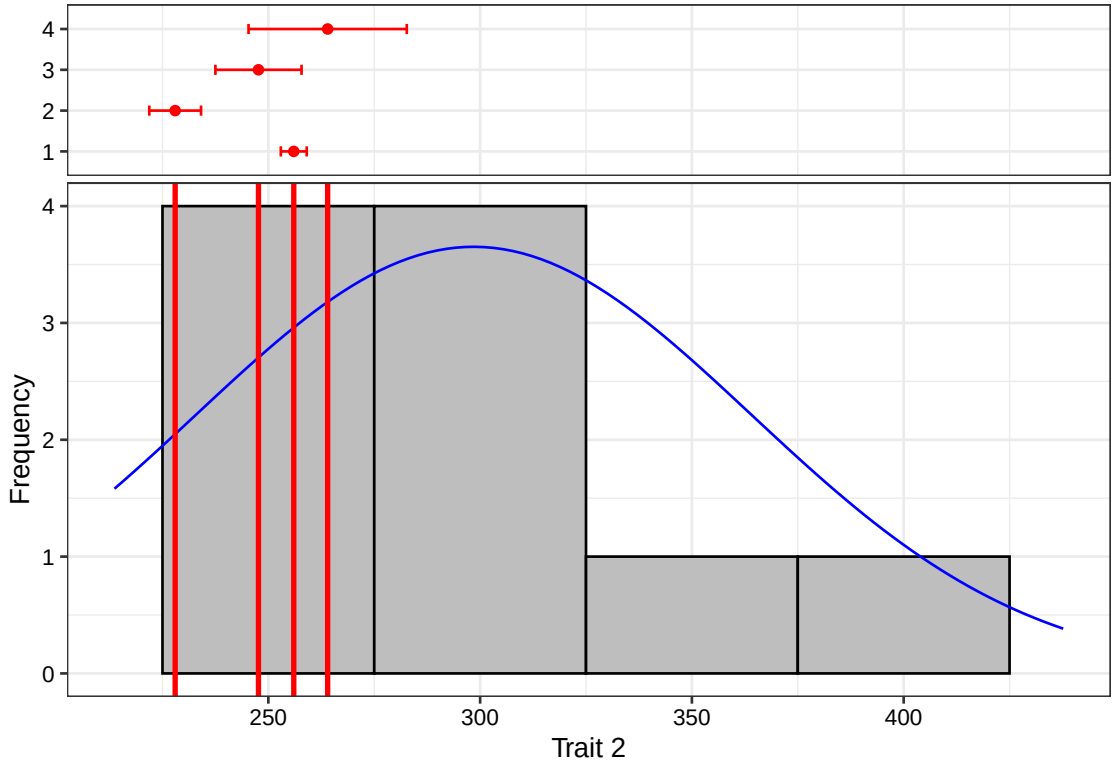
```
plot(freq1)
```




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

```
Warning: Removed 2 rows containing missing values (`geom_bar()`).
```

```
plot(freq2)
```



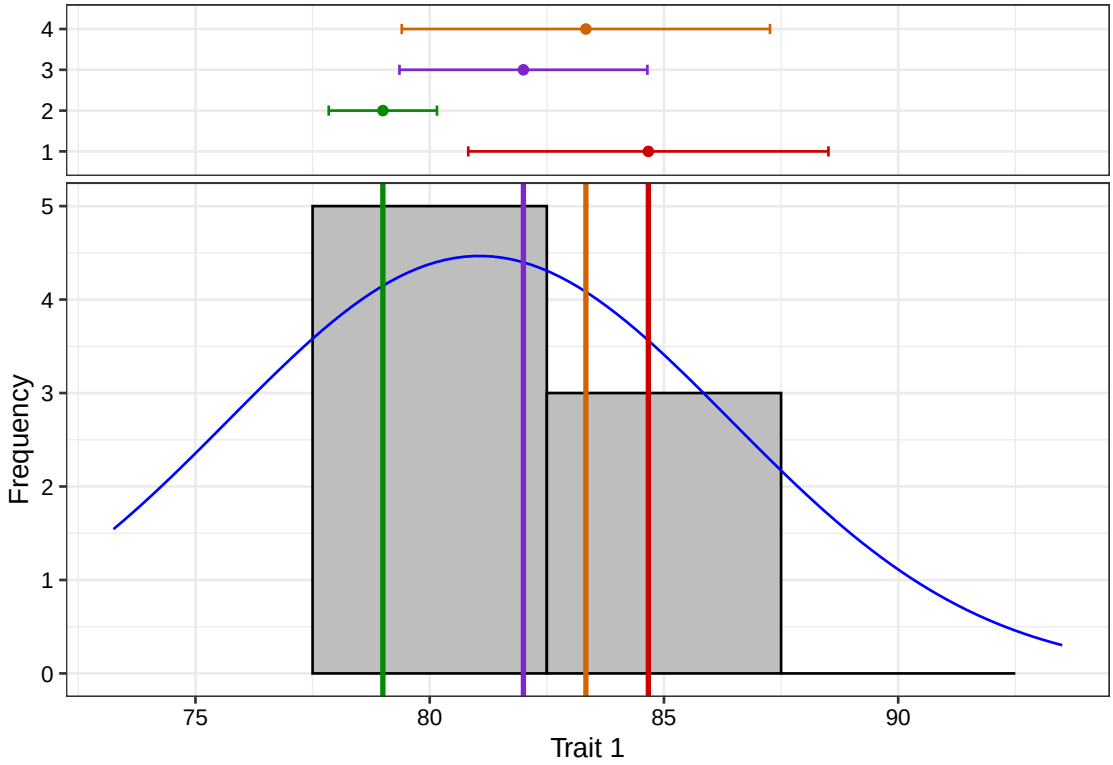
The colours for the check values may be specified using the argument **check.col**.

```
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()`).
```

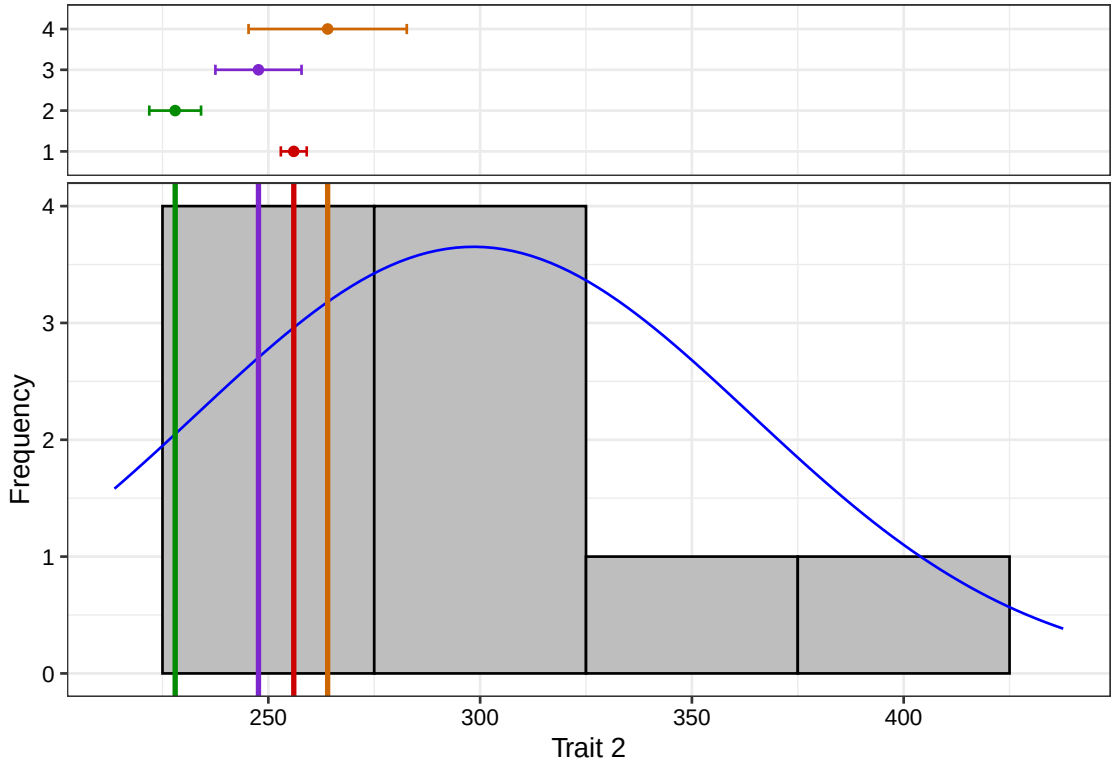
```
plot(freq1)
```




```
# 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)
```

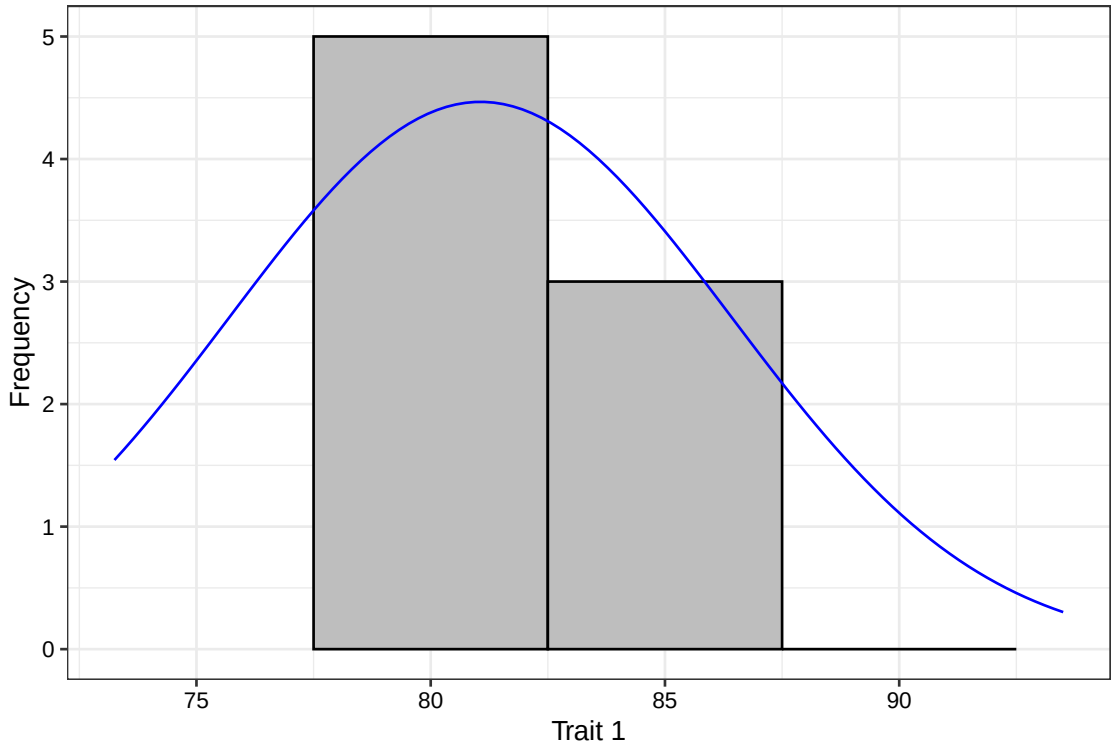


The default the check highlighting can be avoided using the argument **highlight.check = FALSE**.

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

```
Warning: Removed 2 rows containing missing values (`geom_bar()`).
```

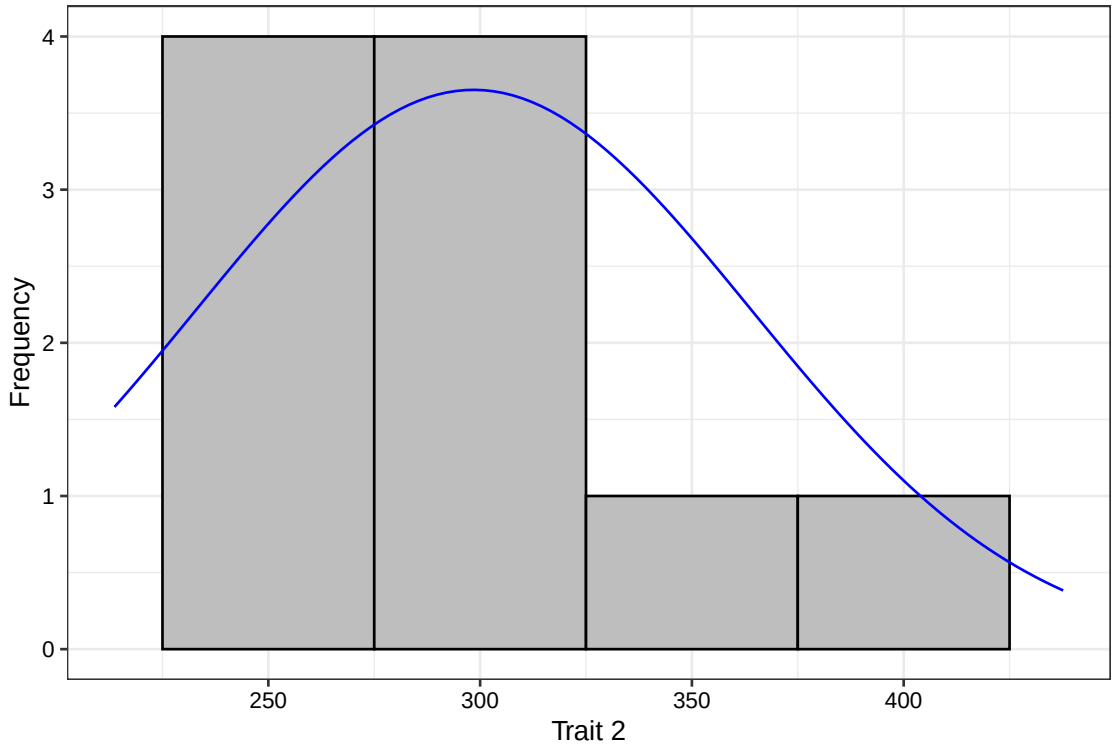
```
plot(freq1)
```




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

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

```
Warning in gva.augmentedRCBD(out1): P-value for "Treatment: Test" is > 0.05. Genetic variability a
this trait.

$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"
```

Negative estimates of variance components if computed are not abnormal. For information on how to deal with these, refer Robinson et al. (1955) and Dudley and Moll (1969).

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"))
```

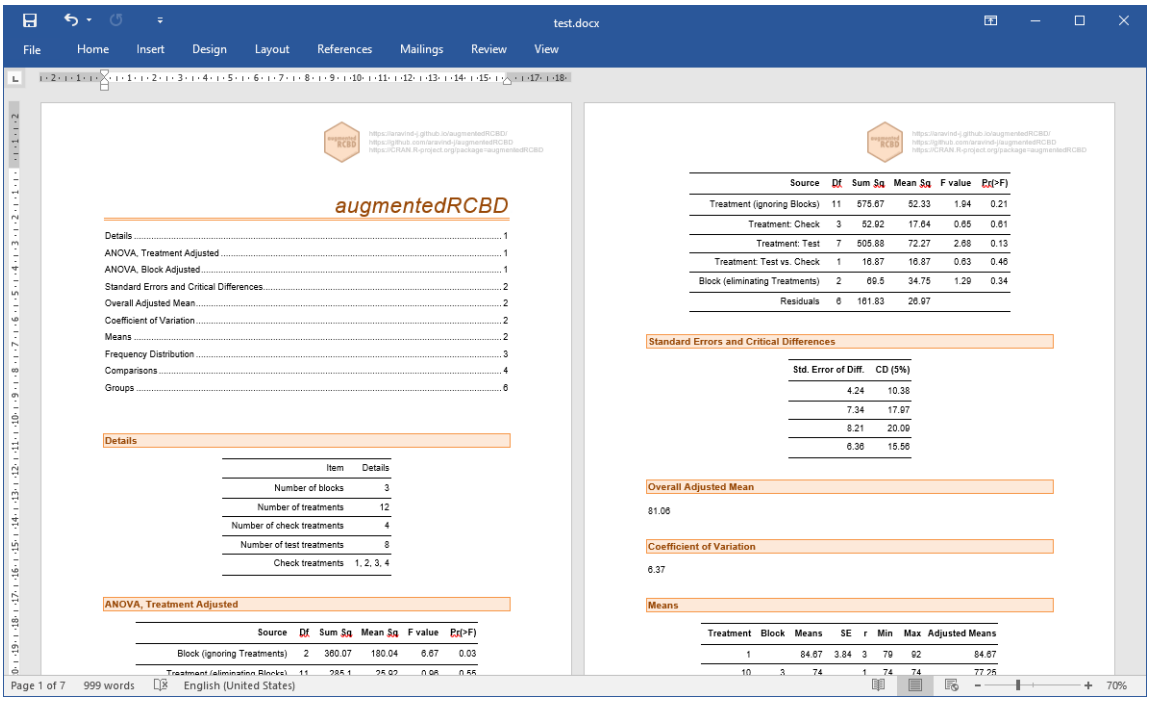


Fig. 6: MS Word report generated with **`report.agumentedRCBD`** function.

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.

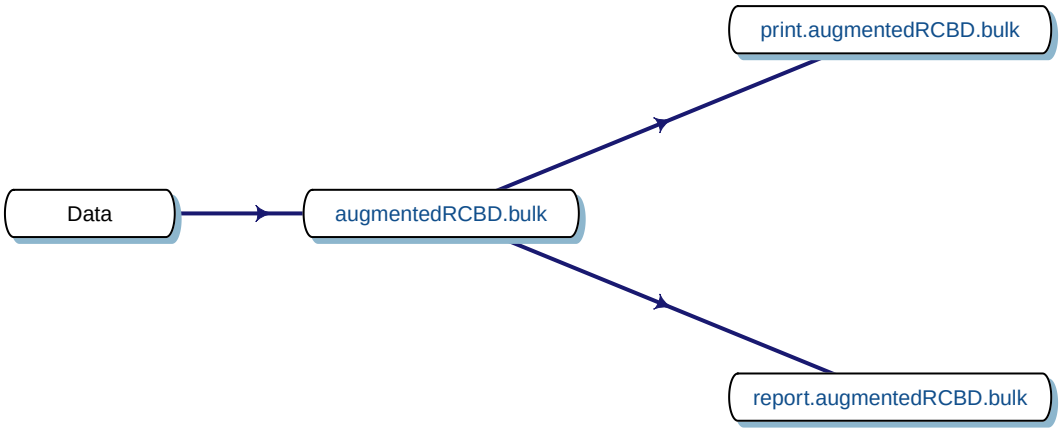


Fig. 7. Workflow for analysis of multiple traits with **`augmentedRCBD`**.

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 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
=========================
                                      Mean.Sq
                              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
ns P > 0.05; * P <= 0.05; ** P <= 0.01

ANOVA, Block Adjusted
=====================
                                    Mean.Sq
                           Source Df    y1          y2
1    Treatment (ignoring Blocks) 11 52.33 ns  5882.50 **
2               Treatment: Check  3 17.64 ns   716.75 ns
3                Treatment: Test  7 72.27 ns  4980.41 **
4      Treatment: Test vs. Check  1 16.87 ns 27694.41 **
5 Block (eliminating Treatments)  2 34.75 ns   638.58 ns
6                      Residuals  6 26.97      286.25
ns P > 0.05; * P <= 0.05; ** P <= 0.01

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 6.70 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
```

```
====================
alpha = 0.05
                                Comparison    y1    y2
1 A Test Treatment and a Control Treatment 16.41 53.45
2                  Control Treatment Means 10.38 33.80
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 Skewness_sig Kurtosis Kurtosis
1    y1    12  81.06      1.55          5.36  73.25  93.50     0.93           ns     3.52
2    y2    12 298.48     18.92         65.55 213.67 437.67     0.74           ns     2.79
ns P > 0.05; * P <= 0.05; ** P <= 0.01


Genetic Variability Analysis
====================
k = 2.063
  Trait   Mean      PV      GV     EV   GCV GCV.category   PCV PCV.category  ECV   hBS hBS.categor
1    y1  81.06   72.27   45.30  26.97  8.30          Low 10.49       Medium 6.41 62.68         Hig
2    y2 298.48 4980.41 4694.16 286.25 22.95         High 23.64         High 5.67 94.25         Hig


Warning Messages
====================


[Frequency Distribution]
y1
Removed 2 rows containing missing values (`geom_bar()`).
y2
Removed 2 rows containing missing values (`geom_bar()`).


[GVA]
y1
P-value for "Treatment: Test" is > 0.05. Genetic variability analysis may not be appropriate for t

Treatment Means
===============
   Treatment    y1     y2
1          1 84.67 256.00
2         10 77.25 437.67
3         11 86.50 299.42
4         12 79.50 288.42
5          2 79.00 228.00
6          3 82.00 247.67
7          4 83.33 264.00
8          5 78.25 293.92
9          6 78.25 382.67
```

```
10         7 93.50 346.42
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
=========================
                                        Mean.Sq
                                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
ns P > 0.05; * P <= 0.05; ** P <= 0.01

ANOVA, Block Adjusted
=====================
                                     Mean.Sq
                             Source Df    y1          y2
1    Treatment (ignoring Blocks) 11 52.33 ns  5882.50 **
2                Treatment: Check  3 17.64 ns   716.75 ns
3                 Treatment: Test  7 72.27 ns  4980.41 **
4      Treatment: Test vs. Check  1 16.87 ns 27694.41 **
5 Block (eliminating Treatments)  2 34.75 ns   638.58 ns
6                       Residuals  6 26.97      286.25
ns P > 0.05; * P <= 0.05; ** P <= 0.01

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 6.70 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
===================
alpha = 0.05
                                Comparison    y1    y2
1 A Test Treatment and a Control Treatment 16.41 53.45
2                  Control Treatment Means 10.38 33.80
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 Skewness_sig Kurtosis Kurtosis
1    y1    12  81.06      1.55          5.36  73.25  93.50     0.93           ns     3.52
2    y2    12 298.48     18.92         65.55 213.67 437.67     0.74           ns     2.79
ns P > 0.05; * P <= 0.05; ** P <= 0.01


Genetic Variability Analysis
====================
k = 2.063
  Trait   Mean      PV      GV     EV   GCV GCV.category   PCV PCV.category  ECV   hBS hBS.categor
1    y1  81.06   72.27   45.30  26.97  8.30          Low 10.49       Medium 6.41 62.68         Hig
2    y2 298.48 4980.41 4694.16 286.25 22.95         High 23.64         High 5.67 94.25         Hig


Warning Messages
====================


[Frequency Distribution]
y1
Removed 2 rows containing missing values (`geom_bar()`).
y2
```

```
Removed 2 rows containing missing values (`geom_bar()`).


[GVA]
y1
P-value for "Treatment: Test" is > 0.05. Genetic variability analysis may not be appropriate for t

Treatment Means
===============
   Treatment    y1     y2
1          1 84.67 256.00
2         10 77.25 437.67
3         11 86.50 299.42
4         12 79.50 288.42
5          2 79.00 228.00
6          3 82.00 247.67
7          4 83.33 264.00
8          5 78.25 293.92
9          6 78.25 382.67
10         7 93.50 346.42
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"))
```

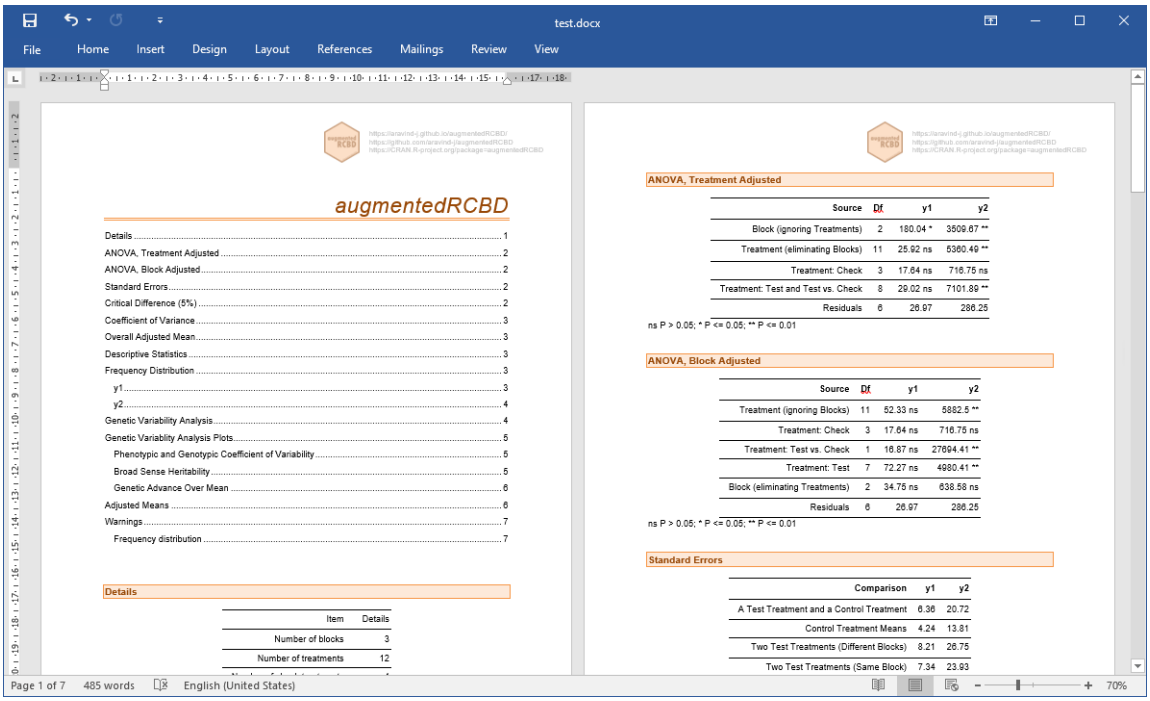


Fig. 8: MS Word report generated with **`report.agumentedRCBD.bulk`** function.

9 Citing `augmentedRCBD`

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

  Aravind, J., Mukesh Sankar, S., Wankhede, D. P., and Kaur, V. (NA).  augmentedRCBD: Analysis of
  Randomised Complete Block Designs. R package version 0.1.5.9000,
  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 K
    note = {R package version 0.1.5.9000},
    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
support the project by citing the package.
```

```
sessionInfo()
```

10 Session Info

```
R Under development (unstable) (2022-10-11 r83083 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 22621)

Matrix products: default

locale:
[1] LC_COLLATE=English_India.utf8  LC_CTYPE=English_India.utf8    LC_MONETARY=English_India.utf8 L
[5] LC_TIME=English_India.utf8

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

other attached packages:
[1] augmentedRCBD_0.1.5.9000 diagram_1.6.5            shape_1.4.6

loaded via a namespace (and not attached):
  [1] RColorBrewer_1.1-3     mathjaxr_1.6-0         rstudioapi_0.14.0-9000 jsonlite_1.8.3
  [6] TH.data_1.1-1          estimability_1.4.1     farver_2.1.1           rmarkdown_2.18
 [11] vctrs_0.5.1            rhub_1.1.2             memoise_2.0.1          RCurl_1.98-1.9
 [16] tinytex_0.42           htmltools_0.5.3        usethis_2.1.6          curl_4.3.3
 [21] bslib_0.4.1            htmlwidgets_1.5.4      desc_1.4.2             testthat_3.1.5
 [26] covr_3.6.1             sandwich_3.0-2         emmeans_1.8.2          zoo_1.8-11
 [31] uuid_1.1-0             mime_0.12              lifecycle_1.0.3        pkgconfig_2.0.3
 [36] R6_2.5.1               fastmap_1.1.0          rcmdcheck_1.4.0        rbibutils_2.2.10
 [41] digest_0.6.30          colorspace_2.0-3       ps_1.7.2               rprojroot_2.0.3
 [46] labeling_0.4.2         fansi_1.0.3            httr_1.4.4             compiler_4.3.0
 [51] withr_2.5.0            praise_1.0.0           DBI_1.1.3              pkgbuild_1.3.1
 [56] MASS_7.3-58.1          rappdirs_0.3.3         sessioninfo_1.2.2      tools_4.3.0
 [61] httpuv_1.6.6           lintr_3.0.2            glue_1.6.2             callr_3.7.3
 [66] rsconnect_0.8.28       grid_4.3.0             reshape2_1.4.4         generics_0.1.3
 [71] data.table_1.14.6      xml2_1.3.3             utf8_1.2.2             pillar_1.8.1
 [76] later_1.3.0            rJava_1.0-6            splines_4.3.0          dplyr_1.0.10
 [81] lattice_0.20-45        survival_3.4-0         tidyselect_1.2.0       miniUI_0.1.1.1
 [86] xfun_0.35              brio_1.1.3             devtools_2.4.5         rex_1.2.1
 [91] rematch_1.0.1          lazyeval_0.2.2         xopen_1.0.0            yaml_2.3.6
 [96] evaluate_0.18          codetools_0.2-18       officer_0.4.4          gdtools_0.2.4
[101] numform_0.7.0          multcompView_0.1-8     cli_3.5.0              xtable_1.8-4
[106] Rdpack_2.4             jquerylib_0.1.4        munsell_0.5.0          processx_3.8.0
[111] Rcpp_1.0.9             coda_0.19-4            XML_3.99-0.12          parallel_4.3.0
[116] pkgdown_2.0.6          ggplot2_3.4.0.9000     assertthat_0.2.1       parsedate_1.3.1
[121] whoami_1.3.0           profvis_0.3.7          urlchecker_1.0.1       bitops_1.0-7
[126] cyclocomp_1.1.0        goodpractice_1.0.4     scales_1.2.1           openxlsx_4.2.5.1
[131] crayon_1.5.2           flextable_0.8.3        clisymbols_1.2.0       rlang_1.0.6
```

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