

Data Analysis with `augmentedRCBD`

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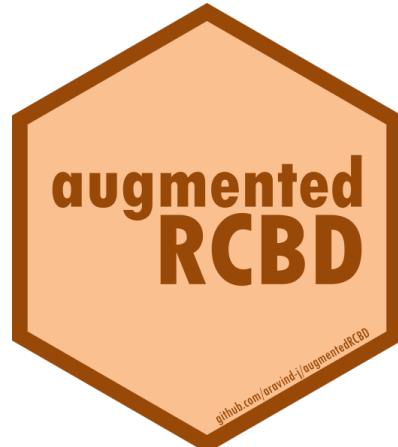
1 Overview

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 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 at [http://www.R-project.org/r-devel/bin/windows/base/](#).
- [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 its 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>

Installers for Supported Platforms

Installers	Size	Date	MD5
RStudio 1.1.456 - Windows Vista/7/8/10	85.8 MB	2018-07-19	24ca3fe
RStudio 1.1.456 - Mac OS X 10.6+ (64-bit)	74.5 MB	2018-07-19	4fc4f4f
RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (32-bit)	89.3 MB	2018-07-19	3493f9d
RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (64-bit)	97.4 MB	2018-07-19	863ae80
RStudio 1.1.456 - Ubuntu 16.04+/Debian 9+ (64-bit)	64.9 MB	2018-07-19	d96e635
RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit)	88.1 MB	2018-07-19	1df56c7
RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit)	90.6 MB	2018-07-19	5e77094

Zip/Tarballs

Zip/tar archives	Size	Date	MD5
RStudio 1.1.456 - Windows Vista/7/8/10	122.9 MB	2018-07-19	659d6b1
RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (32-bit)	90 MB	2018-07-19	63117c1
RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (64-bit)	98.3 MB	2018-07-19	c53c32a
RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit)	88.8 MB	2018-07-19	f4ba256
RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit)	91.4 MB	2018-07-19	c60db64

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.

The screenshot shows the RStudio IDE. The top menu bar includes File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, and Help. Below the menu is a toolbar with various icons for file operations like Open, Save, and Print. A search bar says "Go to file/function". The main area has a tab labeled "Untitled1 x". The code editor window contains the number "1" at the top left. A red circle with the number "2" is overlaid on the right side of the editor area. The status bar at the bottom shows "1:1 (Top Level) R Script". Below the editor is the "Console" tab, which displays the standard R startup message. A red circle with the number "1" is overlaid on the right side of the console output. The console output includes the R version information, copyright notice, platform details, and the standard R welcome message about being free software and having no warranty. It also mentions R's collaborative nature, contributors, and citation information. The message concludes with instructions for demos, help, and quitting R.

```
R version 3.5.1 (2018-07-02) -- "Feather Spray"
Copyright (c) 2018 The R Foundation for Statistical Computing
Platform: i386-w64-mingw32/i386 (32-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[workspace loaded from ~/.RData]

> |
```

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

3.3.1 Console

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

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

```
1+1
```

```
[1] 2
```

3.3.2 Source

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

3.3.3 Environment|History|Connections

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

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

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

3.3.4 Files|Plots|Packages|Help|Viewer

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

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

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

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

4 Some Basics

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

4.1 Working Directory

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

```
# Print current working directory
getwd()

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

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

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

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

4.2 Expression and Assignment

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

```
# Constant
123

[1] 123

# Arithmetic (add two numbers)
1 + 2

[1] 3

# Condition
34 > 25

[1] TRUE

1 == 2

[1] FALSE

# Function call (mean of a series of numbers)
mean(c(25,56,89,35))

[1] 51.25
```

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

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

[1] 3
```

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

4.3 Objects and Functions

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

4.3.1 Vector

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

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

```
# A numeric vector
a <- c(1, 2, 3.3)
class(a)
```

```
[1] "numeric"
str(a)
```

```
num [1:3] 1 2 3.3
length(a)
```

```
[1] 3
```

```
# An integer vector
b <- c(1L, 2L, 3L)
class(b)
```

```
[1] "integer"
str(b)
```

```
int [1:3] 1 2 3
length(b)
```

```
[1] 3
```

The vector mode ‘character’ store text.

```
# A character vector
c <- c("one", "two", "three")
class(c)
```

```
[1] "character"
str(c)
```

```
chr [1:3] "one" "two" "three"
length(c)
```

```
[1] 3
```

The vector mode ‘logical’ stores ‘TRUE’ OR ‘FALSE’ logical data.

```
#logical vector
d <- c(TRUE, TRUE, TRUE, FALSE, TRUE, FALSE)
class(d)

[1] "logical"

str(d)

logi [1:6] TRUE TRUE TRUE FALSE TRUE FALSE
length(d)

[1] 6
```

4.3.2 Factor

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

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

[1] "male"    "female"  "female"  "male"    "male"
is.factor(catg)

[1] FALSE
# Apply the factor function
factor_catg <- factor(catg)

factor_catg

[1] male    female  female  male   male
Levels: female male
is.factor(factor_catg)

[1] TRUE
class(factor_catg)

[1] "factor"
str(factor_catg)

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

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

```
# Conversion of numeric to factor
a <- c(1, 2, 3.3)
class(a)

[1] "numeric"

str(a)

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

```

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

[1] "factor"

str(fac_a)

Factor w/ 3 levels "1","2","3.3": 1 2 3
# Conversion of integer to factor
b <- c(1L, 2L, 3L)
class(b)

[1] "integer"

str(b)

int [1:3] 1 2 3

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

[1] "factor"

str(fac_b)

Factor w/ 3 levels "1","2","3": 1 2 3
# Conversion of character to factor
c <- c("one", "two", "three")
class(c)

[1] "character"

str(c)

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

fac_c <- as.factor(c)
class(fac_c)

[1] "factor"

str(fac_c)

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

```

4.3.3 Matrix

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

```

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

[,1] [,2] [,3] [,4]
[1,]    1     6    11    16
[2,]    2     7    12    17
[3,]    3     8    13    18
[4,]    4     9    14    19

```

```
[5,]    5   10   15   20
class(m)
[1] "matrix" "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 23043 packages available for deployment and use at the official repository, the Comprehensive R Archive Network (CRAN).

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

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

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

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

4.8 Importing and Exporting Tabular Data

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

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

blk	trt	y1	y2
I	1	92	258
I	2	79	224
I	3	87	238
I	4	81	278
I	7	96	347
I	11	89	300
I	12	82	289
II	1	79	260
II	2	81	220
II	3	81	237
II	4	91	227
II	5	79	281
II	9	78	311
III	1	83	250
III	2	77	240
III	3	78	268

blk	trt	y1	y2
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 0.1.7. 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
0.1.5	2021-06-12
0.1.6	2023-05-28

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

Block	Treatment	Trait
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 III	G 4	78	287
Block III	G 8	70	226
Block III	G 6	75	395
Block III	G 10	74	450

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

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

7 Data Analysis for a Single Trait

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

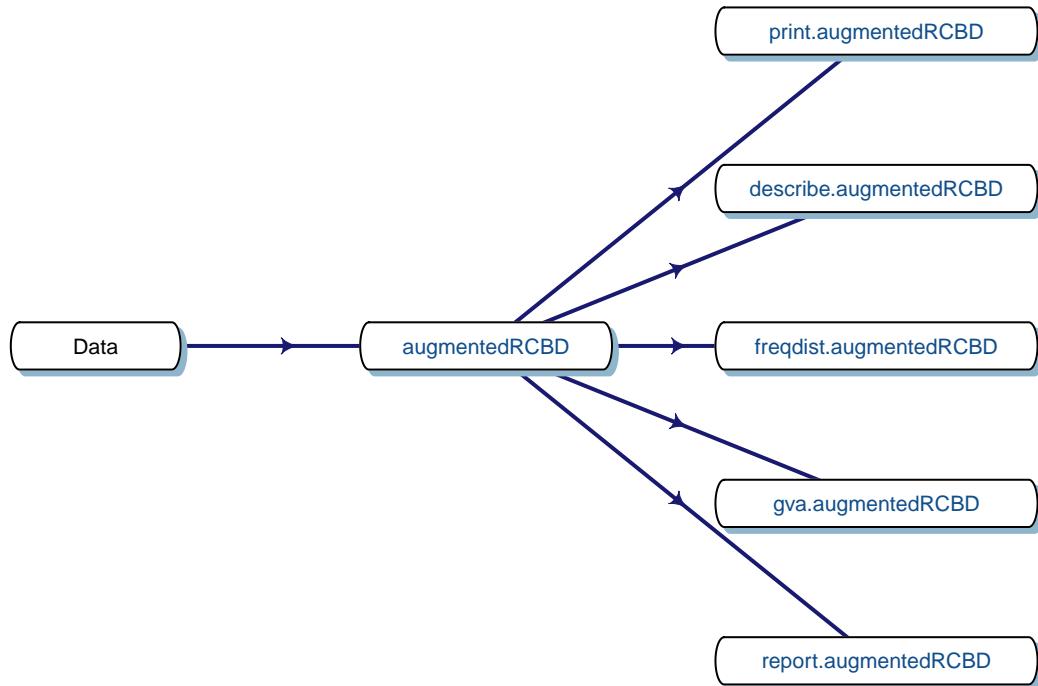


Fig. 4. Workflow for analysis of single traits with `augmentedRCBD`.

7.1 `augmentedRCBD()`

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

```
blk <- c(1, 1, 1, 1, 1, 1, 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		84.67	3.84	3	79.00	92.00	84.67
10	3	74.00	<NA>	1	74.00	74.00	77.25
11	1	89.00	<NA>	1	89.00	89.00	86.50
12	1	82.00	<NA>	1	82.00	82.00	79.50
2		79.00	1.15	3	77.00	81.00	79.00
3		82.00	2.65	3	78.00	87.00	82.00
4		83.33	3.93	3	78.00	91.00	83.33
5	2	79.00	<NA>	1	79.00	79.00	78.25
6	3	75.00	<NA>	1	75.00	75.00	78.25
7	1	96.00	<NA>	1	96.00	96.00	93.50
8	3	70.00	<NA>	1	70.00	70.00	73.25
9	2	78.00	<NA>	1	78.00	78.00	77.25

Comparisons

=====

Method : lsd

	contrast	estimate	SE	df	t.ratio	p.value	sig
treatment1	- treatment2	5.67	4.24	6	1.336	0.230	
treatment1	- treatment3	2.67	4.24	6	0.629	0.553	
treatment1	- treatment4	1.33	4.24	6	0.314	0.764	
treatment1	- treatment5	6.42	6.36	6	1.009	0.352	
treatment1	- treatment6	6.42	6.36	6	1.009	0.352	
treatment1	- treatment7	-8.83	6.36	6	-1.389	0.214	
treatment1	- treatment8	11.42	6.36	6	1.795	0.123	
treatment1	- treatment9	7.42	6.36	6	1.166	0.288	
treatment1	- treatment10	7.42	6.36	6	1.166	0.288	
treatment1	- treatment11	-1.83	6.36	6	-0.288	0.783	
treatment1	- treatment12	5.17	6.36	6	0.812	0.448	
treatment2	- treatment3	-3.00	4.24	6	-0.707	0.506	
treatment2	- treatment4	-4.33	4.24	6	-1.022	0.346	
treatment2	- treatment5	0.75	6.36	6	0.118	0.910	
treatment2	- treatment6	0.75	6.36	6	0.118	0.910	
treatment2	- treatment7	-14.50	6.36	6	-2.280	0.063	
treatment2	- treatment8	5.75	6.36	6	0.904	0.401	
treatment2	- treatment9	1.75	6.36	6	0.275	0.792	
treatment2	- treatment10	1.75	6.36	6	0.275	0.792	
treatment2	- treatment11	-7.50	6.36	6	-1.179	0.283	
treatment2	- treatment12	-0.50	6.36	6	-0.079	0.940	
treatment3	- treatment4	-1.33	4.24	6	-0.314	0.764	
treatment3	- treatment5	3.75	6.36	6	0.590	0.577	
treatment3	- treatment6	3.75	6.36	6	0.590	0.577	
treatment3	- treatment7	-11.50	6.36	6	-1.808	0.121	
treatment3	- treatment8	8.75	6.36	6	1.376	0.218	
treatment3	- treatment9	4.75	6.36	6	0.747	0.483	
treatment3	- treatment10	4.75	6.36	6	0.747	0.483	
treatment3	- treatment11	-4.50	6.36	6	-0.707	0.506	

treatment3 - treatment12	2.50	6.36	6	0.393	0.708
treatment4 - treatment5	5.08	6.36	6	0.799	0.455
treatment4 - treatment6	5.08	6.36	6	0.799	0.455
treatment4 - treatment7	-10.17	6.36	6	-1.598	0.161
treatment4 - treatment8	10.08	6.36	6	1.585	0.164
treatment4 - treatment9	6.08	6.36	6	0.956	0.376
treatment4 - treatment10	6.08	6.36	6	0.956	0.376
treatment4 - treatment11	-3.17	6.36	6	-0.498	0.636
treatment4 - treatment12	3.83	6.36	6	0.603	0.569
treatment5 - treatment6	0.00	8.21	6	0.000	1.000
treatment5 - treatment7	-15.25	8.21	6	-1.857	0.113
treatment5 - treatment8	5.00	8.21	6	0.609	0.565
treatment5 - treatment9	1.00	7.34	6	0.136	0.896
treatment5 - treatment10	1.00	8.21	6	0.122	0.907
treatment5 - treatment11	-8.25	8.21	6	-1.005	0.354
treatment5 - treatment12	-1.25	8.21	6	-0.152	0.884
treatment6 - treatment7	-15.25	8.21	6	-1.857	0.113
treatment6 - treatment8	5.00	7.34	6	0.681	0.521
treatment6 - treatment9	1.00	8.21	6	0.122	0.907
treatment6 - treatment10	1.00	7.34	6	0.136	0.896
treatment6 - treatment11	-8.25	8.21	6	-1.005	0.354
treatment6 - treatment12	-1.25	8.21	6	-0.152	0.884
treatment7 - treatment8	20.25	8.21	6	2.466	0.049 *
treatment7 - treatment9	16.25	8.21	6	1.979	0.095
treatment7 - treatment10	16.25	8.21	6	1.979	0.095
treatment7 - treatment11	7.00	7.34	6	0.953	0.377
treatment7 - treatment12	14.00	7.34	6	1.906	0.105
treatment8 - treatment9	-4.00	8.21	6	-0.487	0.643
treatment8 - treatment10	-4.00	7.34	6	-0.545	0.606
treatment8 - treatment11	-13.25	8.21	6	-1.614	0.158
treatment8 - treatment12	-6.25	8.21	6	-0.761	0.475
treatment9 - treatment10	0.00	8.21	6	0.000	1.000
treatment9 - treatment11	-9.25	8.21	6	-1.126	0.303
treatment9 - treatment12	-2.25	8.21	6	-0.274	0.793
treatment10 - treatment11	-9.25	8.21	6	-1.126	0.303
treatment10 - treatment12	-2.25	8.21	6	-0.274	0.793
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	73.25	5.61	6	59.52	86.98	1
9	77.25	5.61	6	63.52	90.98	12
10	77.25	5.61	6	63.52	90.98	12
5	78.25	5.61	6	64.52	91.98	12
6	78.25	5.61	6	64.52	91.98	12
2	79.00	3.00	6	71.66	86.34	12
12	79.50	5.61	6	65.77	93.23	12
3	82.00	3.00	6	74.66	89.34	12

```

4      83.33 3.00 6    76.00    90.67   12
1      84.67 3.00 6    77.33    92.00   12
11     86.50 5.61 6    72.77   100.23   12
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		256.00	3.06	3	250.00	260.00	256.00
10	3	450.00	<NA>	1	450.00	450.00	437.67
11	1	300.00	<NA>	1	300.00	300.00	299.42
12	1	289.00	<NA>	1	289.00	289.00	288.42
2		228.00	6.11	3	220.00	240.00	228.00
3		247.67	10.17	3	237.00	268.00	247.67
4		264.00	18.68	3	227.00	287.00	264.00
5	2	281.00	<NA>	1	281.00	281.00	293.92
6	3	395.00	<NA>	1	395.00	395.00	382.67
7	1	347.00	<NA>	1	347.00	347.00	346.42
8	3	226.00	<NA>	1	226.00	226.00	213.67
9	2	311.00	<NA>	1	311.00	311.00	323.92

Comparisons

=====

Method : lsd

	contrast	estimate	SE	df	t.ratio	p.value	sig
	treatment1 - treatment2	28.00	13.81	6	2.027	0.089	
	treatment1 - treatment3	8.33	13.81	6	0.603	0.568	
	treatment1 - treatment4	-8.00	13.81	6	-0.579	0.584	
	treatment1 - treatment5	-37.92	20.72	6	-1.830	0.117	
	treatment1 - treatment6	-126.67	20.72	6	-6.113	0.001	***
	treatment1 - treatment7	-90.42	20.72	6	-4.363	0.005	**
	treatment1 - treatment8	42.33	20.72	6	2.043	0.087	
	treatment1 - treatment9	-67.92	20.72	6	-3.278	0.017	*
	treatment1 - treatment10	-181.67	20.72	6	-8.767	0.000	***
	treatment1 - treatment11	-43.42	20.72	6	-2.095	0.081	
	treatment1 - treatment12	-32.42	20.72	6	-1.564	0.169	
	treatment2 - treatment3	-19.67	13.81	6	-1.424	0.204	
	treatment2 - treatment4	-36.00	13.81	6	-2.606	0.040	*
	treatment2 - treatment5	-65.92	20.72	6	-3.181	0.019	*
	treatment2 - treatment6	-154.67	20.72	6	-7.464	0.000	***
	treatment2 - treatment7	-118.42	20.72	6	-5.715	0.001	**
	treatment2 - treatment8	14.33	20.72	6	0.692	0.515	
	treatment2 - treatment9	-95.92	20.72	6	-4.629	0.004	**
	treatment2 - treatment10	-209.67	20.72	6	-10.118	0.000	***

treatment2 - treatment11	-71.42	20.72	6	-3.447	0.014	*
treatment2 - treatment12	-60.42	20.72	6	-2.916	0.027	*
treatment3 - treatment4	-16.33	13.81	6	-1.182	0.282	
treatment3 - treatment5	-46.25	20.72	6	-2.232	0.067	
treatment3 - treatment6	-135.00	20.72	6	-6.515	0.001	***
treatment3 - treatment7	-98.75	20.72	6	-4.766	0.003	**
treatment3 - treatment8	34.00	20.72	6	1.641	0.152	
treatment3 - treatment9	-76.25	20.72	6	-3.680	0.010	*
treatment3 - treatment10	-190.00	20.72	6	-9.169	0.000	***
treatment3 - treatment11	-51.75	20.72	6	-2.497	0.047	*
treatment3 - treatment12	-40.75	20.72	6	-1.967	0.097	
treatment4 - treatment5	-29.92	20.72	6	-1.444	0.199	
treatment4 - treatment6	-118.67	20.72	6	-5.727	0.001	**
treatment4 - treatment7	-82.42	20.72	6	-3.977	0.007	**
treatment4 - treatment8	50.33	20.72	6	2.429	0.051	
treatment4 - treatment9	-59.92	20.72	6	-2.892	0.028	*
treatment4 - treatment10	-173.67	20.72	6	-8.381	0.000	***
treatment4 - treatment11	-35.42	20.72	6	-1.709	0.138	
treatment4 - treatment12	-24.42	20.72	6	-1.178	0.283	
treatment5 - treatment6	-88.75	26.75	6	-3.318	0.016	*
treatment5 - treatment7	-52.50	26.75	6	-1.963	0.097	
treatment5 - treatment8	80.25	26.75	6	3.000	0.024	*
treatment5 - treatment9	-30.00	23.93	6	-1.254	0.257	
treatment5 - treatment10	-143.75	26.75	6	-5.374	0.002	**
treatment5 - treatment11	-5.50	26.75	6	-0.206	0.844	
treatment5 - treatment12	5.50	26.75	6	0.206	0.844	
treatment6 - treatment7	36.25	26.75	6	1.355	0.224	
treatment6 - treatment8	169.00	23.93	6	7.063	0.000	***
treatment6 - treatment9	58.75	26.75	6	2.196	0.070	
treatment6 - treatment10	-55.00	23.93	6	-2.299	0.061	
treatment6 - treatment11	83.25	26.75	6	3.112	0.021	*
treatment6 - treatment12	94.25	26.75	6	3.523	0.012	*
treatment7 - treatment8	132.75	26.75	6	4.962	0.003	**
treatment7 - treatment9	22.50	26.75	6	0.841	0.433	
treatment7 - treatment10	-91.25	26.75	6	-3.411	0.014	*
treatment7 - treatment11	47.00	23.93	6	1.964	0.097	
treatment7 - treatment12	58.00	23.93	6	2.424	0.052	
treatment8 - treatment9	-110.25	26.75	6	-4.121	0.006	**
treatment8 - treatment10	-224.00	23.93	6	-9.362	0.000	***
treatment8 - treatment11	-85.75	26.75	6	-3.205	0.018	*
treatment8 - treatment12	-74.75	26.75	6	-2.794	0.031	*
treatment9 - treatment10	-113.75	26.75	6	-4.252	0.005	**
treatment9 - treatment11	24.50	26.75	6	0.916	0.395	
treatment9 - treatment12	35.50	26.75	6	1.327	0.233	
treatment10 - treatment11	138.25	26.75	6	5.168	0.002	**
treatment10 - treatment12	149.25	26.75	6	5.579	0.001	**
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	213.67	18.27	6	168.95	258.38	12
2	228.00	9.77	6	204.10	251.90	1
3	247.67	9.77	6	223.76	271.57	123
1	256.00	9.77	6	232.10	279.90	1234
4	264.00	9.77	6	240.10	287.90	234
12	288.42	18.27	6	243.70	333.13	345
5	293.92	18.27	6	249.20	338.63	345
11	299.42	18.27	6	254.70	344.13	45
9	323.92	18.27	6	279.20	368.63	56
7	346.42	18.27	6	301.70	391.13	56
6	382.67	18.27	6	337.95	427.38	67
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
=====
Treatment (ignoring Blocks)      Df Sum Sq Mean Sq F value Pr(>F)
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
=====
Control Treatment Means          Std. Error of Diff.  CD (5%)
Two Test Treatments (Same Block) 4.240458 10.37603
Two Test Treatments (Different Blocks) 7.344688 17.97180
A Test Treatment and a Control Treatment 8.211611 20.09309
6.704752 16.40594

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

Comparisons
=====
Method : lsd

```

	contrast	estimate	SE	df	t.ratio	p.value	sig
	treatment1 - treatment2	5.67	4.24	6	1.336	0.230	
	treatment1 - treatment3	2.67	4.24	6	0.629	0.553	
	treatment1 - treatment4	1.33	4.24	6	0.314	0.764	
	treatment1 - treatment5	6.42	6.36	6	1.009	0.352	
	treatment1 - treatment6	6.42	6.36	6	1.009	0.352	
	treatment1 - treatment7	-8.83	6.36	6	-1.389	0.214	
	treatment1 - treatment8	11.42	6.36	6	1.795	0.123	
	treatment1 - treatment9	7.42	6.36	6	1.166	0.288	
	treatment1 - treatment10	7.42	6.36	6	1.166	0.288	
	treatment1 - treatment11	-1.83	6.36	6	-0.288	0.783	
	treatment1 - treatment12	5.17	6.36	6	0.812	0.448	
	treatment2 - treatment3	-3.00	4.24	6	-0.707	0.506	
	treatment2 - treatment4	-4.33	4.24	6	-1.022	0.346	
	treatment2 - treatment5	0.75	6.36	6	0.118	0.910	
	treatment2 - treatment6	0.75	6.36	6	0.118	0.910	
	treatment2 - treatment7	-14.50	6.36	6	-2.280	0.063	
	treatment2 - treatment8	5.75	6.36	6	0.904	0.401	
	treatment2 - treatment9	1.75	6.36	6	0.275	0.792	
	treatment2 - treatment10	1.75	6.36	6	0.275	0.792	
	treatment2 - treatment11	-7.50	6.36	6	-1.179	0.283	
	treatment2 - treatment12	-0.50	6.36	6	-0.079	0.940	
	treatment3 - treatment4	-1.33	4.24	6	-0.314	0.764	
	treatment3 - treatment5	3.75	6.36	6	0.590	0.577	
	treatment3 - treatment6	3.75	6.36	6	0.590	0.577	
	treatment3 - treatment7	-11.50	6.36	6	-1.808	0.121	
	treatment3 - treatment8	8.75	6.36	6	1.376	0.218	
	treatment3 - treatment9	4.75	6.36	6	0.747	0.483	
	treatment3 - treatment10	4.75	6.36	6	0.747	0.483	
	treatment3 - treatment11	-4.50	6.36	6	-0.707	0.506	
	treatment3 - treatment12	2.50	6.36	6	0.393	0.708	
	treatment4 - treatment5	5.08	6.36	6	0.799	0.455	
	treatment4 - treatment6	5.08	6.36	6	0.799	0.455	
	treatment4 - treatment7	-10.17	6.36	6	-1.598	0.161	
	treatment4 - treatment8	10.08	6.36	6	1.585	0.164	
	treatment4 - treatment9	6.08	6.36	6	0.956	0.376	
	treatment4 - treatment10	6.08	6.36	6	0.956	0.376	
	treatment4 - treatment11	-3.17	6.36	6	-0.498	0.636	
	treatment4 - treatment12	3.83	6.36	6	0.603	0.569	
	treatment5 - treatment6	0.00	8.21	6	0.000	1.000	
	treatment5 - treatment7	-15.25	8.21	6	-1.857	0.113	
	treatment5 - treatment8	5.00	8.21	6	0.609	0.565	
	treatment5 - treatment9	1.00	7.34	6	0.136	0.896	
	treatment5 - treatment10	1.00	8.21	6	0.122	0.907	
	treatment5 - treatment11	-8.25	8.21	6	-1.005	0.354	
	treatment5 - treatment12	-1.25	8.21	6	-0.152	0.884	
	treatment6 - treatment7	-15.25	8.21	6	-1.857	0.113	
	treatment6 - treatment8	5.00	7.34	6	0.681	0.521	
	treatment6 - treatment9	1.00	8.21	6	0.122	0.907	
	treatment6 - treatment10	1.00	7.34	6	0.136	0.896	
	treatment6 - treatment11	-8.25	8.21	6	-1.005	0.354	

```

treatment6 - treatment12    -1.25 8.21  6  -0.152  0.884
treatment7 - treatment8     20.25 8.21  6   2.466  0.049 *
treatment7 - treatment9     16.25 8.21  6   1.979  0.095
treatment7 - treatment10    16.25 8.21  6   1.979  0.095
treatment7 - treatment11    7.00  7.34  6   0.953  0.377
treatment7 - treatment12    14.00 7.34  6   1.906  0.105
treatment8 - treatment9    -4.00  8.21  6  -0.487  0.643
treatment8 - treatment10    -4.00  7.34  6  -0.545  0.606
treatment8 - treatment11   -13.25 8.21  6  -1.614  0.158
treatment8 - treatment12    -6.25  8.21  6  -0.761  0.475
treatment9 - treatment10    0.00  8.21  6   0.000  1.000
treatment9 - treatment11   -9.25  8.21  6  -1.126  0.303
treatment9 - treatment12    -2.25  8.21  6  -0.274  0.793
treatment10 - treatment11   -9.25  8.21  6  -1.126  0.303
treatment10 - treatment12   -2.25  8.21  6  -0.274  0.793
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	73.25	5.61	6	59.52	86.98	1
9	77.25	5.61	6	63.52	90.98	12
10	77.25	5.61	6	63.52	90.98	12
5	78.25	5.61	6	64.52	91.98	12
6	78.25	5.61	6	64.52	91.98	12
2	79.00	3.00	6	71.66	86.34	12
12	79.50	5.61	6	65.77	93.23	12
3	82.00	3.00	6	74.66	89.34	12
4	83.33	3.00	6	76.00	90.67	12
1	84.67	3.00	6	77.33	92.00	12
11	86.50	5.61	6	72.77	100.23	12
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								
<hr/>											
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								
<hr/>											
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		256.00	3.06	3	250.00	260.00	256.00
10	3	450.00	<NA>	1	450.00	450.00	437.67
11	1	300.00	<NA>	1	300.00	300.00	299.42
12	1	289.00	<NA>	1	289.00	289.00	288.42
2		228.00	6.11	3	220.00	240.00	228.00
3		247.67	10.17	3	237.00	268.00	247.67
4		264.00	18.68	3	227.00	287.00	264.00
5	2	281.00	<NA>	1	281.00	281.00	293.92

6	3	395.00	<NA>	1	395.00	395.00		382.67
7	1	347.00	<NA>	1	347.00	347.00		346.42
8	3	226.00	<NA>	1	226.00	226.00		213.67
9	2	311.00	<NA>	1	311.00	311.00		323.92

Comparisons

=====

Method : lsd

	contrast	estimate	SE	df	t.ratio	p.value	sig
	treatment1 - treatment2	28.00	13.81	6	2.027	0.089	
	treatment1 - treatment3	8.33	13.81	6	0.603	0.568	
	treatment1 - treatment4	-8.00	13.81	6	-0.579	0.584	
	treatment1 - treatment5	-37.92	20.72	6	-1.830	0.117	
	treatment1 - treatment6	-126.67	20.72	6	-6.113	0.001	***
	treatment1 - treatment7	-90.42	20.72	6	-4.363	0.005	**
	treatment1 - treatment8	42.33	20.72	6	2.043	0.087	
	treatment1 - treatment9	-67.92	20.72	6	-3.278	0.017	*
	treatment1 - treatment10	-181.67	20.72	6	-8.767	0.000	***
	treatment1 - treatment11	-43.42	20.72	6	-2.095	0.081	
	treatment1 - treatment12	-32.42	20.72	6	-1.564	0.169	
	treatment2 - treatment3	-19.67	13.81	6	-1.424	0.204	
	treatment2 - treatment4	-36.00	13.81	6	-2.606	0.040	*
	treatment2 - treatment5	-65.92	20.72	6	-3.181	0.019	*
	treatment2 - treatment6	-154.67	20.72	6	-7.464	0.000	***
	treatment2 - treatment7	-118.42	20.72	6	-5.715	0.001	**
	treatment2 - treatment8	14.33	20.72	6	0.692	0.515	
	treatment2 - treatment9	-95.92	20.72	6	-4.629	0.004	**
	treatment2 - treatment10	-209.67	20.72	6	-10.118	0.000	***
	treatment2 - treatment11	-71.42	20.72	6	-3.447	0.014	*
	treatment2 - treatment12	-60.42	20.72	6	-2.916	0.027	*
	treatment3 - treatment4	-16.33	13.81	6	-1.182	0.282	
	treatment3 - treatment5	-46.25	20.72	6	-2.232	0.067	
	treatment3 - treatment6	-135.00	20.72	6	-6.515	0.001	***
	treatment3 - treatment7	-98.75	20.72	6	-4.766	0.003	**
	treatment3 - treatment8	34.00	20.72	6	1.641	0.152	
	treatment3 - treatment9	-76.25	20.72	6	-3.680	0.010	*
	treatment3 - treatment10	-190.00	20.72	6	-9.169	0.000	***
	treatment3 - treatment11	-51.75	20.72	6	-2.497	0.047	*
	treatment3 - treatment12	-40.75	20.72	6	-1.967	0.097	
	treatment4 - treatment5	-29.92	20.72	6	-1.444	0.199	
	treatment4 - treatment6	-118.67	20.72	6	-5.727	0.001	**
	treatment4 - treatment7	-82.42	20.72	6	-3.977	0.007	**
	treatment4 - treatment8	50.33	20.72	6	2.429	0.051	
	treatment4 - treatment9	-59.92	20.72	6	-2.892	0.028	*
	treatment4 - treatment10	-173.67	20.72	6	-8.381	0.000	***
	treatment4 - treatment11	-35.42	20.72	6	-1.709	0.138	
	treatment4 - treatment12	-24.42	20.72	6	-1.178	0.283	
	treatment5 - treatment6	-88.75	26.75	6	-3.318	0.016	*
	treatment5 - treatment7	-52.50	26.75	6	-1.963	0.097	

treatment5 - treatment8	80.25	26.75	6	3.000	0.024	*
treatment5 - treatment9	-30.00	23.93	6	-1.254	0.257	
treatment5 - treatment10	-143.75	26.75	6	-5.374	0.002	**
treatment5 - treatment11	-5.50	26.75	6	-0.206	0.844	
treatment5 - treatment12	5.50	26.75	6	0.206	0.844	
treatment6 - treatment7	36.25	26.75	6	1.355	0.224	
treatment6 - treatment8	169.00	23.93	6	7.063	0.000	***
treatment6 - treatment9	58.75	26.75	6	2.196	0.070	
treatment6 - treatment10	-55.00	23.93	6	-2.299	0.061	
treatment6 - treatment11	83.25	26.75	6	3.112	0.021	*
treatment6 - treatment12	94.25	26.75	6	3.523	0.012	*
treatment7 - treatment8	132.75	26.75	6	4.962	0.003	**
treatment7 - treatment9	22.50	26.75	6	0.841	0.433	
treatment7 - treatment10	-91.25	26.75	6	-3.411	0.014	*
treatment7 - treatment11	47.00	23.93	6	1.964	0.097	
treatment7 - treatment12	58.00	23.93	6	2.424	0.052	
treatment8 - treatment9	-110.25	26.75	6	-4.121	0.006	**
treatment8 - treatment10	-224.00	23.93	6	-9.362	0.000	***
treatment8 - treatment11	-85.75	26.75	6	-3.205	0.018	*
treatment8 - treatment12	-74.75	26.75	6	-2.794	0.031	*
treatment9 - treatment10	-113.75	26.75	6	-4.252	0.005	**
treatment9 - treatment11	24.50	26.75	6	0.916	0.395	
treatment9 - treatment12	35.50	26.75	6	1.327	0.233	
treatment10 - treatment11	138.25	26.75	6	5.168	0.002	**
treatment10 - treatment12	149.25	26.75	6	5.579	0.001	**
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	213.67	18.27	6	168.95	258.38	12
2	228.00	9.77	6	204.10	251.90	1
3	247.67	9.77	6	223.76	271.57	123
1	256.00	9.77	6	232.10	279.90	1234
4	264.00	9.77	6	240.10	287.90	234
12	288.42	18.27	6	243.70	333.13	345
5	293.92	18.27	6	249.20	338.63	345
11	299.42	18.27	6	254.70	344.13	45
9	323.92	18.27	6	279.20	368.63	56
7	346.42	18.27	6	301.70	391.13	56
6	382.67	18.27	6	337.95	427.38	67
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 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		84.67	3.84	3	79.00	92.00	84.67
10	3	74.00	<NA>	1	74.00	74.00	77.25
11	1	89.00	<NA>	1	89.00	89.00	86.50
12	1	82.00	<NA>	1	82.00	82.00	79.50
2		79.00	1.15	3	77.00	81.00	79.00
3		82.00	2.65	3	78.00	87.00	82.00
4		83.33	3.93	3	78.00	91.00	83.33
5	2	79.00	<NA>	1	79.00	79.00	78.25
6	3	75.00	<NA>	1	75.00	75.00	78.25
7	1	96.00	<NA>	1	96.00	96.00	93.50
8	3	70.00	<NA>	1	70.00	70.00	73.25
9	2	78.00	<NA>	1	78.00	78.00	77.25

Comparisons

Method : lsd

	contrast	estimate	SE	df	t.ratio	p.value	sig
treatment1	- treatment2	5.67	4.24	6	1.336	0.230	
treatment1	- treatment3	2.67	4.24	6	0.629	0.553	
treatment1	- treatment4	1.33	4.24	6	0.314	0.764	
treatment1	- treatment5	6.42	6.36	6	1.009	0.352	
treatment1	- treatment6	6.42	6.36	6	1.009	0.352	
treatment1	- treatment7	-8.83	6.36	6	-1.389	0.214	
treatment1	- treatment8	11.42	6.36	6	1.795	0.123	
treatment1	- treatment9	7.42	6.36	6	1.166	0.288	
treatment1	- treatment10	7.42	6.36	6	1.166	0.288	
treatment1	- treatment11	-1.83	6.36	6	-0.288	0.783	
treatment1	- treatment12	5.17	6.36	6	0.812	0.448	
treatment2	- treatment3	-3.00	4.24	6	-0.707	0.506	
treatment2	- treatment4	-4.33	4.24	6	-1.022	0.346	
treatment2	- treatment5	0.75	6.36	6	0.118	0.910	
treatment2	- treatment6	0.75	6.36	6	0.118	0.910	
treatment2	- treatment7	-14.50	6.36	6	-2.280	0.063	
treatment2	- treatment8	5.75	6.36	6	0.904	0.401	
treatment2	- treatment9	1.75	6.36	6	0.275	0.792	
treatment2	- treatment10	1.75	6.36	6	0.275	0.792	
treatment2	- treatment11	-7.50	6.36	6	-1.179	0.283	
treatment2	- treatment12	-0.50	6.36	6	-0.079	0.940	
treatment3	- treatment4	-1.33	4.24	6	-0.314	0.764	
treatment3	- treatment5	3.75	6.36	6	0.590	0.577	
treatment3	- treatment6	3.75	6.36	6	0.590	0.577	
treatment3	- treatment7	-11.50	6.36	6	-1.808	0.121	
treatment3	- treatment8	8.75	6.36	6	1.376	0.218	
treatment3	- treatment9	4.75	6.36	6	0.747	0.483	

treatment3 - treatment10	4.75	6.36	6	0.747	0.483
treatment3 - treatment11	-4.50	6.36	6	-0.707	0.506
treatment3 - treatment12	2.50	6.36	6	0.393	0.708
treatment4 - treatment5	5.08	6.36	6	0.799	0.455
treatment4 - treatment6	5.08	6.36	6	0.799	0.455
treatment4 - treatment7	-10.17	6.36	6	-1.598	0.161
treatment4 - treatment8	10.08	6.36	6	1.585	0.164
treatment4 - treatment9	6.08	6.36	6	0.956	0.376
treatment4 - treatment10	6.08	6.36	6	0.956	0.376
treatment4 - treatment11	-3.17	6.36	6	-0.498	0.636
treatment4 - treatment12	3.83	6.36	6	0.603	0.569
treatment5 - treatment6	0.00	8.21	6	0.000	1.000
treatment5 - treatment7	-15.25	8.21	6	-1.857	0.113
treatment5 - treatment8	5.00	8.21	6	0.609	0.565
treatment5 - treatment9	1.00	7.34	6	0.136	0.896
treatment5 - treatment10	1.00	8.21	6	0.122	0.907
treatment5 - treatment11	-8.25	8.21	6	-1.005	0.354
treatment5 - treatment12	-1.25	8.21	6	-0.152	0.884
treatment6 - treatment7	-15.25	8.21	6	-1.857	0.113
treatment6 - treatment8	5.00	7.34	6	0.681	0.521
treatment6 - treatment9	1.00	8.21	6	0.122	0.907
treatment6 - treatment10	1.00	7.34	6	0.136	0.896
treatment6 - treatment11	-8.25	8.21	6	-1.005	0.354
treatment6 - treatment12	-1.25	8.21	6	-0.152	0.884
treatment7 - treatment8	20.25	8.21	6	2.466	0.049 *
treatment7 - treatment9	16.25	8.21	6	1.979	0.095
treatment7 - treatment10	16.25	8.21	6	1.979	0.095
treatment7 - treatment11	7.00	7.34	6	0.953	0.377
treatment7 - treatment12	14.00	7.34	6	1.906	0.105
treatment8 - treatment9	-4.00	8.21	6	-0.487	0.643
treatment8 - treatment10	-4.00	7.34	6	-0.545	0.606
treatment8 - treatment11	-13.25	8.21	6	-1.614	0.158
treatment8 - treatment12	-6.25	8.21	6	-0.761	0.475
treatment9 - treatment10	0.00	8.21	6	0.000	1.000
treatment9 - treatment11	-9.25	8.21	6	-1.126	0.303
treatment9 - treatment12	-2.25	8.21	6	-0.274	0.793
treatment10 - treatment11	-9.25	8.21	6	-1.126	0.303
treatment10 - treatment12	-2.25	8.21	6	-0.274	0.793
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	73.25	5.61	6	59.52	86.98	1
9	77.25	5.61	6	63.52	90.98	12
10	77.25	5.61	6	63.52	90.98	12
5	78.25	5.61	6	64.52	91.98	12
6	78.25	5.61	6	64.52	91.98	12
2	79.00	3.00	6	71.66	86.34	12

```

12      79.50 5.61  6    65.77    93.23    12
3       82.00 3.00  6    74.66    89.34    12
4       83.33 3.00  6    76.00    90.67    12
1       84.67 3.00  6    77.33    92.00    12
11      86.50 5.61  6    72.77   100.23    12
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		256.00	3.06	3	250.00	260.00	256.00
10	3	450.00	<NA>	1	450.00	450.00	437.67
11	1	300.00	<NA>	1	300.00	300.00	299.42
12	1	289.00	<NA>	1	289.00	289.00	288.42
2		228.00	6.11	3	220.00	240.00	228.00
3		247.67	10.17	3	237.00	268.00	247.67
4		264.00	18.68	3	227.00	287.00	264.00
5	2	281.00	<NA>	1	281.00	281.00	293.92
6	3	395.00	<NA>	1	395.00	395.00	382.67
7	1	347.00	<NA>	1	347.00	347.00	346.42
8	3	226.00	<NA>	1	226.00	226.00	213.67
9	2	311.00	<NA>	1	311.00	311.00	323.92

Comparisons

Method : lsd

	contrast	estimate	SE	df	t.ratio	p.value	sig
treatment1 - treatment2		28.00	13.81	6	2.027	0.089	
treatment1 - treatment3		8.33	13.81	6	0.603	0.568	
treatment1 - treatment4		-8.00	13.81	6	-0.579	0.584	
treatment1 - treatment5		-37.92	20.72	6	-1.830	0.117	
treatment1 - treatment6		-126.67	20.72	6	-6.113	0.001	***
treatment1 - treatment7		-90.42	20.72	6	-4.363	0.005	**
treatment1 - treatment8		42.33	20.72	6	2.043	0.087	
treatment1 - treatment9		-67.92	20.72	6	-3.278	0.017	*
treatment1 - treatment10		-181.67	20.72	6	-8.767	0.000	***
treatment1 - treatment11		-43.42	20.72	6	-2.095	0.081	
treatment1 - treatment12		-32.42	20.72	6	-1.564	0.169	
treatment2 - treatment3		-19.67	13.81	6	-1.424	0.204	
treatment2 - treatment4		-36.00	13.81	6	-2.606	0.040	*
treatment2 - treatment5		-65.92	20.72	6	-3.181	0.019	*
treatment2 - treatment6		-154.67	20.72	6	-7.464	0.000	***
treatment2 - treatment7		-118.42	20.72	6	-5.715	0.001	**
treatment2 - treatment8		14.33	20.72	6	0.692	0.515	
treatment2 - treatment9		-95.92	20.72	6	-4.629	0.004	**
treatment2 - treatment10		-209.67	20.72	6	-10.118	0.000	***

treatment2 - treatment11	-71.42	20.72	6	-3.447	0.014	*
treatment2 - treatment12	-60.42	20.72	6	-2.916	0.027	*
treatment3 - treatment4	-16.33	13.81	6	-1.182	0.282	
treatment3 - treatment5	-46.25	20.72	6	-2.232	0.067	
treatment3 - treatment6	-135.00	20.72	6	-6.515	0.001	***
treatment3 - treatment7	-98.75	20.72	6	-4.766	0.003	**
treatment3 - treatment8	34.00	20.72	6	1.641	0.152	
treatment3 - treatment9	-76.25	20.72	6	-3.680	0.010	*
treatment3 - treatment10	-190.00	20.72	6	-9.169	0.000	***
treatment3 - treatment11	-51.75	20.72	6	-2.497	0.047	*
treatment3 - treatment12	-40.75	20.72	6	-1.967	0.097	
treatment4 - treatment5	-29.92	20.72	6	-1.444	0.199	
treatment4 - treatment6	-118.67	20.72	6	-5.727	0.001	**
treatment4 - treatment7	-82.42	20.72	6	-3.977	0.007	**
treatment4 - treatment8	50.33	20.72	6	2.429	0.051	
treatment4 - treatment9	-59.92	20.72	6	-2.892	0.028	*
treatment4 - treatment10	-173.67	20.72	6	-8.381	0.000	***
treatment4 - treatment11	-35.42	20.72	6	-1.709	0.138	
treatment4 - treatment12	-24.42	20.72	6	-1.178	0.283	
treatment5 - treatment6	-88.75	26.75	6	-3.318	0.016	*
treatment5 - treatment7	-52.50	26.75	6	-1.963	0.097	
treatment5 - treatment8	80.25	26.75	6	3.000	0.024	*
treatment5 - treatment9	-30.00	23.93	6	-1.254	0.257	
treatment5 - treatment10	-143.75	26.75	6	-5.374	0.002	**
treatment5 - treatment11	-5.50	26.75	6	-0.206	0.844	
treatment5 - treatment12	5.50	26.75	6	0.206	0.844	
treatment6 - treatment7	36.25	26.75	6	1.355	0.224	
treatment6 - treatment8	169.00	23.93	6	7.063	0.000	***
treatment6 - treatment9	58.75	26.75	6	2.196	0.070	
treatment6 - treatment10	-55.00	23.93	6	-2.299	0.061	
treatment6 - treatment11	83.25	26.75	6	3.112	0.021	*
treatment6 - treatment12	94.25	26.75	6	3.523	0.012	*
treatment7 - treatment8	132.75	26.75	6	4.962	0.003	**
treatment7 - treatment9	22.50	26.75	6	0.841	0.433	
treatment7 - treatment10	-91.25	26.75	6	-3.411	0.014	*
treatment7 - treatment11	47.00	23.93	6	1.964	0.097	
treatment7 - treatment12	58.00	23.93	6	2.424	0.052	
treatment8 - treatment9	-110.25	26.75	6	-4.121	0.006	**
treatment8 - treatment10	-224.00	23.93	6	-9.362	0.000	***
treatment8 - treatment11	-85.75	26.75	6	-3.205	0.018	*
treatment8 - treatment12	-74.75	26.75	6	-2.794	0.031	*
treatment9 - treatment10	-113.75	26.75	6	-4.252	0.005	**
treatment9 - treatment11	24.50	26.75	6	0.916	0.395	
treatment9 - treatment12	35.50	26.75	6	1.327	0.233	
treatment10 - treatment11	138.25	26.75	6	5.168	0.002	**
treatment10 - treatment12	149.25	26.75	6	5.579	0.001	**
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	213.67	18.27	6	168.95	258.38	12
2	228.00	9.77	6	204.10	251.90	1
3	247.67	9.77	6	223.76	271.57	123
1	256.00	9.77	6	232.10	279.90	1234
4	264.00	9.77	6	240.10	287.90	234
12	288.42	18.27	6	243.70	333.13	345
5	293.92	18.27	6	249.20	338.63	345
11	299.42	18.27	6	254.70	344.13	45
9	323.92	18.27	6	279.20	368.63	56
7	346.42	18.27	6	301.70	391.13	56
6	382.67	18.27	6	337.95	427.38	67
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		84.67	3.84	3	79.00	92.00	84.67
10	3	74.00	<NA>	1	74.00	74.00	77.25
11	1	89.00	<NA>	1	89.00	89.00	86.50
12	1	82.00	<NA>	1	82.00	82.00	79.50
2		79.00	1.15	3	77.00	81.00	79.00
3		82.00	2.65	3	78.00	87.00	82.00
4		83.33	3.93	3	78.00	91.00	83.33
5	2	79.00	<NA>	1	79.00	79.00	78.25
6	3	75.00	<NA>	1	75.00	75.00	78.25
7	1	96.00	<NA>	1	96.00	96.00	93.50
8	3	70.00	<NA>	1	70.00	70.00	73.25
9	2	78.00	<NA>	1	78.00	78.00	77.25

Comparisons

=====

Method : lsd

	contrast	estimate	SE	df	t.ratio	p.value	sig
treatment1 - treatment2		5.67	4.24	6	1.336	0.230	
treatment1 - treatment3		2.67	4.24	6	0.629	0.553	
treatment1 - treatment4		1.33	4.24	6	0.314	0.764	
treatment1 - treatment5		6.42	6.36	6	1.009	0.352	
treatment1 - treatment6		6.42	6.36	6	1.009	0.352	
treatment1 - treatment7		-8.83	6.36	6	-1.389	0.214	
treatment1 - treatment8		11.42	6.36	6	1.795	0.123	

treatment1 - treatment9	7.42	6.36	6	1.166	0.288
treatment1 - treatment10	7.42	6.36	6	1.166	0.288
treatment1 - treatment11	-1.83	6.36	6	-0.288	0.783
treatment1 - treatment12	5.17	6.36	6	0.812	0.448
treatment2 - treatment3	-3.00	4.24	6	-0.707	0.506
treatment2 - treatment4	-4.33	4.24	6	-1.022	0.346
treatment2 - treatment5	0.75	6.36	6	0.118	0.910
treatment2 - treatment6	0.75	6.36	6	0.118	0.910
treatment2 - treatment7	-14.50	6.36	6	-2.280	0.063
treatment2 - treatment8	5.75	6.36	6	0.904	0.401
treatment2 - treatment9	1.75	6.36	6	0.275	0.792
treatment2 - treatment10	1.75	6.36	6	0.275	0.792
treatment2 - treatment11	-7.50	6.36	6	-1.179	0.283
treatment2 - treatment12	-0.50	6.36	6	-0.079	0.940
treatment3 - treatment4	-1.33	4.24	6	-0.314	0.764
treatment3 - treatment5	3.75	6.36	6	0.590	0.577
treatment3 - treatment6	3.75	6.36	6	0.590	0.577
treatment3 - treatment7	-11.50	6.36	6	-1.808	0.121
treatment3 - treatment8	8.75	6.36	6	1.376	0.218
treatment3 - treatment9	4.75	6.36	6	0.747	0.483
treatment3 - treatment10	4.75	6.36	6	0.747	0.483
treatment3 - treatment11	-4.50	6.36	6	-0.707	0.506
treatment3 - treatment12	2.50	6.36	6	0.393	0.708
treatment4 - treatment5	5.08	6.36	6	0.799	0.455
treatment4 - treatment6	5.08	6.36	6	0.799	0.455
treatment4 - treatment7	-10.17	6.36	6	-1.598	0.161
treatment4 - treatment8	10.08	6.36	6	1.585	0.164
treatment4 - treatment9	6.08	6.36	6	0.956	0.376
treatment4 - treatment10	6.08	6.36	6	0.956	0.376
treatment4 - treatment11	-3.17	6.36	6	-0.498	0.636
treatment4 - treatment12	3.83	6.36	6	0.603	0.569
treatment5 - treatment6	0.00	8.21	6	0.000	1.000
treatment5 - treatment7	-15.25	8.21	6	-1.857	0.113
treatment5 - treatment8	5.00	8.21	6	0.609	0.565
treatment5 - treatment9	1.00	7.34	6	0.136	0.896
treatment5 - treatment10	1.00	8.21	6	0.122	0.907
treatment5 - treatment11	-8.25	8.21	6	-1.005	0.354
treatment5 - treatment12	-1.25	8.21	6	-0.152	0.884
treatment6 - treatment7	-15.25	8.21	6	-1.857	0.113
treatment6 - treatment8	5.00	7.34	6	0.681	0.521
treatment6 - treatment9	1.00	8.21	6	0.122	0.907
treatment6 - treatment10	1.00	7.34	6	0.136	0.896
treatment6 - treatment11	-8.25	8.21	6	-1.005	0.354
treatment6 - treatment12	-1.25	8.21	6	-0.152	0.884
treatment7 - treatment8	20.25	8.21	6	2.466	0.049 *
treatment7 - treatment9	16.25	8.21	6	1.979	0.095
treatment7 - treatment10	16.25	8.21	6	1.979	0.095
treatment7 - treatment11	7.00	7.34	6	0.953	0.377
treatment7 - treatment12	14.00	7.34	6	1.906	0.105
treatment8 - treatment9	-4.00	8.21	6	-0.487	0.643
treatment8 - treatment10	-4.00	7.34	6	-0.545	0.606
treatment8 - treatment11	-13.25	8.21	6	-1.614	0.158

```
treatment8 - treatment12      -6.25 8.21  6  -0.761   0.475
treatment9 - treatment10      0.00 8.21  6   0.000   1.000
treatment9 - treatment11     -9.25 8.21  6  -1.126   0.303
treatment9 - treatment12     -2.25 8.21  6  -0.274   0.793
treatment10 - treatment11    -9.25 8.21  6  -1.126   0.303
treatment10 - treatment12    -2.25 8.21  6  -0.274   0.793
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	73.25	5.61	6	59.52	86.98	1
9	77.25	5.61	6	63.52	90.98	12
10	77.25	5.61	6	63.52	90.98	12
5	78.25	5.61	6	64.52	91.98	12
6	78.25	5.61	6	64.52	91.98	12
2	79.00	3.00	6	71.66	86.34	12
12	79.50	5.61	6	65.77	93.23	12
3	82.00	3.00	6	74.66	89.34	12
4	83.33	3.00	6	76.00	90.67	12
1	84.67	3.00	6	77.33	92.00	12
11	86.50	5.61	6	72.77	100.23	12
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		256.00	3.06	3	250.00	260.00	256.00
10	3	450.00	<NA>	1	450.00	450.00	437.67
11	1	300.00	<NA>	1	300.00	300.00	299.42
12	1	289.00	<NA>	1	289.00	289.00	288.42
2		228.00	6.11	3	220.00	240.00	228.00
3		247.67	10.17	3	237.00	268.00	247.67
4		264.00	18.68	3	227.00	287.00	264.00
5	2	281.00	<NA>	1	281.00	281.00	293.92
6	3	395.00	<NA>	1	395.00	395.00	382.67
7	1	347.00	<NA>	1	347.00	347.00	346.42
8	3	226.00	<NA>	1	226.00	226.00	213.67
9	2	311.00	<NA>	1	311.00	311.00	323.92

Comparisons

```
=====

```

Method : lsd

	contrast	estimate	SE	df	t.ratio	p.value	sig
	treatment1 - treatment2	28.00	13.81	6	2.027	0.089	

treatment1 - treatment3	8.33	13.81	6	0.603	0.568
treatment1 - treatment4	-8.00	13.81	6	-0.579	0.584
treatment1 - treatment5	-37.92	20.72	6	-1.830	0.117
treatment1 - treatment6	-126.67	20.72	6	-6.113	0.001 ***
treatment1 - treatment7	-90.42	20.72	6	-4.363	0.005 **
treatment1 - treatment8	42.33	20.72	6	2.043	0.087
treatment1 - treatment9	-67.92	20.72	6	-3.278	0.017 *
treatment1 - treatment10	-181.67	20.72	6	-8.767	0.000 ***
treatment1 - treatment11	-43.42	20.72	6	-2.095	0.081
treatment1 - treatment12	-32.42	20.72	6	-1.564	0.169
treatment2 - treatment3	-19.67	13.81	6	-1.424	0.204
treatment2 - treatment4	-36.00	13.81	6	-2.606	0.040 *
treatment2 - treatment5	-65.92	20.72	6	-3.181	0.019 *
treatment2 - treatment6	-154.67	20.72	6	-7.464	0.000 ***
treatment2 - treatment7	-118.42	20.72	6	-5.715	0.001 **
treatment2 - treatment8	14.33	20.72	6	0.692	0.515
treatment2 - treatment9	-95.92	20.72	6	-4.629	0.004 **
treatment2 - treatment10	-209.67	20.72	6	-10.118	0.000 ***
treatment2 - treatment11	-71.42	20.72	6	-3.447	0.014 *
treatment2 - treatment12	-60.42	20.72	6	-2.916	0.027 *
treatment3 - treatment4	-16.33	13.81	6	-1.182	0.282
treatment3 - treatment5	-46.25	20.72	6	-2.232	0.067
treatment3 - treatment6	-135.00	20.72	6	-6.515	0.001 ***
treatment3 - treatment7	-98.75	20.72	6	-4.766	0.003 **
treatment3 - treatment8	34.00	20.72	6	1.641	0.152
treatment3 - treatment9	-76.25	20.72	6	-3.680	0.010 *
treatment3 - treatment10	-190.00	20.72	6	-9.169	0.000 ***
treatment3 - treatment11	-51.75	20.72	6	-2.497	0.047 *
treatment3 - treatment12	-40.75	20.72	6	-1.967	0.097
treatment4 - treatment5	-29.92	20.72	6	-1.444	0.199
treatment4 - treatment6	-118.67	20.72	6	-5.727	0.001 **
treatment4 - treatment7	-82.42	20.72	6	-3.977	0.007 **
treatment4 - treatment8	50.33	20.72	6	2.429	0.051
treatment4 - treatment9	-59.92	20.72	6	-2.892	0.028 *
treatment4 - treatment10	-173.67	20.72	6	-8.381	0.000 ***
treatment4 - treatment11	-35.42	20.72	6	-1.709	0.138
treatment4 - treatment12	-24.42	20.72	6	-1.178	0.283
treatment5 - treatment6	-88.75	26.75	6	-3.318	0.016 *
treatment5 - treatment7	-52.50	26.75	6	-1.963	0.097
treatment5 - treatment8	80.25	26.75	6	3.000	0.024 *
treatment5 - treatment9	-30.00	23.93	6	-1.254	0.257
treatment5 - treatment10	-143.75	26.75	6	-5.374	0.002 **
treatment5 - treatment11	-5.50	26.75	6	-0.206	0.844
treatment5 - treatment12	5.50	26.75	6	0.206	0.844
treatment6 - treatment7	36.25	26.75	6	1.355	0.224
treatment6 - treatment8	169.00	23.93	6	7.063	0.000 ***
treatment6 - treatment9	58.75	26.75	6	2.196	0.070
treatment6 - treatment10	-55.00	23.93	6	-2.299	0.061
treatment6 - treatment11	83.25	26.75	6	3.112	0.021 *
treatment6 - treatment12	94.25	26.75	6	3.523	0.012 *
treatment7 - treatment8	132.75	26.75	6	4.962	0.003 **
treatment7 - treatment9	22.50	26.75	6	0.841	0.433

```

treatment7 - treatment10   -91.25 26.75  6  -3.411  0.014   *
treatment7 - treatment11    47.00 23.93  6   1.964  0.097
treatment7 - treatment12   58.00 23.93  6   2.424  0.052
treatment8 - treatment9  -110.25 26.75  6  -4.121  0.006   **
treatment8 - treatment10 -224.00 23.93  6  -9.362  0.000 *** 
treatment8 - treatment11 -85.75 26.75  6  -3.205  0.018   *
treatment8 - treatment12 -74.75 26.75  6  -2.794  0.031   *
treatment9 - treatment10 -113.75 26.75  6  -4.252  0.005   **
treatment9 - treatment11  24.50 26.75  6   0.916  0.395
treatment9 - treatment12  35.50 26.75  6   1.327  0.233
treatment10 - treatment11 138.25 26.75  6   5.168  0.002   **
treatment10 - treatment12 149.25 26.75  6   5.579  0.001   **
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	213.67	18.27	6	168.95	258.38	12
2	228.00	9.77	6	204.10	251.90	1
3	247.67	9.77	6	223.76	271.57	123
1	256.00	9.77	6	232.10	279.90	1234
4	264.00	9.77	6	240.10	287.90	234
12	288.42	18.27	6	243.70	333.13	345
5	293.92	18.27	6	249.20	338.63	345
11	299.42	18.27	6	254.70	344.13	45
9	323.92	18.27	6	279.20	368.63	56
7	346.42	18.27	6	301.70	391.13	56
6	382.67	18.27	6	337.95	427.38	67
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
```

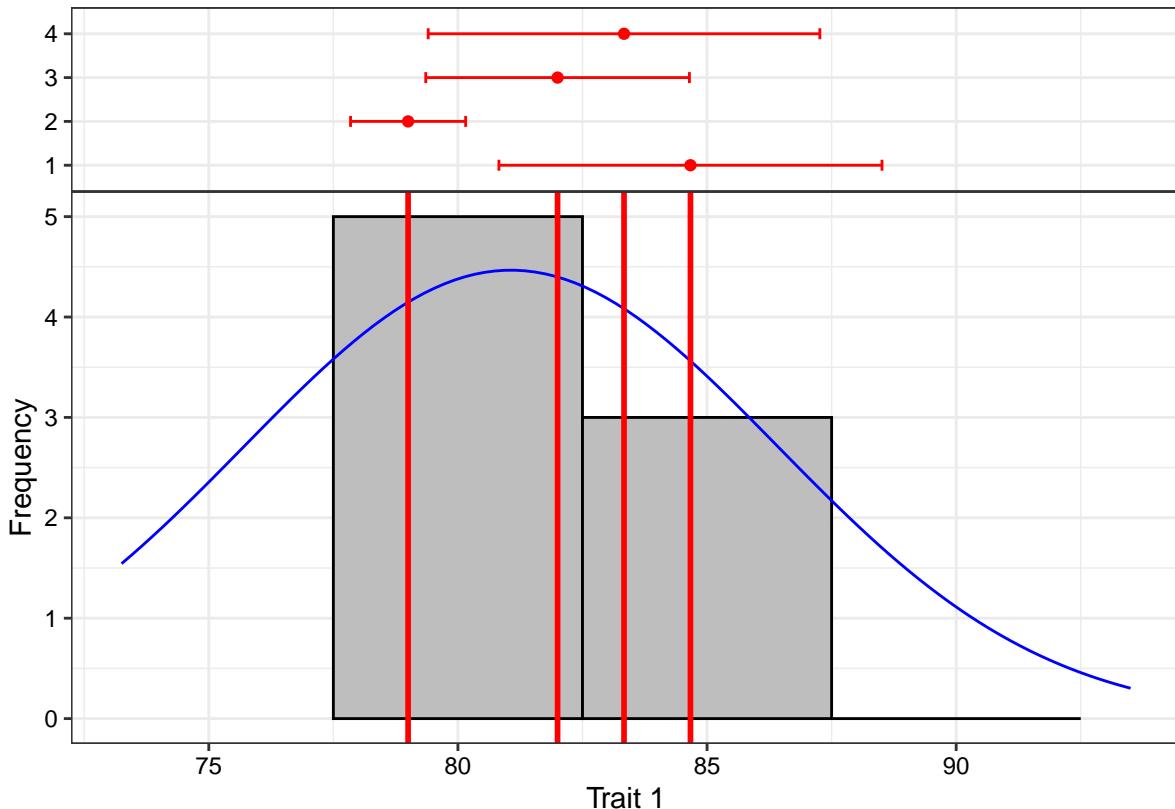
```
2.787997 0.536812
```

```
$`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: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),  
  min.n = 1, right = TRUE) :  
  extra argument 'right' will be disregarded  
Warning: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),  
  min.n = 1, right = TRUE) :  
  extra argument 'right' will be disregarded  
  
Warning: Removed 2 rows containing missing values or values outside the scale range (`geom_bar()`).  
plot(freq1)
```



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

```
Warning: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
```

```

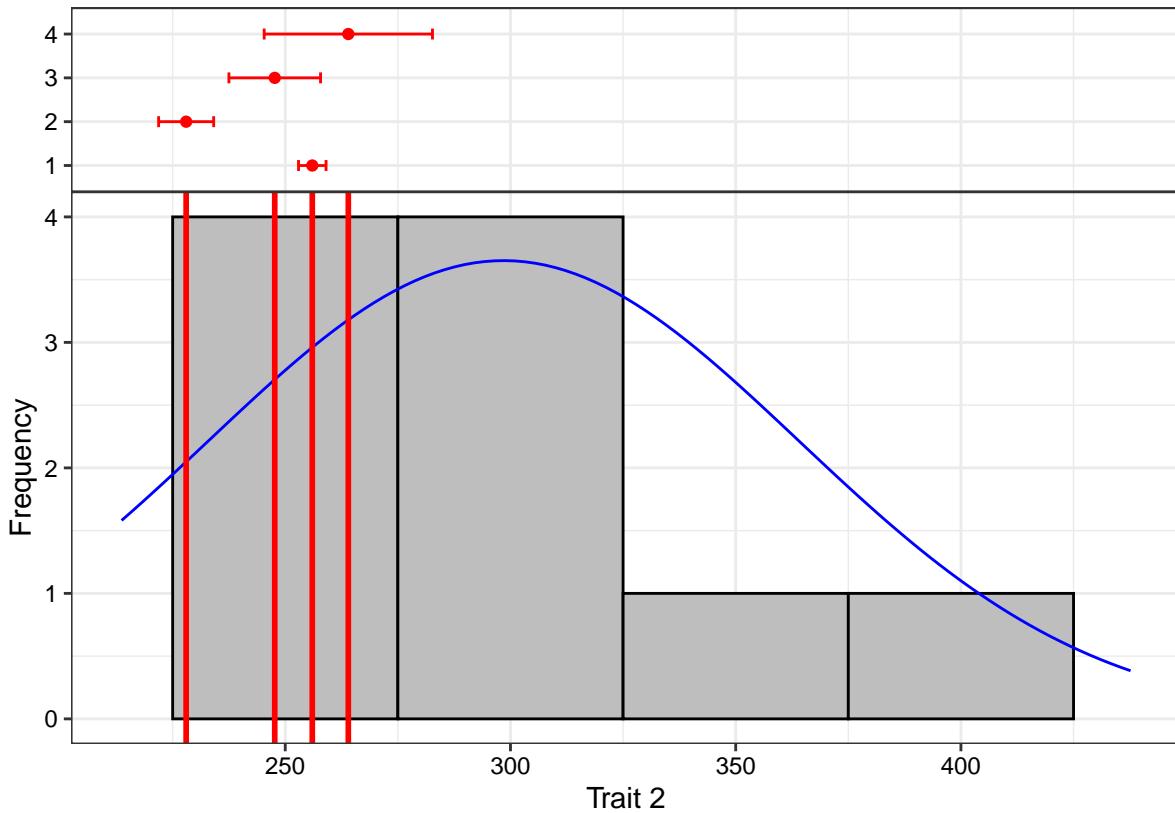
min.n = 1, right = TRUE) :
extra argument 'right' will be disregarded

Warning: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
min.n = 1, right = TRUE) :
extra argument 'right' will be disregarded

Warning: Removed 2 rows containing missing values or values outside the scale range (`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)

```

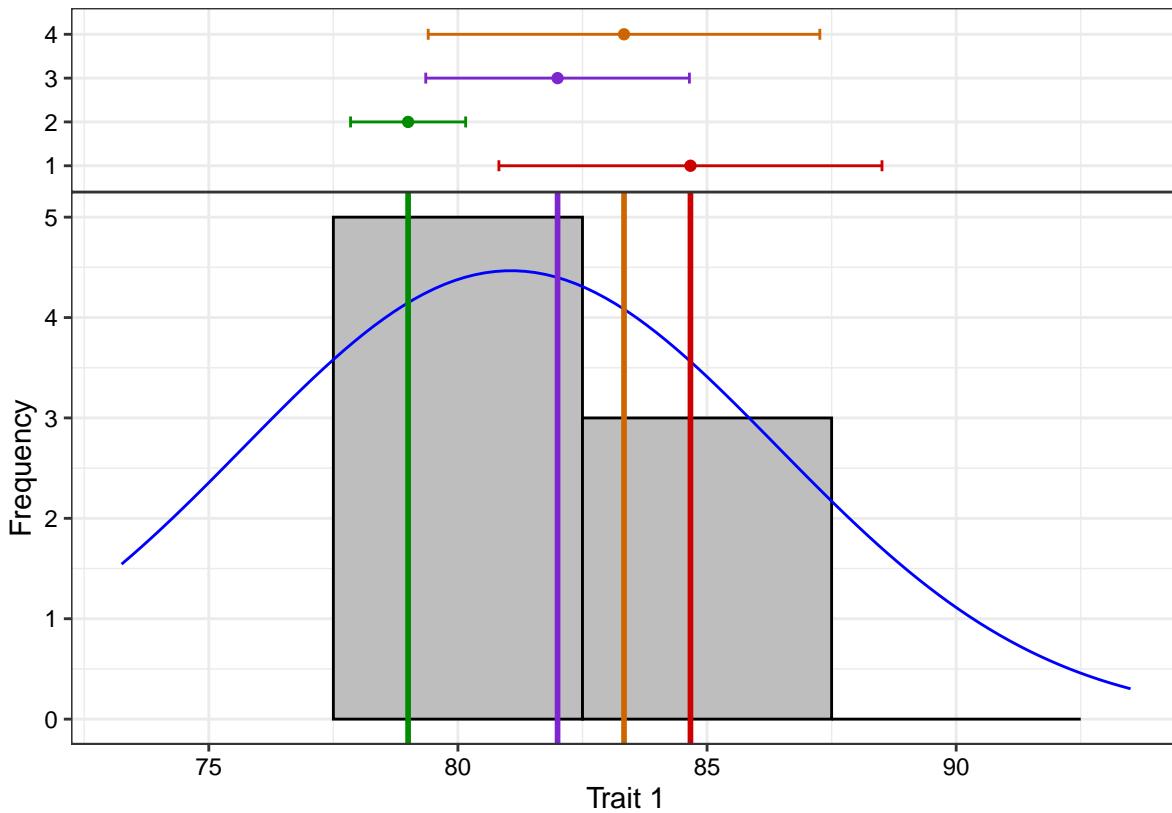
```

Warning: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
min.n = 1, right = TRUE) :
extra argument 'right' will be disregarded
Warning: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
min.n = 1, right = TRUE) :
extra argument 'right' will be disregarded

Warning: Removed 2 rows containing missing values or values outside the scale range (`geom_bar()`).

plot(freq1)

```

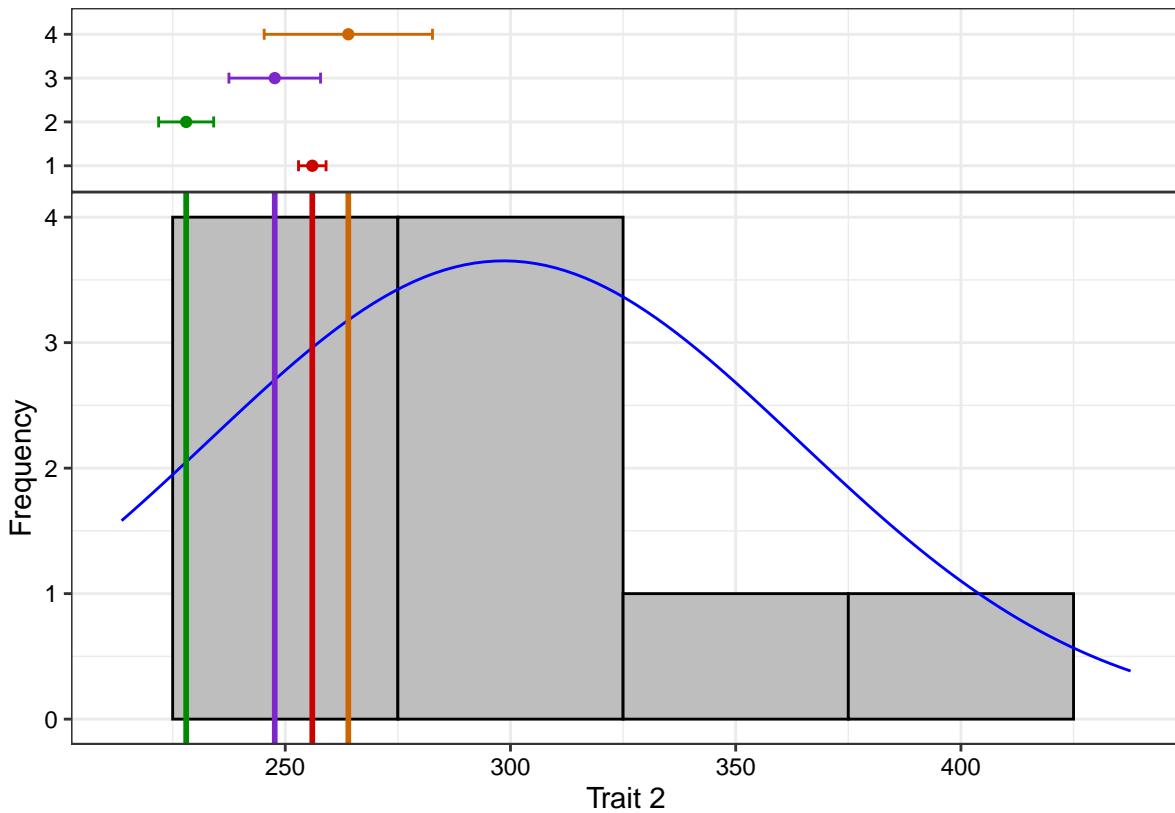


```
# Frequency distribution for variable y2
freq2 <- freqdist.augmentedRCBD(out2, xlab = "Trait 2", check.col = colset)
```

```
Warning: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
  min.n = 1, right = TRUE) :
  extra argument 'right' will be disregarded
```

```
Warning: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
  min.n = 1, right = TRUE) :
  extra argument 'right' will be disregarded
```

```
Warning: Removed 2 rows containing missing values or values outside the scale range (`geom_bar()`).
plot(freq2)
```

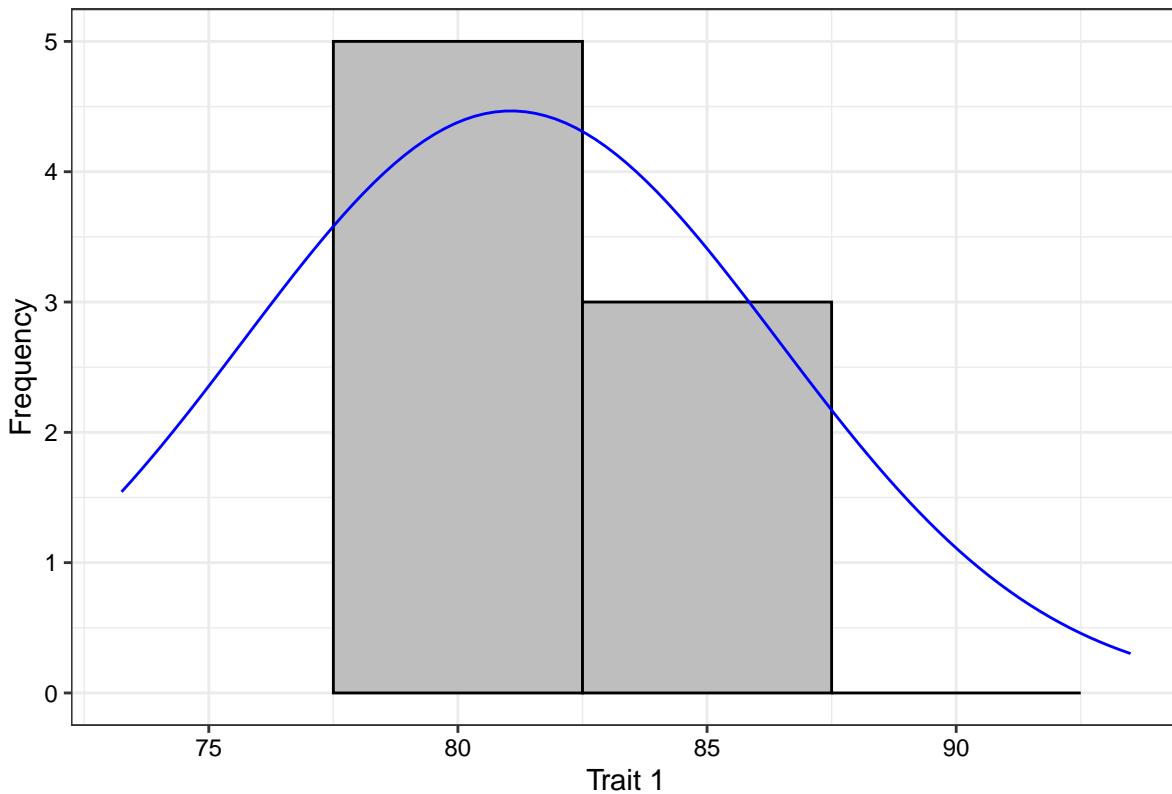


The default the check highlighting can be avoided using the argument `highlight.check = FALSE`.

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

```
Warning: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
  min.n = 1, right = TRUE) :
  extra argument 'right' will be disregarded
Warning: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
  min.n = 1, right = TRUE) :
  extra argument 'right' will be disregarded
```

```
Warning: Removed 2 rows containing missing values or values outside the scale range (`geom_bar()`).
plot(freq1)
```

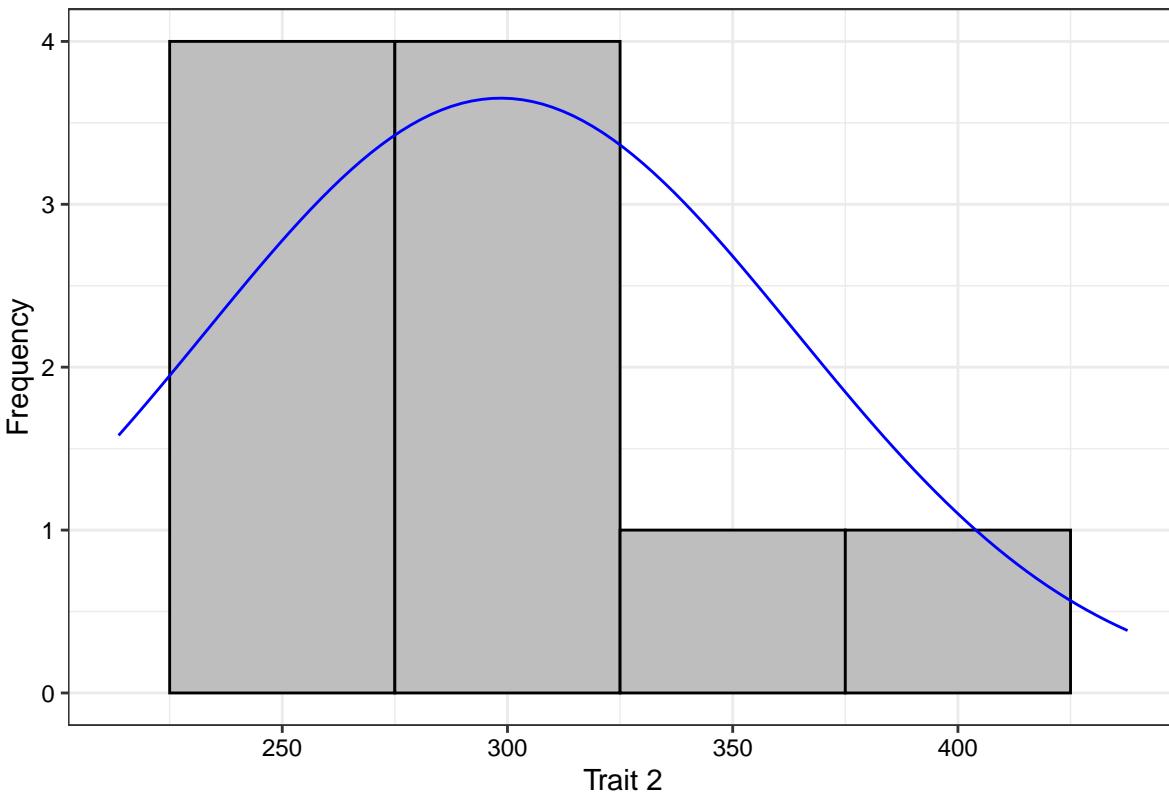


```
# Frequency distribution for variable y2
freq2 <- freqdist.augmentedRCBD(out2, xlab = "Trait 2",
                                 highlight.check = FALSE)
```

Warning: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
 min.n = 1, right = TRUE) :
 extra argument 'right' will be disregarded

Warning: In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
 min.n = 1, right = TRUE) :
 extra argument 'right' will be disregarded

Warning: Removed 2 rows containing missing values or values outside the scale range (`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 Madhavamnenon (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 analysis may not be appropriate for 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.docx"),
                      file.type = "word")

# MS word report for variable y2
report.augmentedRCBD(aug = out2,
                      target = file.path(tempdir(),
                                         "augmentedRCBD output.docx"),
                      file.type = "word")
```

The screenshot shows a Microsoft Word document titled "augmentedRCBD output.docx". The ribbon menu is visible at the top. A logo for "augmentedRCBD" is in the top right. The table of contents lists various sections with page numbers:

Details.....	1
ANOVA, Treatment Adjusted.....	1
ANOVA, Block Adjusted	2
Standard Errors and Critical Differences	2
Overall Adjusted Mean	2
Coefficient of Variation	2
Means.....	2
Frequency Distribution.....	3
Descriptive Statistics	3
Genetic Variability Analysis	4
Comparisons	4
Groups	7
Warnings	7
Frequency Distribution	7
Genetic Variability Analysis	8

The "Details" section is currently selected. It contains a table with the following data:

Item	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

At the bottom, it says "Page 1 of 8 1111 words" and "English (United States)".

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

Alternatively, the analysis results can also be exported to a MS Excel file as follows.

```
# MS excel report for variable y1
report.augmentedRCBD(aug = out1,
                      target = file.path(tempdir()),
```

```
        "augmentedRCBD output.xlsx"),
file.type = "excel")

# MS excel report for variable y2
report.augmentedRCBD(aug = out2,
                      target = file.path(tempdir(),
                                         "augmentedRCBD output.xlsx"),
                      file.type = "excel")
```

The screenshot shows an MS Excel spreadsheet with the following details:

- Title Bar:** Shows "AutoSave Off" and the file name "augmentedRCBD output.xlsx".
- Toolbar:** Standard Excel toolbar with File, Home, Insert, Page Layout, Formulas, Data, Review, View, and Help.
- Cell A1:** Contains the text "augmented RCBD".
- Cells A4 to A6:** Contain URLs:
 - <https://aravind-j.github.io/augmentedRCBD>
 - <https://github.com/aravind-j/augmentedRCBD>
 - <https://CRAN.R-project.org/package=augmentedRCBD>
- Section Headers:**
 - SI.No Sheets**
 - 1 Details**
 - 2 ANOVA, Treatment Adjusted**
 - 3 ANOVA, Block Adjusted**
 - 4 SEs and CDs**
 - 5 Overall Adjusted Mean**
 - 6 Coefficient of Variation**
 - 7 Means**
 - 8 Frequency Distribution**
 - 9 Descriptive Statistics**
 - 10 Genetic Variability Analysis**
 - 11 Comparisons**
 - 12 Groups**
 - 13 Warnings**
- Bottom Navigation:** Includes tabs for Index, Details, ANOVA, Treatment Adjusted, ANOVA, Block Adjusted, SEs, and other options.
- Status Bar:** Shows "Ready" and "Accessibility: Investigate".

Fig. 7: MS Excel report generated with `report.augmentedRCBD` function.

8 Data Analysis for a Multiple Traits

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

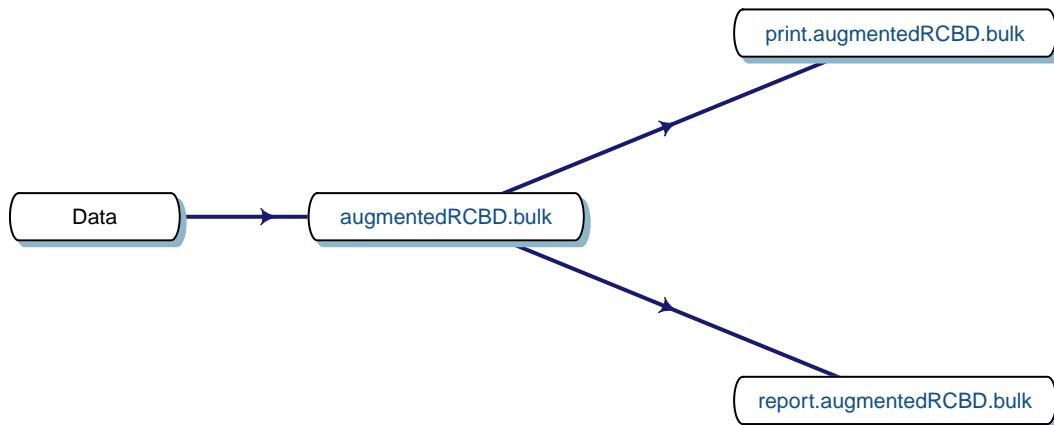


Fig. 8. Workflow for analysis of multiple traits with `augmentedRCBD`.

8.1 `augmentedRCBD.bulk()`

Consider the data frame `data` imported from Table 1 according to the instructions in section 4.8.

```
str(data)
```

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

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

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

However in this case treatment comparisons/grouping by least significant difference or Tukey's honest significant difference method is not computed. Also the output object size is reduced using the `simplify = TRUE` argument in the `augmentedRCBD` function.

The logical arguments `describe`, `freqdist` and `gva` can be used to specify whether to generate the descriptive statistics, frequency distribution plots and genetic variability statistics respectively. If `gva = TRUE`, then plots to compare phenotypic and genotypic coefficient of variation, broad sense heritability and genetic advance over mean between traits are also generated.

```
bout <- augmentedRCBD.bulk(data = data, block = "blk",
                             treatment = "trt", traits = c("y1", "y2"),
                             checks = NULL, alpha = 0.05, describe = TRUE,
```

```

freqdist = TRUE, gva = TRUE,
check.col = c("brown", "darkcyan",
             "forestgreen", "purple"),
console = TRUE)

```

ANOVA for y1 computed (1/2)

ANOVA for y2 computed (2/2)

Augmented Design Details

	Trait	Number of blocks	Number of treatments	Number of check treatments	Number of test treatments	
1	y1	3		12	4	
2	y2	3		12	4	
<hr/>						
Check treatments						
1		1, 2, 3, 4				
2		1, 2, 3, 4				

ANOVA, Treatment Adjusted

Source	Df	Mean.Sq	
		y1	y2
Block (ignoring Treatments)	2	180.04	*
Treatment (eliminating Blocks)	11	25.92	11 5360.49 **
Treatment: Check	3	17.64	3 716.75
Treatment: Test and Test vs. Check	8	29.02	8 7101.89 **
Residuals	6	26.97	6 286.25

P > 0.05; * P <= 0.05; ** P <= 0.01

ANOVA, Block Adjusted

Source	Df	Mean.Sq	
		y1	y2
Treatment (ignoring Blocks)	11	52.33	11 5882.50 **
Treatment: Check	3	17.64	3 716.75
Treatment: Test	7	72.27	7 4980.41 **
Treatment: Test vs. Check	1	16.87	1 27694.41 **
Block (eliminating Treatments)	2	34.75	2 638.58
Residuals	6	26.97	6 286.25

P > 0.05; * P <= 0.05; ** P <= 0.01

Coefficient of Variation

Trait	CV
y1	6.37
y2	6.06

Overall Adjusted Mean

```
Trait Overall.adjusted.mean
y1           81.06
y2          298.48
```

Standard Errors

=====

	Comparison	y1	y2
A Test Treatment and a Control Treatment	6.70	21.84	
Control Treatment Means	4.24	13.81	
Two Test Treatments (Different Blocks)	8.21	26.75	
Two Test Treatments (Same Block)	7.34	23.93	

Critical Difference

=====

alpha = 0.05

	Comparison	y1	y2
A Test Treatment and a Control Treatment	16.41	53.45	
Control Treatment Means	10.38	33.80	
Two Test Treatments (Different Blocks)	20.09	65.46	
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_sig
y1	12	81.06	1.55	5.36	73.25	93.50	0.93		3.52	
y2	12	298.48	18.92	65.55	213.67	437.67	0.74		2.79	

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.category	
y1 †	81.06	72.27	45.30	26.97	8.30		Low	10.49	Medium	6.41	62.68	High
y2	298.48	4980.41	4694.16	286.25	22.95		High	23.64	High	5.67	94.25	High
GA	GAM	GAM.category										
10.99	13.56	Medium										
137.22	45.97	High										

Warning:

† P-value for "Treatment: Test" is > 0.05. Genetic variability analysis may not be appropriate for th

Warning:

† Negative GV detected.

GCV, GCV category, hBS, hBS category, GA, GAM and
GAM category could not be computed.

Warning Messages

```
=====
```

```
[Frequency Distribution]
<y1>
In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
  min.n = 1, right = TRUE) :
  extra argument 'right' will be disregarded
In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
  min.n = 1, right = TRUE) :
  extra argument 'right' will be disregarded
Removed 2 rows containing missing values or values outside the scale range (`geom_bar()`).

<y2>
In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
  min.n = 1, right = TRUE) :
  extra argument 'right' will be disregarded
In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
  min.n = 1, right = TRUE) :
  extra argument 'right' will be disregarded
Removed 2 rows containing missing values or values outside the scale range (`geom_bar()`).
```

[GVA]

<y1>

P-value for "Treatment: Test" is > 0.05. Genetic variability analysis may not be appropriate for this

Treatment Means

```
=====
```

Treatment	Block	y1	y2
1		84.67	256.00
10	3	77.25	437.67
11	1	86.50	299.42
12	1	79.50	288.42
2		79.00	228.00
3		82.00	247.67
4		83.33	264.00
5	2	78.25	293.92
6	3	78.25	382.67
7	1	93.50	346.42
8	3	73.25	213.67
9	2	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

```
=====

```

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

ANOVA, Treatment Adjusted

```
=====

```

Mean.Sq

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

P > 0.05; * P <= 0.05; ** P <= 0.01

ANOVA, Block Adjusted

```
=====

```

Mean.Sq

Source	Df	y1	Df	y2
Treatment (ignoring Blocks)	11	52.33	11	5882.50 **
Treatment: Check	3	17.64	3	716.75
Treatment: Test	7	72.27	7	4980.41 **
Treatment: Test vs. Check	1	16.87	1	27694.41 **
Block (eliminating Treatments)	2	34.75	2	638.58
Residuals	6	26.97	6	286.25

P > 0.05; * P <= 0.05; ** P <= 0.01

Coefficient of Variation

```
=====

```

Trait CV

y1 6.37

y2 6.06

Overall Adjusted Mean

```
=====

```

Trait Overall.adjusted.mean

y1 81.06

y2 298.48

Standard Errors

```
=====

```

Comparison y1 y2

A Test Treatment and a Control Treatment 6.70 21.84

```

Control Treatment Means 4.24 13.81
Two Test Treatments (Different Blocks) 8.21 26.75
Two Test Treatments (Same Block) 7.34 23.93

```

Critical Difference

=====

alpha = 0.05

	Comparison	y1	y2
A Test Treatment and a Control Treatment	16.41	53.45	
Control Treatment Means	10.38	33.80	
Two Test Treatments (Different Blocks)	20.09	65.46	
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_sig
y1	12	81.06	1.55	5.36	73.25	93.50	0.93		3.52	
y2	12	298.48	18.92	65.55	213.67	437.67	0.74		2.79	

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.category
y1 †	81.06	72.27	45.30	26.97	8.30	Low	10.49	Medium	6.41	62.68	High
y2	298.48	4980.41	4694.16	286.25	22.95	High	23.64	High	5.67	94.25	High
GA	GAM	GAM.category									
10.99	13.56	Medium									
137.22	45.97	High									

Warning:

† P-value for "Treatment: Test" is > 0.05. Genetic variability analysis may not be appropriate for th

Warning:

‡ Negative GV detected.

GCV, GCV category, hBS, hBS category, GA, GAM and
GAM category could not be computed.

Warning Messages

=====

[Frequency Distribution]

<y1>

```

In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
  min.n = 1, right = TRUE) :
  extra argument 'right' will be disregarded
In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),

```

```

min.n = 1, right = TRUE) :
extra argument 'right' will be disregarded
Removed 2 rows containing missing values or values outside the scale range (`geom_bar()`).

<y2>
In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
  min.n = 1, right = TRUE) :
extra argument 'right' will be disregarded
In pretty.default(range(x, na.rm = TRUE), n = nclass.Sturges(na.omit(x)),
  min.n = 1, right = TRUE) :
extra argument 'right' will be disregarded
Removed 2 rows containing missing values or values outside the scale range (`geom_bar()`).

```

[GVA]

<y1>

P-value for "Treatment: Test" is > 0.05. Genetic variability analysis may not be appropriate for this

Treatment Means

=====

Treatment	Block	y1	y2
1		84.67	256.00
10	3	77.25	437.67
11	1	86.50	299.42
12	1	79.50	288.42
2		79.00	228.00
3		82.00	247.67
4		83.33	264.00
5	2	78.25	293.92
6	3	78.25	382.67
7	1	93.50	346.42
8	3	73.25	213.67
9	2	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"),
                           file.type = "word")

```

The screenshot shows a Microsoft Word document with the title "augmentedRCBD bulk output.docx" at the top. The ribbon menu includes File, Home, Insert, Draw, Design, Layout, References, Mailings, Review, View, Zotero, and Help. A search bar is also present. The main content area displays a table of contents for the "augmentedRCBD" package, which includes sections like Details, ANOVA, Descriptive Statistics, Frequency Distribution, Genetic Variability Analysis, and Adjusted Means, each with a corresponding page number. The document is in landscape orientation with a light blue background.

	Page Number
Details.....	1
ANOVA, Treatment Adjusted.....	2
ANOVA, Block Adjusted.....	2
Standard Errors.....	2
Critical Difference (5%).....	3
Coefficient of Variance.....	3
Overall Adjusted Mean.....	3
Check Statistics.....	3
y1	3
y2	4
Descriptive Statistics.....	4
Frequency Distribution.....	4
y1	4
y2	5
Genetic Variability Analysis.....	5
Genetic Variability Analysis Plots.....	6
Phenotypic and Genotypic Coefficient of Variability.....	6
Broad Sense Heritability.....	6
Genetic Advance Over Mean.....	7
Adjusted Means.....	7
Warnings.....	8
Frequency Distribution	8
Genetic Variability Analysis.....	8

Details

Page 1 of 8 583 words English (United States) Text Predictions: On Accessibility: Investigate

Fig. 9: MS Word report generated with `report.augmentedRCBD.bulk` function.

Alternatively, the analysis results can also be exported to a MS Excel file as follows.

```
# MS excel report
report.augmentedRCBD.bulk(aug.bulk = bout,
                           target = file.path(tempdir()),
```

```
    "augmentedRCBD bulk output.xlsx"),  
    file.type = "excel")
```

The screenshot shows a Microsoft Excel spreadsheet titled "augmentedRCBD output.xlsx". The spreadsheet has a green header bar with standard menu options: File, Home, Insert, Page Layout, Formulas, Data, Review, View, and Help. The main content area displays a table of contents for the report. Row 1 contains the text "augmented RCBD" inside an orange hexagonal logo. Rows 4 through 6 list URLs: "https://aravind-j.github.io/augmentedRCBD", "https://github.com/aravind-j/augmentedRCBD", and "https://CRAN.R-project.org/package=augmentedRCBD". Row 9 is a header for "SI.No Sheets" with a horizontal line below it. Rows 10 through 22 list 13 items: 1 Details, 2 ANOVA, Treatment Adjusted, 3 ANOVA, Block Adjusted, 4 SEs and CDs, 5 Overall Adjusted Mean, 6 Coefficient of Variation, 7 Means, 8 Frequency Distribution, 9 Descriptive Statistics, 10 Genetic Variability Analysis, 11 Comparisons, 12 Groups, and 13 Warnings. The bottom navigation bar includes tabs for Index, Details, ANOVA, Treatment Adjusted, ANOVA, Block Adjusted, SEs, and more.

Fig. 10: MS Excel report generated with `report.augmentedRCBD.bulk` function.

9 Citing augmentedRCBD

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

Aravind, J., Mukesh Sankar, S., Wankhede, D. P., and Kaur, V. (2025). augmentedRCBD: Analysis of Augmented Randomised Complete Block Designs. R package version 0.1.7.9000, <https://aravind-j.github.io/augmentedRCBD/> <https://cran.r-project.org/package=augmentedRCBD>.

A BibTeX entry for LaTeX users is

```
@Manual{,
  title = {augmentedRCBD: Analysis of Augmented Randomised Complete Block Designs},
  author = {J. Aravind and S. {Mukesh Sankar} and Dhammaprakash Pandhari Wankhede and Vikender Kaur},
  note = {R package version 0.1.7.9000 https://aravind-j.github.io/augmentedRCBD/ https://cran.r-project.org/package=augmentedRCBD},
  year = {2025},
}
```

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

10 Session Info

```
sessionInfo()

R Under development (unstable) (2025-12-09 r89129 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows 11 x64 (build 26200)

Matrix products: default
  LAPACK version 3.12.1

locale:
[1] LC_COLLATE=English_India.utf8  LC_CTYPE=English_India.utf8    LC_MONETARY=English_India.utf8
[4] LC_NUMERIC=C                 LC_TIME=English_India.utf8

time zone: Asia/Calcutta
tzcode source: internal

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

other attached packages:
[1] diagram_1.6.5          shape_1.4.6.1        augmentedRCBD_0.1.7.9000 RCurl_1.98-1.17

loaded via a namespace (and not attached):
[1] Rdpack_2.6.4            bitops_1.0-9          remotes_2.5.0.9000     testthat_3.3.1
[5] sandwich_3.1-1          rlang_1.1.6           magrittr_2.0.4         multcomp_1.4-29
[9] compiler_4.6.0          roxygen2_7.3.3       systemfonts_1.3.1     callr_3.7.6
[13] vctrs_0.6.5             reshape2_1.4.5       numform_0.7.0         stringr_1.6.0
[17] pkgconfig_2.0.3          fastmap_1.2.0        ellipsis_0.3.2        labeling_0.4.3
[21] pander_0.6.6            rmarkdown_2.30       sessioninfo_1.2.3     ps_1.9.1
```

[25] ragg_1.5.0	tinytex_0.58	purrr_1.2.0	xfun_0.54
[29] cachem_1.1.0	uuid_1.2-1	parallel_4.6.0	R6_2.6.1
[33] stringi_1.8.7	RColorBrewer_1.1-3	pkgload_1.4.1	brio_1.1.5
[37] estimability_1.5.1	Rcpp_1.1.0.8.1	knitr_1.50	usethis_3.2.1
[41] zoo_1.8-14	Matrix_1.7-4	splines_4.6.0	tidyselect_1.2.1
[45] rstudioapi_0.17.1	dichromat_2.0-0.1	yaml_2.3.12	codetools_0.2-20
[49] curl_7.0.0	processx_3.8.6	pkgbuild_1.4.8	lattice_0.22-7
[53] tibble_3.3.0	plyr_1.8.9	withr_3.0.2	S7_0.2.1
[57] flextable_0.9.10	askpass_1.2.1	coda_0.19-4.1	evaluate_1.0.5
[61] moments_0.14.1	desc_1.4.3	survival_3.8-3	rJava_1.0-11
[65] zip_2.3.3	xml2_1.5.1	pillar_1.11.1	rsconnect_1.7.0
[69] generics_0.1.4	rprojroot_2.1.1	mathjaxr_2.0-0	ggplot2_4.0.1
[73] scales_1.4.0	xtable_1.8-4	glue_1.8.0	gdtools_0.4.4
[77] emmeans_2.0.0	tools_4.6.0	data.table_1.17.8	openxlsx_4.2.8.1
[81] XML_3.99-0.20	fs_1.6.6	mvtnorm_1.3-3	grid_4.6.0
[85] tidyR_1.3.1	rbibutils_2.4	devtools_2.4.6	cli_3.6.5
[89] textshaping_1.0.4	officer_0.7.2	fontBitstreamVera_0.1.1	dplyr_1.1.4
[93] gtable_0.3.6	digest_0.6.39	fontquiver_0.2.1	TH.data_1.1-5
[97] farver_2.1.2	memoise_2.0.1	htmltools_0.5.9	lifecycle_1.0.4
[101] httr_1.4.7	multcompView_0.1-10	fontLiberation_0.1.0	openssl_2.3.4
[105] MASS_7.3-65			

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