Data Analysis with `augmentedRCBD`

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Contents

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. (1956, 1961). 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 languates 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/.

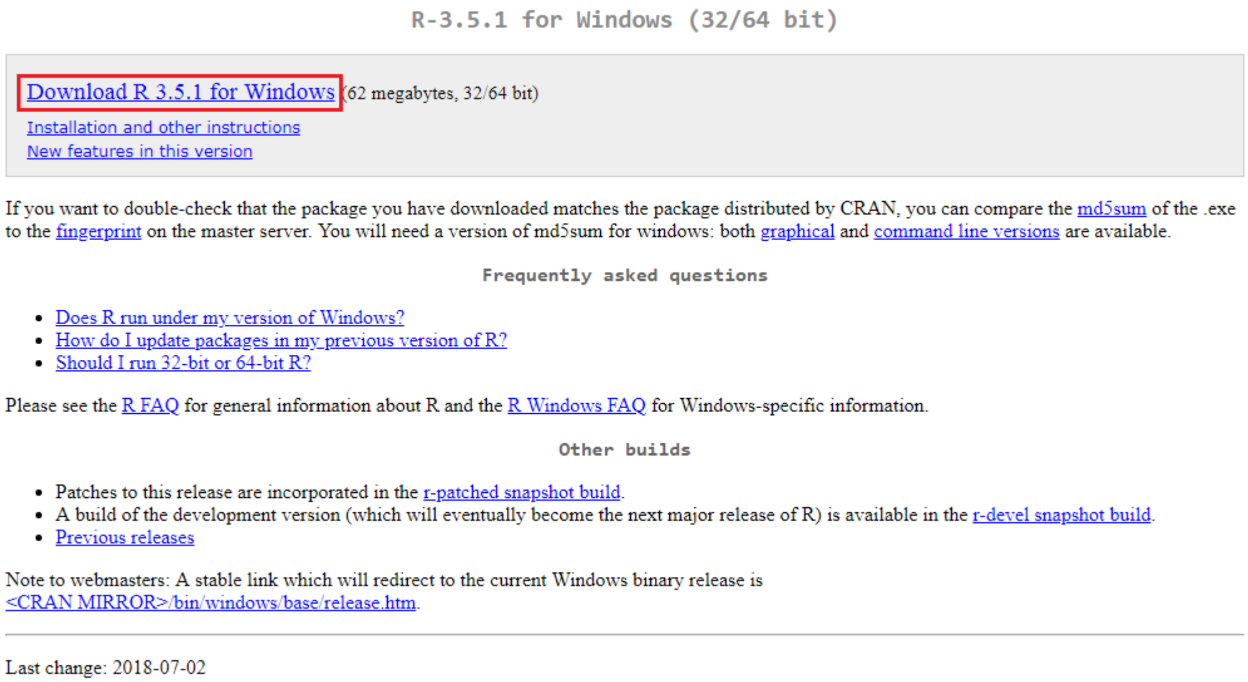
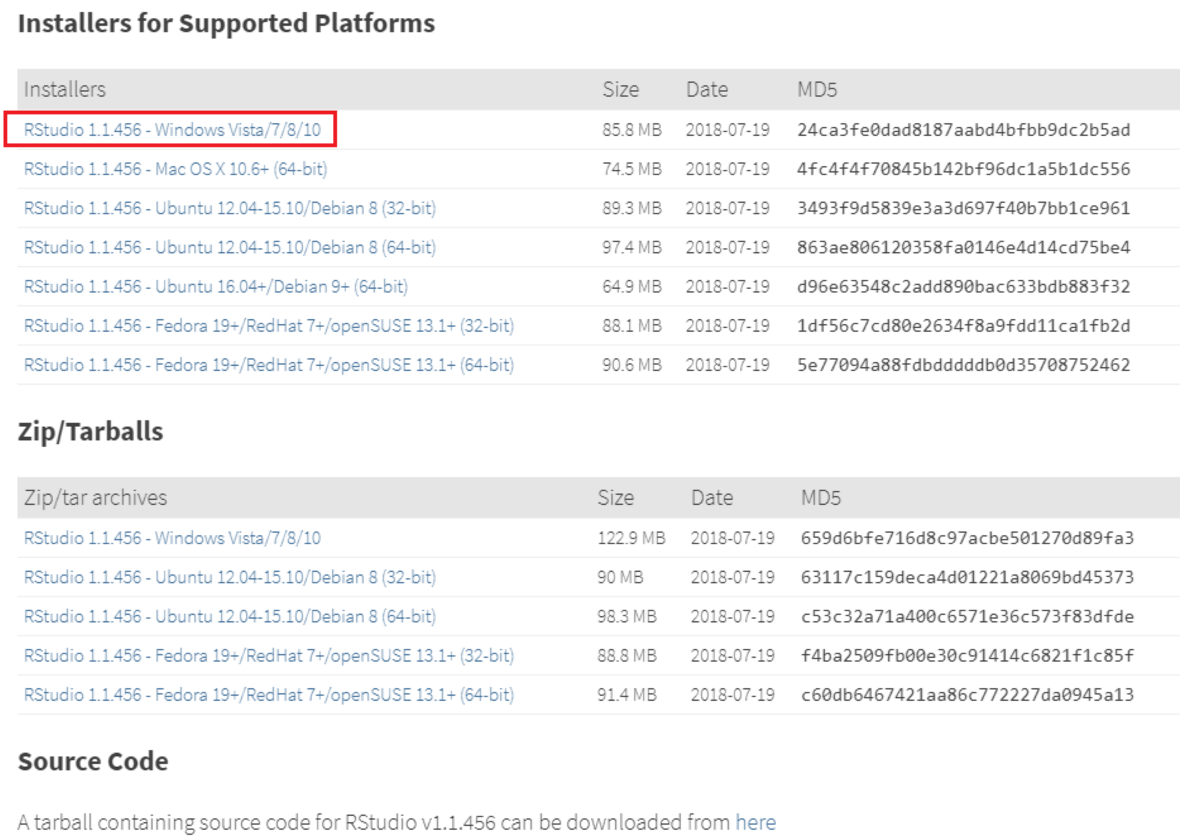


Fig. 1: The `R` download location.

3.2 Installing `RStudio`

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

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



Installers for Supported Platforms

Installers	Size	Date	MD5
RStudio 1.1.456 - Windows Vista/7/8/10	85.8 MB	2018-07-19	24ca3fe0dad8187aabd4bfbb9dc2b5ad
RStudio 1.1.456 - Mac OS X 10.6+ (64-bit)	74.5 MB	2018-07-19	4fc4f4f70845b142bf96dc1a5b1dc556
RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (32-bit)	89.3 MB	2018-07-19	3493f9d5839e3a3d697f40b7bb1ce961
RStudio 1.1.456 - Ubuntu 12.04-15.10/Debian 8 (64-bit)	97.4 MB	2018-07-19	863ae806120358fa0146e4d14cd75be4
RStudio 1.1.456 - Ubuntu 16.04+/Debian 9+ (64-bit)	64.9 MB	2018-07-19	d96e63548c2add890bac633bdb883f32
RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit)	88.1 MB	2018-07-19	1df56c7cd80e2634f8a9fdd11ca1fb2d
RStudio 1.1.456 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit)	90.6 MB	2018-07-19	5e77094a88fdbddddb0d35708752462

Zip/Tarballs

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

Source Code

A tarball containing source code for RStudio v1.1.456 can be downloaded from here

Fig. 2: The `RStudio` download location.

3.3 The `RStudio` Interface

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

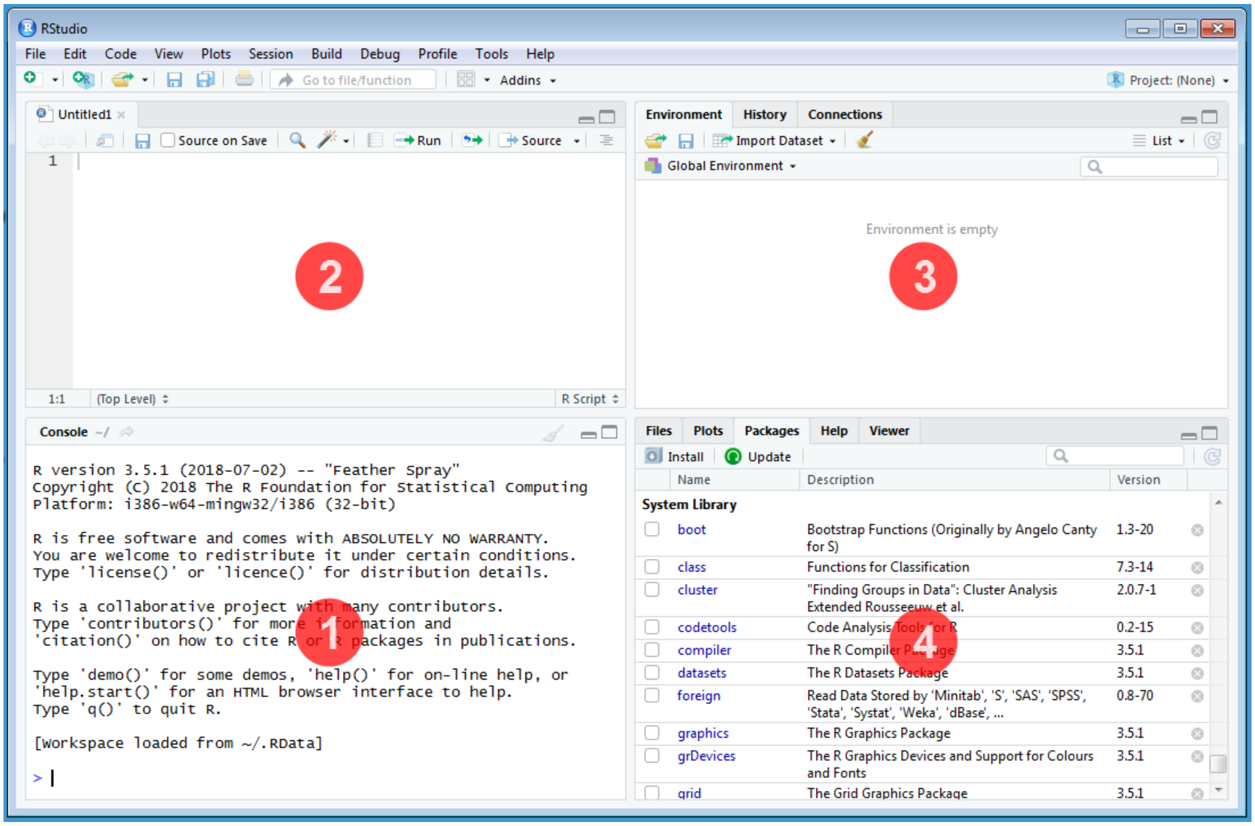


Fig. 3: The default RStudio interface with the four panes.

3.3.1 Console

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

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

```
1+1
```

```
[1] 2
```

3.3.2 Source

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

3.3.3 Environment|History|Connections

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

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

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

3.3.4 Files|Plots|Packages|Help|Viewer

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

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

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

The 'Viewer' tab shows any web content output generated by an `R` code.

4 Some Basics

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

4.1 Working Directory

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

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

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

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

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

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

4.2 Expression and Assignment

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

```
# Constant
123
```

```
[1] 123
```

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

```
[1] 3
```

```
# Condition
34 > 25
```

```
[1] TRUE
```

```
1 == 2
```

```
[1] FALSE
```

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

```
[1] 51.25
```

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

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

```
[1] 3
```

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

4.3 Objects and Functions

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

4.3.1 Vector

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

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

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

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

```
str(a)
```

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

```
length(a)
```

```
[1] 3
```

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

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

```
str(b)
```

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

```
length(b)
```

```
[1] 3
```

The vector mode 'character' store text.

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

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

```
str(c)
```

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

```
length(c)
```

```
[1] 3
```

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

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

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

```
str(d)
```

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

```
length(d)
```

```
[1] 6
```

4.3.2 Factor

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

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

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

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

```
[1] FALSE
```

```
# Apply the factor function
factor_catg <- factor(catg)

factor_catg
```

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

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

```
[1] TRUE
```

```
class(factor_catg)
```

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

```
str(factor_catg)
```

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

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

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

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

```
str(a)
```

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

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

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

```
str(fac_a)
```

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

```
# Conversion of integer to factor
b <- c(1L, 2L, 3L)
class(b)
```

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

```
str(b)
```

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

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

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

```
str(fac_b)
```

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

```
# Conversion of character to factor
c <- c("one","two","three")
class(c)
```

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

```
str(c)
```

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

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

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

```
str(fac_c)
```

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

4.3.3 Matrix

A 'matrix' in `R` is a vector with the attributes '`nrow`' and '`ncol`'.

```r
# 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
```

```r
class(m)
```

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

```r
typeof(m)
```

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

```r
# Dimensions of m
dim(m)
```

```
[1] 5 4
```

4.3.4 List

A 'list' is a containter 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.

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

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

```r
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.

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

```
  L x y          z
1 A 1 1       This
2 B 1 2         is
```

```
3 C 1 3          a
4 D 1 4 data frame
```

```
str(df)
```

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

```
attributes(df)
```

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

$class
[1] "data.frame"

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

```
rownames(df)
```

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

```
colnames(df)
```

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

4.3.6 Functions

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

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

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

```
[1] 2.1
```

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

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

```
[1] 5
```

4.4 Special Elements

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

`NA` (not available) indicates missing data.

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

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

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

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

```
anyNA(x)
```

```
[1] TRUE
```

```
a
```

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

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

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

`Inf` indicates infinity.

```
1/0
```

```
[1] Inf
```

`NaN` (Not a Number) indicates any undefined value.

```
0/0
```

```
[1] NaN
```

4.5 Indexing

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

Consider a vector `a`.

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

```
[1] 1
```

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

```
[1] 2.0 3.3
```

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

```
[1] 3.3 6.7
```

Consider a matrix `m`.

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

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

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

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

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

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

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

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

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

```
b
5
```

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

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

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

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

Consider a list w.

```r
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
```

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

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

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

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

```
w$data
```

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

Consider a data frame `df`.

```
df
```

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

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

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

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

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

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

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

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

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

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

```
[1] 1
```

```
# Indexing by name
df$L
```

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

```
df$z
```

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

4.6 Help Documentation

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

```
?ls
help(ls)

?mean

?setwd
```

4.7 Packages

Packages in R are collections of R functions, data, and compiled code in a well-defined format. They are add-ons which extend the functionality of R and at present, there are 13647 packages available for deployment and use at the official repository, the Comprehensive R Archive Network (CRAN).

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

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

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

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

4.8 Importing and Exporting Tabular Data

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

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

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

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

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

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

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

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

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

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

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

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

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

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

4.9 Additional Resources

To learn more about R, there are upteen number of online tutorials as well as free courses availble. 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:

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

# Install development version from Github

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.

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 2) 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 2: 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 3).

Table 3: 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	Treatment	Trait
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 4).

Table 4: Data from an experiment in augmented RCBD design arranged in long-form (Block and Treatment as numbers).

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

Multiple traits can be added as additional columns (Table 5).

Table 5: 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	Treatment	Trait1	Trait2
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 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`. These objects can then be taken as input by the several functions to print the results to console (`print.augmentedRCBD`), generate descriptive statistics from adjusted means (`describe.augmentedRCBD`), plot frequency distribution (`freqdist.augmentedRCBD`) and computed genetic variability statistics (gva.augmentedRCBD). All these outputs can also be exported as a MS Word report using the `report.augmentedRCBD` function.

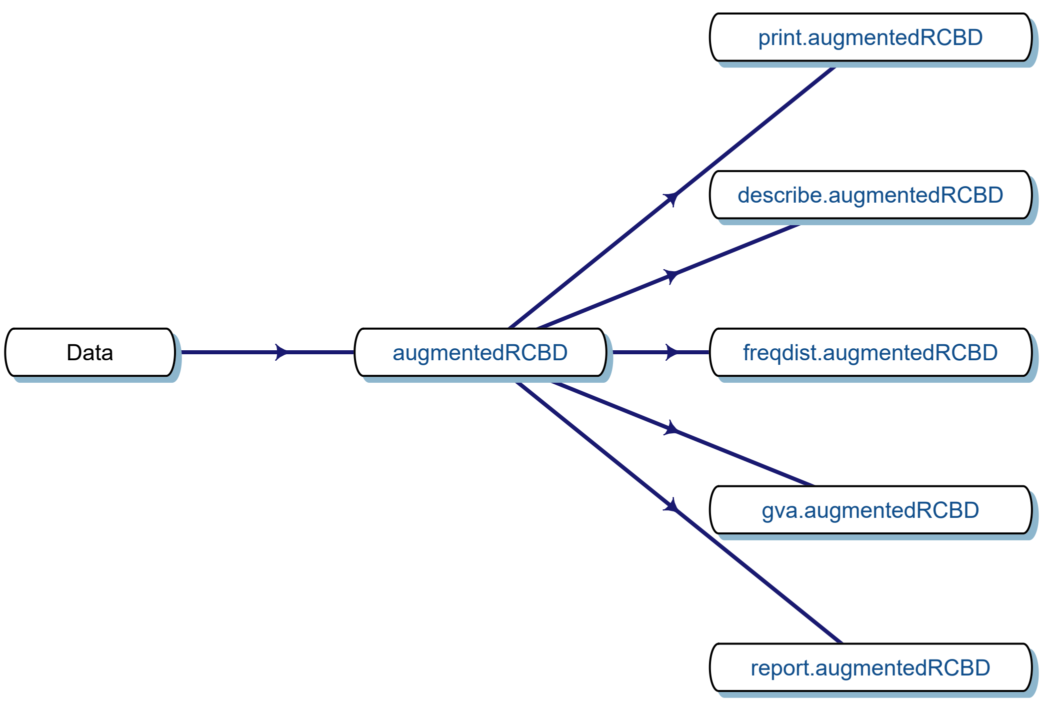


Fig. 4. Workflow for analysis of single traits with augmentedRCBD.

7.1 augmentedRCBD()

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

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

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

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

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

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

```

Augmented Design Details
========================

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

ANOVA, Treatment Adjusted
=========================
                                     Df Sum Sq Mean Sq F value Pr(>F)
Block (ignoring Treatments)           2  360.1  180.04   6.675 0.0298 *
Treatment (eliminating Blocks)       11  285.1   25.92   0.961 0.5499
  Treatment: Check                    3   52.9   17.64   0.654 0.6092
  Treatment: Test and Test vs. Check  8  232.2   29.02   1.076 0.4779
Residuals                             6  161.8   26.97
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

Treatment Means
```

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

Coefficient of Variation
========================
6.372367

Overall Adjusted Mean
=====================
81.0625

Standard Errors
===================
                                         Std. Error of Diff.  CD (5%)
Control Treatment Means                             4.240458 10.37603
Two Test Treatments (Same Block)                    7.344688 17.97180
Two Test Treatments (Different Blocks)              8.211611 20.09309
A Test Treatment and a Control Treatment            6.360687 15.56404

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

Method : lsd

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

```r
class(out1)
```

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

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

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

```

Augmented Design Details
========================

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

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

Block (ignoring Treatments)          **
Treatment (eliminating Blocks)       ***
  Treatment: Check
  Treatment: Test and Test vs. Check ***
Residuals
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

ANOVA, Block Adjusted
=====================
                               Df Sum Sq Mean Sq F value   Pr(>F)
Treatment (ignoring Blocks)    11  64708    5883  20.550 0.000707 ***
  Treatment: Check              3   2150     717   2.504 0.156116
  Treatment: Test               7  34863    4980  17.399 0.001366 **
  Treatment: Test vs. Check     1  27694   27694  96.749 6.36e-05 ***
Block (eliminating Treatments)  2   1277     639   2.231 0.188645
Residuals                       6   1718     286
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

```
10          7      1 347.0000        NA  1 347 347       346.4167
11          8      3 226.0000        NA  1 226 226       213.6667
12          9      2 311.0000        NA  1 311 311       323.9167

Coefficient of Variation
========================
6.057617

Overall Adjusted Mean
=====================
298.4792

Standard Errors
===================
                                          Std. Error of Diff.  CD (5%)
Control Treatment Means                              13.81424 33.80224
Two Test Treatments (Same Block)                     23.92697 58.54719
Two Test Treatments (Different Blocks)               26.75117 65.45775
A Test Treatment and a Control Treatment             20.72137 50.70336

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

Method : lsd

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

```r
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.

```r
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 ...
```

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

```r
# Results for variable y1
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
```

```

Augmented Design Details
========================

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

ANOVA, Treatment Adjusted
=========================
                                     Df Sum Sq Mean Sq F value Pr(>F)
Block (ignoring Treatments)           2  360.1  180.04   6.675 0.0298 *
Treatment (eliminating Blocks)       11  285.1   25.92   0.961 0.5499
  Treatment: Check                    3   52.9   17.64   0.654 0.6092
  Treatment: Test and Test vs. Check  8  232.2   29.02   1.076 0.4779
Residuals                             6  161.8   26.97
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

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

Coefficient of Variation
========================
6.372367
```

```
Overall Adjusted Mean
=====================
81.0625

Standard Errors
===================
                                          Std. Error of Diff.  CD (5%)
Control Treatment Means                              4.240458 10.37603
Two Test Treatments (Same Block)                     7.344688 17.97180
Two Test Treatments (Different Blocks)               8.211611 20.09309
A Test Treatment and a Control Treatment             6.360687 15.56404

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

Method : lsd

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

```r
class(out1)
```

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

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

```
Augmented Design Details
========================

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

ANOVA, Treatment Adjusted
=========================
                                    Df Sum Sq Mean Sq F value   Pr(>F)
Block (ignoring Treatments)          2   7019    3510  12.261 0.007597
Treatment (eliminating Blocks)      11  58965    5360  18.727 0.000920
  Treatment: Check                   3   2150     717   2.504 0.156116
```

```
  Treatment: Test and Test vs. Check  8  56815    7102  24.810 0.000473
Residuals                             6   1717     286

Block (ignoring Treatments)          **
Treatment (eliminating Blocks)       ***
  Treatment: Check
  Treatment: Test and Test vs. Check ***
Residuals
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

ANOVA, Block Adjusted
=====================
                               Df Sum Sq Mean Sq F value   Pr(>F)
Treatment (ignoring Blocks)    11  64708    5883  20.550 0.000707 ***
  Treatment: Check              3   2150     717   2.504 0.156116
  Treatment: Test               7  34863    4980  17.399 0.001366 **
  Treatment: Test vs. Check     1  27694   27694  96.749 6.36e-05 ***
Block (eliminating Treatments)  2   1277     639   2.231 0.188645
Residuals                       6   1718     286
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

Coefficient of Variation
========================
6.057617

Overall Adjusted Mean
=====================
298.4792

Standard Errors
===================
                                         Std. Error of Diff.  CD (5%)
Control Treatment Means                             13.81424 33.80224
Two Test Treatments (Same Block)                    23.92697 58.54719
Two Test Treatments (Different Blocks)              26.75117 65.45775
A Test Treatment and a Control Treatment            20.72137 50.70336
```

```
Treatment Groups
==================

Method : lsd

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

```r
class(out2)
```

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

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

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

```
Augmented Design Details
========================

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

ANOVA, Treatment Adjusted
=========================
                                     Df Sum Sq Mean Sq F value Pr(>F)
Block (ignoring Treatments)           2  360.1  180.04   6.675 0.0298 *
Treatment (eliminating Blocks)       11  285.1   25.92   0.961 0.5499
  Treatment: Check                    3   52.9   17.64   0.654 0.6092
  Treatment: Test and Test vs. Check  8  232.2   29.02   1.076 0.4779
Residuals                             6  161.8   26.97
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

ANOVA, Block Adjusted
=====================
```

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

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

Coefficient of Variation
========================
6.372367

Overall Adjusted Mean
=====================
81.0625

Standard Errors
===================
                                           Std. Error of Diff.  CD (5%)
Control Treatment Means                               4.240458 10.37603
Two Test Treatments (Same Block)                      7.344688 17.97180
Two Test Treatments (Different Blocks)                8.211611 20.09309
A Test Treatment and a Control Treatment              6.360687 15.56404

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

Method : lsd

   Treatment Adjusted Means       SE df lower.CL  upper.CL Group
8          8       73.25000 5.609598  6 59.52381  86.97619     1
9          9       77.25000 5.609598  6 63.52381  90.97619    12
10        10       77.25000 5.609598  6 63.52381  90.97619    12
5          5       78.25000 5.609598  6 64.52381  91.97619    12
6          6       78.25000 5.609598  6 64.52381  91.97619    12
2          2       79.00000 2.998456  6 71.66304  86.33696    12
12        12       79.50000 5.609598  6 65.77381  93.22619    12
3          3       82.00000 2.998456  6 74.66304  89.33696    12
```

```
4           4       83.33333 2.998456  6 75.99637  90.67029    12
1           1       84.66667 2.998456  6 77.32971  92.00363    12
11         11       86.50000 5.609598  6 72.77381 100.22619    12
7           7       93.50000 5.609598  6 79.77381 107.22619     2
```

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

```

Augmented Design Details
========================

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

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

Block (ignoring Treatments)          **
Treatment (eliminating Blocks)       ***
  Treatment: Check
  Treatment: Test and Test vs. Check ***
Residuals
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

ANOVA, Block Adjusted
=====================
                               Df Sum Sq Mean Sq F value   Pr(>F)
Treatment (ignoring Blocks)    11  64708    5883  20.550 0.000707 ***
  Treatment: Check              3   2150     717   2.504 0.156116
  Treatment: Test               7  34863    4980  17.399 0.001366 **
  Treatment: Test vs. Check     1  27694   27694  96.749 6.36e-05 ***
Block (eliminating Treatments)  2   1277     639   2.231 0.188645
Residuals                       6   1718     286
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Treatment Means
===============
   Treatment Block    Means        SE r Min Max Adjusted Means
1          1        256.0000  3.055050 3 250 260        256.0000
2         10      3 450.0000        NA 1 450 450        437.6667
3         11      1 300.0000        NA 1 300 300        299.4167
```

```
4         12     1 289.0000        NA 1 289 289       288.4167
5          2       228.0000  6.110101 3 220 240       228.0000
6          3       247.6667 10.170764 3 237 268       247.6667
7          4       264.0000 18.681542 3 227 287       264.0000
8          5     2 281.0000        NA 1 281 281       293.9167
9          6     3 395.0000        NA 1 395 395       382.6667
10         7     1 347.0000        NA 1 347 347       346.4167
11         8     3 226.0000        NA 1 226 226       213.6667
12         9     2 311.0000        NA 1 311 311       323.9167

Coefficient of Variation
========================
6.057617

Overall Adjusted Mean
=====================
298.4792

Standard Errors
===================
                                          Std. Error of Diff.  CD (5%)
Control Treatment Means                              13.81424 33.80224
Two Test Treatments (Same Block)                     23.92697 58.54719
Two Test Treatments (Different Blocks)               26.75117 65.45775
A Test Treatment and a Control Treatment             20.72137 50.70336

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

Method : lsd

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

7.2 print.augmentedRCBD()

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

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

```
Augmented Design Details
========================
```

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

ANOVA, Treatment Adjusted
=========================
                                     Df Sum Sq Mean Sq F value Pr(>F)
Block (ignoring Treatments)           2  360.1  180.04   6.675 0.0298 *
Treatment (eliminating Blocks)       11  285.1   25.92   0.961 0.5499
  Treatment: Check                    3   52.9   17.64   0.654 0.6092
  Treatment: Test and Test vs. Check  8  232.2   29.02   1.076 0.4779
Residuals                             6  161.8   26.97
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

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

Coefficient of Variation
========================
6.372367

Overall Adjusted Mean
=====================
81.0625

Standard Errors
===================
```

```
                                          Std. Error of Diff.  CD (5%)
Control Treatment Means                              4.240458 10.37603
Two Test Treatments (Same Block)                     7.344688 17.97180
Two Test Treatments (Different Blocks)               8.211611 20.09309
A Test Treatment and a Control Treatment             6.360687 15.56404

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

Method : lsd

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

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

```


Augmented Design Details
========================

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

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

Block (ignoring Treatments)          **
Treatment (eliminating Blocks)       ***
  Treatment: Check
  Treatment: Test and Test vs. Check ***
Residuals
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ANOVA, Block Adjusted
=====================
                               Df Sum Sq Mean Sq F value   Pr(>F)    
Treatment (ignoring Blocks)    11  64708    5883  20.550 0.000707 ***
  Treatment: Check              3   2150     717   2.504 0.156116    
  Treatment: Test               7  34863    4980  17.399 0.001366 ** 
  Treatment: Test vs. Check     1  27694   27694  96.749 6.36e-05 ***
Block (eliminating Treatments)  2   1277     639   2.231 0.188645    
Residuals                       6   1718     286                     
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

Coefficient of Variation
========================
6.057617

Overall Adjusted Mean
=====================
298.4792

Standard Errors
===================
                                         Std. Error of Diff.  CD (5%)
Control Treatment Means                             13.81424 33.80224
Two Test Treatments (Same Block)                    23.92697 58.54719
Two Test Treatments (Different Blocks)              26.75117 65.45775
A Test Treatment and a Control Treatment            20.72137 50.70336

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

Method : lsd

   Treatment Adjusted Means        SE df lower.CL upper.CL    Group
8          8       213.6667 18.274527  6 168.9505 258.3828   12    
2          2       228.0000  9.768146  6 204.0982 251.9018   1     
3          3       247.6667  9.768146  6 223.7649 271.5685   123   
1          1       256.0000  9.768146  6 232.0982 279.9018   1234  
```

```
4          4       264.0000  9.768146  6 240.0982 287.9018   234
12        12       288.4167 18.274527  6 243.7005 333.1328    345
5          5       293.9167 18.274527  6 249.2005 338.6328    345
11        11       299.4167 18.274527  6 254.7005 344.1328     45
9          9       323.9167 18.274527  6 279.2005 368.6328      56
7          7       346.4167 18.274527  6 301.7005 391.1328      56
6          6       382.6667 18.274527  6 337.9505 427.3828       67
10        10       437.6667 18.274527  6 392.9505 482.3828        7
```

7.3 describe.augmentedRCBD()

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

```r
# 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
```

```r
# 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
```

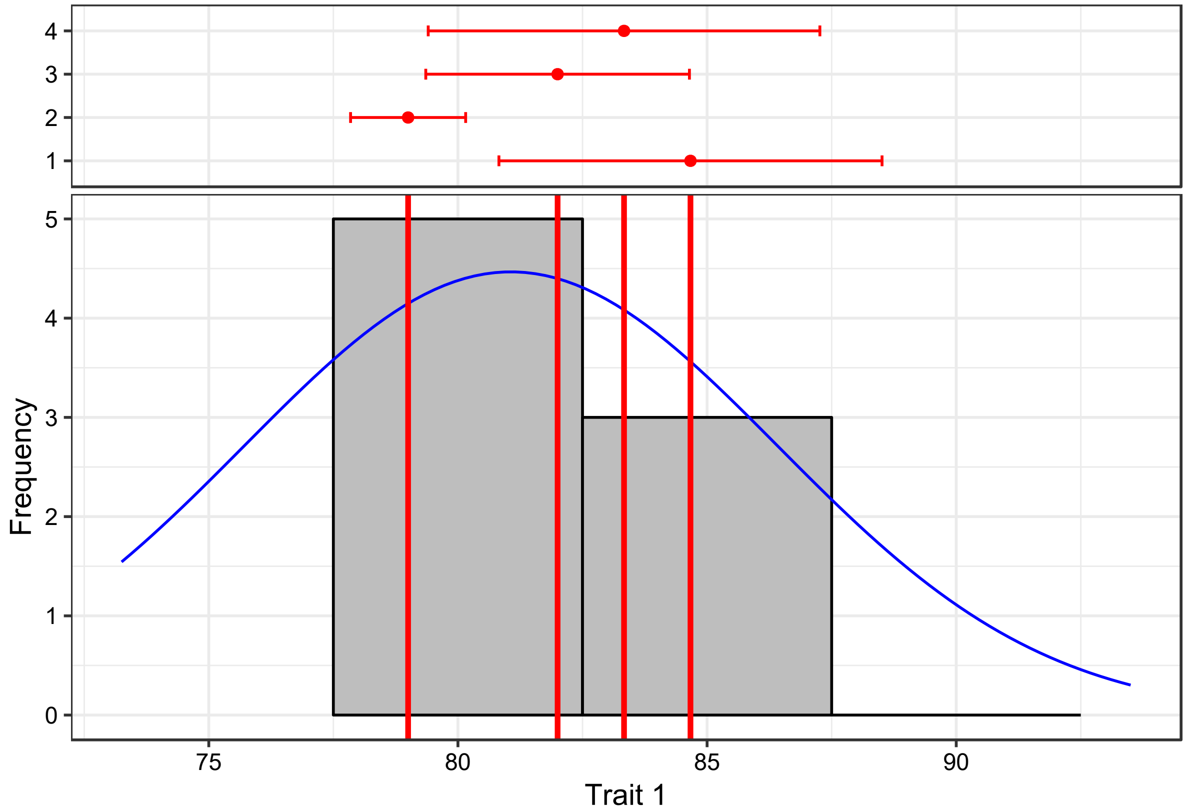
7.4 `freqdist.augmentedRCBD()`

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

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

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

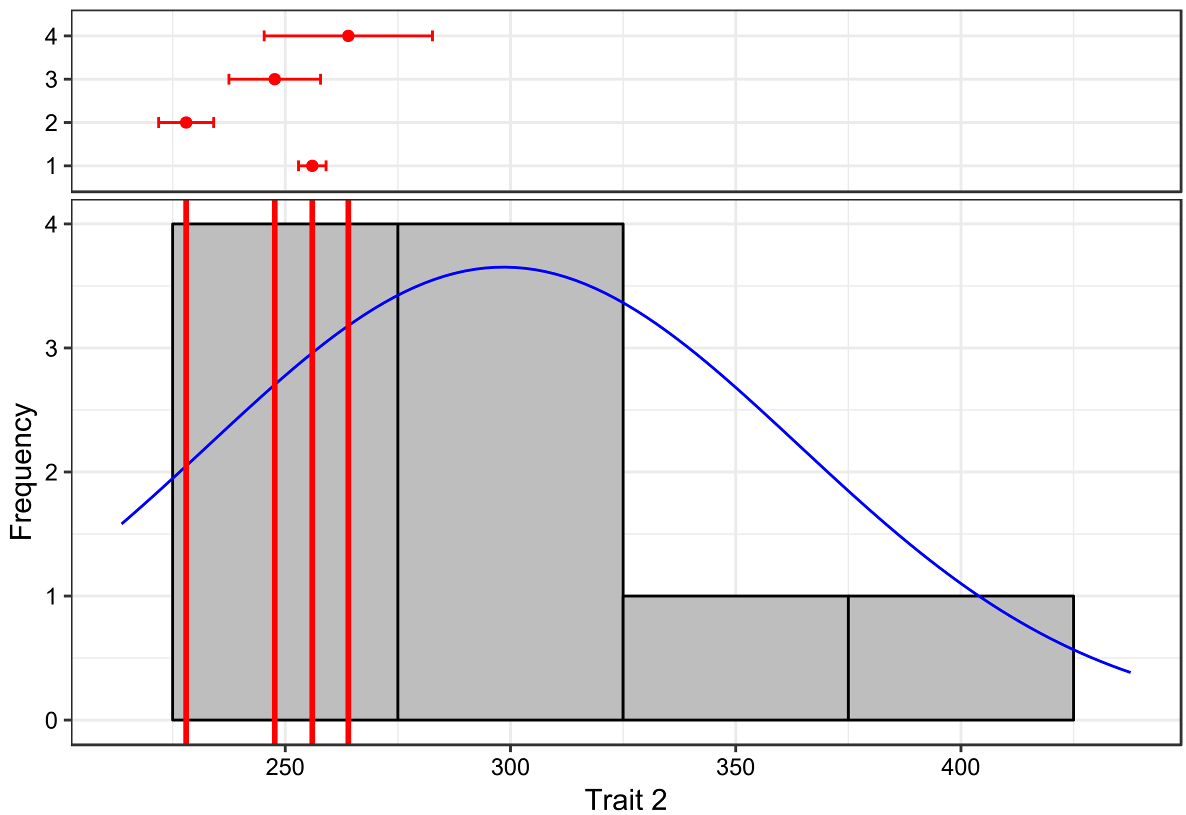
```r
plot(freq1)
```




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

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

```r
plot(freq2)
```



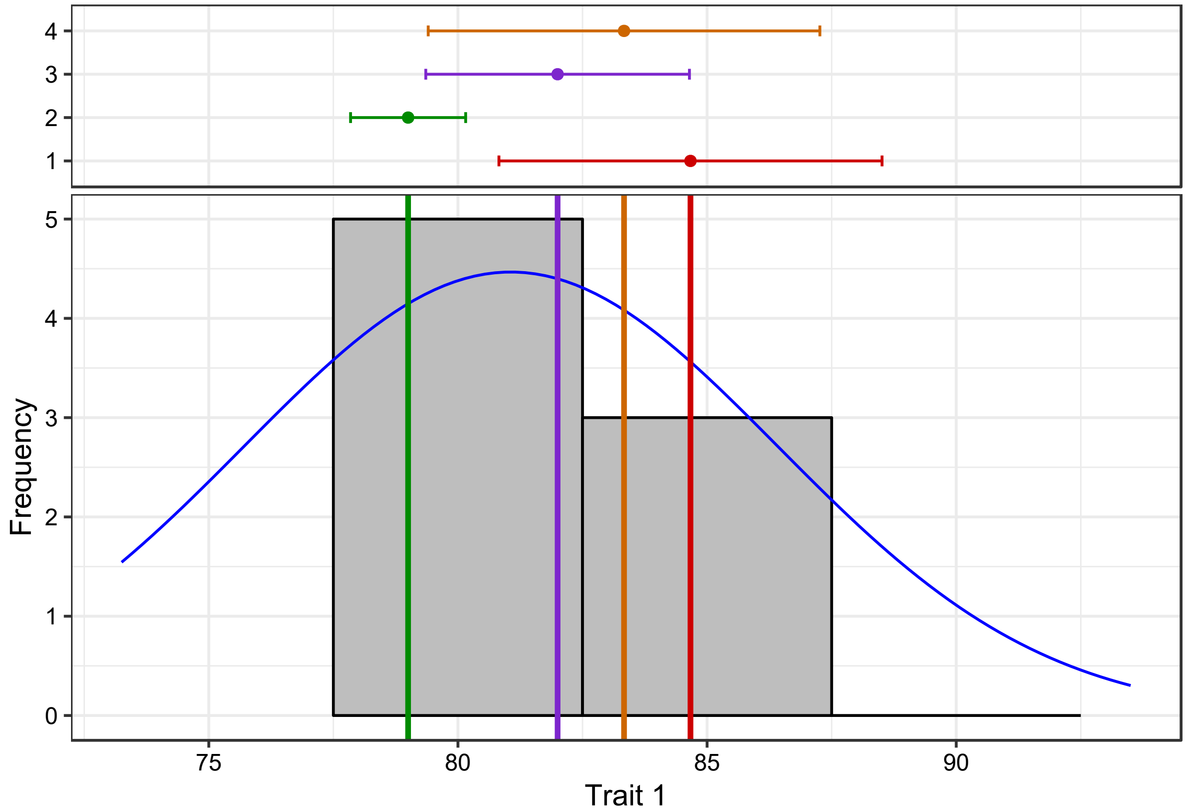
The colours for the check values may be specified using the argument `check.col`.

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

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

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

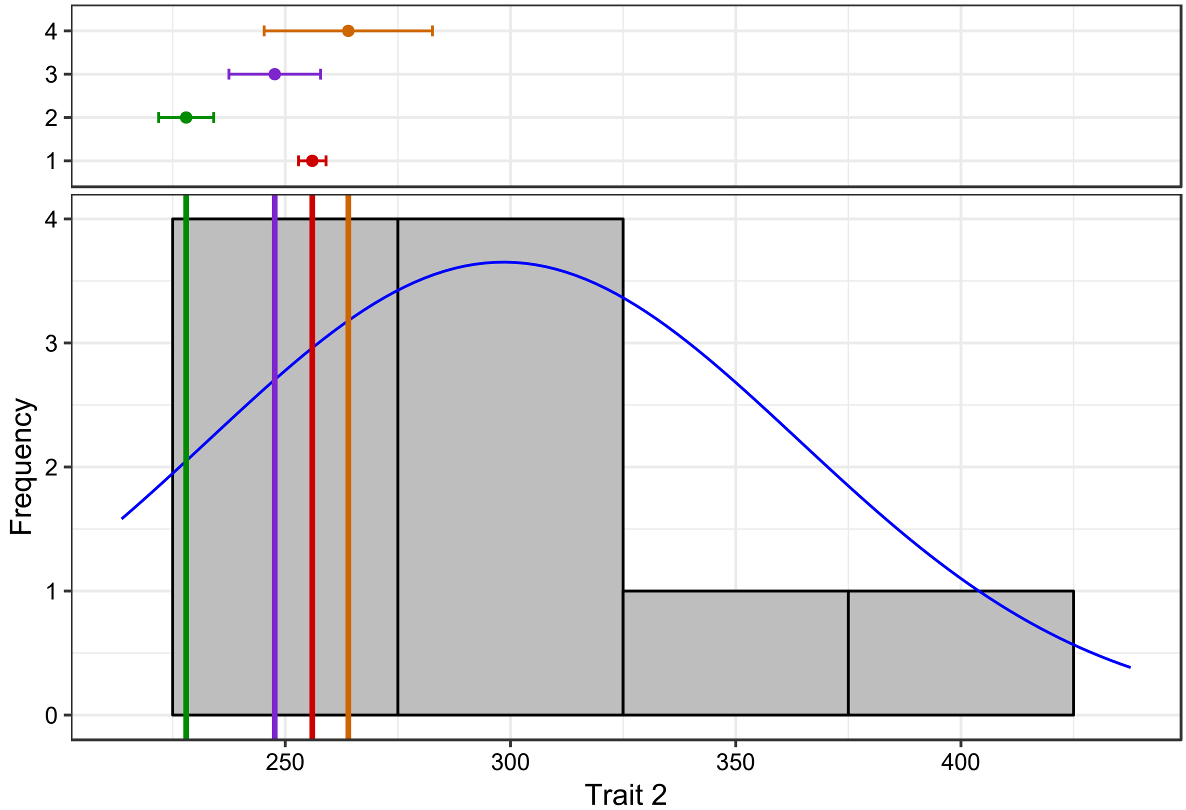
```
plot(freq1)
```




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

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

```
plot(freq2)
```

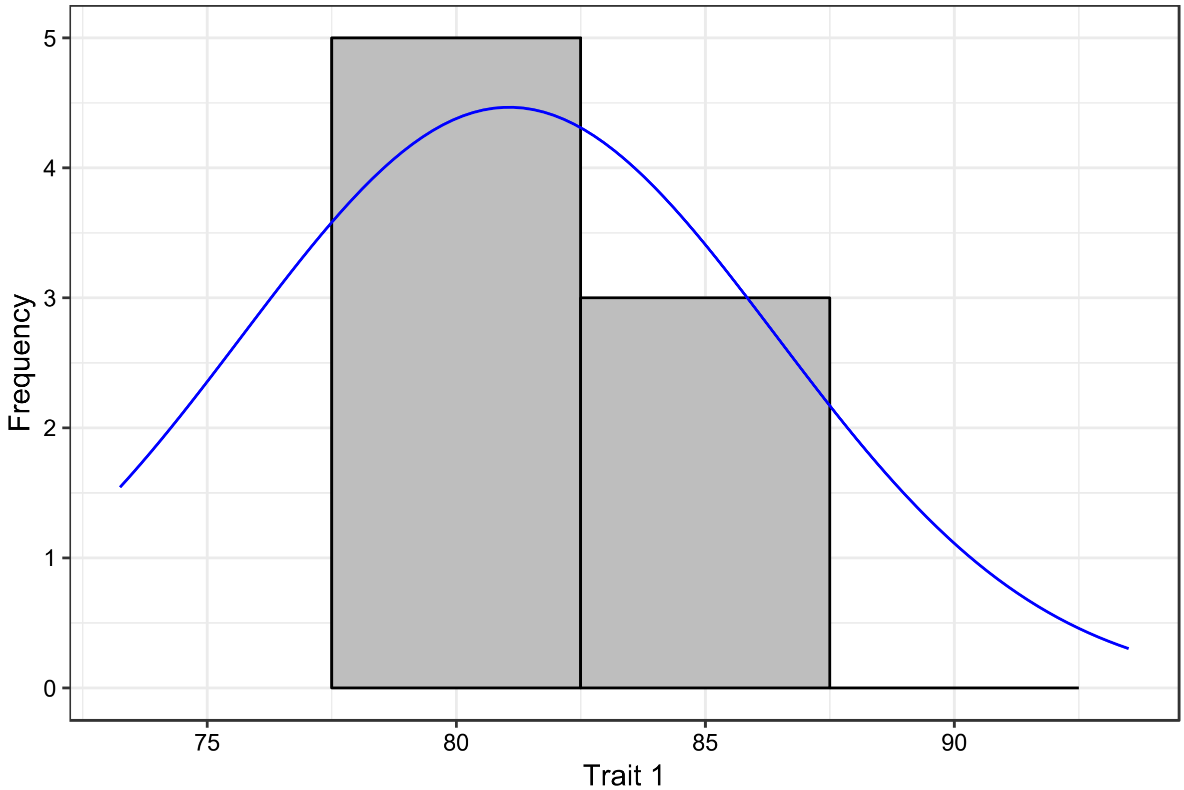


The default the check highlighting can be avoided using the argument `highlight.check = FALSE`.

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

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

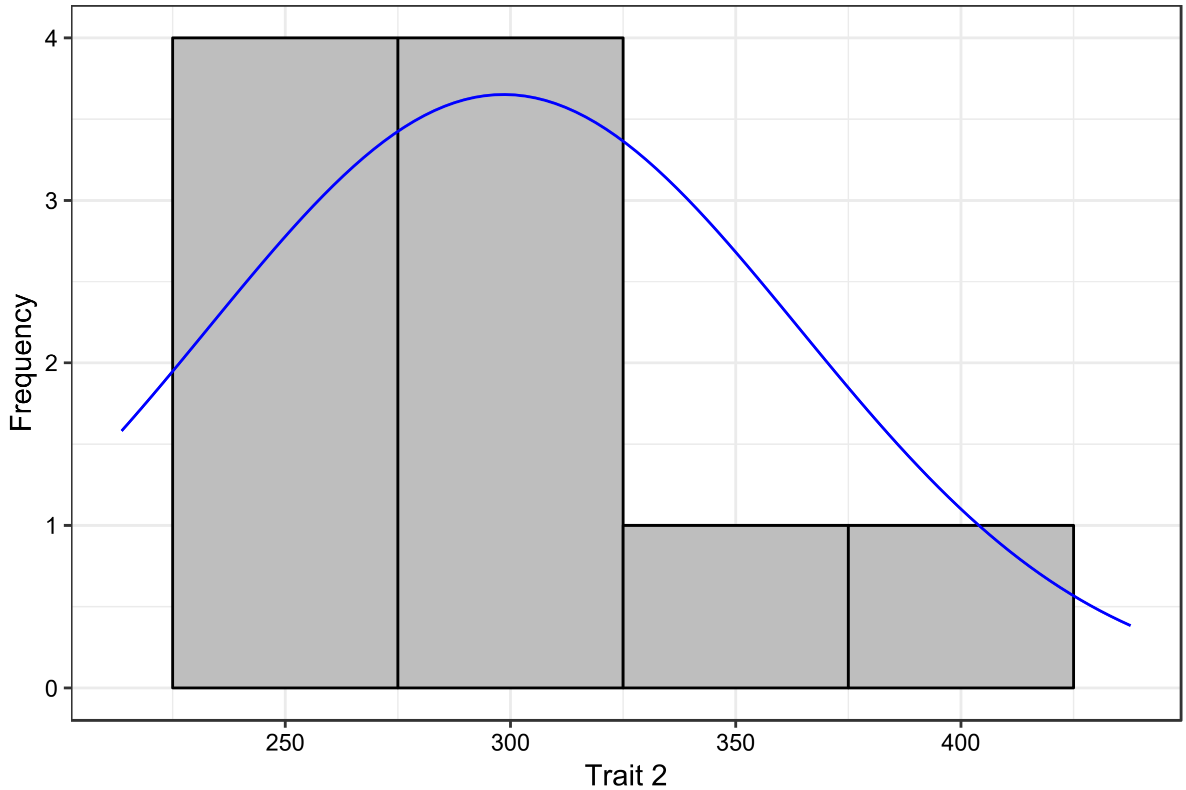
```
plot(freq1)
```




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

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

```r
plot(freq2)
```



7.5 `gva.augmentedRCBD()`

The genetic variability statistics such as mean, phenotypic variation, genotypic variation,

7.5 `report.augmentedRCBD()`

8 Data Analysis for a Multiple Traits

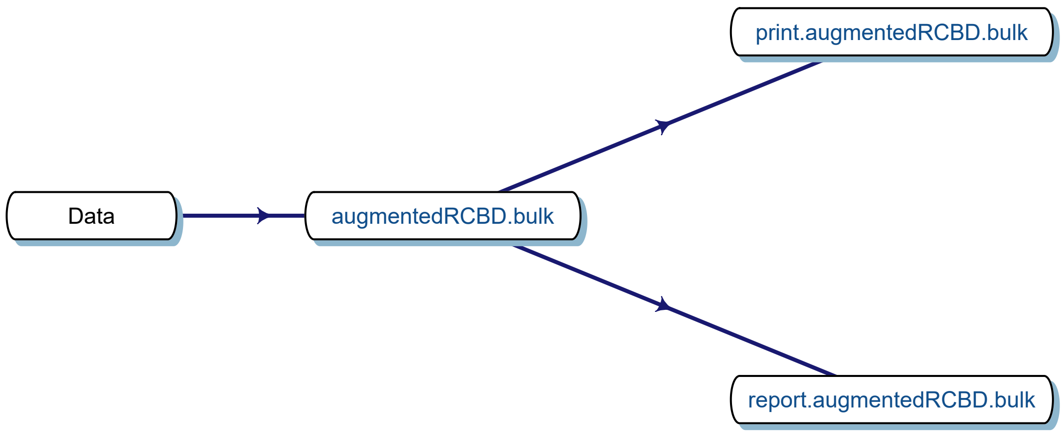


Fig. 5. Workflow for analysis of multiple traits with `augmentedRCBD`.

Then the package can be loaded using the function

```
library(augmentedRCBD)
```

9 Citing augmentedRCBD

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

  Aravind, J., Mukesh Sankar, S., Wankhede, D. P., and Kaur, V.
  (2019).  augmentedRCBD: Analysis of Augmented Randomised
  Complete Block Designs. R package version 0.1.0.9000,
  https://aravind-j.github.io/augmentedRCBD/https://cran.r-project.org/package=augmentedRCBD.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {augmentedRCBD: Analysis of Augmented Randomised Complete Block Designs},
    author = {J. Aravind and S. {Mukesh Sankar} and Dhammaprakash Pandhari Wankhede and Vikender Kaur},
    year = {2019},
    note = {R package version 0.1.0.9000},
    note = {https://aravind-j.github.io/augmentedRCBD/},
    note = {https://cran.r-project.org/package=augmentedRCBD},
  }

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

10 Session Info

```
sessionInfo()
```

```
R Under development (unstable) (2018-10-27 r75507)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows >= 8 x64 (build 9200)

Matrix products: default

locale:
[1] LC_COLLATE=English_India.1252  LC_CTYPE=English_India.1252
[3] LC_MONETARY=English_India.1252 LC_NUMERIC=C
[5] LC_TIME=English_India.1252

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

other attached packages:
[1] diagram_1.6.4            shape_1.4.4
[3] augmentedRCBD_0.1.0.9000

loaded via a namespace (and not attached):
 [1] Rcpp_1.0.0         mvtnorm_1.0-8      lattice_0.20-38
```

```
 [4] multcompView_0.1-7 zoo_1.8-4          assertthat_0.2.0
 [7] rprojroot_1.3-2    digest_0.6.18      R6_2.3.0
[10] plyr_1.8.4         backports_1.1.2    evaluate_0.12
[13] coda_0.19-2        ggplot2_3.1.0      highr_0.7
[16] pillar_1.3.0       Rdpack_0.10-3      gdtools_0.1.7
[19] rlang_0.3.0.1      lazyeval_0.2.1     multcomp_1.4-8
[22] uuid_0.1-2         rstudioapi_0.8     Matrix_1.2-15
[25] flextable_0.4.6    rmarkdown_1.10     desc_1.2.0
[28] labeling_0.3       moments_0.14       splines_3.6.0
[31] stringr_1.3.1      munsell_0.5.0      tinytex_0.9
[34] compiler_3.6.0     xfun_0.4           pkgconfig_2.0.2
[37] base64enc_0.1-3    htmltools_0.3.6    tidyselect_0.2.5
[40] tibble_1.4.2       codetools_0.2-15   crayon_1.3.4
[43] dplyr_0.7.8        withr_2.1.2        MASS_7.3-51.1
[46] grid_3.6.0         xtable_1.8-3       gtable_0.2.0
[49] magrittr_1.5       scales_1.0.0       bibtex_0.4.2
[52] zip_1.0.0          estimability_1.3   stringi_1.2.4
[55] reshape2_1.4.3     bindrcpp_0.2.2     testthat_2.0.1
[58] xml2_1.2.0         sandwich_2.5-0     TH.data_1.0-9
[61] tools_3.6.0        glue_1.3.0         officer_0.3.2
[64] purrr_0.2.5        emmeans_1.3.0      pkgload_1.0.2
[67] survival_2.43-3    yaml_2.2.0         colorspace_1.3-2
[70] gbRd_0.4-11        knitr_1.20         bindr_0.1.1
```

References

Anscombe, F. J., and Glynn, W. J. (1983). Distribution of the kurtosis statistic b_2 for normal samples. *Biometrika* 70, 227–234. doi:10.1093/biomet/70.1.227.

D'Agostino, R. B. (1970). Transformation to normality of the null distribution of g_1. *Biometrika* 57, 679–681. doi:10.1093/biomet/57.3.679.

Federer, W. T. (1956). Augmented (or hoonuiaku) designs. *The Hawaiian Planters' Record* LV(2), 191–208.

Federer, W. T. (1961). Augmented designs with one-way elimination of heterogeneity. *Biometrics* 17, 447–473. doi:10.2307/2527837.

Tippmann, S. (2015). Programming tools: Adventures with R. *Nature News* 517, 109. doi:10.1038/517109a.