

# **Biometry Hub Internship**

By Ziyang Wang



# Week 1

First glance

## R-Studio

Introduction to R and  
RStudio

## R package-ggplot2

Plot construction and  
customize layout



## Experimental Design

Definitions and terms,  
different design types  
and practices

## Communication

Attending Peter's  
presentation, and statistical  
meeting with Jing and Shiyu



# R and RStudio

The introduction



## RStudio 08/Jul/2019

- R Studio user interface
- Basic definitions (variables, packages, functions)
- Exploring data frames
- Data management
- Graphics

[Learn More](#)

[Learn More](#)



```

1 2+3+2
2 #Practice
3 #Practice1
4 8/2
5
6 #2
7 (210*1290)/(sqrt(1367^3))
8
9 #Find the answer
10 sqrt(9)
11 log(20)
12 exp(20)
13 abs(-10)
14 round(3.1298376198712,digits=5)
15
16 #Find the volume of a water tank
17 pi*(1.19^2)*4.28
18
19 2*a
20
21 #Practice
22

```

## Calculations

9:17

(Top Level) ↴

Console

Terminal ×

Jobs ×

~/

[1] 4

```

>
> #2
> (210*1290)/(sqrt(1367^3))
[1] 5.359894
>
```

#Find the answer

sqrt(9)

[1] 3

log(20)

[1] 2.995732

exp(20)

[1] 485165195

abs(-10)

[1] 10

```

> round(3.1298376198712,digits=5)
```

## User interface

Environment History Connections

Import Dataset

Global Environment

values

city	chr [1:3]	"Chengdu"	"Queensland"	"Tok
col	"unique"			
h	num [1:5]	2	4	6
r	num [1:5]	1	2	3
T	int [1:5]	1	2	3
v	num [1:5]	6.28	50.27	169.65
vec.rep	chr [1:9]	"Z"	"Y"	"W"
x	num [1:20]	7.36	65.84	5.57
z	num [1:3]	NA	3	5

Files Plots Packages Help Viewer

R Data Input

Find in Topic

read.table [utils]

R Docu

## Data Input

### Description

Reads a file in table format and creates a data frame from it, with cases corresponding to lines and variables corresponding to fields in the file.

### Usage

```

read.table(file, header = FALSE, sep = "", quote = "\"\"", 
          dec = ".", numerals = c("allow.loss", "warn.loss", "no.loss"),
          row.names, col.names, as.is = !stringsAsFactors,
          na.strings = "NA", colClasses = NA, nrow = -1,
          skip = 0, check.names = TRUE, fill = !blank.lines.skip,
          strip.white = FALSE, blank.lines.skip = TRUE,
          comment.char = "#",
          allowEscapes = FALSE, flush = FALSE,
          stringsAsFactors = default.stringsAsFactors(),
          fileEncoding = "", encoding = "unknown", text, skipNul = FALSE)
```

```

read.csv(file, header = TRUE, sep = ",", quote = "\"\"", 
         dec = ".", fill = TRUE, comment.char = "", ...)
```

```

read.csv2(file, header = TRUE, sep = ";", quote = "\"\"", 
          dec = ";", fill = TRUE, comment.char = "", ...)
```

```

read.delim(file, header = TRUE, sep = "\t", quote = "\"\"", 
           dec = ".", fill = TRUE, comment.char = "", ...)
```

## Search for help

## Packages



**ggplot2**  
A handy R package

## ggplot( )+layers

- ❖ Graphs creation
- ❖ numerical & categorical data
- ❖ Customization- color, symbol, size, and transparency.

Example plot 1

Example plot 2

## Microsoft Office

The consequences of today are determined by the actions of the past. To change your future, alter your decisions today.



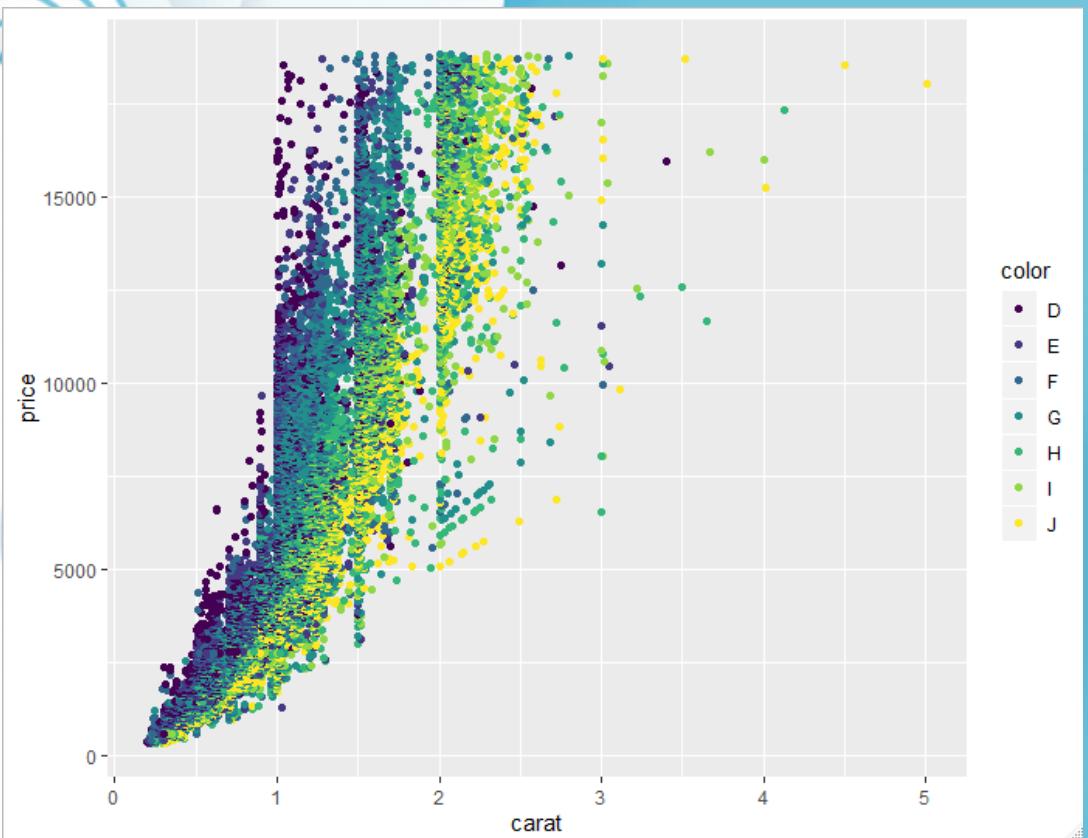
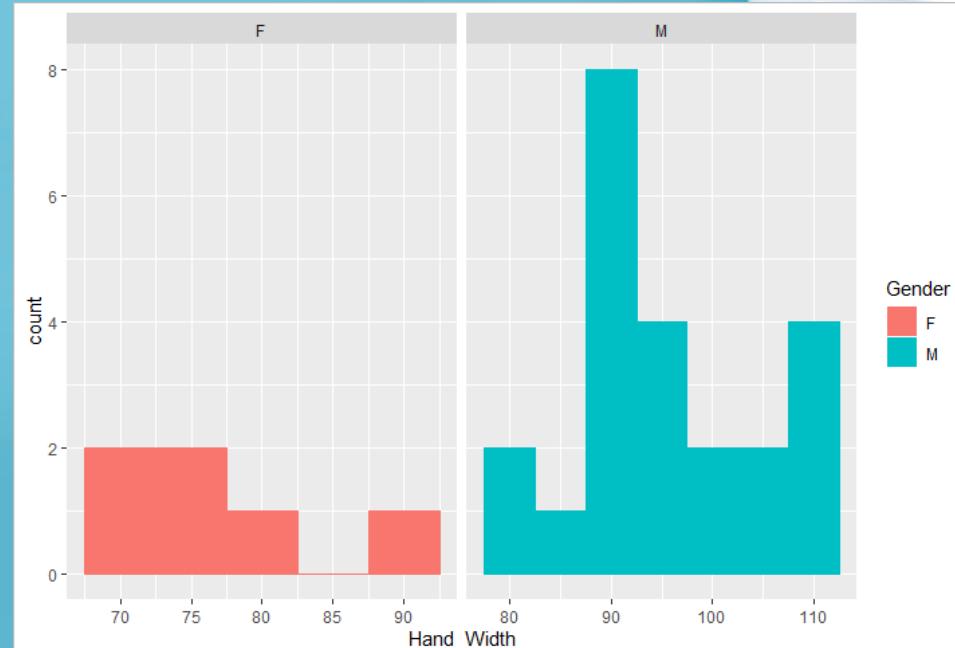
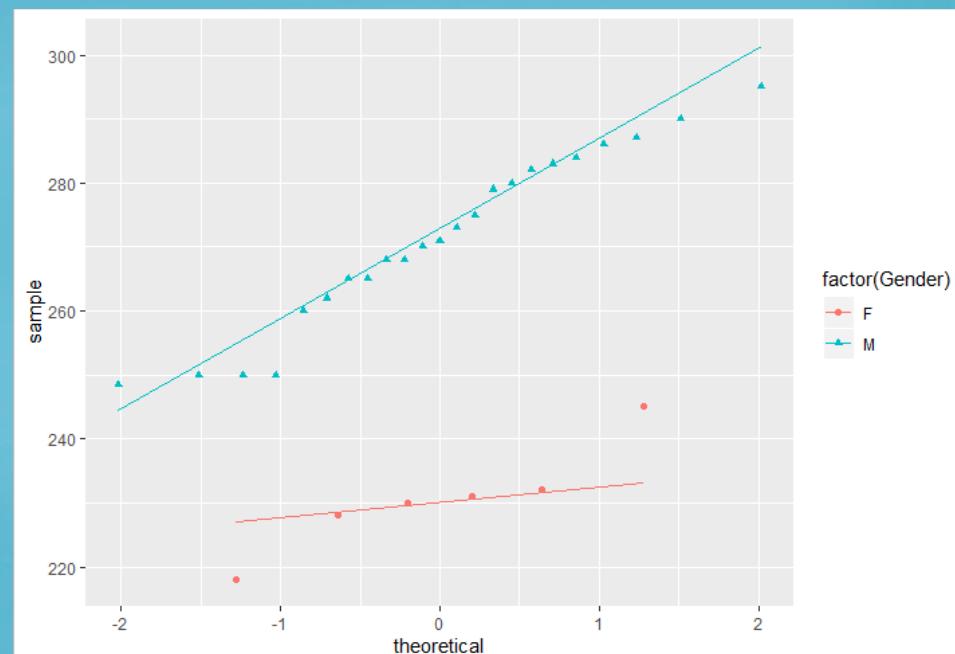


Figure 1. A scatter plot generated by ggplot() function using in-build R dataset "diamond"

```
(p <- ggplot(data = diamonds,
  mapping =
    aes(x=carat,y=price))+  
  geom_point(aes(color=color)))
```



Histogram showing the hand width(mm) of females and males

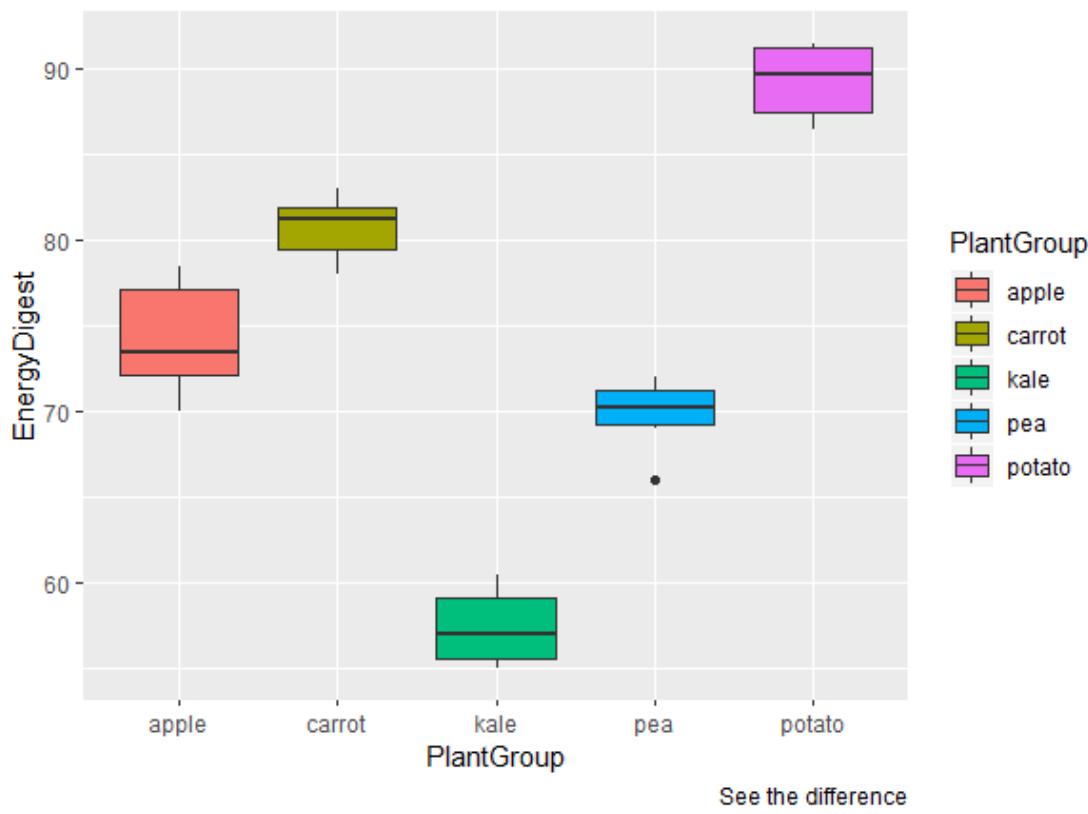


Normal QQ-plot of the Foot length (mm) of females and males

## Unknown

Boxplot of EnergyDigest ability

Fiber dataset



Boxplot showing the energy digestibility % for each plant diet

```
fiber <- read.csv(  
  file = "D:/Firefox download/Rstudio/Energydigestability1.csv")  
  
view(fiber)  
  
(p0 <- ggplot(data = fiber,  
               mapping = aes(PlantGroup,EnergyDigest)))  
  
(p01 <- p0+ geom_boxplot(aes(fill=PlantGroup),  
                           outlier.shape = 19,  
                           outlier.size = 1.5))  
  
(p02 <- p01 +  
  labs(title = "Boxplot of EnergyDigest ability",  
       subtitle = "Fiber dataset",  
       caption = "See the difference",  
       tag = "Unknown"))
```



# Agronomic experiment

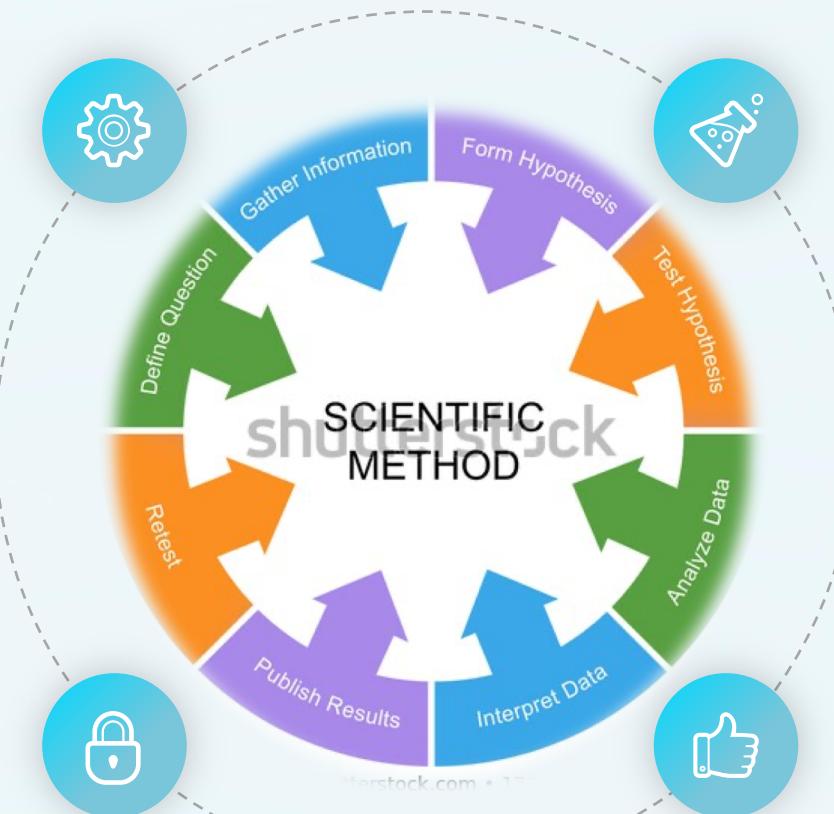
The planning and designing

## Terms and definitions

Populations, samples, treatments, experimental and observational units, replication

## Planning experiments

# of treatment, levels of treatment, blocking, natural gradient



## Designing experiments

CRD, RCBD, Latin Square, Factorial, Split-plot

## Design-agricolae R package

Use R coding to adopt your design  
Residual degree of freedom

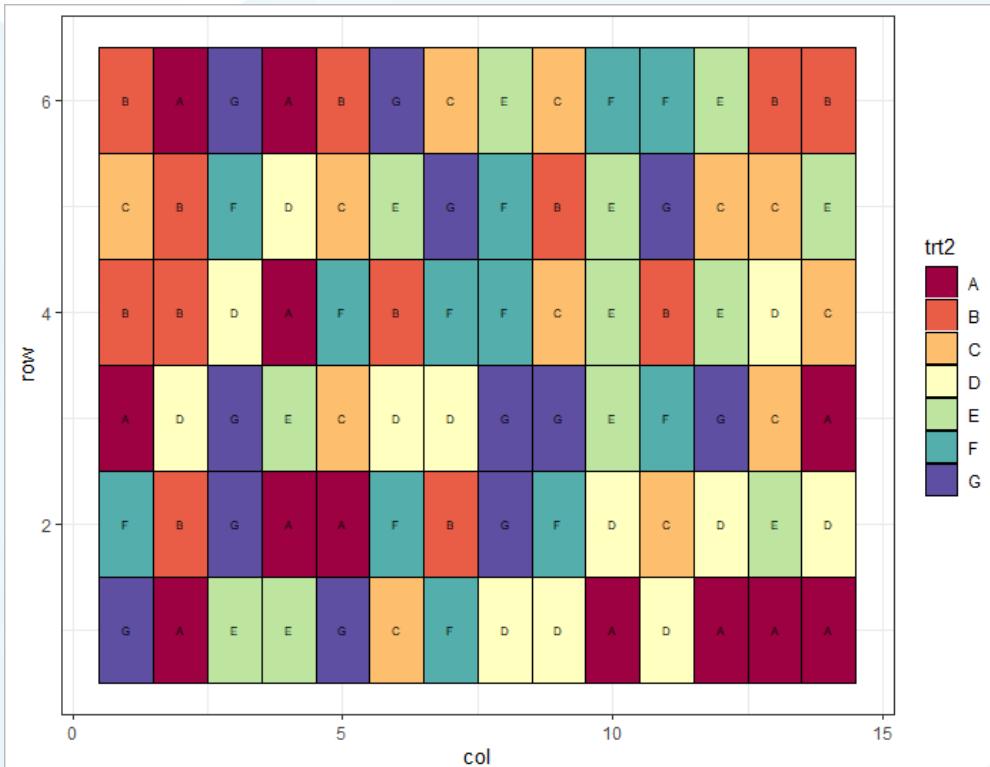


Figure 2. A completely randomized design

```

trt2 <- c("A", "B", "C", "D", "E", "F", "G")
rep2 <- 12
E2 <- design.crd(trt2, r = rep2)
des.e2 <- E2$book

plot.des(design.obj=des.e2, design="crd",
         nrows=6, ncols=14, plot.fac="trt2")

```

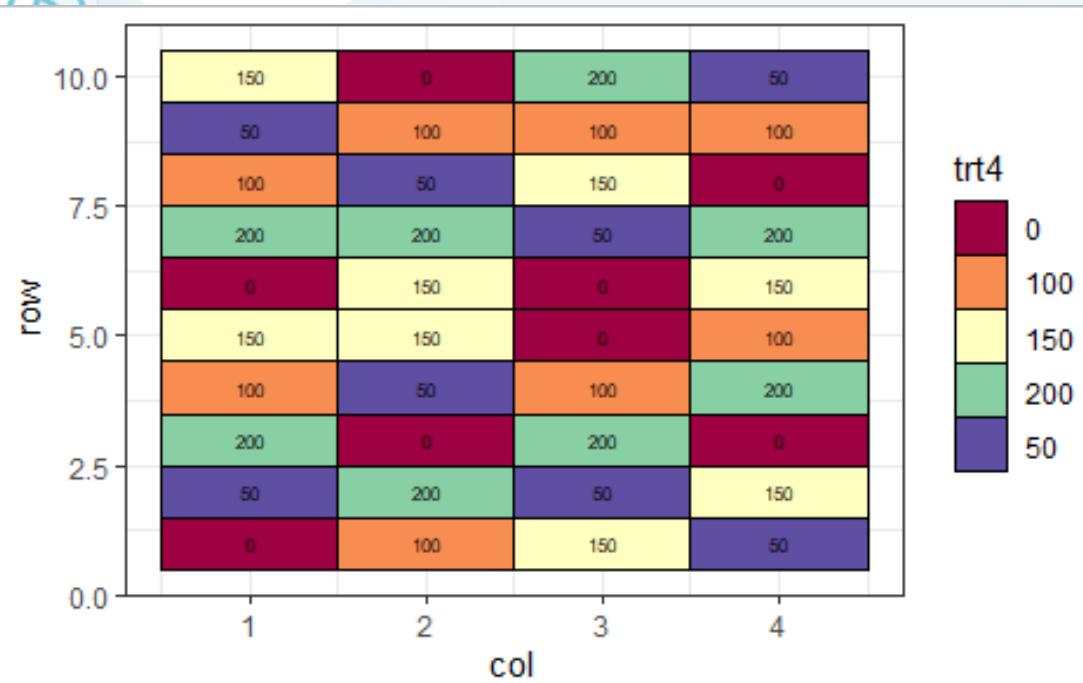
Source of Variation		df
trt2		6
Residual		77
Total		83

Figure 3. The skeletal ANOVA table

```

satab(design.obj = des.e2, design ="crd")
write.csv(des.e2, "e2.csv", row.names=FALSE)

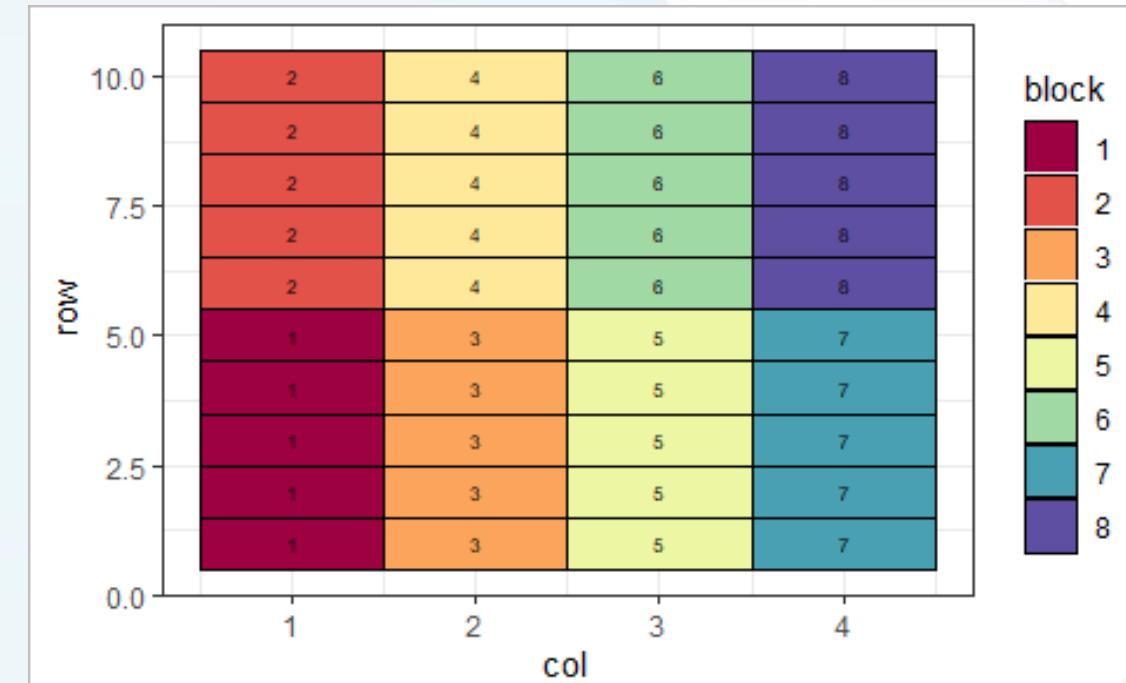
```



```
trt4 <- c("0","50","100","150","200")
rep4 <- 8
E4 <- design.rcbd(trt4, r = rep4)
des.e4 <- E4$book

plot.des(design.obj=des.e4, design="rcbd",
         nrows=10, ncols=4, plot.fac="trt4")
```

Figure 4. A design frame based on Randomized Complete Block design

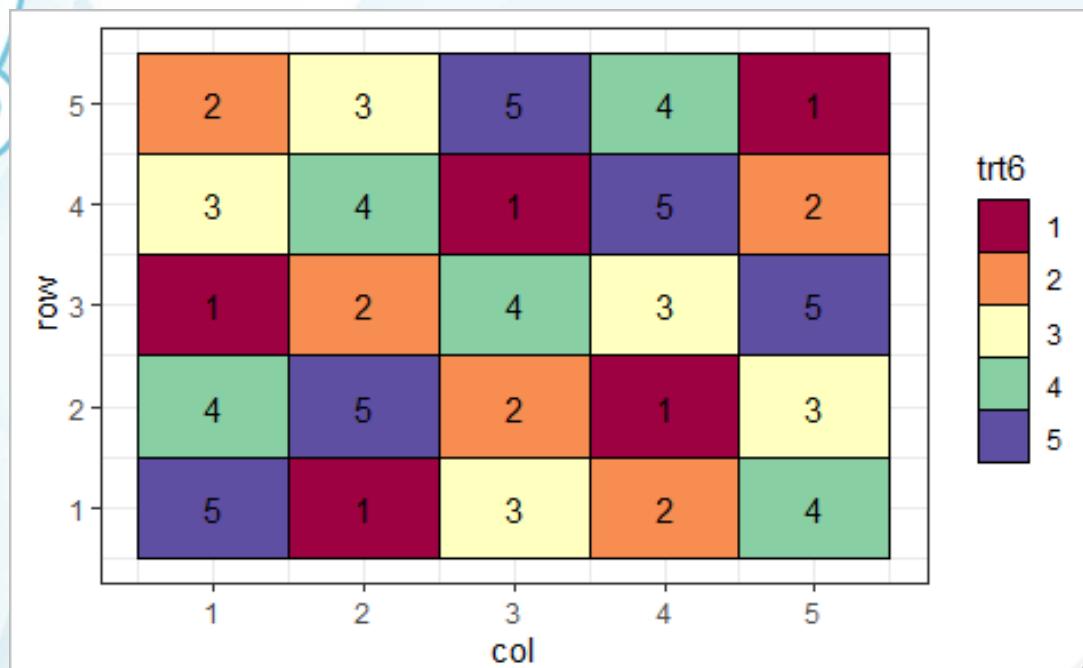


```
plot.des(design.obj=des.e4, design="rcbd",
         nrows=10, ncols=4, plot.fac="block")

satab(design.obj = des.e4, design = "rcbd")
```

Source of Variation	df
<hr/>	
Block stratum	7
trt4	4
Residual	28
Total	39

Figure 5. A design frame based on Latin Square



```
trt6 <- c("1", "2", "3", "4", "5")
E6 <- design.lsd(trt6)
des.e6 <- E6$book

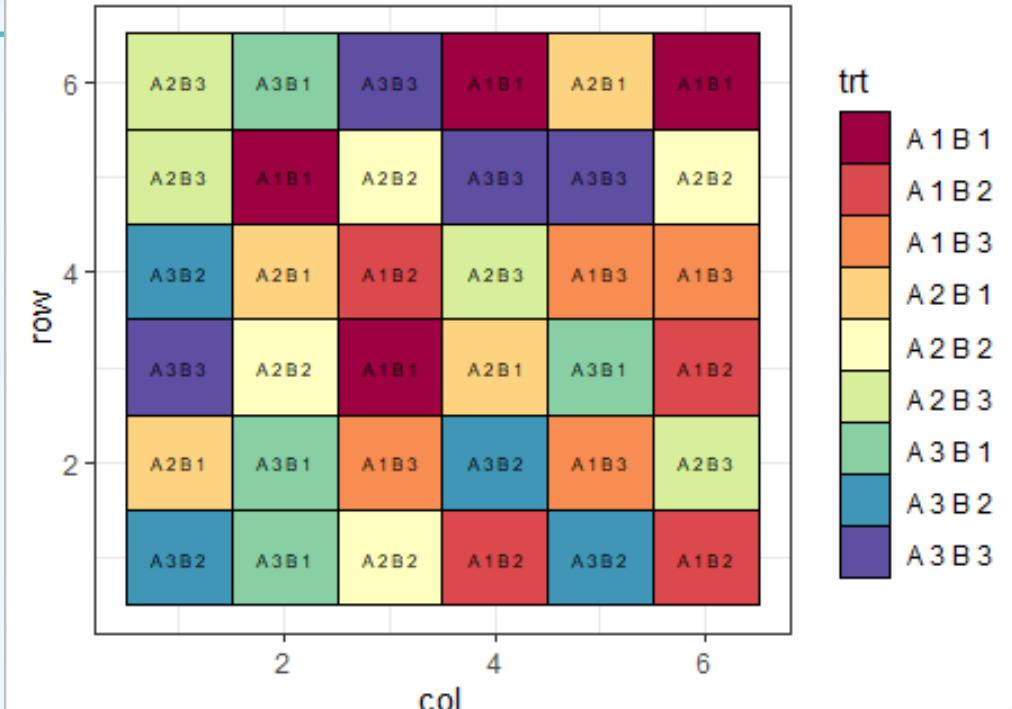
plot.des(design.obj=des.e6, design="lsd",
         nrows=5, ncols=5, plot.fac="trt6")

satab(design.obj = des.e6, design = "lsd")

write.csv(des.e6, "e6.csv", row.names=FALSE)
```

Source of Variation	df
Row	4
Column	4
trt6	4
Residual	12
Total	24

Figure 6. A design frame based on Factorial CRD



```
trt7 <- c(3,3)
rep7 <- 4
E7 <- design.ab(trt7, r = rep7, design = "crd")
des.e7 <- E7$book

plot.des(design.obj=des.e7, design="fac",
         nrows=6, ncols=6, plot.fac="trt")

satab(design.obj = des.e7, design = "faccrd")

write.csv(des.e7, "e7.csv", row.names=FALSE)
```

Source of Variation	df
A	2
B	2
AB	4
Residual	27
Total	35



# Meetings & Presentations

With biometry staffs

Statistical meeting is important for efficient communication in project, note taking skills are very important



Peter Josef Kasprzak  
Presentation- Yield Estimation  
by Computer Program



Lachlan Mitchell  
Digit recognition by  
MINIST



Jing and Shiyu  
CSA project-plant pathogen  
WGCNA analysis-Transcriptional  
factor



# Week 2

Digging further

# O2 Week 2 overview

Further exploration



## Exploring RStudio

- R vs GenStat 19<sup>th</sup>
- Shiny App

f    t    in    g+

## Statistical meetings

- Principles of experimental design
- Principles of statistical inference in practical applications
- The importance of sampling

f    t    in    g+



# Experimental design

Helena Oakey

## Biofuel potential of barley straw

- From field biomass to ethanol – not economic
- Need more efficient sugar release – find the gene responsible for high sugar release

## Spatial row-column design

- 648 elite varieties, 5 replicates
- no repeating of the same variety in the same row and column.

## Field variation and Lab variation

Samples re-randomized in the lab

Consider variation between various batches



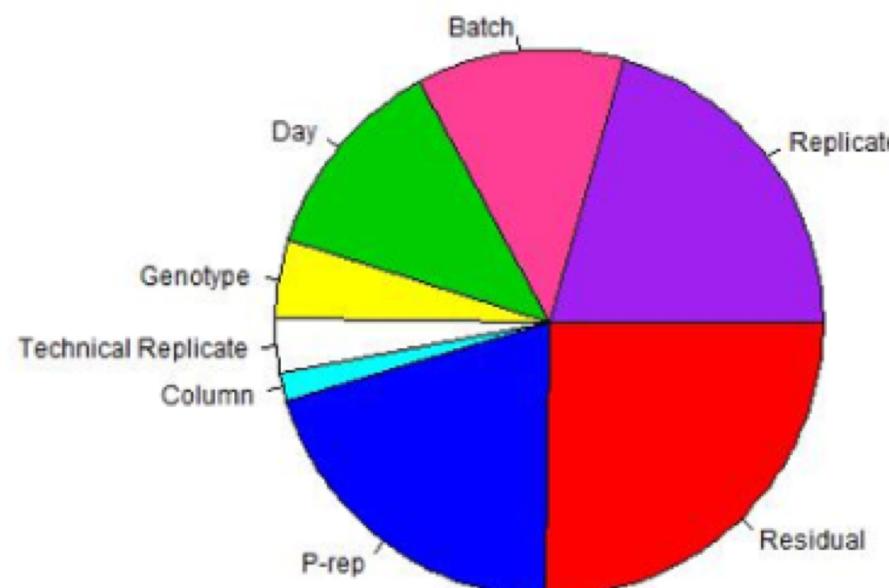
### Source of variation

In-lab re-randomization  
reduced the variation brought  
by varieties



Max - 20  
varieties





TERM	%
Replicate	20.6
Batch	12.2
Day	12.3
Genotype	4.6
Technical Rep	3.2
Column	1.6
P-prep	20.2
Residual	25.3

## PDSA Cycle



- ❖ Questions
- ❖ Experiment conduction
- ❖ Scope
- ❖ Analyze data and draw conclusion
- ❖ Implement changes

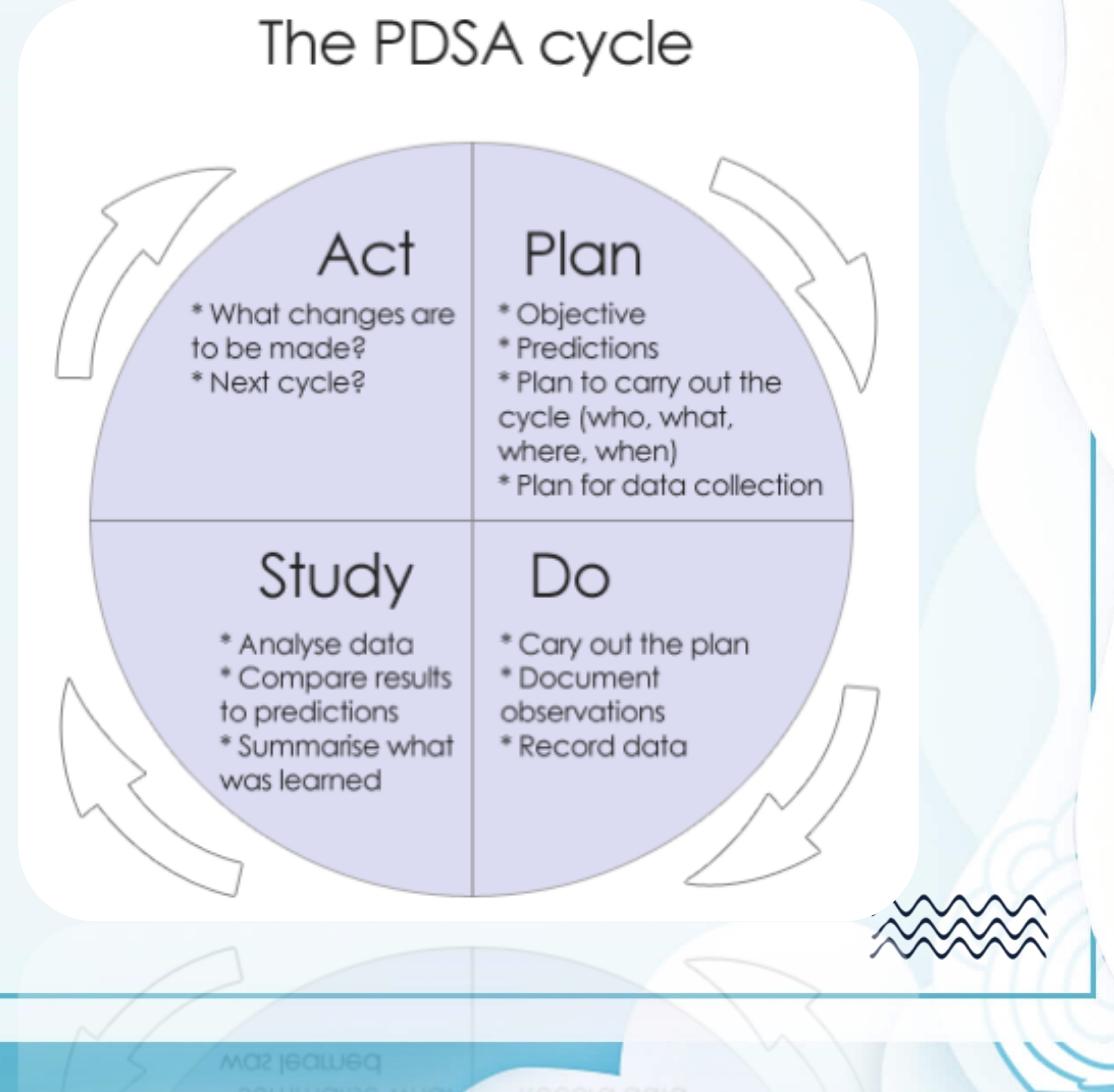
## Accuracy of estimators

- ❖ Group means, SEs
- ❖ T-test

## Blocking design

- ❖ grouping things that have similar result together

## The PDSA cycle





# Sampling design

Peter Josef Kasprzak



Sampling and  
Randomisation  
Why?



Infinite and Finite  
design-based and model-based  
inference in survey sampling



Sampling types  
Descriptive, analytical  
and pattern sampling

**Importance to detect the errors of estimators**, and use proper sampling protocols

Central limit theorem & SLLN (Strong law of large numbers)



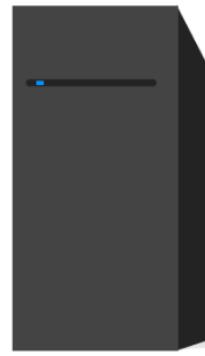
Build interactive web apps  
straight from R

Shiny packages & Shiny dashboard

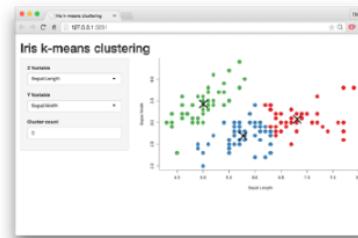


Customize with CSS and  
HTML

# R Studio Shiny app



Server Instructions



User Interface (UI)



# ShinyApp elements

## App template

The shortest viable shiny app



```
library(shiny)  
ui <- fluidPage()  
  
server <- function(input, output) {}  
  
shinyApp(ui = ui, server = server)
```



Input

Use input values  
with input\$



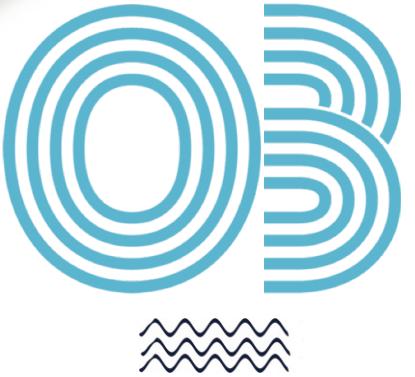
Output

Save objects to  
display to output\$



Display

Build objects to  
display with  
render\*()



# Week 3

Please enter your title



## «Practical Statistics and Experimental Design for Plant and Crop Science»

Book reading



### Basic statistical calculations

- ❖ Population/sample mean, median, variance.
- ❖ Corrected sum of squares( $S_{xx}$ ).
- ❖ SD,CV
- ❖ Weighted mean, harmonic mean



### Type of variables

- Continuous, discrete and categorical variables.



### Basic summary

- ❖ Frequency distributions
- ❖ Histograms, boxplot, stem-leaf plot
- ❖ Quartiles and ranges





# Linear mixed effect models

Sam Rogers

## Linear models

Linear model:

$$Y = X\beta + \varepsilon$$

Linear mixed model:

$$Y = X\beta + Z\mu + \varepsilon$$



Learn more

## LME4

Open source (free to use)

Cannot specify residual correlation structure

Cannot incorporate market based relationship matrices

Limited variance structure available for random effect

## ASReml-R

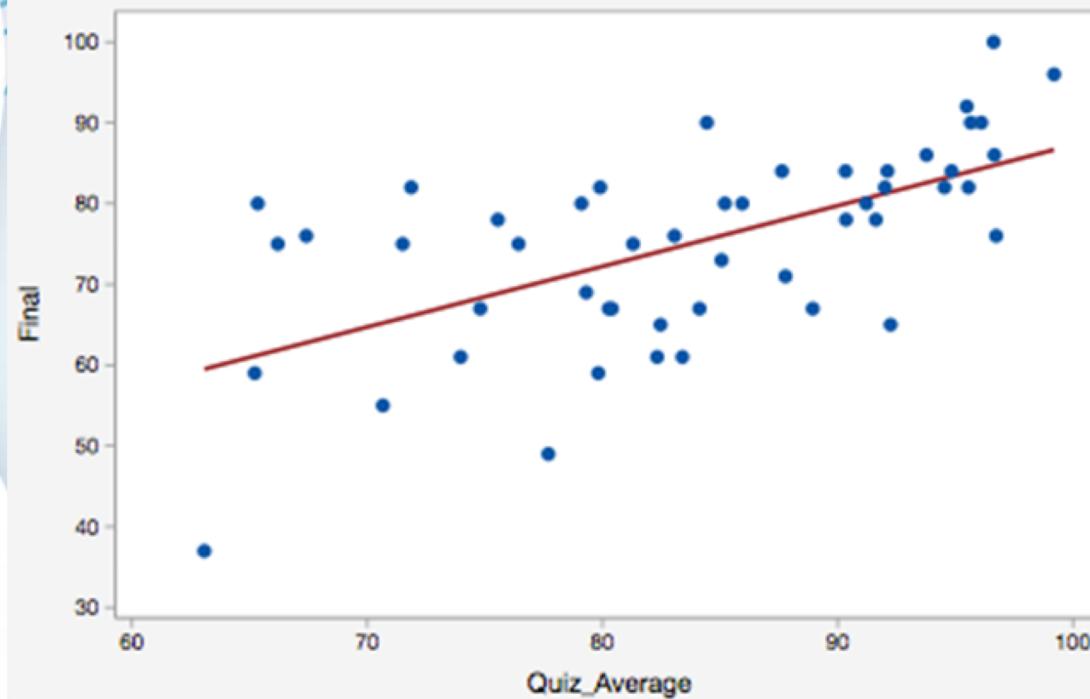
Close source (have to pay for access)

Can specify residual correlation structure

Can incorporate market based relationship matrices

Flexible variance structure available for random effect

Fitted Line Plot for Linear Model



## Linear model

$$Y = X\beta + \varepsilon$$

Pseudo normalized phonological diversity

Pseudo distance from origin

- Pseudo language family
- 1
  - 2
  - 3
  - 4
  - 5
  - 6
  - 7
  - 8
  - 9
  - 10
  - 11
  - 12
  - 13
  - 14
  - 15

## Linear mixed model

$$Y = X\beta + Z\mu + \varepsilon$$



# Optimal Design

Julian Taylor



## Package OD

A R package used to design proper experiments to reduce experimental cost



## Optimal Design

In the design of experiments, optimal designs are a class of experimental designs that are optimal with respect to some statistical criterion.



# The End

THINKS FOR YOUR LISTING

