

MA50259: Statistical Design of Investigations

Coursework 1 (2024)

Disclaimer:

AI software (RStudio built-in Co-Pilot and ChatGPT) are used in this coursework for code, RMarkdown formatting, and explanation suggestions, debugging purposes.

Part 1: Baking Powder Experiment

In an experiment to study the effect of the amount of baking powder in a biscuit dough upon the rise heights (measured in centimetre) of the biscuits, four levels of baking powder were tested and four replicate biscuits were made with each level in a random order. The results are shown in the table below (tsp stands for teaspoon)

.25 tsp	0.5 tsp	.75 tsp	1 tsp
11.4	27.8	47.6	61.6
11.0	29.2	47.0	62.4
11.3	26.8	47.3	63.0
9.5	26.0	45.5	63.9

1. What is the experimental unit and which type of experimental design is this?

Answer:

Definition of an *experimental unit*: The item under study upon which something is changed. This could be things, human subjects, or just a point in time.

The *experimental unit* in this experiment is each individual biscuit.

Definition of a *experimental design*: A collection of experiments or runs that is planned in advance of the actual execution. The particular runs selected in an experimental design will depend upon the purpose of the design.

This type of experimental design is known as completely randomised design (CRD).

2. Read-in the data in the table above in R as a `data.frame` in such a way that it can be used by the `lm` function without any modification, that is, your data frame should have 2 columns and 16 rows. The variables in the dataframe should be called `riseht` and `type`. The data frame should be called `biscuits`

```
options(width = 50)
biscuits <- data.frame(riseht=c(11.4,11.0,11.3,9.5,27.8,29.2,26.8,26.0,47.6,47.0
                              ,47.3,45.5,61.6,62.4,63.0,63.9),
                      type=rep(c(0.25,0.5,0.75,1),each=4))
biscuits$type <- factor(biscuits$type)
```

3. Construct in R, the design matrix \mathbf{X} corresponding to the model:

$$y_{ij} = \mu + \tau_j + \epsilon_{ij}$$

where $\tau_{0.25}, \tau_{0.50}, \tau_{0.75}$ and $\tau_{1.0}$ are the effects of the levels of the baking powder. All $\epsilon_{ij} \sim N(0, \sigma^2)$ and are mutually independent.

```
y <- biscuits$riseht
t <- length(unique(factor(biscuits$type))) # number of treatments
r <- nrow(biscuits)/t # number of replicates per treatment
n <- nrow(biscuits) # total number of experimental units
levels <- unique(factor(biscuits$type)) # levels of the baking powder
fact <- gl(t,r,labels=levels) # factor variable
Z <- model.matrix(~fact-1) # matrix Z as the means model of a CRD
X <- cbind(1,Z) # design matrix X as the treatment effects model of a CRD

# naming the columns
colnames(X) <- c("reference", "0.25 tsp", "0.50 tsp", "0.75 tsp", "1.00 tsp")

# Display the design matrix X
kable(X, align = "c", caption = "Design Matrix X")
```

Table 1: Design Matrix X

reference	0.25 tsp	0.50 tsp	0.75 tsp	1.00 tsp
1	1	0	0	0
1	1	0	0	0
1	1	0	0	0
1	1	0	0	0
1	0	1	0	0
1	0	1	0	0
1	0	1	0	0
1	0	1	0	0
1	0	0	1	0
1	0	0	1	0
1	0	0	1	0
1	0	0	0	1
1	0	0	0	1
1	0	0	0	1
1	0	0	0	1

4. How many unknown parameters are in the model?

Answer:

5 unknown parameters:

- i. One reference rise height of the biscuit when there is no treatment μ
- ii. Four treatment effects τ_i for $i = 1, 2, 3, 4$

5. Find the rank of the design matrix \mathbf{X} . You should justify your answer.

```
cat("Rank of design matrix X: ", qr(X)$rank)
```

```
## Rank of design matrix X: 4
```

Answer:

The rank of the design matrix \mathbf{X} is 4. This is because the design matrix \mathbf{X} has 5 columns and the rank of a matrix is the maximum number of linearly independent column vectors in the matrix. The first column of \mathbf{X} is a column of ones, and thus the remaining 4 columns are dependent on the first column but not to one another. Therefore, the rank of \mathbf{X} is 4 as shown in the QR decomposition of \mathbf{X} above.

6. Perform the analysis of variance to test the hypothesis of no treatment effect. You should do the computations using the theory given in the lectures and not simply use the command `aov`.

```
# The ANOVA table is computed using the following steps:
# Calculate grand mean
grand_mean <- mean(y)

# Calculate the total sum of squares (SSTotal)
SSTotal <- sum((y - grand_mean)^2)

# Calculate the treatment sum of squares (SSTreatment)
means <- tapply(y, biscuits$type, mean)
SSTreatment <- sum(r*means^2) - n*grand_mean^2

# Calculate the error sum of squares (SSError)
SSError <- SSTotal - SSTreatment

# Alternative code for SSError
# t(matrix(y,ncol=1))%*(diag(n)-(1/n)*rep(1,n)%*t(rep(1,n)))%*matrix(y,ncol= 1)

# Calculate the degrees of freedom for the treatment (dfTreatment)
dfTreatment <- t - 1

# Calculate the degrees of freedom for the error (dfError)
dfError <- n - t

# Calculate the mean square for the treatment (MSTreatment)
MSTreatment <- SSTreatment/dfTreatment

# Calculate the mean square for the error (MSError)
MSError <- SSError/dfError

# Calculate the F-statistic
F_stat <- MSTreatment/MSError
```

```
# Calculate the p-value
p_value <- 1 - pf(F_stat,dfTreatment,dfError)

kable(
  data.frame(
    Source = c("Treatment", "Error", "Total"),
    `Sum of Squares` = c(SSTreatment, SSEerror, SSTtotal),
    `Degrees of Freedom` = c(dfTreatment, dfError, n - 1),
    `Mean Square` = c(round(MSTreatment, 4), round(MSEerror, 4), ""),
    `F-statistic` = c(round(F_stat, 4), "", ""),
    `p-value` = c(sprintf("%.2e", p_value), "", "")
  ),
  align = "c"
)
```

Source	Sum.of.Squares	Degrees.of.Freedom	Mean.Square	F.statistic	p.value
Treatment	6145.7319	3	2048.5773	1822.6452	3.33e-16
Error	13.4875	12	1.124		
Total	6159.2194	15			

Answer:

The hypothesis test is as follows:

The null hypothesis, H_0 : $\tau_1 = \tau_2 = \tau_3 = \tau_4$.

The alternative hypothesis, H_a : at least two of the τ s differs.

Let the significance level be $\alpha = 0.05$. The null hypothesis is that there is no treatment effect, that is, $\tau_1 = \tau_2 = \tau_3 = \tau_4$. The alternative hypothesis is that at least one of the τ s are not equal. Given that we obtained a p-value of 3.33×10^{-16} , which is less than the significance level of 0.05 (5% is commonly used in a typical hypothesis test), we reject the null hypothesis and conclude that there is a treatment effect.

7. Formulate a contrast to test the hypothesis that increase in rise height is a linear function of the increase in baking powder in the dough, and test this hypothesis.

```
# Contrast Reference: https://online.stat.psu.edu/stat555/node/73/

# Formulate the contrast
# Since we are testing whether the increase in rise height is a linear function of the
# increase in baking powder in the dough, we can use the contrast:
linear_contrast_c <- c(0, -3, -1, 1, 3)
ginverse <- rbind(0, cbind(0, solve(t(Z) %*% Z)))
beta <- ginverse %*% t(X) %*% y

# Calculate the contrast estimate
contrast_estimate <- linear_contrast_c %*% beta

# Calculate the standard error of the contrast estimate
# The standard error of the contrast estimate is calculated using the formula:
```

```

# SE = sqrt(MSError * sum(c^2)/t)
# Refer: https://websites.umich.edu/~gonzo/coursenotes/file3.pdf page 3-3
SE_contrast_estimate <- sqrt(MSError * sum(linear_contrast_c^2)/t)

# Calculate the t-statistic
t_stat <- contrast_estimate / SE_contrast_estimate

# Calculate the p-value in a two-tailed test
# Refer: https://www.geeksforgeeks.org/how-to-calculate-the-p-value-of-a-t-score-in-r/
p_value_contrast <- 2 * pt(-abs(t_stat), dfError)

kable(
  data.frame(
    Contrast = c("Contrast Test"),
    `Contrast Estimate` = round(contrast_estimate, 2),
    `Contrast Standard Error` = round(SE_contrast_estimate, 2),
    `t-Statistic` = round(t_stat, 2),
    `p-Value` = sprintf("%.2e", p_value_contrast)
  ),
  align = "c"
)

```

Contrast	Contrast.Estimate	Contrast.Standard.Error	t.Statistic	p.Value
Contrast Test	175.18	2.37	73.89	2.51e-17

Answer:

A contrast is a linear combination $\mathbf{c}^T \beta = c_0 \mu + \sum_{i=1}^t c_i \tau_i$ of the treatment means, where $\sum_{i=0}^t c_i = 0$.

A contrast allows us to test the hypothesis that increase in rise height is a linear function of the increase in baking powder in the dough.

Let $c_0 = 0$ as we are only interested to check for presence of a linear trend due to varying the amount of baking powder used.

Since we are testing whether the increase in rise height is a linear function of the increase in baking powder in the dough, we can use the contrast:

$$\mathbf{c} = (0, -3, -1, 1, 3)$$

which is a classical orthogonal contrast coefficients for testing the linear trend in the treatment means. This also fulfils the requirement that the sum of the contrast weights is equal to zero $\sum \mathbf{c} = 0 - 3 - 1 + 1 + 3 = 0$.

The contrast weights are chosen such that the first treatment level is weighted by -3, the second treatment level is weighted by -1, the third treatment level is weighted by 1, and the fourth treatment level is weighted by 3. Doing so allows the τ_2 and τ_3 to serve as a pivot point for the linear trend, while multiplying τ_1 by -3 allows us to “pull” the contrast value down, and multiplying τ_4 by 3 allows us to “push” the contrast value up. Thus allows symmetrical distribution of the contrast weights around the pivot point, making it suitable to check a simple linear trend.

Setting up our hypothesis test:

Let:

The null hypothesis, H_0 : $\tau_1 = \tau_2 = \tau_3 = \tau_4$.

The alternative hypothesis, H_a : at least two of the τ s differs.

Calculating beta:

From the equation:

$$\mathbf{X}^T \mathbf{X} \boldsymbol{\beta} = \mathbf{X}^T \mathbf{y}$$

we can rewrite the equation to find $\tilde{\boldsymbol{\beta}}$ as:

$$\tilde{\boldsymbol{\beta}} = (\mathbf{X}^T \mathbf{X})^- \mathbf{X}^T \mathbf{y}$$

where $(\mathbf{X}^T \mathbf{X})^-$ is the generalized inverse of $\mathbf{X}^T \mathbf{X}$.

A generalized inverse of a square matrix \mathbf{A} is another square matrix \mathbf{A}^- satisfying

$$\mathbf{A} \mathbf{A}^- \mathbf{A} = \mathbf{A}$$

The generalized inverse of a non-full rank matrix is used to estimate the variance of the experimental error using the technique

$$(\mathbf{X}^T \mathbf{X})^- = \begin{pmatrix} 0 & 0 \\ 0 & (\mathbf{Z}^T \mathbf{Z})^{-1} \end{pmatrix}$$

where \mathbf{X} is the design matrix and \mathbf{Z} is the matrix of means.

```
kable(means, col.names = c("Treatment Level", "Means Within Individual Treatment Levels"), align = "c")
```

Treatment Level	Means Within Individual Treatment Levels
0.25	10.800
0.5	27.450
0.75	46.850
1	62.725

The contrast estimates to 175.18 using the formula:

$$c^T \hat{\boldsymbol{\beta}} = 0 + c^T \hat{\tau}_i = \text{contrast weight} \times \text{mean within individual treatment levels} = (-3 \times 10.800) + (-1 \times 27.450) + (1 \times 46.850) + (3 \times 62.725) = 175.18$$

Next, we calculate the standard error of the contrast using the formula:

$$\text{standard error (contrast)} = \sqrt{MSE \times \frac{\sum_{i=1}^t c_i^2}{\text{no. of treatment levels checked in this contrast}}} = \sqrt{1.124 \times \frac{(-3)^2 + (-1)^2 + (1)^2 + (3)^2}{4}} = 2.37$$

where

MSE = mean square error

c_i = contrast weight

t = number of treatments

The t-statistic is calculated using the formula:

$$t = \frac{\text{contrast estimate}}{\text{standard error (contrast)}} = \frac{175.18}{2.37} = 73.89$$

The p-value is calculated using a t-score of 73.89 and 12 degrees of freedom ($n-t = 16-4 = 12$). We obtain a p-value of 2.51×10^{-17} , which is less than the significance level of 0.05 (*5% is commonly used in a typical hypothesis test*). Therefore, we reject the null hypothesis and conclude that there is a linear trend in the treatment means given that the p-value is less than 0.05 ($2.51 \times 10^{-17} < 0.05$).

8. Estimate the variance σ^2 of the experimental error.

```
# Estimate the variance of the experimental error
# The variance of the experimental error is estimated using the formula:
# \hat{\sigma}^2 = SSE / (n - t)

# Formulate the ginverse for non-full rank treatment model
SSE_matrix_method <- t(y) %*% (diag(n) - X %*% ginverse %*% t(X)) %*% y
variance_of_experimental_error <- round(SSE_matrix_method / (n - t), 4)
cat("Variance of the experimental error: ", variance_of_experimental_error)
```

```
## Variance of the experimental error: 1.124
```

Answer:

The variance of the experimental error is estimated to be 1.124 using the formula $\hat{\sigma}^2 = \frac{SSE}{n-t}$.

Sum of Square Error (SSE) is calculated using the formula

$$\mathbf{y}^T (\mathbf{I} - \mathbf{X}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T) \mathbf{y}$$

where:

- \mathbf{y} is the response vector
 - \mathbf{I} is the identity matrix
 - n is the total number of experimental units
 - t is the number of treatments.
-

9. Discuss whether the assumptions for the considered linear model are justified.

Answer:

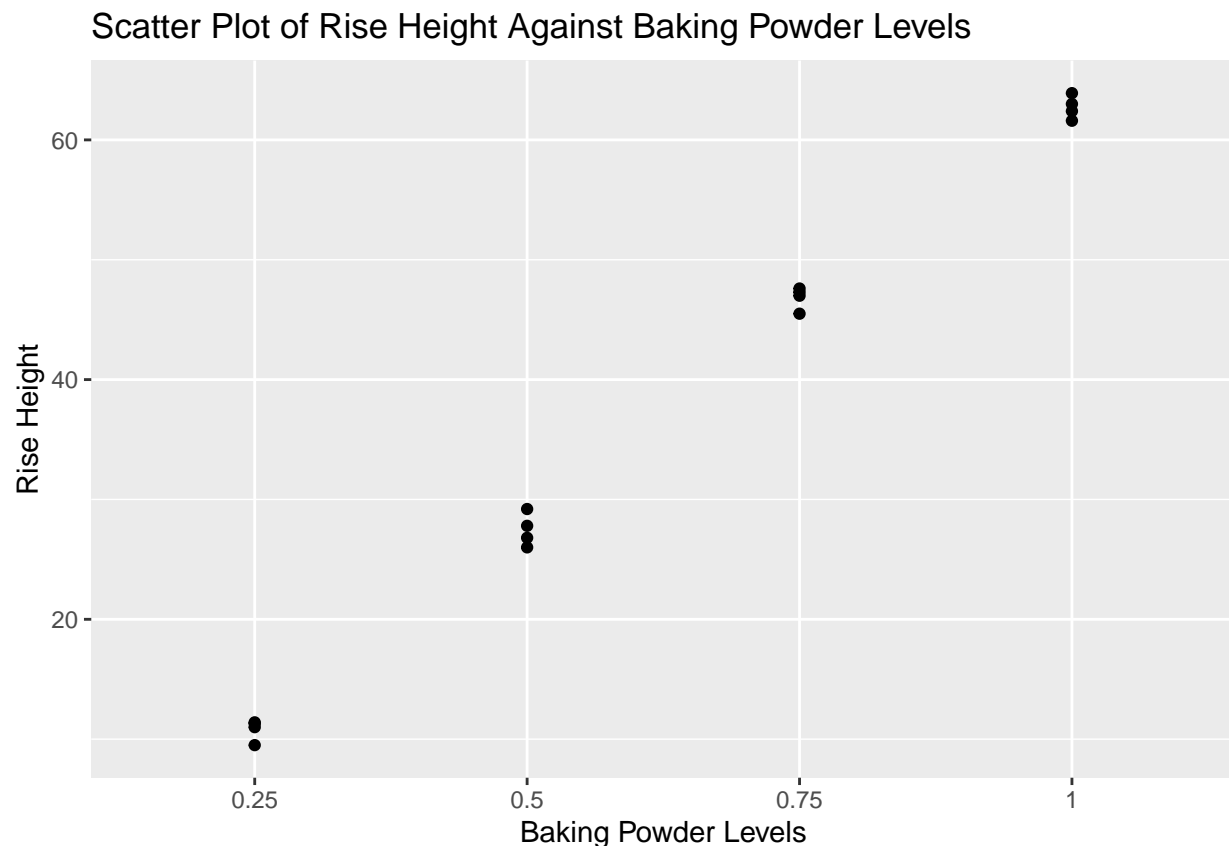
The assumptions for the considered linear model are:

Assumption 1: There is an additive effect of the treatment levels on the means, e.g. $\mu_i = \mu + \tau_i$.

The assumption is justified as based on our contrast test, we have found that there is a linear trend in the treatment means. This means that the increase in rise height is a linear function of the increase in baking powder in the dough.

Not to mention a simple scatter plot also shows a linear trend in the treatment means as we increase the amount of baking powder in the dough.

```
library(ggplot2)
ggplot(biscuits, aes(x=type, y=riseht)) +
  geom_point() +
  labs(title="Scatter Plot of Rise Height Against Baking Powder Levels", x="Baking Powder Levels", y="Rise Height")
```

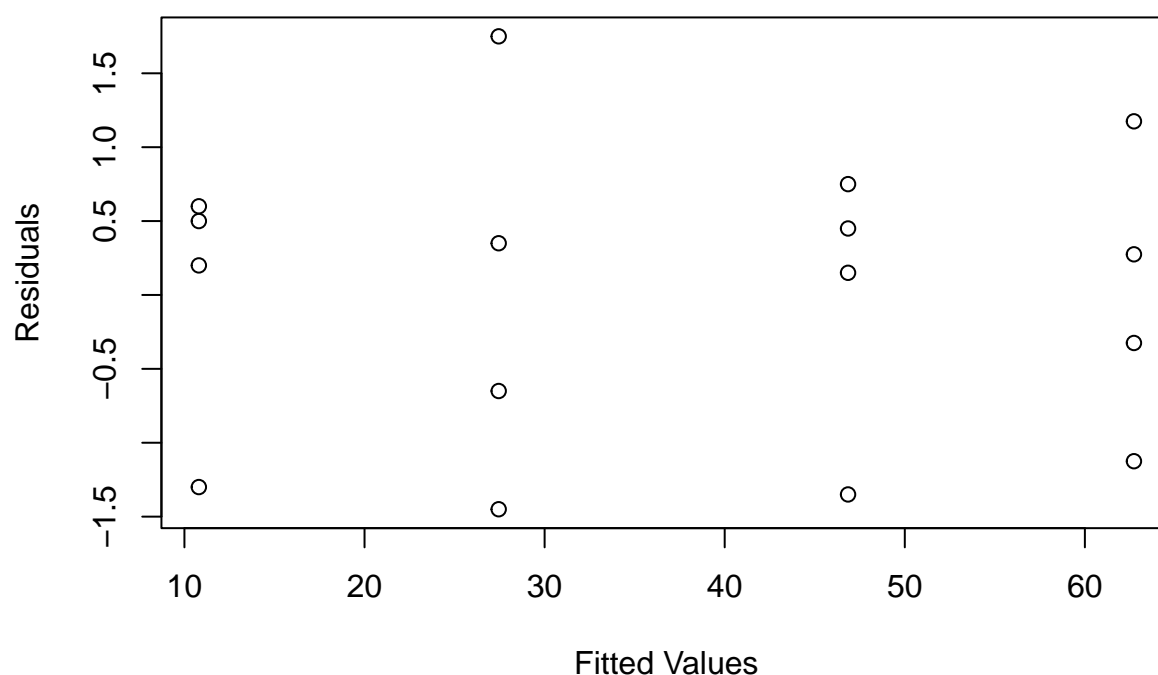


Assumption 2: If the units are homogeneous, the probability distribution of the response y_{ij} or the experimental error ϵ_{ij} , under the same treatment level, is the same.

To check the assumption of homogeneity of variance, we can use the residuals vs fitted values plot. The residuals vs fitted values plot will help us to assess whether the variance of the residual is consistent across all levels of the independent variable. If the variance of the residuals is consistent across all levels of the independent variable, then the assumption of homogeneity of variance is met.

```
residuals <- residuals(aov(riseht ~ type, data = biscuits))
plot(fitted(aov(riseht ~ type, data = biscuits)), residuals, xlab = "Fitted Values", ylab = "Residuals")
```


Residuals vs Fitted Values

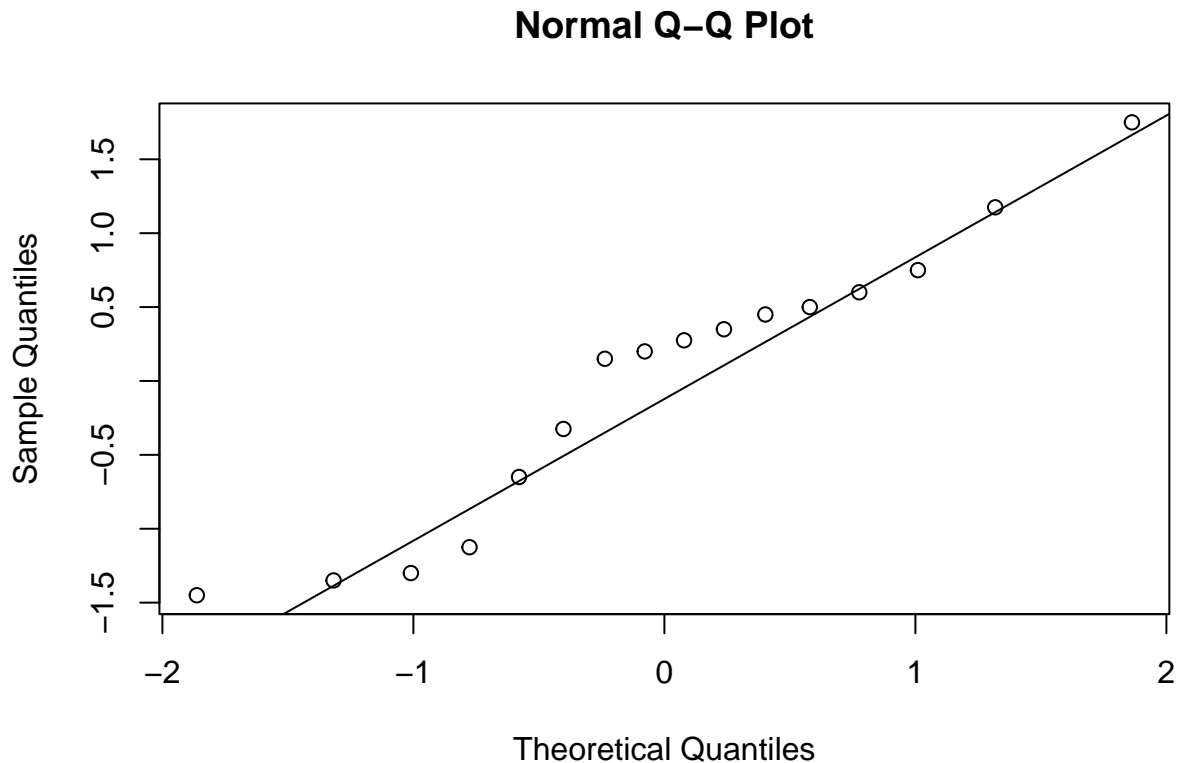


As shown in the residuals vs fitted values plot, the variance of the residuals is fairly consistent (no significant deviation on the datapoint observed) across all levels of the independent variable. This suggests that the assumption of homogeneity of variance is met.

Assumption 3: The probability distribution of the response y_{ij} or the experimental error ϵ_{ij} , is Gaussian.

A QQ plot can be used to check the whether the residuals are normally distributed (Gaussian). If the residuals are normally distributed, the points in the QQ plot will fall approximately along a straight line.

```
qqnorm(residuals)
qqline(residuals)
```



As shown in the QQ plot, the points at both tails of the QQ points falls approximately along the straight line (*Observe the 3 points when theoretical quantiles are less than -1 and the 3 points when theoretical quantiles more than 1*). This suggests that the residuals are normally distributed.

-
10. If the dough were made in batches and the four replicate biscuit rise heights in each column (shown in the table above) were all from the same batch, would your answer to (a) be different? How could the data be analysed if this were the case?
-

Answer:

It would change the nature of the experiment as we lost the advantages gained due to randomisation. Randomisation is important as it helps to ensure that each individual treatment groups are comparable and that the effects observed are due to treatments rather than any underlying differences between the treatment groups. If the biscuits are made all from the same batches, this introduces the possibility of batch-to-batch variation influencing the results. It might have confound the effects of the baking powder, making it harder for us to isolate the true effect of each treatment level of the baking powder.

The assumption of independence of the errors ϵ_{ij} would be violated. This is because the errors ϵ_{ij} would not be independent of one another. In other words, the error associated from one experimental unit (biscuit) should not be influence by error of any other biscuit for it to be considered independent. However, if the biscuits are made all from the same batches, that meant that all replicate within treatments come from the same batch and are thus manufactured under the same conditions (e.g. same temperature, same humidity, same manufacturing equipment used etc.). This would introduce the possibility of correlated error, as conditions within a batch could affect all the biscuits in a similar way.

In this case, the data could be analysed using a randomised complete block design where the blocks would be the batches of dough and the treatments would be the levels of the baking powder. This would allow us to account for the batch-to-batch variation by ensuring that all treatments are represented within each batch.

Part 2: Free fall of Papers of Different Dimension

In this part of the coursework you will design a factorial experiment, collect the data and then analyse it. You will carry out this experiment to identify how different design factors influence the free fall time of a piece of paper.

Experimental Units

In this experiment each experimental unit will correspond to a single piece of paper. Replicates will mean you will have to use as many papers of different dimension as needed.

Instructions

In this experiment you will need to drop many pieces of paper from a certain height. Please follow the following instructions:

- Use white printer paper (if needed you can use the university printer papers).
- Label your papers according to the factor variables (described below) and the replicate number.
- Perform the experiment in a large open space, mostly isolated from wind.
- Always allow the papers to fall approximately from the same height, straight towards the floor.
- You can do some practice before starting the main experiment, but I recommend to use different papers for this. The practice papers can be used more than once.
- Do not do all the experiment in one go. Take a few breaks to make sure your arm does not get tired and always use the same arm for the experiment.
- Recycle all the paper after finishing the experiment.

Response

Time in seconds (time to be recorded to the nearest whole second) of the free fall of the paper. To measure the free fall time, follow the following instructions:

- Locate a position from where you would drop the piece of paper. You can mark that with your bag/other item. Stand there and drop the piece of paper from a certain height. Use your mobile/ a stopwatch to record the free fall time of the paper.
- Record the times in seconds (time to be recorded to the nearest whole second) in a spreadsheet making reference to each level of the factor.
- If anything goes wrong, for example if the paper touches your body before falling down, repeat that particular run with a different (pristine) paper.
- Repeat the experiment by dropping the pieces of paper from (approximately) the same height every time.

Factor variables

- Factor 1 (length of the paper): (2 levels) 5 cm, 6 cm. You can measure the length using a ruler.
- Factor 2 (Width of the paper): (2 levels) 5.5 cm, 6.5 cm. You can measure the width using a ruler.

Randomization

Remember to assign the factor level combinations to the experimental units (the piece of paper) completely at random. You can do this in R using the `sample` function. For example, for a balanced design with $r = 3$ replicates, you can assign the level combinations to a total of 12 papers using the following command

```
f<-rep(c("5,5.5","6,5.5","5,6.5","6,6.5"),each=3)
sample(f,12)
```

```
## [1] "5,6.5" "5,6.5" "5,6.5" "6,6.5" "6,6.5"
## [6] "5,5.5" "5,5.5" "6,5.5" "6,5.5" "6,6.5"
## [11] "6,5.5" "5,5.5"
```

The experiment will be balanced in the sense that each factor level combination will have the same number of replicates r but you will have to determine the number of replicates. For this, consider the model with interactions:

$$y_{ijk} = \mu + \tau_i + \alpha_j + \gamma_{ij} + \epsilon_{ijk}$$

where $\tau_{3.5}, \tau_{4.5}$ are the effects of the two different lengths of the papers, α_3, α_4 are the effects of the two different widths of the papers, γ_{ij} are the effects of the interactions. All $\epsilon_{ijk} \sim N(0, \sigma^2)$ and are mutually independent.

Before running the main experiment, you will need to perform a simple pilot experiment in order to estimate the variance parameter σ^2 . You should perform $n_{pilot} = 10$ runs with 10 different papers of length 5 cm and width 5.5 cm.

Specifically of length 5 cm and width 5.5 cm respectively. Denote by t_1, \dots, t_{10} the observed times in seconds. You should estimate the variance in the usual way, that is,

$$\hat{\sigma}^2 = \frac{1}{n_{pilot} - 1} \sum_{i=1}^{10} (t_i - \bar{t})^2$$

- a) Report your 10 observations from the pilot experiment as well as your estimated value of σ^2 .

```
# Pilot experiment
pilot_raw <- c(3.28, 3.52, 3.56, 3.54, 3.66, 3.62, 2.98, 3.10, 3.28, 2.98)

# Round to nearest whole second
pilot <- round(pilot_raw)

kable(
  data.frame(
    `Number of Observations` = 1:10,
    `Free Fall Time` = pilot_raw,
    `Free Fall Time Rounded to Nearest Second` = pilot
  ),
  align = "c"
)
```

Number.of.Observations	Free.Fall.Time	Free.Fall.Time.Rounded.to.Nearest.Second
1	3.28	3
2	3.52	4
3	3.56	4
4	3.54	4
5	3.66	4
6	3.62	4
7	2.98	3
8	3.10	3
9	3.28	3
10	2.98	3

```
# Estimating the variance of the experimental error using the given formula
variance_of_experimental_error_pilot <- round(sum((pilot - mean(pilot))^2) / (length(pilot) - 1), 4)
variance_of_experimental_error_pilot
```

```
## [1] 0.2778
```

- b) Denote $\Delta_5 := \mu_{5,5.5} - \mu_{5,6.5}$ and $\Delta_6 := \mu_{6,5.5} - \mu_{6,6.5}$ where μ_{ij} is the mean response for length $i \in \{5, 6\}$ and width $j \in \{5.5, 6.5\}$. State the null and the alternative hypotheses for a two-sided test of $\Delta_5 = \Delta_6$. Let $\Delta = |\Delta_5 - \Delta_6|$. We would like to detect an absolute difference $\Delta = 1$ with high power. Determine the number of replicates r necessary to achieve at least 90% power using a significance level $\alpha = 0.05$.

```
library(daewr)
# Power calculation
rmin <- 2
rmax <- 10
alpha <- 0.05
delta <- 1
nlev <- c(2,2)
nreps <- c(rmin:rmax)
power <- Fpower2(alpha, nlev, nreps, delta, sqrt(variance_of_experimental_error_pilot))
kable(power, align = "c")
```

alpha	a	b	nreps	Delta	sigma	powera	powerb
0.05	2	2	2	1	0.5270674	0.5301904	0.5301904
0.05	2	2	3	1	0.5270674	0.8199333	0.8199333
0.05	2	2	4	1	0.5270674	0.9353680	0.9353680
0.05	2	2	5	1	0.5270674	0.9781197	0.9781197
0.05	2	2	6	1	0.5270674	0.9929472	0.9929472
0.05	2	2	7	1	0.5270674	0.9978177	0.9978177
0.05	2	2	8	1	0.5270674	0.9993476	0.9993476
0.05	2	2	9	1	0.5270674	0.9998106	0.9998106
0.05	2	2	10	1	0.5270674	0.9999464	0.9999464

Answer:

The null hypothesis, $H_0: \Delta_5 = \Delta_6$.

The alternative hypothesis, $H_a: \Delta_5 \neq \Delta_6$.

We would like to detect an absolute difference $\Delta = 1$ with high power. The number of replicates r necessary to achieve at least 90% power using a significance level $\alpha = 0.05$ is $nrep = 4$.

```
# Generating the data
set.seed(37) # Set seed for reproducibility
f<-rep(c("5,5.5","6,5.5","5,6.5","6,6.5"),each=4)
sample(f,16)

## [1] "6,5.5" "6,6.5" "6,5.5" "5,5.5" "5,5.5"
## [6] "6,6.5" "5,5.5" "5,6.5" "5,6.5" "5,6.5"
## [11] "6,5.5" "6,6.5" "5,6.5" "6,5.5" "5,5.5"
## [16] "6,6.5"

# Inputting the collect data into a dataframe (Exclude the non-rounded observed values)
df <- data.frame(
  `Length` = c(6, 6, 6, 5, 5, 6, 5, 5, 5, 5, 6, 6, 5, 6, 5, 6),
  `Width` = c(5.5, 6.5, 5.5, 5.5, 5.5, 6.5, 5.5, 6.5, 6.5, 6.5, 5.5, 6.5, 6.5, 5.5, 5.5, 6.5),
  `Fall_Time` = c(3, 3, 4, 4, 3, 3, 3, 3, 3, 3, 4, 3, 4, 4, 4, 4)
)

# Displaying the collected data in a table
kable(
  data.frame(
    `Number of Observations` = 1:16,
    `Length` = c(6, 6, 6, 5, 5, 6, 5, 5, 5, 5, 6, 6, 5, 6, 5, 6),
    `Width` = c(5.5, 6.5, 5.5, 5.5, 5.5, 6.5, 5.5, 6.5, 6.5, 6.5, 5.5, 6.5, 6.5, 5.5, 5.5, 6.5),
    `Observed_Value` = c(3.35, 3.45, 3.57, 3.58, 3.45, 3.3, 3.2, 3.16, 2.85, 3.07, 3.4, 3.72, 3.2, 3.7,
    `Observed_Value_Rounded` = c(3, 3, 4, 4, 3, 3, 3, 3, 3, 3, 4, 3, 4, 4, 4, 4)
  ),
  align = "c"
)
```

Number.of.Observations	Length	Width	Observed_Value	Observed_Value_Rounded
1	6	5.5	3.35	3
2	6	6.5	3.45	3
3	6	5.5	3.57	4
4	5	5.5	3.58	4
5	5	5.5	3.45	3
6	6	6.5	3.30	3
7	5	5.5	3.20	3
8	5	6.5	3.16	3
9	5	6.5	2.85	3
10	5	6.5	3.07	3
11	6	5.5	3.40	3
12	6	6.5	3.72	4
13	5	6.5	3.20	3
14	6	5.5	3.70	4
15	5	5.5	3.68	4
16	6	6.5	3.98	4

Number.of.Observations	Length	Width	Observed_Value	Observed_Value_Rounded
------------------------	--------	-------	----------------	------------------------

- c) Use ANOVA and your collected data to test if length of paper has a significant effect. Clearly state the hypotheses you are testing. Repeat the test but now consider width instead of length of paper.

Answer:

For a two-factor factorial:

The means model:

$$y_{ijk} = \mu_{ij} + \epsilon_{ijk}$$

where:

- i represents the level of the first factor
- j represents the level of the second factor
- k represents the replicate number
- μ_{ij} represents the expected response in the (i, j) th cell

and its corresponding effects model: #TODO: Retype this

$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \epsilon_{ijk}$$

where:

- α_i (length of paper) and β_j (width of paper) are the main treatment effects.
- γ_{ij} is the interaction effect between the cell mean, μ_{ij} and $\mu + \alpha_i + \beta_j$.
- ϵ_{ijk} is the experimental error such that $E(\epsilon_{ijk}) = 0$ and $\epsilon \sim MVN(0, \sigma^2 I)$.

```
# Creating the design matrix X
# Define factor variables
# length_of_paper <- df %>% mutate(length = as.factor(length))
# width_of_paper <- factor(c(5.5, 6.5))
#
# # Create interaction
# inter <- interaction(length_of_paper, width_of_paper, sep = ",")
#
# # Create the design matrix
# X1 <- model.matrix(~length_of_paper - 1, df)
# X2 <- model.matrix(~width_of_paper - 1, df)
# X3 <- model.matrix(~inter - 1, df)
#
# X <- rbind(X1, X2, X3)
# colnames(X)[1] <- "(intercept)"
# X

# Alternative method
length <- factor(df$Length)
width <- factor(df$Width)
```

```

paper_model <- as.formula("~ length * width")
X_paper <- model.matrix(paper_model)

time <- c(3, 3, 4, 4, 3, 3, 3, 3, 3, 3, 3, 4, 3, 4, 4, 4)
factor_combination <- data.frame(
  length = c(6, 6, 6, 5, 5, 6, 5, 5, 5, 5, 6, 6, 5, 6, 5, 6),
  width = c(5.5, 6.5, 5.5, 5.5, 5.5, 6.5, 5.5, 6.5, 6.5, 6.5, 5.5, 6.5, 6.5, 5.5, 5.5, 6.5)
)
exp_results <- data.frame(time, factor_combination)

exp_results$length <- factor(exp_results$length)
exp_results$width <- factor(exp_results$width)

exp_model <- aov(time ~ length * width, data = exp_results)

test_results <- anova(exp_model)
test_results

```

```

## Analysis of Variance Table
##
## Response: time
##
##           Df Sum Sq Mean Sq F value Pr(>F)
## length      1   0.25    0.25      1  0.337
## width       1   0.25    0.25      1  0.337
## length:width 1   0.25    0.25      1  0.337
## Residuals   12   3.00    0.25

```

Answer:

The hypothesis test for the length of paper is as follows:

The null hypothesis, $H_0: \tau_5 = \tau_6$. The alternative hypothesis, $H_a: \tau_5 \neq \tau_6$.

The hypothesis test for the width of paper is as follows:

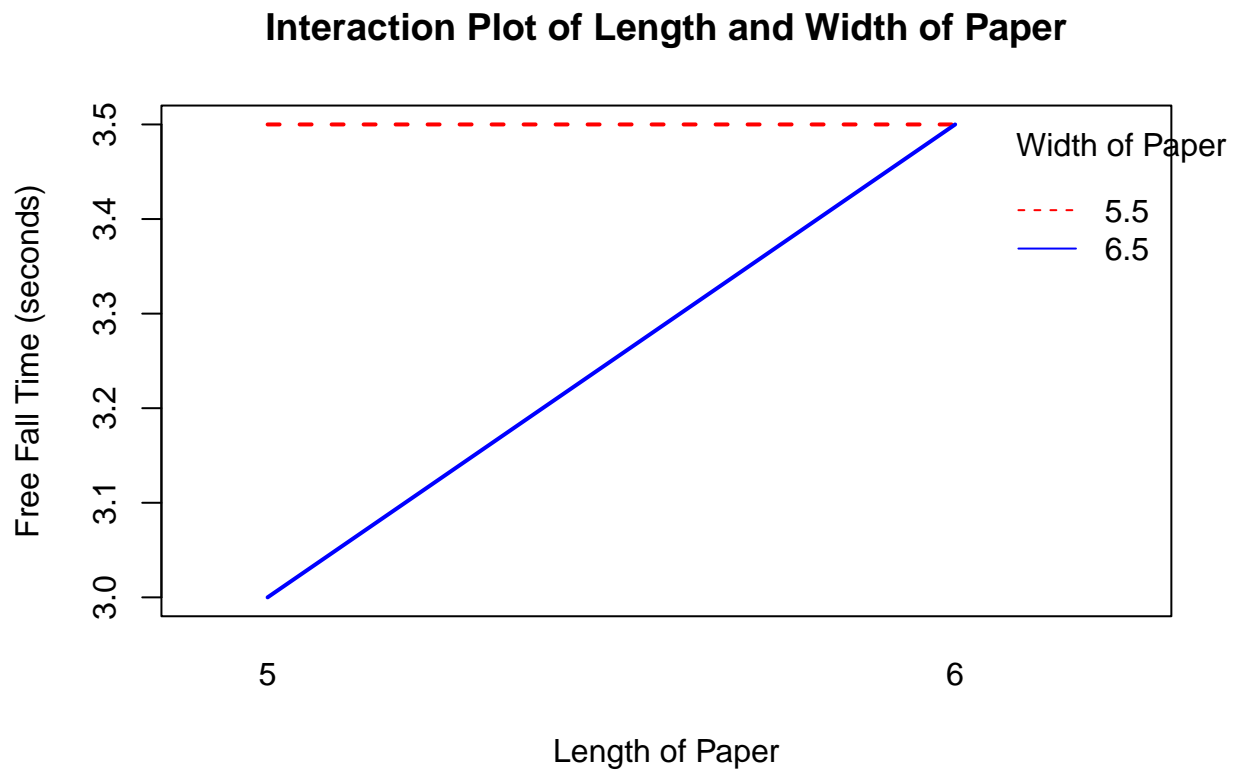
The null hypothesis, $H_0: \alpha_{5.5} = \alpha_{6.5}$. The alternative hypothesis, $H_a: \alpha_{5.5} \neq \alpha_{6.5}$.

The p-value for the standalone effect of the length of the paper τ_i is 0.337 which is greater than the significance level of 0.05. Therefore, we fail to reject the null hypothesis and conclude that the length of the paper does not have a significant effect on the free fall time of the paper.

The p-value for the standalone effect of the width of the paper α_j is 0.337 which is greater than the significance level of 0.05. Therefore, we fail to reject the null hypothesis and conclude that the width of the paper does not have a significant effect on the free fall time of the paper.

- d) Use the previous ANOVA table to comment on if the interaction effect is significant or not. Clearly state the hypotheses you are testing to check if the interaction effect is significant or not. Also, comment on the same using an appropriate plot. Mention any lurking variables one needs to be aware of.
-


```
# Interaction plot
interaction.plot(exp_results$length
, exp_results$width
, exp_results$time
, xlab = "Length of Paper"
, ylab = "Free Fall Time (seconds)"
, trace.label = "Width of Paper"
, legend = TRUE
, col = c("red", "blue")
, lwd = 2
# , type = "b"
, main = "Interaction Plot of Length and Width of Paper"
)
```



Answer:

The hypothesis test for the interaction effect is as follows:

The null hypothesis, $H_0: \gamma_{ij} = 0$. The alternative hypothesis, $H_a: \gamma_{ij} \neq 0$.

The p-value for the interaction effect γ_{ij} is 0.337 which is greater than the significance level of 0.05. Therefore, we fail to reject the null hypothesis and conclude that the interaction effect is not significant.