Lifestyle Choices and Level of Lung Cancer - A Statistical Inquiry

2023-05-04

Introduction

Hello everyone, we are Group - 4, our Team members are Osama, Vishra, Mansi and Zahra. Allow me to share some insights about the dataset we have chosen, which is about Lung Cancer prediction and can be found on Kaggle accessible via https://www.kaggle.com/datasets/thedevastator/cancer-patients-and-air-pollution-a-new-link

Deaths due to lung cancer is common in the world where smoking and exposure to environmental toxins are two significant risk factors. This data set contains 26 variables and 1000 rows where 1 variable is numerical (age) and rest of them are categorical variables counted on scales of 1 to 7 or 1 to 8. The data set was published in Journal - Nature Medicine, where 462,000 people residing in 2 areas where one area had a lower rate of pollution, and the other area included a higher rate of pollution were followed for 6 years.

Objective

The overall objective of this project is to advance knowledge of the intricate connection between lifestyle choices and lung cancer risk to offer insights that can guide public health initiatives and prevention methods.

Purpose

The Purpose of this study is to understand different variables and how different lifestyle factors can contribute or influence the level of lung cancer.

Research Design

A Quantitative approach has been used for this study where a correlation type of research design has been implemented using secondary data collected over an average of 6 years from a community residing in China where relationship between lifestyle factors and level of pollution has been analysed.

Exploratory Data Analysis

We will perform exploratory data analysis of our data set to understand the distribution of data, existing null values, existence of duplicate values and understand the relationship of different variables with each other and their relationship with the target variable. It enables us to precisely understand the variables and summarize the key insights for statistical interpretation of the hypothesis defined. It enables a thorough comprehension of the data set , the definition or rejection of hypotheses.

Reading the dataset

```
df <- read.csv("~/cancer patient data sets.csv")
head(df)
```

```
##   index Patient.Id Age Gender Air.Pollution Alcohol.use Dust.Allergy
## 1     0         P1  33      1             2           4            5
## 2     1        P10  17      1             3           1            5
## 3     2       P100  35      1             4           5            6
## 4     3      P1000  37      1             7           7            7
## 5     4       P101  46      1             6           8            7
## 6     5       P102  35      1             4           5            6
##   OccuPational.Hazards Genetic.Risk chronic.Lung.Disease Balanced.Diet Obesity
## 1                    4            3                    2             2       4
## 2                    3            4                    2             2       2
## 3                    5            5                    4             6       7
## 4                    7            6                    7             7       7
## 5                    7            7                    6             7       7
## 6                    5            5                    4             6       7
##   Smoking Passive.Smoker Chest.Pain Coughing.of.Blood Fatigue Weight.Loss
## 1       3              2          2                 4       3           4
## 2       2              4          2                 3       1           3
## 3       2              3          4                 8       8           7
## 4       7              7          7                 8       4           2
## 5       8              7          7                 9       3           2
## 6       2              3          4                 8       8           7
##   Shortness.of.Breath Wheezing Swallowing.Difficulty Clubbing.of.Finger.Nails
## 1                   2        2                     3                        1
## 2                   7        8                     6                        2
## 3                   9        2                     1                        4
## 4                   3        1                     4                        5
## 5                   4        1                     4                        2
## 6                   9        2                     1                        4
##   Frequent.Cold Dry.Cough Snoring  Level
## 1             2         3       4    Low
## 2             1         7       2 Medium
## 3             6         7       2   High
## 4             6         7       5   High
## 5             4         2       3   High
## 6             6         7       2   High
```

Shape of the dataset

```
dim(df)
```

```
## [1] 1000   26
```

Checking for null values

```
colSums(is.na(df))
```

```
##                    index               Patient.Id                      Age
##                        0                        0                        0
##                   Gender            Air.Pollution              Alcohol.use
##                        0                        0                        0
##             Dust.Allergy     OccuPational.Hazards             Genetic.Risk
##                        0                        0                        0
##     chronic.Lung.Disease            Balanced.Diet                  Obesity
##                        0                        0                        0
##                  Smoking           Passive.Smoker               Chest.Pain
##                        0                        0                        0
##        Coughing.of.Blood                  Fatigue              Weight.Loss
##                        0                        0                        0
##      Shortness.of.Breath                 Wheezing    Swallowing.Difficulty
##                        0                        0                        0
## Clubbing.of.Finger.Nails            Frequent.Cold                Dry.Cough
##                        0                        0                        0
##                  Snoring                    Level
##                        0                        0
```

Checking for duplicates

```
df[duplicated(df),]
```

```
##  [1] index                    Patient.Id               Age
##  [4] Gender                   Air.Pollution            Alcohol.use
##  [7] Dust.Allergy             OccuPational.Hazards     Genetic.Risk
## [10] chronic.Lung.Disease     Balanced.Diet            Obesity
## [13] Smoking                  Passive.Smoker           Chest.Pain
## [16] Coughing.of.Blood        Fatigue                  Weight.Loss
## [19] Shortness.of.Breath      Wheezing                 Swallowing.Difficulty
## [22] Clubbing.of.Finger.Nails Frequent.Cold            Dry.Cough
## [25] Snoring                  Level
## <0 rows> (or 0-length row.names)
```

Checking the data types of all columns

```
str(df)
```

```
## ’data.frame’:    1000 obs. of  26 variables:
##  $ index                   : int  0 1 2 3 4 5 6 7 8 9 ...
##  $ Patient.Id              : chr  "P1" "P10" "P100" "P1000" ...
##  $ Age                     : int  33 17 35 37 46 35 52 28 35 46 ...
##  $ Gender                  : int  1 1 1 1 1 1 2 2 2 1 ...
##  $ Air.Pollution           : int  2 3 4 7 6 4 2 3 4 2 ...
##  $ Alcohol.use             : int  4 1 5 7 8 5 4 1 5 3 ...
##  $ Dust.Allergy            : int  5 5 6 7 7 6 5 4 6 4 ...
##  $ OccuPational.Hazards    : int  4 3 5 7 7 5 4 3 5 2 ...
##  $ Genetic.Risk            : int  3 4 5 6 7 5 3 2 6 4 ...
##  $ chronic.Lung.Disease    : int  2 2 4 7 6 4 2 3 5 3 ...
##  $ Balanced.Diet           : int  2 2 6 7 7 6 2 4 5 3 ...
##  $ Obesity                 : int  4 2 7 7 7 7 4 3 5 3 ...
##  $ Smoking                 : int  3 2 2 7 8 2 3 1 6 2 ...
##  $ Passive.Smoker          : int  2 4 3 7 7 3 2 4 6 3 ...
##  $ Chest.Pain              : int  2 2 4 7 7 4 2 3 6 4 ...
##  $ Coughing.of.Blood       : int  4 3 8 8 9 8 4 1 5 4 ...
##  $ Fatigue                 : int  3 1 8 4 3 8 3 3 1 1 ...
##  $ Weight.Loss             : int  4 3 7 2 2 7 4 2 4 2 ...
##  $ Shortness.of.Breath     : int  2 7 9 3 4 9 2 2 3 4 ...
##  $ Wheezing                : int  2 8 2 1 1 2 2 4 2 6 ...
##  $ Swallowing.Difficulty   : int  3 6 1 4 4 1 3 2 4 5 ...
##  $ Clubbing.of.Finger.Nails: int  1 2 4 5 2 4 1 2 6 4 ...
##  $ Frequent.Cold           : int  2 1 6 6 4 6 2 3 2 2 ...
##  $ Dry.Cough               : int  3 7 7 7 2 7 3 4 4 1 ...
##  $ Snoring                 : int  4 2 2 5 3 2 4 3 1 5 ...
##  $ Level                   : chr  "Low" "Medium" "High" "High" ...
```

Research Question

Which lifestyle factor has the highest influence on the level of lung cancer?

Null hypothesis

There is no significant relationship between the variables depicting lifestyle choices and the level of lung cancer.

Alternate hypothesis

There is a significant relationship between the variables depicting lifestyle choices and the level of lung cancer.

Target variable - Level of Cancer

Here, after understanding the data from EDA and research question along with forming a hypothesis for the data set, we need to convert categorical columns into categorical data so that statistical tests can be performed efficiently and it becomes easier to further do hypothesis testing and data visualization of the variables.

Converting the categorical columns into categorical data

```
# Convert columns 4 to n to factors
df[, 4:(ncol(df))] <- lapply(df[, 4:(ncol(df))], factor)
# Print the structure of the dataframe
str(df)
```

```
## ’data.frame':    1000 obs. of  26 variables:
##  $ index                   : int  0 1 2 3 4 5 6 7 8 9 ...
##  $ Patient.Id              : chr  "P1" "P10" "P100" "P1000" ...
##  $ Age                     : int  33 17 35 37 46 35 52 28 35 46 ...
##  $ Gender                  : Factor w/ 2 levels "1","2": 1 1 1 1 1 1 2 2 2 1 ...
##  $ Air.Pollution           : Factor w/ 8 levels "1","2","3","4",..: 2 3 4 7 6 4 2 3 4 2 ...
##  $ Alcohol.use             : Factor w/ 8 levels "1","2","3","4",..: 4 1 5 7 8 5 4 1 5 3 ...
##  $ Dust.Allergy            : Factor w/ 8 levels "1","2","3","4",..: 5 5 6 7 7 6 5 4 6 4 ...
##  $ OccuPational.Hazards    : Factor w/ 8 levels "1","2","3","4",..: 4 3 5 7 7 5 4 3 5 2 ...
##  $ Genetic.Risk            : Factor w/ 7 levels "1","2","3","4",..: 3 4 5 6 7 5 3 2 6 4 ...
##  $ chronic.Lung.Disease    : Factor w/ 7 levels "1","2","3","4",..: 2 2 4 7 6 4 2 3 5 3 ...
##  $ Balanced.Diet           : Factor w/ 7 levels "1","2","3","4",..: 2 2 6 7 7 6 2 4 5 3 ...
##  $ Obesity                 : Factor w/ 7 levels "1","2","3","4",..: 4 2 7 7 7 7 4 3 5 3 ...
##  $ Smoking                 : Factor w/ 8 levels "1","2","3","4",..: 3 2 2 7 8 2 3 1 6 2 ...
##  $ Passive.Smoker          : Factor w/ 8 levels "1","2","3","4",..: 2 4 3 7 7 3 2 4 6 3 ...
##  $ Chest.Pain              : Factor w/ 9 levels "1","2","3","4",..: 2 2 4 7 7 4 2 3 6 4 ...
##  $ Coughing.of.Blood       : Factor w/ 9 levels "1","2","3","4",..: 4 3 8 8 9 8 4 1 5 4 ...
##  $ Fatigue                 : Factor w/ 8 levels "1","2","3","4",..: 3 1 7 4 3 7 3 3 1 1 ...
##  $ Weight.Loss             : Factor w/ 8 levels "1","2","3","4",..: 4 3 7 2 2 7 4 2 4 2 ...
##  $ Shortness.of.Breath     : Factor w/ 8 levels "1","2","3","4",..: 2 7 8 3 4 8 2 2 3 4 ...
##  $ Wheezing                : Factor w/ 8 levels "1","2","3","4",..: 2 8 2 1 1 2 2 4 2 6 ...
##  $ Swallowing.Difficulty   : Factor w/ 8 levels "1","2","3","4",..: 3 6 1 4 4 1 3 2 4 5 ...
##  $ Clubbing.of.Finger.Nails: Factor w/ 9 levels "1","2","3","4",..: 1 2 4 5 2 4 1 2 6 4 ...
##  $ Frequent.Cold           : Factor w/ 7 levels "1","2","3","4",..: 2 1 6 6 4 6 2 3 2 2 ...
##  $ Dry.Cough               : Factor w/ 7 levels "1","2","3","4",..: 3 7 7 7 2 7 3 4 4 1 ...
##  $ Snoring                 : Factor w/ 7 levels "1","2","3","4",..: 4 2 2 5 3 2 4 3 1 5 ...
##  $ Level                   : Factor w/ 3 levels "High","Low","Medium": 2 3 1 1 1 1 2 2 3 3 ...
```

Lets do descriptive statistics of the data frame to understand essential elements of the data set and the summary will help in making an informed decision about the data sample and its measurements.

Summary of the dataset

```
summary(df)
```

```
##      index        Patient.Id             Age        Gender  Air.Pollution
##  Min.   :  0.0   Length:1000        Min.   :14.00   1:598   6      :326  
##  1st Qu.:249.8   Class  :character   1st Qu.:27.75   2:402   2      :201  
##  Median :499.5   Mode   :character   Median :36.00           3      :173  
##  Mean   :499.5                      Mean   :37.17           1      :141  
##  3rd Qu.:749.2                      3rd Qu.:45.00           4      : 90  
##  Max.   :999.0                      Max.   :73.00           7      : 30  
##                                                             (Other): 39  
##   Alcohol.use   Dust.Allergy OccuPational.Hazards Genetic.Risk
##  2      :202   7      :405   7      :365          1: 40       
##  8      :188   4      :133   3      :151          2:212
##  7      :167   5      :111   2      :132          3:173
##  1      :152   6      :110   5      :130          4: 40
##  5      : 90   3      :101   4      :112          5:100
##  3      : 80   2      : 70   1      : 50          6:108
##  (Other):121   (Other): 70   (Other): 60          7:327
##  chronic.Lung.Disease Balanced.Diet Obesity    Smoking    Passive.Smoker
##  1: 50                1: 40         1: 70   2      :222   2      :284
##  2:173                2:231         2:140   7      :207   7      :187
##  3:141                3:173         3:193   1      :181   4      :161
##  4:141                4: 61         4:191   3      :172   3      :140
##  5: 80                5: 40         5: 20   8      : 89   8      :108
##  6:308                6:159         6: 30   6      : 60   1      : 60
##  7:107                7:296         7:356   (Other): 69   (Other): 60
##    Chest.Pain  Coughing.of.Blood    Fatigue     Weight.Loss
##  7      :296   7      :187       3      :212   2      :280
##  4      :191   4      :172       2      :211   7      :230
##  2      :181   3      :171       4      :180   3      :150
##  3      :153   2      :121       1      :110   1      :121
##  1      : 80   8      :119       8      :109   5      :100
##  6      : 40   1      : 71       5      : 89   4      : 60
##  (Other): 59   (Other):159       (Other): 89   (Other): 59
##  Shortness.of.Breath    Wheezing   Swallowing.Difficulty
##  2      :243         2      :240   1      :221
##  6      :201         5      :171   4      :189
##  3      :140         4      :163   2      :160
##  4      : 90         1      :149   5      :110
##  7      : 89         7      :139   8      :110
##  5      : 87         6      : 68   6      : 91
##  (Other):150         (Other): 70   (Other):119
##  Clubbing.of.Finger.Nails Frequent.Cold Dry.Cough Snoring    Level
##  2      :240             1:139         1:119     1:170   High  :365
##  4      :220             2:192         2:251     2:300   Low   :303
##  1      :131             3:230         3:101     3:211   Medium:332
##  5      :120             4:180         4:141     4:131
##  3      :100             5: 20         5:131     5:139
##  9      : 80             6:170         6: 89     6: 39
##  (Other):109             7: 69         7:168     7: 10
```

Our chosen significance level is 0.05 (Standard). As our sample size is 1000 rows and 26 variables of which are categorical variables except age, we are doing fisher's exact test by doing a contingency table of each column with our target variable. Fisher's test will also give us a simulated p-value for the size of the data set hence we are using this test rather than using any other statistical testing.

Performing statistical tests to know the significant variables

```
# Define the column names of interest
cols <- c("Age","Gender", "Air.Pollution", "Alcohol.use", "Dust.Allergy",
          "OccuPational.Hazards", "Genetic.Risk", "chronic.Lung.Disease",
          "Balanced.Diet", "Obesity", "Smoking", "Passive.Smoker",
          "Chest.Pain", "Coughing.of.Blood", "Fatigue", "Weight.Loss",
          "Shortness.of.Breath", "Wheezing", "Swallowing.Difficulty",
```

```r
          "Clubbing.of.Finger.Nails", "Frequent.Cold", "Dry.Cough",
          "Snoring")

# Create an empty list to store the test results
fisher_results <- list()

# Iterate over each column and perform Fisher's exact test
for (col in cols) {
  # Create a contingency table of the column and the target column
  cont_table <- table(df[, col], df$Level)
  # Perform Fisher's exact test
  fisher_result <- fisher.test(cont_table, simulate.p.value = TRUE, B = 1000)
  # Store the test result in the list
  fisher_results[[col]] <- fisher_result}
# Print the test results
fisher_results
```

```
## $Age
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Gender
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Air.Pollution
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Alcohol.use
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Dust.Allergy
##
##  Fisher’s Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $OccuPational.Hazards
##
##  Fisher’s Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Genetic.Risk
##
##  Fisher’s Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $chronic.Lung.Disease
##
##  Fisher’s Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Balanced.Diet
##
##  Fisher’s Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
```

```
## $Obesity
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Smoking
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Passive.Smoker
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Chest.Pain
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Coughing.of.Blood
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Fatigue
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
```

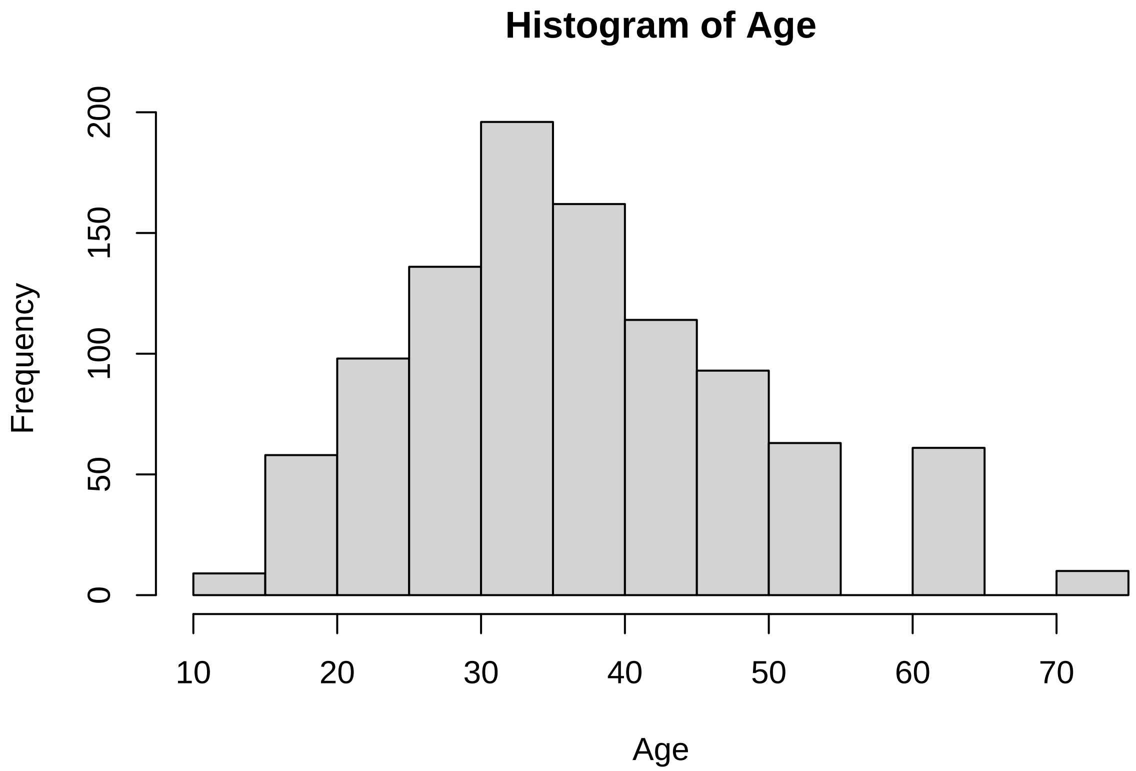
```
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Weight.Loss
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Shortness.of.Breath
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Wheezing
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Swallowing.Difficulty
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Clubbing.of.Finger.Nails
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
```

```
##
##
## $Frequent.Cold
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Dry.Cough
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
##
##
## $Snoring
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1000 replicates)
##
## data:  cont_table
## p-value = 0.000999
## alternative hypothesis: two.sided
```

After seeing the Fisher's Exact test results we can see that a simulated p-value has been generated based on the 1000 replicates for the dataset, in all the variables the simulated p-value is lesser than chosen significance 0.05 hence we can understand from this that there is a significant association between the variables and the target variable.

Plotting the histogram of the numerical variable

```
hist(df$Age, main = "Histogram of Age", xlab = "Age")
```



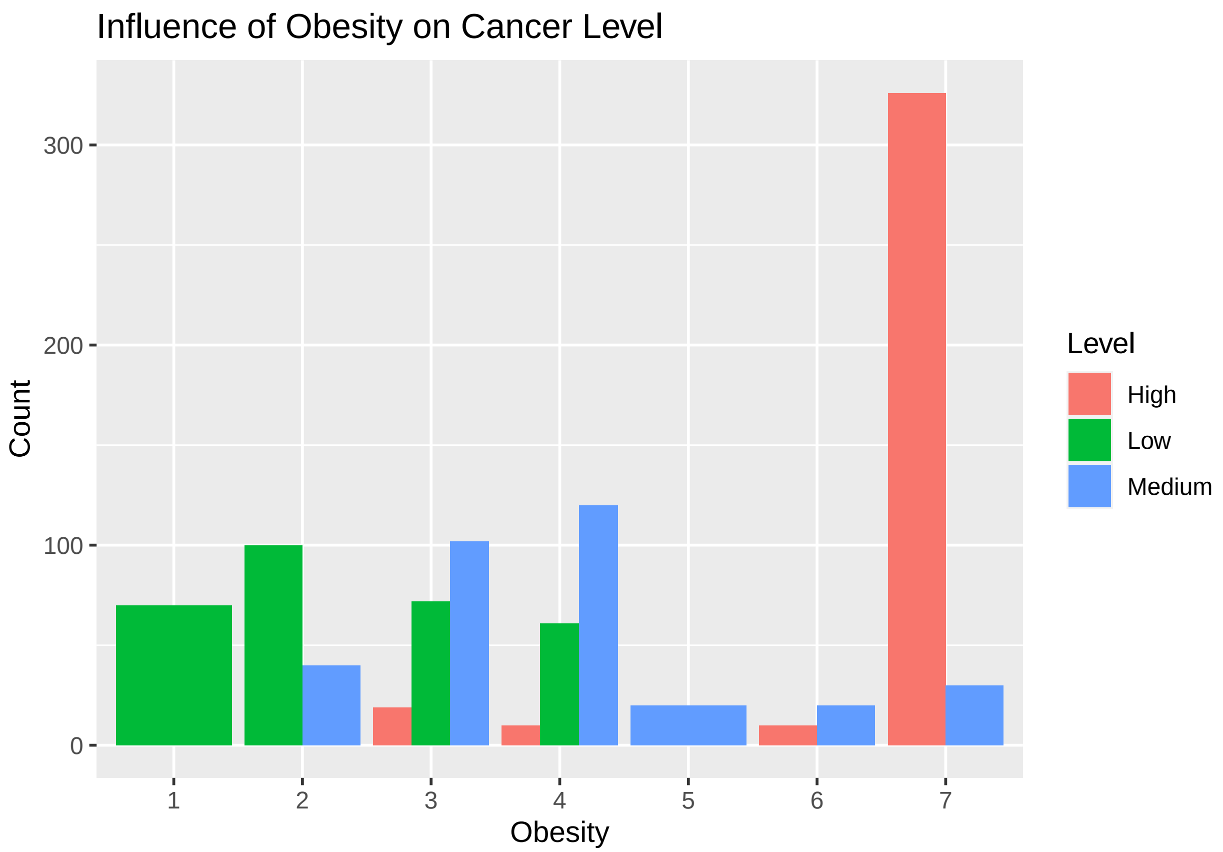
The histogram showcases the distribution of participants based on their age where the highest count lies between 30-35 years of age.

In order to understand the effect of lifestyle variables on the level of lung cancer we are going to plot few plots which will help us understand the target variable's association with other lifestyle variables.

Checking the influence of Obesity on the level of cancer

```
library(ggplot2)

ggplot(df, aes(x = Obesity, fill = Level)) +
  geom_bar(position = "dodge") +
  labs(title = "Influence of Obesity on Cancer Level",
       x = "Obesity",
       y = "Count",
       fill = "Level")
```

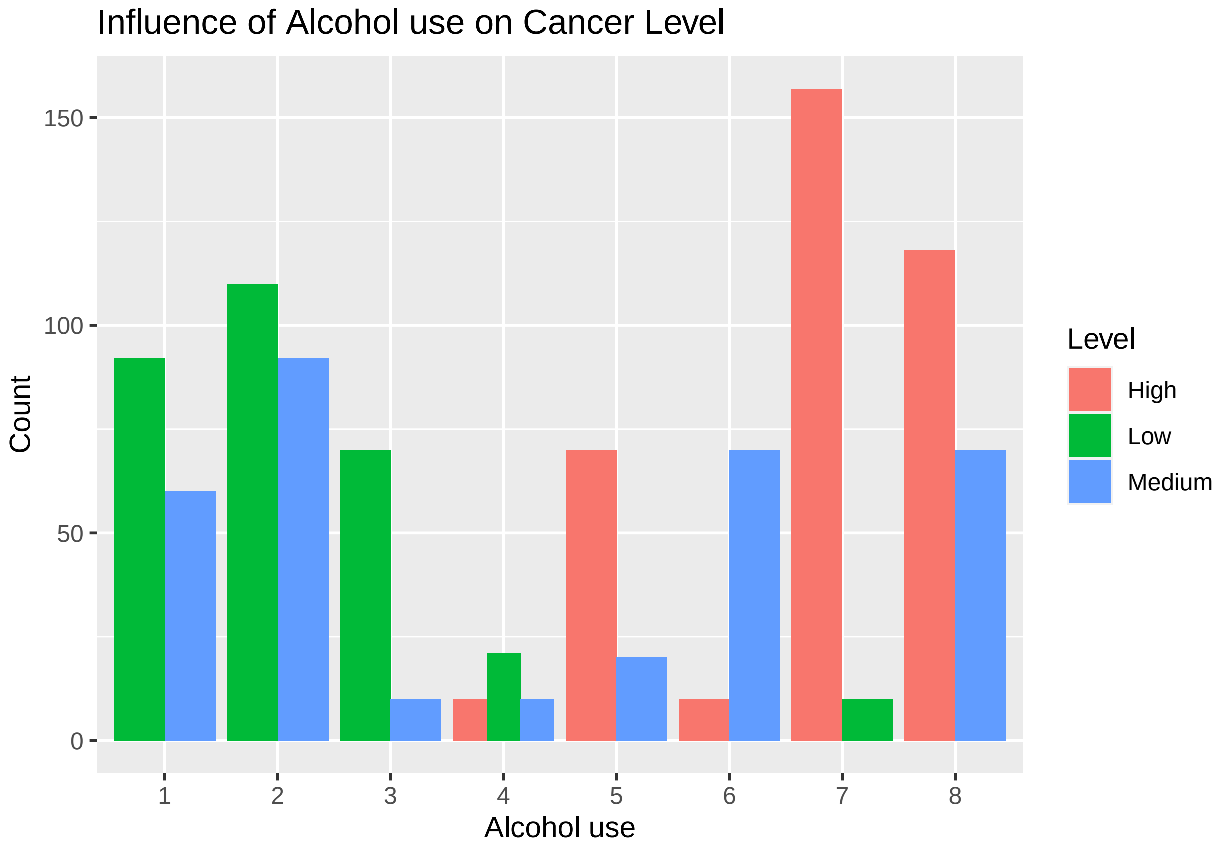


The graph represents the relationship between the level of cancer and obesity. As obesity increases the risk of cancer increases.

Checking the influence of Alcohol use on the level of cancer

```
library(ggplot2)

ggplot(df, aes(x = Alcohol.use, fill = Level)) +
  geom_bar(position = "dodge") +
  labs(title = "Influence of Alcohol use on Cancer Level",
       x = "Alcohol use",
       y = "Count",
       fill = "Level")
```

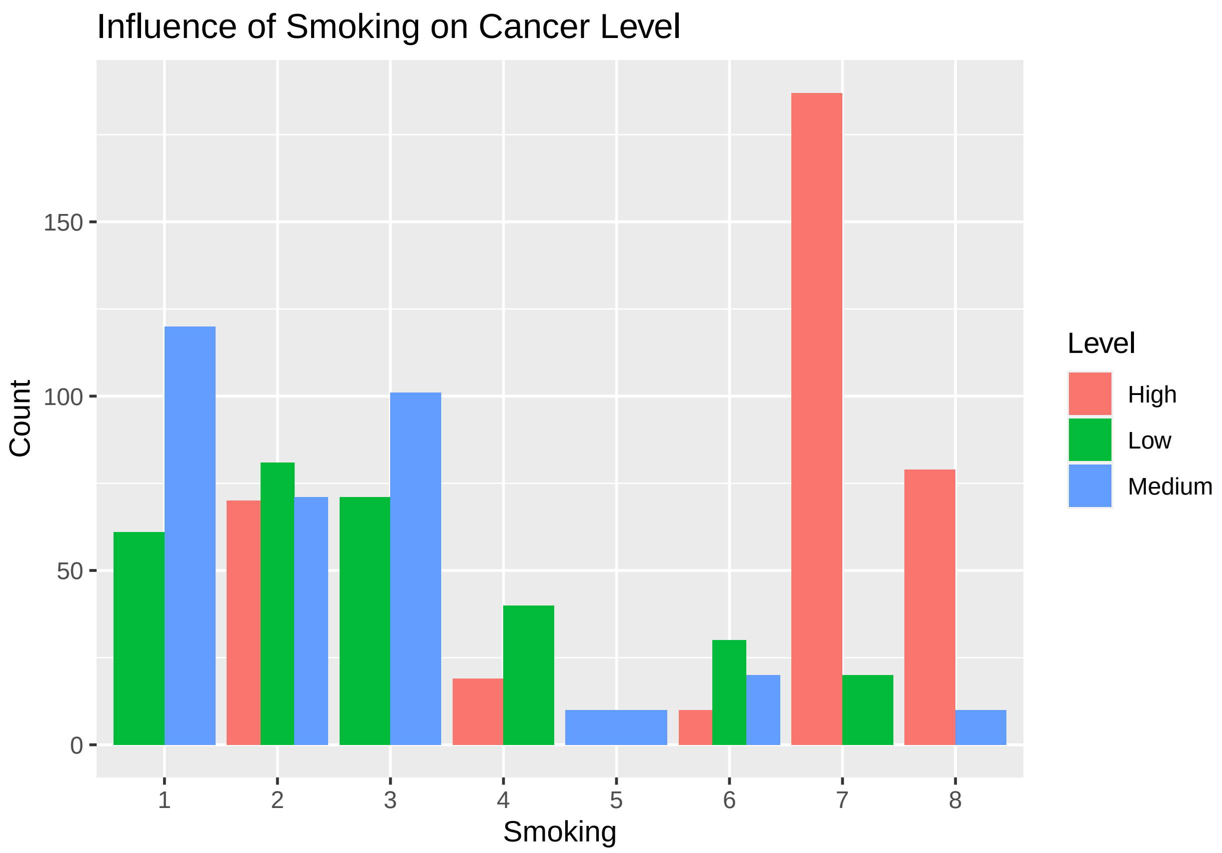


The graph represents the relationship between the level of cancer and Alcohol Consumption. The risk of cancer increases with increased consumption of alcohol.

Checking the influence of Smoking on the level of cancer

```
library(ggplot2)

ggplot(df, aes(x = Smoking, fill = Level)) +
  geom_bar(position = "dodge") +
  labs(title = "Influence of Smoking on Cancer Level",
       x = "Smoking",
       y = "Count",
       fill = "Level")
```

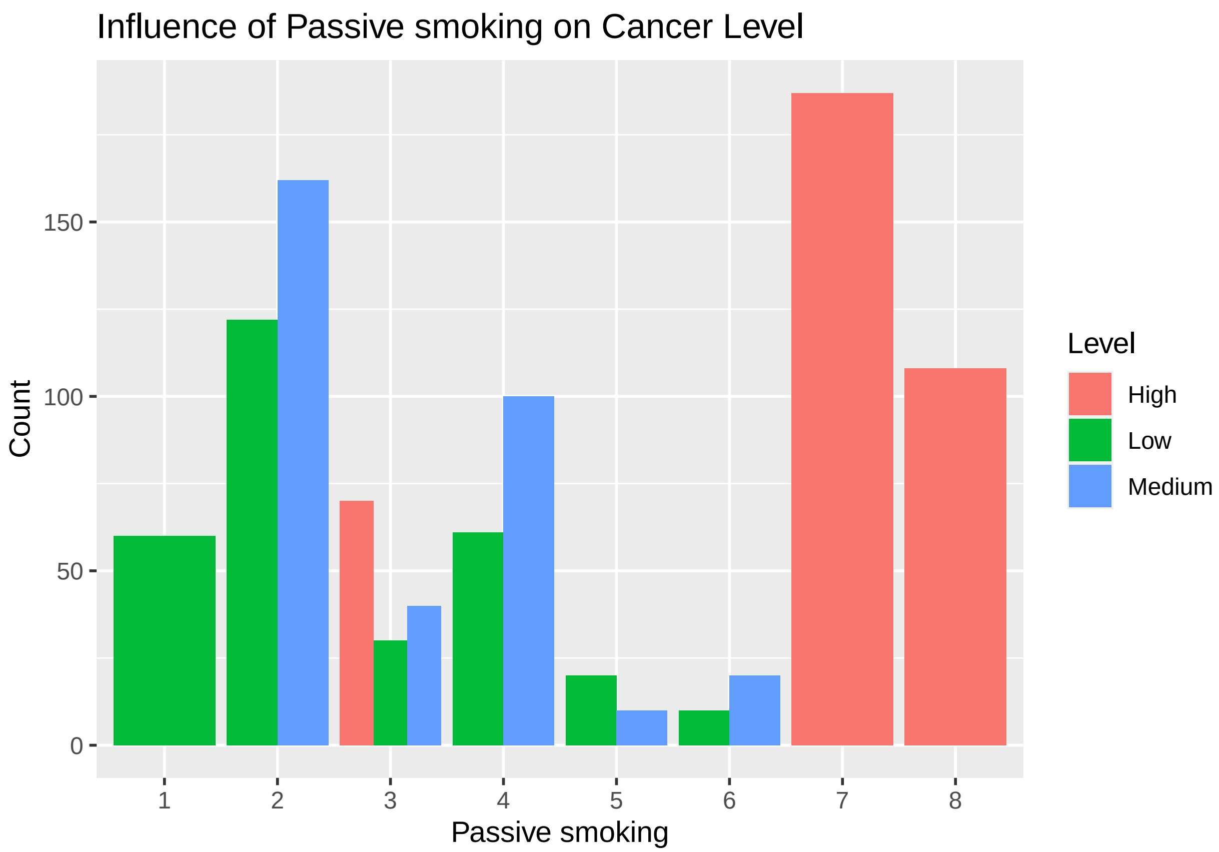


The graph represents the relationship between the level of cancer and Smoking. The relationship seems to be non-linear as we can see a high level of cancer for both lower and higher level of smoking.

Checking the influence of Passive Smoking on the level of cancer

```
library(ggplot2)

ggplot(df, aes(x = Passive.Smoker, fill = Level)) +
  geom_bar(position = "dodge") +
  labs(title = "Influence of Passive smoking on Cancer Level",
       x = "Passive smoking",
       y = "Count",
       fill = "Level")
```

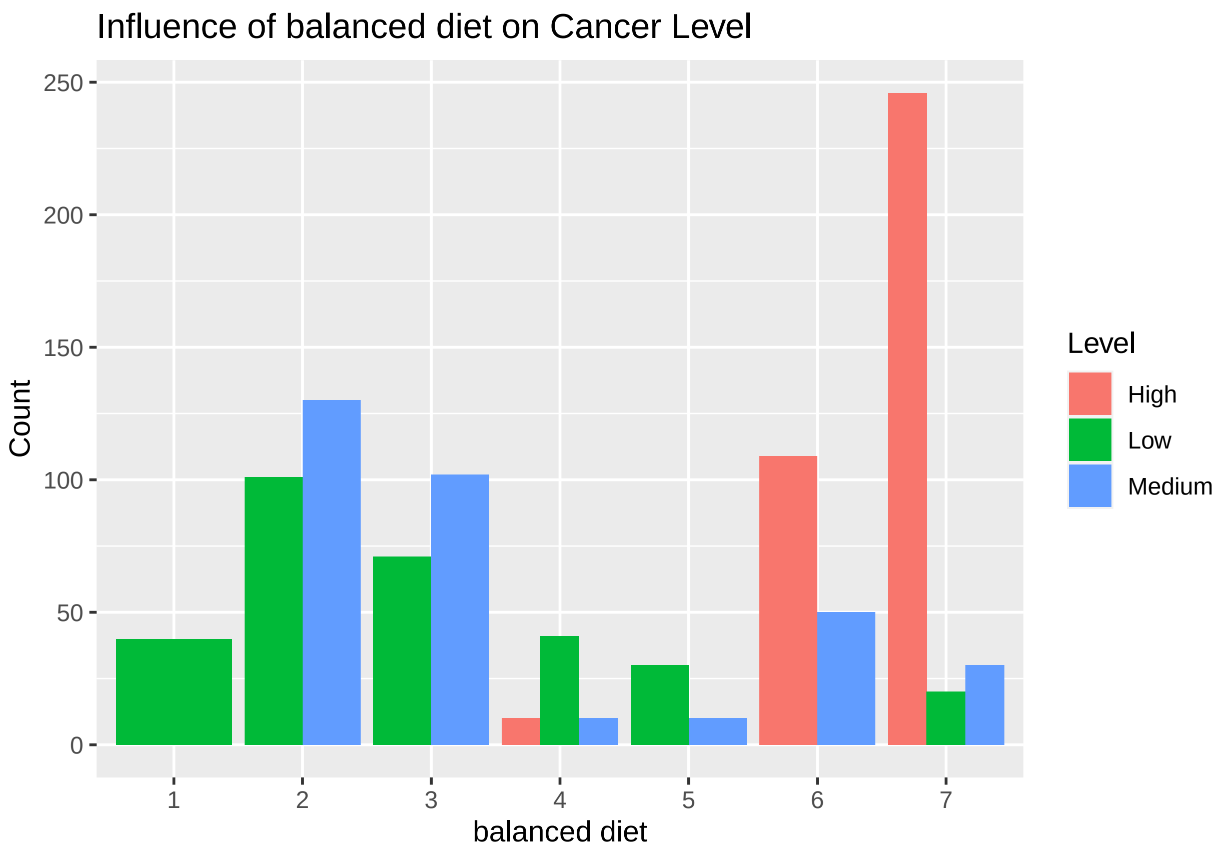


The graph represents the relationship between the level of Cancer and Exposure to Passive Smoking. High exposure to passive smoking increases the probability of cancer occurrence.

Checking the influence of Balanced Diet on the level of cancer

```
library(ggplot2)

ggplot(df, aes(x = Balanced.Diet, fill = Level)) +
  geom_bar(position = "dodge") +
  labs(title = "Influence of balanced diet on Cancer Level",
       x = "balanced diet",
       y = "Count",
       fill = "Level")
```



The graph represents the relationship between the level of Cancer and Balanced Diet. Higher exposure to non-balanced diet can contribute to an increase in the level of cancer.

We have understood the association between lifestyle variables and target column, now lets build a Logistic Regression model between the lifestyle variables and level of cancer which will give us more comprehensive understanding to draw a conclusion for the hypothesis.

Building LR model between Obesity and level of cancer

```
library(nnet)

# create a multinomial logistic regression model
model <- multinom(Level ~ Obesity, data = df)
```

```
## # weights:  24 (14 variable)
## initial  value 1098.612289
## iter  10 value 549.337082
## iter  20 value 540.902570
## iter  30 value 540.760559
## iter  30 value 540.760558
## final  value 540.760558
## converged
```

```r
# print the summary of the model
summary(model)
```

```
## Call:
## multinom(formula = Level ~ Obesity, data = df)
##
## Coefficients:
##        (Intercept) Obesity2    Obesity3   Obesity4  Obesity5     Obesity6
## Low      48.622453  8.35696 -47.2907281 -46.814371 -41.82667 -100.2646659
## Medium    1.044304 55.01916   0.6363283   1.440646  43.90001   -0.3511818
##          Obesity7
## Low    -58.769988
## Medium  -3.429844
##
## Std. Errors:
##        (Intercept)  Obesity2  Obesity3  Obesity4    Obesity5     Obesity6
## Low      1.9894325 0.9071667 1.9980858 2.0044687 1.65405e-13 1.934666e-14
## Medium   0.2148083 0.9071667 0.2889442 0.3325593 5.93432e-14 3.755526e-01
##         Obesity7
## Low    6.8636945
## Medium 0.2627627
##
## Residual Deviance: 1081.521
## AIC: 1109.521
```

Building LR model between Alcohol.use and level of cancer

```r
library(nnet)

# create a multinomial logistic regression model
model <- multinom(Level ~ Alcohol.use, data = df)
```

```
## # weights:  27 (16 variable)
## initial  value 1098.612289
## iter  10 value 580.564270
## iter  20 value 554.218435
## iter  30 value 553.369081
## final  value 553.368099
## converged
```

```r
# print the summary of the model
summary(model)
```

```
## Call:
## multinom(formula = Level ~ Alcohol.use, data = df)
##
## Coefficients:
##        (Intercept) Alcohol.use2 Alcohol.use3 Alcohol.use4 Alcohol.use5
## Low       18.95791    -3.430968    -3.546743    -18.21597    -46.73226
## Medium    18.53047    -3.182217    -5.065211    -18.53047    -19.78323
##        Alcohol.use6 Alcohol.use7 Alcohol.use8
## Low       -33.09842    -21.71158    -37.68378
## Medium    -16.58455    -34.06716    -19.05266
##
## Std. Errors:
##        (Intercept) Alcohol.use2 Alcohol.use3 Alcohol.use4 Alcohol.use5
## Low       58.21500     198.1427     231.2007     58.21597 2.825502e-04
## Medium    58.21497     198.1427     231.2008     58.21632 5.821544e+01
##        Alcohol.use6 Alcohol.use7 Alcohol.use8
## Low       348.96589     58.21578     4.411072
## Medium     58.21569    184.22022    58.215136
##
## Residual Deviance: 1106.736
## AIC: 1138.736
```

Building LR model between Smoking and level of cancer

```
library(nnet)

# create a multinomial logistic regression model
model <- multinom(Level ~ Smoking, data = df)
```

```
## # weights:  27 (16 variable)
## initial  value 1098.612289
## iter  10 value 690.699600
## iter  20 value 670.738086
## iter  30 value 670.433416
## final  value 670.433028
## converged
```

```
# print the summary of the model
summary(model)
```

```
## Call:
## multinom(formula = Level ~ Smoking, data = df)
##
## Coefficients:
##        (Intercept)  Smoking2  Smoking3  Smoking4   Smoking5  Smoking6  Smoking7
## Low       20.52885 -20.38289 -3.099091 -19.78440 -14.331537 -19.43023 -22.76422
## Medium    21.20547 -21.19129 -3.423273 -35.03639   4.287428 -20.51232 -38.77456
##         Smoking8
## Low    -37.24543
## Medium -23.27233
##
## Std. Errors:
##        (Intercept) Smoking2 Smoking3  Smoking4     Smoking5 Smoking6  Smoking7
## Low       61.34649 61.34666 12.60226  61.34695 7.389782e-06 61.34727  61.34686
## Medium    61.34649 61.34667 12.60227 219.86679 9.227678e-04 61.34738 286.80132
##         Smoking8
## Low    271.57497
## Medium  61.34724
```

```
##
## Residual Deviance: 1340.866
## AIC: 1372.866
```

Building LR model between Passive smoking and level of cancer

```
library(nnet)

# create a multinomial logistic regression model
model <- multinom(Level ~ Passive.Smoker, data = df)
```

```
## # weights:  27 (16 variable)
## initial  value 1098.612289
## iter  10 value 499.421839
## iter  20 value 484.283449
## iter  30 value 483.888740
## final  value 483.888338
## converged
```

```
# print the summary of the model
summary(model)
```

```
## Call:
## multinom(formula = Level ~ Passive.Smoker, data = df)
##
## Coefficients:
##        (Intercept) Passive.Smoker2 Passive.Smoker3 Passive.Smoker4
## Low      28.245308       -10.61677      -29.092606       -13.15657
## Medium   -6.954208        24.86632        6.394592        22.53724
##        Passive.Smoker5 Passive.Smoker6 Passive.Smoker7 Passive.Smoker8
## Low          -7.650585       -8.428063       -45.33670       -61.96155
## Medium       26.855784       27.464601       -14.31672       -25.02818
##
## Std. Errors:
##        (Intercept) Passive.Smoker2 Passive.Smoker3 Passive.Smoker4
## Low      100.34931        22.48496       100.34945        191.0484
## Medium    81.17122        30.94434        81.17133        165.5426
##        Passive.Smoker5 Passive.Smoker6 Passive.Smoker7 Passive.Smoker8
## Low           25.46411        25.46124     305.9281232    1.906292e-06
## Medium        25.52957        25.53247       0.6267271    8.002591e-06
##
## Residual Deviance: 967.7767
## AIC: 999.7767
```

Building LR model between Balanced Diet and level of cancer

```
library(nnet)

# create a multinomial logistic regression model
model <- multinom(Level ~ Balanced.Diet, data = df)
```

```
## # weights:  24 (14 variable)
## initial  value 1098.612289
## iter  10 value 632.065297
## iter  20 value 617.757539
## iter  30 value 617.451738
## iter  30 value 617.451737
## final  value 617.451737
## converged
```

```
# print the summary of the model
summary(model)
```

```
## Call:
## multinom(formula = Level ~ Balanced.Diet, data = df)
##
## Coefficients:
##        (Intercept) Balanced.Diet2 Balanced.Diet3 Balanced.Diet4 Balanced.Diet5
## Low       41.41700      -28.16453      -32.22668      -40.00604      -6.898585
## Medium   -15.74085       29.24567       25.29343       15.74069      49.160878
##        Balanced.Diet6 Balanced.Diet7
## Low         -83.87628      -43.92654
## Medium       14.96146       13.63676
##
## Std. Errors:
##        (Intercept) Balanced.Diet2 Balanced.Diet3 Balanced.Diet4 Balanced.Diet5
## Low       14.98650       60.32640       17.55607       14.98904       1.082252
## Medium    12.84564       62.42862       16.01270       12.85091       1.082252
##        Balanced.Diet6 Balanced.Diet7
## Low      2.703842e-10       14.98764
## Medium   1.284643e+01       12.84665
##
## Residual Deviance: 1234.903
## AIC: 1262.903
```

We can observe that of all the above Logistic Regression models done for the 5 variables with the target variable, one can observe that passive smoking, alcohol.use and obesity have the lowest AIC value and residual deviance which interprets that Logistic regression is a good fit for the data.

We tried different combinations of the 5 lifestyle variables to build a LR model with the best AIC value in order to understand the best fit and complexity for the given data.

Building LR model with the best AIC value

```
library(nnet)
# create a multinomial logistic regression model
model <- multinom(Level ~ Obesity*Alcohol.use+Passive.Smoker, data = df)
```

```
## # weights:  192 (126 variable)
## initial  value 1098.612289
## iter  10 value 39.736520
## iter  20 value 0.254536
## iter  30 value 0.054253
## iter  40 value 0.014627
## iter  50 value 0.006378
## iter  60 value 0.002288
## iter  70 value 0.000343
## final  value 0.000053
## converged
```

```
# print the summary of the model
summary(model)
```

```
## Warning in sqrt(diag(vc)): NaNs produced
```

```
## Call:
## multinom(formula = Level ~ Obesity * Alcohol.use + Passive.Smoker,
##     data = df)
##
## Coefficients:
##        (Intercept)  Obesity2   Obesity3  Obesity4  Obesity5  Obesity6
## Low       275.8987 -181.1207   7.449124 -127.0576 -82.38104 -185.8409
## Medium   -271.0347  218.1575 -70.203855  107.0235 126.90453  147.6832
##          Obesity7 Alcohol.use2 Alcohol.use3 Alcohol.use4 Alcohol.use5
## Low    -126.48358   -25.810043   -53.274739     21.02724   -131.95468
## Medium   80.19865     4.209199     8.844643    -11.44146     63.45679
##        Alcohol.use6 Alcohol.use7 Alcohol.use8 Passive.Smoker2 Passive.Smoker3
## Low     -61.5547608     45.88816    -100.3075       -144.1007      0.07784804
## Medium   -0.4983999     50.07927     100.8446        229.7059     97.59189475
##        Passive.Smoker4 Passive.Smoker5 Passive.Smoker6 Passive.Smoker7
## Low          -111.2311       -139.1129       -40.81522      -286.30764
## Medium        303.9139        144.4611       117.94351       -22.87267
##        Passive.Smoker8 Obesity2:Alcohol.use2 Obesity3:Alcohol.use2
## Low         -229.03104              146.4954             -112.7190
## Medium       -10.65449             -181.8890              199.6543
##        Obesity4:Alcohol.use2 Obesity5:Alcohol.use2 Obesity6:Alcohol.use2
## Low                 101.3771                     0                     0
## Medium             -127.6404                     0                     0
##        Obesity7:Alcohol.use2 Obesity2:Alcohol.use3 Obesity3:Alcohol.use3
## Low                        0              17.39137             -369.2219
## Medium                     0             -68.31761              317.3870
##        Obesity4:Alcohol.use3 Obesity5:Alcohol.use3 Obesity6:Alcohol.use3
## Low                 208.1664                     0                     0
## Medium             -238.4680                     0                     0
##        Obesity7:Alcohol.use3 Obesity2:Alcohol.use4 Obesity3:Alcohol.use4
## Low                        0                     0                     0
## Medium                     0                     0                     0
##        Obesity4:Alcohol.use4 Obesity5:Alcohol.use4 Obesity6:Alcohol.use4
## Low                 180.2751                     0            -159.24790
## Medium              -36.9554                     0              25.51393
##        Obesity7:Alcohol.use4 Obesity2:Alcohol.use5 Obesity3:Alcohol.use5
## Low                        0                     0                     0
## Medium                     0                     0                     0
##        Obesity4:Alcohol.use5 Obesity5:Alcohol.use5 Obesity6:Alcohol.use5
## Low                        0             -28.11711             -26.59295
## Medium                     0              31.90572             122.16922
##        Obesity7:Alcohol.use5 Obesity2:Alcohol.use6 Obesity3:Alcohol.use6
## Low                -77.24462              31.37326                     0
## Medium             -90.61815              67.37114                     0
##        Obesity4:Alcohol.use6 Obesity5:Alcohol.use6 Obesity6:Alcohol.use6
## Low                -88.83727             -54.26392                     0
## Medium            -117.29950              94.99880                     0
##        Obesity7:Alcohol.use6 Obesity2:Alcohol.use7 Obesity3:Alcohol.use7
## Low                 50.17317             138.16378                     0
## Medium             -45.56884             -86.16221                     0
##        Obesity4:Alcohol.use7 Obesity5:Alcohol.use7 Obesity6:Alcohol.use7
## Low                        0                     0                     0
## Medium                     0                     0                     0
##        Obesity7:Alcohol.use7 Obesity2:Alcohol.use8 Obesity3:Alcohol.use8
## Low                -92.27562                     0             -247.9375
## Medium             136.24148                     0              100.7293
##        Obesity4:Alcohol.use8 Obesity5:Alcohol.use8 Obesity6:Alcohol.use8
## Low                154.76651                     0                     0
## Medium             -80.02892                     0                     0
##        Obesity7:Alcohol.use8
## Low                -7.136512
## Medium             80.144160
##
## Std. Errors:
##        (Intercept) Obesity2     Obesity3 Obesity4     Obesity5     Obesity6
## Low       9371.841 2400.495 1.064348e-09 11697.18 2.132204e-11          NaN
## Medium   11350.859 2891.300 4.572753e-22 11697.18 3.043912e-16 1.153708e-42
##            Obesity7 Alcohol.use2 Alcohol.use3 Alcohol.use4 Alcohol.use5
## Low    1.063737e-02 1.307496e-16     2400.495 1.623419e-67 1.190800e-11
## Medium 1.504163e+04 5.187005e-17     2891.300 1.153708e-42 3.043912e-16
##        Alcohol.use6 Alcohol.use7 Alcohol.use8 Passive.Smoker2 Passive.Smoker3
## Low      0.01064082 1.618637e-40    11697.179        11697.18    3.671773e-06
## Medium   0.01064082 6.738173e+03     8634.235        11697.18    3.671777e-06
##        Passive.Smoker4 Passive.Smoker5 Passive.Smoker6 Passive.Smoker7
## Low         0.01063737    1.507266e-19        2400.495    3.586013e-65
## Medium      0.01063737    2.925298e-27        2891.300    5.187240e+04
##        Passive.Smoker8 Obesity2:Alcohol.use2 Obesity3:Alcohol.use2
## Low       1.618637e-40          1.307497e-16          6.797467e-25
## Medium    3.757392e+04          5.187005e-17          8.969291e-25
##        Obesity4:Alcohol.use2 Obesity5:Alcohol.use2 Obesity6:Alcohol.use2
## Low             9.075894e-28                     0                     0
## Medium          9.075893e-28                     0                     0
##        Obesity7:Alcohol.use2 Obesity2:Alcohol.use3 Obesity3:Alcohol.use3
## Low                        0              2400.495          1.577276e-82
## Medium                     0              2891.300          4.567722e-22
##        Obesity4:Alcohol.use3 Obesity5:Alcohol.use3 Obesity6:Alcohol.use3
## Low             2.215777e-55                     0                     0
## Medium         2.122176e-126                     0                     0
##        Obesity7:Alcohol.use3 Obesity2:Alcohol.use4 Obesity3:Alcohol.use4
## Low                        0                     0                     0
## Medium                     0                     0                     0
##        Obesity4:Alcohol.use4 Obesity5:Alcohol.use4 Obesity6:Alcohol.use4
## Low             1.623419e-67                     0         7.983574e-132
## Medium          1.623419e-67                     0          1.153708e-42
##        Obesity7:Alcohol.use4 Obesity2:Alcohol.use5 Obesity3:Alcohol.use5
## Low                        0                     0                     0
## Medium                     0                     0                     0
##        Obesity4:Alcohol.use5 Obesity5:Alcohol.use5 Obesity6:Alcohol.use5
## Low                        0          1.654608e-19         5.292023e-112
## Medium                     0          3.043912e-16          1.812284e-64
##        Obesity7:Alcohol.use5 Obesity2:Alcohol.use6 Obesity3:Alcohol.use6
## Low             1.190800e-11          3.671777e-06                     0
## Medium          4.000867e-37          3.671777e-06                     0
##        Obesity4:Alcohol.use6 Obesity5:Alcohol.use6 Obesity6:Alcohol.use6
## Low             2.358432e-86          5.374667e-54                     0
## Medium         1.371735e-112          2.925298e-27                     0
##        Obesity7:Alcohol.use6 Obesity2:Alcohol.use7 Obesity3:Alcohol.use7
## Low               0.01063737         2.430725e-103                     0
## Medium            0.01063737         2.430764e-103                     0
##        Obesity4:Alcohol.use7 Obesity5:Alcohol.use7 Obesity6:Alcohol.use7
## Low                        0                     0                     0
## Medium                     0                     0                     0
##        Obesity7:Alcohol.use7 Obesity2:Alcohol.use8 Obesity3:Alcohol.use8
## Low             1.618637e-40                     0         1.843189e-138
## Medium          6.738173e+03                     0          1.516616e-55
##        Obesity4:Alcohol.use8 Obesity5:Alcohol.use8 Obesity6:Alcohol.use8
## Low                 11697.18                     0                     0
## Medium              11697.18                     0                     0
##        Obesity7:Alcohol.use8
## Low             7.329741e-67
## Medium          9.362783e+03
##
## Residual Deviance: 0.0001064186
## AIC: 132.0001
```

Results

The results of P-value for each variable in the dataset by doing Fisher's exact test gives an interpretation that all the variables show a significant association with the target variable. Hence, with the help of Logistic regression model, When compared individually passive smoking has the lowest AIC value and Residual deviance hence showing highest association with the target variable and when we finally combine different lifestyle variables to attain a lower AIC value and lower deviance, obesity, Alcohol.Use and Passive smoking variables together can predict a good model fit while giving lowest AIC score and lower residual deviance.

Looking at this statistical testing and above results, we can reject the null hypothesis and prove that there is a significant association between the lifestyle variables (highest association with passive smoking) and the level of cancer thus answering the research question.