

# INTRODUCTION TO DATA SCIENCE

**Applying ML classification algorithms on obesity levels based on eating habits and physical condition Data Set**

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## Obesity-Prediction-Data-Science

### Problem Description:

The problem statement given to us is as follows : " Applying ML Classification algorithms on the data set and getting inferences from the data using appropriate ML algorithms. " We collected the dataset [Estimation of obesity levels based on eating habits and physical condition Data Set](#) from the [UCL Machine Learning Repository]Official publication of the research that provides data can be accessed from [here.\(https://archive.ics.uci.edu/ml/index.php\)](https://archive.ics.uci.edu/ml/index.php).

### Aim:

We will predict levels of obesity using various types of machine learning classification models to our dataset to make relevant predictions on which factors influences obesity.

### Data Set Information:

This dataset include data for the estimation of obesity levels in individuals from the countries of Mexico, Peru and Colombia, based on their eating habits and physical condition. The data contains 17 attributes and 2111 records, the records are labeled with the class variable NObsesity (Obesity Level), that allows classification of the data using the values of Insufficient Weight, Normal Weight, Overweight Level I, Overweight Level II, Obesity Type I, Obesity Type II and

Obesity Type III. 77% of the data was generated synthetically using the Weka tool and the SMOTE filter, 23% of the data was collected directly from users through a web platform.

Data Set Characteristics		Multivariate
Attribute Characteristics	Integer	
Associated Tasks	Classification, Regression, Clustering	
Number of Instances	2111	
Number of Attributes	17	
Missing Values?	N/A	
Area	Life	
Date Donated	2019-08-27	
Number of Web Hits	105220	

More information regarding the dataset like - csv files , attribute information and processing done on the dataset is given in the subsequent pages.

### Attribute information

1. What is your gender? (**Gender**) = Female, Male
2. What is your age? (**Age**) = Numeric value
3. What is your height? (**Height**) = Numeric value in meters
4. What is your weight? (**Weight**) = Numeric value in Kilograms
5. Has a family member suffered or suffers from  
overweight(**family\_history\_with\_overweight**)? = Yes, No
6. Do you eat high caloric food frequently? (**FAVC**) = Yes, No
7. Do you usually eat vegetables in your meals? (**FCVC**) = 1-3 follow by usually meal
8. How many main meals do you have daily? (**NCP**) = Between 1 y 2, 3, more than 4
9. Do you eat any food between meal? (**CAEC**) = No, Sometimes, Frequently, Always
10. Do you smoke? (**Smoke**) = Yes, No
11. How much water do you drink daily? (**CH20**) = less than a liter, between 1 and 2L, more than 2 L
12. Do you monitor the calories you eat daily? (**SCC**) = Yes, No
13. How often do you have physical activity? (**FAF**) = I do not have, 1 or 2 days, 2 or 4 days, 4 or 5 day
14. How much time do you use technological devices? (**TUE**) = 0-2 hours, 3-5 hours, more than 5 hours
15. How often do you drink alcohol? (**CALC**) = I don't drink, Sometimes, Frequently, Always
16. Which transportation do you usually use? (**MTRANS**) = Automobile, Motorbike, Bike Public Transportation, Walking

## Imports

We have imported the following libraries to perform EDA, preprocessing, classification and regression

```
In [1]: #import packages
import csv
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from scipy import stats
```

First of all, we will read the csv file **ObesityDataSet\_raw\_and\_data\_sinthetic.csv** with the help of panda libraries

```
In [2]: #read data
df = pd.read_csv("ObesityDataSet_raw_and_data_sinthetic.csv")
```

```
In [3]: df.head()
```

	Gender	Age	Height	Weight	family_history_with_overweight	FAVC	FCVC	NCP	CAEC	SMC
0	Female	21.0	1.62	64.0		yes	no	2.0	3.0	Sometimes
1	Female	21.0	1.52	56.0		yes	no	3.0	3.0	Sometimes
2	Male	23.0	1.80	77.0		yes	no	2.0	3.0	Sometimes
3	Male	27.0	1.80	87.0		no	no	3.0	3.0	Sometimes
4	Male	22.0	1.78	89.8		no	no	2.0	1.0	Sometimes

Applying the head function on dataframe which contains the csv file, we get the first 5 records.

## Data Cleaning

```
In [4]: df = df.rename(columns={'NObeyesdad': 'result'})
```

We will rename the last column which tells the type of obesity of the person from NObeyesdad to result

```
In [5]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2111 entries, 0 to 2110
Data columns (total 17 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   Gender            2111 non-null   object  
 1   Age               2111 non-null   float64 
 2   Height            2111 non-null   float64 
 3   Weight            2111 non-null   float64 
 4   family_history_with_overweight  2111 non-null   object  
 5   FAVC              2111 non-null   object  
 6   FCVC              2111 non-null   float64 
 7   NCP               2111 non-null   float64 
 8   CAEC              2111 non-null   object  
 9   SMOKE             2111 non-null   object  
 10  CH20              2111 non-null   float64 
 11  SCC               2111 non-null   object  
 12  FAF               2111 non-null   float64 
 13  TUE               2111 non-null   float64 
 14  CALC              2111 non-null   object  
 15  MTRANS             2111 non-null   object  
 16  result             2111 non-null   object  
dtypes: float64(8), object(9)
memory usage: 280.5+ KB
```

In [6]: `df.shape`

Out[6]: (2111, 17)

In [7]: `df.isnull().sum()`  
*# no data cleaning required*

Out[7]:

Gender	0
Age	0
Height	0
Weight	0
family_history_with_overweight	0
FAVC	0
FCVC	0
NCP	0
CAEC	0
SMOKE	0
CH20	0
SCC	0
FAF	0
TUE	0
CALC	0
MTRANS	0
result	0

dtype: int64

- Using the shape function we obtain the following inference:-
  - Number of Rows which is the number of records - 2111
  - Number of Columns which is the number of attributes- 17
- Using the info function we got to know that the data loads as text and float objects for most of the objects. However we know that some are float, categorical and ordinal

- Using the isnull().sum() function we infer that all of the records are unique and contain no null values
- Height and Weight are included however they have a direct correlation to each other and our target variable

**After the analysis of the csv file we come to the conclusion that no data cleaning is required as no null values or missing values are present**

## Exploratory Data Analysis

- Exploratory data analysis (EDA) is an approach to analyzing data sets to summarize their main characteristics, often with visual methods.
- We will analyse the attributes of the dataset and summarize the variables, visualizing it and study about the relationship between two variables and plot the data using **matplotlib library** and **seaborn library**

These are the plots we are going to see below for the various attributes of the dataset

- **Histogram** is for quantitative data – the number of bars depends on the user or to the software. It is an approximate representation of numerical data distribution.
- **Bar Chart** is for categorical data – the number of bars depends on the number of categories
- **Scatter Plot** is yet another way of representation of attributes of a dataset. It is basically a type of plot or mathematical diagram which uses cartesian coordinates for the display of values. It uses two variables for a set of data , one on the X-axis and one on the Y-axis. In scatter plot , data is represented in form of points on the cartesian plane , with one variable determining the position on the horizontal axis and the other variable determining the position on the vertical axis

```
In [8]: def count_values(dataset, cat_variable, order = None):
    """
    Function: Counts values in each category and displays them on a plot.

    Parameters: Dataset, category feature, and order of appearance (order is optional)
    """
    ax = sns.countplot(x = cat_variable, data = dataset, palette = sns.cubehelix_palette
        for p in ax.patches:
            ax.annotate(f"\n{p.get_height()}", (p.get_x()+0.2, p.get_height()),
                        ha = "center", va = "top", color = "white", size = 10)

    plt.title(f"Number of items in each {cat_variable} category")
    plt.show()
```

**count\_values** function takes the parameter dataset i.e. the dataframe which contains the csv file, an attribute of the csv file and the order we want to see in the plot.

- For example- Gender has two values male and female so [male,female] can be our order as well as [female,male].
- The function plots a bar graph i.e. it is used for categorical data.
- The function uses **seaborn** and **matplotlib** libraries.

```
In [9]: def plot_distribution(dataset, feature):
    """
        Function: Computes and displays distribution of features with continuous values; plots histogram with mean and median lines.

        Parameters: Dataset and feature with continuous values.
    """
    plt.hist(dataset[feature], bins = "fd")

    plt.axvline(dataset[feature].mean(), color = "red", label = "mean")
    plt.axvline(dataset[feature].median(), color = "orange", label = "median")

    plt.xlabel(f"{feature}")
    plt.ylabel("Count")
    plt.legend()
    plt.title(f"Distribution of values in {feature}")
    plt.show()
```

**plot\_distibution** function takes the dataframe of csv file and attribute of the dataset. It does not require any order as it uses continuous values.

- The function plots a histogram and also displays mean and median of the attirbute.
- The function uses **matplotlib** library

```
In [10]: def cross_plot(dataset, lead_category, sup_category, order = None, hue_order= None):
    """
        Function: Plots interaction between two categorical variables.

        Parameters: Dataset, lead category, supplemental category, and order of appearance
    """

    ax = sns.countplot(x = lead_category, hue = sup_category, data = dataset, order =
        for p in ax.patches:
            ax.annotate(f"\n{p.get_height()}", (p.get_x()+0.2, p.get_height()),
                        ha = "center", va = "top", color = "white", size = 10)

    plt.title(f"Number of items in each {lead_category} with respect to {sup_category}")
    plt.show()
```

**cross\_plot** uses 5 parameters. First being the dataframe of the csv file, second the leading attribute which will be plotted on X-axis, third the supplemental attribute which will be plotted with respect to the result and then the orders of lead attribute and supplemental attribute respectively.

- It is a plot between two categorical variables
- It plots a bar graph where each value of X-axis has n no. of bars where n is equal to the order of supplemental attribute.
- The function uses **seaborn** library.

```
In [11]: def cmp_plot(dataset, lead_category, sup_category, order = None):
    """
    Function: Plots interaction between numerical and categorical variables.

    Parameters: Dataset, lead category, supplemental category, and order of appearance
    """

    ax = sns.histplot(data= dataset, x=sup_category, hue=lead_category, palette= "rocket")
    plt.show()
```

**cmp\_plot** has the dataset, lead attribute, supplemental attribute and order of lead attribute as parameters.

- It plots between numerical and categorical variable.
- It plots a histogram.
- The function uses **seaborn** library.

```
In [12]: sns.axes_style("darkgrid")
sns.set(rc={'figure.figsize':(17 ,11.27)})
```

## Obesity Levels

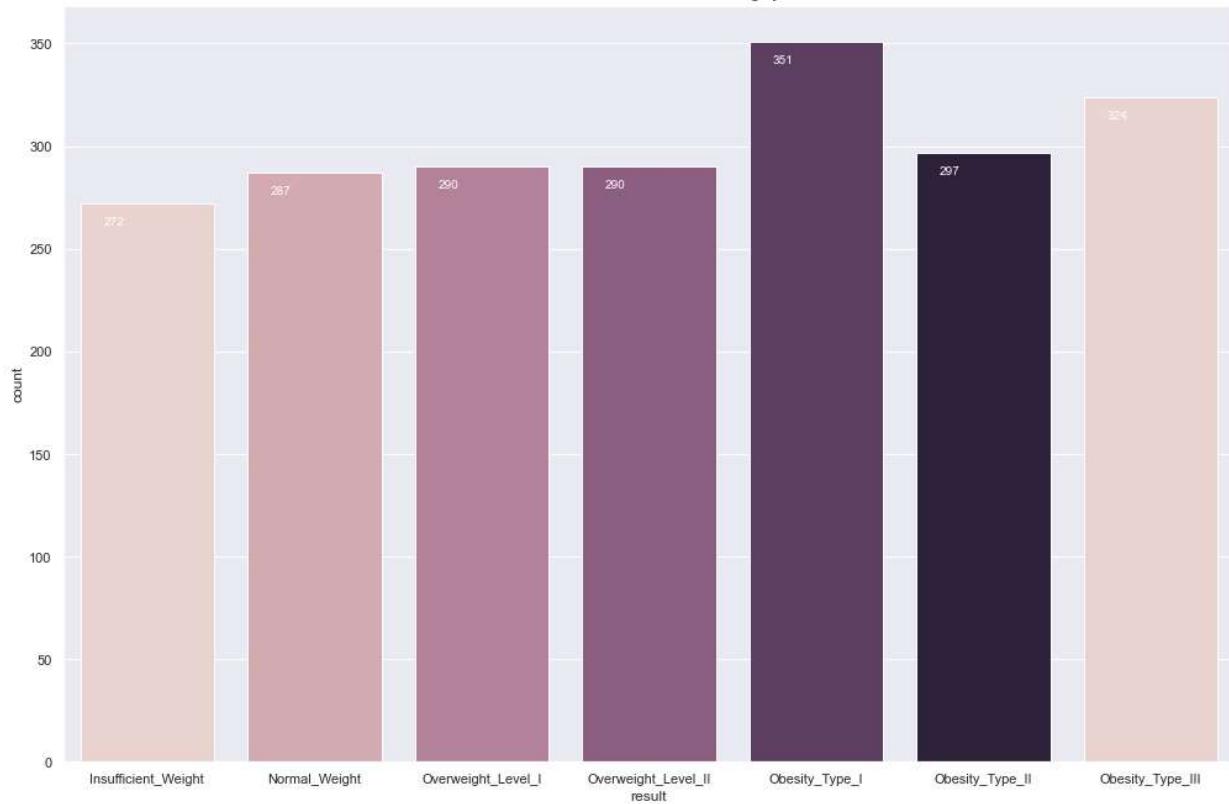
```
In [13]: weight_order= ["Insufficient_Weight", "Normal_Weight", "Overweight_Level_I", "Overwei
```

- It is the different values we can see in the result column also known as **obesity levels** hence this order will be used in **cross\_plot** and **cmp\_plot** function for the lead attribute.

## Result

```
In [14]: count_values(df, "result", weight_order)
```

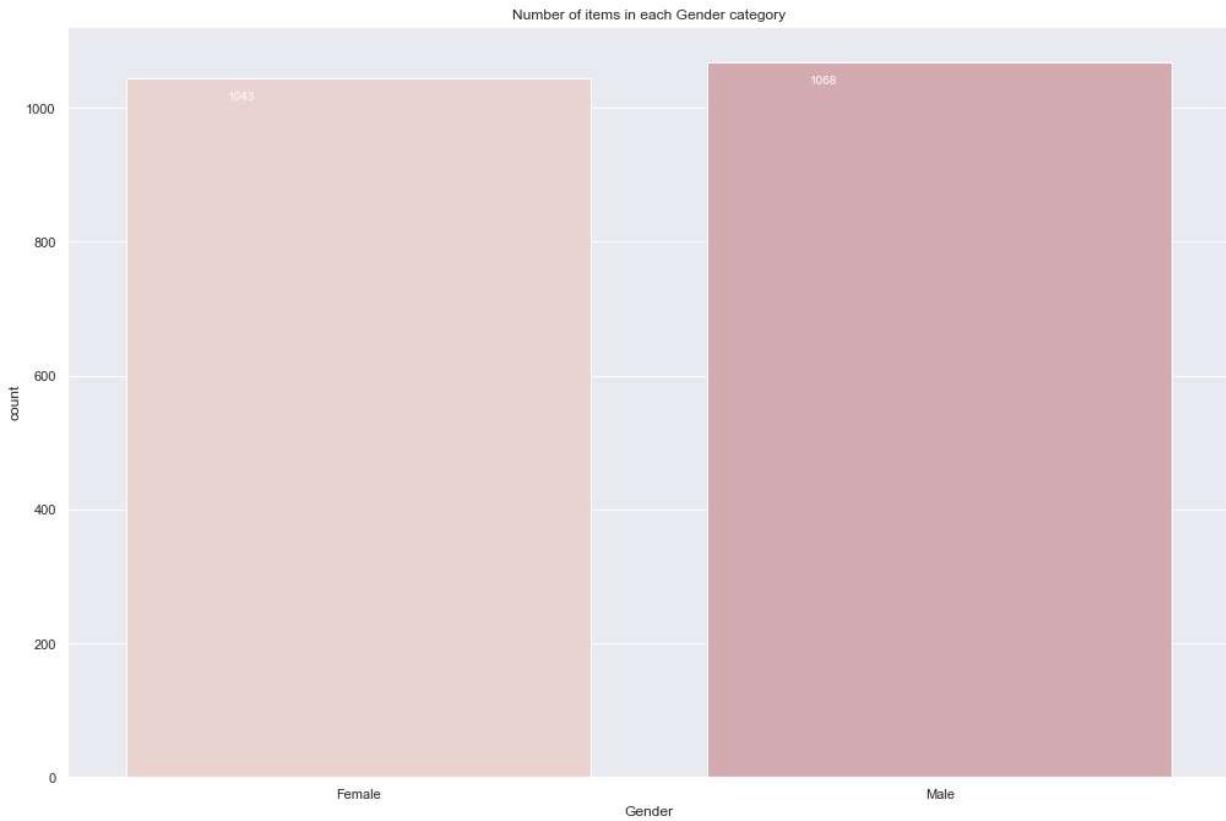
Number of items in each result category



- 351 instances belong to "obesity\_type\_1"; more than 250 instances belong to "insufficient\_weight" class.
- The plot shows the dataset is balanced; only "Obese Type I" class slightly outnumber the other categories.

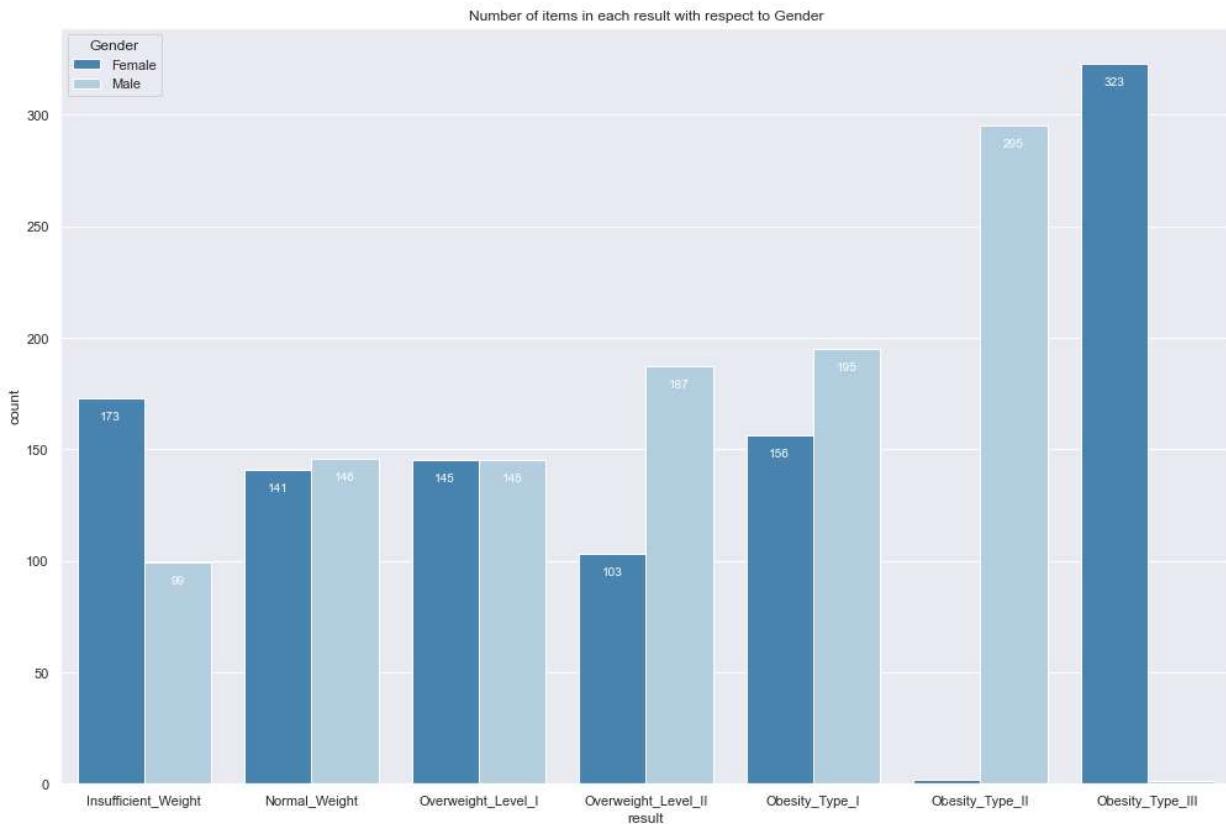
## Gender

```
In [15]: count_values(df, "Gender")
```



- There are almost an equal number of females and males in the dataset. Data is available for slightly more men than women but this does not make it imbalanced.

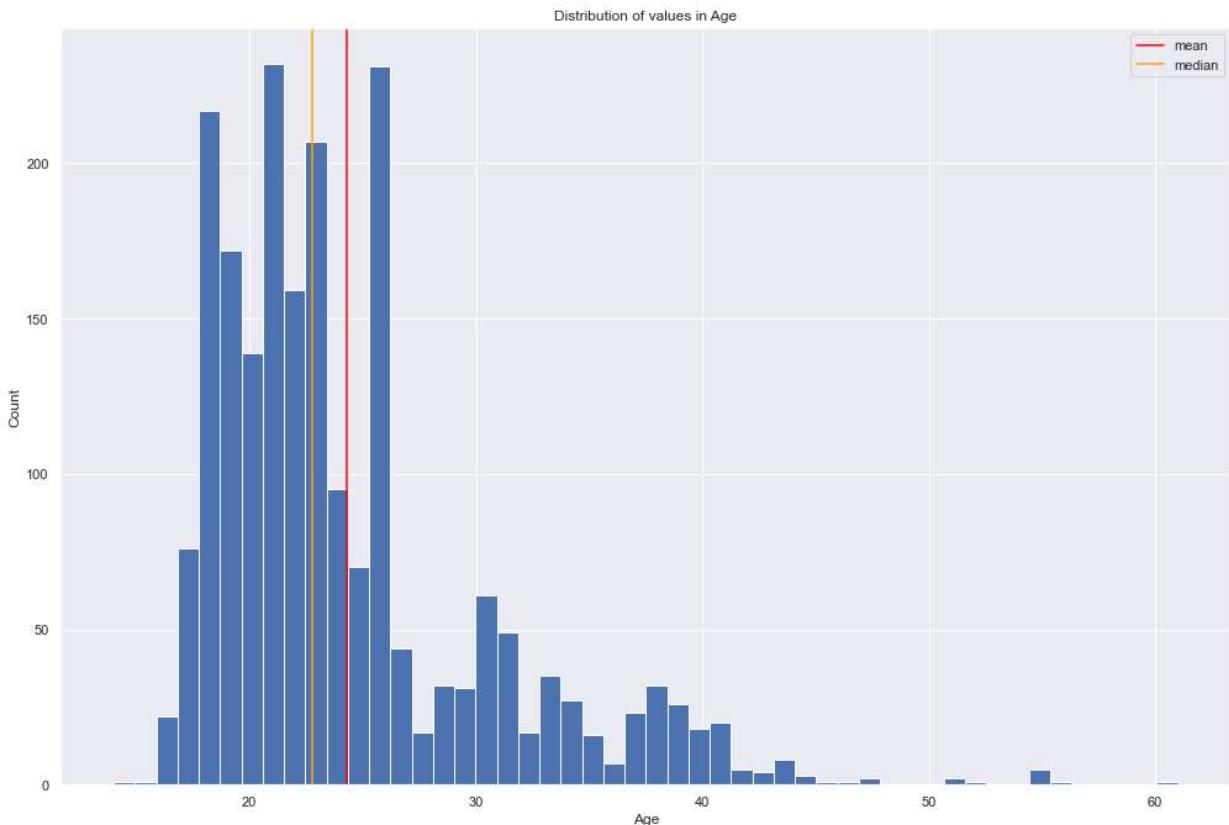
```
In [16]: cross_plot(df, "result", "Gender", weight_order)
```



- Women are more likely to have "Insufficient weight" than men. On the other hand, there are more obese men than women, save in the last, extreme obesity category.
- Females do not have "obesity\_type\_2". males do not have "obesity\_type\_3"

## Age

In [17]: `plot_distribution(df, "Age")`



In [18]: `df["Age"].describe()`

Out[18]:

count	2111.000000
mean	24.312600
std	6.345968
min	14.000000
25%	19.947192
50%	22.777890
75%	26.000000
max	61.000000

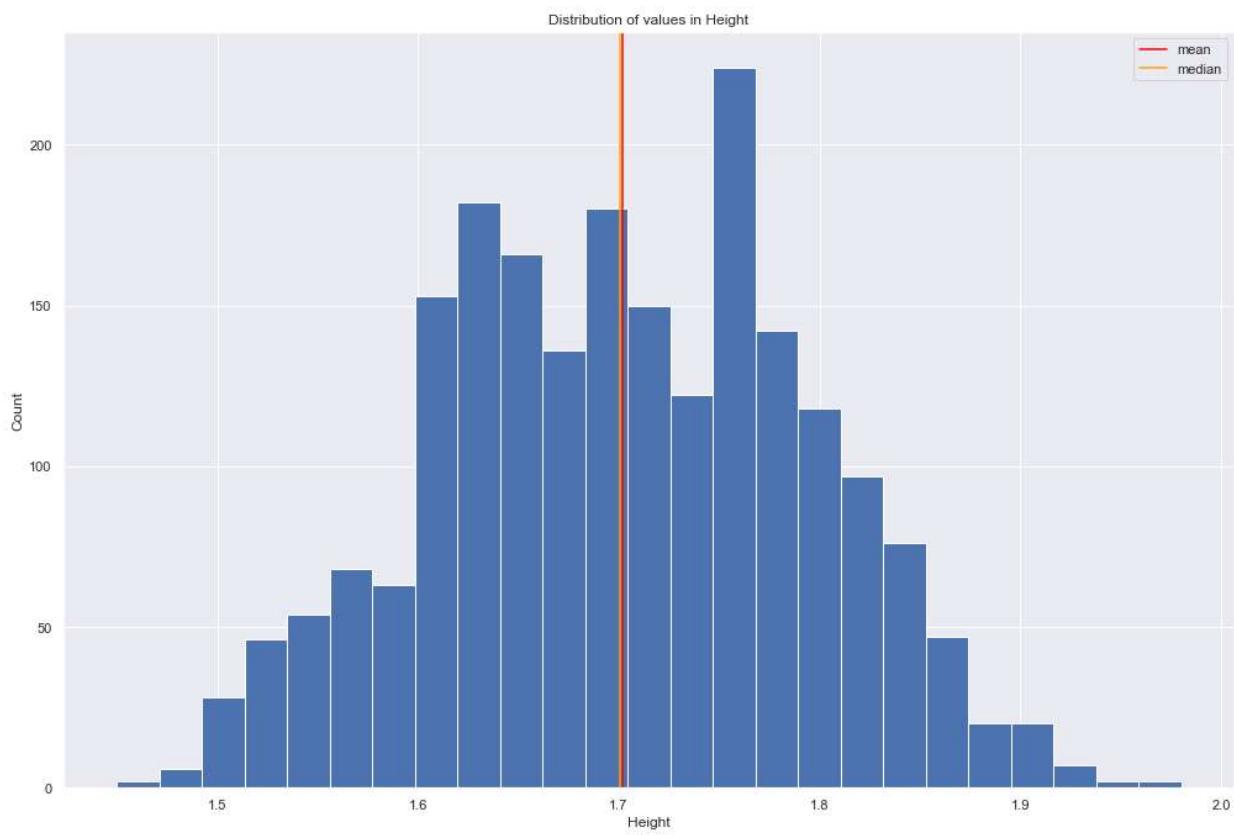
Name: Age, dtype: float64

- We can see that mostly young people were joined the survey.
- Top 3 ages: 21, 18, 19

## Height & Weight

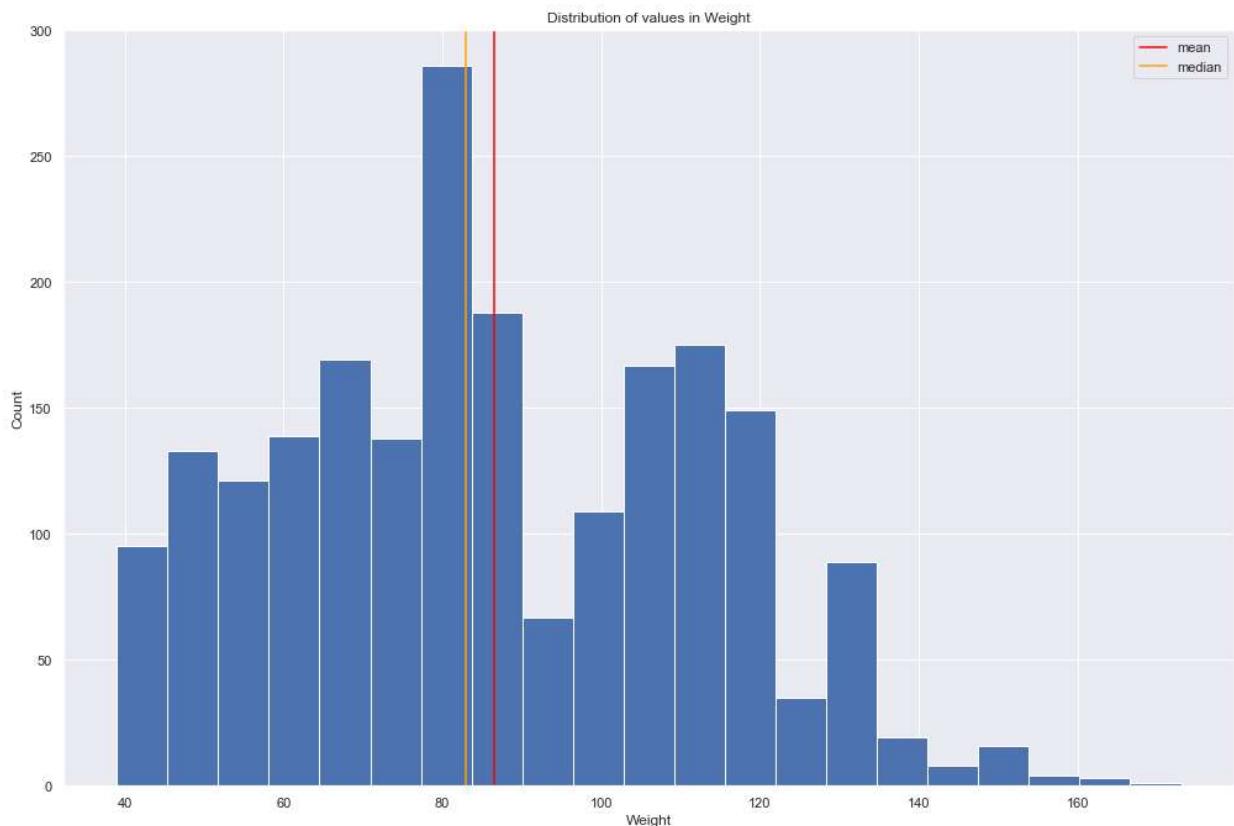
In [19]: `plot_distribution(df, "Height")`

## project



- Most people are 1.60 m - 1.85 m tall. Both mean and median values are around 1.70.

```
In [20]: plot_distribution(df, "Weight")
```



- The mean and the median are shifted to the left because of the larger number of people weighting 80 kg.

In [21]:

```
# Obesity is calculated by BMI
# Body Mass Index (BMI) = Weight/(Height)^2
# Correlation Between Height & Weight

sns.lmplot(x='Weight', y='Height', data=df, height= 8, line_kws={'color': 'red'})
plt.title("Scatter Plot with Linear fit");
```



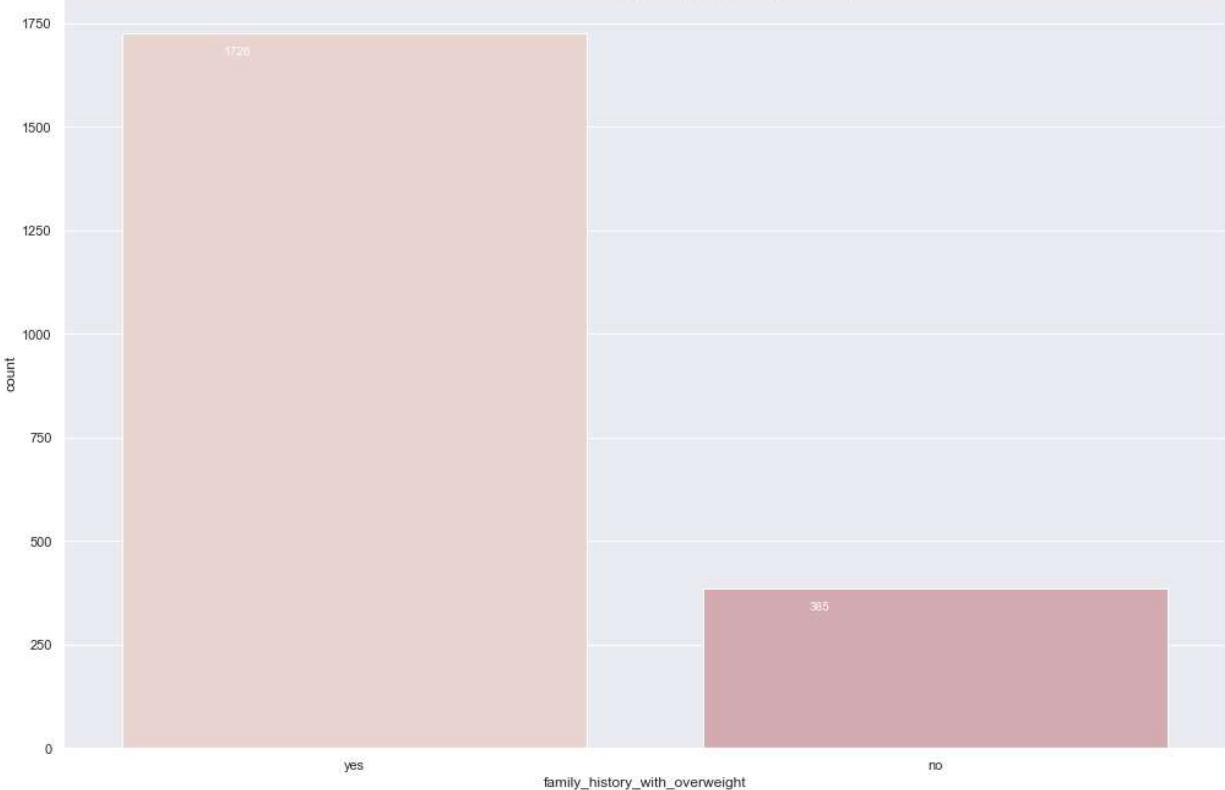
- The red line shows that there is a positive correlation between them, which means an increase in one variable leads to an increase in the other. In other words, taller people are more likely to weight more.

## Family History

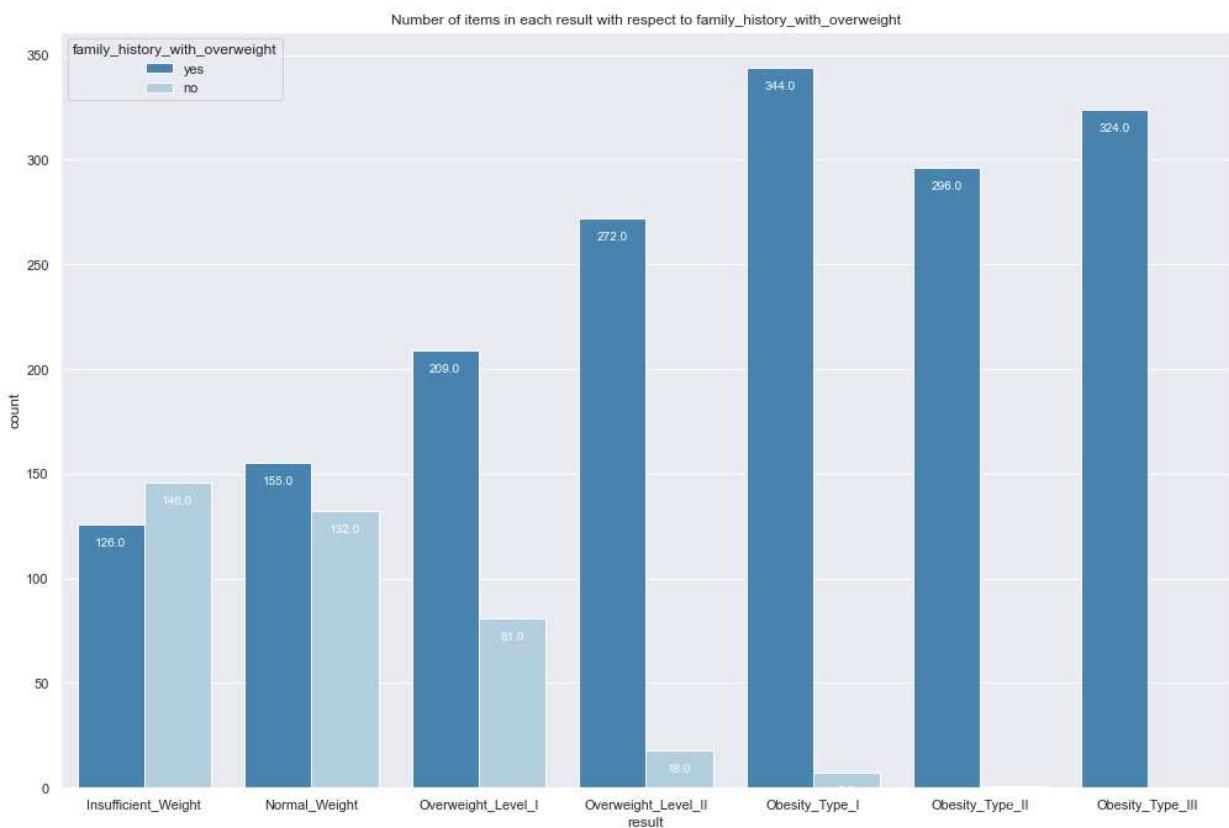
In [22]:

```
count_values(df, "family_history_with_overweight")
```

Number of items in each family\_history\_with\_overweight category



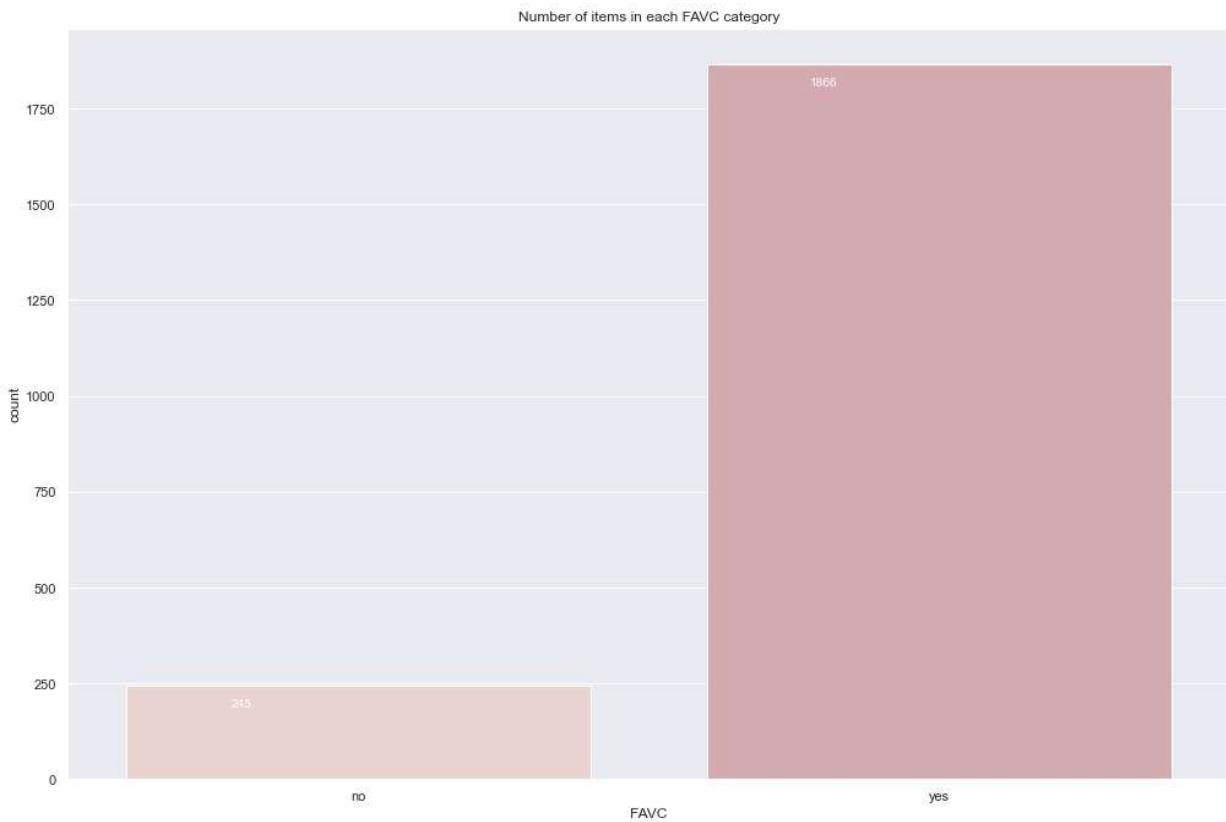
```
In [23]: cross_plot(df, "result", "family_history_with_overweight", weight_order)
```



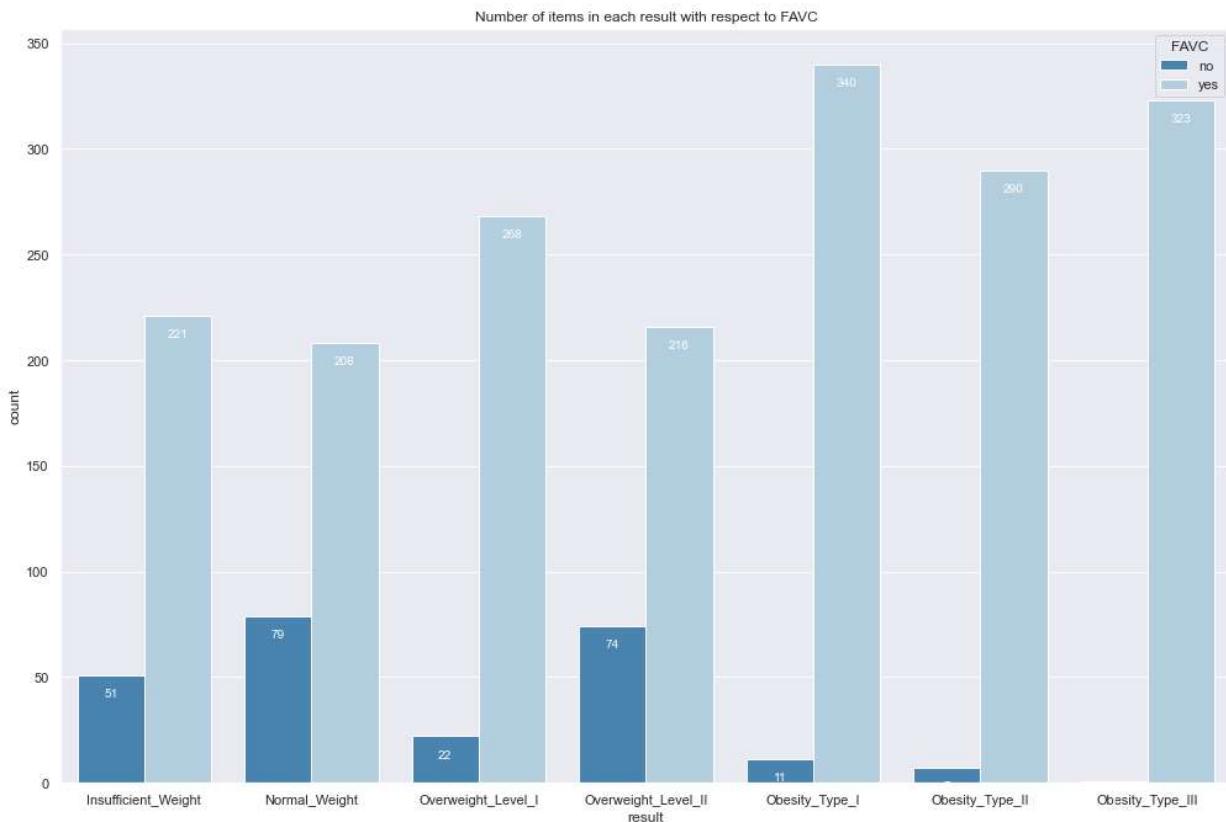
- All those categorised as overweight or obese had family members suffering from weight problems.

## High caloric food Consumption

In [24]: `count_values(df, "FAVC")`



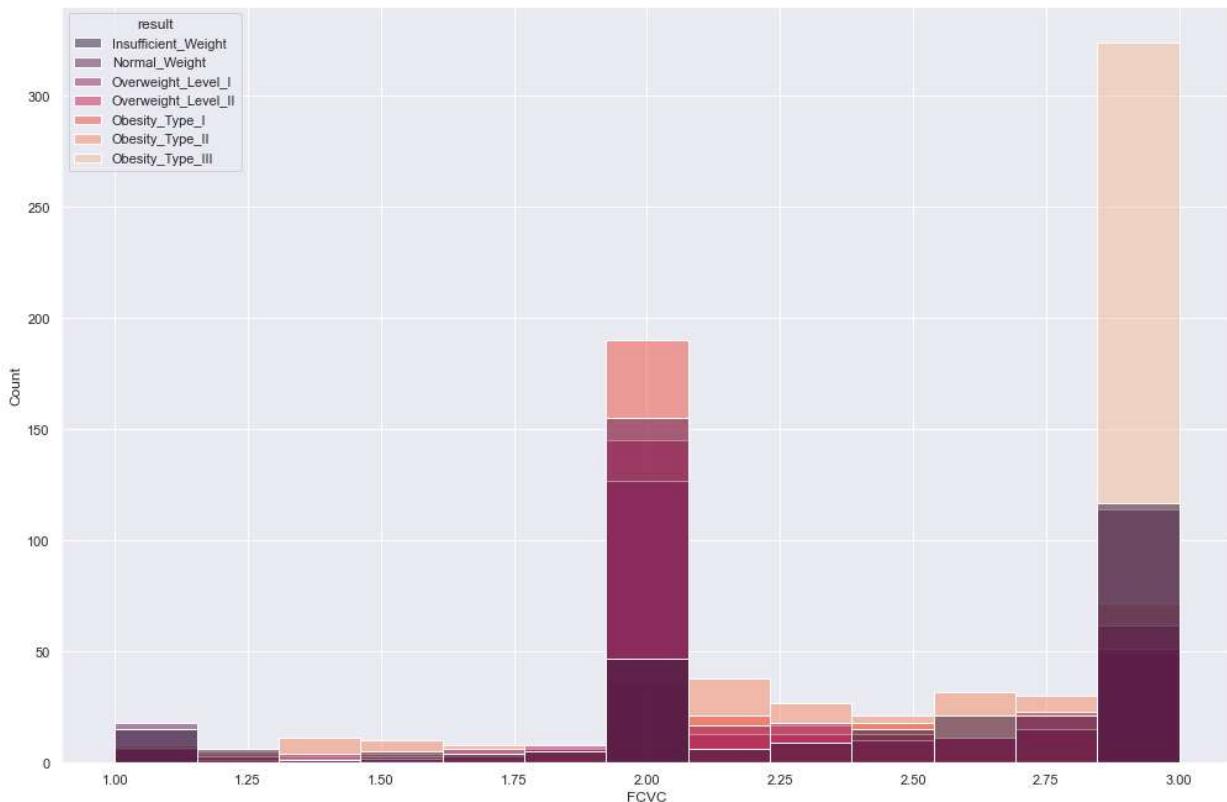
In [25]: `cross_plot(df, "result", "FAVC", weight_order)`



## Consumption of Vegetables

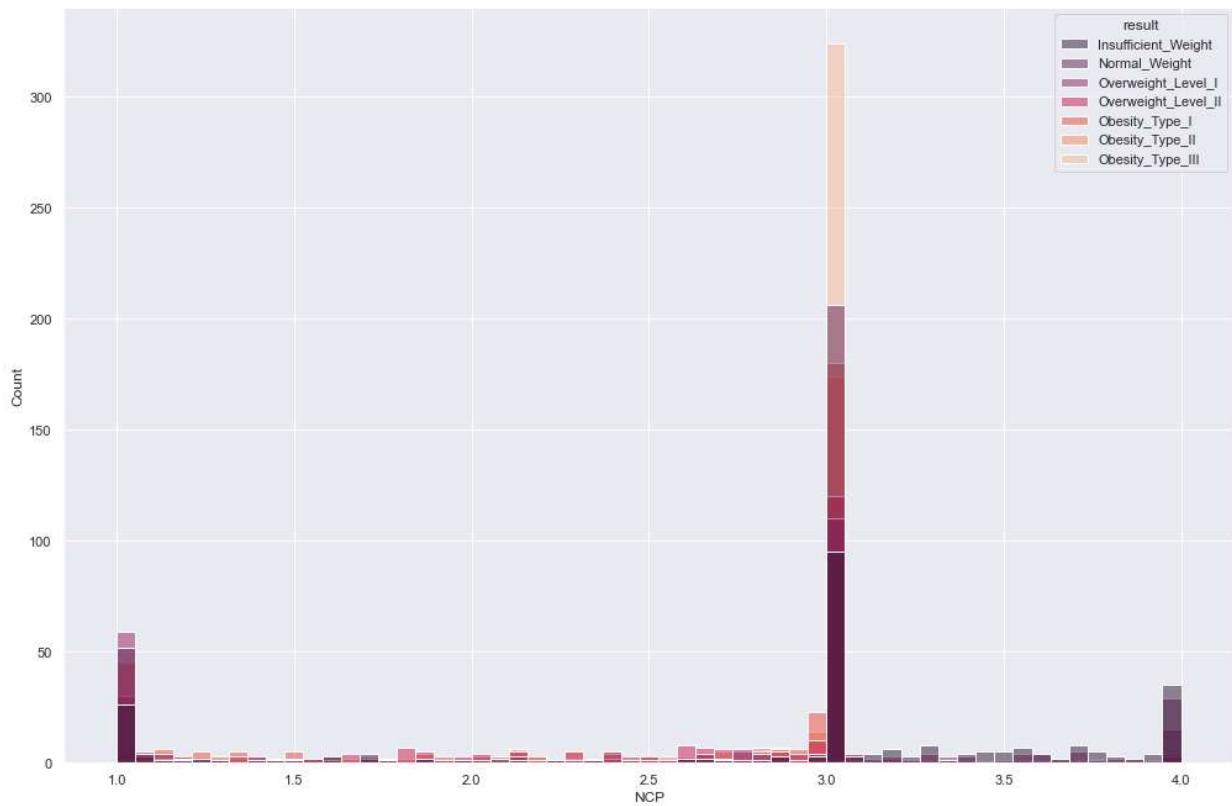
- "FCVC" column denotes if people consume vegetables.
- It could be assumed that "3" means "Always", "2" - "Sometimes", and "1" - "Never", but it is not clear what the values inbetween mean.

```
In [26]: cmp_plot(df, "result", "FCVC", weight_order)
```



## Meals per day

```
In [27]: cmp_plot(df, "result", "NCP", weight_order)
```



In [28]: `df["NCP"].describe()`

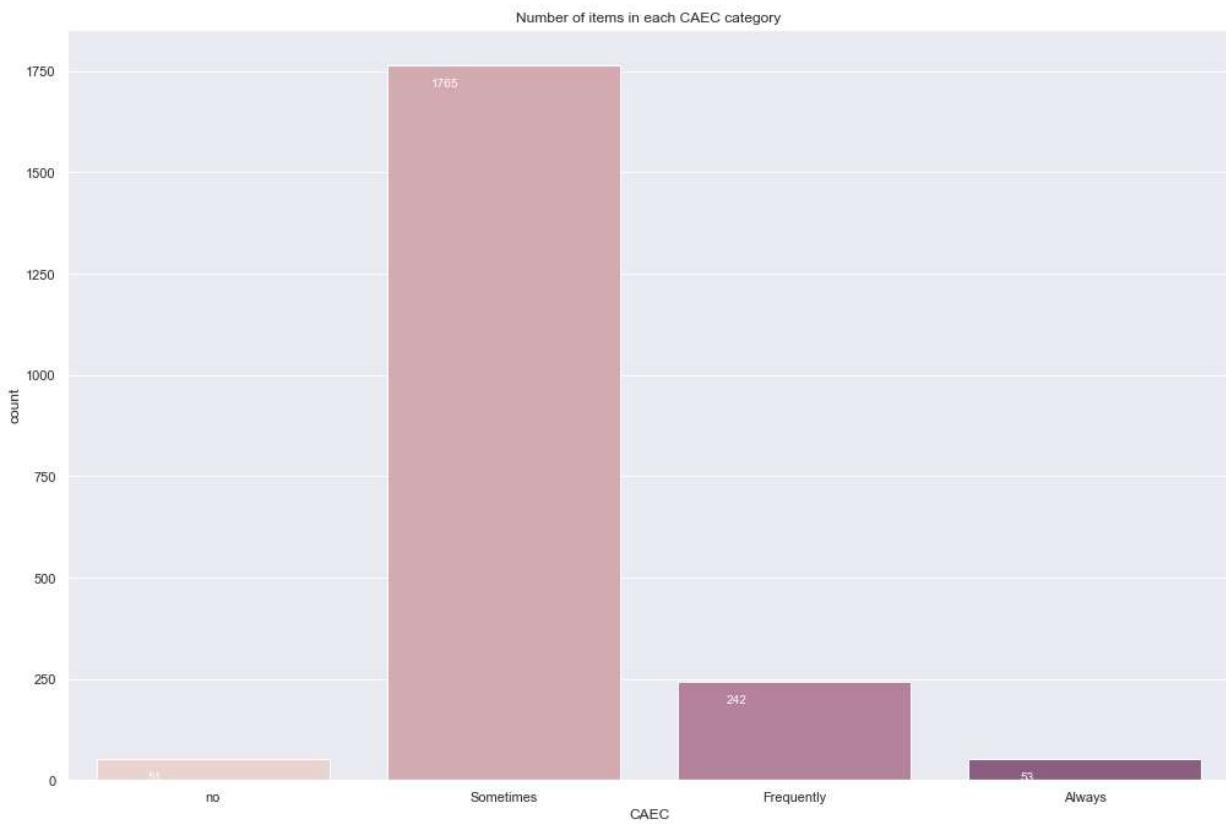
Out[28]:

count	2111.000000
mean	2.685628
std	0.778039
min	1.000000
25%	2.658738
50%	3.000000
75%	3.000000
max	4.000000
Name:	NCP, dtype: float64

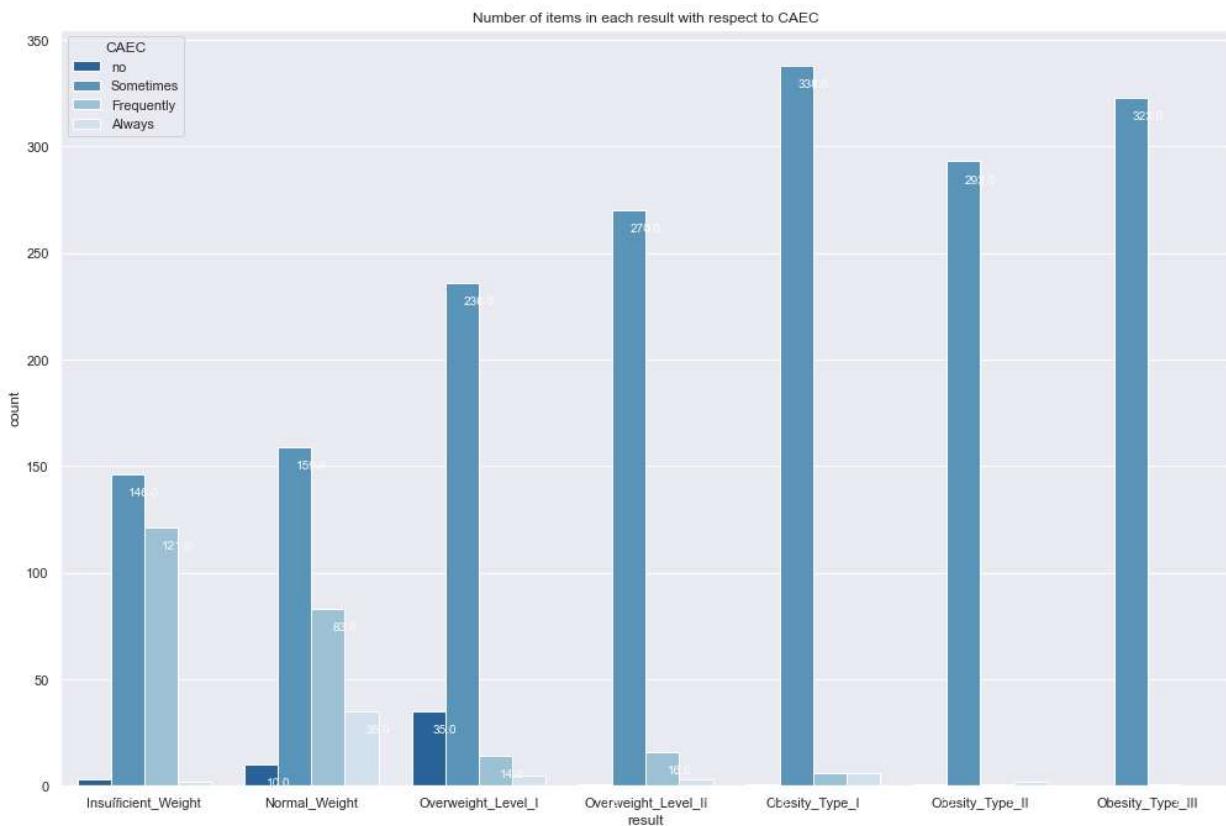
- From the above plot we can infer that most of the obese type people have meals more than 3 times.

## Food between meals

In [29]: `count_values(df, "CAEC", ["no", "Sometimes", "Frequently", "Always"])`



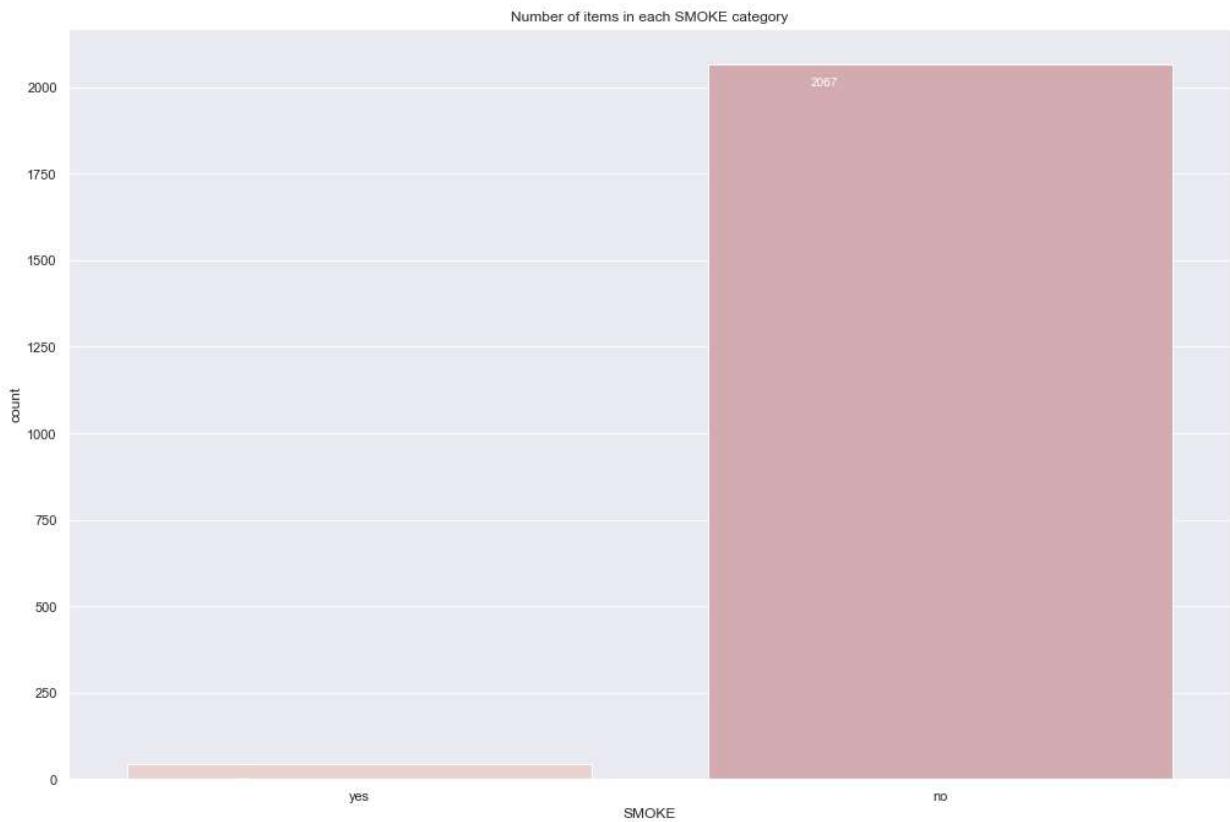
```
In [30]: cross_plot(df, "result", "CAEC", weight_order, hue_order= ["no", "Sometimes", "Frequen
```



- Most of those who have food between meals sometimes are found to be in obesity type 1-3 range and overweiht levels.

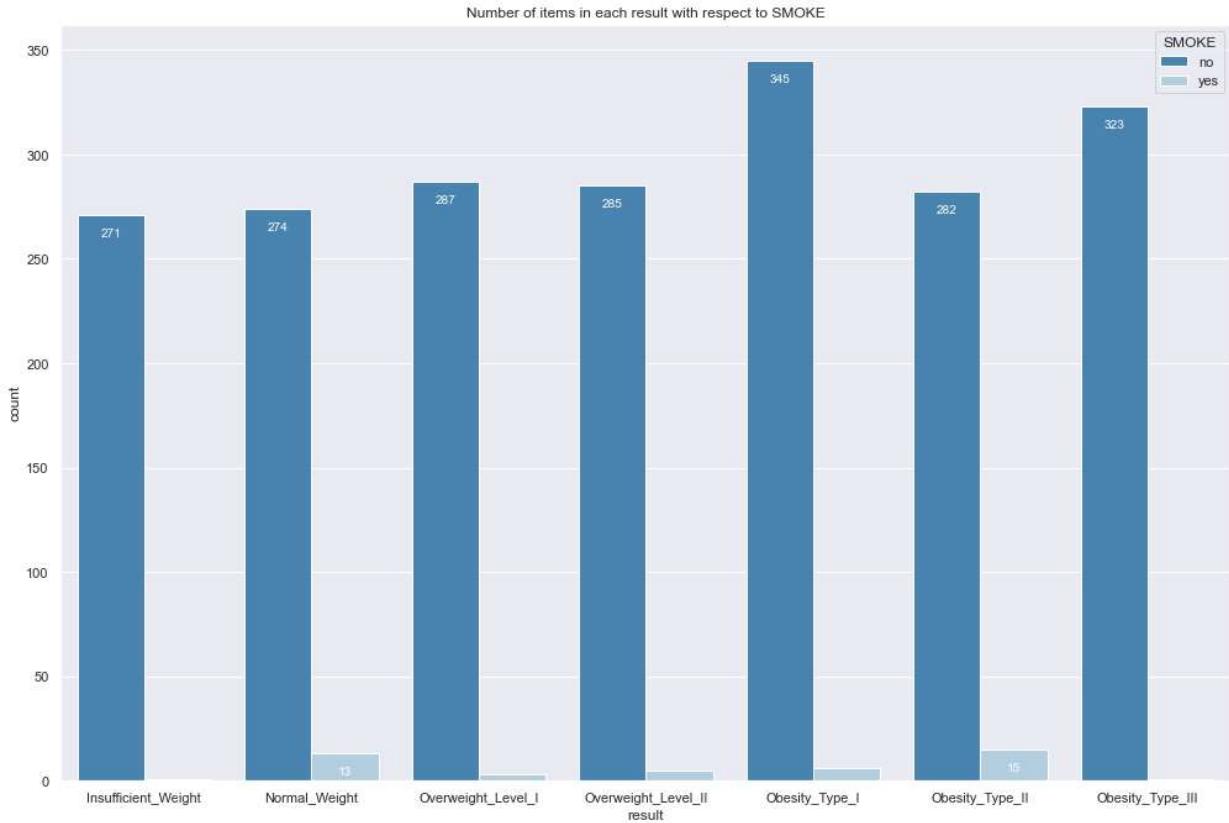
## Smoke

```
In [31]: count_values(df, "SMOKE", ["yes", "no"])
```



- Most of the people in the survey are non-smokers which makes it difficult to find inference about smokers.

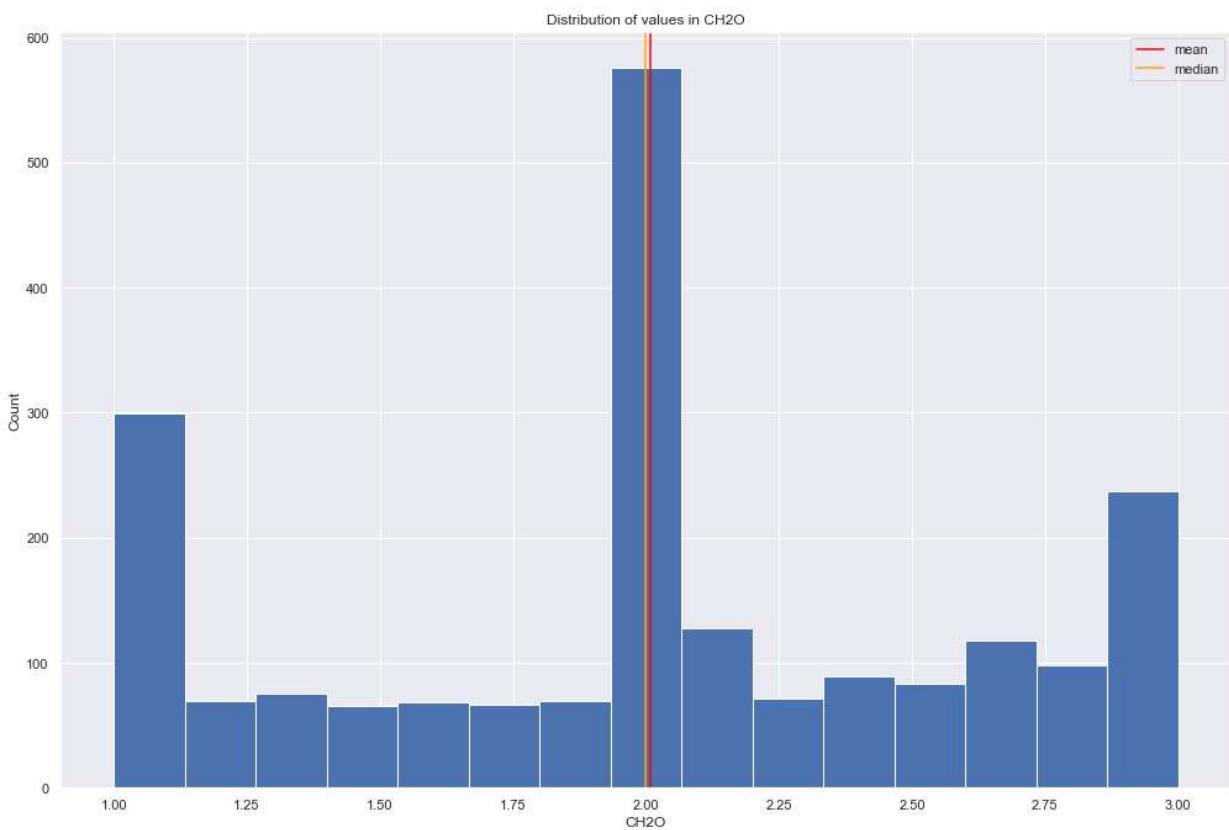
```
In [32]: cross_plot(df, "result", "SMOKE", weight_order)
```



- Analysing the plot we understand that non-smoking does not have any effect on obesity or insufficient weight as all the attributes are ranging from 270-345 hence not much deviation

## Water Intake

```
In [33]: plot_distribution(df, "CH20")
```

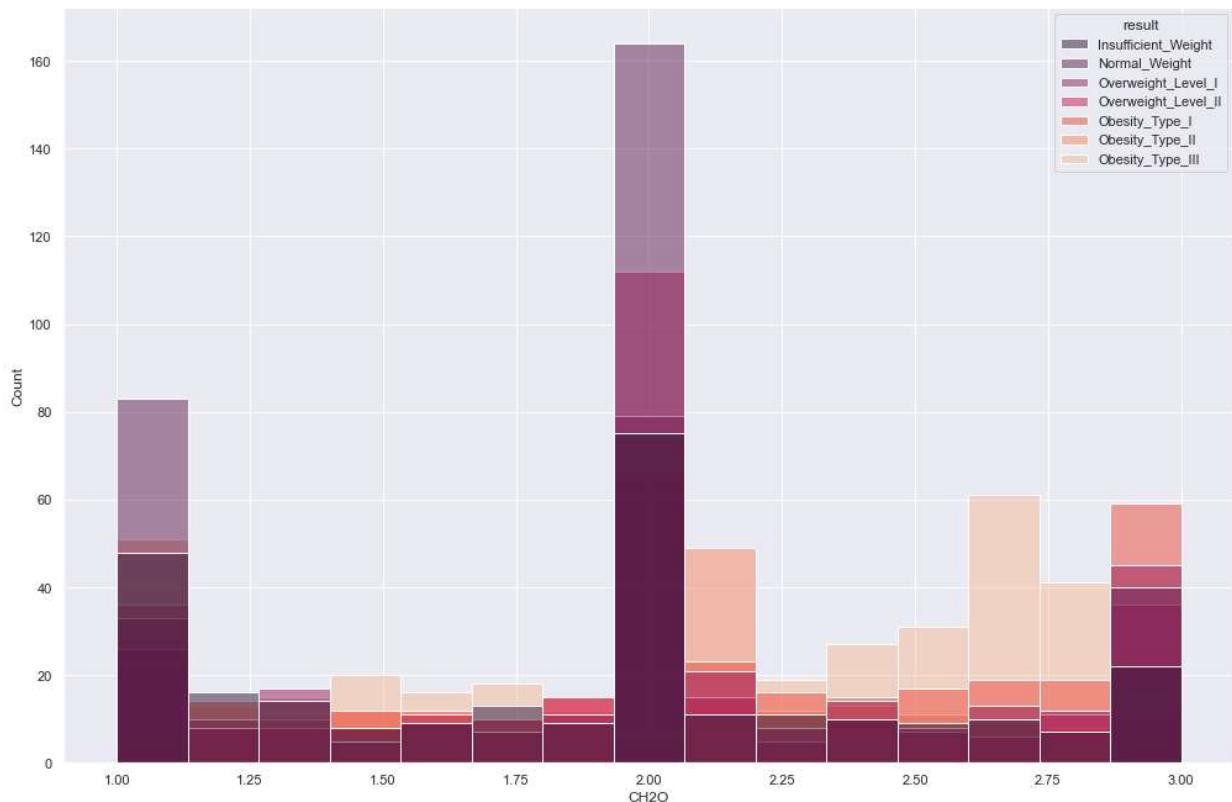


```
In [34]: df["CH2O"].describe()
```

```
Out[34]: count    2111.000000
mean      2.008011
std       0.612953
min      1.000000
25%      1.584812
50%      2.000000
75%      2.477420
max      3.000000
Name: CH2O, dtype: float64
```

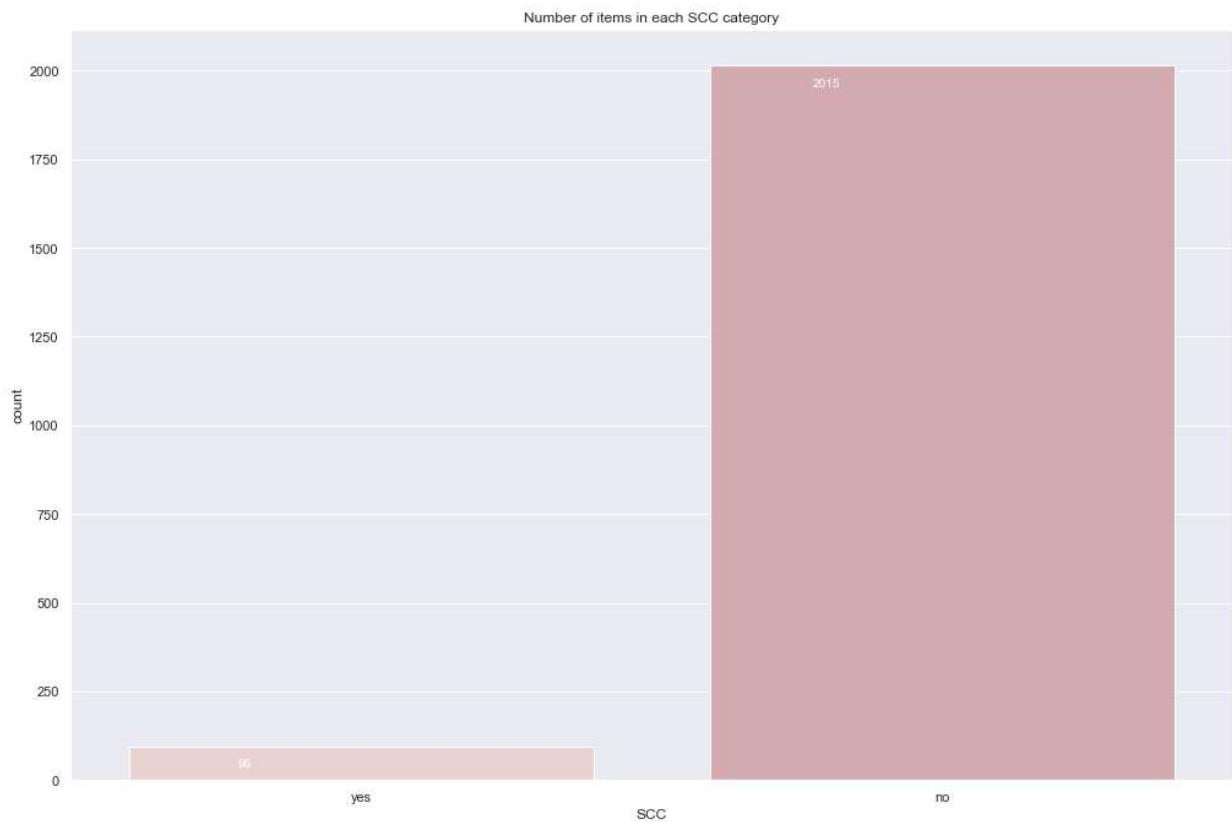
- According to the distribution and statistics we can infer that most of the people in the survey drink 2 litres of water and there is no one who drinks less than a litre

```
In [35]: cmp_plot(df, "result", "CH2O", weight_order)
```



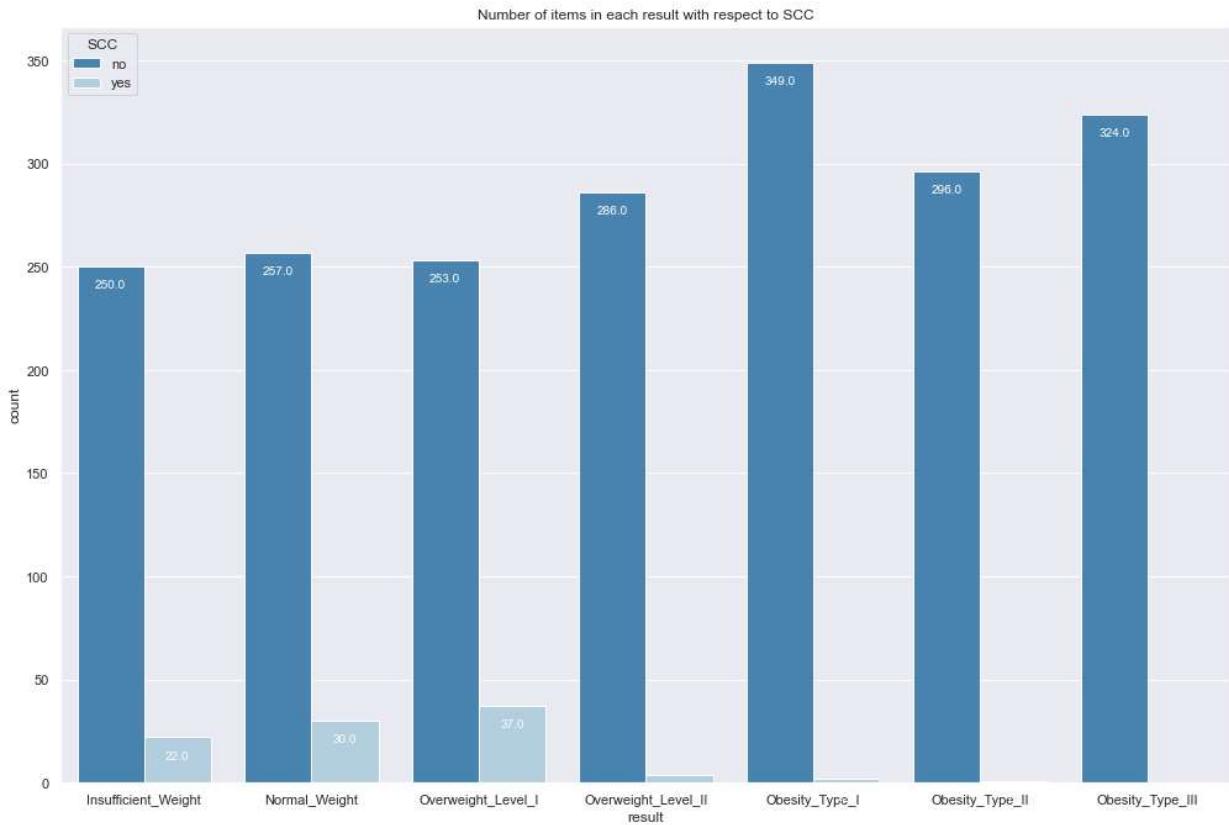
## Record Calories intake

```
In [36]: count_values(df, "SCC", ["yes", "no"])
```



- Most of the people who took part in the survey did not record their daily calories intake

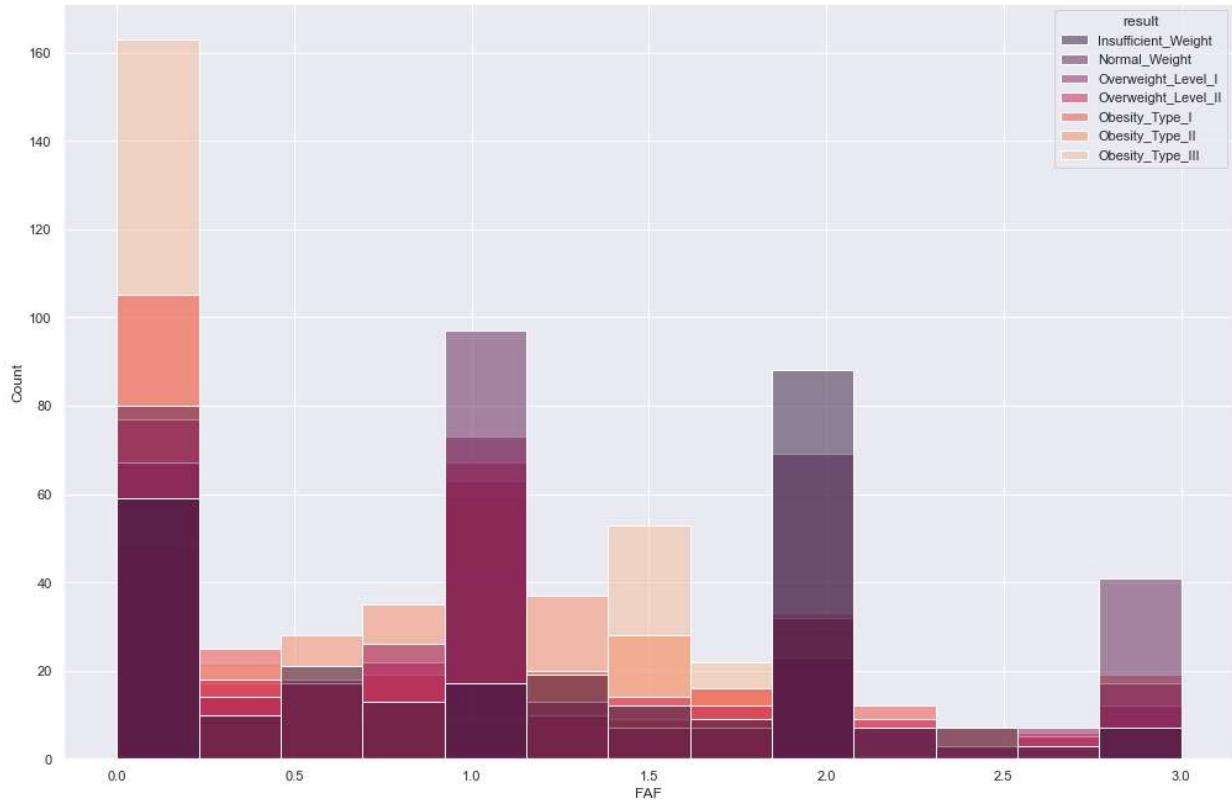
In [37]: `cross_plot(df, "result", "SCC", weight_order,)`



- Majority of the people who recorded their daily calories intake were either insufficient weight or normal weight or overweight but the majority of those who did not measure their calories intake belong to overweight and obesity categories

## Physical Activity

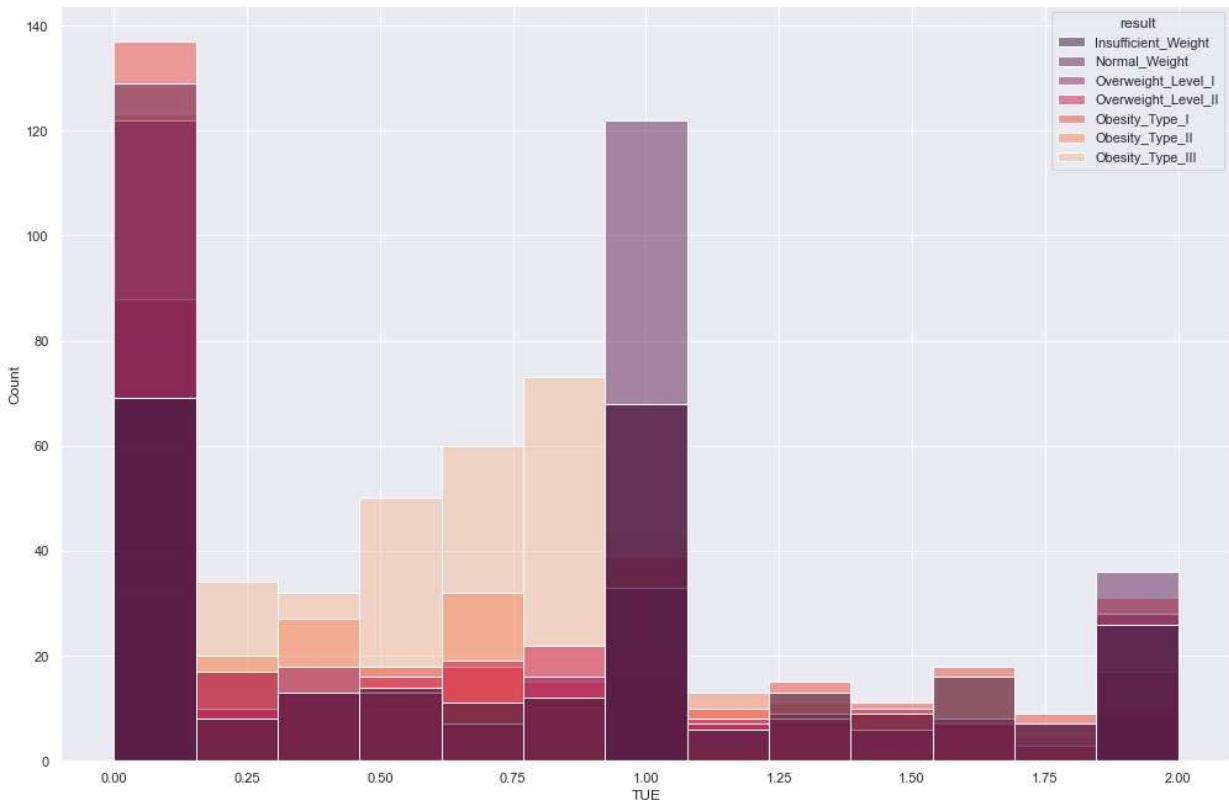
In [38]: `cmp_plot(df, "result", "FAF", weight_order)`



- People who do not do physical activity more than 2 days a week suffer from Obesity type-3, type-2 and type-1

## Use of technological devices

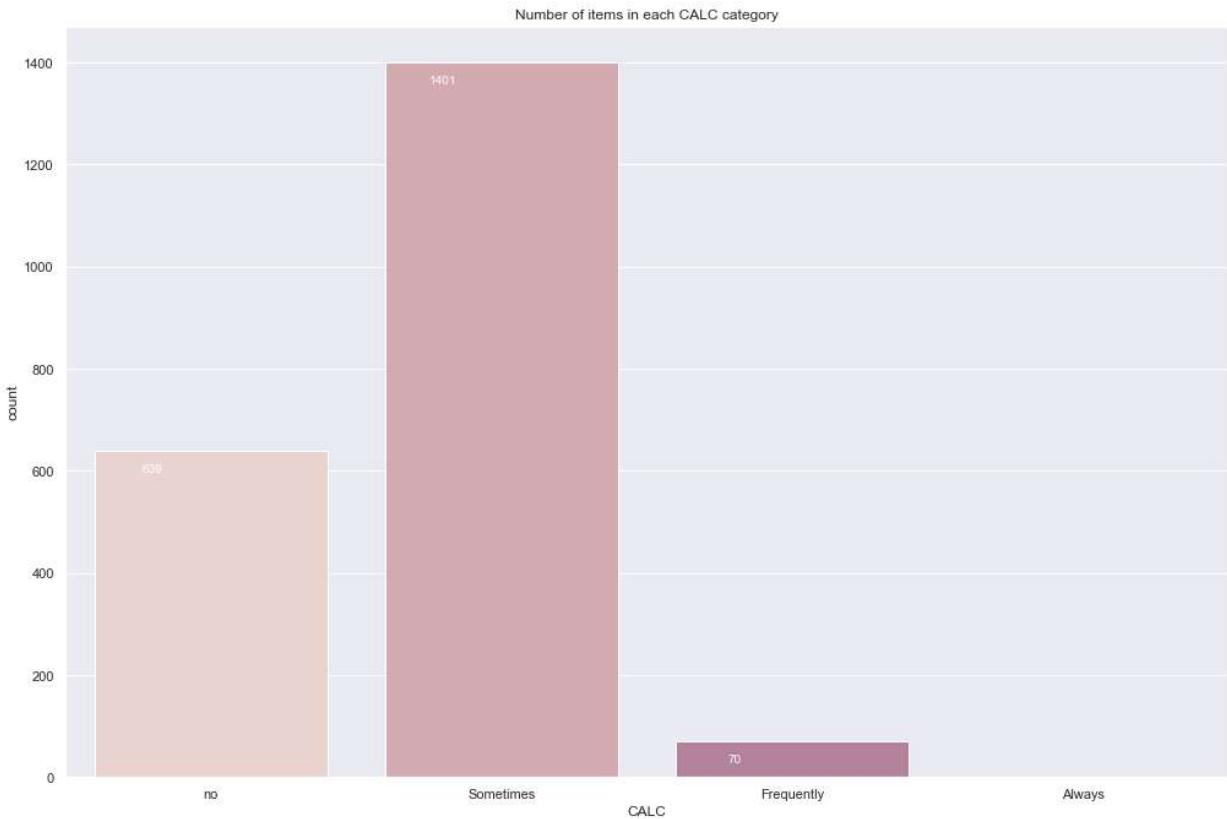
```
In [39]: cmp_plot(df, "result", "TUE", weight_order)
```



- The plot shows that most of the people suffering from obesity type 1 to 3 do not use technological device more than hour.

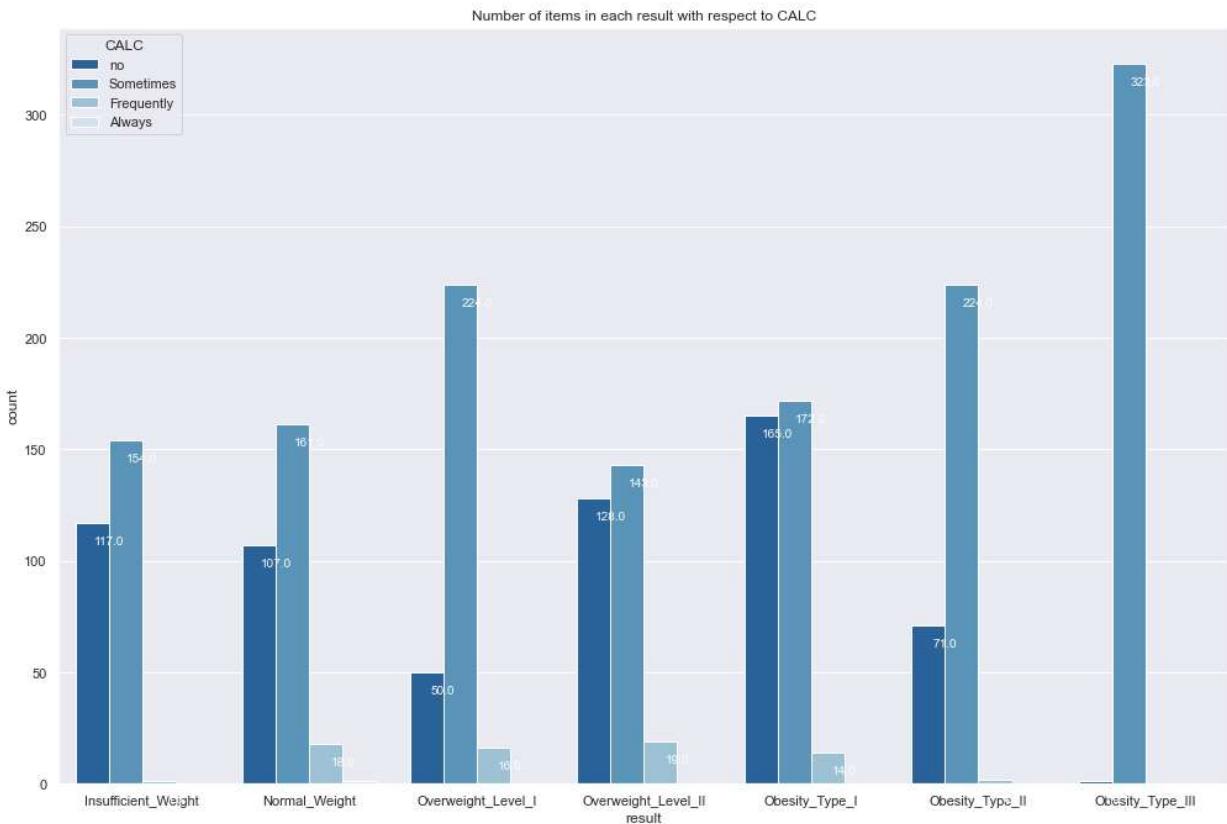
## Alcohol Consumption

```
In [40]: count_values(df, "CALC", ["no", "Sometimes", "Frequently", "Always"])
```



- Most of the people who took part in survey either did not consume alcohol or consumed sometimes.

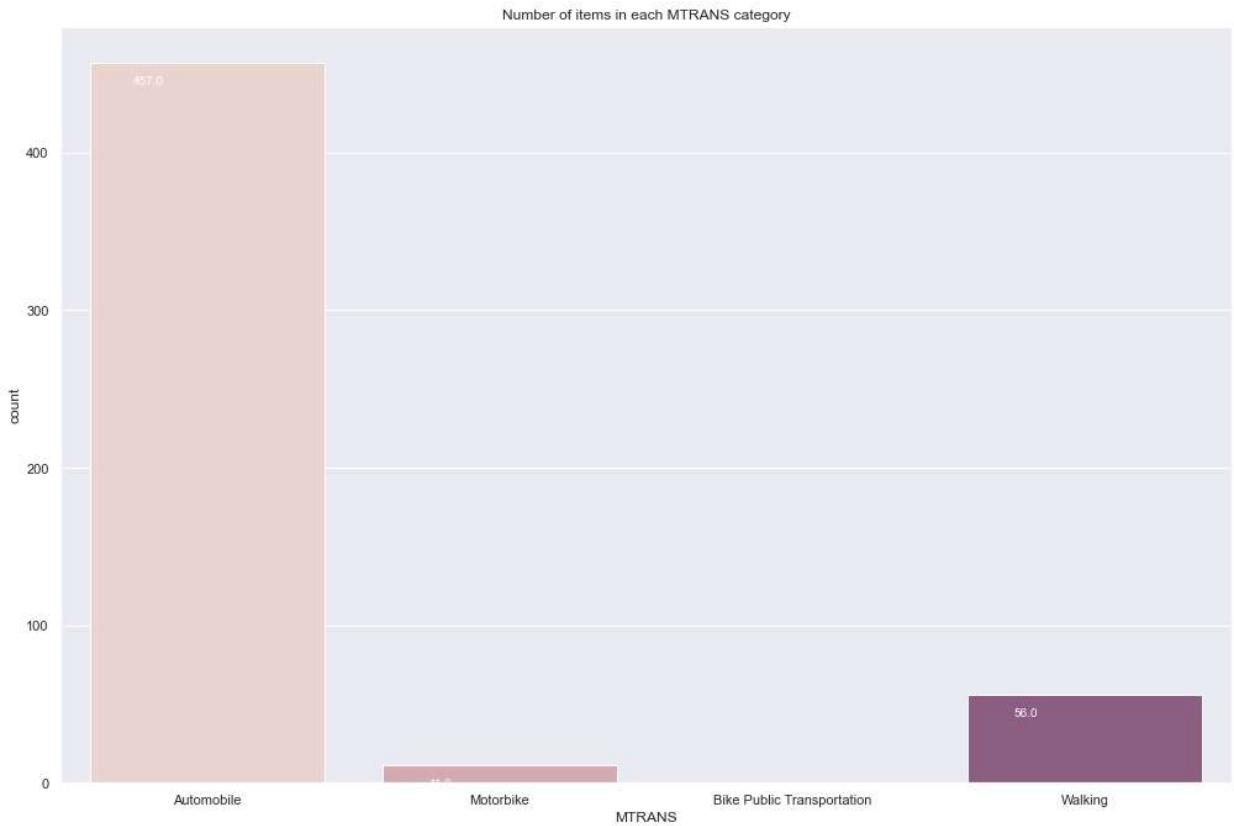
```
In [41]: cross_plot(df, "result", "CALC", weight_order, hue_order= ["no", "Sometimes", "Frequen
```



- Most of the people who consumed alcohol "sometimes" are suffering from obesity , specially from obesity type 3

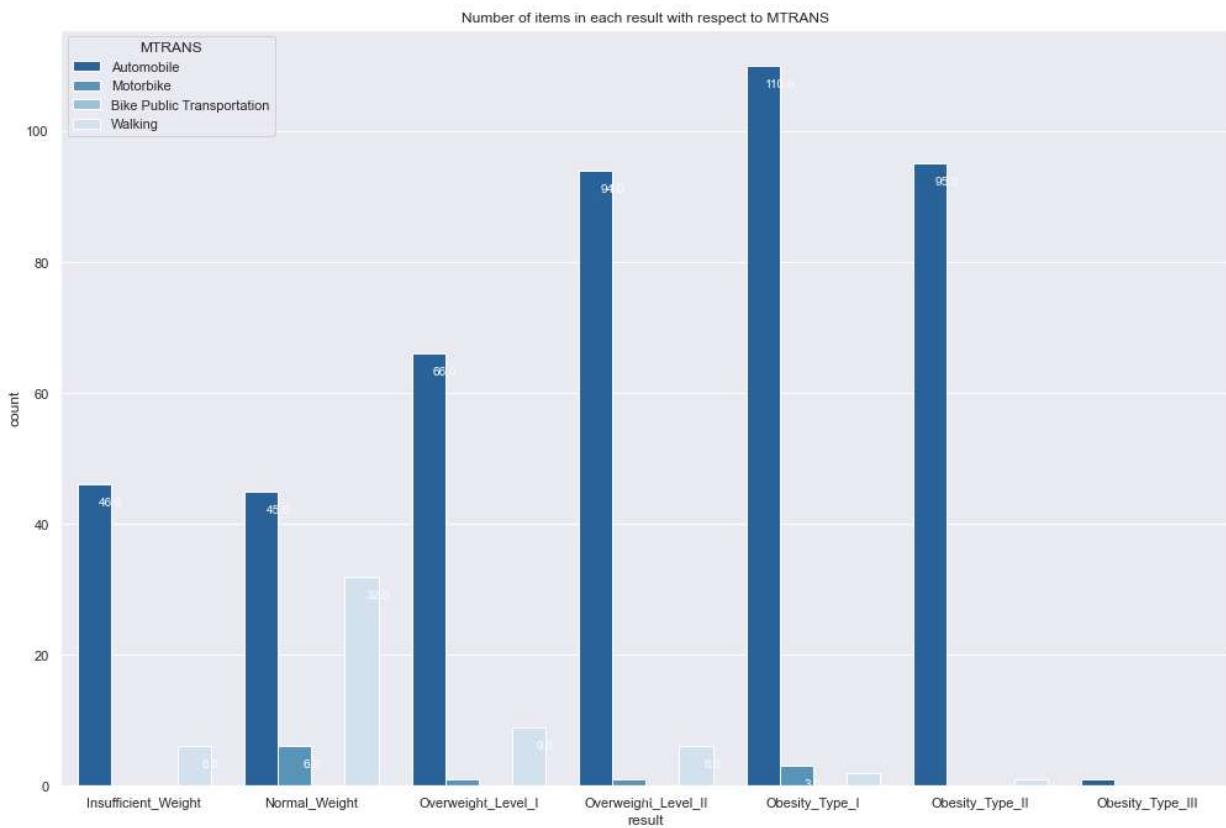
## Transportation

```
In [42]: count_values(df, "MTRANS", ["Automobile","Motorbike","Bike Public Transportation","Wa]
```



- Most of the people who took part in the survey used automobile

```
In [43]: cross_plot(df, "result", "MTRANS", weight_order,[ "Automobile","Motorbike","Bike Public
```



- Majority of the people who prefer walking belong to insufficient to overweight category i.e. people who walk to commute from one place to another are not suffering from obesity

## Correlation

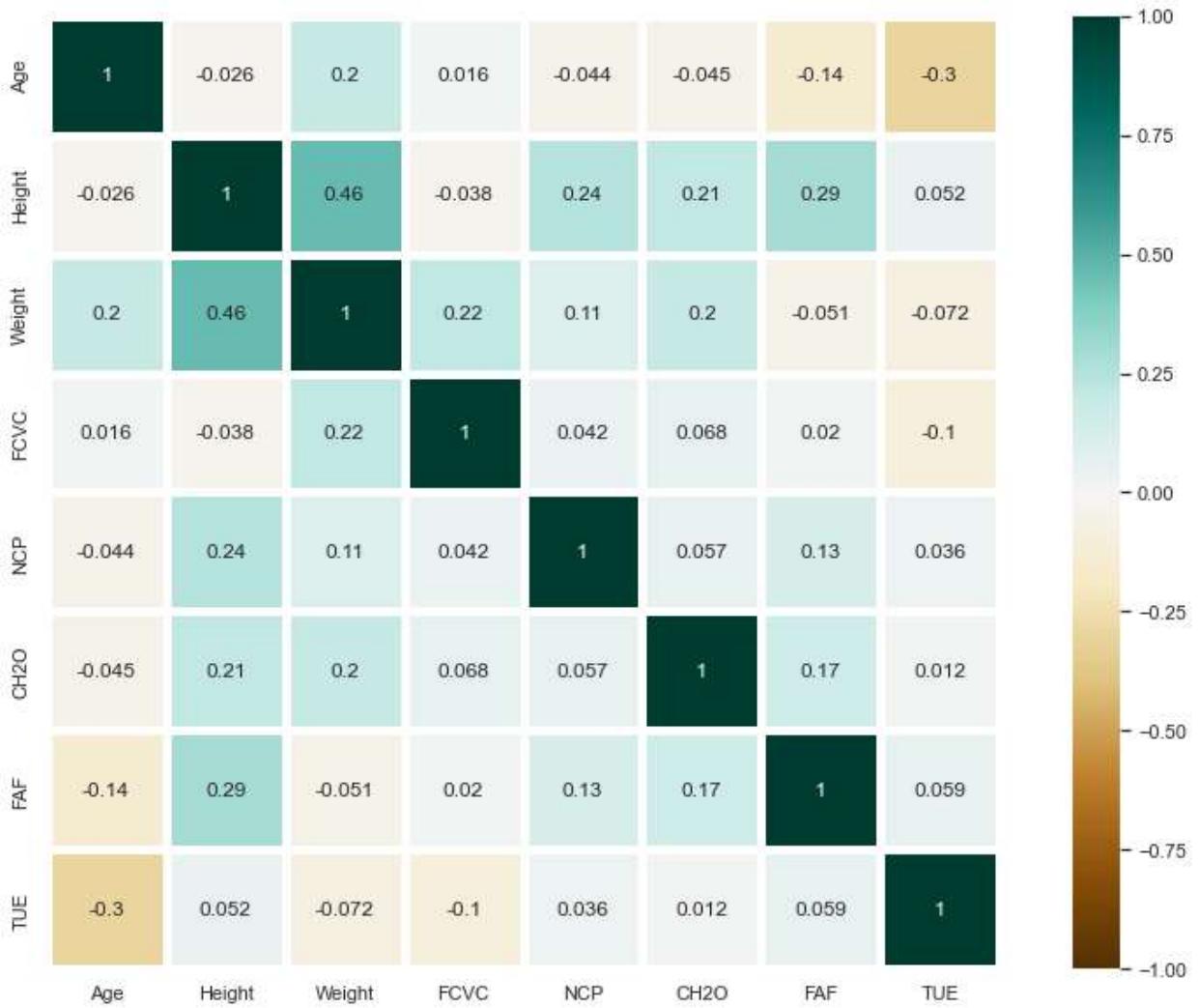
Correlation is a statistical measure that expresses the extent to which two variables are linearly related (meaning they change together at a constant rate). It's a common tool for describing simple relationships without making a statement about cause and effect. We can determine that there are two types of correlation :

- Positive correlation** : In positive correlation , if one variable increases then the other variable increases and same if one variable decreases then the other variable decreases. The slope of the fitting line in such a case would be positive.
- Negative correlation** : In negative correlation , the inverse relationship is there between the correlated variables , that is if one variable increases/decreases then the other variable decreases/increases.

Here we are using the **heatmap function** of the **seaborn library** to obtain the correlation between attributes of the dataset.

```
In [44]: plt.figure(figsize = (15, 10))
sns.heatmap(df.corr(), annot=True, square=True, center=0, vmin=-1, vmax=1,
            cmap='BrBG', linewidths=5)
```

```
Out[44]: <AxesSubplot:>
```

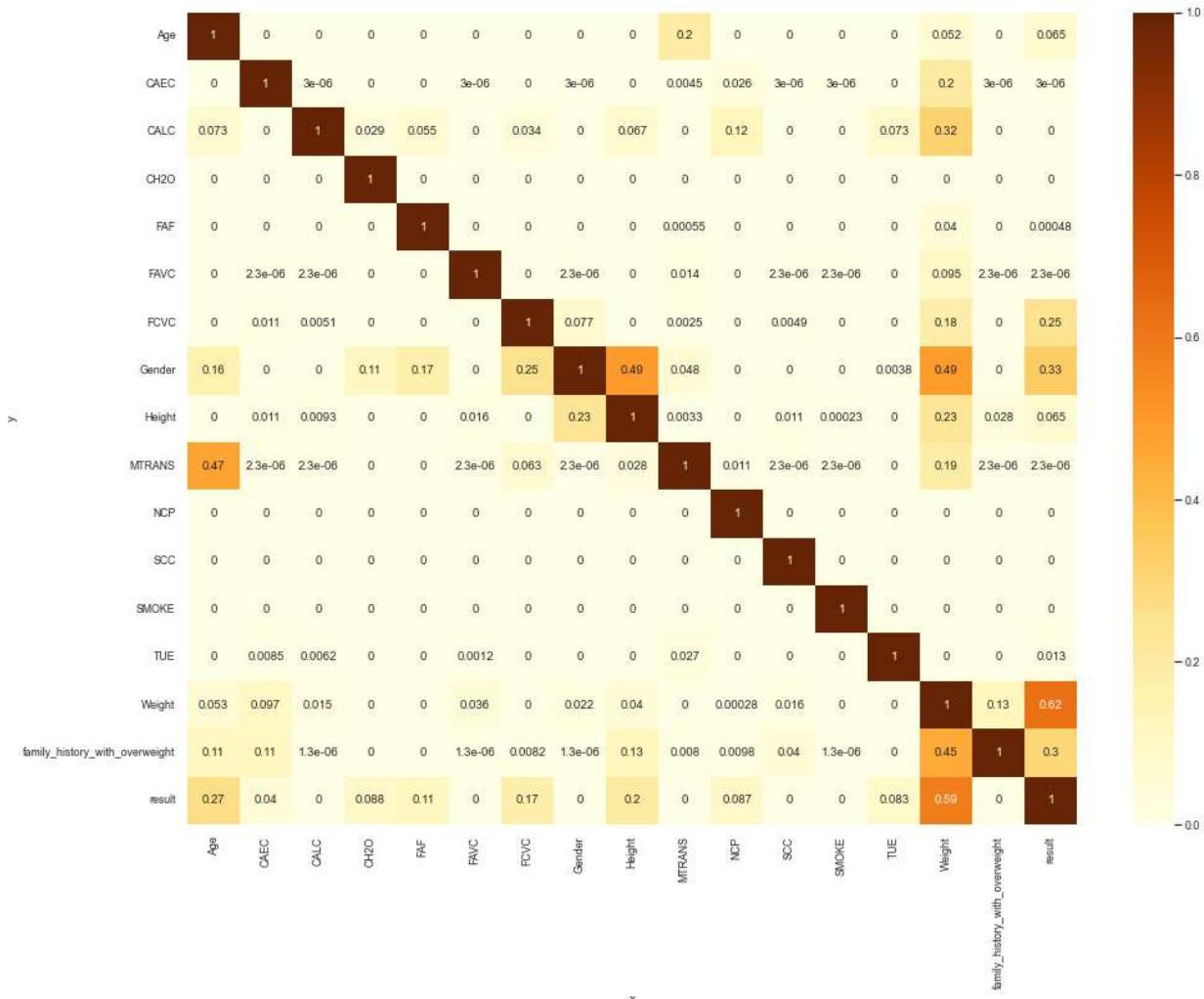


The PPS is an asymmetric, data-type-agnostic score that can detect linear or non-linear relationships between two columns. The score ranges from 0 (no predictive power) to 1 (perfect predictive power). It can be used as an alternative to the correlation (matrix).

```
In [45]: import ppscore as pps
import warnings
warnings.filterwarnings("ignore")

matrix_df = pps.matrix(df).pivot(columns='x', index='y', values='ppscore')

sns.set(font_scale=0.8)
plt.figure(figsize=(16,12))
sns.heatmap(matrix_df, annot=True, cmap = sns.color_palette("YlOrBr", as_cmap=True))
plt.show()
```



## Inferences about the dataset

- The dataset contains integer and float values, it also contains text objects.
- The data did not require any cleaning as there were no null or missing values.
- The dataset had all type of people in the survey from insufficient weight to obesity type 3 and every type had almost an equal no. of people except obesity type 1 which had more people with respect to other categories.
- There were almost equal no. of people of both genders and women are more likely to have insufficient weight whereas men suffer from obesity.
- People with family history of obesity were either overweight or obese.
- Majority of the people in the survey were non-smokers hence little inference about smokers were made.
- Most of the people do no record their daily calories intake.
- The correlation matrix which is only applicable on numerical data showed that height and weight are highly correlated.
- We can calculate PPS for both numerical and categorical variable and it not only shows linear relation but also quadratic or logarithmic.
- The PPS matrix shows that following attributes are highly dependant on each other:-
  - weight and result

- weight and family\_history\_with\_overweight
- age and mode of transport
- gender and height
- gender and weight
- gender and result

## Data Preprocessing

Pre-processing refers to the transformations applied to our data before feeding it to the algorithm. Data Preprocessing is a technique that is used to convert the raw data into a clean data set.

### Need of Data Preprocessing:-

- For achieving better results from the applied model in Machine Learning projects the format of the data has to be in a proper manner. Some specified Machine Learning model needs information in a specified format, for example, Random Forest algorithm does not support null values, therefore to execute random forest algorithm null values have to be managed from the original raw data set, as we already checked earlier our dataset does not have any null value.
- Data is limited so model will need to perform well with limited amount of data
- Model will need to handle dummy variables well and not be dependent on ratio data
- The ordinal variables may or may not be helpful to the model
- The data is pretty wide but not very deep, so reducing the factors may be necessary.

### Making a new dataframe

```
In [46]: df_prep = df.copy()
ord_feature_list= ["Gender", "family_history_with_overweight",
                   "FAVC", "CAEC", "SMOKE", "SCC", "CALC", "MTRANS"]
```

### Encode Labels

- Encode categorical features as an integer array.
- The input to this transformer should be an array-like of integers or strings, denoting the values taken on by categorical (discrete) features. The features are converted to ordinal integers. This results in a single column of integers (0 to n\_categories - 1) per feature.

```
In [47]: #encoding
from sklearn.preprocessing import OrdinalEncoder
df_ord=df_prep[ord_feature_list]

enc = OrdinalEncoder()
enc.fit(df_ord)
df_ord_arr=enc.transform(df_ord)
```

```
encoded_cat_df=pd.DataFrame(df_ord_arr, columns=ord_feature_list)
encoded_cat_df
```

Out[47]:

	Gender	family_history_with_overweight	FAVC	CAEC	SMOKE	SCC	CALC	MTRANS	result	
0	0.0		1.0	0.0	2.0	0.0	0.0	3.0	3.0	1.0
1	0.0		1.0	0.0	2.0	1.0	1.0	2.0	3.0	1.0
2	1.0		1.0	0.0	2.0	0.0	0.0	1.0	3.0	1.0
3	1.0		0.0	0.0	2.0	0.0	0.0	1.0	4.0	5.0
4	1.0		0.0	0.0	2.0	0.0	0.0	2.0	3.0	6.0
...	...		...	...	...	...	...	...	...	
2106	0.0		1.0	1.0	2.0	0.0	0.0	2.0	3.0	4.0
2107	0.0		1.0	1.0	2.0	0.0	0.0	2.0	3.0	4.0
2108	0.0		1.0	1.0	2.0	0.0	0.0	2.0	3.0	4.0
2109	0.0		1.0	1.0	2.0	0.0	0.0	2.0	3.0	4.0
2110	0.0		1.0	1.0	2.0	0.0	0.0	2.0	3.0	4.0

2111 rows × 9 columns

## Changes

- **Gender column** - Female is represented by 0 and male is represented by 1.
- **family\_history\_with\_overweight** - yes is represented by 1 and no is represented by 0.
- Other categorical variables are changed in a similar fashion.

```
In [48]: train_df_final = pd.concat( [df[df.columns.difference(ord_feature_list)] , encoded_cat
```

## Train - Test split

- Split arrays or matrices into random train and test subsets.
- **Why we are doing this** : We are splitting the dataset into train and test so that we can pass them through different ML algorithms which we will proceed for in the further sections. The **training dataset** is given to the algorithm and on the basis of the training dataset , prediction of the **test dataset** takes place.

In [49]:

```
# split df to X and Y
from sklearn.model_selection import train_test_split

y = train_df_final.loc[:, 'result'].values
X = train_df_final.drop('result', axis=1)

# split data into 80-20 for training set / test set
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, stratify = X_train.shape, X_test.shape, y_train.shape, y_test.shape)
```

```
Out[49]: ((1688, 16), (423, 16), (1688,), (423,))
```

We have 1688 rows out of 2111 rows as training dataset and 423 rows as test dataset.

## Normalize Data

- Data normalization is the systematic process of grouping similar values into one common value, bringing greater context and accuracy to your marketing database. Basically, data normalization formats your data to look and read the same across all records in a database. Here all the values will be between 0 and 1.
- **Why are we doing this-** Normalization is a good technique to use when you do not know the distribution of your data or when you know the distribution is not Gaussian (a bell curve). Normalization is useful when your data has varying scales and the algorithm you are using does not make assumptions about the distribution of your data, such as k-nearest neighbors and artificial neural networks.

```
In [50]: #normalization(make all values bet. 0-1)
```

```
from sklearn.preprocessing import MinMaxScaler
scaler = MinMaxScaler()
scaler.fit(X_train)

X_train_normalized_arr=scaler.transform(X_train)
X_train_normalized_df=pd.DataFrame(X_train_normalized_arr, columns=X_train.columns.to_list())

X_test_normalized_arr=scaler.transform(X_test)
X_test_normalized_df=pd.DataFrame(X_test_normalized_arr, columns=X_test.columns.to_list())
```

```
In [51]: X_train_normalized_df
```

Out[51]:

	Age	CH2O	FAF	FCVC	Height	NCP	TUE	Weight	Gender	family_h
0	0.245550	0.206025	0.047985	1.000000	0.412658	0.666667	0.376538	0.539261	0.0	
1	0.191489	0.500000	0.333333	1.000000	0.377358	0.000000	1.000000	0.164021	0.0	
2	0.533806	0.502597	0.108438	0.851228	0.566038	0.666667	0.209528	0.656324	1.0	
3	0.159611	0.675604	0.082277	1.000000	0.679002	0.666667	0.456680	0.929958	0.0	
4	0.190119	0.501785	0.419850	1.000000	0.532655	0.666667	0.208558	0.129869	0.0	
...	...	...	...	...	...	...	...	...	...	...
1683	0.234043	0.500000	0.666667	0.500000	0.226415	0.000000	0.000000	0.131217	0.0	
1684	0.207358	0.500000	0.543971	0.268752	0.578815	0.666667	0.315711	0.642361	1.0	
1685	0.094117	0.693195	0.514877	1.000000	0.538606	0.666667	0.450033	0.720039	0.0	
1686	0.170139	0.328041	0.142590	1.000000	0.534458	0.921842	0.277983	0.097514	0.0	
1687	0.148936	1.000000	0.333333	0.500000	0.320755	0.000000	0.000000	0.254233	1.0	

1688 rows × 16 columns

--	--

In [52]: X\_test\_normalized\_df

Out[52]:

	Age	CH2O	FAF	FCVC	Height	NCP	TUE	Weight	Gender	family_h
0	0.187546	0.500000	0.030781	0.500000	0.502432	0.666667	0.733248	0.300884	1.0	
1	0.122464	0.256018	0.101241	0.814396	0.174204	0.587628	0.001615	0.203847	0.0	
2	0.253601	0.011664	0.016977	1.000000	0.304645	0.666667	0.500000	0.517432	0.0	
3	0.136989	0.693995	0.283572	1.000000	0.671326	0.666667	0.328246	0.936148	0.0	
4	0.425532	1.000000	0.666667	0.500000	0.452830	0.666667	0.000000	0.369048	1.0	
...	...	...	...	...	...	...	...	...	...	...
418	0.085106	0.500000	1.000000	0.500000	0.660377	0.666667	0.000000	0.270635	1.0	
419	0.172086	0.548375	0.181521	0.674373	0.666287	0.666667	0.338440	0.552174	1.0	
420	0.124806	0.791082	0.666667	0.560093	0.585528	1.000000	0.755305	0.134257	1.0	
421	0.085106	0.500000	0.666667	0.000000	0.339623	0.666667	1.000000	0.196826	0.0	
422	0.127660	0.500000	0.333333	0.000000	0.603774	0.000000	0.500000	0.254233	1.0	

423 rows × 16 columns

--	--

Both the training dataset and test dataset have now values of all attributes between 0 and 1.

We are importing necessary libraries from **sklearn** which will help us in various classification which we are going to perform ahead.

```
In [53]: #import necessary libraries
from sklearn.model_selection import StratifiedShuffleSplit
from sklearn.model_selection import GridSearchCV
from sklearn.tree import DecisionTreeClassifier, plot_tree
from sklearn.metrics import accuracy_score, roc_curve, confusion_matrix, classification_report
from sklearn.naive_bayes import GaussianNB, MultinomialNB, ComplementNB, CategoricalNB
from sklearn.svm import LinearSVC, SVC
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
import scikitplot as skplt
```

## Cross-validation (k-fold)

- Randomly partition the data into k mutually exclusive subsets, each approximately equal size
- At i-th iteration, use Di as test set and others as training set.

```
In [54]: # cross-validation with 10 splits
cv = StratifiedShuffleSplit(n_splits=10, random_state = 42, test_size=0.2)
```

The function below will display test scores and return result string and indexes of false samples.

```
In [55]: def display_test_scores(test, pred, prob):
    print("\n\n    TEST SCORES\n")
    print("=====-----\n")

    #print accuracy
    accuracy = accuracy_score(test, pred)
    print("ACCURACY: {:.4f}\n".format(accuracy))
    print("\n")
    print("-----\n")

    #print confusion matrix
    print ("CONFUSION MATRIX:\n")
    conf_mat = confusion_matrix(test, pred)
    cm_df = pd.DataFrame(conf_mat)

    #draw cm

    sns.heatmap(cm_df, annot=True)
    plt.ylabel('Actual label')
    plt.xlabel('Predicted label')
    plt.show()
    print("\n")
    print("\n")
    print("-----\n")

    #print FP, FN
    print("FALSE POSITIVES:\n")
    fp = conf_mat[1][0]
    pos_labels = conf_mat[1][0]+conf_mat[1][1]
    print("{} out of {} positive labels {:.4f}%\n".format(fp, pos_labels, fp/pos_labels))
    print("\n")
    print("-----\n")
```

```

print("FALSE NEGATIVES:\n")
fn = conf_mat[0][1]
neg_labels = conf_mat[0][1]+conf_mat[0][0]
print("{} out of {} negative labels {:.4f}%\n".format(fn, neg_labels, fn/neg_labels))
print("\n")
print("-----\n")

#roc
roc = roc_auc_score(test, prob, multi_class="ovr", average="macro")
print("ROC-AUC score:{:.4f}%\n".format(roc))
print("\n")

skplt.metrics.plot_roc(pred, prob)
plt.show()

print("-----\n")

#print classification report
print("PRECISION, RECALL, F1 scores:\n\n")
print("{}\n".format(classification_report(test, pred)))

false_indexes = np.where(test != pred)
return false_indexes

```

# Machine Learning

## Classification

In [56]: X\_train= X\_train\_normalized\_df  
X\_test= X\_test\_normalized\_df

In [57]: # decesion tree  
# Naive bayes  
# SVM  
# KNN  
# Logistic Regression  
# Random Forest

### Decision Tree

Decision Tree is also the most commonly used approach that are used for supervised learning. One of the benefits of Decision Tree is that it can solve both regression and classification tasks.

- Root node:-It is starting/initial node of the tree. It represents the entire sample and it further gets split into child nodes(interior nodes)
- Interior nodes:-the interior nodes represents the features of the dataset and its branches represent the decision rules that need to be taken.
- Leaf Nodes:- It is used to represent the outcome of the regression classification model.

In [58]: #parameters  
param\_grid = {'criterion':['gini', 'entropy'],

```

        "class_weight": [None, "balanced"],
    }

#Decision Tree
grid_1 = GridSearchCV(DecisionTreeClassifier(random_state=0), param_grid, verbose=False)
grid_1.fit(X_train, y_train)

#print best scores
print("The best parameters are %s with a score of %0.4f"
      % (grid_1.best_params_, grid_1.best_score_))

#prediction results
y_pred = grid_1.predict(X_test)
y_prob = grid_1.predict_proba(X_test)
display_test_scores(y_test, y_pred, y_prob)

```

The best parameters are {'class\_weight': 'balanced', 'criterion': 'entropy'} with a score of 0.9470

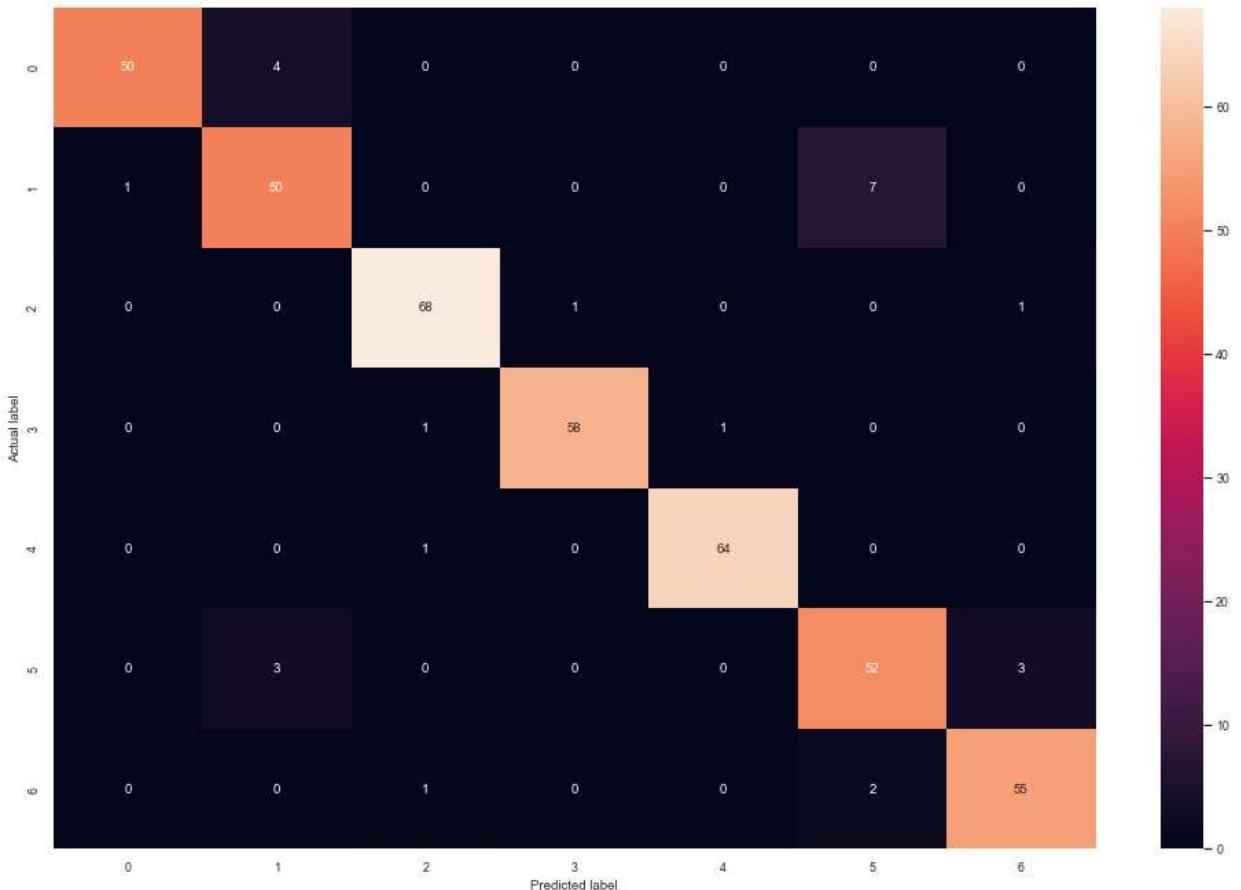
## TEST SCORES

=====

ACCURACY: 0.9385

-----

## CONFUSION MATRIX:



---

**FALSE POSITIVES:**

1 out of 51 positive labels (0.0196%)

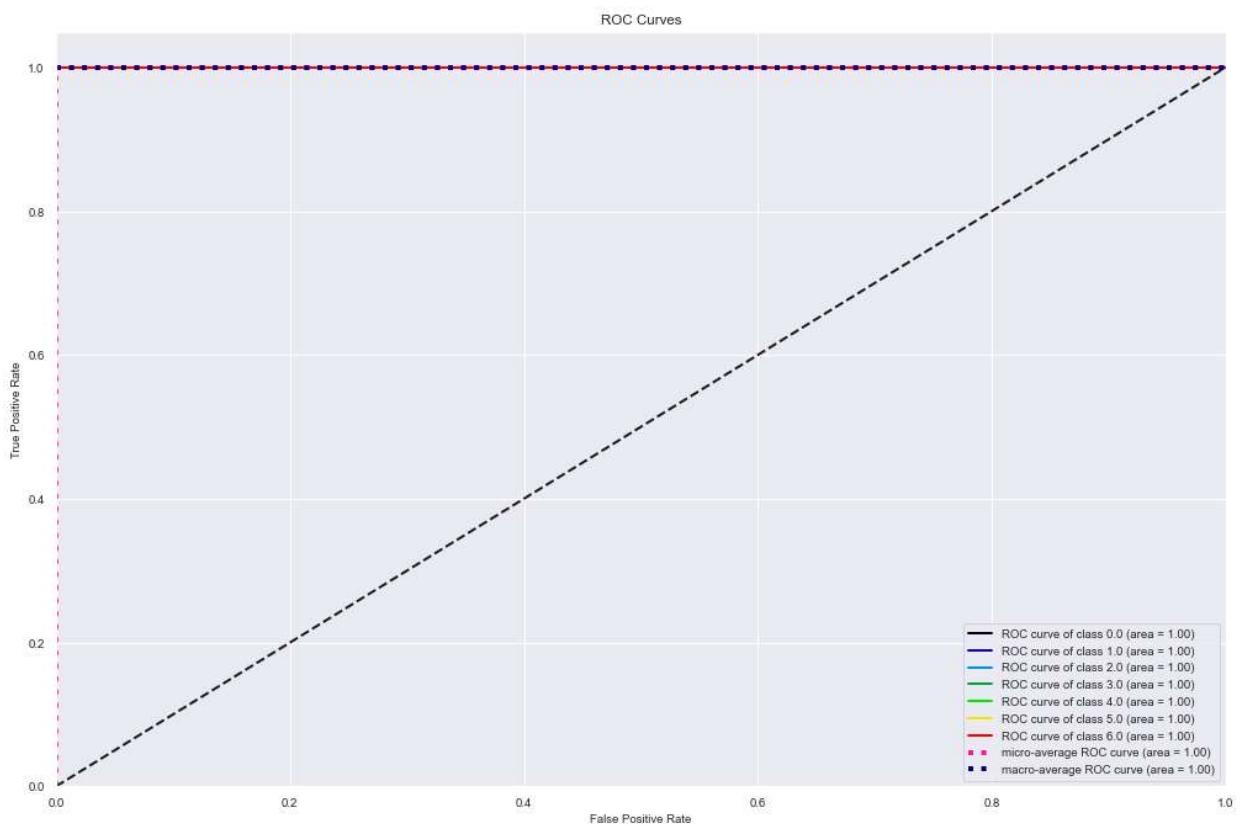
---

**FALSE NEGATIVES:**

4 out of 54 negative labels (0.0741%)

---

ROC-AUC score: (0.9631%)

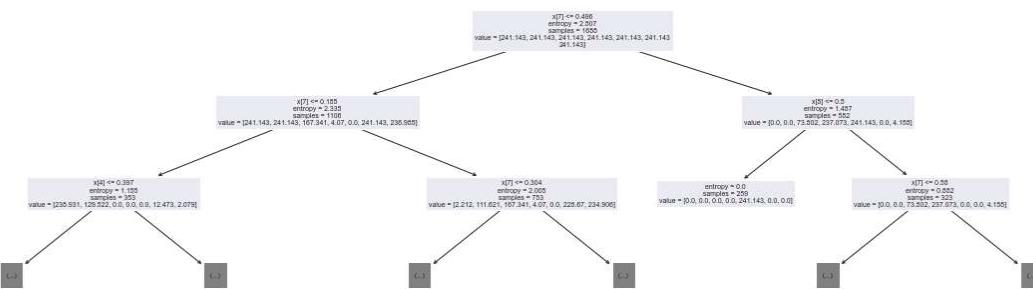


PRECISION, RECALL, F1 scores:

	precision	recall	f1-score	support
0.0	0.98	0.93	0.95	54
1.0	0.88	0.86	0.87	58
2.0	0.96	0.97	0.96	70
3.0	0.98	0.97	0.97	60
4.0	0.98	0.98	0.98	65
5.0	0.85	0.90	0.87	58
6.0	0.93	0.95	0.94	58
accuracy			0.94	423
macro avg	0.94	0.94	0.94	423
weighted avg	0.94	0.94	0.94	423

Out[58]: (array([ 20, 49, 58, 69, 84, 91, 123, 140, 150, 152, 214, 216, 260, 263, 264, 268, 279, 284, 289, 299, 306, 328, 362, 403, 405, 421], dtype=int64),)

```
In [59]: plt.figure(figsize = (22, 6))
plot_tree(grid_1.best_estimator_, max_depth= 2)
plt.show()
```



## Inference

- In decision tree we use entropy as a parameter to infer the best result here the entropy or information gain is the best suited value for calculating the prediction with accuracy.
- The attribute with the highest information gain will produce the best split as it's doing the best job at classifying the training data according to its target classification the attribute x[7] value as shown in the graph that is Weight is that attribute.

## Naive-Bayes

Naive Bayes classifiers are a collection of classification algorithms based on Bayes' Theorem. It is not a single algorithm but a family of algorithms where all of them share a common principle, i.e. every pair of features being classified is independent of each other.

- **Bayes Theorem**--Bayes Theorem finds the probability of an event occurring given the probability of another event that has already occurred.

- **Gaussian Naive Bayes**-In Gaussian Naive Bayes, continuous values associated with each feature are assumed to be distributed according to a Gaussian distribution.
- A Gaussian distribution is also called Normal distribution. When plotted, it gives a bell shaped curve which is symmetric about the mean of the feature values

```
In [60]: # Naive-Bayes with different approaches
nb_list = [ GaussianNB(), MultinomialNB(), ComplementNB()]

for nb in nb_list:
    print("\n\n-----", str(nb), "-----")

    # parameters
    parameters = {}

    # grid search for parameters
    grid_2 = GridSearchCV(estimator=nb, param_grid=parameters, cv=cv, n_jobs=-1)
    grid_2.fit(X_train, y_train)

    # print best scores
    print("The best parameters are {} with a score of {:.4f}\n"
          .format(grid_2.best_params_, grid_2.best_score_))

    # prediction results
    y_pred = grid_2.predict(X_test)
    y_prob = grid_2.predict_proba(X_test)

    # print accuracy metrics
    display_test_scores(y_test, y_pred, y_prob)
```

----- GaussianNB() -----  
 The best parameters are {} with a score of 0.5754

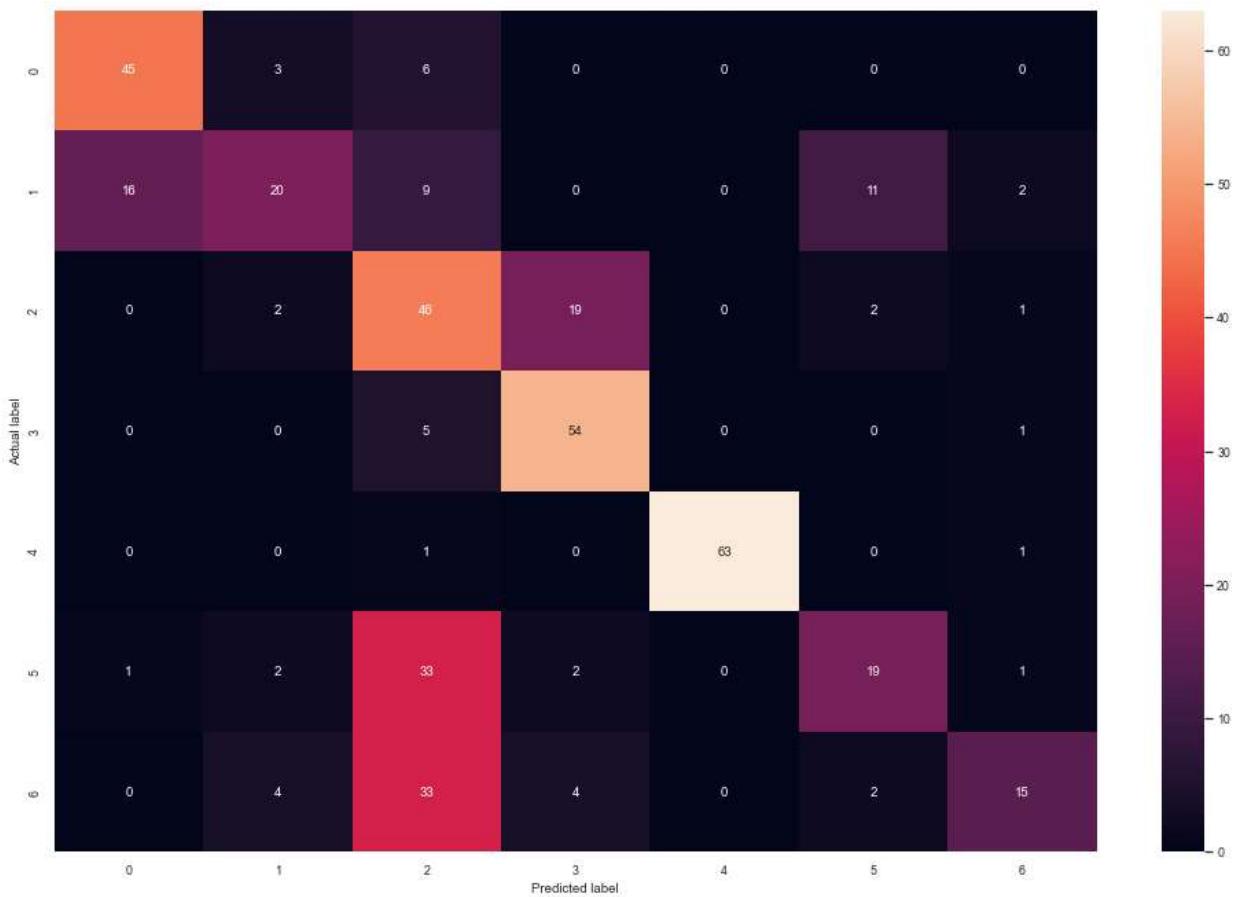
TEST SCORES

=====

ACCURACY: 0.6194

=====

CONFUSION MATRIX:




---

#### FALSE POSITIVES:

16 out of 36 positive labels (0.4444%)

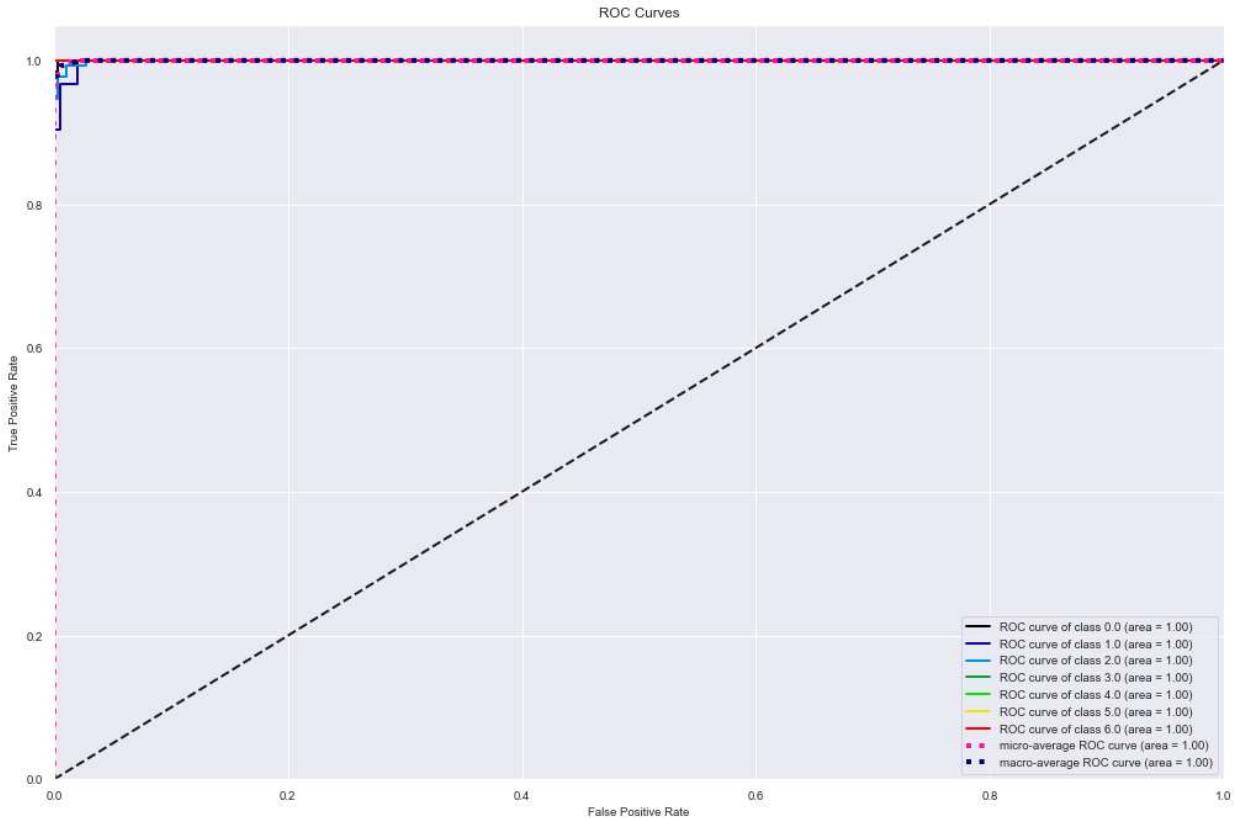
---

#### FALSE NEGATIVES:

3 out of 48 negative labels (0.0625%)

---

ROC-AUC score: (0.9236%)



-----  
PRECISION, RECALL, F1 scores:

	precision	recall	f1-score	support
0.0	0.73	0.83	0.78	54
1.0	0.65	0.34	0.45	58
2.0	0.35	0.66	0.45	70
3.0	0.68	0.90	0.78	60
4.0	1.00	0.97	0.98	65
5.0	0.56	0.33	0.41	58
6.0	0.71	0.26	0.38	58
accuracy			0.62	423
macro avg	0.67	0.61	0.60	423
weighted avg	0.66	0.62	0.61	423

----- MultinomialNB() -----

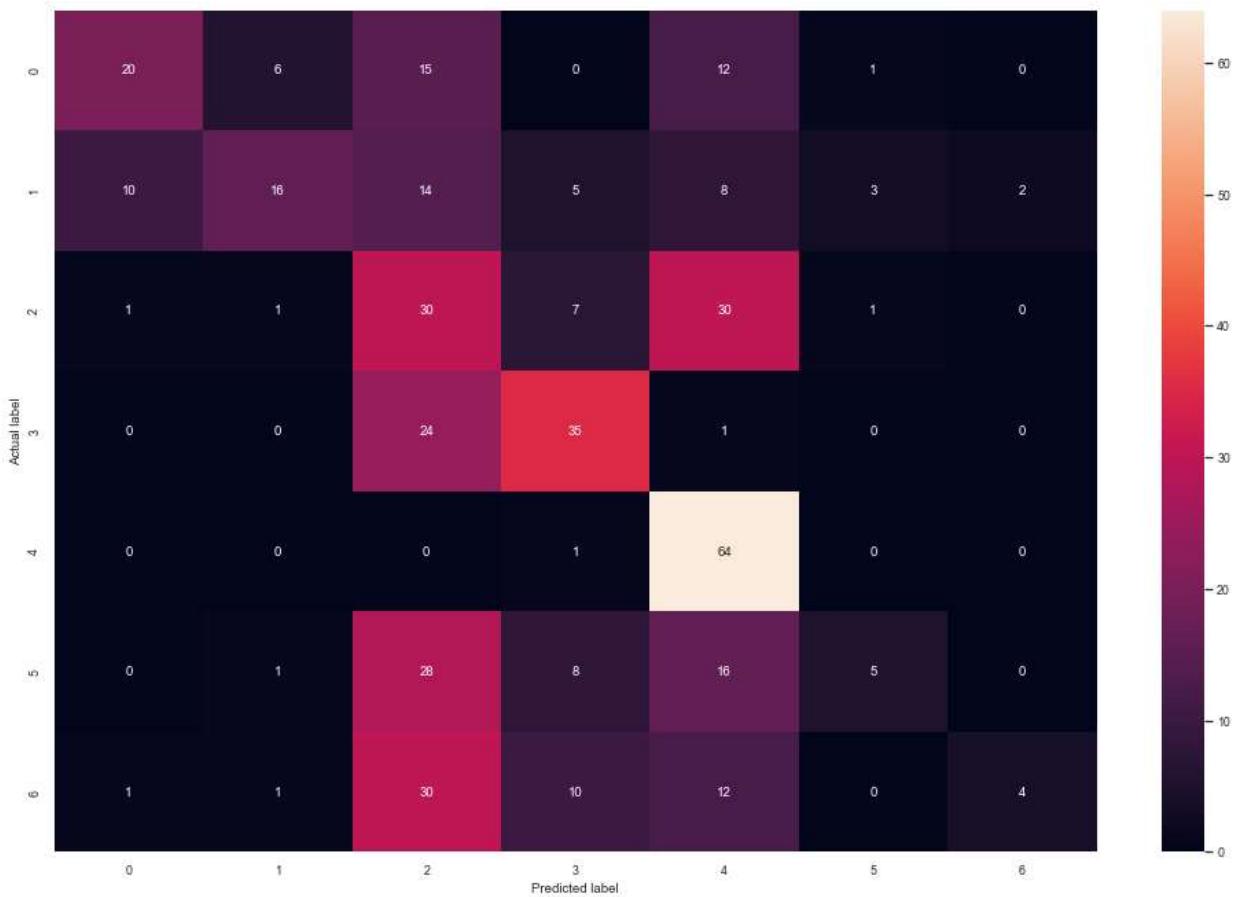
The best parameters are {} with a score of 0.4071

TEST SCORES

=====

ACCURACY: 0.4113

-----  
CONFUSION MATRIX:



---

**FALSE POSITIVES:**

10 out of 26 positive labels (0.3846%)

---

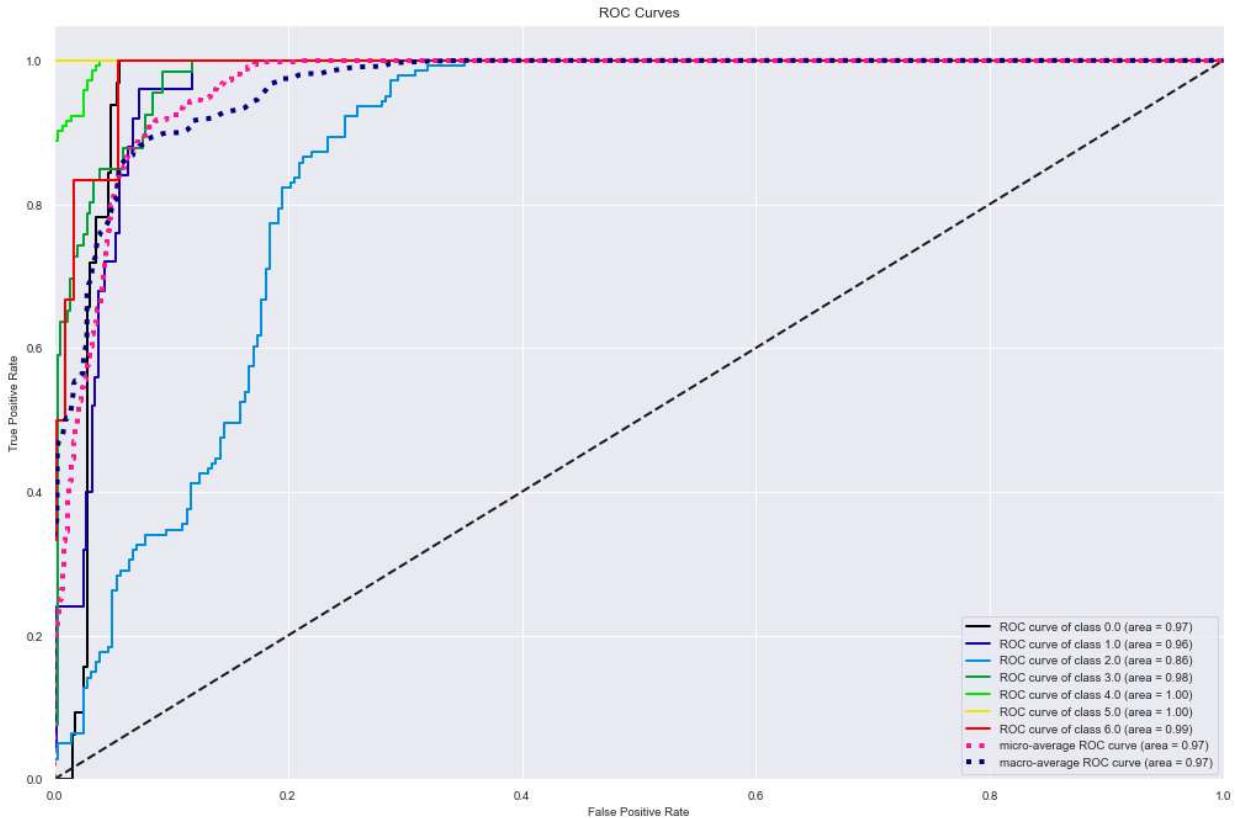
---

**FALSE NEGATIVES:**

6 out of 26 negative labels (0.2308%)

---

ROC-AUC score: (0.8253%)



---

PRECISION, RECALL, F1 scores:

	precision	recall	f1-score	support
0.0	0.62	0.37	0.47	54
1.0	0.64	0.28	0.39	58
2.0	0.21	0.43	0.28	70
3.0	0.53	0.58	0.56	60
4.0	0.45	0.98	0.62	65
5.0	0.50	0.09	0.15	58
6.0	0.67	0.07	0.12	58
accuracy			0.41	423
macro avg	0.52	0.40	0.37	423
weighted avg	0.51	0.41	0.37	423

---

----- ComplementNB() -----

The best parameters are {} with a score of 0.3899

TEST SCORES

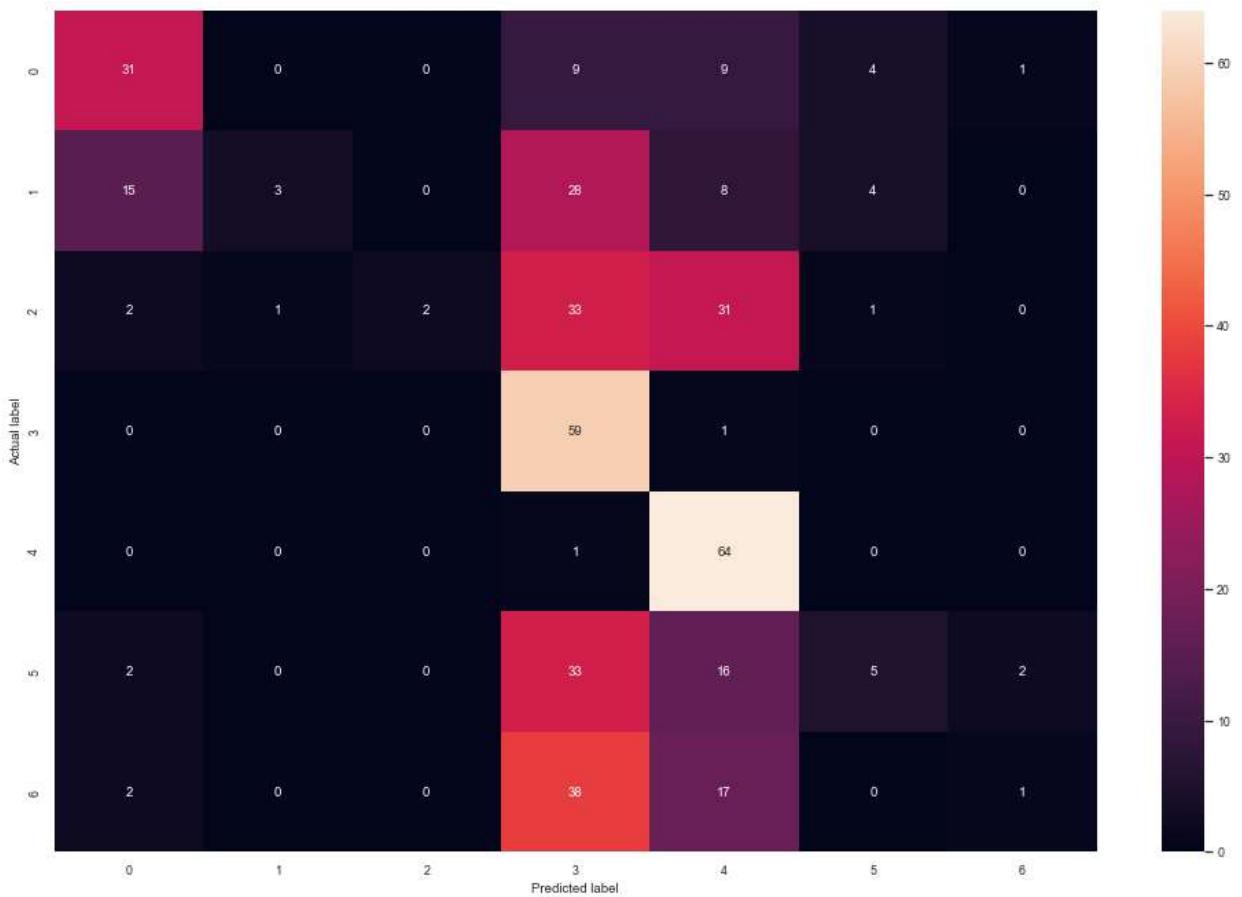
---

ACCURACY: 0.3901

---

---

CONFUSION MATRIX:




---

#### FALSE POSITIVES:

15 out of 18 positive labels (0.8333%)

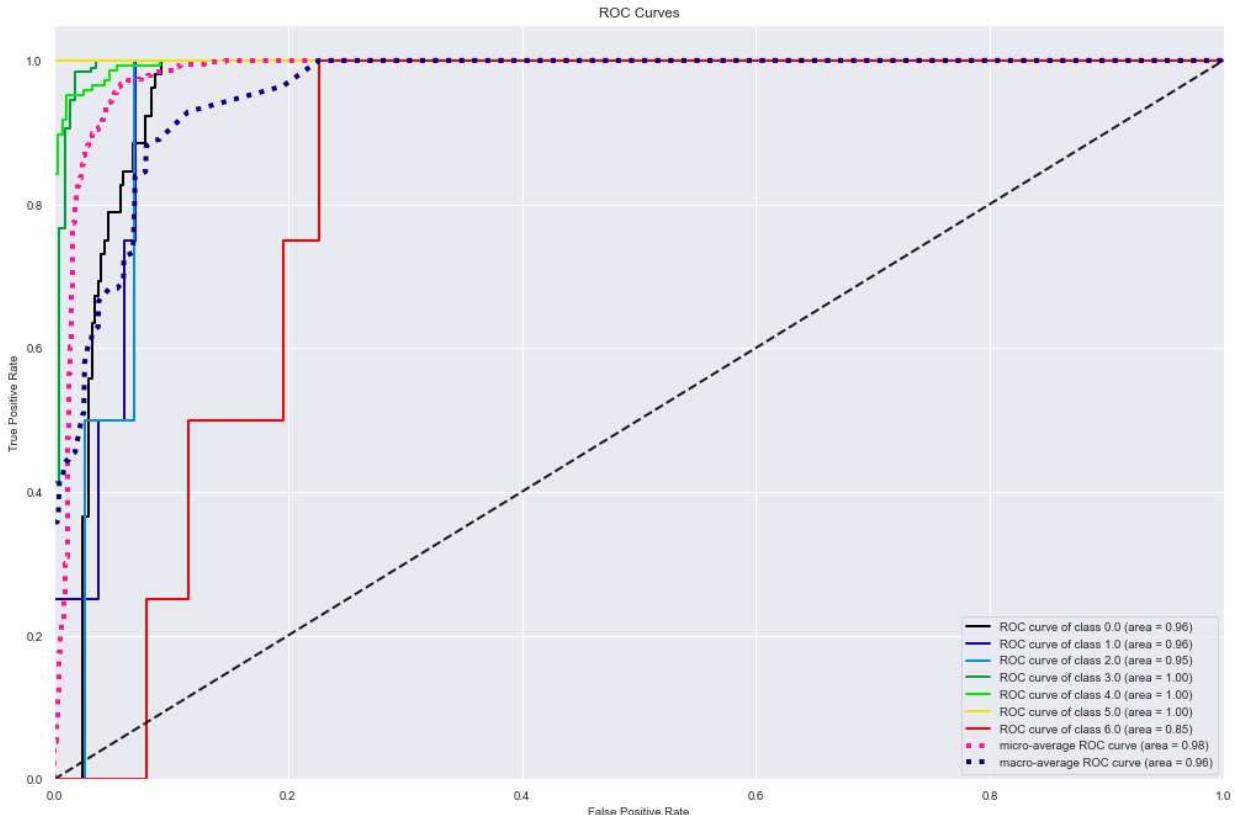
---

#### FALSE NEGATIVES:

0 out of 31 negative labels (0.0000%)

---

ROC-AUC score: (0.8287%)



PRECISION, RECALL, F1 scores:

	precision	recall	f1-score	support
0.0	0.60	0.57	0.58	54
1.0	0.75	0.05	0.10	58
2.0	1.00	0.03	0.06	70
3.0	0.29	0.98	0.45	60
4.0	0.44	0.98	0.61	65
5.0	0.36	0.09	0.14	58
6.0	0.25	0.02	0.03	58
accuracy			0.39	423
macro avg	0.53	0.39	0.28	423
weighted avg	0.54	0.39	0.28	423

## Inference

- Using the dataset we have calculated Gaussian, Multinomial are complemented and it can be clearly seen that the best accuracy was given by gaussian naive bayes.
- Biggest disadvantage is that the requirement of predictors to be independent, but here the contrary example is Weight. This is the reason for low score.

## Support Vector Machine

Support Vector Machine(SVM) is a supervised machine learning algorithm used for both classification and regression. Though we say regression problems as well its best suited for

classification. The objective of SVM algorithm is to find a hyperplane in an N-dimensional space that distinctly classifies the data points. The dimension of the hyperplane depends upon the number of features. If the number of input features is two, then the hyperplane is just a line. If the number of input features is three, then the hyperplane becomes a 2-D plane. It becomes difficult to imagine when the number of features exceeds three. The best hyperplane is the one that represents the largest separation or margin between the two classes. So we choose the hyperplane whose distance from it to the nearest data point on each side is maximized.

```
In [61]: # SVM classifier
svm = SVC(tol=1e-5, random_state=0, probability=True)

# parameters
parameters = {
    'kernel': ['linear', 'poly', 'rbf', 'sigmoid'],
    'C': [0.01, 0.1, 1, 10, 100],
}

# grid search for parameters
grid_3 = GridSearchCV(estimator=svm, param_grid=parameters, cv=cv, n_jobs=-1)
grid_3.fit(X_train, y_train)

# print best scores
print("The best parameters are %s with a score of %0.4f\n"
      % (grid_3.best_params_, grid_3.best_score_))

# prediction results
y_pred = grid_3.predict(X_test)
y_prob = grid_3.predict_proba(X_test)

# print accuracy metrics
display_test_scores(y_test, y_pred, y_prob)
```

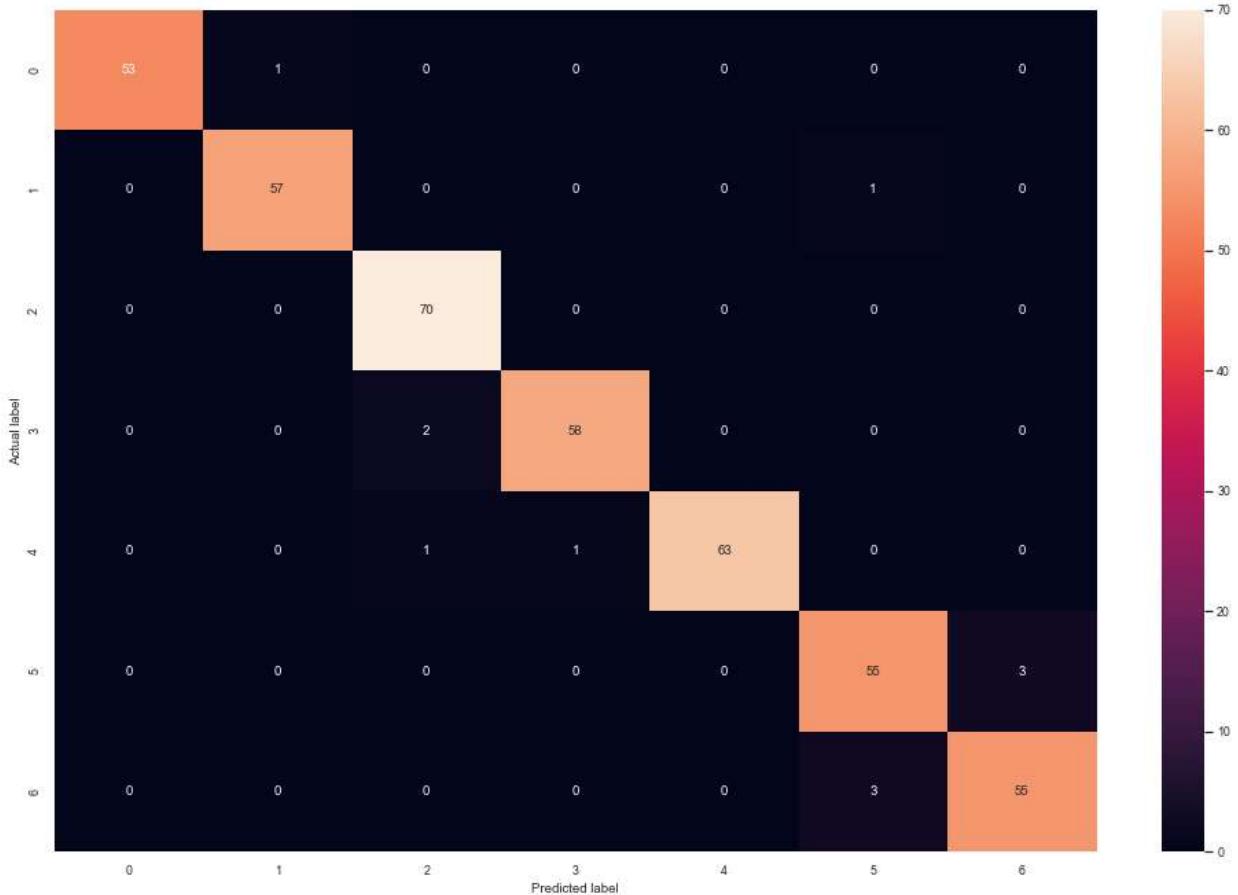
The best parameters are {'C': 100, 'kernel': 'linear'} with a score of 0.9583

TEST SCORES

=====

ACCURACY: 0.9716

CONFUSION MATRIX:



---

**FALSE POSITIVES:**

0 out of 57 positive labels (0.0000%)

---

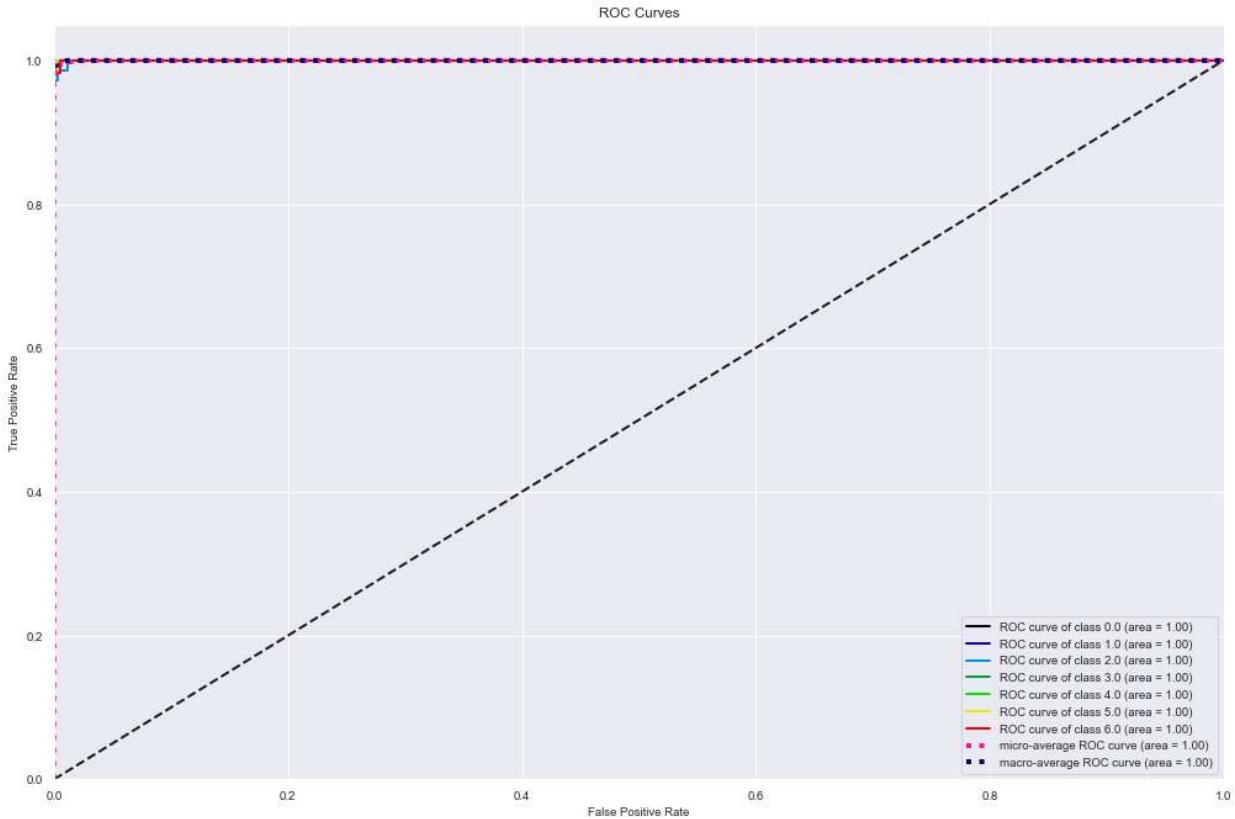
---

**FALSE NEGATIVES:**

1 out of 54 negative labels (0.0185%)

---

ROC-AUC score: (0.9981%)



PRECISION, RECALL, F1 scores:

	precision	recall	f1-score	support
0.0	1.00	0.98	0.99	54
1.0	0.98	0.98	0.98	58
2.0	0.96	1.00	0.98	70
3.0	0.98	0.97	0.97	60
4.0	1.00	0.97	0.98	65
5.0	0.93	0.95	0.94	58
6.0	0.95	0.95	0.95	58
accuracy			0.97	423
macro avg	0.97	0.97	0.97	423
weighted avg	0.97	0.97	0.97	423

```
Out[61]: (array([ 21,  59,  69,  84, 123, 144, 309, 320, 328, 337, 364, 403],  
           dtype=int64),)
```

## K-Nearest Neighbours

The k-nearest neighbours classifier (KNN) is a non-parametric supervised machine learning algorithm. It's distance-based: it classifies objects based on their proximate neighbors' classes.

The k-nearest neighbours algorithm is also non-linear. In contrast to simpler models like linear regression, it will work well with data in which the relationship between the independent variable (x) and the dependent variable (y) is not a straight line.

```
In [62]: knn = KNeighborsClassifier()  
# parameters
```

```
parameters = {
    "algorithm": ["auto", "ball_tree", "kd_tree", "brute"],
    "n_neighbors": list(range(0, 25)),
    "metric": ['euclidean', 'manhattan', 'chebyshev'],
    "p": [1,2],
}

# grid search for parameters
grid_4 = GridSearchCV(estimator=knn, param_grid=parameters, cv=cv, n_jobs=-1)
grid_4.fit(X_train, y_train)

# print best scores
print("The best parameters are %s with a score of %0.4f\n"
      % (grid_4.best_params_, grid_4.best_score_))

# prediction results
y_pred = grid_4.predict(X_test)
y_prob = grid_4.predict_proba(X_test)

# print accuracy metrics
display_test_scores(y_test, y_pred, y_prob)
```

The best parameters are {'algorithm': 'auto', 'metric': 'manhattan', 'n\_neighbors': 3, 'p': 1} with a score of 0.8420

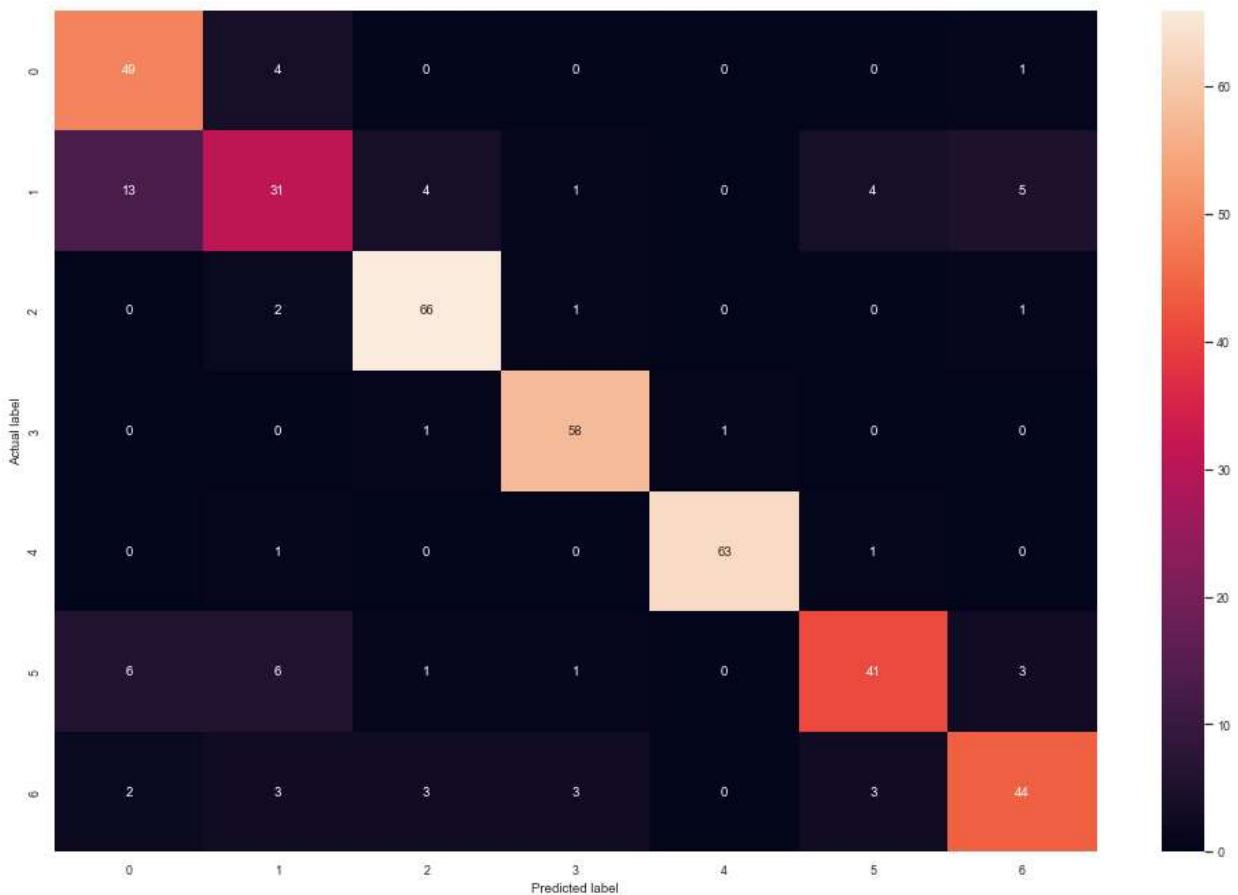
## TEST SCORES

---

ACCURACY: 0.8322

---

CONFUSION MATRIX:



---

**FALSE POSITIVES:**

13 out of 44 positive labels (0.2955%)

---

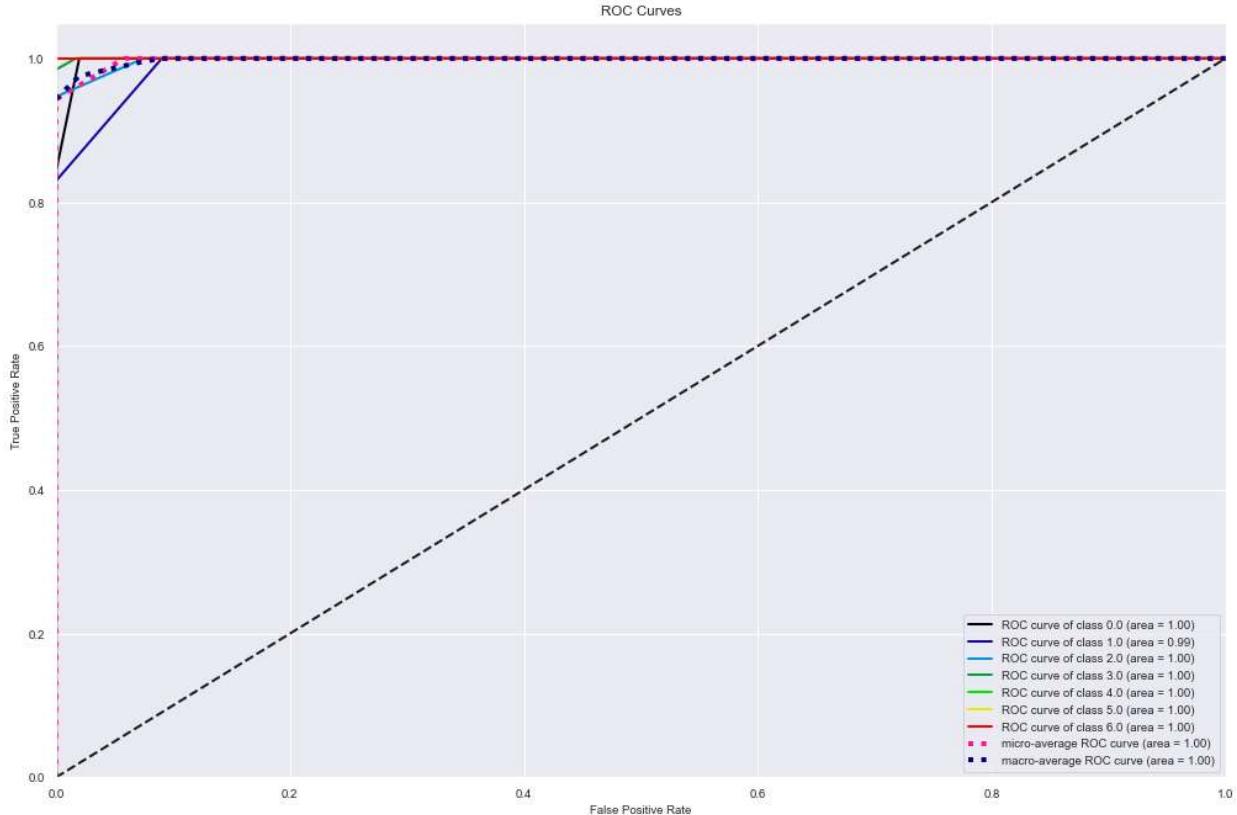
---

**FALSE NEGATIVES:**

4 out of 53 negative labels (0.0755%)

---

ROC-AUC score: (0.9478%)



PRECISION, RECALL, F1 scores:

	precision	recall	f1-score	support
0.0	0.70	0.91	0.79	54
1.0	0.66	0.53	0.59	58
2.0	0.88	0.94	0.91	70
3.0	0.91	0.97	0.94	60
4.0	0.98	0.97	0.98	65
5.0	0.84	0.71	0.77	58
6.0	0.81	0.76	0.79	58
accuracy			0.83	423
macro avg	0.83	0.83	0.82	423
weighted avg	0.83	0.83	0.83	423

```
Out[62]: (array([  0,  10,  20,  23,  25,  32,  33,  40,  49,  55,  56,  57,  63,
       65,  69,  75,  82,  84,  89,  91,  98, 103, 107, 109, 113, 122,
      123, 125, 126, 128, 152, 173, 183, 184, 186, 189, 193, 209, 214,
      223, 232, 244, 251, 264, 270, 279, 286, 292, 295, 304, 306, 309,
      315, 320, 328, 330, 335, 351, 354, 364, 366, 370, 372, 383, 384,
      393, 399, 409, 418, 421, 422], dtype=int64),)
```

## Logistic Regression

Logistic regression is used to obtain odds ratio in the presence of more than one explanatory variable. The procedure is quite similar to multiple linear regression, with the exception that the response variable is binomial. The result is the impact of each variable on the odds ratio of the

observed event of interest. The main advantage is to avoid confounding effects by analyzing the association of all variables together.

```
In [63]: logit = LogisticRegression(solver='lbfgs', random_state=0)
# parameters
parameters = {
    "penalty":['l1', 'l2'],
    "C": [0.01, 0.1, 1, 10, 100],
    "max_iter": [250],
    "penalty":["l1","l2"]
}

# grid search for parameters
grid_5 = GridSearchCV(estimator=logit, param_grid=parameters, cv=cv, n_jobs=-1)
grid_5.fit(X_train, y_train)

# print best scores
print("The best parameters are %s with a score of %0.4f\n"
      % (grid_5.best_params_, grid_5.best_score_))

# prediction results
y_pred = grid_5.predict(X_test)
y_prob = grid_5.predict_proba(X_test)

# print accuracy metrics
display_test_scores(y_test, y_pred, y_prob)
```

The best parameters are {'C': 100, 'max\_iter': 250, 'penalty': 'l2'} with a score of 0.9151

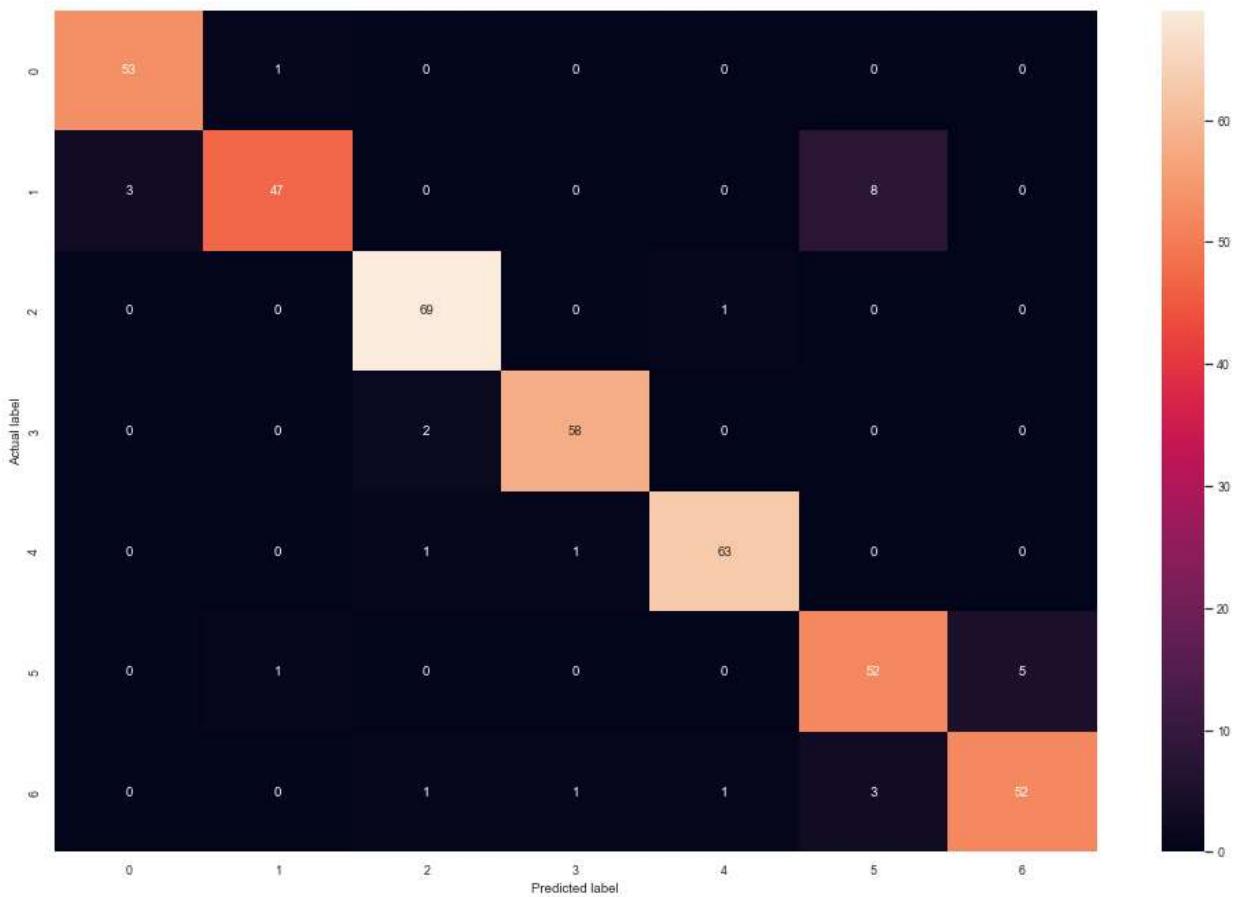
#### TEST SCORES

---

ACCURACY: 0.9314

---

CONFUSION MATRIX:



---

**FALSE POSITIVES:**

3 out of 50 positive labels (0.0600%)

---

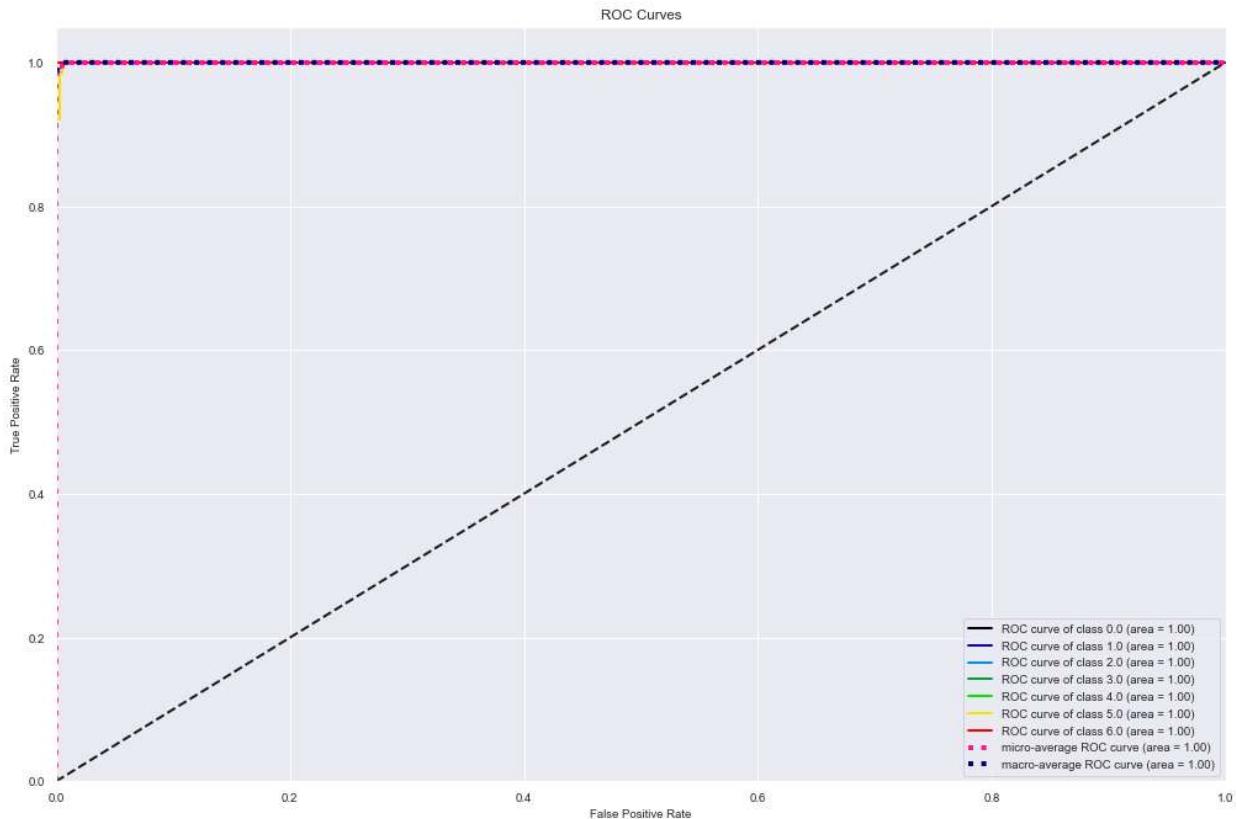
---

**FALSE NEGATIVES:**

1 out of 54 negative labels (0.0185%)

---

ROC-AUC score: (0.9925%)



PRECISION, RECALL, F1 scores:

	precision	recall	f1-score	support
0.0	0.95	0.98	0.96	54
1.0	0.96	0.81	0.88	58
2.0	0.95	0.99	0.97	70
3.0	0.97	0.97	0.97	60
4.0	0.97	0.97	0.97	65
5.0	0.83	0.90	0.86	58
6.0	0.91	0.90	0.90	58
accuracy			0.93	423
macro avg	0.93	0.93	0.93	423
weighted avg	0.93	0.93	0.93	423

```
Out[63]: (array([ 21,  22,  23,  37,  55,  57,  59,  69,  84, 120, 123, 128, 133,
       140, 144, 169, 209, 212, 231, 279, 286, 309, 320, 328, 340, 354,
       364, 371, 421], dtype=int64),)
```

## Inference

- From this model we can infer that it can be used for multiclass classifications also therefore this model was the one with the most close prediction, and Logistic Regression can derive confidence level (about its prediction), whereas KNN can only output the labels.

## Random Forest

The random forest is a classification algorithm consisting of many decision trees. It uses bagging and features randomness when building each individual tree to try to create an uncorrelated forest of trees whose prediction by committee is more accurate than that of any individual tree.

```
In [64]: rf = RandomForestClassifier(random_state=0)

# parameters
parameters = {
    "bootstrap": [True, False],
    "max_features": [None, "sqrt", "log2"],
    "class_weight": [None, "balanced", "balanced_subsample"],
    "max_samples": [None, 0.3, 0.5, 0.7, 0.9],
    "n_estimators": [10, 100, 200],
    'criterion': ['gini', 'entropy'],

}

# grid search for parameters
grid_6 = GridSearchCV(estimator=rf, param_grid=parameters, cv=cv, n_jobs=-1)
grid_6.fit(X_train, y_train)

# print best scores
print("The best parameters are %s with a score of %0.4f"
      % (grid_6.best_params_, grid_6.best_score_))

# prediction results
y_pred = grid_6.predict(X_test)
y_prob = grid_6.predict_proba(X_test)

# print accuracy metrics
display_test_scores(y_test, y_pred, y_prob)
```

The best parameters are {'bootstrap': True, 'class\_weight': 'balanced\_subsample', 'criterion': 'entropy', 'max\_features': None, 'max\_samples': None, 'n\_estimators': 200} with a score of 0.9624

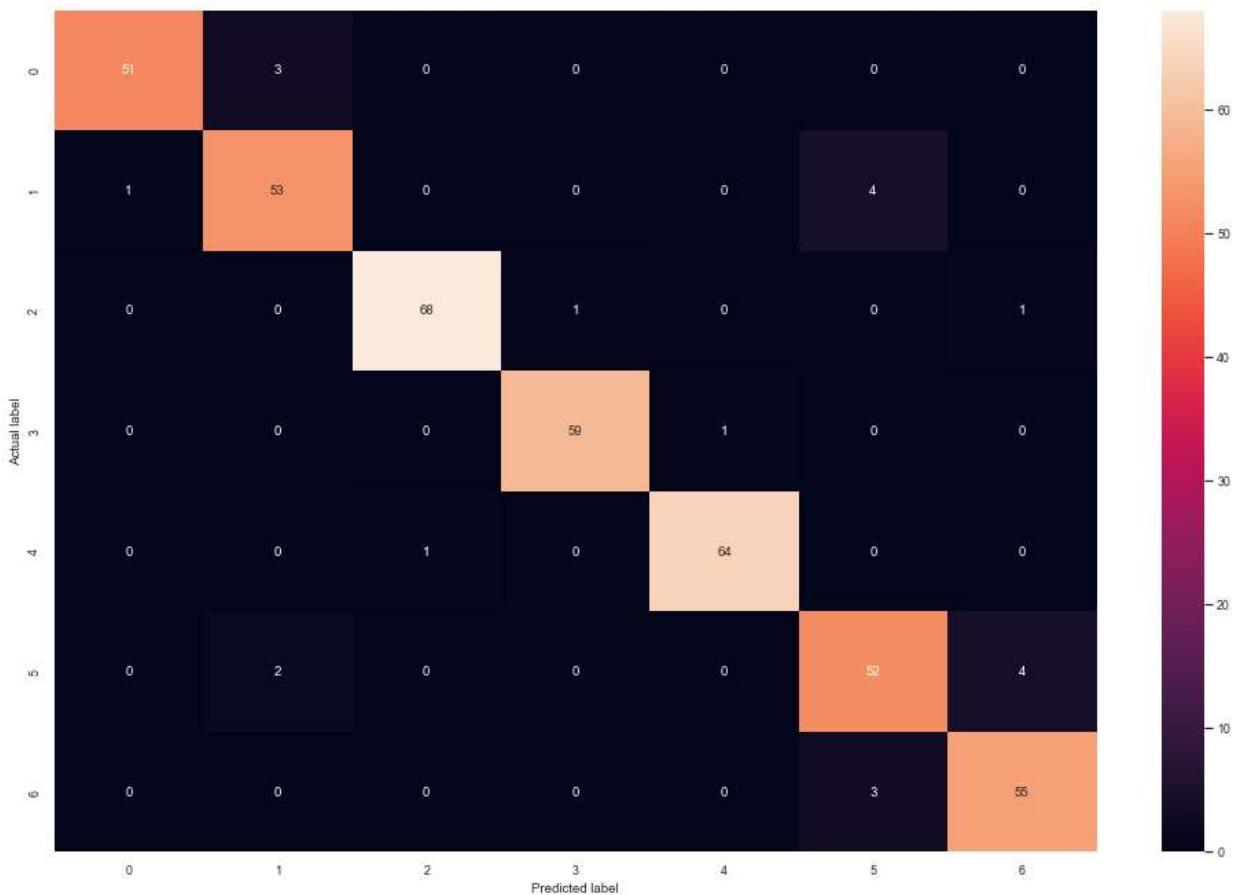
## TEST SCORES

---

ACCURACY: 0.9504

---

CONFUSION MATRIX:



---

**FALSE POSITIVES:**

1 out of 54 positive labels (0.0185%)

---

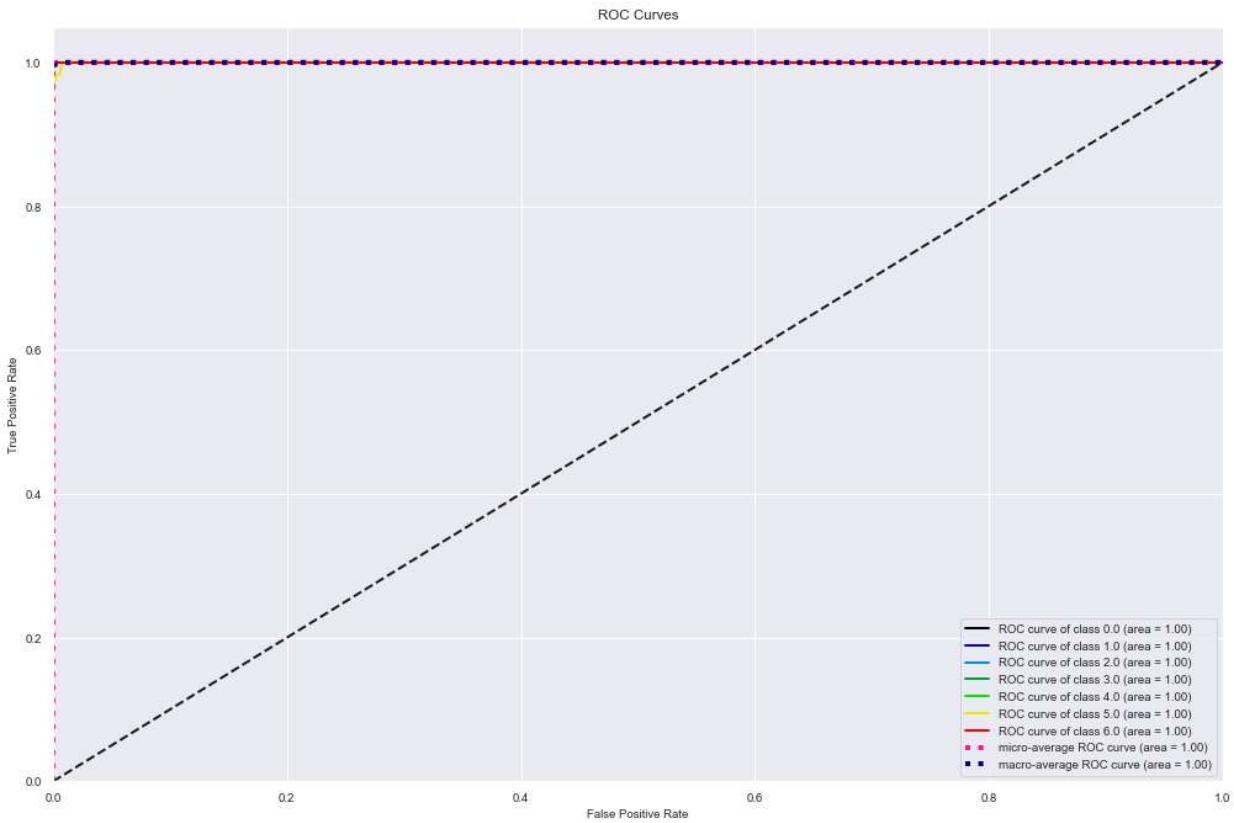
---

**FALSE NEGATIVES:**

3 out of 54 negative labels (0.0556%)

---

ROC-AUC score: (0.9961%)



PRECISION, RECALL, F1 scores:

	precision	recall	f1-score	support
0.0	0.98	0.94	0.96	54
1.0	0.91	0.91	0.91	58
2.0	0.99	0.97	0.98	70
3.0	0.98	0.98	0.98	60
4.0	0.98	0.98	0.98	65
5.0	0.88	0.90	0.89	58
6.0	0.92	0.95	0.93	58
accuracy			0.95	423
macro avg	0.95	0.95	0.95	423
weighted avg	0.95	0.95	0.95	423

```
Out[64]: array([ 49,  69,  84,  91, 123, 140, 164, 214, 263, 264, 268, 279, 284,
   289, 306, 328, 345, 360, 362, 403, 421], dtype=int64),)
```

```
In [65]: feature_imp = pd.Series(grid_6.best_estimator_.feature_importances_, index=X_train.columns)

# Creating a bar plot
sns.barplot(x=feature_imp.index, y=feature_imp, palette=sns.cubehelix_palette(start=.5,
```

- # Add Labels to your graph
 

```
plt.xticks(rotation=45, horizontalalignment='right')
```
- plt.tight\_layout()
 

```
plt.show()
```



## Inference

- From this model we can infer that our prediction is most dependent on weight followed by height and gender.

```
In [66]: import pandas as pd

data = {'Accuracy': [0.9385, 0.6194, 0.9716, 0.8322, 0.9314, 0.9504],
        'ROC_AUC': [0.9631, 0.9236, 0.9981, 0.9478, 0.9931, 0.9961],
        'Precision':[0.94, 0.66, 0.97, 0.83, 0.93, 0.95],
        'Recall':[0.94, 0.62, 0.97, 0.83, 0.93, 0.95],
        'F1-Score':[0.94, 0.61, 0.97, 0.83, 0.93, 0.95]};

df = pd.DataFrame(data, index=['Decision Tree', 'Naive Bayes(Gaussian)', 'SVM', 'k-Nearest Neighbour', 'Logistic Regression', 'Random Forest classifier'])
print(df)
```

	Accuracy	ROC_AUC	Precision	Recall	F1-Score
Decision Tree	0.9385	0.9631	0.94	0.94	0.94
Naive Bayes(Gaussian)	0.6194	0.9236	0.66	0.62	0.61
SVM	0.9716	0.9981	0.97	0.97	0.97
k-Nearest Neighbour	0.8322	0.9478	0.83	0.83	0.83
Logistic Regression	0.9314	0.9931	0.93	0.93	0.93
Random Forest classifier	0.9504	0.9961	0.95	0.95	0.95

## Conclusion

- Our result is most dependant on weight i.e it is the most significant attribute, which we inferred from Random Forest Classifier.

- Out of all the classifications, Support Vector Machine is the most accurate whereas Naive Bayes is the least accurate.
- We have classified the data with best accuracy of 97.17%

## References

[1] Palechor, F. M., & de la Hoz Manotas, A. (2019). Dataset for estimation of obesity levels based on eating habits and physical condition in individuals from Colombia, Peru and Mexico. Data in Brief, 104344.