c03

July 17, 2022

1 CARDIO CATCH DISEASES

1.1 0. INTRODUCTION

1.1.1 0.1 Planning

Input

- Create a tool that increases the diagnostic accuracy;
- Database with patient diagnoses;

Output

- Model with stable accuracy for all situationsPerformance of the model;
- Most important patient characteristics;
- Tool that can be easy used by health specialists;

Tasks

1. What information is important for predicting heart problems?
    - Is blood pressure the most important parameter?
2. Performance of the model:
    - Can accuracy alone solve this problem?
    - What is the minimum value required for a model used in health problems?
3. Action Plan:
    - User-friendly website to enter patient data and return forecast

1.1.2 0.2 Imports

[ ]:
```
import pickle
import numpy    as np
import pandas   as pd
import seaborn  as sns
import sweetviz as sv

from IPython.core.display       import HTML, Image
from typing                     import Union
from sklearn.model_selection    import train_test_split, KFold
from matplotlib                 import pyplot               as plt
```

```
from sklearn.preprocessing      import MinMaxScaler, RobustScaler

from sklearn.ensemble           import RandomForestClassifier,␣
↪ExtraTreesClassifier, AdaBoostClassifier, GradientBoostingClassifier

from yellowbrick.features       import Rank1D
from boruta                     import BorutaPy

from xgboost                    import XGBClassifier
from lightgbm                   import LGBMClassifier
from catboost                   import CatBoostClassifier


from sklearn.feature_selection  import RFE
from sklearn.naive_bayes        import GaussianNB
from sklearn.metrics            import accuracy_score, precision_score,␣
↪recall_score, f1_score, roc_auc_score
from sklearn.linear_model       import LogisticRegression
from sklearn.neighbors          import KNeighborsClassifier
from sklearn.preprocessing      import MinMaxScaler, RobustScaler
```

1.1.3 0.3 Helper Functions

```
[ ]: def numerical_metrics(numerical_attributes: Union[int, float]):
         """Shows the main values for descriptive statistics in numerical variables.

         Args:
             numerical_attributes ([float64 and int64]): [Insert all numerical␣
     ↪attributes in the dataset]

         Returns:
             [dataframe]: [A dataframe with mean, median, std deviation, skewness,␣
     ↪kurtosis, min, max and range]
         """

         data_mean = pd.DataFrame(numerical_attributes.apply(np.mean)).T
         data_median = pd.DataFrame(numerical_attributes.apply(np.median)).T
         data_std = pd.DataFrame(numerical_attributes.apply(np.std)).T
         data_min = pd.DataFrame(numerical_attributes.apply(min)).T
         data_max = pd.DataFrame(numerical_attributes.apply(max)).T
         data_range = pd.DataFrame(numerical_attributes.apply(lambda x: x.max() - x.
     ↪min())).T
         data_q1 = pd.DataFrame(numerical_attributes.apply(lambda x: np.quantile(x, .
     ↪25))).T
```

```
    data_q3 = pd.DataFrame(numerical_attributes.apply(lambda x: np.quantile(x, .
↪75))).T
    data_skew = pd.DataFrame(numerical_attributes.apply(lambda x: x.skew())).T
    data_kurtosis = pd.DataFrame(numerical_attributes.apply(lambda x: x.
↪kurtosis())).T

    num_attributes = pd.
↪concat([data_min,data_max,data_range,data_mean,data_median, data_q1,␣
↪data_q3,data_std,data_skew,data_kurtosis]).T.reset_index()
    num_attributes.columns =␣
↪['Attributes','Min','Max','Range','Mean','Median','Q1','Q3', 'St␣
↪deviation','Skewness','Kurtosis']

    return num_attributes
```

[ ]:
```
def categorical_metrics(data: Union[int, str], col: str):
    """
    Shows the the absolute and percent values in categorical variables.

    Args:
        data ([dataframe]): [Insert all categorical attributes in the dataset]

    Returns:
        [dataframe]: [A dataframe with absolute and percent values]
    """

    return pd.DataFrame({'absolute': data[col].value_counts(), 'percent %':␣
↪data[col].value_counts(normalize = True) * 100 })
```

[ ]:
```
def cat_convert(data: Union[int, float]):
     """
     Revert the Encoding on Categorical Features

     Args:
        data ([dataframe]): [Insert all categorical attributes in the dataset]

     Returns:
        data ([dataframe]): [Categorical Dataframe]
     """

     data['gender'] = data['gender'].apply(lambda x: 'woman' if x == 1 else␣
↪'man')

     data['smoker'] = data['smoker'].apply(lambda x: 'yes' if x == 1 else 'no')
```

```
    data['alcohol_intake'] = data['alcohol_intake'].apply(lambda x: 'yes' if x␣
↪== 1 else 'no')

    data['physical_activity'] = data['physical_activity'].apply(lambda x:␣
↪'yes' if x == 1 else 'no')

    data['cardio_result'] = data['cardio'].apply(lambda x: 'yes' if x == 1␣
↪else 'no')

    data['cholesterol'] = data['cholesterol'].apply(lambda x: 'normal' if x ==␣
↪1 else
                                                    'above normal' if x == 2␣
↪else
                                                    'well above normal')

    data['glucose'] = data['glucose'].apply(lambda x: 'normal' if x == 1 else
                                            'above normal' if x == 2 else
                                            'well above normal')

    return data
```

[ ]:
```
def jupyter_settings():
    %matplotlib inline
    %pylab inline
    plt.style.use('tableau-colorblind10')
    plt.rcParams['figure.figsize'] = [25, 12]
    plt.rcParams['font.size'] = 24
    display(HTML('<style>.container { width:100% !important; }</style>'))
    pd.options.display.max_columns = None
    pd.options.display.max_rows = None
    pd.set_option('display.expand_frame_repr', False)
    sns.set()

jupyter_settings()
```

```
%pylab is deprecated, use %matplotlib inline and import the required libraries.
Populating the interactive namespace from numpy and matplotlib
```

```
<IPython.core.display.HTML object>
```

[ ]:
```
def multiple_kdeplots(df: Union[int, float, str], rows: int, cols: int):
    """
    Shows a matrix with kdeplots of selected features.

    Args:
        df ([dataframe]): [Insert all categorical attributes in the dataset]
        rows ([int]): [Insert the number of rows of the subplot]
```

```
        cols ([int]): [Insert the number of columns of the subplot]

    Returns:
        [Image]: [A matrix plot with kdeplots]
    """

    for i, col in enumerate(df.columns, 1):
        plt.subplot(rows, cols, i)
        ax = sns.kdeplot(data = df, x = col)
        plt.ylabel('')

    return ax
```

[ ]:
```
def multiple_boxplots(df: Union[int, float, str], rows: int, cols: int):
    """
    Shows a matrix with boxplots of selected features.

    Args:
        df ([dataframe]): [Insert all categorical attributes in the dataset]
        rows ([int]): [Insert the number of rows of the subplot]
        cols ([int]): [Insert the number of columns of the subplot]

    Returns:
        [Image]: [A matrix plot with boxplots]
    """

    for i, col in enumerate(df.columns, 1):
        plt.subplot(rows, cols, i)
        ax = sns.boxplot(data = df, x = col)
        plt.ylabel('')

    return ax
```

[ ]:
```
def metrics_df(models, target: str, X_train: Union[int, float, str], y_train:␣
 ↪Union[int, float, str], X_val: Union[int, float, str], y_val: Union[int,␣
 ↪float, str], verbose = True):
    """Return Metrics of the model

    Args:
        model: [ML model for metrics evaluation]
        target[str]: [Target feature name]
        X_train[dataframe]: [Train variables]
        y_train[list]: [Target feature list]
        X_val[dataframe]: [Validation variables]
        y_val[list]: [Target feature list]
        verbose[bool]: [print training]
```

```python
    Returns:
        [DataFrame]: [Dataframe with metrics]
    """
    print('Please, wait a moment - Doing ML')
    model_df = []
    i = 1
    j = len(models)

    for model in models:
        model_name = type(model).__name__
        if verbose == True:
            print(f"Training model {i}/{j} -> " + model_name)
        model.fit(X_train, y_train)

        # probabilities prediction
        yhat = model.predict(X_val)

        # accuracy
        accuracy = accuracy_score(y_val, yhat)

        # precision
        precision = precision_score(y_val, yhat)

        # recall
        recall = recall_score(y_val, yhat)

        # f1 score
        f1 = f1_score(y_val, yhat)

        # roc auc
        roc_auc = roc_auc_score(y_val, yhat)

        i += 1

        df_result = pd.DataFrame({'Model_Name': model_name,
                                  'Accuracy': accuracy,
                                  'Precision': precision,
                                  'Recall': recall,
                                  'F1-Score': f1,
                                  'ROCAUC': roc_auc}, index = [0])

        model_df.append(df_result)
        final_result = pd.concat(model_df)
    print('Finished, check the results')

    return final_result
```

[ ]:
```python
def cross_validation(models, target: str, X_train: Union[int, float, str],␣
↪y_train: Union[int, float, str], kfold: int = 5, verbose: bool = True):
    """Return CV result

    Args:
        model: [ML model for CV]
        target[str]: [Target feature name]
        X_train[dataframe]: [Train variables]
        y_train[list]: [Target feature list]
        kfold[int]: [Number of data splits]
        verbose[bool]: [print folding]

    Returns:
        [DataFrame]: [Dataframe for CV]
    """
    print('Please, wait a moment, Doing CV')
    folds = KFold(n_splits = kfold, shuffle = True, random_state = 42)
    accuracy_list = []
    precision_list = []
    recall_list = []
    f1_list = []
    roc_auc_list = []

    model_df = []
    j = 1
    l = len(models)

    for model in models:
        model_name = type(model).__name__
        if verbose == True:
            print(f"Folding model {j}/{l} -> " + model_name)

        for train_cv, val_cv in folds.split(X_train, y_train):
            X_train_fold = X_train.iloc[train_cv]
            y_train_fold = y_train.iloc[train_cv]
            X_val_fold = X_train.iloc[val_cv]
            y_val_fold = y_train.iloc[val_cv]

            # fit model
            model.fit(X_train_fold, y_train_fold)

            # predict probabilities
            yhat = model.predict(X_val_fold)

            data = X_val_fold.copy()
            data[target] = y_val_fold.copy()
```

```
            # accuracy
            accuracy = accuracy_score(y_val_fold, yhat)
            accuracy_list.append(accuracy)

            # precision
            precision = precision_score(y_val_fold, yhat)
            precision_list.append(precision)

            # recall
            recall = recall_score(y_val_fold, yhat)
            recall_list.append(recall)

            # f1 score
            f1 = f1_score(y_val_fold, yhat)
            f1_list.append(f1)

            # roc auc
            roc_auc = roc_auc_score(y_val_fold, yhat)
            roc_auc_list.append(roc_auc)


        df_result = pd.DataFrame({'Model_Name': (model_name),
                                  'Accuracy Mean': np.mean(accuracy_list).
↪round(3),
                                  'Accuracy STD': np.std(accuracy_list).
↪round(3),
                                  'Precision Mean': np.mean(precision_list).
↪round(3),
                                  'Precision STD': np.std(precision_list).
↪round(3),
                                  'Recall Mean': np.mean(recall_list).round(3),
                                  'Recall STD': np.std(recall_list).round(3),
                                  'F1 Score Mean': np.mean(f1_list).round(3),
                                  'F1 Score STD': np.std(f1_list).round(3),
                                  'ROCAUC Mean': np.mean(roc_auc_list).round(3),
                                  'ROCAUC STD': np.std(roc_auc_list).round(3)},␣
↪index = [0])

        j += 1

        model_df.append(df_result)
        cv_result = pd.concat(model_df)
    print('Finished, check the results')

    return cv_result
```

1.1.4 0.4 Settings

```
[ ]: # round
pd.options.display.float_format = '{:.3f}'.format

seed = 42

homepath = '/home/gutto/Repos/Cardio-Catch-Diseases/'
```

1.1.5 0.5 Data

This dataset is avaliable here.

There are 3 types of input features:

Objective: factual information;

Examination: results of medical examination;

Subjective: information given by the patient.

Data fields

- **Age:** *Objective Feature* | Age in days
- **Height:** *Objective Feature* | Height in cm
- **Weight:** *Objective Feature* | Weight in kg
- **Gender:** *Objective Feature* | Biological gender, can be Male or Female, 1- Woman, 2- Man
- **Systolic blood pressure (ap_hi):** *Examination Feature*
- **Diastolic blood pressure (ap_lo):** *Examination Feature*
- **Cholesterol:** *Examination Feature* | Can be classified as 1: normal, 2: above normal, 3: well above normal
- **Glucose:** *Examination Feature* | Can be classified as 1: normal, 2: above normal, 3: well above normal
- **Smoking:** *Subjective Feature* | Can be smoke or binary
- **Alcohol intake:** *Subjective Feature* | Can be alco or binary
- **Physical activity:** *Subjective Feature* | Can be active or binary
- **Presence or absence of cardiovascular disease:** *Target Variable* | Can be cardio or binary

```
[ ]: df_raw = pd.read_csv(homepath + '/data/raw/cardio_train.csv', sep = ';')

df_raw.to_pickle(homepath + 'data/processed/df_raw.pkl')
```

1.2 1. DATA DESCRIPTION

1.2.1 1.1 Dataset First Look

```
[ ]: df1 = pd.read_pickle(homepath + 'data/processed/df_raw.pkl')
```

```
[ ]: df1.head().T
```

```
[ ]:                     0          1          2          3          4
     id                0.000      1.000      2.000      3.000      4.000
     age           18393.000  20228.000  18857.000  17623.000  17474.000
     gender            2.000      1.000      1.000      2.000      1.000
     height          168.000    156.000    165.000    169.000    156.000
     weight           62.000     85.000     64.000     82.000     56.000
     ap_hi           110.000    140.000    130.000    150.000    100.000
     ap_lo            80.000     90.000     70.000    100.000     60.000
     cholesterol       1.000      3.000      3.000      1.000      1.000
     gluc              1.000      1.000      1.000      1.000      1.000
     smoke             0.000      0.000      0.000      0.000      0.000
     alco              0.000      0.000      0.000      0.000      0.000
     active            1.000      1.000      0.000      1.000      0.000
     cardio            0.000      1.000      1.000      1.000      0.000
```

```
[ ]: df1.rename(columns = {'gluc': 'glucose', 'alco': 'alcohol_intake', 'smoke':␣
      ↪'smoker', 'alco': 'alcohol_intake', 'active': 'physical_activity'}, inplace␣
      ↪= True)
```

1.2.2 1.2 Data Dimensions

```
[ ]: print(f'Number of rows: {df1.shape[0]} \nNumber of columns: {df1.shape[1]}')
```

```
Number of rows: 70000
Number of columns: 13
```

1.2.3 1.3 Check Data

```
[ ]: df1.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 70000 entries, 0 to 69999
Data columns (total 13 columns):
 #   Column             Non-Null Count  Dtype
---  ------             --------------  -----
 0   id                 70000 non-null  int64
 1   age                70000 non-null  int64
 2   gender             70000 non-null  int64
 3   height             70000 non-null  int64
 4   weight             70000 non-null  float64
 5   ap_hi              70000 non-null  int64
 6   ap_lo              70000 non-null  int64
 7   cholesterol        70000 non-null  int64
 8   glucose            70000 non-null  int64
 9   smoker             70000 non-null  int64
 10  alcohol_intake     70000 non-null  int64
 11  physical_activity  70000 non-null  int64
 12  cardio             70000 non-null  int64
```

```
dtypes: float64(1), int64(12)
memory usage: 6.9 MB
```

1.2.4 1.4 Change Units

[ ]:
```
# Converting Age from days to years
df1['age'] = df1['age'].apply(lambda x: x / 365)
df1['age'] = df1['age'].astype(int)

# Converting Height from cm to m
df1['height'] = df1['height'].apply(lambda x: x / 100)
```

1.2.5 1.5 Descriptive Statistics

1.5.1 SweetViz Report

[ ]:
```
feature_config = sv.FeatureConfig(skip = 'id', force_cat = ['gender',␣
↪'cholesterol', 'glucose', 'smoker', 'alcohol_intake', 'physical_activity'])
report_1 = sv.analyze([df1, 'Cardio Catch Diseases'], 'cardio', feature_config)

report_1.show_notebook(layout = 'vertical', scale = 0.9)
```

```
                                                   |          | [  0%]   00:00 -> (?␣
↪left)
```

```
<IPython.core.display.HTML object>
```

Report Insights

Target

1. `cardio`
   - the feature is balanced (50/50);
   - highest correlation ratios is `age`(0.24) and `weight`(0.18);
   - `cholesterol` and `glucose` seems to be a little relevant to the target;

Numerical Features

2. `age`
   - should be in year, not days;
   - highest correlation ratios are `cardio`(0.24) and `glucose`(0.16);
   - negative skewed curve;
   - negative kurtosis(platykurtic);
3. `height`
   - should be in m, not cm;
   - highest correlation ratios are `weight`(0.29), `gender`(0.5) and `smoker`(0.19);
   - negative skewed curve;
   - positive kurtosis(leptokurtic);
4. `weight`
   - highest correlation ratios are `height`(0.29), `cardio`(0.18) and `gender`(0.16);
   - positive skewed curve;

- positive kurtosis(leptokurtic);
- Highest weight is 200kg and min 10 **need attention**;

5. `ap_hi` (systolic blood pressure)
   - no strong correlation to be cited;
   - positive skewed curve;
   - positive kurtosis(leptokurtic);
   - avg and median are ok;
   - Highest weight is 16020 and min -150 **need attention**;
6. `ap_lo` (diastolic blood pressure)
   - no strong correlation to be cited;
   - positive skewed curve;
   - positive kurtosis(leptokurtic);
   - avg and median are ok;
   - Highest weight is 11000 and min -70 **need attention**;

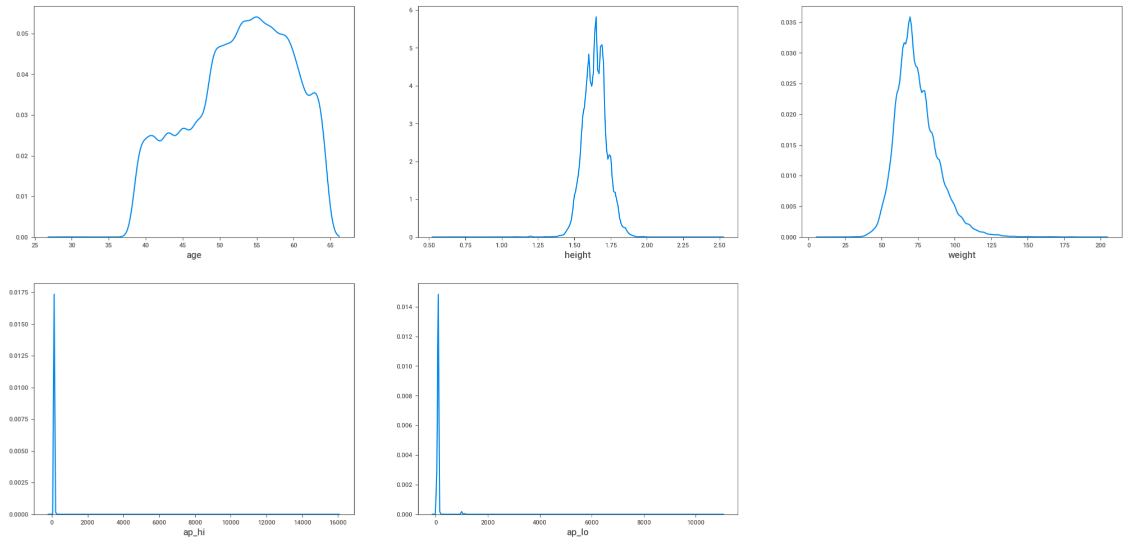
Categorical Features

7. `gender`
   - unbalanced (65/35) but seems to be the normal in reality;
   - highest correlation ratios are `smoker`(0.19) and `height`(0.5);
8. `cholesterol`
   - unbalanced (75/14/12) but seems to be the normal in reality;
   - highest correlation ratios are `glucose`(0.19) and `age`(0.16);
9. `glucose`
   - unbalanced (85/8/7) but seems to be the normal in reality;
   - highest correlation ratios are `smoker`(0.14) and `height`(0.12);
10. `smoker`
    - unbalanced (91/9) but seems to be the normal in reality;
    - highest correlation ratios are `gender`(0.19), `smoker`(0.16) and `height`(0.19);
11. `alcohol_intake`
    - unbalanced (95/5) but seems to be the 'normal' in reality;
    - highest correlation ratios are `smoker`(0.16) and `height`(0.09);
12. `physical_activity`
    - unbalanced (80/20) but seems to be the normal in reality;
    - no strong correlation to be cited, this feature can be possibly dropped in the future steps;

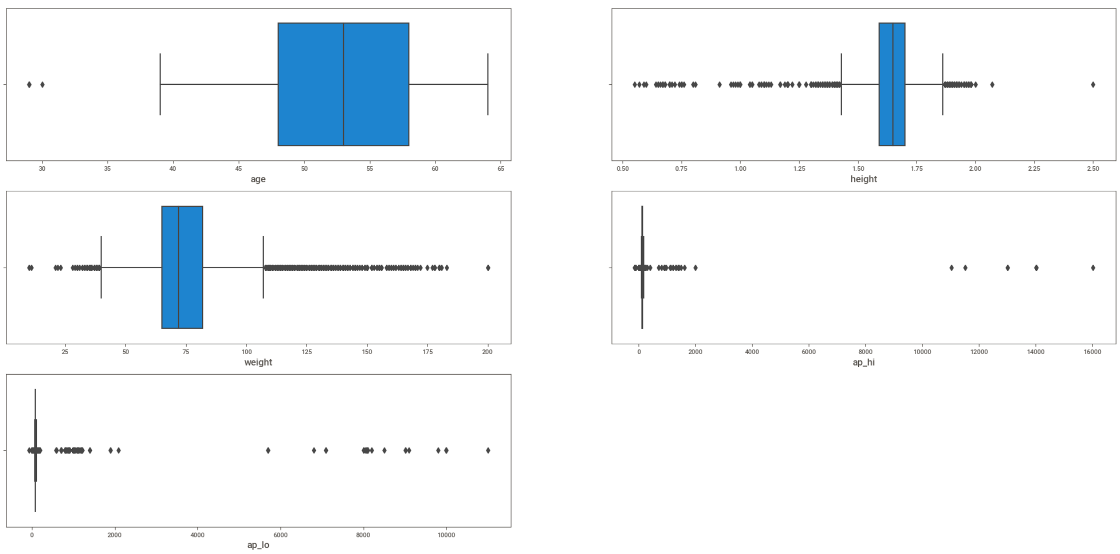
1.5.2 Numerical Attributes

[ ]:
```
num_attributes = df1[['age', 'height', 'weight', 'ap_hi', 'ap_lo']]
```

[ ]:
```
multiple_kdeplots(num_attributes, 2, 3);
```



[ ]:
```
multiple_boxplots(num_attributes, 3, 2);
```



To-do: Outliers Study

1.5.3 Categorical Attributes

[ ]:
```
df1_cat = df1.copy()

df1_cat = cat_convert(df1_cat)
```

```
cat_attributes = df1_cat[['gender', 'cholesterol', 'glucose', 'smoker',
↪'alcohol_intake', 'physical_activity', 'cardio', 'cardio_result']]
cat_attributes.head()
```

```
[ ]:   gender        cholesterol glucose smoker alcohol_intake physical_activity
    cardio cardio_result
    0    man             normal  normal     no             no               yes
    0            no
    1  woman  well above normal  normal     no             no               yes
    1           yes
    2  woman  well above normal  normal     no             no                no
    1           yes
    3    man             normal  normal     no             no               yes
    1           yes
    4  woman             normal  normal     no             no                no
    0            no
```

```
categorical_metrics(cat_attributes, 'gender')
```

```
[ ]:        absolute  percent %
    woman     45530     65.043
    man       24470     34.957
```

```
categorical_metrics(cat_attributes, 'cholesterol')
```

```
[ ]:                    absolute  percent %
    normal                 52385     74.836
    above normal            9549     13.641
    well above normal       8066     11.523
```

```
categorical_metrics(cat_attributes, 'glucose')
```

```
[ ]:                    absolute  percent %
    normal                 59479     84.970
    well above normal       5331      7.616
    above normal            5190      7.414
```

```
categorical_metrics(cat_attributes, 'smoker')
```

```
[ ]:      absolute  percent %
    no      63831     91.187
    yes      6169      8.813
```

```
categorical_metrics(cat_attributes, 'alcohol_intake')
```

```
[ ]:      absolute  percent %
    no      66236     94.623
```

yes	3764	5.377

[ ]:
```
categorical_metrics(cat_attributes, 'physical_activity')
```

[ ]:

	absolute	percent %
yes	56261	80.373
no	13739	19.627

That info is strange, I believed that the percentage of people who exercised would be much lower

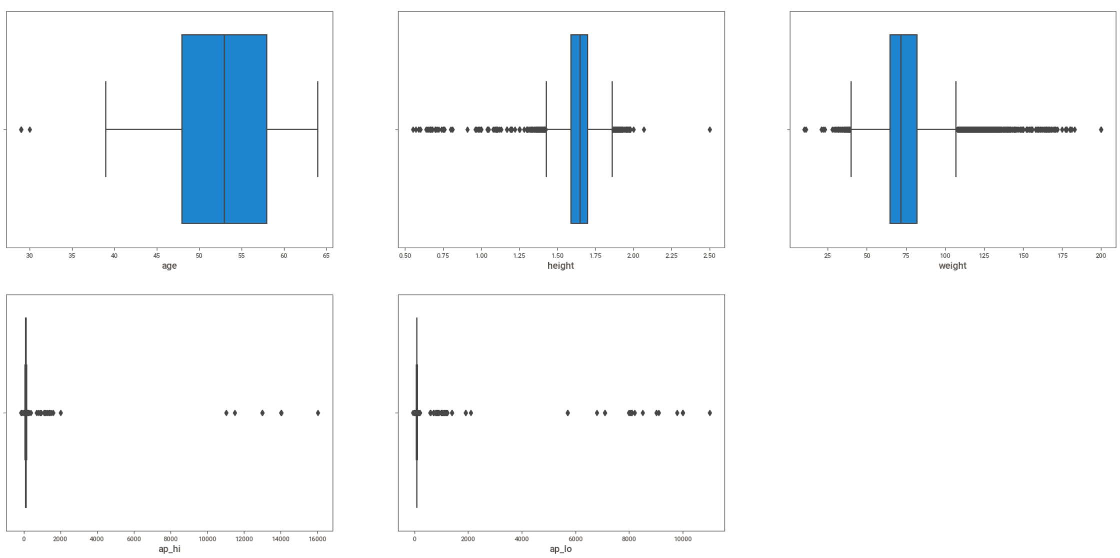
[ ]:
```
categorical_metrics(cat_attributes, 'cardio_result')
```

[ ]:

	absolute	percent %
no	35021	50.030
yes	34979	49.970

1.2.6 1.6 Data Filtering

[ ]:
```
multiple_boxplots(df1[['age', 'height', 'weight', 'ap_hi', 'ap_lo']], 2, 3);
```



1.6.1 ap_hi and ap_lo

1. There are a lot of values at pressures above 400, 500, my theory is that this would be a typo where the person who measured would have added an extra 0 unintentionally.
2. Negative pressure values can be another typo, where add one - accidentally

[ ]:
```
df1[df1['ap_hi'] >= 400].head(3)
```

```
[ ]:         id  age  gender  height  weight  ap_hi  ap_lo  cholesterol  glucose
    smoker  alcohol_intake  physical_activity  cardio
    1876  2654  41       1   1.600  60.000    902     60            1        1
    0              0                  1       0
    2014  2845  62       2   1.670  59.000    906      0            1        1
    0              0                  1       0
    4817  6822  39       1   1.680  63.000    909     60            2        1
    0              0                  1       0
```

```
[ ]: df1[df1['ap_hi'] < 0].head(3)
```

```
[ ]:           id  age  gender  height  weight  ap_hi  ap_lo  cholesterol  glucose
    smoker  alcohol_intake  physical_activity  cardio
    4607    6525   41       1   1.650  78.000   -100     80            2        1
    0              0                  1       0
    16021  22881   60       2   1.610  90.000   -115     70            1        1
    0              0                  1       0
    20536  29313   42       1   1.530  54.000   -100     70            1        1
    0              0                  1       0
```

```
[ ]: df1[df1['ap_lo'] >= 400].head(3)
```

```
[ ]:       id  age  gender  height  weight  ap_hi  ap_lo  cholesterol  glucose
    smoker  alcohol_intake  physical_activity  cardio
    228  314   47       2   1.830  98.000    160   1100            1        2
    1              0                  1       1
    241  334   60       2   1.570  60.000    160   1000            2        1
    0              0                  0       1
    260  357   49       1   1.500  83.000    140    800            1        1
    0              0                  1       1
```

```
[ ]: df1[df1['ap_lo'] < 0].head(3)
```

```
[ ]:           id  age  gender  height  weight  ap_hi  ap_lo  cholesterol  glucose
    smoker  alcohol_intake  physical_activity  cardio
    60106  85816   61       1   1.670  74.000     15    -70            1        1
    0              0                  1       1
```

```
[ ]: df1['ap_hi'] = df1['ap_hi'].apply(lambda x: (x/10) if (x > 400) else x)
     df1['ap_hi'] = df1['ap_hi'].apply(lambda x: (-x) if (x < 0) else x)
     df1['ap_lo'] = df1['ap_lo'].apply(lambda x: (x/10) if (x > 400) else x)
     df1['ap_lo'] = df1['ap_lo'].apply(lambda x: (-x) if (x < 0) else x)
```

Considering that diastolic pressure values higher than 350 and less than 70 and systolic pressure values higher than 250 and less than 40 are practically impossible even in cases of patients with hypotension or hypertensive crisis, these lines will be removed in this project.

[ ]:
```
len(df1[df1['ap_hi'] < 70])
```

[ ]: 183

[ ]:
```
len(df1[df1['ap_hi'] > 350])
```

[ ]: 9

[ ]:
```
len(df1[df1['ap_lo'] > 250])
```

[ ]: 24

[ ]:
```
len(df1[df1['ap_lo'] < 30])
```

[ ]: 52

[ ]:
```
# ap_hi
df1 = df1[df1['ap_hi'].between(70, 350)]

# ap_lo
df1 = df1[df1['ap_lo'].between(40, 250)]
```

1.6.2 Age

[ ]:
```
age_min = df1['age'].min()
age_max = df1['age'].max()

print(f'The youngest client is {age_min} years old and the oldest is {age_max}.
↪')
```

```
The youngest client is 29 years old and the oldest is 64.
```

Everything seems right around here

1.6.3 Height

In general, people with dwarfism are shorter than 1.45 meters for men and 1.40 meters for women. Values less than 1 meter are considered extremely rare, and will be removed from this database as they are possibly typos.

[ ]:
```
df1['height'].min()
```

[ ]: 0.55

[ ]:
```
df_height = df1.loc[df1['height'] < 1]
len(df_height)
```

[ ]: 26

[ ]:
```
df_height
```

[ ]:
```
          id  age  gender  height  weight   ap_hi   ap_lo  cholesterol  glucose
smoker  alcohol_intake  physical_activity  cardio
224       309  59        2   0.760  55.000 120.000  80.000            1        1
0               0                 1       0
8171    11662  48        2   0.970 170.000 160.000 100.000           1        1
1               0                 1       1
12770   18218  53        1   0.750 168.000 120.000  80.000            1        1
1               0                 1       1
13265   18928  61        2   0.710  68.000 120.000  80.000            3        1
0               0                 1       0
14323   20459  60        1   0.670  57.000 120.000  90.000            1        1
0               0                 1       1
15167   21686  43        1   0.700  68.000 120.000  80.000            1        1
0               0                 0       0
16699   23859  53        2   0.740  98.000 140.000  90.000            1        1
0               0                 1       1
22542   32207  39        1   0.680  65.000 100.000  60.000            1        1
0               0                 0       0
22723   32456  64        1   0.550  81.000 130.000  90.000            1        1
0               0                 1       1
23913   34186  52        1   0.810 156.000 140.000  90.000            1        1
0               0                 1       0
27384   39156  41        1   0.800 178.000 140.000  90.000            3        3
0               0                 1       1
27603   39462  57        1   0.640  61.000 130.000  70.000            1        1
0               0                 1       0
28737   41075  54        1   0.910  55.000 140.000  90.000            1        1
0               0                 1       1
29157   41661  52        1   0.600  69.000 110.000  70.000            1        1
0               0                 0       0
32098   45832  42        1   0.720  74.000 150.000  90.000            1        1
0               0                 1       1
33607   48009  53        2   0.650  72.000 130.000  80.000            1        1
0               0                 0       0
44490   63545  52        1   0.650  60.000 120.000  80.000            1        1
0               0                 1       0
46319   66161  57        2   0.680  71.000 120.000  80.000            1        1
0               0                 1       0
47352   67631  63        1   0.750  75.000 120.000  80.000            1        1
0               0                 1       0
50789   72476  39        2   0.670  60.000 110.000  80.000            1        1
1               1                 1       0
51459   73386  42        2   0.700  69.000 120.000  80.000            1        1
0               0                 0       0
53344   76116  56        2   0.670  80.000 120.000  80.000            1        1
0               0                 0       1
56022   79917  58        1   0.960  59.000  90.000  60.000            1        1
```

```
0                0                   1       1
64115   91523   50        1   0.590  57.600 125.000  67.000            1         1
0                0                   0       0
65302   93223   50        1   0.990  60.000  90.000  60.000            1         1
0                0                   1       0
66643   95141   51        1   0.570  61.000 130.000  90.000            1         1
0                0                   1       1
```

[ ]:
```
df1.drop(df1[df1['height'] < 1].index, inplace = True)
```

One of the sports with the tallest players is basketball, in which the biggest player who ever played in the NBA, Gheorghe Muresan, was 2.31m tall. Height values above this are very rare and will be removed from df1.

Reference

[ ]:
```
df1['height'].max()
```

[ ]: 2.5

[ ]:
```
df1.loc[df1['height'] > 2]
```

[ ]:
```
          id  age  gender  height  weight   ap_hi   ap_lo  cholesterol  glucose
smoker  alcohol_intake  physical_activity  cardio
6486    9223   58        1   2.500  86.000 140.000 100.000            3         1
0                0                   1       1
21628   30894   52        2   2.070  78.000 100.000  70.000            1         1
0                1                   1       0
```

[ ]:
```
df1.drop(df1[df1['height'] == 2.5].index, inplace = True)
```

1.6.4 Weight

[ ]:
```
df1['weight'].max()
```

[ ]: 200.0

[ ]:
```
df1['weight'].min()
```

[ ]: 10.0

Values less than 35 kg look weird in this dataset, so they will be removed

[ ]:
```
df_weight = df1.loc[df1['weight'] < 35]
len(df_weight)
```

[ ]: 20

[ ]:
```
df_weight
```

[ ]:
```
          id  age  gender  height  weight   ap_hi   ap_lo  cholesterol  glucose  \
smoker  alcohol_intake  physical_activity  cardio
3752     5306   42       1   1.200  30.000 110.000  70.000            1        1
0               0                  1       0
14722   21040   62       1   1.430  34.000 100.000  70.000            1        1
0               0                  1       0
16906   24167   47       2   1.700  31.000 150.000  90.000            2        2
0               0                  1       1
18559   26503   49       1   1.600  30.000 120.000  80.000            1        1
0               0                  1       1
22016   31439   42       1   1.460  32.000 100.000  70.000            1        1
0               0                  0       0
26806   38312   63       1   1.570  23.000 110.000  80.000            1        1
0               0                  1       0
29488   42156   55       2   1.770  22.000 120.000  80.000            1        1
1               1                  1       0
33511   47872   57       1   1.530  34.000 110.000  70.000            3        3
0               0                  1       1
33817   48318   59       2   1.780  11.000 130.000  90.000            1        1
0               0                  1       1
34276   48976   40       2   1.280  28.000 120.000  80.000            1        1
0               0                  1       0
35314   50443   54       1   1.460  32.000 130.000  80.000            1        2
0               0                  0       0
38417   54851   59       1   1.540  32.000 110.000  60.000            1        1
0               0                  1       0
41905   59853   58       1   1.430  30.000 103.000  61.000            2        1
0               0                  1       0
48080   68667   52       1   1.430  33.000 100.000  60.000            1        1
0               0                  1       0
51837   73914   54       2   1.390  34.000 120.000  70.000            1        1
0               0                  1       0
55852   79686   64       1   1.520  34.000 140.000  90.000            1        1
0               0                  1       1
57858   82567   51       2   1.650  10.000 180.000 110.000            2        2
0               0                  1       1
60188   85931   59       1   1.620  21.000 120.000  80.000            2        1
0               0                  1       1
60699   86650   51       1   1.710  29.000 110.000  70.000            2        1
0               0                  1       1
65082   92896   62       1   1.450  33.000 130.000 100.000            2        1
0               0                  1       1
```

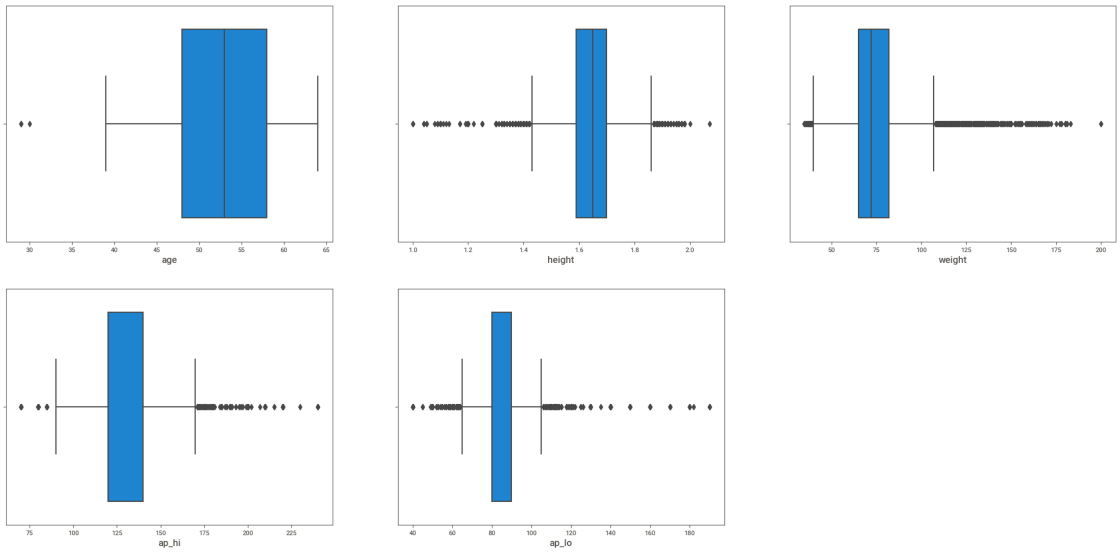
[ ]:
```python
df1.drop(df1[df1['weight'] < 35].index, inplace = True)
```

1.6.5 After Filtering

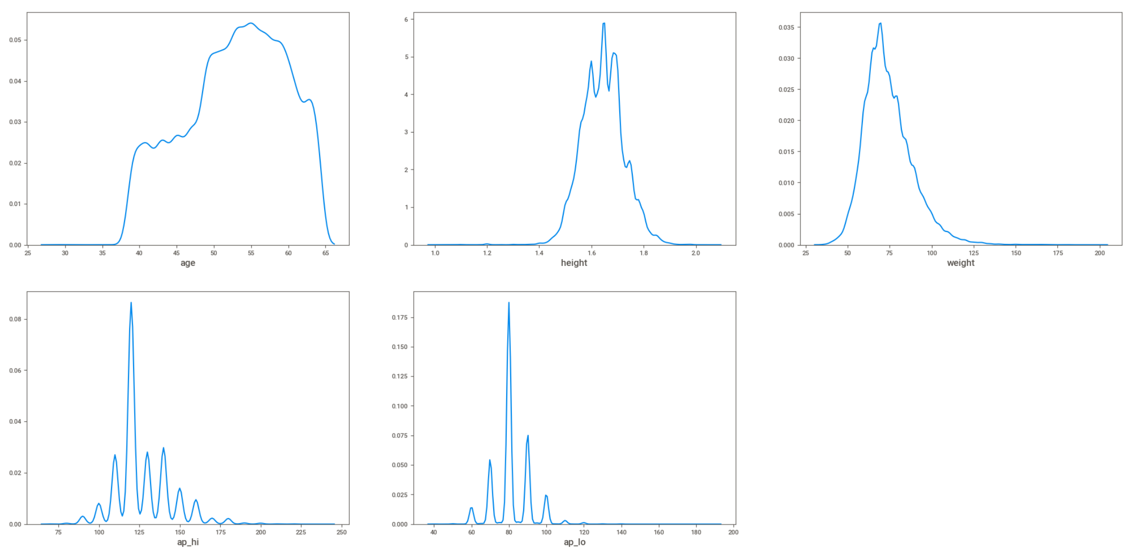
```
[ ]: rows_lost = 70000 - len(df1)
     print(f'In the data filtering, {rows_lost} rows  have been removed')
```

```
In the data filtering, 317 rows  have been removed
```

```
[ ]: multiple_boxplots(df1[['age', 'height', 'weight', 'ap_hi', 'ap_lo']], 2, 3);
```




```
[ ]: multiple_kdeplots(df1[['age', 'height', 'weight', 'ap_hi', 'ap_lo']], 2, 3);
```



1.2.7 1.7 Save State

[ ]:
```
df1.to_pickle(homepath + 'data/processed/df1.pkl')
```

1.3 2. FEATURE ENGINEERING

1.3.1 2.1 Load Checkpoint

[ ]:
```
df2 = pd.read_pickle(homepath + 'data/processed/df1.pkl')
```

1.3.2 2.2 Systolic and Diastolic Pressure

I noticed something interesting in the descriptive statistics, **some diastolic pressure values are higher than systolic pressure values**. My theory is: In the construction of this database someone inserted the values of these two columns swapped because the value of the systolic pressure is, by definition, greater than the diastolic pressure.

[ ]:
```
df2['pulse_pressure_range'] = df2['ap_hi'] - df2['ap_lo']

df2['systolic_pressure'] = df2[['ap_hi', 'ap_lo', 'pulse_pressure_range']].
 ↪apply(lambda x: x['ap_hi'] if x['pulse_pressure_range'] >= 0                                                                     ␣
 ↪            else (x['ap_hi'] + (x['pulse_pressure_range']*(-1))), axis = 1)


df2['diastolic_pressure'] = df2[['ap_hi', 'ap_lo', 'pulse_pressure_range']].
 ↪apply(lambda x: x['ap_lo'] if x['pulse_pressure_range'] >= 0                                                                     ␣
 ↪            else (x['ap_lo'] + (x['pulse_pressure_range'])), axis = 1)

df2['pulse_pressure_range'] = df2['pulse_pressure_range'].apply(lambda x: x if␣
 ↪x >= 0 else -x)
```

1.3.3 2.3 Blood Pressure

According to the American Heart Association, the ideal blood pressure range is 120/80 mm Hg. A person's blood pressure is expressed in two values – 120 and 80 in the previous case. The first value is the systolic blood pressure, while the value after the slash '/' symbol is the diastolic blood pressure.

- **Systolic blood pressure**: This unit indicates how much pressure blood exerts on the arterial walls when the heart beats at the time of measurement. This is when the heart pumps blood out of the heart and circulates it to various organs in the body.
- **Diastolic blood pressure**: This unit indicates how much pressure is exerted on the arterial walls when the heart rests between two beats. This is the period during which the heart opens its chamber to fill with blood.

In general, systolic blood pressure receives more medical attention. It is also an important risk factor for cardiovascular disease in older people. It is widely observed that systolic blood pressure increases steadily with age due to the increased stiffness of large arteries and plaque formation in the blood vessels. Under normal circumstances, blood pressure approaching 300 is hazardous. In various health forums, individuals have reported having experienced blood pressure above 250. Most of these individuals have also reported suffering from extreme medical conditions, such as a heavy buzzing in the ears, uncontrollably intense headaches, dizziness, and even loss of consciousness.

Reference

A sudden fall in blood pressure can be dangerous. A change of just 20 mm Hg — a drop from 110 systolic to 90 mm Hg systolic, for example, can cause dizziness and fainting when the brain fails to receive enough blood. And big drops, such as those caused by uncontrolled bleeding, severe infections or allergic reactions, can be life-threatening.

Reference

Blood pressure can be classified into four categories based on the readings from a sphygmomanometer:

- **Hypotension**: Systolic pressure reading lower than 90 and diastolic lower than 60;
- **Normal**: Systolic pressure reading between 90-120 and diastolic pressure reading between 60-80 is considered normal;
- **Pre-high blood pressure**: Systolic pressure reading between 120-140 and diastolic pressure reading between 80-90 is considered a slightly elevated level of blood pressure;
- **High blood pressure**: Systolic pressure reading between 140-180 and diastolic pressure reading between 90-100 is considered to be a high blood pressure condition;
- **Hypertensive crisis**: If one's systolic pressure exceeds 180 or diastolic pressure crosses 100, it is a stage that requires immediate medical attention.

[ ]:
```
df2['blood_pressure'] = df2.apply(lambda x:  'hypothension' if␣
↪(x['systolic_pressure'] < 90) and (x['diastolic_pressure'] < 60)
                                        else 'normal' if␣
↪(x['systolic_pressure'] >= 90 and x['systolic_pressure'] <= 120) and␣
↪(x['diastolic_pressure'] >= 60 and x['diastolic_pressure'] <= 80)
                                        else 'prehigh_blood_pressure' if␣
↪(x['systolic_pressure'] > 120 and x['systolic_pressure'] <= 140) or␣
↪(x['diastolic_pressure'] > 80 and x['diastolic_pressure'] <= 90)
                                        else 'high_blood_pressure' if␣
↪(x['systolic_pressure'] > 140 and x['systolic_pressure'] <= 180) or␣
↪(x['diastolic_pressure'] > 90 and x['diastolic_pressure'] <= 100)
                                        else 'hypertensive_crisis' if␣
↪(x['systolic_pressure'] > 180) and (x['diastolic_pressure'] > 100)
                                        else 'need_an_analysis', axis = 1)
```

[ ]:
```
categorical_metrics(df2, 'blood_pressure')
```

[ ]:

	absolute	percent %
normal	38785	55.659
prehigh_blood_pressure	24750	35.518
high_blood_pressure	5823	8.356
hypertensive_crisis	157	0.225

```
need_an_analysis              155       0.222
hypothension                   13       0.019
```

1.3.4 2.3 Pulse Pressure

A normal pulse pressure range is between 40 and 60 mm Hg, values below 40 are considered low and above 60 high. Low pulse pressure can indicate decreased cardiac output. It's often observed in people with heart failure.As people age, it's common for their pulse pressure measurement to increase. This can be due to high blood pressure or atherosclerosis, fatty deposits that build up on your arteries. Additionally, iron deficiency anemia and hyperthyroidism can lead to an increase in pulse pressure.

Reference

[ ]:
```
df2['pulse_pressure'] = df2['pulse_pressure_range'].apply(lambda x: 'low' if (x␣
↪>= 0) and (x < 40)
                                                                      else 'normal' if (x␣
↪>= 40) and (x < 60)
                                                                      else 'high')
```

[ ]:
```
categorical_metrics(df2, 'pulse_pressure')
```

[ ]:
```
        absolute  percent %
normal     50728     72.798
high       11692     16.779
low         7263     10.423
```

1.3.5 2.4 BMI and Body Mass

The body mass index (BMI) is a measure that uses your height and weight to work out if your weight is healthy, it can be calculated with person's weight in kilograms divided by the square of height in meters. A high or low BMI may be an indicator of poor diet, varying activity levels or high stress but normal bmi, alone, doesn't mean healthy.

The BMI result will fit into one of 5 bands:

Underweight	Normal	Overweight	Obese	Extremely Obese
Under 18.5	Between 18.5 and 24.9	Between 25 and 29.9	Between 30 and 39.9	40 or over

Health problems associated with a BMI in the obesity include:

- type 2 diabetes;
- stroke;
- heart disease;
- high blood pressure.

Health problems associated with a BMI in the underweight:

- weakened immuned system;
- anaemia;
- palpitations.

Reference

[ ]:
```
# BMI
df2['bmi'] = round(df2['weight']/(df2['height']**2), 1)

df2['body_mass'] = df2['bmi'].apply(lambda x: 'underweight' if (x < 18.5)
                                    else  'normal' if (x >= 18.5) and (x <␣
↪25)
                                    else  'overweight' if (x >= 25) and (x␣
↪< 30)
                                    else  'obese' if (x >= 30) and (x < 40)
                                    else 'extremely_obese')
```

[ ]:
```
categorical_metrics(df2, 'body_mass')
```

[ ]:

	absolute	percent %
overweight	25451	36.524
normal	25100	36.020
obese	16656	23.903
extremely_obese	1869	2.682
underweight	607	0.871

1.3.6 2.5 Period of Life

Reference

[ ]:
```
age_min = df2['age'].min()
age_max = df2['age'].max()

print(f'The smallest age in this dataset is {age_min} years.\nThe highest age␣
↪in this dataset is {age_max} years.')
```

```
The smallest age in this dataset is 29 years.
The highest age in this dataset is 64 years.
```

[ ]:
```
df2['period_of_life'] = df2['age'].apply(lambda x: 'early_adulthood' if (x >=␣
↪29) and (x < 40)
                                          else   'middle_adulthood')
```

[ ]:
```
categorical_metrics(df2, 'period_of_life')
```

[ ]:

	absolute	percent %
middle_adulthood	67905	97.448
early_adulthood	1778	2.552

1.3.7 2.5 Drop Columns

```
[ ]: df2.drop(columns = ['ap_hi', 'ap_lo', 'pulse_pressure_range'], inplace = True)
```

1.3.8 2.6 Save State

```
[ ]: df2.to_pickle(homepath + 'data/processed/df2.pkl')
```

1.4 3. EXPLORATORY DATA ANALYSIS

1.4.1 3.1 Load Checkpoint

```
[ ]: df3 = pd.read_pickle(homepath + 'data/processed/df2.pkl')
```

```
[ ]: df3.columns
```

```
[ ]: Index(['id', 'age', 'gender', 'height', 'weight', 'cholesterol', 'glucose',
            'smoker', 'alcohol_intake', 'physical_activity', 'cardio',
            'systolic_pressure', 'diastolic_pressure', 'blood_pressure',
            'pulse_pressure', 'bmi', 'body_mass', 'period_of_life'],
           dtype='object')
```

```
[ ]: feature_config = sv.FeatureConfig(skip = 'id', force_cat = ['gender',␣
      ↪'cholesterol', 'glucose', 'smoker', 'alcohol_intake', 'physical_activity',␣
      ↪'blood_pressure', 'body_mass', 'period_of_life'])
     report_2 = sv.analyze([df2, 'Cardio Catch Diseases'], 'cardio', feature_config)

     report_2.show_notebook(layout = 'vertical', scale = 0.9)
```

```
                                                 |          | [  0%]   00:00 -> (?␣
 ↪left)
```

```
<IPython.core.display.HTML object>
```

1.4.2 3.2 Save State

```
[ ]: df3.to_pickle(homepath + 'data/processed/df3.pkl')
```

1.5 4. DATA PREPARATION

1.5.1 4.1 Load Checkpoint

```
[ ]: df4 = pd.read_pickle(homepath + 'data/processed/df3.pkl')
```

1.5.2 4.2 Split Data

[ ]:
```
# Train -> 70%
# Test -> 20%
# Validation -> 10%
x_train, x_test = train_test_split(df4, test_size = 0.2, random_state = seed)

# if train = 80% x dataset, then val = 0.1/0.8 = 0.125
# 0.125 x 0.8 = 0.1
x_train, x_val = train_test_split(df4, test_size = 0.125, random_state = seed)
```

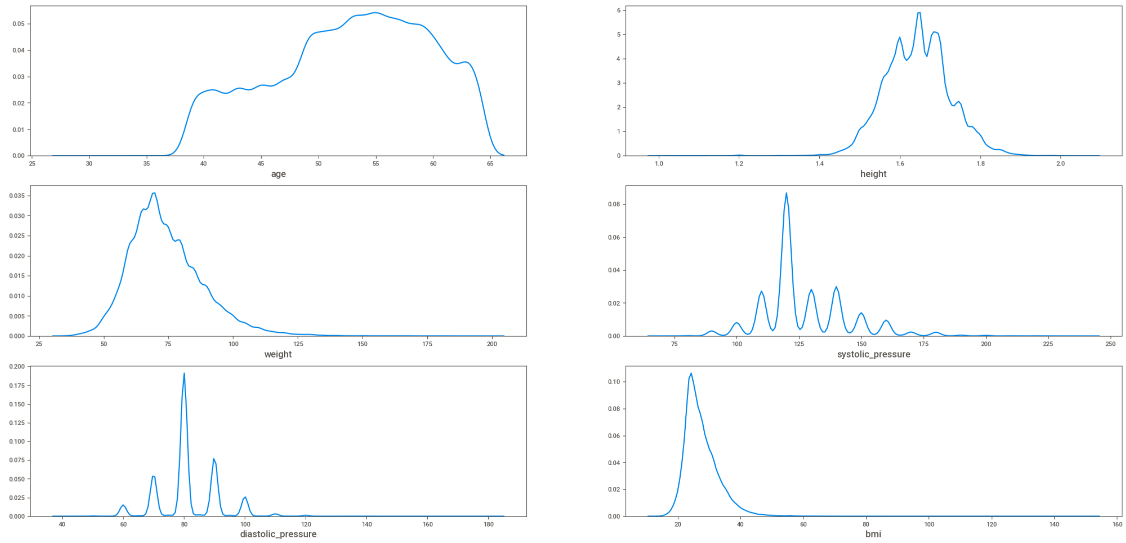
1.5.3 4.3 Encoding

[ ]:
```
# Ordinal Encoding
bp_encoding = {'need_an_analysis': 0, 'hypothension': 1, 'normal': 2,␣
↪'prehigh_blood_pressure': 3, 'high_blood_pressure': 4, 'hypertensive_crisis':
↪ 5}
pp_encoding = {'measurement_error': 0, 'low': 1, 'normal': 2, 'high': 3}
bm_encoding = {'underweight': 1, 'normal': 2, 'overweight': 3, 'obese': 4,␣
↪'extremely_obese': 5}
pl_encoding = {'early_adulthood': 1, 'middle_adulthood': 2}

# One Hot Encoding
x_train, x_test, x_val = [pd.get_dummies(dataframe, prefix = ['gender'],␣
↪columns = ['gender']) for dataframe in [x_train, x_test, x_val]]



for df in [x_train, x_test, x_val]:
    df['blood_pressure'] = df['blood_pressure'].map(bp_encoding)
    df['pulse_pressure'] = df['pulse_pressure'].map(pp_encoding)
    df['body_mass'] = df['body_mass'].map(bm_encoding)
    df['period_of_life'] = df['period_of_life'].map(pl_encoding)
```

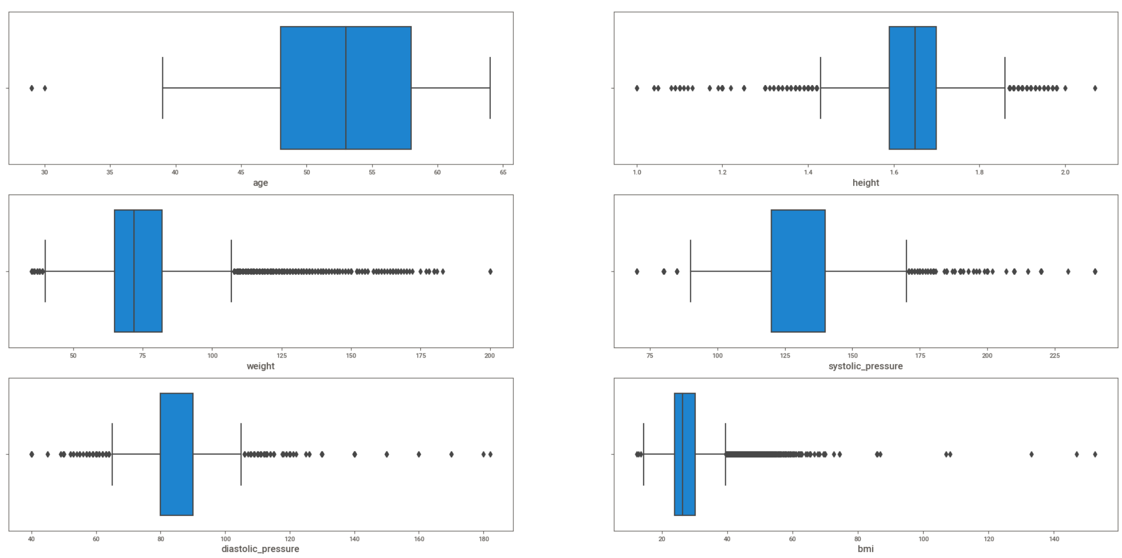
1.5.4 4.4 Rescaling

[ ]:
```
num_attributes = df4[['age', 'height', 'weight', 'systolic_pressure',␣
↪'diastolic_pressure', 'bmi']]
```

[ ]:
```
multiple_kdeplots(num_attributes, 3, 2);
```




```
[ ]: multiple_boxplots(num_attributes, 3, 2);
```



1. Without Outlier and With Normal Distribution: Standard Scaler (Mean and std deviation)
2. With Outliers and Normal Distribution: Robust Scaler (Quartile)
3. Without Normal Distribution: MinMax Scaler

```
[ ]: # scaler
mms = MinMaxScaler()
rs = RobustScaler()
```

```
min_max_scaler = ['age', 'height', 'systolic_pressure', 'diastolic_pressure',␣
↪'bmi']
robust_scaler = ['weight']

for col in min_max_scaler:
    pickle.dump(mms, open(homepath + f'src/features/{col}_scaler.pkl', 'wb'))
    for dataframe in [x_train, x_test, x_val]:
        dataframe[[col]] = mms.fit_transform(dataframe[[col]].values)

for col in robust_scaler:
    pickle.dump(rs, open(homepath + f'src/features/{col}_scaler.pkl', 'wb'))
    for dataframe in [x_train, x_test, x_val]:
        dataframe[[col]] = rs.fit_transform(dataframe[[col]].values)
```

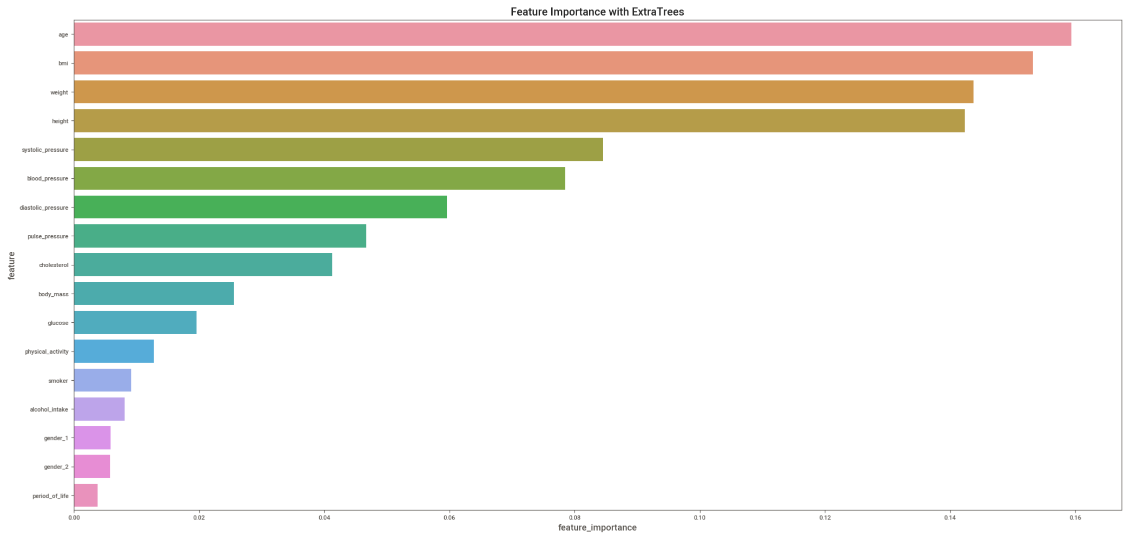
1.5.5 4.5 Split X and y

[ ]:
```
# target: cardio
y_train, y_test, y_val = [dataframe['cardio'] for dataframe in [x_train,␣
↪x_test, x_val]]
ids_train, ids_test, ids_val = [dataframe['id'] for dataframe in [x_train,␣
↪x_test, x_val]]
X_train, X_test, X_val = [dataframe.drop(columns = ['cardio', 'id']) for␣
↪dataframe in [x_train, x_test, x_val]]
```

1.5.6 4.6 Feature Importance

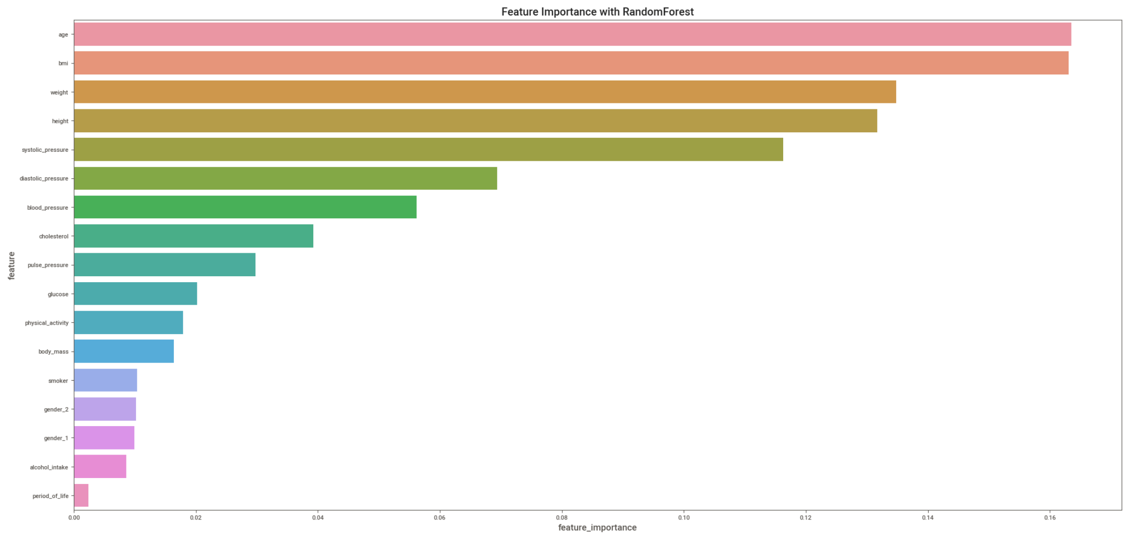
4.6.1 Feature Importance with ExtraTrees

[ ]:
```
et_importance = ExtraTreesClassifier(n_estimators = 100, random_state = seed,␣
↪n_jobs = 6)
et_importance.fit(X_train, y_train)

# feature importance dataframe
feature_selection = pd.DataFrame({'feature': X_train.
↪columns,'feature_importance': et_importance.feature_importances_})\
                                .sort_values('feature_importance', ascending =␣
↪False).reset_index(drop = True)

# plot feature importance
ax = sns.barplot(x = 'feature_importance', y = 'feature', data =␣
↪feature_selection, orient = 'h')
ax.set_title('Feature Importance with ExtraTrees');
```



4.6.2 Feature Importance with RandomForest

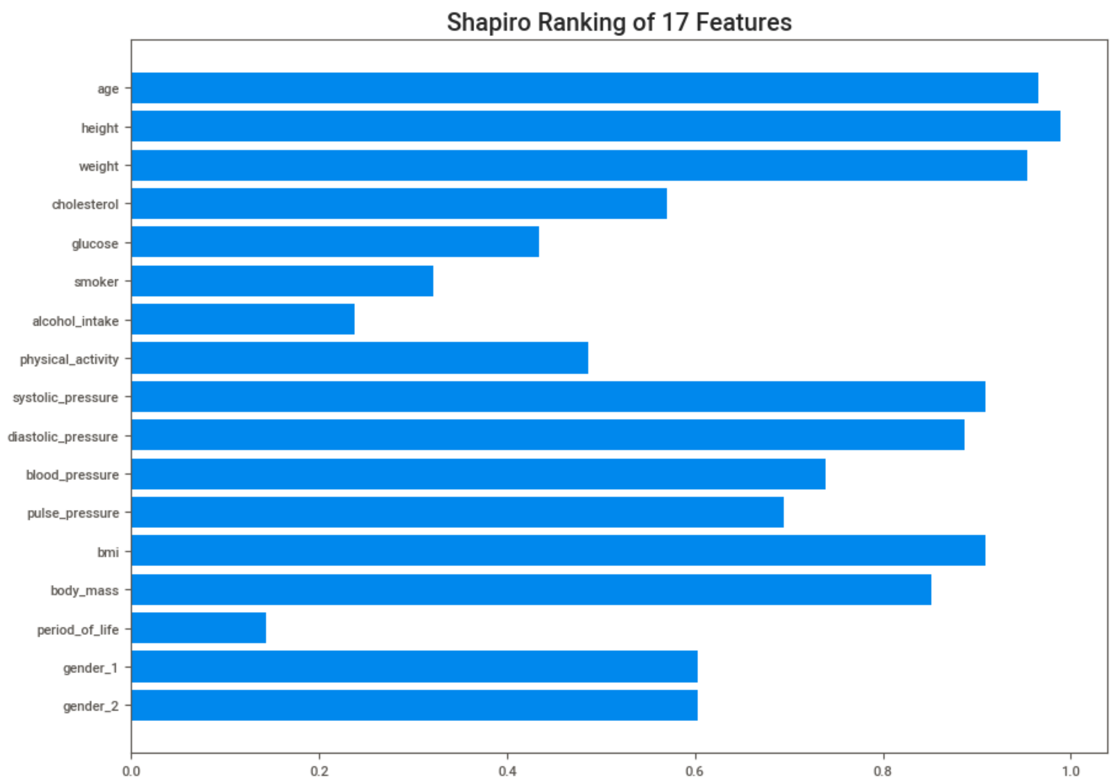
[ ]:
```
rf_importance = RandomForestClassifier(n_estimators = 100, random_state = seed, n_jobs = 6)
rf_importance.fit(X_train, y_train)

# feature importance dataframe
feature_selection = pd.DataFrame({'feature': X_train.columns,'feature_importance': rf_importance.feature_importances_})\
                                    .sort_values('feature_importance', ascending = False).reset_index(drop = True)

# plot feature importance
ax = sns.barplot(x = 'feature_importance', y = 'feature', data = feature_selection, orient = 'h')
ax.set_title('Feature Importance with RandomForest');
```



4.6.3 Rank Features

[ ]:
```python
visualizer_1d = Rank1D(algorithm = 'shapiro', size = (1024, 768))
visualizer_1d.fit(X_train, y_train)
visualizer_1d.transform(X_train)
visualizer_1d.finalize();
```

```
/home/gutto/Repos/Cardio-Catch-Diseases/.venv/lib/python3.9/site-
packages/scipy/stats/morestats.py:1681: UserWarning: p-value may not be accurate
for N > 5000.
  warnings.warn("p-value may not be accurate for N > 5000.")
```



To-do:

- p-value alert

4.6.4 Boruta

[ ]:
```
rf_boruta = RandomForestClassifier(n_estimators = 500, n_jobs = 6, random_state␣
↪= seed)

boruta = BorutaPy(rf_boruta, n_estimators = 'auto', random_state = seed).
↪fit(X_train.values, y_train.values)
```

[ ]:
```
cols_selected = boruta.support_.tolist()

cols_selected_boruta = X_train.iloc[:, cols_selected].columns.to_list()

cols_not_selected_boruta = list(np.setdiff1d(X_train.columns,␣
↪cols_selected_boruta))
```

[ ]:
```
cols_selected_boruta
```

[ ]:
```
['age', 'systolic_pressure', 'bmi']
```

[ ]:
```
cols_not_selected_boruta
```

[ ]:
```
['alcohol_intake',
 'blood_pressure',
 'body_mass',
 'cholesterol',
 'diastolic_pressure',
 'gender_1',
 'gender_2',
 'glucose',
 'height',
 'period_of_life',
 'physical_activity',
 'pulse_pressure',
 'smoker',
 'weight']
```

1.5.7 4.7 Save State

[ ]:
```
X_train.to_pickle(homepath + 'data/processed/X_train.pkl')
X_test.to_pickle(homepath + 'data/processed/X_test.pkl')
X_val.to_pickle(homepath + 'data/processed/X_val.pkl')
y_train.to_pickle(homepath + 'data/processed/y_train.pkl')
y_test.to_pickle(homepath + 'data/processed/y_test.pkl')
y_val.to_pickle(homepath + 'data/processed/y_val.pkl')
ids_train.to_pickle(homepath + 'data/processed/ids_train.pkl')
ids_test.to_pickle(homepath + 'data/processed/ids_test.pkl')
ids_val.to_pickle(homepath + 'data/processed/ids_val.pkl')
```

1.6 5. MACHINE LEARNING MODELLING

[ ]:
```
X_train = pd.read_pickle(homepath + 'data/processed/X_train.pkl')
X_val = pd.read_pickle(homepath + 'data/processed/X_val.pkl')
y_train = pd.read_pickle(homepath + 'data/processed/y_train.pkl')
y_val = pd.read_pickle(homepath + 'data/processed/y_val.pkl')
```

[ ]:
```
models = [
          RandomForestClassifier(random_state = seed, n_jobs = 7),
          ExtraTreesClassifier(random_state = seed, n_jobs = 7),
          GaussianNB(),
          XGBClassifier(random_state = seed, n_jobs = 7, eval_metric =␣
 ↪'logloss', use_label_encoder = False),
          CatBoostClassifier(random_state = seed, verbose = False),
          AdaBoostClassifier(random_state = seed),
          LGBMClassifier(random_state = seed, n_jobs = 7),
          KNeighborsClassifier(n_neighbors = 7, n_jobs = 7),
          GradientBoostingClassifier(random_state = seed)
```

```
         ]
```

[ ]:
```
metrics_result = metrics_df(models, 'cardio', X_train, y_train, X_val, y_val)
```

```
Please, wait a moment - Doing ML
Training model 1/9 -> RandomForestClassifier
Training model 2/9 -> ExtraTreesClassifier
Training model 3/9 -> GaussianNB
Training model 4/9 -> XGBClassifier
Training model 5/9 -> CatBoostClassifier
Training model 6/9 -> AdaBoostClassifier
Training model 7/9 -> LGBMClassifier
Training model 8/9 -> KNeighborsClassifier
Training model 9/9 -> GradientBoostingClassifier
Finished, check the results
```

[ ]:
```
metrics_result
```

[ ]:

	Model_Name	Accuracy	Precision	Recall	F1-Score	ROCAUC
0	RandomForestClassifier	0.717	0.719	0.715	0.717	0.717
0	ExtraTreesClassifier	0.710	0.701	0.736	0.718	0.710
0	GaussianNB	0.686	0.646	0.827	0.725	0.686
0	XGBClassifier	0.723	0.730	0.709	0.719	0.723
0	CatBoostClassifier	0.721	0.721	0.723	0.722	0.721
0	AdaBoostClassifier	0.721	0.767	0.637	0.696	0.721
0	LGBMClassifier	0.731	0.749	0.697	0.722	0.731
0	KNeighborsClassifier	0.703	0.704	0.705	0.704	0.703
0	GradientBoostingClassifier	0.726	0.753	0.675	0.712	0.726

[ ]:
```
cv_result = cross_validation(models, 'cardio', X_train, y_train)
```

```
Please, wait a moment, Doing CV
Folding model 1/9 -> RandomForestClassifier
Folding model 2/9 -> ExtraTreesClassifier
Folding model 3/9 -> GaussianNB
Folding model 4/9 -> XGBClassifier
Folding model 5/9 -> CatBoostClassifier
Folding model 6/9 -> AdaBoostClassifier
Folding model 7/9 -> LGBMClassifier
Folding model 8/9 -> KNeighborsClassifier
Folding model 9/9 -> GradientBoostingClassifier
Finished, check the results
```

[ ]:
```
cv_result
```

[ ]:
```
                    Model_Name  Accuracy Mean  Accuracy STD  Precision Mean  \
 Precision STD  Recall Mean  Recall STD  F1 Score Mean  F1 Score STD  ROCAUC Mean  \
```

```
ROCAUC STD
0      RandomForestClassifier          0.712         0.004            0.715
0.004        0.705        0.005          0.710         0.004        0.712
0.004
0        ExtraTreesClassifier          0.706         0.008            0.709
0.008        0.699        0.009          0.704         0.008        0.706
0.008
0                  GaussianNB          0.712         0.010            0.721
0.019        0.691        0.014          0.705         0.007        0.712
0.010
0               XGBClassifier          0.717         0.013            0.729
0.022        0.691        0.012          0.709         0.010        0.717
0.013
0          CatBoostClassifier          0.721         0.014            0.734
0.022        0.693        0.012          0.713         0.011        0.721
0.014
0          AdaBoostClassifier          0.723         0.014            0.740
0.024        0.687        0.016          0.712         0.010        0.723
0.014
0              LGBMClassifier          0.725         0.014            0.743
0.023        0.689        0.015          0.714         0.011        0.725
0.014
0        KNeighborsClassifier          0.722         0.015            0.737
0.026        0.690        0.015          0.713         0.011        0.722
0.015
0  GradientBoostingClassifier          0.723         0.015            0.740
0.025        0.691        0.014          0.714         0.011        0.723
0.015
```

1.7 6. HYPERPARAMETER FINE TUNNING

1.8 7. BUSINESS TRANSLATION