

# Project Name : Cardiovascular(Heart) Diseases Risk Prediction Using ML

By

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## Importing Libraries

In [6]:

```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
sns.set_theme(color_codes=True)
```

## Importing Dataset

In [7]:

```
print("Importing data....")
df = pd.read_csv(r"C:\Users\md naiyer azam\Desktop\Dataset files\CVD_cleaned.csv")
print("Sucessfully imported...")
```

```
Importing data....
Sucessfully imported...
```

In [8]:

```
df.head() # it is used to give first five row
```

Out[8]:

	General_Health	Checkup	Exercise	Heart_Disease	Skin_Cancer	Other_Cancer	Depression	Diabetes
0	Poor	Within the past 2 years	No	No	No	No	No	No
1	Very Good	Within the past year	No	Yes	No	No	No	Yes
2	Very Good	Within the past year	Yes	No	No	No	No	Yes
3	Poor	Within the past year	Yes	Yes	No	No	No	Yes
4	Good	Within the past year	No	No	No	No	No	No

## Data Preprocessing Part 1

In [9]:

```
#Check the number of unique value from all of the object datatype
df.select_dtypes(include='object').nunique()
```

Out[9]:

```
General_Health      5
Checkup             5
Exercise            2
Heart_Disease       2
Skin_Cancer         2
Other_Cancer        2
Depression          2
Diabetes            4
Arthritis           2
Sex                 2
Age_Category       13
Smoking_History     2
dtype: int64
```

## Exploratory Data Analysis

In [10]:

```
# list of categorical variables to plot
cat_vars = ['General_Health', 'Checkup', 'Exercise', 'Skin_Cancer', 'Other_Cancer',
            'Depression', 'Diabetes', 'Arthritis', 'Sex', 'Age_Category', 'Smoking_History']

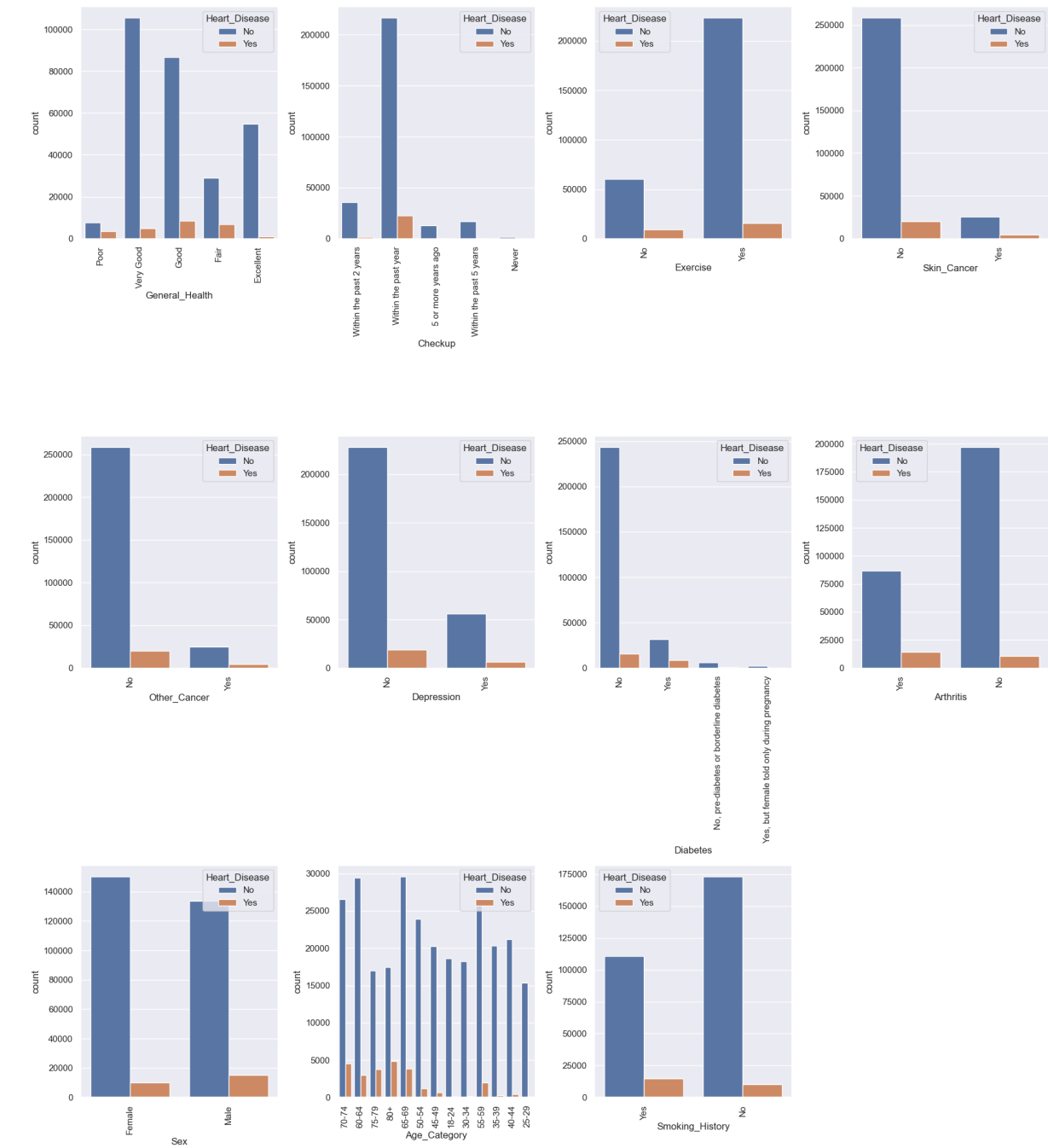
# create figure with subplots
fig, axs = plt.subplots(nrows=3, ncols=4, figsize=(18, 20))
axs = axs.flatten()

# create barplot for each categorical variable
for i, var in enumerate(cat_vars):
    sns.countplot(x=var, hue='Heart_Disease', data=df, ax=axs[i])
    axs[i].set_xticklabels(axs[i].get_xticklabels(), rotation=90)

# adjust spacing between subplots
fig.tight_layout()

# remove the 12th subplot
fig.delaxes(axs[11])

# show plot
plt.show()
```



In [11]:

```
import warnings
warnings.filterwarnings("ignore")
# get list of categorical variables
cat_vars = ['General_Health', 'Checkup', 'Exercise', 'Skin_Cancer', 'Other_Cancer',
            'Depression', 'Diabetes', 'Arthritis', 'Sex', 'Age_Category', 'Smoking_History']

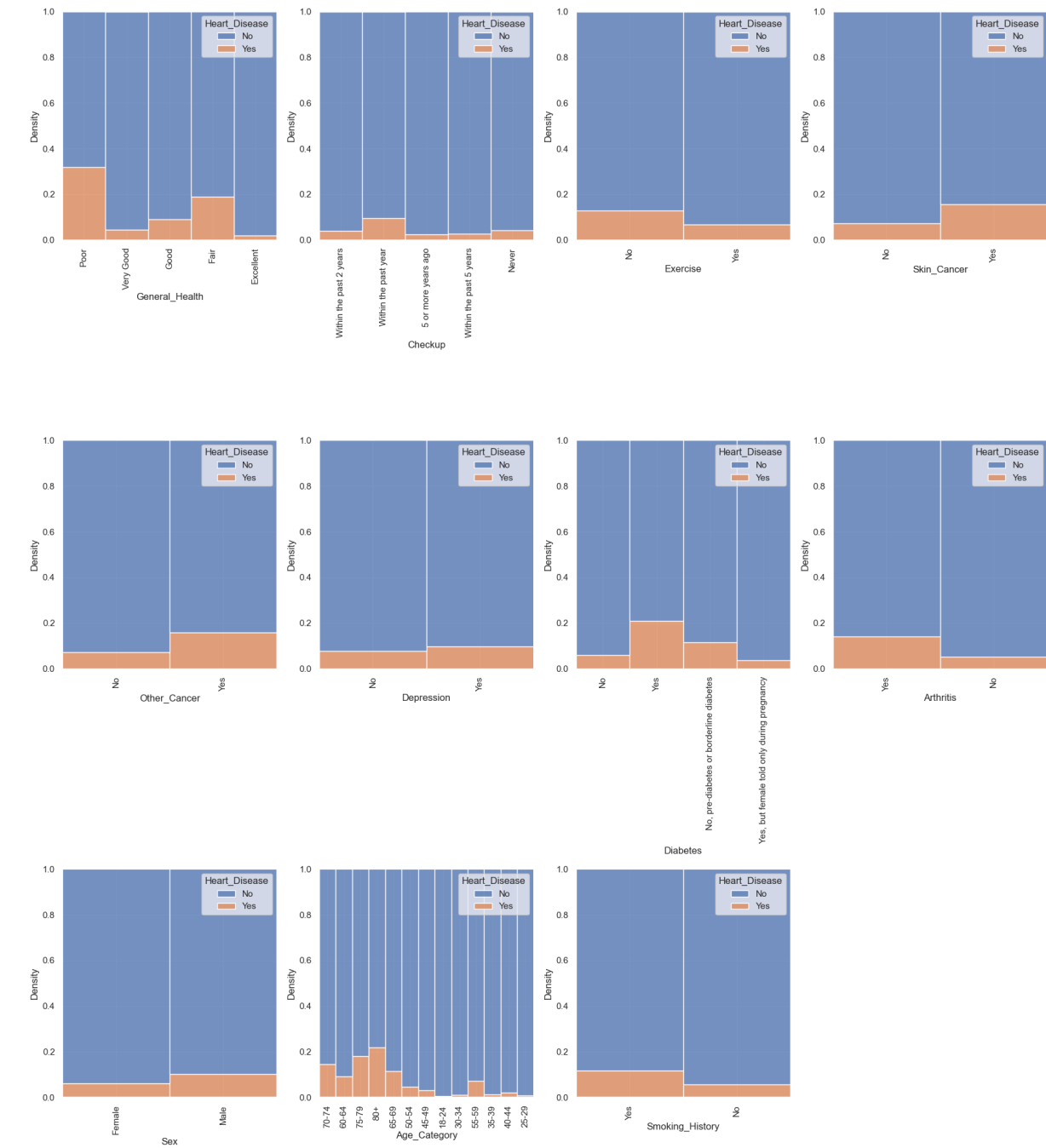
# create figure with subplots
fig, axs = plt.subplots(nrows=3, ncols=4, figsize=(18, 20))
axs = axs.flatten()

# create histplot for each categorical variable
for i, var in enumerate(cat_vars):
    sns.histplot(x=var, hue='Heart_Disease', data=df, ax=axs[i], multiple="fill", kde=False, element='step')
    axs[i].set_xticklabels(df[var].unique(), rotation=90)
    axs[i].set_xlabel(var)

# adjust spacing between subplots
fig.tight_layout()

# remove the 12th subplot
fig.delaxes(axs[11])

# show plot
plt.show()
```



In [12]:

```
# Specify the maximum number of categories to show individually
max_categories = 5

cat_vars = ['General_Health', 'Checkup', 'Exercise', 'Skin_Cancer', 'Other_Cancer',
            'Depression', 'Diabetes', 'Arthritis', 'Sex', 'Age_Category', 'Smoking_History', 'Heart_Health']

# Create a figure and axes
fig, axs = plt.subplots(nrows=3, ncols=4, figsize=(22, 22))

# Create a pie chart for each categorical variable
for i, var in enumerate(cat_vars):
    if i < len(axs.flat):
        # Count the number of occurrences for each category
        cat_counts = df[var].value_counts()

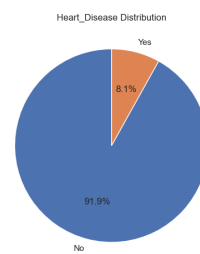
        # Group categories beyond the top max_categories as 'Other'
        if len(cat_counts) > max_categories:
            cat_counts_top = cat_counts[:max_categories]
            cat_counts_other = pd.Series(cat_counts[max_categories:].sum(), index=['Other'])
            cat_counts = cat_counts_top.append(cat_counts_other)

        # Create a pie chart
        axs.flat[i].pie(cat_counts, labels=cat_counts.index, autopct='%1.1f%%', startangle=90)

        # Set a title for each subplot
        axs.flat[i].set_title(f'{var} Distribution')

# Adjust spacing between subplots
fig.tight_layout()

# Show the plot
plt.show()
```





In [13]:

```

num_vars = ['Height_(cm)', 'Weight_(kg)', 'BMI', 'Alcohol_Consumption',
            'Fruit_Consumption', 'Green_Vegetables_Consumption', 'FriedPotato_Consumption']

fig, axs = plt.subplots(nrows=3, ncols=3, figsize=(20, 10))
axs = axs.flatten()

for i, var in enumerate(num_vars):
    sns.boxplot(x=var, data=df, ax=axs[i])

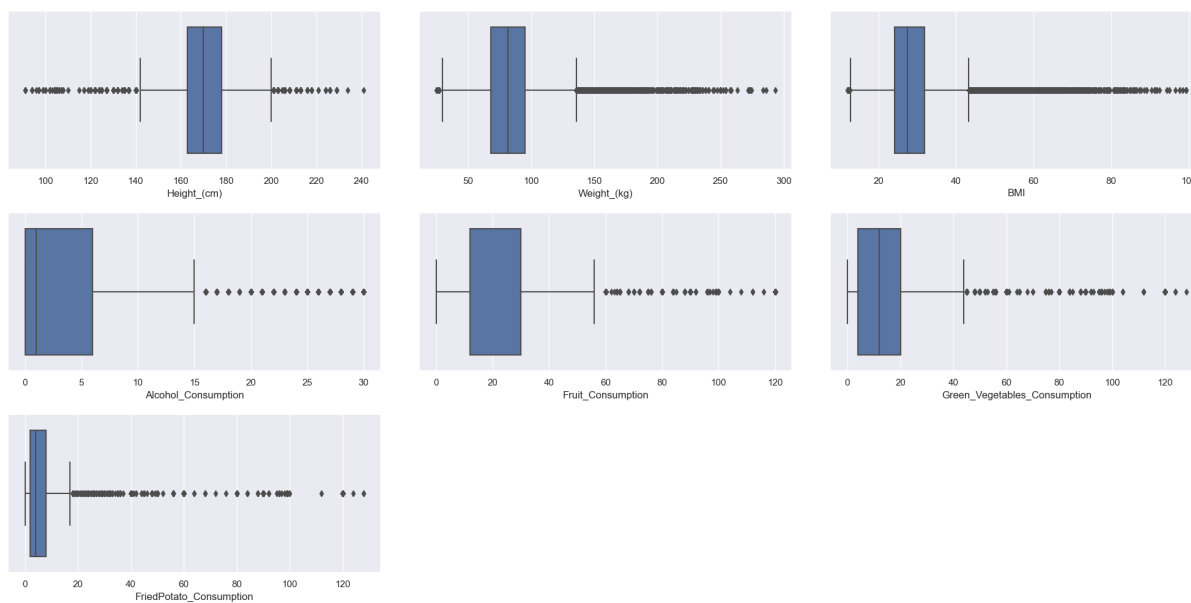
fig.tight_layout()

# remove the 8th subplot
fig.delaxes(axs[7])

# remove the 9th subplot
fig.delaxes(axs[8])

plt.show()

```



In [14]:

```

num_vars = ['Height_(cm)', 'Weight_(kg)', 'BMI', 'Alcohol_Consumption',
            'Fruit_Consumption', 'Green_Vegetables_Consumption', 'FriedPotato_Consumption']

fig, axs = plt.subplots(nrows=3, ncols=3, figsize=(20, 20))
axs = axs.flatten()

for i, var in enumerate(num_vars):
    sns.boxplot(y=var, x='Heart_Disease', data=df, ax=axs[i])

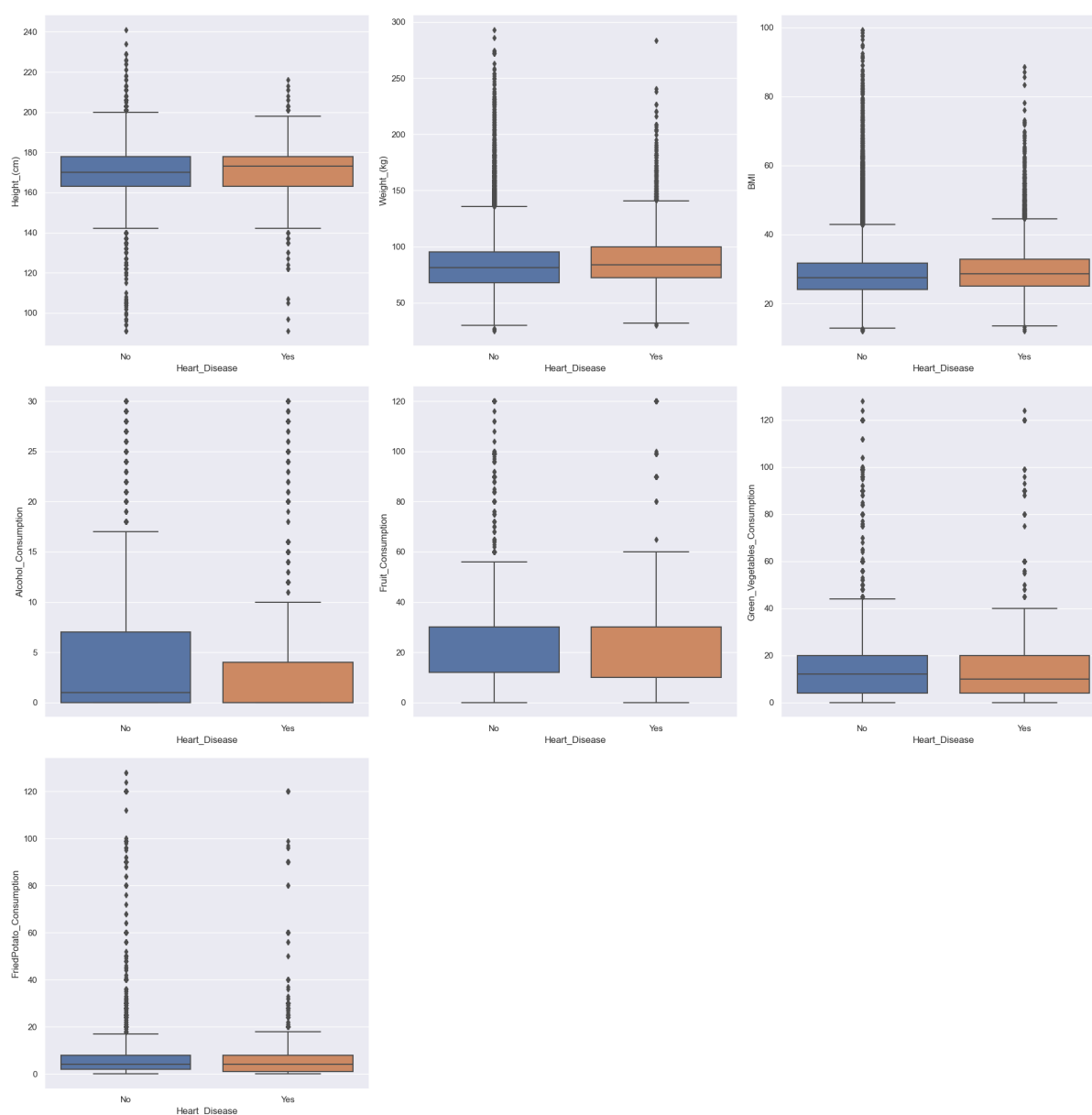
fig.tight_layout()

# remove the 8th subplot
fig.delaxes(axs[7])

# remove the 9th subplot
fig.delaxes(axs[8])

plt.show()

```



In [15]:

```

num_vars = ['Height_(cm)', 'Weight_(kg)', 'BMI', 'Alcohol_Consumption',
            'Fruit_Consumption', 'Green_Vegetables_Consumption', 'FriedPotato_Consumption']

fig, axs = plt.subplots(nrows=3, ncols=3, figsize=(20, 10))
axs = axs.flatten()

for i, var in enumerate(num_vars):
    sns.violinplot(x=var, data=df, ax=axs[i])

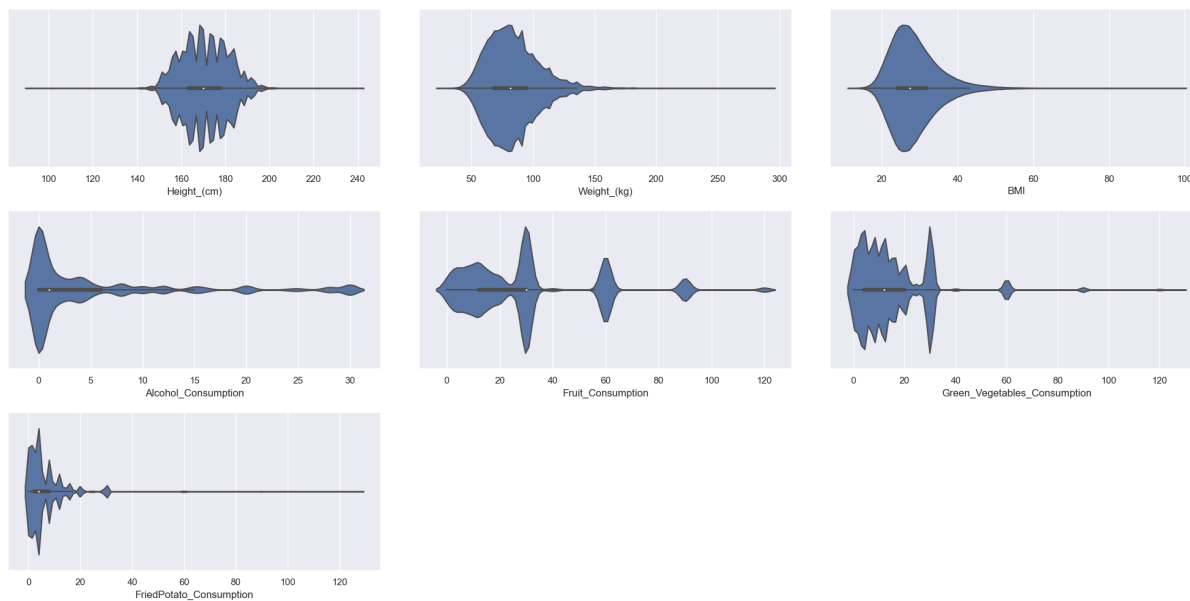
fig.tight_layout()

# remove the 8th subplot
fig.delaxes(axs[7])

# remove the 9th subplot
fig.delaxes(axs[8])

plt.show()

```



In [16]:

```

num_vars = ['Height_(cm)', 'Weight_(kg)', 'BMI', 'Alcohol_Consumption',
            'Fruit_Consumption', 'Green_Vegetables_Consumption', 'FriedPotato_Consumption']

fig, axs = plt.subplots(nrows=3, ncols=3, figsize=(20, 20))
axs = axs.flatten()

for i, var in enumerate(num_vars):
    sns.violinplot(y=var, data=df, x='Heart_Disease', ax=axs[i])

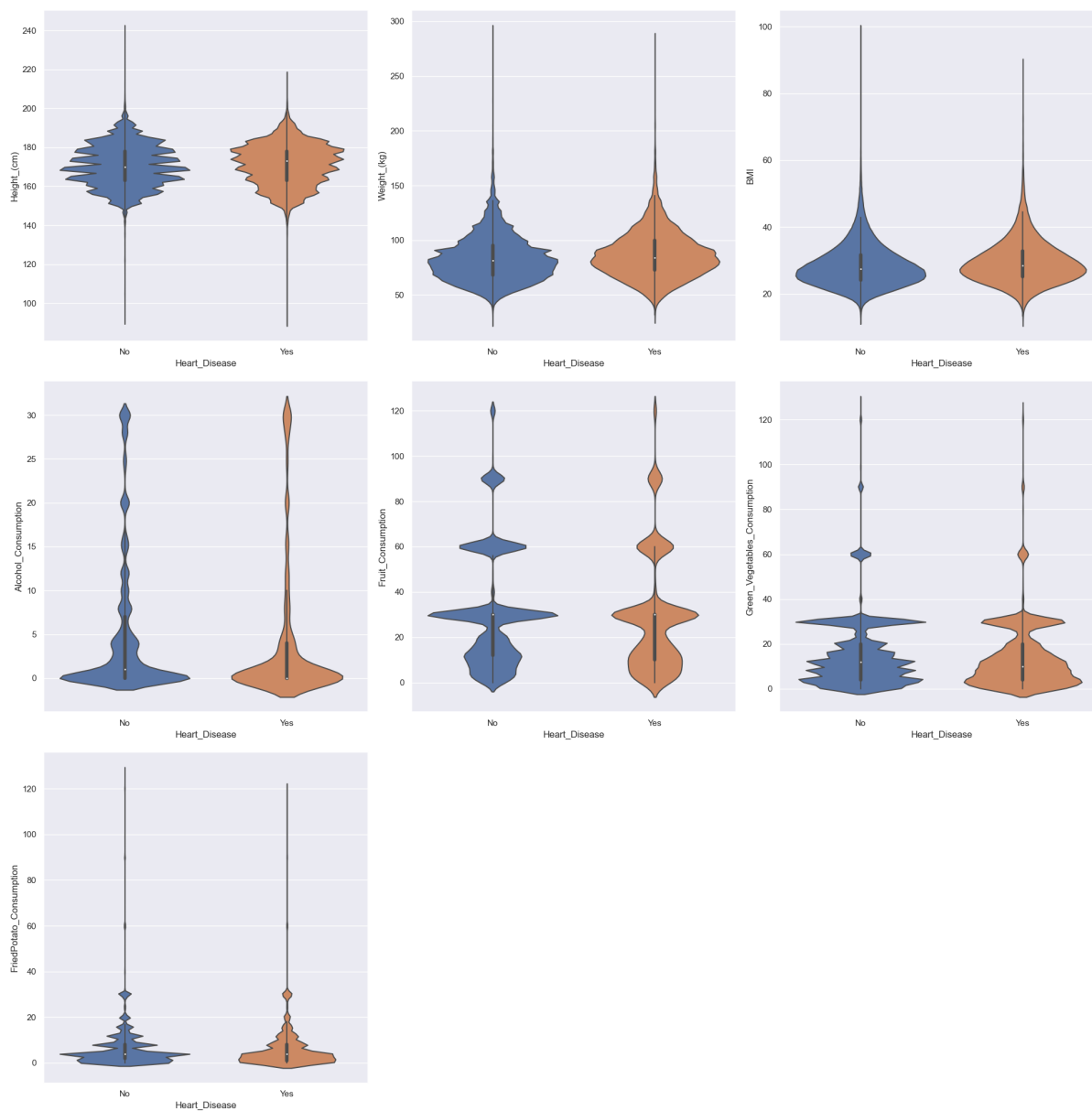
fig.tight_layout()

# remove the 8th subplot
fig.delaxes(axs[7])

# remove the 9th subplot
fig.delaxes(axs[8])

plt.show()

```



## Data Preprocessing Part 2

In [17]:

```
#Check missing value
check_missing = df.isnull().sum() * 100 / df.shape[0]
check_missing[check_missing > 0].sort_values(ascending=False)
```

Out[17]:

```
Series([], dtype: float64)
```

## Label Encoding for each Object datatype

In [18]:

```
# Loop over each column in the DataFrame where dtype is 'object'
for col in df.select_dtypes(include=['object']).columns:

    # Print the column name and the unique values
    print(f"{col}: {df[col].unique()}")
```

```
General_Health: ['Poor' 'Very Good' 'Good' 'Fair' 'Excellent']
Checkup: ['Within the past 2 years' 'Within the past year' '5 or more years ago'
'Within the past 5 years' 'Never']
Exercise: ['No' 'Yes']
Heart_Disease: ['No' 'Yes']
Skin_Cancer: ['No' 'Yes']
Other_Cancer: ['No' 'Yes']
Depression: ['No' 'Yes']
Diabetes: ['No' 'Yes' 'No, pre-diabetes or borderline diabetes'
'Yes, but female told only during pregnancy']
Arthritis: ['Yes' 'No']
Sex: ['Female' 'Male']
Age_Category: ['70-74' '60-64' '75-79' '80+' '65-69' '50-54' '45-49' '18-24' '30-34'
'55-59' '35-39' '40-44' '25-29']
Smoking_History: ['Yes' 'No']
```

In [19]:

```
from sklearn import preprocessing

# Loop over each column in the DataFrame where dtype is 'object'
for col in df.select_dtypes(include=['object']).columns:

    # Initialize a LabelEncoder object
    label_encoder = preprocessing.LabelEncoder()

    # Fit the encoder to the unique values in the column
    label_encoder.fit(df[col].unique())

    # Transform the column using the encoder
    df[col] = label_encoder.transform(df[col])

    # Print the column name and the unique encoded values
    print(f"{col}: {df[col].unique()}")
```

```
General_Health: [3 4 2 1 0]
Checkup: [2 4 0 3 1]
Exercise: [0 1]
Heart_Disease: [0 1]
Skin_Cancer: [0 1]
Other_Cancer: [0 1]
Depression: [0 1]
Diabetes: [0 2 1 3]
Arthritis: [1 0]
Sex: [0 1]
Age_Category: [10 8 11 12 9 6 5 0 2 7 3 4 1]
Smoking_History: [1 0]
```

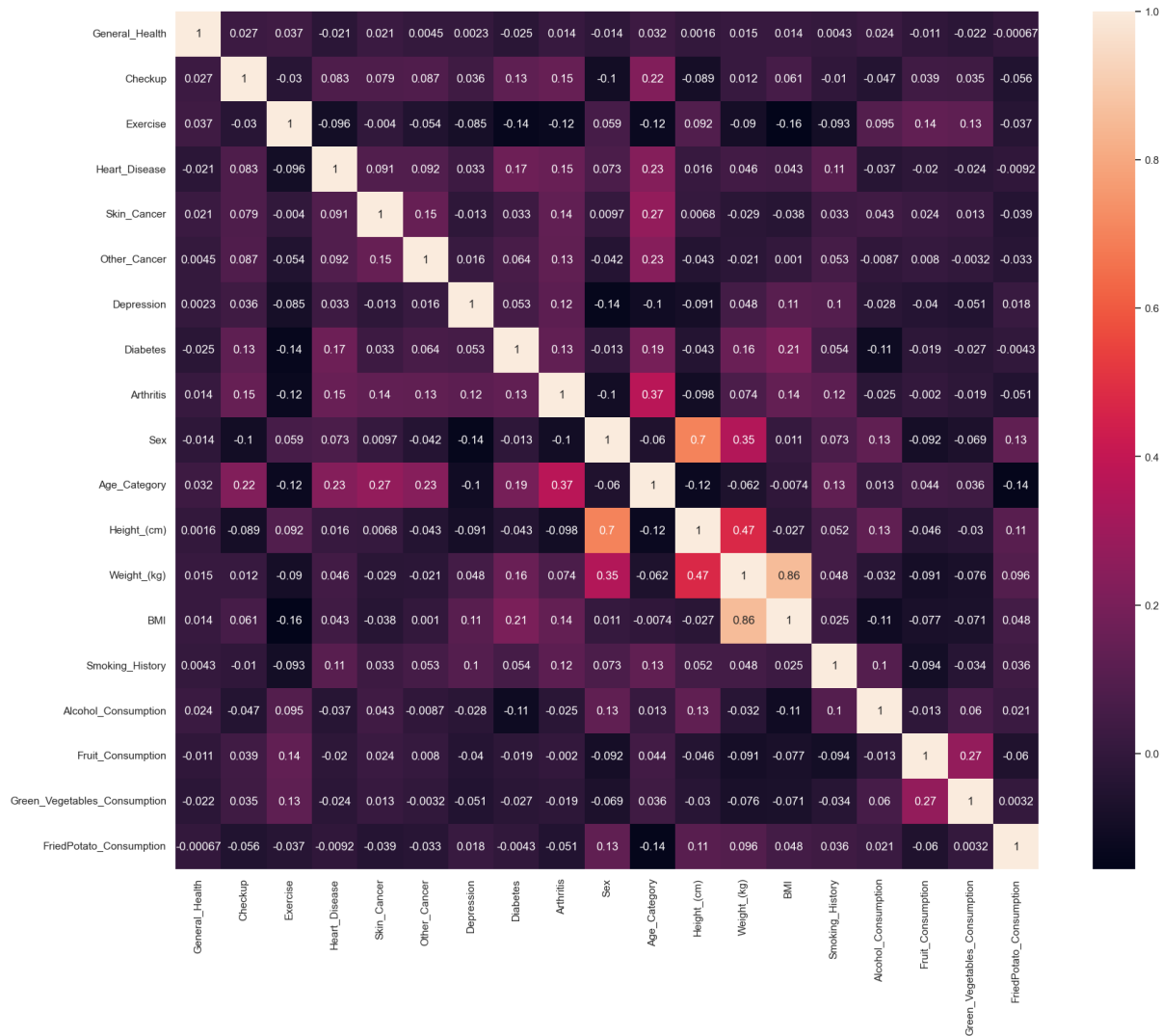
## Correlation Heatmap

In [20]:

```
#Correlation Heatmap (print the correlation score each variables)
plt.figure(figsize=(20, 16))
sns.heatmap(df.corr(), fmt='.2g', annot=True)
```

Out[20]:

<AxesSubplot: >



## Train Test Split

In [21]:

```
from sklearn.model_selection import train_test_split
# Select the features (X) and the target variable (y)
X = df.drop('Heart_Disease', axis=1)
y = df['Heart_Disease']

# Split the data into training and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=0)
```

## Remove the Outlier from train data using IQR

In [22]:

```
# Define the columns for which you want to remove outliers
selected_columns = ['Height(cm)', 'Weight(kg)', 'BMI', 'Alcohol_Consumption',
                    'Fruit_Consumption', 'Green_Vegetables_Consumption', 'FriedPotato_Consumption']

# Calculate the IQR for the selected columns in the training data
Q1 = X_train[selected_columns].quantile(0.25)
Q3 = X_train[selected_columns].quantile(0.75)
IQR = Q3 - Q1

# Set a threshold value for outlier detection (e.g., 1.5 times the IQR)
threshold = 1.5

# Find the indices of outliers based on the threshold
outlier_indices = np.where(
    (X_train[selected_columns] < (Q1 - threshold * IQR)) |
    (X_train[selected_columns] > (Q3 + threshold * IQR))
)[0]

# Remove the outliers from the training data and corresponding labels
X_train = X_train.drop(X_train.index[outlier_indices])
y_train = y_train.drop(y_train.index[outlier_indices])
```

## Decision Tree

In [23]:

```
from sklearn.tree import DecisionTreeClassifier
dtree = DecisionTreeClassifier(random_state=0, max_depth=12, min_samples_leaf=2, min_samples_split=2)
dtree.fit(X_train, y_train)
```

Out[23]:

```
DecisionTreeClassifier
DecisionTreeClassifier(class_weight='balanced', max_depth=12,
                      min_samples_leaf=2, random_state=0)
```

In [24]:

```
from sklearn.metrics import accuracy_score
y_pred = dtree.predict(X_test)
print("Accuracy Score :", round(accuracy_score(y_test, y_pred)*100, 2), "%")
```

Accuracy Score : 71.45 %

In [25]:

```
from sklearn.metrics import accuracy_score, f1_score, precision_score, recall_score, jaccard_score
print('F-1 Score : ', (f1_score(y_test, y_pred, average='micro')))
print('Precision Score : ', (precision_score(y_test, y_pred, average='micro')))
print('Recall Score : ', (recall_score(y_test, y_pred, average='micro')))
print('Jaccard Score : ', (jaccard_score(y_test, y_pred, average='micro')))
```

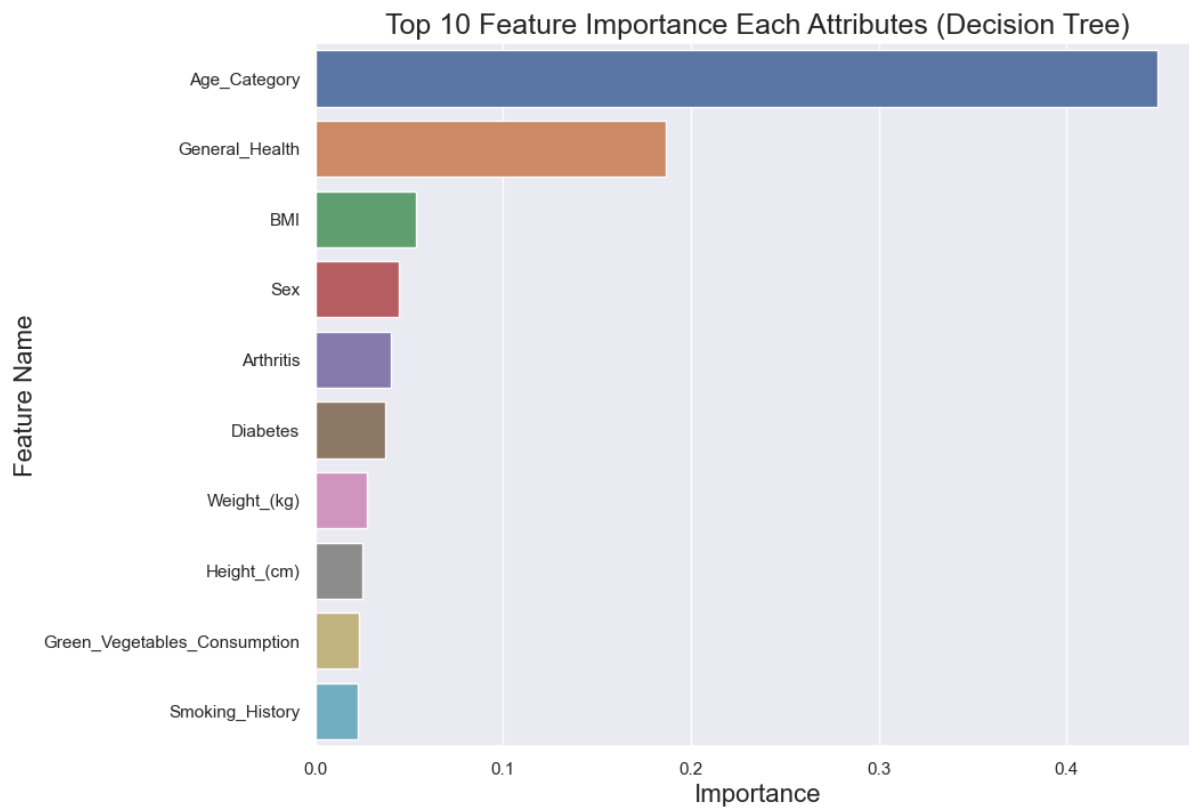
F-1 Score : 0.7144938563403539  
Precision Score : 0.7144938563403539  
Recall Score : 0.7144938563403539  
Jaccard Score : 0.5558074225194253



In [26]:

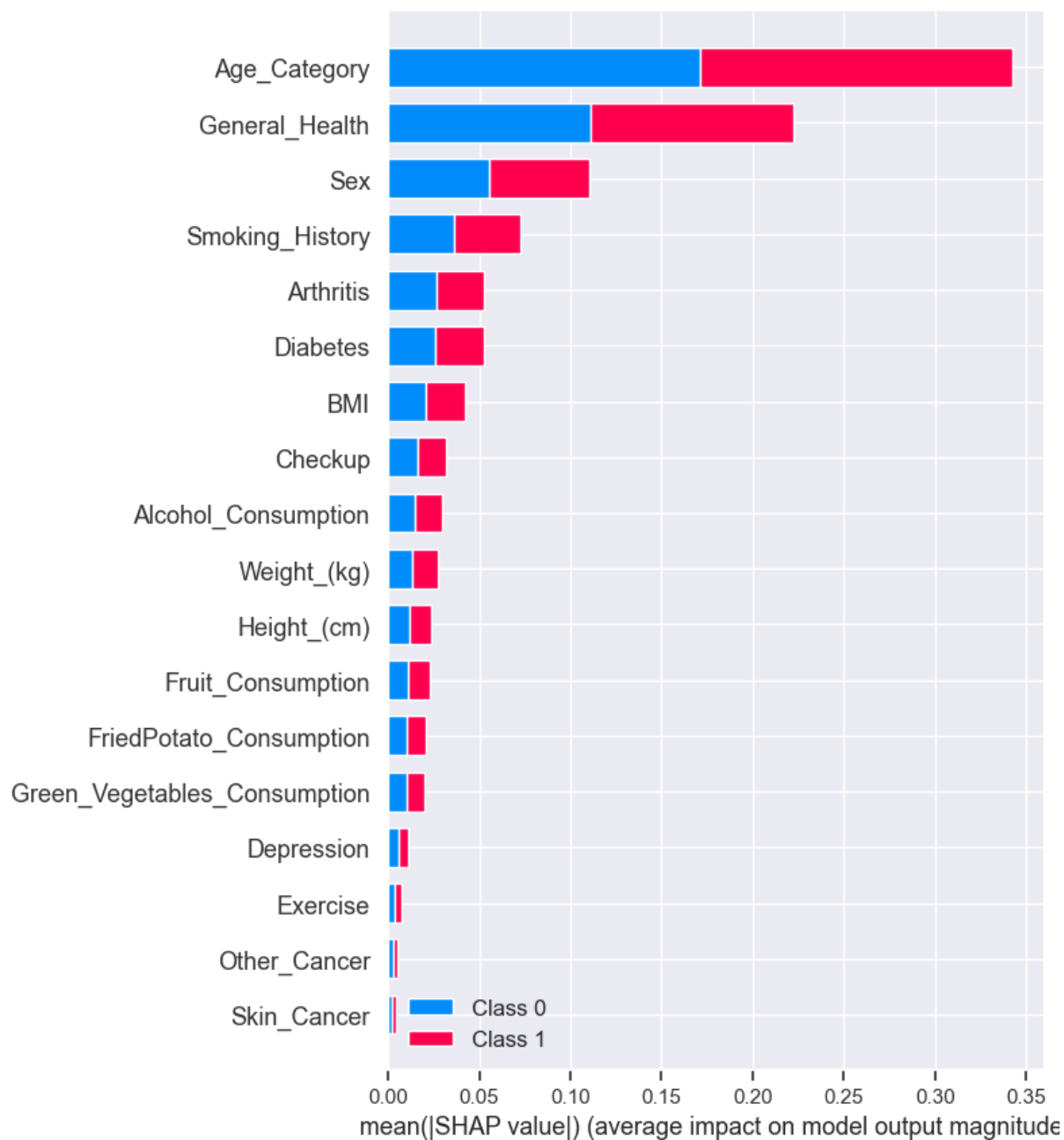
```
imp_df = pd.DataFrame({
    "Feature Name": X_train.columns,
    "Importance": dtree.feature_importances_
})
fi = imp_df.sort_values(by="Importance", ascending=False)

fi2 = fi.head(10)
plt.figure(figsize=(10,8))
sns.barplot(data=fi2, x='Importance', y='Feature Name')
plt.title('Top 10 Feature Importance Each Attributes (Decision Tree)', fontsize=18)
plt.xlabel ('Importance', fontsize=16)
plt.ylabel ('Feature Name', fontsize=16)
plt.show()
```



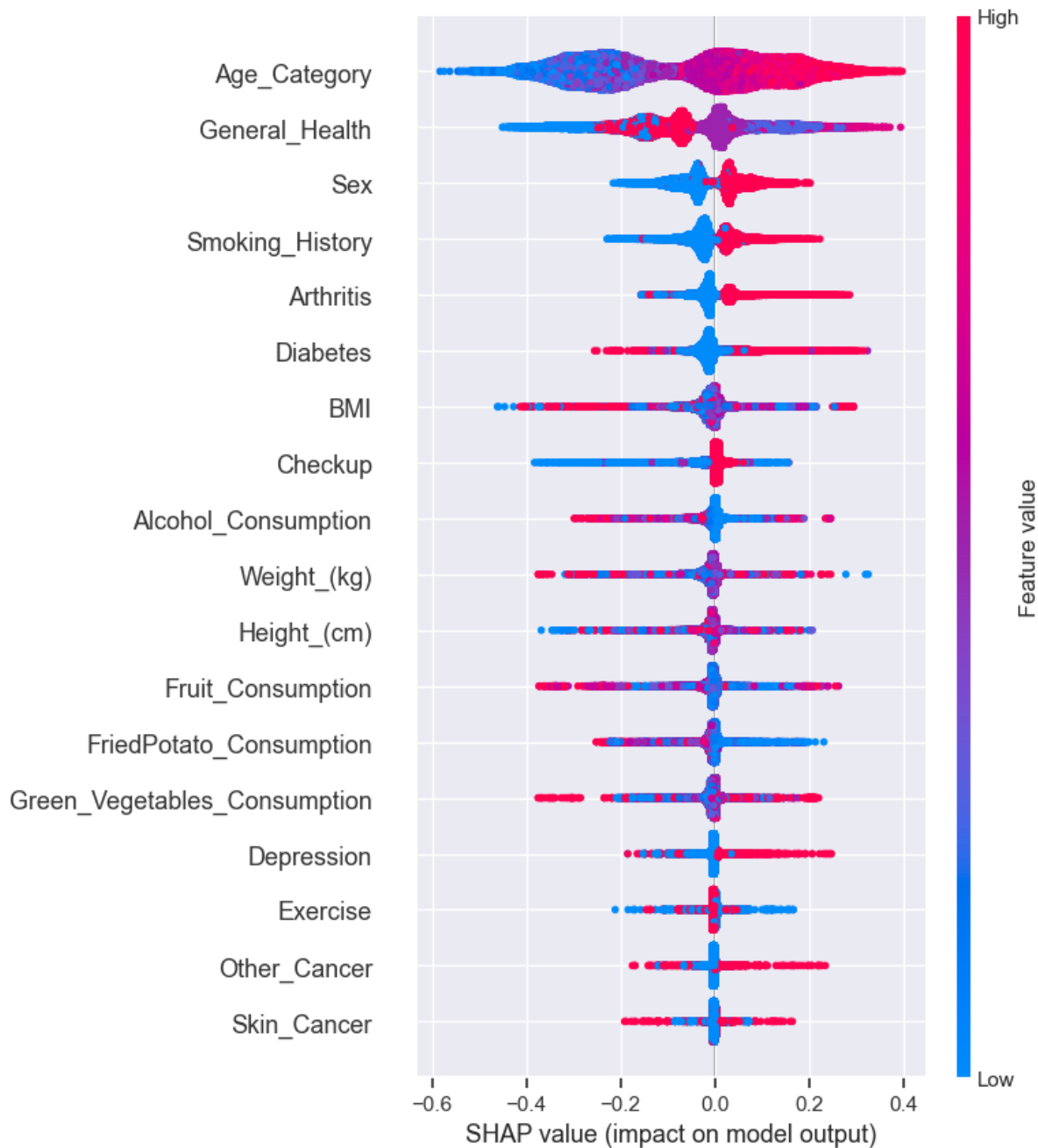
In [29]:

```
import shap
explainer = shap.TreeExplainer(dtree)
shap_values = explainer.shap_values(X_test)
shap.summary_plot(shap_values, X_test)
```



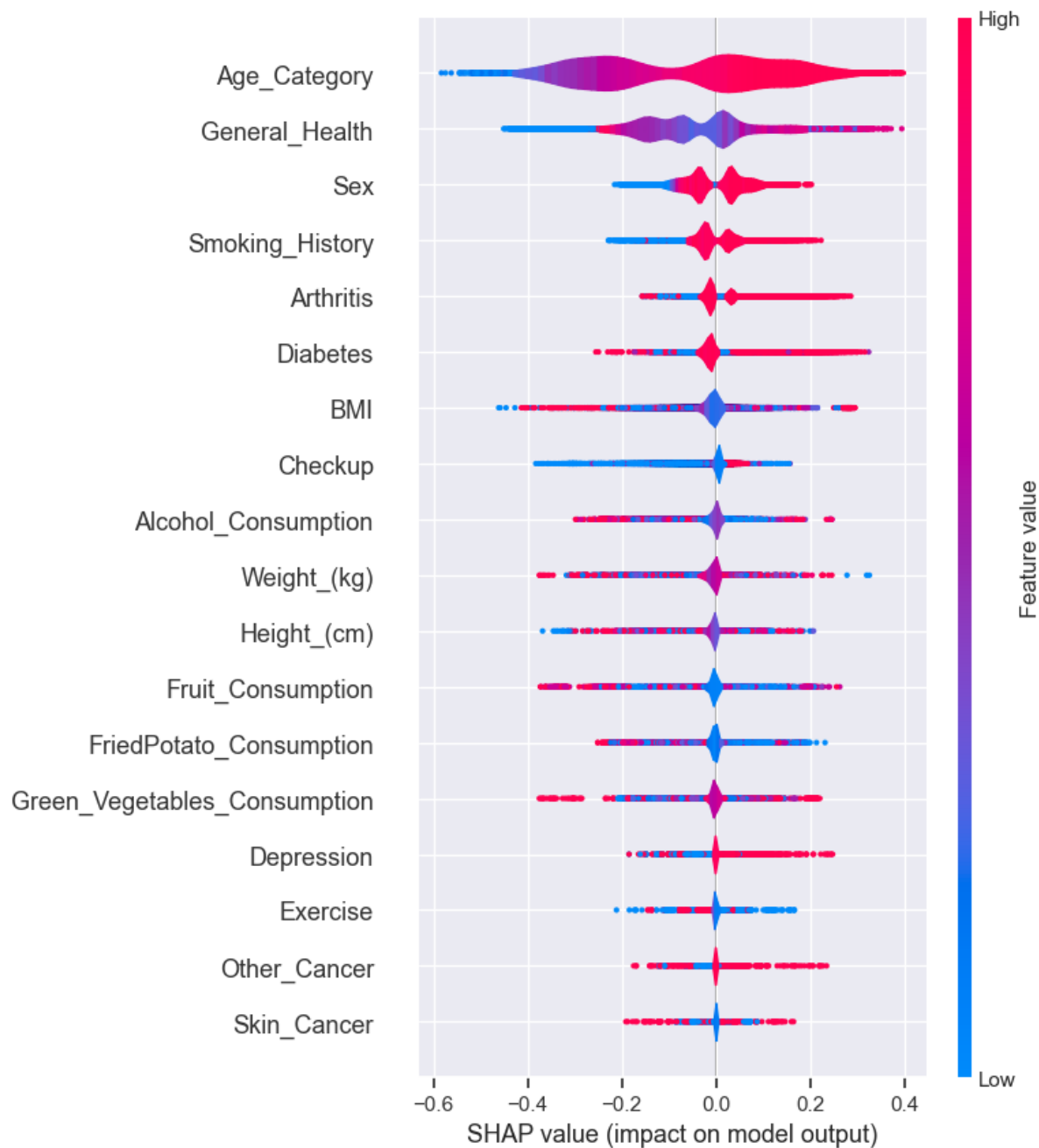
In [30]:

```
# compute SHAP values
explainer = shap.TreeExplainer(dtree)
shap_values = explainer.shap_values(X_test)
shap.summary_plot(shap_values[1], X_test.values, feature_names = X_test.columns)
```



In [31]:

```
# compute SHAP values
explainer = shap.TreeExplainer(dtree)
shap_values = explainer.shap_values(X_test)
shap.summary_plot(shap_values[1], X_test.values, feature_names = X_test.columns, plot_type="violin")
```

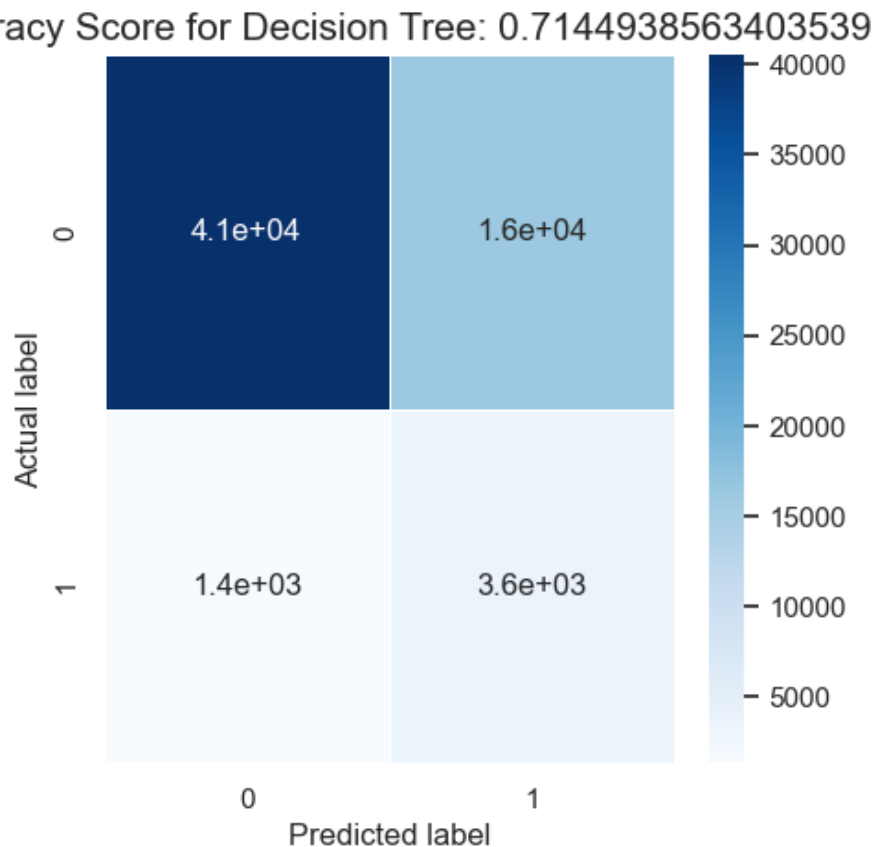


In [32]:

```
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_pred)
plt.figure(figsize=(5,5))
sns.heatmap(data=cm,linewidths=.5, annot=True, cmap = 'Blues')
plt.ylabel('Actual label')
plt.xlabel('Predicted label')
all_sample_title = 'Accuracy Score for Decision Tree: {0}'.format(dtree.score(X_test, y_test))
plt.title(all_sample_title, size = 15)
```

Out[32]:

Text(0.5, 1.0, 'Accuracy Score for Decision Tree: 0.7144938563403539')



In [33]:

```
from sklearn.metrics import roc_curve, roc_auc_score
y_pred_proba = dtree.predict_proba(X_test)[:][:,1]

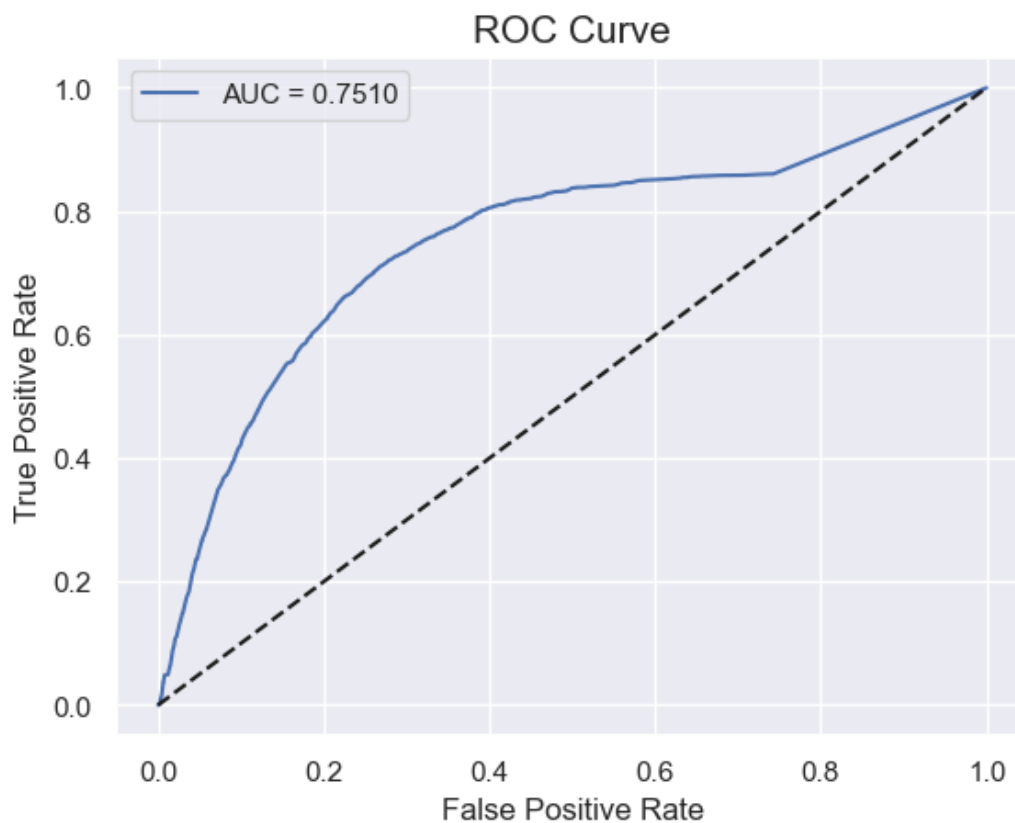
df_actual_predicted = pd.concat([pd.DataFrame(np.array(y_test), columns=['y_actual']), pd.DataFrame(
df_actual_predicted.index = y_test.index

fpr, tpr, tr = roc_curve(df_actual_predicted['y_actual'], df_actual_predicted['y_pred_proba'])
auc = roc_auc_score(df_actual_predicted['y_actual'], df_actual_predicted['y_pred_proba'])

plt.plot(fpr, tpr, label='AUC = %0.4f' %auc)
plt.plot(fpr, fpr, linestyle = '--', color='k')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve', size = 15)
plt.legend()
```

Out[33]:

<matplotlib.legend.Legend at 0x251f2aad660>



## Random Forest

In [34]:

```
from sklearn.ensemble import RandomForestClassifier
rfc = RandomForestClassifier(random_state=0, max_features='sqrt', n_estimators=200, class_weight='balanced')
rfc.fit(X_train, y_train)
```

Out[34]:

```
RandomForestClassifier
RandomForestClassifier(class_weight='balanced', n_estimators=200,
                        random_state=0)
```

In [35]:

```
y_pred = rfc.predict(X_test)
print("Accuracy Score :", round(accuracy_score(y_test, y_pred)*100, 2), "%")
```

Accuracy Score : 91.91 %

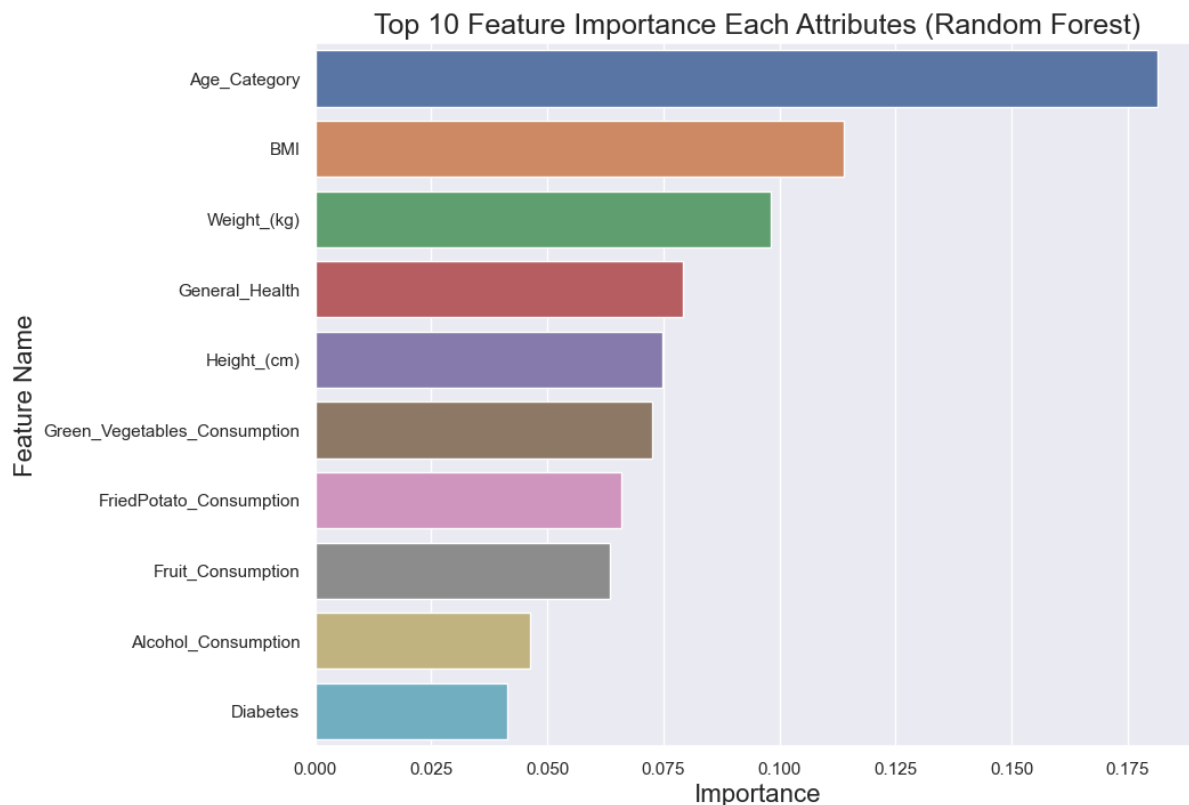
In [36]:

```
from sklearn.metrics import accuracy_score, f1_score, precision_score, recall_score, jaccard_score,
print('F-1 Score : ',(f1_score(y_test, y_pred, average='micro')))
print('Precision Score : ',(precision_score(y_test, y_pred, average='micro')))
print('Recall Score : ',(recall_score(y_test, y_pred, average='micro')))
print('Jaccard Score : ',(jaccard_score(y_test, y_pred, average='micro')))
print('Log Loss : ',(log_loss(y_test, y_pred)))
```

F-1 Score : 0.9191044341195707  
Precision Score : 0.9191044341195707  
Recall Score : 0.9191044341195707  
Jaccard Score : 0.8503175173735922  
Log Loss : 2.9157717373106866

In [37]:

```
imp_df = pd.DataFrame({  
    "Feature Name": X_train.columns,  
    "Importance": rfc.feature_importances_  
})  
fi = imp_df.sort_values(by="Importance", ascending=False)  
  
fi2 = fi.head(10)  
plt.figure(figsize=(10,8))  
sns.barplot(data=fi2, x='Importance', y='Feature Name')  
plt.title('Top 10 Feature Importance Each Attributes (Random Forest)', fontsize=18)  
plt.xlabel ('Importance', fontsize=16)  
plt.ylabel ('Feature Name', fontsize=16)  
plt.show()
```



## End of the code

**\*\*Thank You! \*\***