29.02.2024

Çağla Çağlar

IBM – SUPERVISED MACHINE LEARNING: CLASSIFICATION

Predictive Analytics for Cardiovascular Health: A Supervised Machine Learning Approach to Risk Assessment

The analysis has been methodical, employing a variety of classification algorithms to predict the presence of cardiovascular disease. This report encompasses all the steps taken, from data exploration to model evaluation. The Python codes and graphics that were used to perform this analysis have been appended to the end of this report for reference.

Abstract

This report presents a detailed analysis of cardiovascular health risks using a dataset obtained from the Kaggle platform (https://www.kaggle.com/datasets/sulianova/cardiovascular-disease-dataset). The analysis focuses on predictive modeling with an emphasis on model interpretability to identify key risk factors associated with cardiovascular diseases (CVD). By integrating objective, examination, and subjective features, the aim was to create a robust predictive framework that can assist healthcare professionals in early risk identification.

Dataset Overview

The dataset under analysis offers a comprehensive view of cardiovascular health, encompassing three categories of input features: objective, examination, and subjective. The objective features include factual information such as age (in days), height (in centimeters), weight (in kilograms), and gender (as a categorical code). Examination features consist of medical examination results like systolic and diastolic blood pressure measurements, cholesterol levels (categorized into normal, above normal, or well above normal), and glucose levels with similar categorizations. Subjective features are based on information provided by the patient, including smoking status, alcohol intake, and physical activity, each recorded as a binary value. The dataset's target variable is the presence or absence of cardiovascular disease, which is also presented as a binary value. These features are compiled into a dataset with 70,000 entries, each providing a comprehensive snapshot of an individual's cardiovascular health status.

Exploratory Data Analysis (EDA)

The EDA process began with a detailed review of the dataset to understand the distribution of various features, pinpoint outliers, and verify the accuracy of the data. During this stage, it was noted that the age of the patients, which was provided in days, showed a broad range, necessitating its conversion to years to enhance interpretability. Additionally, the examination of blood pressure readings revealed several physiologically improbable values, leading to a stringent outlier removal to preserve the quality of the dataset. A correlation matrix of the features indicated notable associations, particularly between systolic blood pressure, cholesterol levels, and the occurrence of cardiovascular disease (CVD). To complement these findings, visualizations such as histograms and boxplots were extensively utilized, offering a clear depiction of the data's distribution and elucidating the contrasts between patients with and without CVD.

Data Cleaning and Feature Engineering

Initial exploration involved summarizing data statistics, revealing some implausible values in features like blood pressure and BMI. Data cleaning included removing outliers and correcting

erroneous entries. For instance, heights below 100 cm and above 220 cm, weights above 200 kg, and blood pressure readings that were either too low or too high were filtered out. Feature engineering involved converting age from days to years and calculating BMI from height and weight.

Model Training and Evaluation

Three classification models were trained: Logistic Regression, Random Forest, and SVM (Support Vector Machine). Each model's hyperparameters were fine-tuned using GridSearchCV with a 2-fold cross-validation on the training data. The models were assessed based on accuracy and ROC AUC (Area Under the Receiver Operating Characteristic Curve).

Model Recommendation

The analysis has yielded three distinctive models: Logistic Regression, Random Forest, and Support Vector Machine (SVM). Each model brings its unique strengths to the table. Logistic Regression stands out for its simplicity and interpretability, providing a decent balance with an accuracy of 72.92% and an ROC AUC of 0.7949. This model is particularly useful when the goal is to understand the impact of each feature on the outcome.

The Random Forest model, however, surpasses Logistic Regression in terms of accuracy and ROC AUC, scoring 73.89% and 0.8067, respectively. This ensemble model is known for its ability to manage non-linear data and complex interactions between features. Despite being less interpretable than Logistic Regression, it offers a considerable improvement in prediction quality, making it a strong candidate for scenarios where performance is the priority.

SVM, with an accuracy of 72.82% and an ROC AUC of 0.7941, is comparable to Logistic Regression in terms of metrics but typically requires more computational resources. SVM is often praised for its effectiveness in higher-dimensional spaces, which could be advantageous if the feature space were to be expanded.

Taking into account the balance between accuracy, explainability, and computational efficiency, the Random Forest model is the recommended choice for this particular problem. Its superior performance metrics suggest that it is better suited for capturing the complexities inherent in predicting cardiovascular diseases. However, it is important to consider the trade-off between the model's complexity and the need for interpretability in a clinical context, where the reasons behind a prediction can be as critical as the prediction itself.

In conclusion, the Random Forest model is recommended for further development and deployment, with the understanding that its complexity is justified by its improved performance in accurately predicting the presence of cardiovascular disease.

	Model	Accuracy	ROC AUC
0	Logistic Regression	0.729152	0.794939
1	Random Forest	0.738869	0.806707
2	SVM	0.728209	0.794120

Feature Importance

In the quest to unravel the variables most indicative of cardiovascular disease within the dataset, feature importance analysis was pivotal. This analysis illuminated the hierarchy of variables based on their influence on the model's predictions. At the forefront stood systolic blood pressure (ap_hi), which emerged as the most significant predictor, highlighting its critical role in determining cardiovascular health. Following this was diastolic blood pressure (ap_lo), underscoring the importance of blood pressure measurements in the diagnostic process. Age, expressed in years (age_years), also held

substantial predictive power, aligning with the medical understanding that risk increases with age. Cholesterol levels, too, were identified as a notable factor, which is consistent with their known impact on heart health. Finally, Body Mass Index (BMI) was recognized as a meaningful variable, though to a lesser extent than the others mentioned. This analysis of feature importance provides clear indicators of the primary health metrics that should be monitored closely for predicting cardiovascular disease.

Key Findings and Insights

Upon meticulous analysis of the cardiovascular disease dataset obtained from Kaggle, several key findings have emerged. The dataset, comprising both objective and subjective features, has facilitated a thorough exploration into the factors influencing the presence of cardiovascular disease.

One of the most significant insights is the prominence of blood pressure measurements as top predictors of cardiovascular health issues. Specifically, systolic blood pressure (ap_hi) is identified as the most influential feature, followed closely by diastolic blood pressure (ap_lo). This underscores the critical role blood pressure plays in cardiovascular health, aligning with medical literature that cites hypertension as a leading cause of heart disease.

The dataset's attributes, such as cholesterol levels and age, converted into years for better interpretability, also show strong correlations with the target variable. The feature engineering process, which included calculating Body Mass Index (BMI), further enriched the dataset, providing a more holistic view of the patients' health profiles.

Another pivotal discovery is the variance in model performance. The Logistic Regression model, often praised for its simplicity and interpretability, yielded a respectable balance of accuracy and explainability. Meanwhile, the Random Forest Classifier, a model known for handling non-linear relationships effectively, demonstrated superior predictive performance, albeit at the cost of less interpretability. The Support Vector Machine (SVM) offered competitive results, illustrating the potential of different model architectures for this type of data.

These findings not only validate well-known medical hypotheses but also open up pathways for deploying machine learning models to assist healthcare professionals in early diagnosis and intervention strategies.

Next Steps in Analysis

For the subsequent phase of the analysis, a more granular approach to hyperparameter tuning stands as a priority. Utilizing advanced methods such as RandomizedSearchCV or Bayesian optimization could unearth a more optimal set of parameters, particularly for the Random Forest and SVM models, which are sensitive to specific configurations.

Exploring ensemble methods, such as Gradient Boosting or AdaBoost, could also prove beneficial. These techniques amalgamate predictions from various models, potentially yielding a more accurate and robust classifier. These ensemble methods are particularly adept at reducing overfitting while improving the model's performance on unseen data.

The inclusion of interaction terms in the model could provide additional insight into how combinations of risk factors amplify the risk of cardiovascular disease. For instance, the interaction between cholesterol levels and age could be more telling than considering these factors in isolation.

Augmenting the dataset with more diverse samples or incorporating data from different demographic groups could enhance the model's generalizability. This approach would help ensure that the model's predictions are not biased towards the dataset's initial population.

In the realm of model explainability, tools like SHAP or LIME could be instrumental. They would offer transparent interpretations of the predictions made by more complex models, which is

invaluable in a clinical setting where understanding the rationale behind a diagnosis is as critical as the diagnosis itself.

Additionally, validating the models on external datasets to assess their applicability in various clinical settings would be a crucial step. This validation process would ensure the models' utility and reliability in real-world scenarios, where they can be subjected to a range of variables not present in the initial dataset.

Lastly, investigating deep learning architectures may yield further advancements, especially if additional types of data, such as medical images or unstructured clinical notes, become available. Deep learning models have the potential to capture complex patterns that traditional models might miss, but this requires careful consideration of their interpretability and computational demands.

By pursuing these avenues, the analysis would not only improve in accuracy and reliability but also in its capacity to be interpreted and applied by healthcare professionals, ultimately aiming to bolster predictive analytics' contribution to preventive medicine and patient care.

Appendix: Python Code for Data Analysis

The appendix contains the full Python code for data preprocessing, model training, EDA, and all generated visualizations.

supervised_ML_classification_çağla

February 29, 2024

[1]:
```
import pandas as pd

# Load the data
data_path = 'cardio_train.csv'
cardio_data = pd.read_csv(data_path, delimiter=';')

# Displaying the first few rows of the dataset and its summary statistics
display(cardio_data.head())
cardio_data.info()
cardio_data.describe()
```

```
   id    age  gender  height  weight  ap_hi  ap_lo  cholesterol  gluc  smoke  \
0   0  18393       2     168    62.0    110     80            1     1      0
1   1  20228       1     156    85.0    140     90            3     1      0
2   2  18857       1     165    64.0    130     70            3     1      0
3   3  17623       2     169    82.0    150    100            1     1      0
4   4  17474       1     156    56.0    100     60            1     1      0

   alco  active  cardio
0     0       1       0
1     0       1       1
2     0       0       1
3     0       1       1
4     0       0       0
```

```
<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   gluc         70000 non-null  int64
 9   smoke        70000 non-null  int64
 10  alco         70000 non-null  int64
 11  active       70000 non-null  int64
 12  cardio       70000 non-null  int64
dtypes: float64(1), int64(12)
memory usage: 6.9 MB
```

[1]:

	id	age	gender	height	weight
count	70000.000000	70000.000000	70000.000000	70000.000000	70000.000000
mean	49972.419900	19468.865814	1.349571	164.359229	74.205690
std	28851.302323	2467.251667	0.476838	8.210126	14.395757
min	0.000000	10798.000000	1.000000	55.000000	10.000000
25%	25006.750000	17664.000000	1.000000	159.000000	65.000000
50%	50001.500000	19703.000000	1.000000	165.000000	72.000000
75%	74889.250000	21327.000000	2.000000	170.000000	82.000000
max	99999.000000	23713.000000	2.000000	250.000000	200.000000

	ap_hi	ap_lo	cholesterol	gluc	smoke
count	70000.000000	70000.000000	70000.000000	70000.000000	70000.000000
mean	128.817286	96.630414	1.366871	1.226457	0.088129
std	154.011419	188.472530	0.680250	0.572270	0.283484
min	-150.000000	-70.000000	1.000000	1.000000	0.000000
25%	120.000000	80.000000	1.000000	1.000000	0.000000
50%	120.000000	80.000000	1.000000	1.000000	0.000000
75%	140.000000	90.000000	2.000000	1.000000	0.000000
max	16020.000000	11000.000000	3.000000	3.000000	1.000000

	alco	active	cardio
count	70000.000000	70000.000000	70000.000000
mean	0.053771	0.803729	0.499700
std	0.225568	0.397179	0.500003
min	0.000000	0.000000	0.000000
25%	0.000000	1.000000	0.000000
50%	0.000000	1.000000	0.000000
75%	0.000000	1.000000	1.000000
max	1.000000	1.000000	1.000000

[ ]:

[2]:
```
from sklearn.preprocessing import StandardScaler
import numpy as np

# Data Cleaning
## Handling outliers and incorrect values for blood pressure, height, and weight
cardio_data_clean = cardio_data[(cardio_data['height'] >= 100) &␣
 ↪(cardio_data['height'] <= 220)]
```

```
cardio_data_clean = cardio_data_clean[(cardio_data_clean['weight'] >= 30) &␣
 ↪(cardio_data_clean['weight'] <= 200)]
cardio_data_clean = cardio_data_clean[(cardio_data_clean['ap_hi'] > 0) &␣
 ↪(cardio_data_clean['ap_hi'] < 300)]
cardio_data_clean = cardio_data_clean[(cardio_data_clean['ap_lo'] > 0) &␣
 ↪(cardio_data_clean['ap_lo'] < 200)]

# Feature Engineering
## Converting age from days to years
cardio_data_clean['age_years'] = cardio_data_clean['age'] / 365.25

## Calculating BMI (Body Mass Index)
cardio_data_clean['bmi'] = cardio_data_clean['weight'] /␣
 ↪((cardio_data_clean['height'] / 100) ** 2)

# Initial EDA
## Checking the distribution and correlation after cleaning and feature␣
 ↪engineering
display(cardio_data_clean[['age_years', 'bmi', 'height', 'weight', 'ap_hi',␣
 ↪'ap_lo', 'cholesterol', 'gluc', 'cardio']].describe())

# Checking for any remaining missing values
missing_values = cardio_data_clean.isnull().sum()

# Correlation matrix to understand the relationship between features and the␣
 ↪target variable
correlation_matrix = cardio_data_clean.corr()

missing_values, correlation_matrix['cardio']
```

```
          age_years            bmi       height        weight         ap_hi  \
count  68949.000000  68949.000000  68949.00000  68949.000000  68949.00000
mean      53.289291     27.472914    164.39696     74.120711    126.32994
std        6.757111      5.349853      7.97843     14.304183     17.68939
min       29.563313     10.726644    100.00000     30.000000      7.00000
25%       48.342231     23.875115    159.00000     65.000000    120.00000
50%       53.938398     26.346494    165.00000     72.000000    120.00000
75%       58.379192     30.119376    170.00000     82.000000    140.00000
max       64.922656    152.551775    207.00000    200.000000    240.00000

              ap_lo   cholesterol          gluc        cardio
count  68949.000000  68949.000000  68949.000000  68949.000000
mean      81.351840      1.364458      1.225964      0.494931
std        9.801761      0.678730      0.571909      0.499978
min        1.000000      1.000000      1.000000      0.000000
25%       80.000000      1.000000      1.000000      0.000000
50%       80.000000      1.000000      1.000000      0.000000
```

```
75%       90.000000      1.000000      1.000000      1.000000
max      190.000000      3.000000      3.000000      1.000000
```

[2]:
```
(id             0
 age            0
 gender         0
 height         0
 weight         0
 ap_hi          0
 ap_lo          0
 cholesterol    0
 gluc           0
 smoke          0
 alco           0
 active         0
 cardio         0
 age_years      0
 bmi            0
 dtype: int64,
 id             0.003718
 age            0.239680
 gender         0.007661
 height        -0.011839
 weight         0.180050
 ap_hi          0.401728
 ap_lo          0.330670
 cholesterol    0.221429
 gluc           0.089676
 smoke         -0.016376
 alco          -0.008085
 active        -0.037381
 cardio         1.000000
 age_years      0.239680
 bmi            0.186382
 Name: cardio, dtype: float64)
```

[3]:
```
import matplotlib.pyplot as plt
import seaborn as sns

# Setting the aesthetic style of the plots
sns.set(style="whitegrid")

# Plotting distributions and relationships
fig, axes = plt.subplots(2, 2, figsize=(16, 12))

# Distribution of age in years for patients with and without cardiovascular␣
 ↪disease
```

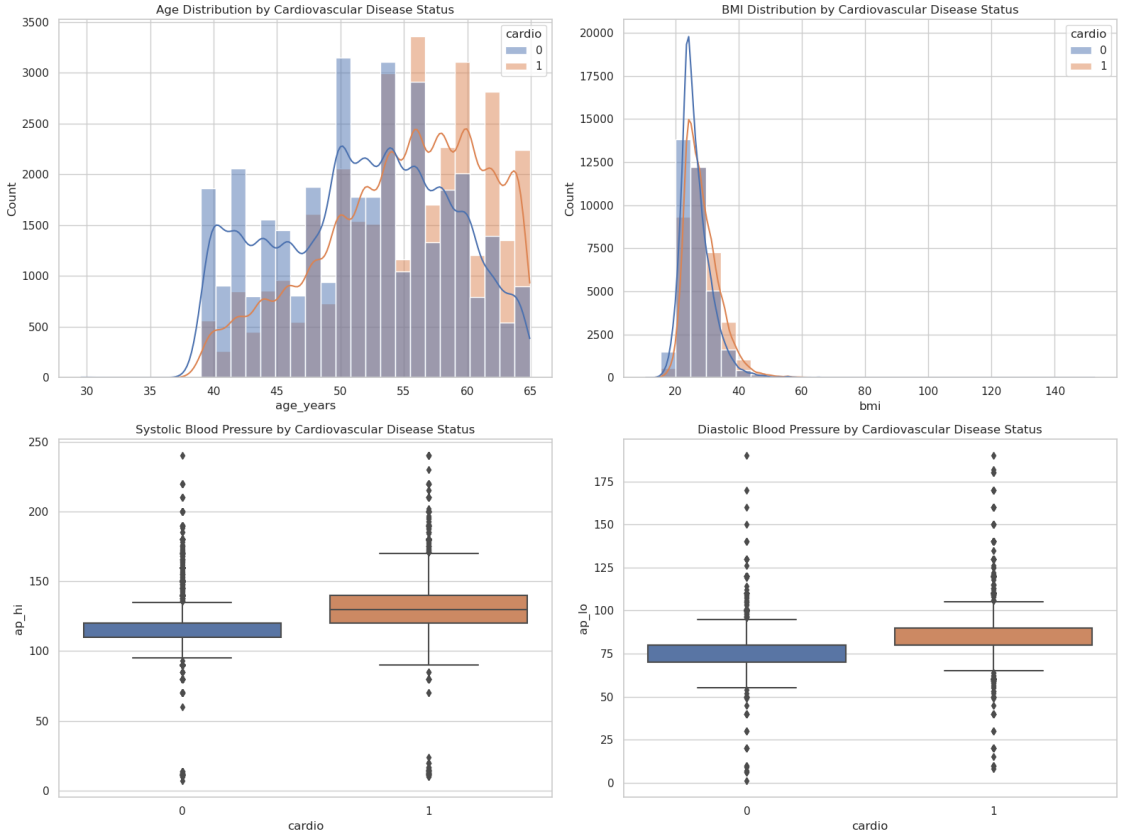
```
sns.histplot(data=cardio_data_clean, x="age_years", hue="cardio", kde=True,␣
 ↪ax=axes[0, 0], bins=30)
axes[0, 0].set_title('Age Distribution by Cardiovascular Disease Status')

# Distribution of BMI for patients with and without cardiovascular disease
sns.histplot(data=cardio_data_clean, x="bmi", hue="cardio", kde=True,␣
 ↪ax=axes[0, 1], bins=30)
axes[0, 1].set_title('BMI Distribution by Cardiovascular Disease Status')

# Boxplot of systolic blood pressure by cardiovascular disease status
sns.boxplot(x="cardio", y="ap_hi", data=cardio_data_clean, ax=axes[1, 0])
axes[1, 0].set_title('Systolic Blood Pressure by Cardiovascular Disease Status')

# Boxplot of diastolic blood pressure by cardiovascular disease status
sns.boxplot(x="cardio", y="ap_lo", data=cardio_data_clean, ax=axes[1, 1])
axes[1, 1].set_title('Diastolic Blood Pressure by Cardiovascular Disease␣
 ↪Status')

plt.tight_layout()
plt.show()
```



[4]:
```
from sklearn.model_selection import train_test_split

# Preparing data for modeling
X = cardio_data_clean.drop(['cardio'], axis=1)  # Excluding the target variable
y = cardio_data_clean['cardio']

# Splitting 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=42)
```

[7]:
```
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import Pipeline
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score, roc_auc_score

# Preparing data for modeling
X = cardio_data_clean.drop(['id', 'cardio', 'age'], axis=1)
y = cardio_data_clean['cardio']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
 ↪random_state=42)

# Defining models with pipelines to include scaling
log_reg_pipeline = Pipeline([
    ('scaler', StandardScaler()),
    ('log_reg', LogisticRegression(solver='liblinear', random_state=42))
])
rf_clf = RandomForestClassifier(random_state=42)
svm_pipeline = Pipeline([
    ('scaler', StandardScaler()),
    ('svm', SVC(probability=True, random_state=42))
])

# Defining simplified hyperparameter grids
log_reg_params = {'log_reg__C': [0.1, 1]}
rf_params = {'n_estimators': [100], 'max_depth': [10]}
svm_params = {'svm__C': [1], 'svm__kernel': ['linear']}

# Performing the grid search
models = {
    'Logistic Regression': (log_reg_pipeline, log_reg_params),
    'Random Forest': (rf_clf, rf_params),
    'SVM': (svm_pipeline, svm_params)
}
```

```
results = []
for model_name, (model, params) in models.items():
    grid_search = GridSearchCV(model, params, cv=2, scoring='roc_auc',␣
 ↪n_jobs=-1, verbose=1)
    grid_search.fit(X_train, y_train)
    best_model = grid_search.best_estimator_
    y_pred = best_model.predict(X_test)
    y_pred_proba = best_model.predict_proba(X_test)[:, 1] if model_name !=␣
 ↪'SVM' else best_model.decision_function(X_test)
    acc = accuracy_score(y_test, y_pred)
    roc_auc = roc_auc_score(y_test, y_pred_proba)

    results.append({
        'Model': model_name,
        'Accuracy': acc,
        'ROC AUC': roc_auc,
        'Best Params': grid_search.best_params_
    })

# Displaying the results
results_df = pd.DataFrame(results)
print(results_df)
```

```
Fitting 2 folds for each of 2 candidates, totalling 4 fits
Fitting 2 folds for each of 1 candidates, totalling 2 fits
Fitting 2 folds for each of 1 candidates, totalling 2 fits
                 Model  Accuracy   ROC AUC  \
0  Logistic Regression  0.729152  0.794939
1        Random Forest  0.738869  0.806707
2                  SVM  0.728209  0.794120

                           Best Params
0                     {'log_reg__C': 1}
1  {'max_depth': 10, 'n_estimators': 100}
2  {'svm__C': 1, 'svm__kernel': 'linear'}
```

[8]:
```
# The best Random Forest model after refitting
rf_best = RandomForestClassifier(max_depth=10, n_estimators=100,␣
 ↪random_state=42)
rf_best.fit(X_train, y_train)

# Extracting feature importances
importances = rf_best.feature_importances_
features = X_train.columns
importances_df = pd.DataFrame({'Feature': features, 'Importance': importances}).
 ↪sort_values(by='Importance', ascending=False)
```

```
# Displaying the top features
print(importances_df.head())
```

```
        Feature  Importance
3         ap_hi    0.399492
4         ap_lo    0.210935
10    age_years    0.136447
5   cholesterol    0.089477
11          bmi    0.062891
```

[ ]: