



Research article

Enhancing cardiovascular disease prediction: A hybrid machine learning approach integrating oversampling and adaptive boosting techniques

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Appendix 1 (All Algorithm)

Algorithm 1 SmoteR(D,tE,o,u,k)

1. Initialize empty sets:

- rareHD to store instances with high relevance of heart disease ($\phi(y) > tE$) and $y = 1$
- rareNHD to store instances with high relevance of no heart disease ($\phi(y) > tE$) and $y = 0$
- newCasesHD to store synthetic cases for rareHD
- newCasesNHD to store synthetic cases for rareNHD
- newCases as the concatenation of newCasesHD and newCasesNHD
- normCases as the set for under-sampling

2. For each instance (x, y) in D :

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- If $\phi(y) > tE$ and $y = 1$, add (x, y) to rareHD ○ If $\phi(y) > tE$ and $y = 0$, add (x, y) to rareNHD
 - 3. Generate synthetic cases for rareHD: ○ $\text{newCasesHD} = \text{genSynthCases}(\text{rareHD}, \%o, k)$
 - 4. Generate synthetic cases for rareNHD:
 - $\text{newCasesNHD} = \text{genSynthCases}(\text{rareNHD}, \%o, k)$
 - 5. Concatenate newCasesHD and newCasesNHD: ○ $\text{newCases} = \text{newCasesHD} \cup \text{newCasesNHD}$
 - 6. Determine the number of cases for under-sampling:
 - $\text{nrNorm} = \%u \text{ of } |\text{newCases}|$
 - 7. Randomly select cases from $D\{\text{rareHD} \cup \text{rareNHD}\}$ for under-sampling:
 - $\text{normCases} = \text{random sample of nrNorm cases from } D\{\text{rareHD} \cup \text{rareNHD}\}$
 - 8. Return the concatenated synthetic and under-sampled cases:
 - Return $\text{newCases} \cup \text{normCases}$
- end
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Algorithm 2 for XGB

1. Import the essential libraries:
 - `pandas as pd` ○ `numpy as np` ○ `xgboost as xgb`
 - `train_test_split` from `sklearn.model_selection` ○ `accuracy_score` from `sklearn.metrics`
2. Load the heart disease dataset into a pandas DataFrame.
3. Pre-process the data:
 - Perform data cleaning and handle missing values. ○ Conduct feature selection based on domain knowledge or statistical techniques.
 - Normalize or standardize the features if necessary. ○ Divided the data into training with testing sets using `train_test_split()` function, considering stratification if needed.
4. Define the XGBoost model:
 - Set the hyperparameters for the XGBoost model, such as the number of trees, learning rate, and maximum depth.
 - Optionally, perform cross-validation or grid search for hyperparameter tuning.
5. Train the model: ○ Fit the XGBoost model using the training data.
6. Evaluate the model:
 - Make predictions on the testing data using the trained model. ○ Compute evaluation metrics specific to heart disease prediction, such as accuracy, precision, recall, and F1-score. ○ Analyze the performance of the model and consider any issues, such as overfitting or underfitting.
7. Interpret the results:

- Investigate the importance of features in predicting heart disease. ○ Identify any patterns or relationships between features and the target variable.
 - Consider the impact of individual features on the model's predictions.
8. Iterate and refine:
- Based on the results, iterate and refine the model by adjusting hyperparameters, modifying feature engineering techniques, or exploring different algorithms.
 - Consider additional techniques like ensemble methods or addressing class imbalance if necessary.
- end

Algorithm 3 for ET

1. Import the necessary libraries:
 - pandas as pd ○ numpy as np
 - ExtraTreesClassifier starting sklearn.ensemble ○ train_test_split after sklearn.model_selection ○ accuracy_score, confusion_matrix from sklearn.metrics
 2. Load the heart disease dataset into a pandas DataFrame:
 - data = pd.read_csv('heart_disease_data.csv')
 3. Pre-process the data:
 - Separate the features (X) from the target variable (y). ○ Splitting data's into training with testing sets use train_test_split() function, considering stratification if needed.
 4. Define the Extra Trees model:
 - Initialize the ExtraTreesClassifier model.
 5. Train the model: ○ Fit the Extra Trees model using the training data.
 6. Make predictions: ○ Generate predictions for the testing data using the trained model.
 7. Evaluate the model:
 - Compute the accurate model by comparing predicted labels with the actual labels.
 - Generate the confusion matrix to assess the outcome of the model.
 8. Print the accuracy and confusion matrix:
 - Print the accuracy score.
 - Print the confusion matrix.
- End

Algorithm 4 for RF

1. Import the necessary libraries:
 - o pandas as pd o numpy as np
 - o RandomForestClassifier after sklearn.ensemble o train_test_split after sklearn.model_selection o accuracy_score, confusion_matrix from sklearn.metrics
2. Load the heart disease dataset into a pandas DataFrame:
 - o data = pd.read_csv('heart_disease_data.csv')
3. Preprocess the data:
 - o Separate the features (X) from the target variable (y). o Divide the data into training with testing sets use train_test_split() function, considering stratification if needed.
4. Define the Random Forest model:
 - o Initialize the RandomForestClassifier model.
5. Train the model: o Fit the Random Forest model using the training data.
6. Make predictions: o Generate predictions for the testing data using the trained model.
7. Evaluate the model:
 - o Compute the accurate model through comparing the predicted labels with the actual labels.
 - o Generate the confusion matrix to assess the performance of the model.
8. Print the accuracy and confusion matrix:
 - o Print the accuracy score.
 - o Print the confusion matrix.

End

Algorithm 5 for AdaBoost

1. Input:
 - o Training input data: $(x_1, y_1), (x_2, y_2), \dots, (x_n, y_n)$, where x_i represents the features of the i th patient and y_i is the corresponding label (+1 for heart disease present, -1 for heart disease not present). o Number of iterations: T
2. Output:
 - o Boosted hypothesis for heart disease prediction: $H(x)$
3. Step 1: Initialize weights for training samples o Set $D_1(n) = 1/N$ for all n , where N is the total number of training samples.
4. Step 2: Iterate T times o For $t = 1$ to T:

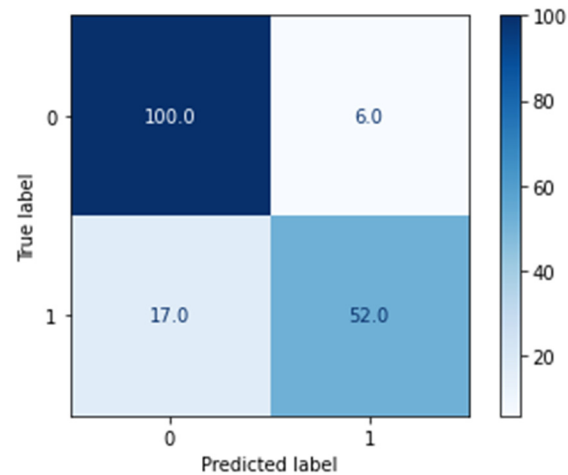
Appendix 2 (Validation)

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Random Forest Results

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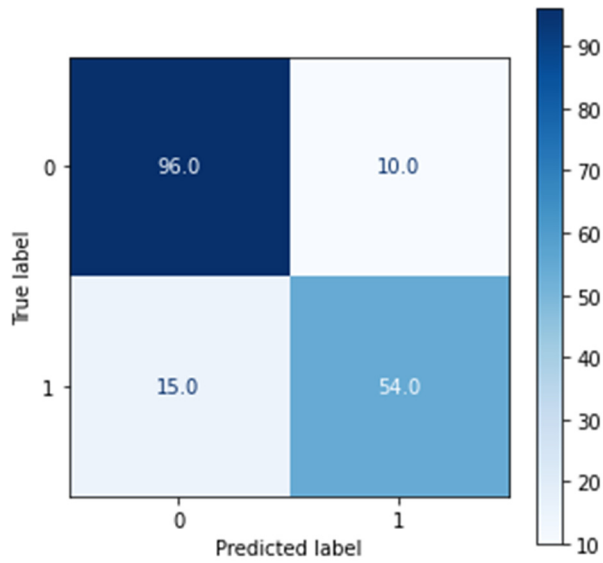
Accuracy [with RF]: 86.85714285714286 %
 Recall [with RF]: 75.36231884057972 %
 precision [with RF]: 89.65517241379311 %
 MCC [with RF]: 0.723628103990507



AdaBoost Random Forest Results

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Accuracy [AdaBoost with RF]: 85.71428571428571 %
 Recall [AdaBoost with RF]: 78.26086956521739 %
 precision [AdaBoost with RF]: 84.375 %
 MCC [AdaBoost with RF]: 0.6983678802480235

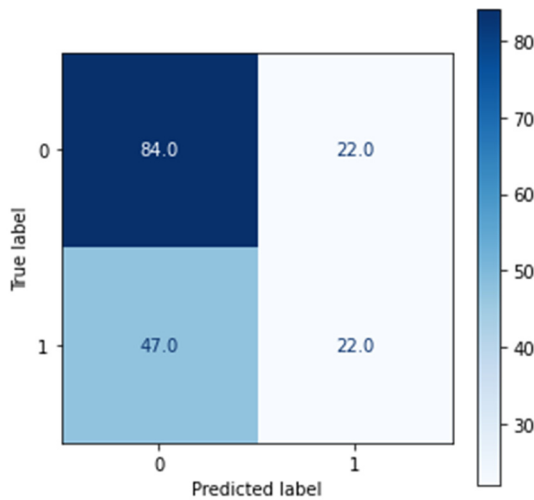


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Logistic Regression Results

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Accuracy [with LR]: 60.57142857142858 %
 Recall [with LR]: 31.88405797101449 %
 precision [with LR]: 50.0 %
 MCC [with LR]: 0.1253674928685844

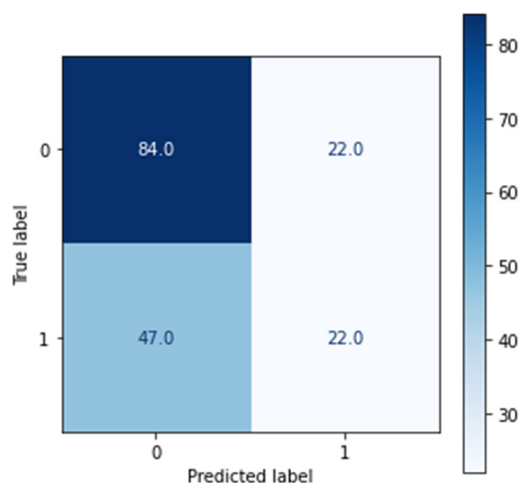


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AdaBoost LR Results

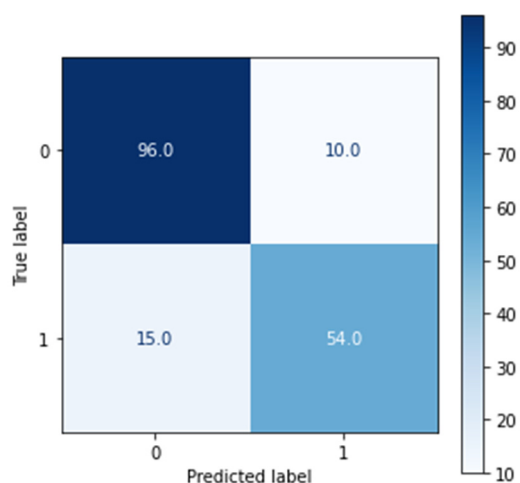
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Accuracy [AdaBoost with LogisticRegression]: 60.57142857142858 %
 Recall [AdaBoost with LogisticRegression]: 31.88405797101449 %
 precision [AdaBoost with LogisticRegression]: 50.0 %
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 MCC [AdaBoost with LR]: 0.1253674928685844



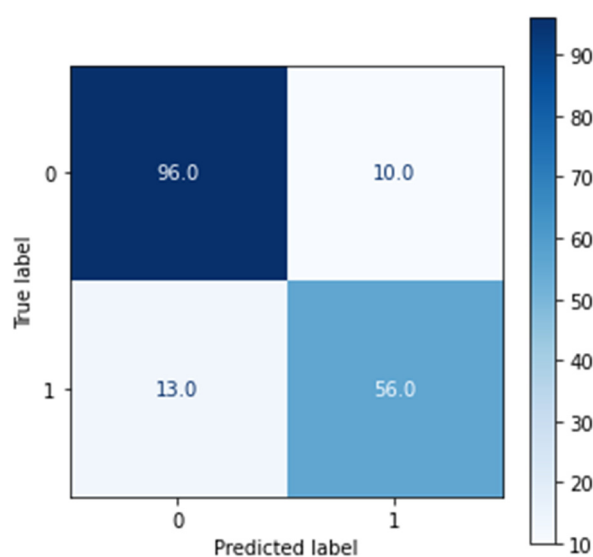
Extra Tree Results

Accuracy [with ET]: 85.71428571428571 %
 Recall [with ET]: 78.26086956521739 %
 precision [with ET]: 84.375 %
 MCC [with ET]: 0.6983678802480235



Extra TreeForest Results

Accuracy [AdaBoost with ET]: 86.85714285714286 %
 Recall [AdaBoost with ET]: 81.15942028985508 %
 precision [AdaBoost with ET]: 84.84848484848484 %
 MCC [AdaBoost with ET]: 0.7232119465299363

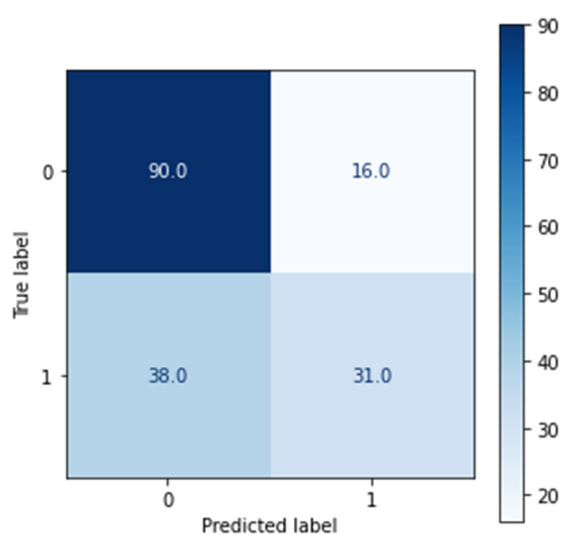


XGB Results

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Accuracy [ with ET]: 69.14285714285714 %
Recall [ with ET]: 44.927536231884055 %
precision [ with ET]: 65.95744680851064 %
MCC [ with ET]: 0.328945049232401
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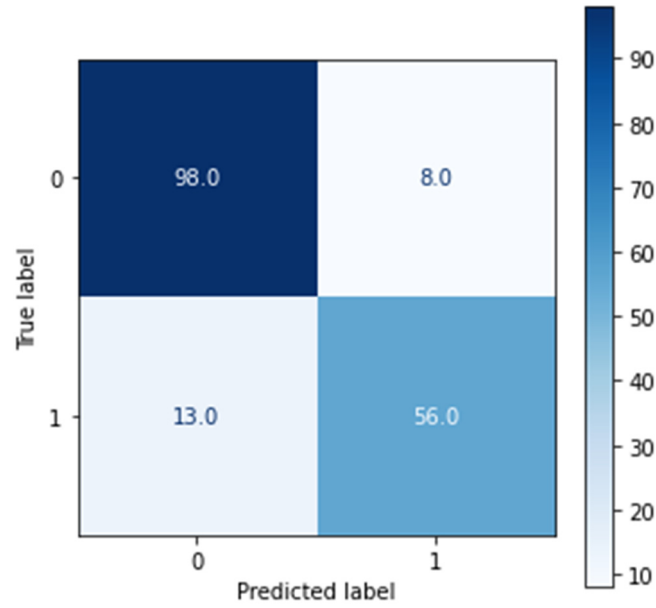


XGB TreeForest Results

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Accuracy [AdaBoost with XGB]: 88.0 %
Recall [AdaBoost with XGB]: 81.15942028985508 %
precision [AdaBoost with XGB]: 87.5 %
MCC [ AdaBoost with XGB]: 0.7469234539641157
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