week_7_bootstrap_grid_search

October 12, 2023

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[]: import pandas as pd # standard
    import numpy as np # standard
    from sklearn import tree # package to make decision tree
    from sklearn.metrics import accuracy score # for accuracy calculation
    from sklearn.metrics import balanced_accuracy_score
    from sklearn.metrics import roc_auc_score
    import matplotlib.pyplot as plt
    import seaborn as sns
    import thermogram_utilities
    import warnings
    warnings.filterwarnings("ignore")
[]: df = pd.read_excel("/Users/avery/OneDrive/Documents/GitHub/
     →Clinical_TLB_2023-2024/lung_cancer_tlb.xlsx")
    # replace NA with control

df['CancerType'])
    # keep only Control and Adenocarcinoma for analysis
    df_tree = df[(df['CancerType'] == 'Control') | (df['CancerType'] == __
     df_tree = df_tree.reset_index(drop=True)
[]: # length of df
    num_rows = df_tree.shape[0]
    # number of bootstraps
    total_bootstraps = 15
    # create results df
    hyperparameter_tuning_df = pd.DataFrame(columns=["max_depth", "max_features",_
     ⇔'min_leaves', "balanced_accuracy", 'auc'])
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best_combination_df = pd.DataFrame(columns=["max_depth", "max_features",_
 ⇔'min_leaves', "balanced_accuracy", 'auc'])
# create array of all indices in full data set
all_indices = np.arange(num_rows)
# columns to drop
drop_cols = ['sample_id', 'pub_id', 'CancerType']
# loop to bootstrap and validate many times
for i in range(total_bootstraps):
    hyperparameter_tuning_df = pd.DataFrame(columns=["max_depth",__

¬"max_features", 'min_leaves', "balanced_accuracy", 'auc'])

    # sample indices with replacement of df
    train_indices = np.random.choice(num_rows, num_rows, replace = True)
    # get the train set using the indices
    train_set = df_tree.iloc[train_indices, : ]
    # get the indices not selected
    test_indices = np.setdiff1d(all_indices, train_indices)
    # use not selected indices as the train set
    test_set = df_tree.iloc[test_indices, : ]
    for depth in range(1, 16):
        for features in range(1, 452, 5):
            for leaves in range (1,6):
                # initialize decision tree
                clf = tree.DecisionTreeClassifier(max_depth= depth,__

max_features=features, min_samples_leaf= leaves)
                # train and test tree
                clf = clf.fit( train_set.drop(drop_cols, axis = 1),__

¬train_set['CancerType'])
                test_predictions = clf.predict(test_set.drop(drop_cols, axis =_
 →1))
                # calculate balanced accuracy
                balanced_acc = balanced_accuracy_score(test_set['CancerType'],__
 →test_predictions)
                # get probabilities
                test_probabilities = clf.predict_proba(test_set.drop(drop_cols,_
 \Rightarrowaxis = 1))
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# test decision tree
                     test_predictions = clf.predict(test_set.drop(drop_cols, axis =__
      \hookrightarrow 1))
                     # calculate weighted accuracy
                     balanced acc = balanced accuracy score(test set['CancerType'],
      →test_predictions)
                     # calculate AUC
                     auc = roc_auc_score(test_set['CancerType'] == 'Control',__
      ⇔test_probabilities[:, 1])
                     # append to results df
                     hyperparameter_tuning_df.loc[len(hyperparameter_tuning_df)] =__
      →[depth, features, leaves, balanced_acc, auc]
         best_combination_df = pd.concat([best_combination_df,__
      hyperparameter_tuning_df.sort_values('balanced_accuracy', ascending=False).
      \hookrightarrowhead(1)])
    C:\Users\avery\AppData\Local\Temp\ipykernel_14236\1892828419.py:61:
    FutureWarning: The behavior of DataFrame concatenation with empty or all-NA
    entries is deprecated. In a future version, this will no longer exclude empty or
    all-NA columns when determining the result dtypes. To retain the old behavior,
    exclude the relevant entries before the concat operation.
      best_combination_df = pd.concat([best_combination_df,
    hyperparameter_tuning_df.sort_values('balanced_accuracy',
    ascending=False).head(1)])
[]: best_combination_df.sort_values('balanced_accuracy', ascending=False).head(5)
     {\it \#best\_combination\_df.to\_excel("BSCV\_Results.xlsx")}
[]:
           max_depth max_features min_leaves balanced_accuracy
                                                                          auc
     6041
                14.0
                                            2.0
                                                          0.826087 0.806238
                             126.0
                 9.0
     3650
                              11.0
                                            1.0
                                                          0.824405 0.824405
     3686
                 9.0
                              46.0
                                            2.0
                                                          0.820513 0.850427
     1377
                 4.0
                              11.0
                                            3.0
                                                          0.814935 0.852814
     4572
                11.0
                              21.0
                                            3.0
                                                          0.808421 0.810526
[]: best_combination_df.sort_values('balanced_accuracy', ascending=False).head(1)
     max_depth = int(best_combination_df.sort_values('balanced_accuracy',__
      →ascending=False).iloc[0, 0])
     max_features = int(best_combination_df.sort_values('balanced_accuracy',__
      ⇒ascending=False).iloc[0, 1])
```

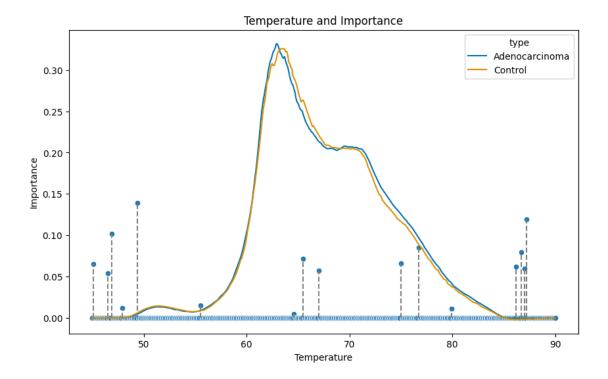
```
min_leaves = int(best_combination_df.sort_values('balanced_accuracy',_
      →ascending=False).iloc[0, 2])
     print(max_depth, max_features, min_leaves)
     clf = tree.DecisionTreeClassifier(max_depth= max_depth,__
      →max features=max features, min samples leaf= min leaves)
     # train and test tree
     clf = clf.fit( df_tree.drop(drop_cols, axis = 1), df_tree['CancerType'])
     feature_importance1 = clf.feature_importances_
     temps = df_tree.drop(['CancerType', 'sample_id', 'pub_id'], axis = 1).columns.
     ⇔str.replace('T', '')
     temps = temps.astype(float)
     feature_importance = pd.DataFrame({"Temperature":temps, "Importance":
      →feature_importance1})
    14 126 2
[]: df_long = pd.melt(df_tree, id_vars=['sample id', 'pub_id', 'CancerType'],
      ovar_name='temp', value_name='dsp' )
     median_df = thermogram_utilities.median_curve(df_long, 'CancerType', 'temp', u

    dsp')

     median_df['temperature'] = median_df['temperature'].str.replace('T', '').
      ⇔astype(float)
[]: # pivot variable importance df to long
     plt.figure(figsize=(10, 6))
     # create a bar plot
     sns.scatterplot(data=feature_importance, x='Temperature', y='Importance')
     p = sns.lineplot(data=median_df, x='temperature', y='median', hue='type', u
      ⇔palette='colorblind')
     for index, row in feature_importance.iterrows():
         x_value = row['Temperature']
         y_value = row['Importance']
         # Add a vertical line from the point to the x-axis
         plt.plot([x_value, x_value], [0, y_value], color='gray', linestyle='--')
     # add labels and title
     plt.xlabel('Temperature')
```

```
plt.ylabel('Importance')
plt.title('Temperature and Importance')
\verb|c:\Users\avery\AppData\Local\Programs\Python\Python310\lib\site-|
packages\seaborn\_oldcore.py:1498: FutureWarning: is_categorical_dtype is
deprecated and will be removed in a future version. Use isinstance(dtype,
CategoricalDtype) instead
  if pd.api.types.is_categorical_dtype(vector):
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c:\Users\avery\AppData\Local\Programs\Python\Python310\lib\site-
packages\seaborn\ oldcore.py:1119: FutureWarning: use inf_as_na option is
deprecated and will be removed in a future version. Convert inf values to NaN
before operating instead.
  with pd.option_context('mode.use_inf_as_na', True):
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deprecated and will be removed in a future version. Convert inf values to NaN
before operating instead.
  with pd.option_context('mode.use_inf_as_na', True):
```

[]: Text(0.5, 1.0, 'Temperature and Importance')



[]: df_tree.shape

[]: (123, 454)