week_8_BSCV_RF

October 18, 2023

[ ]:
```
import pandas as pd # standard
import numpy as np # standard
from sklearn.ensemble import RandomForestClassifier
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'] = np.where(df['CancerType'].isna(), 'Control',␣
 ↪df['CancerType'])

# get location of cut off values
lower_column_index = df.columns.get_loc("T51")
upper_column_index = df.columns.get_loc("T85.1")
label_column_index = df.columns.get_loc("CancerType")

column_indices = np.arange(lower_column_index, upper_column_index)
column_indices = np.append(column_indices, 0)
column_indices = np.append(column_indices, 1)



column_indices = np.append(column_indices, label_column_index)

df = df.iloc[:, column_indices]
```

```
# keep only Control and Adenocarcinoma for analysis
df_tree = df[(df['CancerType'] == 'Control') | (df['CancerType'] ==␣
 ↪'Adenocarcinoma')]
df_tree = df_tree.reset_index(drop=True)
```

[ ]:
```
# set up for feature importance

#    create temps to append to df
temps = df_tree.drop(['CancerType', 'sample_id', 'pub_id'], axis = 1).columns.
 ↪str.replace('T', '')
temps = temps.astype(float)

#    create df
feature_importance = pd.DataFrame({"Temperature":temps})

# create performace df: balanced accuracy, auc
performance_metrics = pd.DataFrame(columns=['Weighted Accuracy', 'AUC'])

# set number of bootstraps
total_bootstraps = 100

# length of df
num_rows = df_tree.shape[0]

# 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 for specified iterations
for i in range(total_bootstraps):

    # randomly select indices to use as train set
    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 indices not included in train_indices to use as test set
    test_indices =     test_indices = np.setdiff1d(all_indices, train_indices)

    # get test set using test indices
    test_set = df_tree.iloc[test_indices, :]

    # initialize random forest (default settings)
    clf = RandomForestClassifier()
```

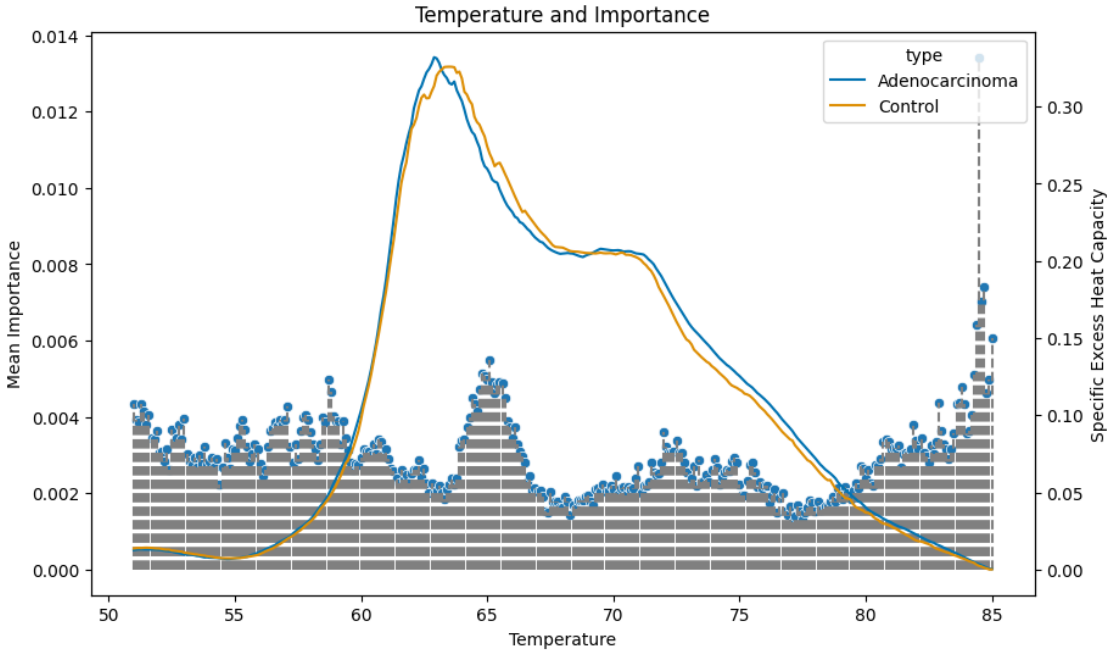
```
    # train forest
    clf.fit(train_set.drop(drop_cols, axis = 1), train_set['CancerType'])

    # get probabilities
    test_probabilities = clf.predict_proba(test_set.drop(drop_cols, axis = 1))

    # test decision tree
    test_predictions = clf.predict(test_set.drop(drop_cols, axis = 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 accuracy, auc to results df
    performance_metrics.loc[len(performance_metrics)] = [balanced_acc, auc]

    feature_importance[i] = clf.feature_importances_
```

[ ]:
```
df_long = pd.melt(df_tree, id_vars=['sample_id', 'pub_id', 'CancerType'],␣
 ↪var_name='temp', value_name='dsp' )

median_df = thermogram_utilities.median_curve(df_long, 'CancerType', 'temp',␣
 ↪'dsp')

median_df['temperature'] = median_df['temperature'].str.replace('T', '').
 ↪astype(float)

feature_importance_long = pd.melt(feature_importance, id_vars=['Temperature'],␣
 ↪var_name='Fold', value_name='Importance' )
feature_importance.iloc[:, 1:].mean(axis=1)

temps = temps.astype(float)
mean_feature_importance = pd.DataFrame({"Temperature":temps, "Mean Importance":␣
 ↪feature_importance.iloc[:, 1:].mean(axis=1)
})
```

[ ]:
```
plt.figure(figsize=(10, 6))

# create a bar plot
sns.scatterplot(data=mean_feature_importance, x='Temperature', y="Mean␣
 ↪Importance")
```

```
for index, row in mean_feature_importance.iterrows():
    x_value = row['Temperature']
    y_value = row["Mean Importance"]

    # Add a vertical line from the point to the x-axis
    plt.plot([x_value, x_value], [0, y_value], color='gray', linestyle='--')


ax2 = plt.gca().twinx()

p = sns.lineplot(data=median_df, x='temperature', y='median',ax=ax2,␣
 ↪hue='type', palette='colorblind')


# add labels and title
plt.xlabel('Temperature')
plt.ylabel('Mean Importance')
ax2.set_ylabel('Specific Excess Heat Capacity')
plt.title('Temperature and Importance')
```

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



[ ]:
```
sns.boxplot(data=performance_metrics['Weighted Accuracy'], width=0.3)
```

```
# Add points to the boxplot using the swarmplot function
sns.swarmplot(data=performance_metrics['Weighted Accuracy'], color='red',␣
↪size=8)
```

[ ]: <Axes: ylabel='Weighted Accuracy'>