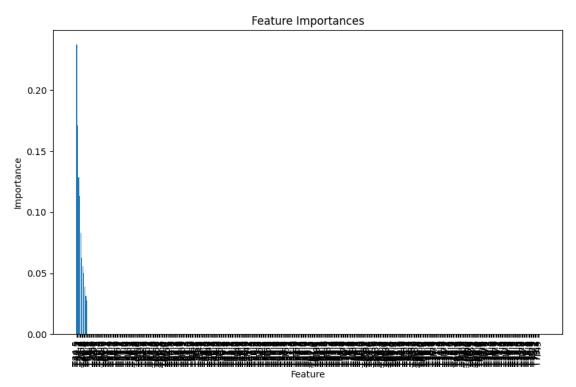
week_6_variable_importance

October 4, 2023

```
[]: 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.model_selection import StratifiedKFold # stratified k fold indices
    #from sklearn.tree import export graphviz
    #import graphviz
    import warnings
    # Suppress all warnings
    warnings.filterwarnings("ignore")
[]: # read in data
    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'] == __
     []: # create empty df to store cv results
    # define the number of splits and random seed for StratifiedKFold
    n_splits = 5
    random_seed = 42
    skf = StratifiedKFold(n_splits=n_splits, random_state=random_seed, shuffle=True)
    # Initialize lists to store train and test indices
    train_indices_list = []
```

```
test_indices_list = []
# loop through the splits and extract train and test indices
for train indices, test_indices in skf.split(df_tree, df_tree['CancerType']):
    # append train and test indices to their lists
    train_indices_list.append(train_indices)
    test_indices_list.append(test_indices)
# access the rows of the thermogram df using the indices
for fold in range(n splits):
    # get training and testing dataframes
    train_df = df_tree.iloc[train_indices_list[fold]].drop(['sample_id',__
 \rightarrow'pub_id'], axis = 1)
    test_df = df_tree.iloc[test_indices_list[fold]].drop(['sample_id',_
 \hookrightarrow'pub id'], axis = 1)
    # train the decision tree using the train set
    clf = tree.DecisionTreeClassifier()
    clf = clf.fit( train_df.drop('CancerType', axis = 1),__
 →train_df['CancerType'])
    # predict the train set / test set
    train_predictions = clf.predict(train_df.drop('CancerType', axis = 1))
    test_predictions = clf.predict(test_df.drop('CancerType', axis = 1))
    # compare predictions to labels
    test_accuracy = accuracy_score(test_predictions, test_df['CancerType'])
    train_accuracy = accuracy_score(train_predictions, train_df['CancerType'])
    # store train/test indices and accuracy
    performance_metrics.loc[len(performance_metrics)] =__
 →[train_indices_list[fold], test_indices_list[fold], train_accuracy, ___
 →test_accuracy]
    feature_importance = clf.feature_importances_
```



```
x_positions = range(0, len(sorted_feature_names), 10)
x_labels = [sorted_feature_names[i] for i in x_positions]
plt.xticks(x_positions, x_labels)

plt.xlabel('Feature')
plt.ylabel('Importance')
plt.title('Feature Importances')
plt.show()
```

Peature Importances 0.20 - 0.15 - 0.00 184.5 - 0.10 - 0.00 - 0.

