week 8 truncated temps

October 16, 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/

Glinical_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("T50")
     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]
```

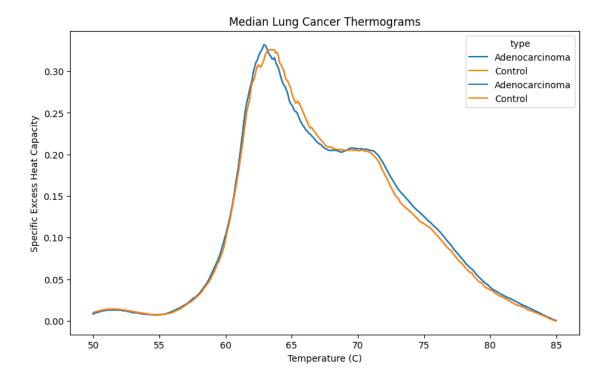
```
# keep only Control and Adenocarcinoma for analysis
    df_tree = df[(df['CancerType'] == 'Control') | (df['CancerType'] ==__
     df tree = df tree.reset index(drop=True)
[]: temps = df_tree.drop(['CancerType', 'sample_id', 'pub_id'], axis = 1).columns.
     ⇔str.replace('T', '')
    temps = temps.astype(float)
    feature_importance = pd.DataFrame({"Temperature":temps})
    # length of df
    num_rows = df_tree.shape[0]
     # number of bootstraps
    total bootstraps = 100
    # create results df
    performance_metrics = pd.DataFrame(columns=['Weighted 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):
         # 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, : ]
         # train decision tree
        clf = tree.DecisionTreeClassifier()
         clf = 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))
```

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# 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_tree = clf.feature_importances_
         feature_importance[i] = feature_importance_tree
[]: 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', __

    dsp')

     median_df['temperature'] = median_df['temperature'].str.replace('T', '').
      ⇔astype(float)
[]: plt.figure(figsize=(10, 6)) # Adjust the figure size if needed
     sns.lineplot(data=median_df, x='temperature', y='median', hue='type', u
      ⇔palette='colorblind')
     ax = plt.gca()
     # Plot the lines with different colors for 'type'
     sns.lineplot(data=median_df, x='temperature', y='median', hue='type')
     # Add ribbons for each 'type' with different colors
     '''for _, row in median_df.iterrows():
         ax.fill_between([row['temperature']], row['lower_q'], row['upper_q'], __
     ⇔alpha=0.3, color='grey')'''
     plt.xlabel('Temperature (C)')
     plt.ylabel('Specific Excess Heat Capacity')
     plt.title('Median Lung Cancer Thermograms')
```

[]: Text(0.5, 1.0, 'Median Lung Cancer Thermograms')

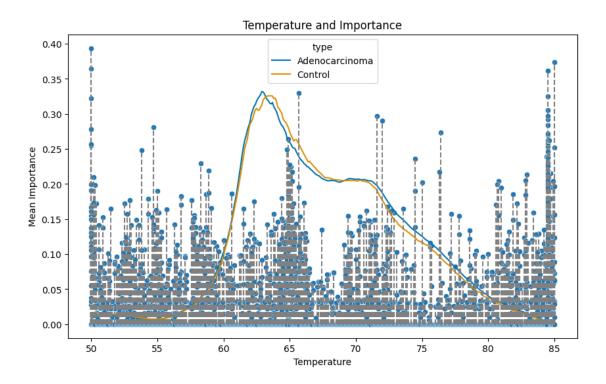


```
ovar_name='Fold', value_name='Importance' )
    feature_importance.iloc[:, 1:].mean(axis=1)
    temps = temps.astype(float)
    mean_feature_importance = pd.DataFrame({"Temperature":temps, "Mean Importance":_
      })
[]: plt.figure(figsize=(10, 6))
    # create a bar plot
    sns.scatterplot(data=feature_importance_long, 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_long.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='--')
```

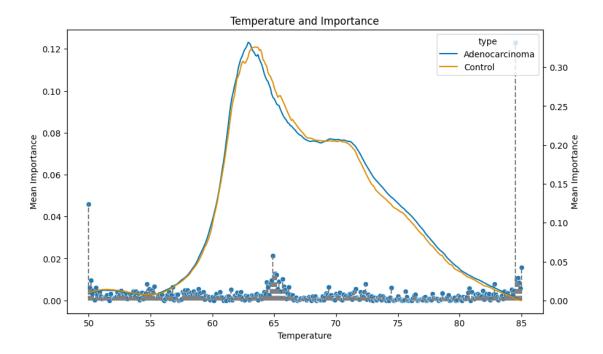
[]: feature_importance_long = pd.melt(feature_importance, id_vars=['Temperature'],__

```
# add labels and title
plt.xlabel('Temperature')
plt.ylabel('Mean Importance')
plt.title('Temperature and Importance')
```

[]: Text(0.5, 1.0, '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', usize=8)
```

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

