Lead, Cadmium, Total Mercury, Selenium, and Manganese in file PBCD_J

April 13, 2023

0.0.1 Lead, Cadmium, Total Mercury, Selenium, and Manganese in file PBCD_J

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Gets rid of all rows that contain NA values and outputs the cleaned data to "Clean PBCD_J_J.xlsx"

[1]:
```python
import os
import numpy as np
import pandas as pd
from scipy import stats
import seaborn as sns
import statsmodels.api as sm
%matplotlib inline

result_dir = '~/Environmental Health Project - Part 2/result'
data_dir = '~/Environmental Health Project - Part 2/data'
in_file_name = 'PBCD_J.xlsx'
out_file_name = 'Clean PBCD_J.xlsx'

in_file_full_name = os.path.join(data_dir, in_file_name)
out_file_full_name = os.path.join(result_dir, out_file_name)

data_in = pd.read_excel(in_file_full_name)
data = data_in.drop(['Unnamed: 0'], axis = 1)
data_no_na = data.dropna()
data_no_na.to_excel(out_file_full_name)
```

```
C:\Users\kecoc\anaconda3\lib\site-packages\openpyxl\styles\stylesheet.py:226:
UserWarning: Workbook contains no default style, apply openpyxl's default
  warn("Workbook contains no default style, apply openpyxl's default")
```

Computes the pearson correlation coefficient between every pair of variables and exports coefficients that are greater than 0.5 and less than 0.999 as a CSV file.

[2]:

```
in_file_name = 'Clean PBCD_J.xlsx'
out_file_name = "PBCD_J_Filtered_Pearson_Correlation_Coefficient.csv"

in_file_full_name = os.path.join(result_dir, in_file_name)
out_file_full_name = os.path.join(result_dir, out_file_name)

data_in = pd.read_excel(in_file_full_name)
data = data_in.drop(['Unnamed: 0', 'SEQN'], axis = 1)

column_points = data.columns #Gets the labels for the final data frame
length = len(column_points) #Gets the amount of labels of the dataframe for the␣
 ↪column and index so the final dataframe can be shaped correctly
values = [] #Creates an empty list that the pearson correlation coefficients␣
 ↪will be stored in

for h in column_points: #Calculates the pearson correlation coefficient for␣
 ↪every pair of columns
    for k in column_points:
        res = stats.pearsonr(data[h], data[k])
        values.append(res.statistic) #Stores the pearson correlation␣
 ↪coefficient for each pair of columns in the values list

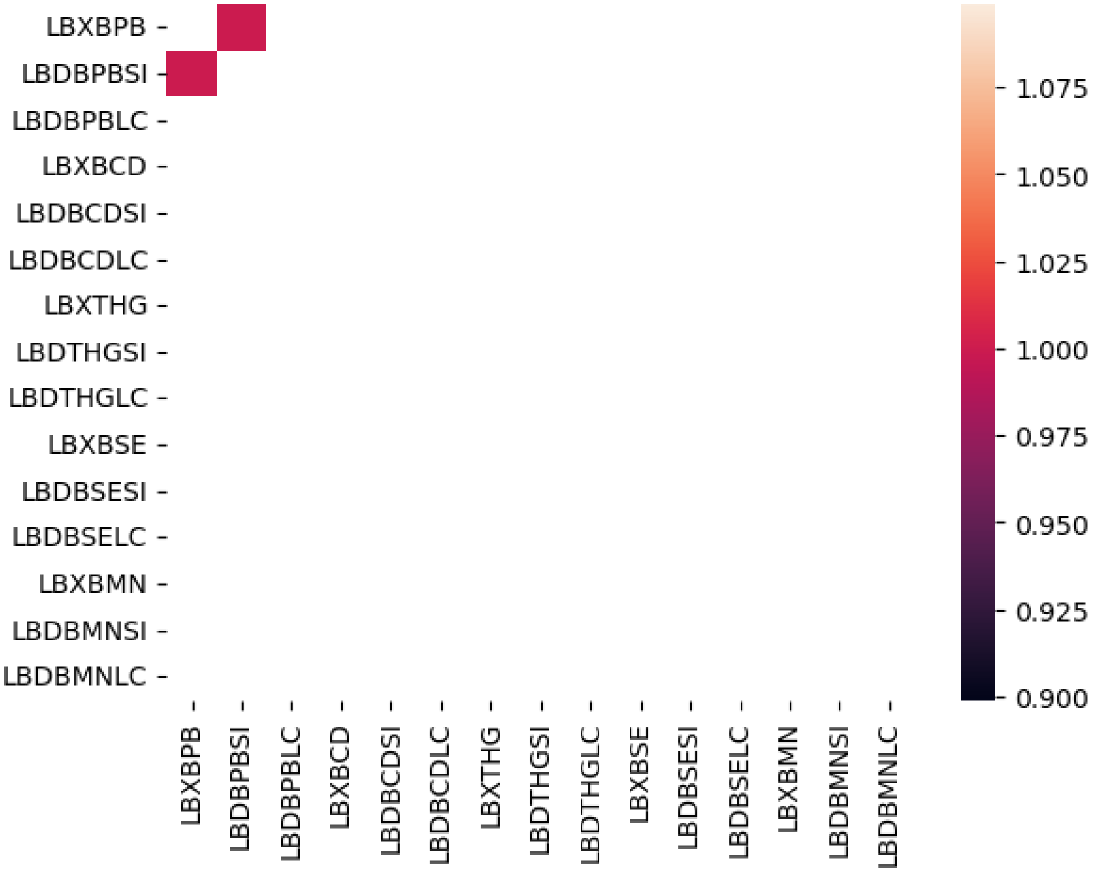
reshaped_values = np.array(values).reshape(length,length) #Creates a reshaped␣
 ↪numpy array using the values list
matrix = pd.DataFrame(reshaped_values, index = column_points, columns =␣
 ↪column_points) #Creates a dataframe of the pearson correlation coefficient␣
 ↪with the variables as the index and column

filtered_matrix = matrix[(matrix > 0.50) & (matrix < 0.999)] #Filters the␣
 ↪matrix to only show the values greater than 0.50 and less than 0.999

print("Heatmap of the filtered pearson correlation coefficient values")
print(sns.heatmap(filtered_matrix)) #Creates a heatmap of the filtered values
filtered_matrix.to_csv(out_file_full_name) #Outputs the filtered matrix to a␣
 ↪csv file
```

```
Heatmap of the filtered pearson correlation coefficient values
AxesSubplot(0.125,0.11;0.62x0.77)
```

```
C:\Users\kecoc\anaconda3\lib\site-packages\scipy\stats\_stats_py.py:4424:
ConstantInputWarning: An input array is constant; the correlation coefficient is
not defined.
  warnings.warn(stats.ConstantInputWarning(msg))
```



Computes the p-values for the F statistic as well as the R^2 values for each pair of variables and exports the R2 values that are greater than 0.5 and less than 0.999 as a CSV file.

[3]:
```
out_file_name = "PBCD_J_Filtered_R^2_values.csv"
out_file_full_name = os.path.join(result_dir, out_file_name)

P_values = [] #Creates an empty list that the P-values of the F statistic will␣
 ↪be stored in
R_squared_values = [] #Creates an empty list that the R^2 values will be stored␣
 ↪in

for h in column_points: #Calculates the pvalue of the f-statistic and r^2 value␣
 ↪for each pair of variables
    for k in column_points:
        X2 = sm.add_constant(data[h])
        est = sm.OLS(data[k],X2)
        est2 = est.fit()
        P_values.append(est2.f_pvalue) #Appends the pvalue of the f-statistic␣
 ↪to the p_values list
        R_squared_values.append(est2.rsquared) #Appends the r^2 value to the␣
 ↪R_squared_values list

reshaped_p_values = np.array(P_values).reshape(length,length) #Reshapes the␣
 ↪P_value list into a numpy array of the correct shape
p_value_matrix = pd.DataFrame(reshaped_p_values, index = column_points, columns␣
 ↪= column_points) #Creates a dataframe of the P_values array with the␣
 ↪variable names as the columns and indexs

reshaped_R_squared_values = np.array(R_squared_values).reshape(length,length)␣
 ↪#Reshapes the R_squared_values list into a numpy array of the correct shape
R_squared_values_matrix = pd.DataFrame(reshaped_R_squared_values, index =␣
 ↪column_points, columns = column_points) #Creates a dataframe of the␣
 ↪R_squared_values array with the variable names as the columns and indexs

filtered_matrix = R_squared_values_matrix[(R_squared_values_matrix > 0.50) &␣
 ↪(R_squared_values_matrix < 0.999)] #Filters the R_squared_values matrix to␣
 ↪only show values greater than 0.50 and less than 0.999

print("HeatMap of filtered R^2 values")
print(sns.heatmap(filtered_matrix))
filtered_matrix.to_csv(out_file_full_name) #Outputs the filtered matrix to a␣
 ↪csv file
```

```
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packages\statsmodels\regression\linear_model.py:1825: RuntimeWarning: invalid
value encountered in double_scalars
  return self.mse_model/self.mse_resid
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HeatMap of filtered R^2 values
AxesSubplot(0.125,0.11;0.62x0.77)
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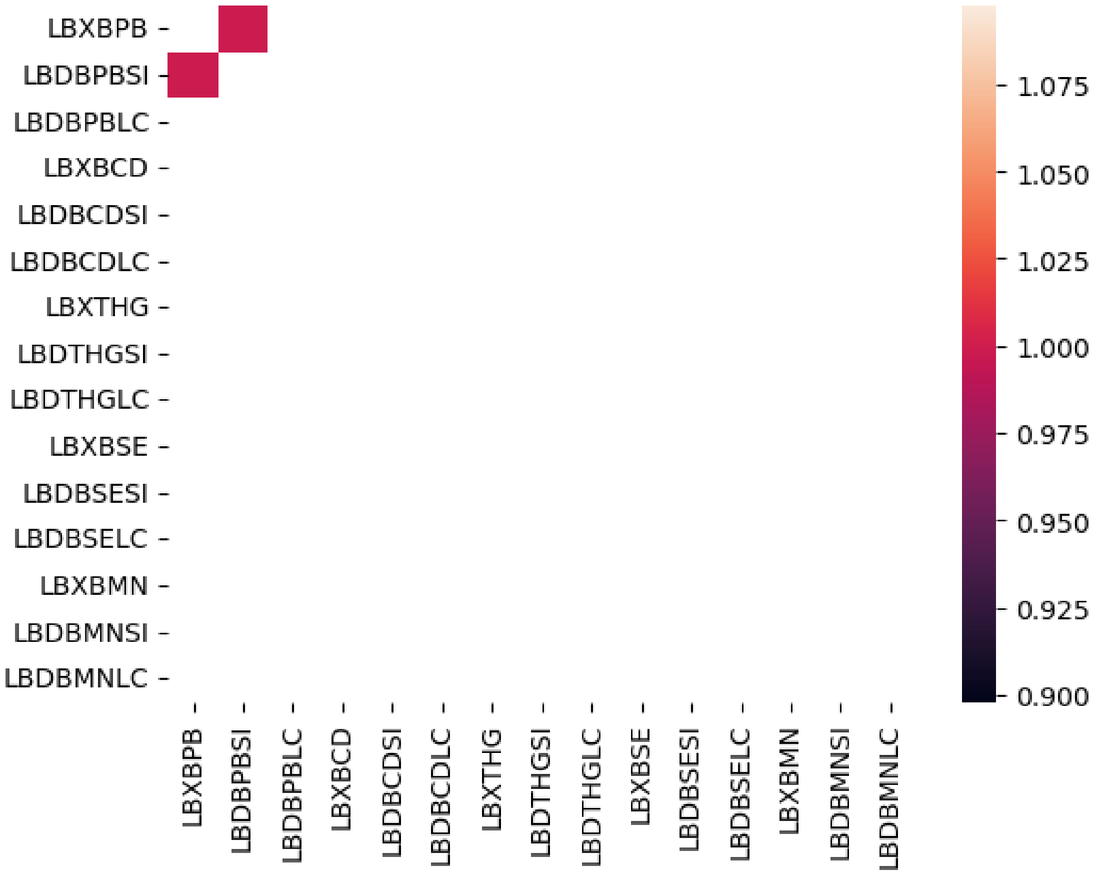

The filtered pearson correlation coefficient heatmap indicates that there is a strong positive relationship between the variables LBXBPB and LBDBPBSI. These values being correlated makes sense as they are just two different ways of measuring blood lead levels. LBXBPB measures blood lead in (ug/dL) while LBDBPBSI measures blood lead in (umol/L). The other pairs of variables don't show a strong positive correlation.