

Assignment #1 – CPSC 552

DataFrames in Python

Pandas library in Python provides a class to store and process two dimensional data (like an Excel sheet) called “DataFrame”. We can read an Excel file into a dataframe, or lists, dictionaries, and other dataframes can be put in a dataframe.

The general form of the dataframe creation is:

pandas.DataFrame(data, index, columns, dtype, copy)

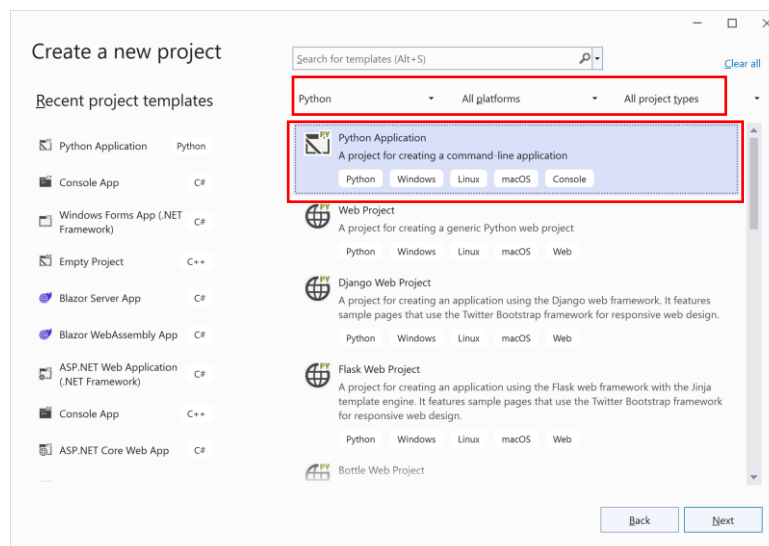
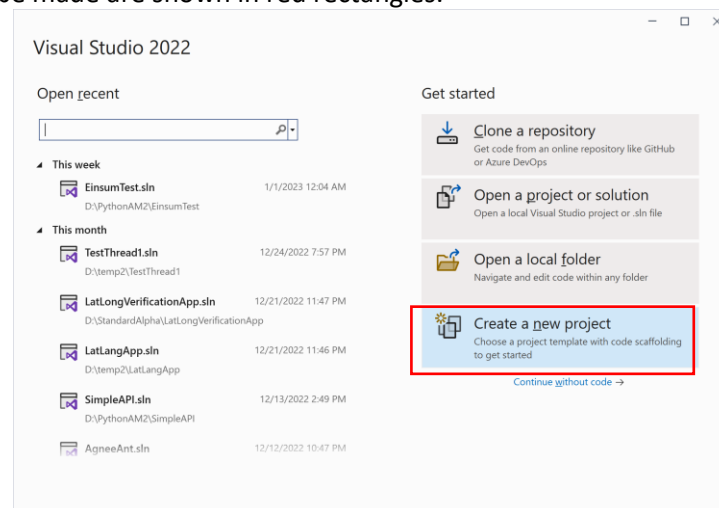
data – it can be a numpy ndarray, list, dictionary or another dataframe.

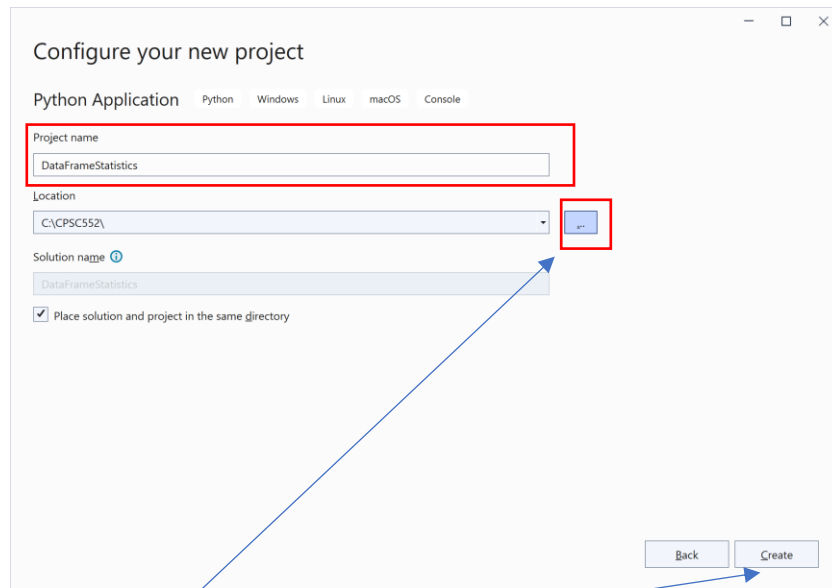
columns - default is - np.arange(n) i.e., column 0, column 1,...,column n-1. Named columns can be passed as well.

dtype - data type of each column.

copy - this is used for copying of data, the default is false.

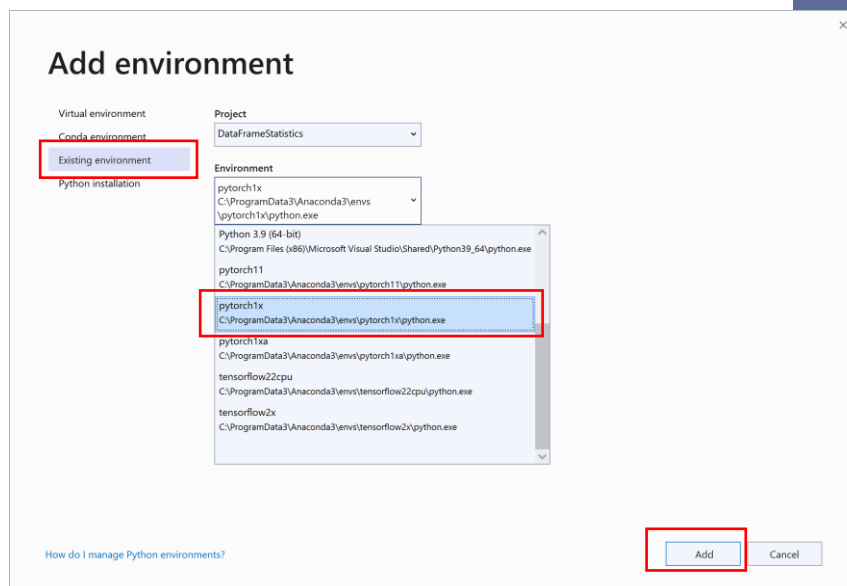
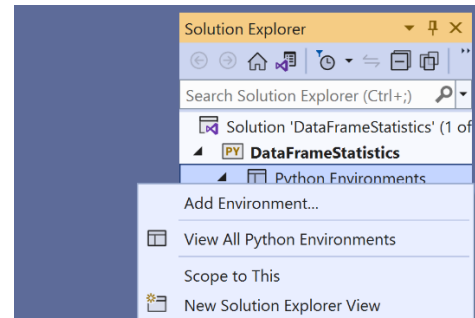
Example: Launch Visual Studio and create a Python application called **DataFrameStatistics** as shown below. Selections to be made are shown in red rectangles.



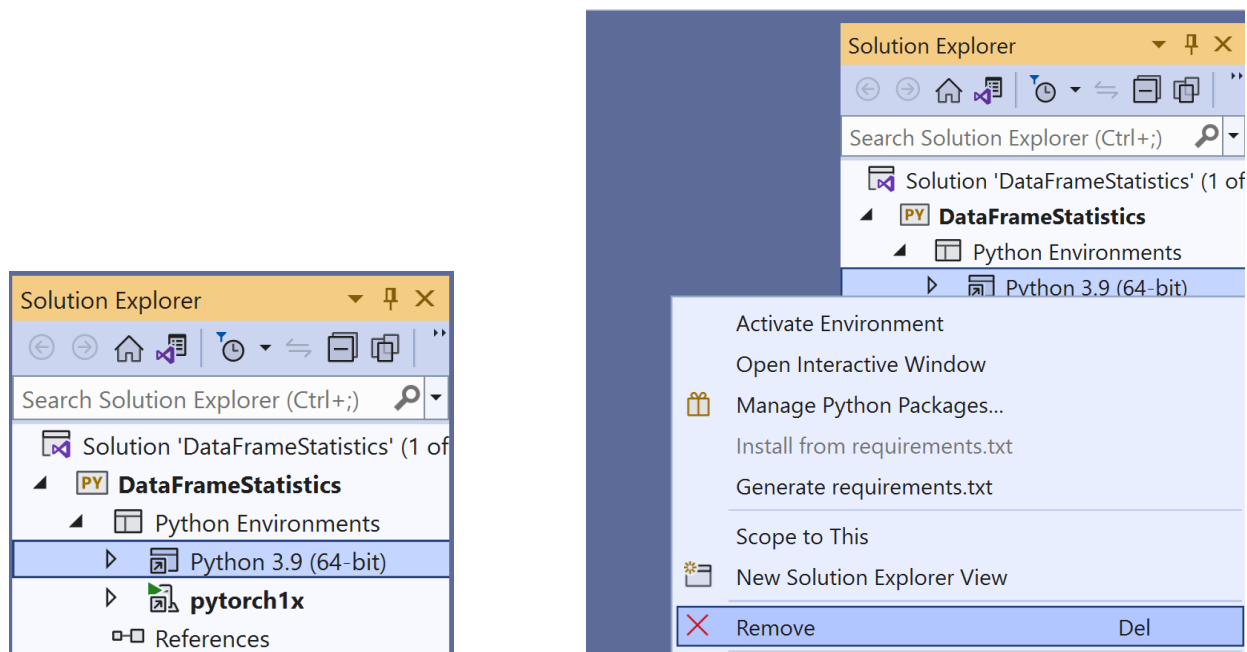


Click on the three dotted button to create a folder called CPSC552 to store the project on the C drive. Once you click the Create button, the project will be created for you.

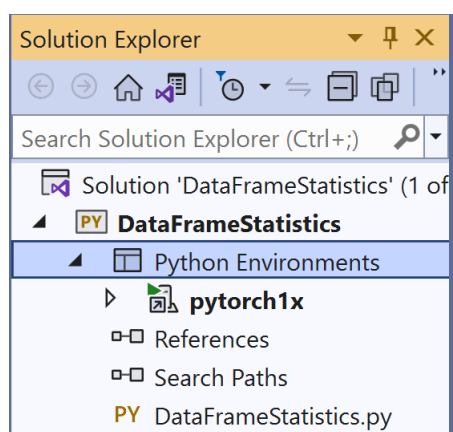
Next, you need to set the proper Python environment e.g., **Pytorch1x** in Visual Studio. Right click on Python Environments (under Solution explorer) and choose Add Environment.



If multiple environments show up under the environments in solution explorer, remove the environment other than “pytorch1x” by right clicking on it and choosing “remove environment”.



Removing a Python environment only removes it from the project and not your computer so it is safe to remove an environment. Make sure that only one environment e.g., “pytorch1x” is shown in bold under environments in Visual Studio (see below).



We will analyze the statistics in the PimaIndians diabetes dataset. This dataset is originally from the National Institute of Diabetes and Digestive and Kidney Diseases. The objective of the dataset is to diagnostically predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset. All patients here are females at least 21 years old of Pima Indian heritage.

There are 768 rows and 9 columns. The last column called outcome indicates if the person has diabetes or not.

```

C:\WINDOWS\system32\cmd.exe
(768, 9)
  Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  DiabetesPedigreeFunction  Age  Outcome
0           6        148             72             35         0    33.6              0.627   50         1
1           1         85             66             29         0    26.6              0.351   31         0
2           8        183             64              0         0    23.3              0.672   32         1
3           1         89             66             23        94    28.1              0.167   21         0
4           0        137             40             35       168    43.1              2.288   33         1
Press any key to continue . . .

```

Type the following code in DataFrameStatistics.py file. Type up to each print statement and then run the program to examine and understand the output it generates. You will have to change the location of the csv file to the folder where you have downloaded the file from the kiwi web site (unzip the dataset zip file after downloading from the kiwi web site).

```

import sys
import numpy as np
import pandas as pd

def main():
    df=pd.read_csv('D:/PythonAM/Data/diabetes_temp.csv')
    pd.set_option('display.max_columns', None) # to display all columns
    print(df.shape)

    print(df.head()) # first set of rows
    print(df.tail()) # last set of rows

    print(df.info()) # null, not null and data type of each column

    print(df.dtypes) # data types of each column

    print("Null values\n",df.isna().sum())
    print("Duplicate values", df.duplicated().sum()) # duplicate values

    # remove null data rows and duplicate rows
    dfn = df.dropna()
    print(dfn.shape)
    df_clean = dfn.drop_duplicates()
    print(df_clean.shape)

    column_headers = list(df.columns.values)
    print("Column Headings :", column_headers)

    # last column is outcome, lets remove it from the columns list
    # so that we can compute correlation between the data columns
    data_columns = column_headers[0:-1]
    print(data_columns)

    data_corr = df_clean[data_columns].corr() # correlation between columns
    print(data_corr)

    # determine the highest correlations for a feature
    corr_data = df_clean.corr().abs()
    cbmi = corr_data["BMI"]

```

```

corrbmi = cbmi.sort_values(ascending = False)
print("sorted correlations-----")
print(corrbmi)

print(df_clean.describe())

print(df_clean.nunique())

# print unique values of Pregnancies
print(df_clean['Pregnancies'].unique())

# combining columns from one dataframe to another new dataframe
seriesBMI = df["BMI"]
seriesGlucose = df["Glucose"]
seriesOutcome = df["Outcome"]
dfnew = pd.concat([seriesBMI, seriesGlucose, seriesOutcome], axis=1)
print(dfnew.head)

#---filtering or removing rows from a dataframe based on criteria
dffiltered = dfnew[dfnew['Glucose'] <= 180]
print(len(dffiltered))
print(dffiltered.head())

# change Outcome column 1 and 0 classes to 1 and 2
dfnew['Outcome'] = dfnew['Outcome'].map(lambda x: 1 if x == 1 else 2)
print(dfnew.head)

# access a particular row, column data in a dataframe
d1 = dfnew.iloc[25,1] # glucose value in row 25
print(d1)

# select 10-13 rows into a new dataframe
d2 = dfnew.iloc[10:14,:]
print(d2.head())

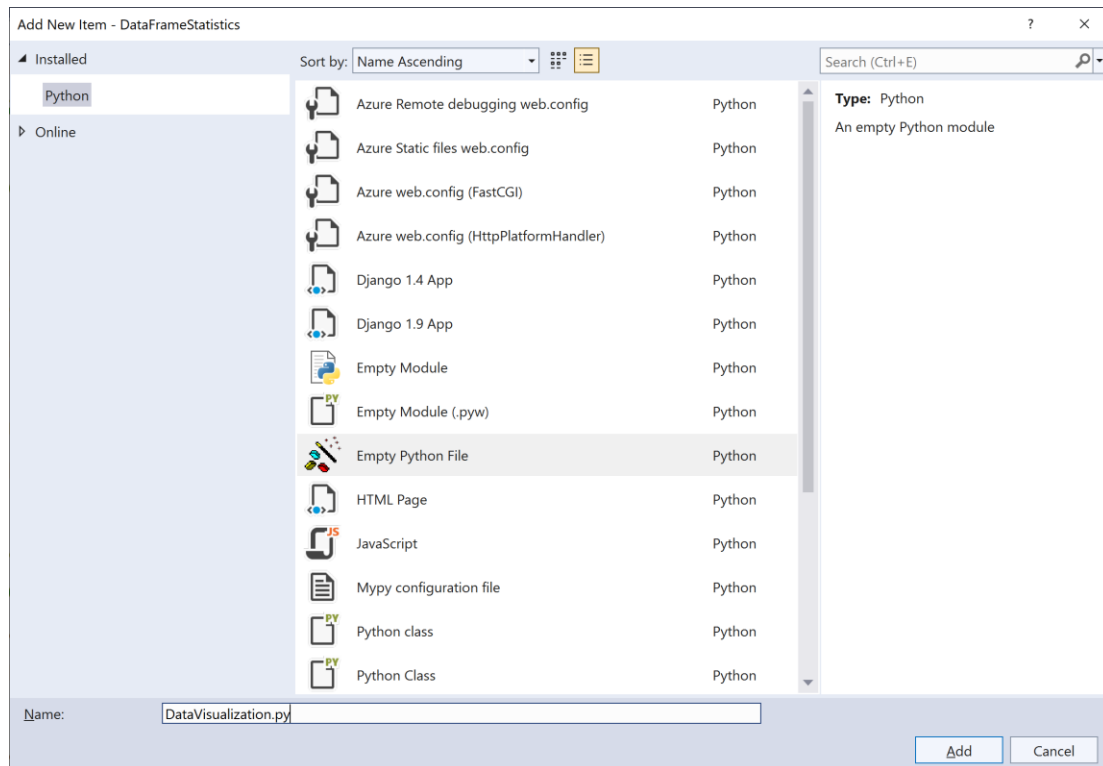
# select 10-13 rows into a new dataframe and reset index
d3 = dfnew.iloc[10:14,:].reset_index()
print(d3.head())

# select 10-13 rows into a new dataframe and reset index
# drop=True to avoid old index being kept
d3 = dfnew.iloc[10:14,:].reset_index(drop=True)
print(d3.head())

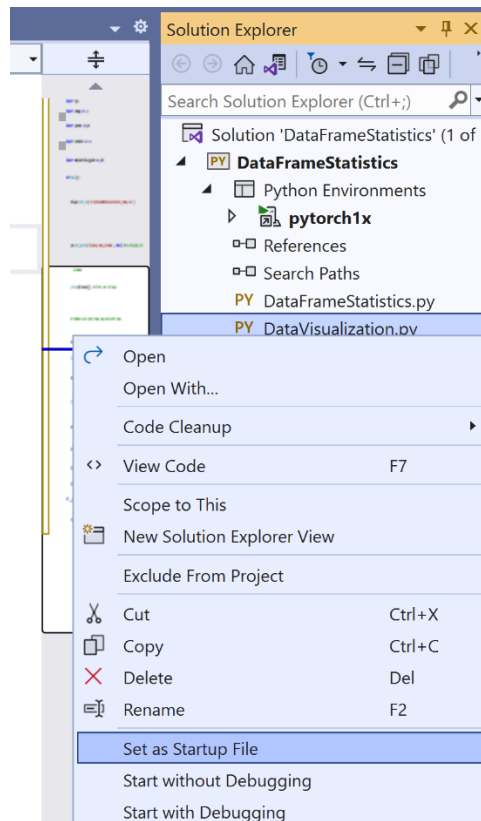
if __name__ == "__main__":
    sys.exit(int(main() or 0))

```

The above code shows how data can be read into a dataframe and do cleanup and determine basic statistics on the data. We also try to visualize the data in order to better understand the data distributions. Add another file to the project called DataVisualization.py by right clicking on the project name and choosing add new item as shown below.



Set the DataVisulaization.py as the startup file by right clicking on it in the solution explorer and choosing “set as startup file” as shown below.



Type the following code in DataVisualization.py. Type up to each plt.show() statement and then run the program to see the visualization it produces.

```
import sys
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt

# pip install seaborn

def main():
    df=pd.read_csv('D:/PythonAM/Data/diabetes_temp.csv')
    pd.set_option('display.max_columns', None) # to display all columns
    print(df.head()) # first set of rows
    # remove null data rows and duplicate rows
    dfn = df.dropna()
    print(dfn.shape)
    dfc = dfn.drop_duplicates()
    print(dfc.shape)

    dfc.Age.plot(color="blue",kind="hist", bins=20)
    plt.xlabel("Age")
    plt.ylabel("frequency")
    plt.show()

    dfc.hist(column='Age', by='Outcome') # histogram by group
    plt.show()

    df2= dfc[["Age", "Glucose"]]
    df2.plot(kind='hist',
             alpha=0.7,
             bins=30,
             title='Histogram Of Age,Glucose',
             rot=45,
             grid=True,
             figsize=(12,8),
             fontsize=15,
             color=['#ff0000', '#00ff00'])
    plt.xlabel('Age/Glucose')
    plt.ylabel("Count");
    plt.show()

    sns.countplot(x="Outcome", data=dfc)
    plt.show()
    print(dfc.Outcome.value_counts()) # outcome counts

    sizes=dfc.Pregnancies.value_counts().values[0:9]
    labels=dfc.Pregnancies.value_counts().index[0:9]
    colors=["green", "pink", "yellow", "purple", "grey", "blue", "plum", "orange",
"red"]
    plt.pie(sizes,data=dfc,labels=labels,colors=colors,radius=1.5)
    plt.show()

    df2=(dfc.columns[0:-1]) # remove outcomes column
```

```
dfc.hist(df2,bins=50, figsize=(20,15))
plt.show()

sns.heatmap(dfc[df2].corr(),annot=True)
plt.show()

if __name__ == "__main__":
    sys.exit(int(main() or 0))
```

The different Visualizations that appear are shown below (you will need to x out each plot in order to see the next plot).

