COMP40370 Practical 1

DATA EXPLORATION AND PREPROCESSING (Part B)

In [56]:
```
import pandas as pd
import numpy as np
from sklearn import svm
import os
import sys
import seaborn as sns
import matplotlib
import matplotlib.pyplot as plt
import scipy as sp
from sklearn.model_selection import train_test_split
from math import sqrt
from sklearn.metrics import mean_squared_error
```

Load 2 seperate Dataframes with 2 csv file.

In [57]:
```
df1 = pd.read_csv('diabetes1.csv')
df1.head(5)
```

Out[57]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72.0	35	0	33.6	0.627	50	1
1	1	85	66.0	29	0	26.6	0.351	31	0
2	8	183	64.0	0	0	23.3	0.672	32	1
3	1	89	66.0	23	94	28.1	0.167	21	0
4	0	137	40.0	35	168	43.1	2.288	15	1

In [58]:
```
df2 = pd.read_csv('ages.csv')
df2.head(5)
```

Out[58]:

	Age	AgeGroup
0	1	Children
1	2	Children

	Age	AgeGroup
2	3	Children
3	4	Children
4	5	Children

Question 1: Outliers removal and transformation

a. What are the kurtosis and skewness values of the Insulin attribute?

```
In [59]: df1['Insulin'].skew()
```

```
Out[59]: 2.268393486537506
```

```
In [60]: df1['Insulin'].kurtosis()
```

```
Out[60]: 7.265911343503076
```

b. Filter the dataframe and select only the rows where Insulin is not equal to 0

```
In [61]: filtered_df = df1[df1['Insulin'] != 0]
         filtered_df
```

Out[61]:

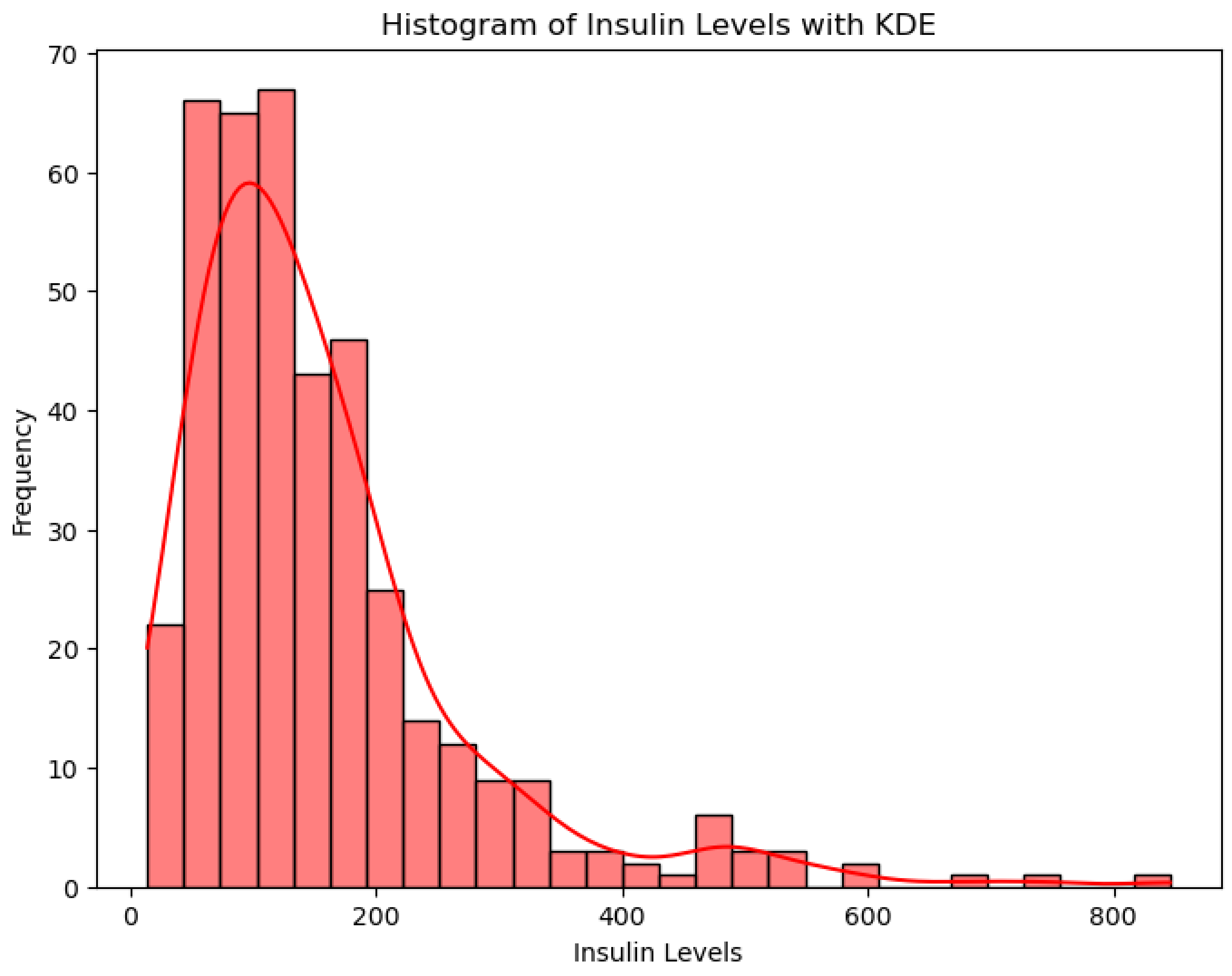
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
3	1	89	66.0	23	94	28.1	0.167	21	0
4	0	137	40.0	35	168	43.1	2.288	15	1
6	3	78	50.0	32	88	31.0	0.248	26	1
8	2	197	70.0	45	543	30.5	0.158	53	1
13	1	189	60.0	23	846	30.1	0.398	59	1
...	...	...	...	...	...	...	...	...	...
778	2	129	74.0	26	205	33.2	0.591	25	0
781	1	140	74.0	26	180	24.1	0.828	23	0
782	1	144	82.0	46	180	46.1	0.335	46	1

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
785	2	121	70.0	32	95	39.1	0.886	23	0
786	7	129	68.0	49	125	38.5	0.439	43	1

404 rows × 9 columns

c. Draw the histogram of Insulin column along with kernel density estimation (KDE) curb.

```
In [62]: plt.figure(figsize=(8, 6))
         sns.histplot(data=filtered_df, x='Insulin', kde=True, color='red')
         plt.xlabel('Insulin Levels')
         plt.ylabel('Frequency')
         plt.title('Histogram of Insulin Levels with KDE')
         plt.show()
```

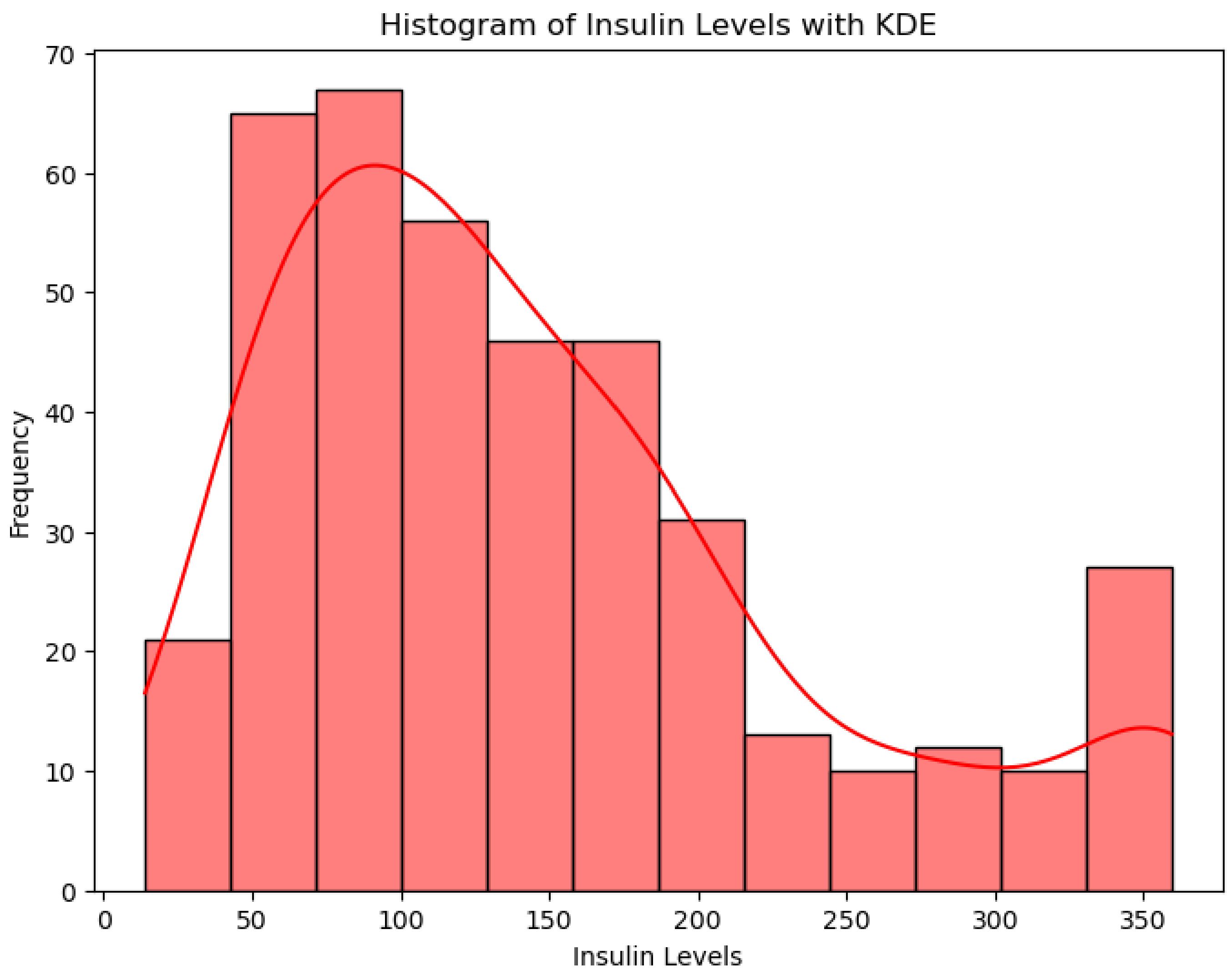


d. Identify outliers of Insulin using Inter Quartile Range (IQR) approach and impute them with min and max values appropriately. Then draw the histogram again to observe the difference

In [63]:
```
Q1 = filtered_df['Insulin'].quantile(0.25)
Q3 = filtered_df['Insulin'].quantile(0.75)
iqr = Q3-Q1
print(f'Interquartile Range (IQR): {iqr}')
```

```
Interquartile Range (IQR): 113.0
```

```
In [64]: lower_bound = Q1 - 1.5 * iqr
         upper_bound = Q3 + 1.5 * iqr
         outliers = filtered_df[(filtered_df['Insulin'] < lower_bound) | (filtered_df['Insulin'] > upper_bound)]
         filtered_df.loc[filtered_df['Insulin'] < lower_bound, 'Insulin'] = lower_bound
         filtered_df.loc[filtered_df['Insulin'] > upper_bound, 'Insulin'] = upper_bound
         plt.figure(figsize=(8, 6))
         sns.histplot(data=filtered_df, x='Insulin', kde=True, color='red')
         plt.xlabel('Insulin Levels')
         plt.ylabel('Frequency')
         plt.title('Histogram of Insulin Levels with KDE')
         plt.show()
```



```
In [65]: outliers.shape
```

```
Out[65]: (25, 9)
```

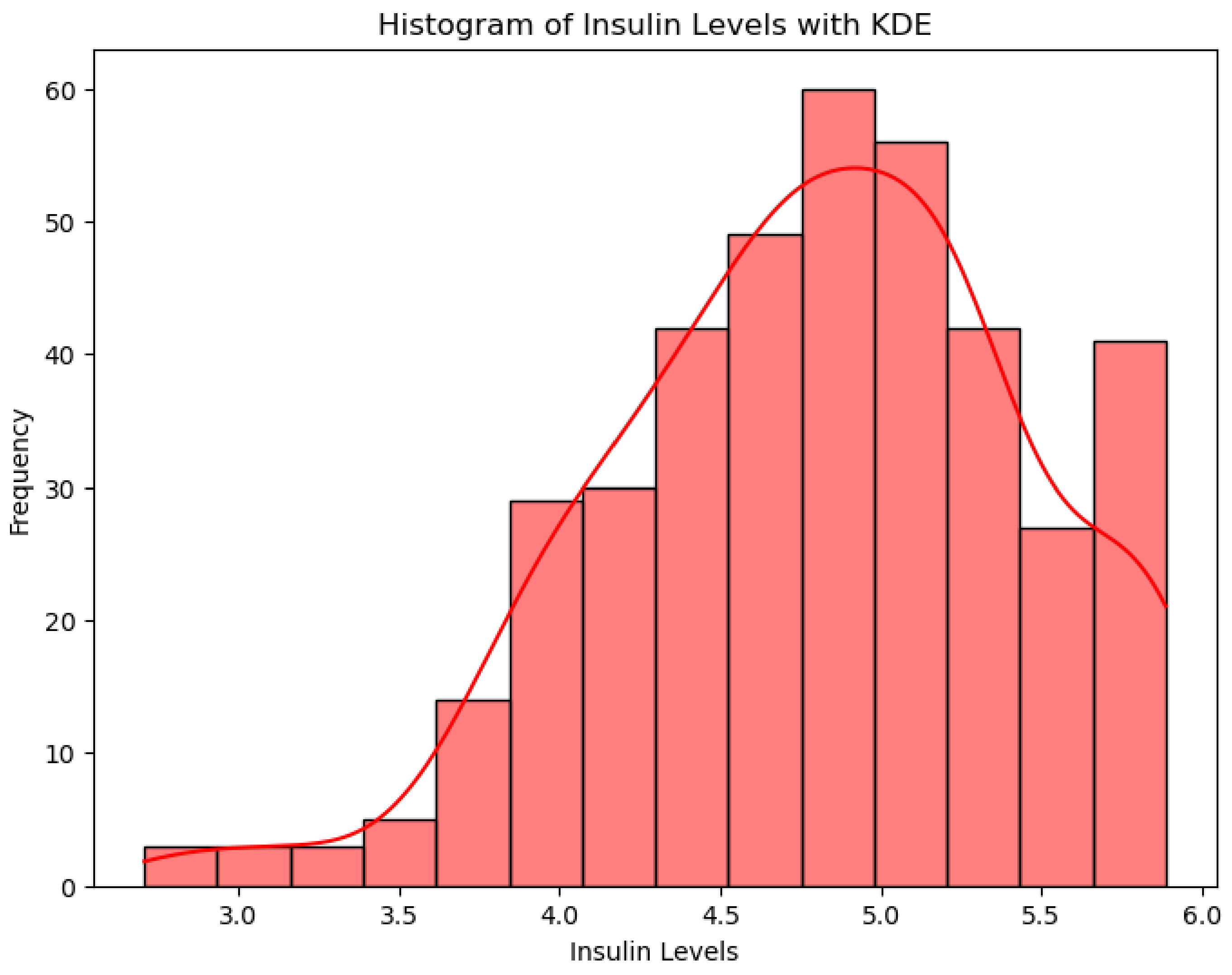
e.Transform Insulin column using loge (x+1) formula to make the Insulin values follow the normal distribution.

```
In [66]: filtered_df['Insulin_transformed'] = np.log1p(filtered_df['Insulin'])
         plt.figure(figsize=(8, 6))
         sns.histplot(data=filtered_df, x='Insulin_transformed', kde=True, color='red')
```

```python
plt.xlabel('Insulin Levels')
plt.ylabel('Frequency')
plt.title('Histogram of Insulin Levels with KDE')
plt.show()
```

```
/var/folders/8d/_9zyyhjn6cn7qy_8qqjt15cm0000gn/T/ipykernel_14604/3468122585.py:1: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a
-view-versus-a-copy
  filtered_df['Insulin_transformed'] = np.log1p(filtered_df['Insulin'])
```



f. Find the kurtosis and skewness of Insulin after the transformation

```
In [67]: filtered_df['Insulin_transformed'].skew()
```

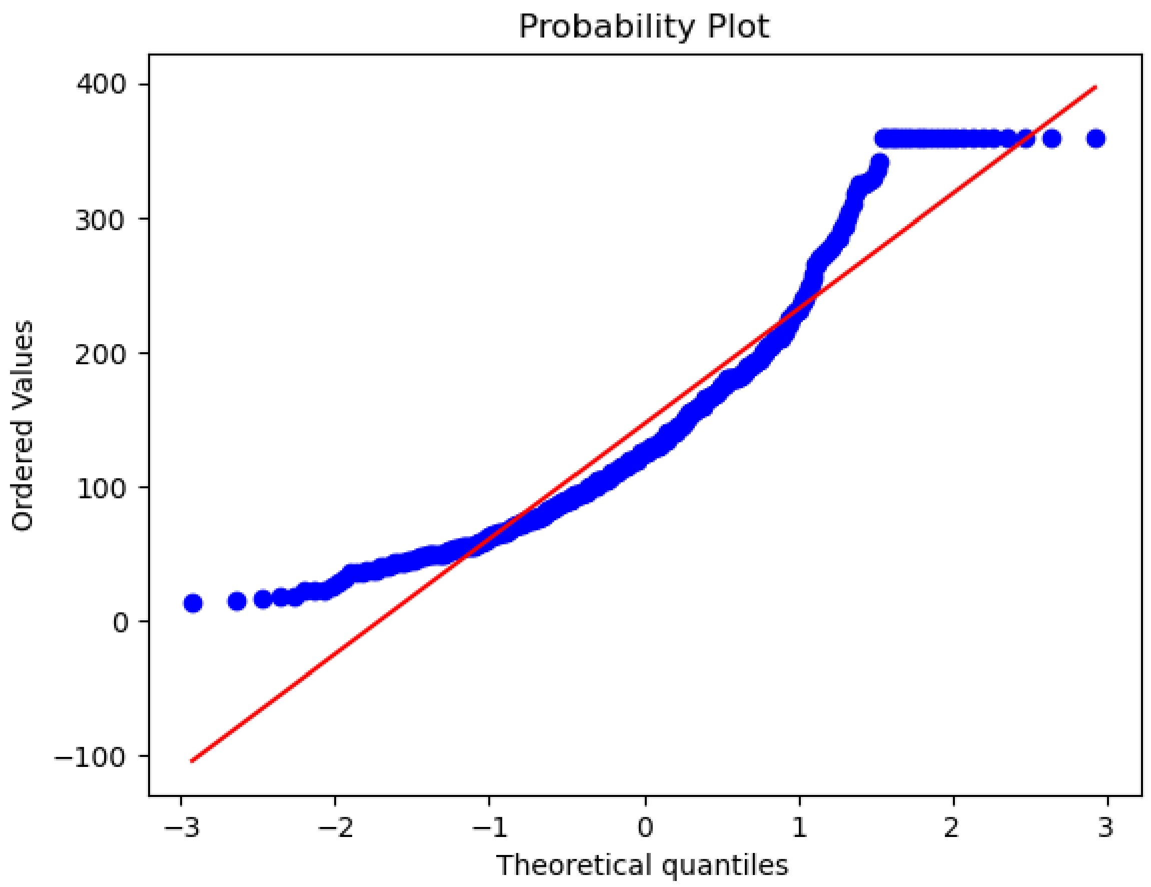
```
Out[67]: -0.39424325557435635
```

```
In [68]: filtered_df['Insulin_transformed'].kurtosis()
```

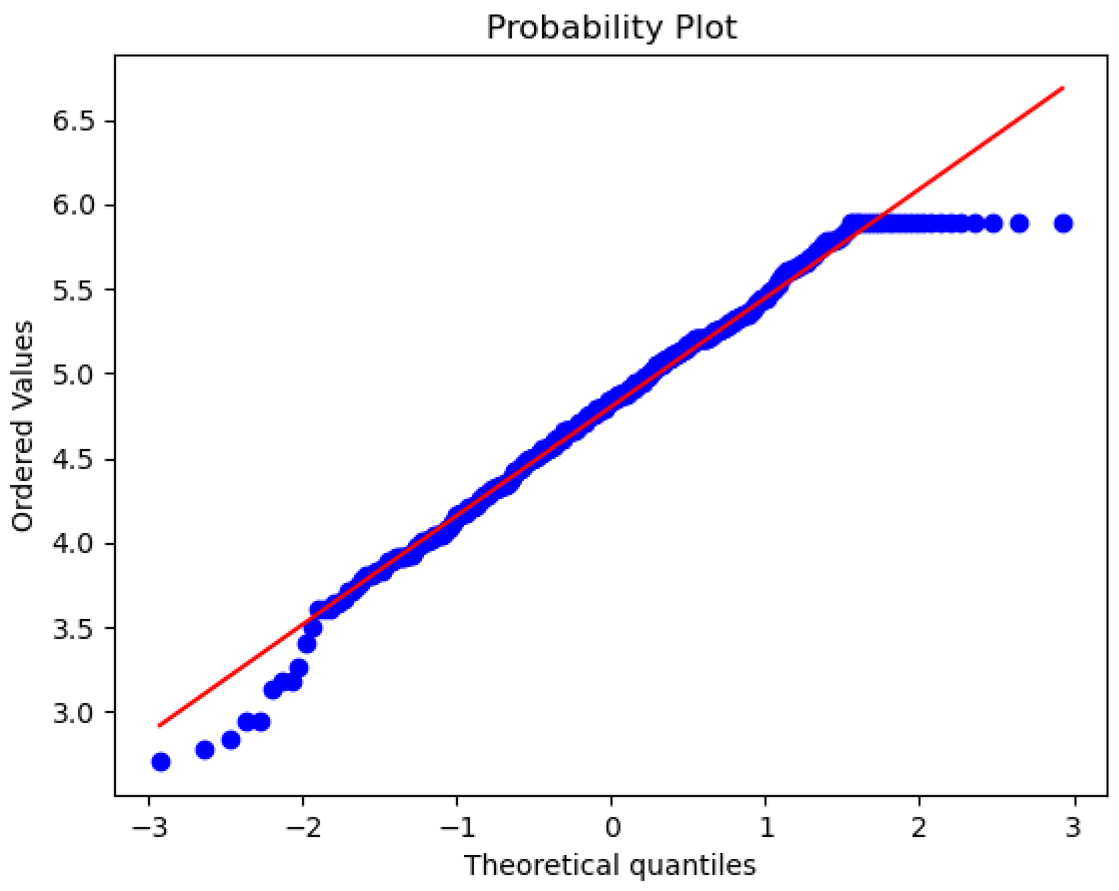
```
Out[68]: 0.04668578356986641
```

g. Use a QQ-plot to compare before and after the loge (x+1) transformation for Insulin column.

```
In [69]: import pylab
         import scipy.stats as stats
         stats.probplot(filtered_df['Insulin'], dist="norm", plot=pylab)
         pylab.show()
```



```
In [70]: stats.probplot(filtered_df['Insulin_transformed'], dist="norm", plot=pylab)
         pylab.show()
```



h. Similarly detect and correct outliers in the 'Glucose','BloodPressure' and 'SkinThickness' columns.

In [71]:
```
Q1 = filtered_df['Glucose'].quantile(0.25)
Q3 = filtered_df['Glucose'].quantile(0.75)
iqr = Q3-Q1
print(f'Interquartile Range (IQR) for "Glucose" : {iqr}')
```

```
Interquartile Range (IQR) for "Glucose" : 44.0
```

In [72]:
```
lower_bound = Q1 - 1.5 * iqr
upper_bound = Q3 + 1.5 * iqr
outliers = filtered_df[(filtered_df['Glucose'] < lower_bound) | (filtered_df['Glucose'] > upper_bound)]
filtered_df.loc[filtered_df['Glucose'] < lower_bound, 'Glucose'] = lower_bound
filtered_df.loc[filtered_df['Glucose'] > upper_bound, 'Glucose'] = upper_bound
```

In [73]:
```
Q1 = filtered_df['BloodPressure'].quantile(0.25)
Q3 = filtered_df['BloodPressure'].quantile(0.75)
iqr = Q3-Q1
print(f'Interquartile Range (IQR) for "BloodPressure" : {iqr}')
```

```
Interquartile Range (IQR) for "BloodPressure" : 16.0
```

In [74]:
```
lower_bound = Q1 - 1.5 * iqr
upper_bound = Q3 + 1.5 * iqr
outliers = filtered_df[(filtered_df['BloodPressure'] < lower_bound) | (filtered_df['BloodPressure'] > upper_bound)]
filtered_df.loc[filtered_df['BloodPressure'] < lower_bound, 'BloodPressure'] = lower_bound
filtered_df.loc[filtered_df['BloodPressure'] > upper_bound, 'BloodPressure'] = upper_bound
```

In [75]:
```
Q1 = filtered_df['SkinThickness'].quantile(0.25)
Q3 = filtered_df['SkinThickness'].quantile(0.75)
iqr = Q3-Q1
print(f'Interquartile Range (IQR) for "SkinThickness" : {iqr}')
```

```
Interquartile Range (IQR) for "SkinThickness" : 16.0
```

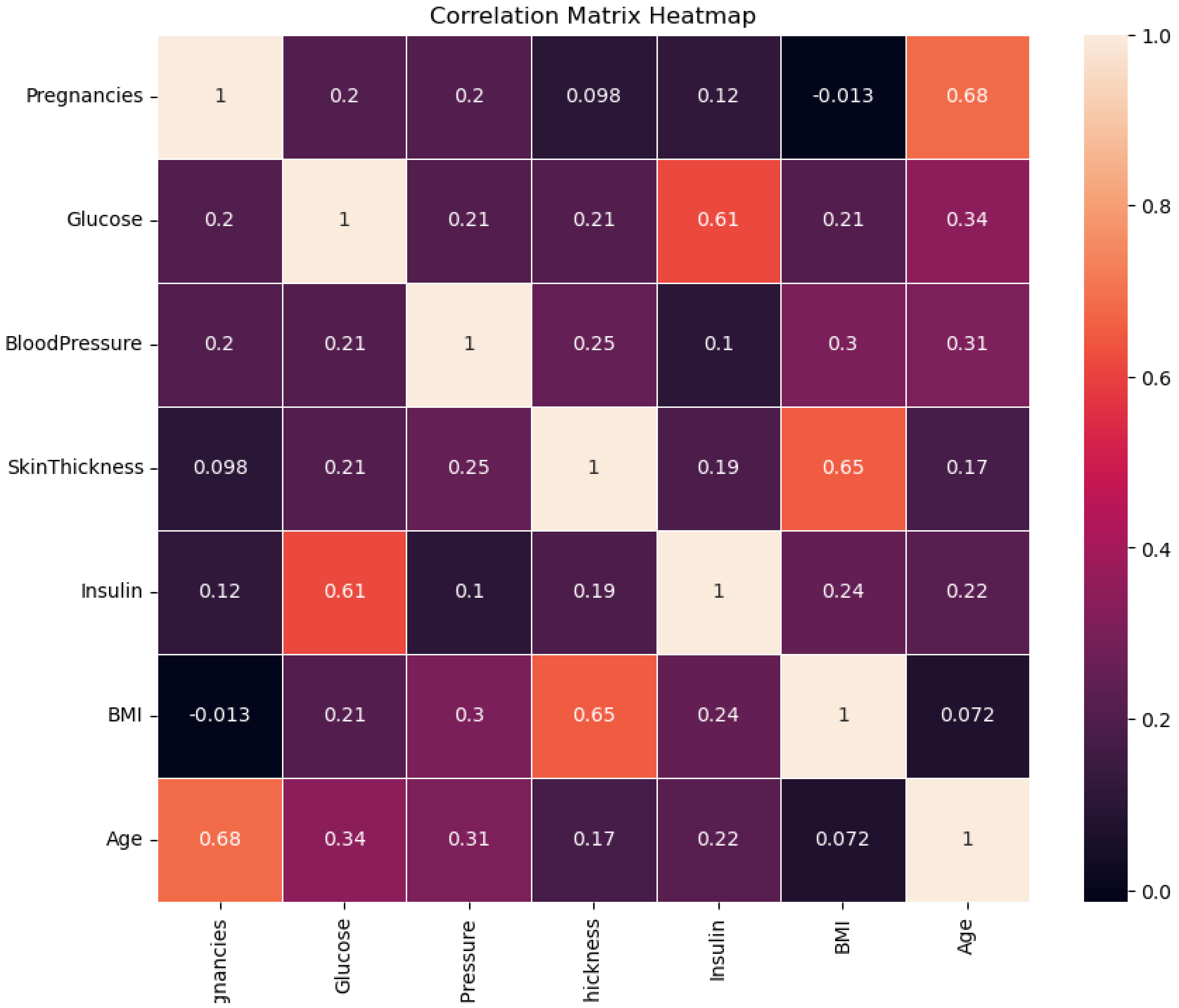
In [76]:
```
lower_bound = Q1 - 1.5 * iqr
upper_bound = Q3 + 1.5 * iqr
outliers = filtered_df[(filtered_df['SkinThickness'] < lower_bound) | (filtered_df['SkinThickness'] > upper_bound)]
filtered_df.loc[filtered_df['SkinThickness'] < lower_bound, 'SkinThickness'] = lower_bound
filtered_df.loc[filtered_df['SkinThickness'] > upper_bound, 'SkinThickness'] = upper_bound
outliers
```

Out[76]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome	Insulin_transformed
445	0	180	78.0	63	14.0	59.4	2.42	25	1	2.70805

i.Display the correlation matrix using the seaborn heatmap function between continuous variables; Pregnancies, Glocose, BloodPressure, SkinThickness, Insulin, BMI, Age.

In [77]:
```
plt.figure(figsize=(10, 8))
sns.heatmap(filtered_df[['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI', 'Age']].corr(),
plt.title('Correlation Matrix Heatmap')
plt.show()
```



	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Age
Pregnancies	1	0.2	0.2	0.098	0.12	-0.013	0.68
Glucose	0.2	1	0.21	0.21	0.61	0.21	0.34
BloodPressure	0.2	0.21	1	0.25	0.1	0.3	0.31
SkinThickness	0.098	0.21	0.25	1	0.19	0.65	0.17
Insulin	0.12	0.61	0.1	0.19	1	0.24	0.22
BMI	-0.013	0.21	0.3	0.65	0.24	1	0.072
Age	0.68	0.34	0.31	0.17	0.22	0.072	1

Question 2: Data processing

a. Group the patients by number of pregnancies, along with their average BloodPressure.

In [78]:
```
filtered_df.groupby('Pregnancies')['BloodPressure'].mean().reset_index()
```

Out[78]:

	Pregnancies	BloodPressure
0	0	73.263158
1	1	68.468085
2	2	66.107692
3	3	70.177778
4	4	70.458333
5	5	73.300000
6	6	67.052632
7	7	72.476190
8	8	78.285714
9	9	80.666667
10	10	81.600000
11	11	81.600000
12	12	74.400000
13	13	86.666667
14	14	78.000000
15	15	70.000000
16	17	72.000000

b. Group the patients by number of pregnancies, along with the average age, sum of all ages in that group, and the count of patients in that group

```
In [79]: filtered_df.groupby('Pregnancies')['Age'].agg(['mean','sum','count']).reset_index()
```

Out[79]:

	Pregnancies	mean	sum	count
0	0	24.258621	1407	58
1	1	27.122449	2658	98
2	2	25.194030	1688	67
3	3	28.244444	1271	45
4	4	30.407407	821	27
5	5	34.666667	728	21
6	6	38.368421	729	19
7	7	42.761905	898	21
8	8	44.714286	626	14
9	9	46.583333	559	12
10	10	48.000000	288	6
11	11	48.400000	242	5
12	12	46.800000	234	5
13	13	46.333333	139	3
14	14	46.000000	46	1
15	15	43.000000	43	1
16	17	47.000000	47	1

c. Add a new column named ‘BMI/Age’ with the value of BMI over the Age, without using any loops.

```
In [80]: filtered_df['BMI/Age'] = filtered_df['BMI']/filtered_df['Age']
```

```
/var/folders/8d/_9zyyhjn6cn7qy_8qqjt15cm0000gn/T/ipykernel_14604/2231514930.py:1: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead
```

```
See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a
-view-versus-a-copy
  filtered_df['BMI/Age'] = filtered_df['BMI']/filtered_df['Age']
```

d. Without looping the rows, add a new column named ‘risk’ with the following rules:

a. High: if BMI > 45 and BloodPressure > 100

b. Medium: if 30 < BMI < 45 and BloodPressure < 100

c. Low: if BMI < 30

d. Unknown: otherwise

In [81]:
```python
filtered_df['risk'] = 'Unknown'
filtered_df.loc[(filtered_df['BMI'] > 45) & (filtered_df['BloodPressure'] > 100), 'risk'] = 'High'
filtered_df.loc[(30 < filtered_df['BMI']) & (filtered_df['BMI'] < 45) & (filtered_df['BloodPressure'] < 100), 'risk'] =
filtered_df.loc[filtered_df['BMI'] < 30, 'risk'] = 'Low'
```

```
/var/folders/8d/_9zyyhjn6cn7qy_8qqjt15cm0000gn/T/ipykernel_14604/1078664258.py:1: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a
-view-versus-a-copy
  filtered_df['risk'] = 'Unknown'
```

e. The file named ages.csv provides the age group names. Merge the two dataframes by the age, the resulted dataframe must contain all the columns of diabetes.csv, in addition to their age group in the column named ‘AgeGroup’.

In [82]:
```python
filtered_df = filtered_df.merge(df2[['Age', 'AgeGroup']], on='Age', how='left')
filtered_df
```

Out[82]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome	Insulin_transformed	BMI/Age
0	1	89	66.0	23	94.0	28.1	0.167	21	0	4.553877	1.338095
1	0	137	40.0	35	168.0	43.1	2.288	15	1	5.129899	2.873333
2	3	78	50.0	32	88.0	31.0	0.248	26	1	4.488636	1.192308
3	2	197	70.0	45	359.5	30.5	0.158	53	1	5.887492	0.575472
4	1	189	60.0	23	359.5	30.1	0.398	59	1	5.887492	0.510169
...	...	...	...	...	...	...	...	...	...	...	...
399	2	129	74.0	26	205.0	33.2	0.591	25	0	5.327876	1.328000

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome	Insulin_transformed	BMI/Age
400	1	140	74.0	26	180.0	24.1	0.828	23	0	5.198497	1.047826
401	1	144	82.0	46	180.0	46.1	0.335	46	1	5.198497	1.002174
402	2	121	70.0	32	95.0	39.1	0.886	23	0	4.564348	1.700000
403	7	129	68.0	49	125.0	38.5	0.439	43	1	4.836282	0.895349

404 rows × 13 columns

f. one-hot encode the categorical variable ‘AgeGroup’ and add the resulting columns to diabetes.cvs, and remove AgeGroup.

In [83]:
```
encoded_agegroup = pd.get_dummies(filtered_df['AgeGroup'], prefix='AgeGroup')
final_df = pd.concat([filtered_df, encoded_agegroup], axis=1)
final_df.drop('AgeGroup', axis=1, inplace=True)
final_df.to_csv('diabetes_updated.csv', index=False)
```