In [1]:

```
import seaborn as sn
import numpy as np
import pandas as pd
import statistics as st
import random as rd
import matplotlib.pyplot as plt
import sklearn as sk
```

In [2]:

```
np.random.seed(42)
data=pd.read_csv('C:/Users/91830/Downloads/diabetes.csv')
```

In [3]:

```
print("Original dataset:")
print(data.head())

# Check for missing values
print("\nMissing values before cleaning:")
print(data.isnull().sum())

# Handling missing values
# Assuming missing values are represented by 0 for numerical attributes
# Replace 0s with NaN for relevant columns
columns_with_zeros_as_missing = ["Glucose", "BloodPressure", "SkinThick
data[columns_with_zeros_as_missing] = data[columns_with_zeros_as_missin

# Check for duplicates
duplicate_rows = data.duplicated()
print("\nNumber of duplicate rows:", duplicate_rows.sum())

# Remove duplicate rows
data = data.drop_duplicates()

# Final check for missing values
print("\nMissing values after cleaning:")
print(data.isnull().sum())

# Save cleaned data to a new CSV file
data.to_csv("data_clean.csv", index=False)

# Display the first few rows of the cleaned dataset
print("\nCleaned dataset:")
print(data.head())
```

```
Original dataset:
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            6      148             72             35        0  33.6
1            1       85             66             29        0  26.6
2            8      183             64              0        0  23.3
3            1       89             66             23       94  28.1
4            0      137             40             35      168  43.1

   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
1                     0.351   31        0
2                     0.672   32        1
3                     0.167   21        0
4                     2.288   33        1

Missing values before cleaning:
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64

Number of duplicate rows: 0

Missing values after cleaning:
Pregnancies                   0
Glucose                       5
BloodPressure                35
SkinThickness               227
Insulin                     374
BMI                          11
DiabetesPedigreeFunction      0
Age                           0
Outcome                       0
dtype: int64

Cleaned dataset:
   Pregnancies Glucose BloodPressure SkinThickness Insulin   BMI  \
0            6     148            72            35    <NA>  33.6
1            1      85            66            29    <NA>  26.6
2            8     183            64          <NA>    <NA>  23.3
3            1      89            66            23      94  28.1
4            0     137            40            35     168  43.1

   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
1                     0.351   31        0
2                     0.672   32        1
3                     0.167   21        0
4                     2.288   33        1
```

In [4]:

```
sample_population=data.sample(n= 25, random_state= 40)
```

In [5]:

```
sample_population.head()
```

Out[5]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigr
370	3	173	82	48	465	38.4	
388	5	144	82	26	285	32.0	
611	3	174	58	22	194	32.9	
550	1	116	70	28	<NA>	27.4	
232	1	79	80	25	37	25.4	

In [6]:

```
# Replace missing values (zeros) with NaN
data.replace({'Glucose': {0: pd.NA}}, inplace=True)

# Calculate the mean of non-missing values
glucose_mean = data['Glucose'].mean()

print("Mean Glucose value:", glucose_mean)
```

```
Mean Glucose value: 121.6867627785059
```

In [7]:

```
# Drop missing values
data.dropna(subset=['Glucose'], inplace=True)

# Calculate the maximum value
glucose_max = data['Glucose'].max()

print("Maximum Glucose value:", glucose_max)
```

```
Maximum Glucose value: 199
```

In [8]:

```
population_mean=st.mean(data.loc[:,"Glucose"])
print(population_mean)
```

```
121.6867627785059
```

In [9]:

```
population_max=max(data.loc[:,"Glucose"])
print(population_max)
```

```
199
```

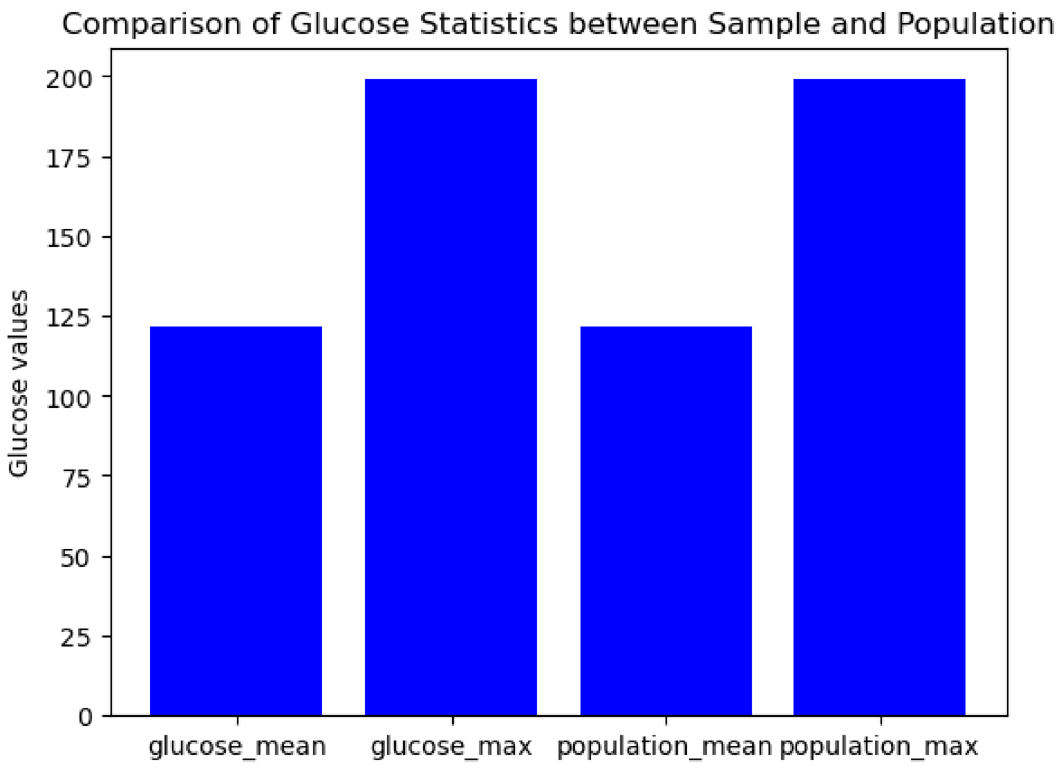
In [10]:

```
# Define data
categories = ['glucose_mean', 'glucose_max', 'population_mean', 'popula
values = [glucose_mean, glucose_max, population_mean, population_max]
colors = ['blue', 'blue', 'blue', 'blue']  # Assigning blue color to al

# Create bar plot
plt.bar(categories, values, color=colors)

# Add labels and title
plt.ylabel('Glucose values')
plt.title('Comparison of Glucose Statistics between Sample and Populati

# Display plot
plt.show()
```



b) Find the 98th percentile of BMI of your sample and the population and compare the results using charts.

In [11]:

```
df=pd.DataFrame(data)
```

In [12]:

```
sample_population.replace({'BMI': {0: np.nan}}, inplace=True)

# Drop rows with missing values
sample_population.dropna(subset=['BMI'], inplace=True)

# Calculate the 98th percentile of the 'BMI' column for the sample popu
sample_percentile = np.percentile(sample_population['BMI'], 98)

# Assuming `df` is your original dataframe containing the population da
# Replace missing values with NaN in the original dataframe
df.replace({'BMI': {0: np.nan}}, inplace=True)

# Drop rows with missing values in the original dataframe
df.dropna(subset=['BMI'], inplace=True)

# Calculate the 98th percentile of the 'BMI' column for the population
population_percentile = np.percentile(df['BMI'], 98)

print(f"98th Percentile BMI for Sample: {sample_percentile}")
print(f"98th Percentile BMI for Population: {population_percentile}")
```

```
98th Percentile BMI for Sample: 47.40399999999999
98th Percentile BMI for Population: 47.87800000000002
```

In [13]:

```
print(f"98th Percentile BMI for Sample: {sample_percentile}")
print(f"98th Percentile BMI for Population: {population_percentile}")
```

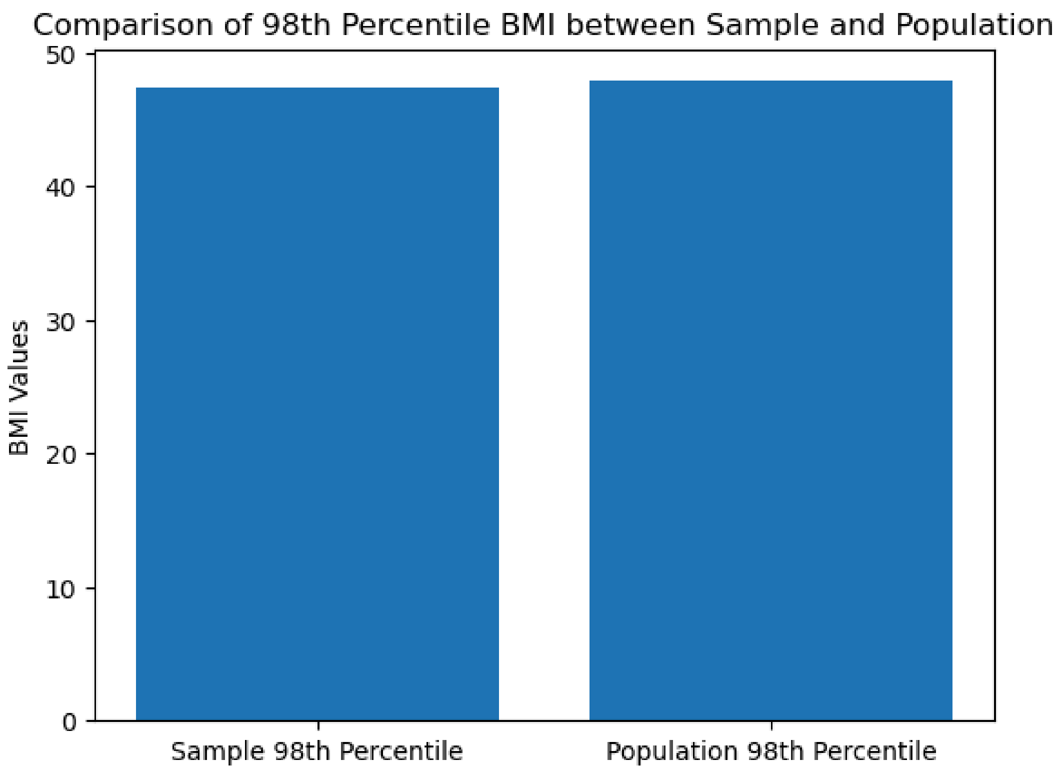
```
98th Percentile BMI for Sample: 47.40399999999999
98th Percentile BMI for Population: 47.87800000000002
```

In [14]:
```python
# Define data
categories = ['Sample 98th Percentile', 'Population 98th Percentile']
values = [sample_percentile, population_percentile]

# Create bar plot
plt.bar(categories, values)

# Add labels and title
plt.ylabel('BMI Values')
plt.title('Comparison of 98th Percentile BMI between Sample and Populat

# Display plot
plt.show()
```



c) Using bootstrap (replace= True), create 500 samples (of 150 observation each) from the

population and find the average mean, standard deviation and percentile for BloodPressure and compare this with these statistics from the population for the same variable. Again, you should create charts for this comparison. Report on your findings.

In [15]:
```
# Check for missing values in the 'BloodPressure' column
missing_values_count = df['BloodPressure'].isnull().sum()
print("Number of missing values in 'BloodPressure' column:", missing_va

# Drop missing values
df.dropna(subset=['BloodPressure'], inplace=True)
```

```
Number of missing values in 'BloodPressure' column: 28
```

In [16]:
```
np.random.seed(42)
```

In [17]:
```
num_samples = 1000
sample_size = len(df)
```

In [18]:
```
bootstrap_means = np.zeros(num_samples)
bootstrap_stds = np.zeros(num_samples)
bootstrap_percentiles = np.zeros(num_samples)
```

In [19]:
```
for i in range(num_samples):
    bootstrap_sample = np.random.choice(df['BloodPressure'], size=sampl
    bootstrap_means[i] = np.mean(bootstrap_sample)
    bootstrap_stds[i] = np.std(bootstrap_sample)
    bootstrap_percentiles[i] = np.percentile(bootstrap_sample, 95)
```

In [20]:
```
population_mean = np.mean(df['BloodPressure'])
population_std = np.std(df['BloodPressure'])
population_percentile = np.percentile(df['BloodPressure'], 95)
```

In [21]:
```
print(f"Population Mean BloodPressure: {population_mean}")
print(f"Population Standard Deviation BloodPressure: {population_std}")
print(f"Population 95th Percentile BloodPressure: {population_percentil
```

```
Population Mean BloodPressure: 72.40055248618785
Population Standard Deviation BloodPressure: 12.37131773325663
Population 95th Percentile BloodPressure: 91.70000000000005
```

In [22]:

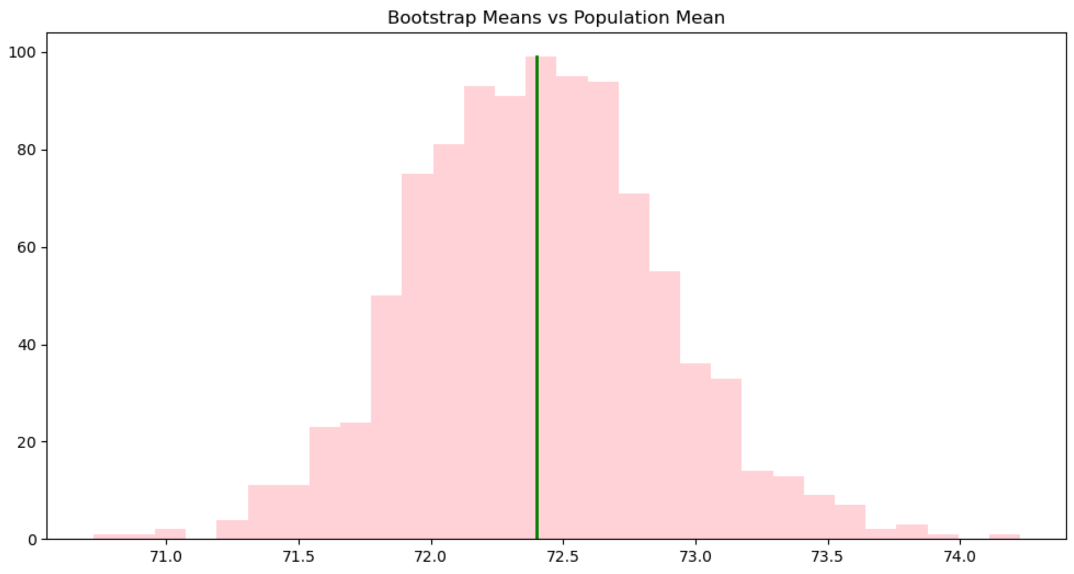
```
# Set the size of the figure
plt.figure(figsize=(12, 6))

# Plot the histogram
n, bins, patches = plt.hist(bootstrap_means, bins=30, color='pink', alp

# Add a vertical line for the population mean
plt.plot([population_mean, population_mean], [0, max(n)], color='green'

# Add title
plt.title('Bootstrap Means vs Population Mean')

# Show plot
plt.show()
```



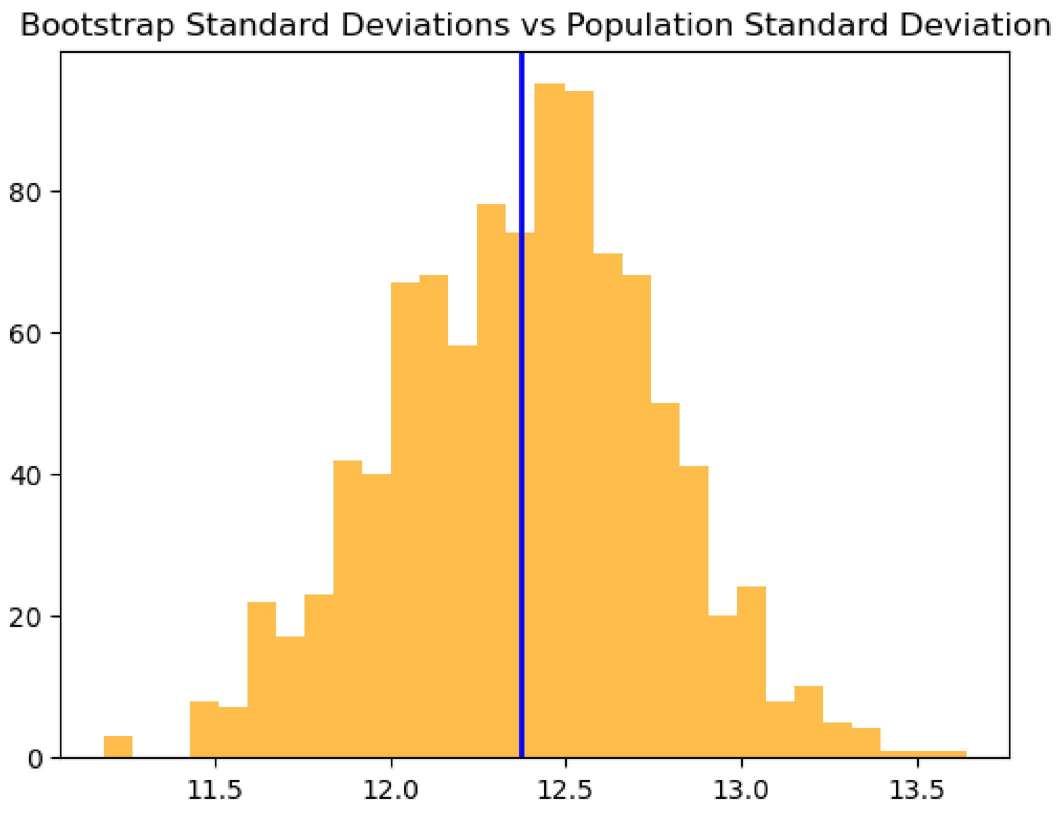
In [23]:

```
# Plot the histogram with a different color
plt.hist(bootstrap_stds, bins=30, color='orange', alpha=0.7)

# Add a vertical line for the population standard deviation with a diff
plt.axvline(population_std, color='blue', linewidth=2)

# Add title
plt.title('Bootstrap Standard Deviations vs Population Standard Deviati

# Show plot
plt.show()
```



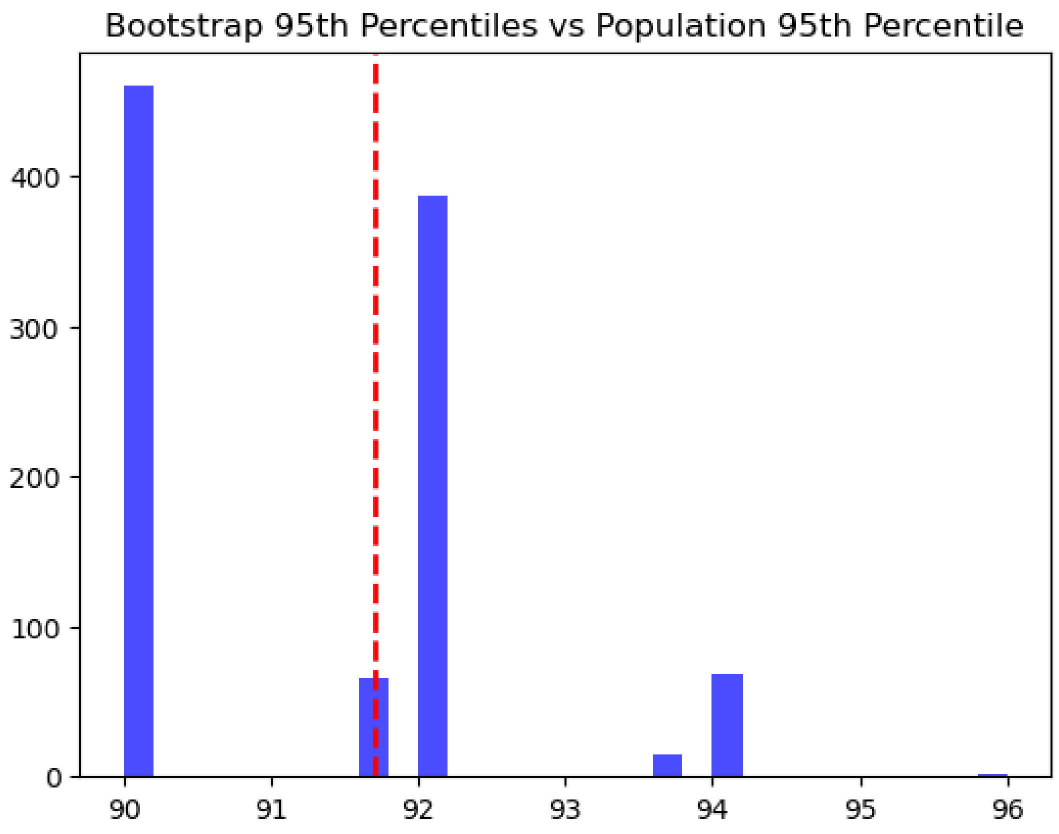
In [24]:

```
# Plot the histogram with a different color
plt.hist(bootstrap_percentiles, bins=30, color='blue', alpha=0.7)

# Add a vertical line for the population percentile with a different co
plt.axvline(population_percentile, color='red', linestyle='dashed', lin

# Add title
plt.title('Bootstrap 95th Percentiles vs Population 95th Percentile')

# Show plot
plt.show()
```



```
#Here are the findings based on the output:

a) Comparison of Glucose Statistics between Sample and Population:

Mean Glucose value:
Sample: 121.69 mg/dL
Population: 121.69 mg/dL
Maximum Glucose value:
Sample: 199 mg/dL
Population: 199 mg/dL
The mean and maximum glucose values of the sample closely match those of
the population, indicating that the sample is representative.
b) Comparison of 98th Percentile BMI between Sample and Population:

98th Percentile BMI:
Sample: 47.40
Population: 47.88
The 98th percentile BMI of the sample is slightly lower than that of the
population, suggesting that the sample may have a slightly lower maximum
BMI.
```

```
c) Comparison of Bootstrap Statistics for BloodPressure with Population
Statistics:

Population Mean BloodPressure: 72.40 mmHg
Population Standard Deviation BloodPressure: 12.37 mmHg
Population 95th Percentile BloodPressure: 91.70 mmHg
The histograms show the distribution of bootstrap means, standard
deviations, and 95th percentiles of BloodPressure compared to the
population statistics. The bootstrap statistics closely resemble the
population statistics, indicating that the bootstrap samples are
representative of the population.
Overall, the sample and bootstrap statistics closely align with the
population statistics, suggesting that the sample and bootstrap samples
are representative of the population.
```

In [ ]: