Homework 5: Application of CLT

Total : 100 pts This is an individual assignment.

There is only one part. **You can use python to solve some numerical calculations.** but make sure to show your steps.

In [2]:

```
import numpy as np
import numpy.random as npr
import random
import itertools

import pandas as pd

import matplotlib.pyplot as plt
%matplotlib inline
# plt.style.use('ggplot')

import scipy.stats as stats
```

Description

Provide analytical solutions to the problems below and upload your answers as a PDF. (There is no need to type your answers -- just scan your handwritten solutions with an app like CamScanner or Scannable.)

- **Central limit Theorem is abbreviated as CLT.**

Problem 1

(10 pt) A population has a mean of $\mu = 100$ and a standard deviation of $\sigma = 15$. You take a random sample of size $ n = 60$.

- Compute the expected mean and standard deviation of the sample mean distribution.

Problem 1 Solution:

(1) Expected Mean of Sample Mean Distribution:

$\mu_{\bar{x}} = \mu = 100$

(2) Standard Deviation (Standard Error) of Sample Mean Distribution:

$\sigma_{\bar{x}} = \frac{\sigma}{\sqrt{n}} = \frac{15}{\sqrt{60}} \approx 1.9365$

Problem 2:

(10pt, 5 pt each) A university's exam scores are normally distributed with a mean of 75 and a standard deviation of 12.

- What is the probability that a randomly selected student scores above 80?
- If we take a random sample of 50 students, what is the probability that their average score is above 80?

Problem 2 Solution:

Given:

- Population mean: $\mu = 75$
- Population standard deviation: $\sigma = 12$

(1) Probability a randomly selected student scores above 80:

Let X be the exam score of a randomly selected student. We want:

$ P(X > 80) = 1 - P(X \leq 80) $

Then, using Python, the calculated probability is approximately 0.3385.

In [3]:
```
prob_above_80 = 1 - stats.norm.cdf(80, loc=75, scale=12)
print(prob_above_80)
```

```
0.3384611195106897
```

(2) Probability the average score of 50 students is above 80:

By the Central Limit Theorem (CLT), the distribution of sample means will be normally distributed with:

- Mean: $\mu_{\bar{x}} = \mu = 75$
- Standard deviation : $ \sigma_{\bar{x}} = \frac{\sigma}{\sqrt{n}} = \frac{12}{\sqrt{50}} \approx 1.6971 $

We want the probability:

$ P(\bar{x} > 80) = 1 - P(\bar{x} \leq 80) $

Calculate using Python, and the probability is approximately 0.0016.

In [4]:
```
prob_sample_mean_above_80 = 1 - stats.norm.cdf(80, loc=75, scale=12/np.sqrt(50))
print(prob_sample_mean_above_80)
```

```
0.0016081146550637193
```

Problem 3:

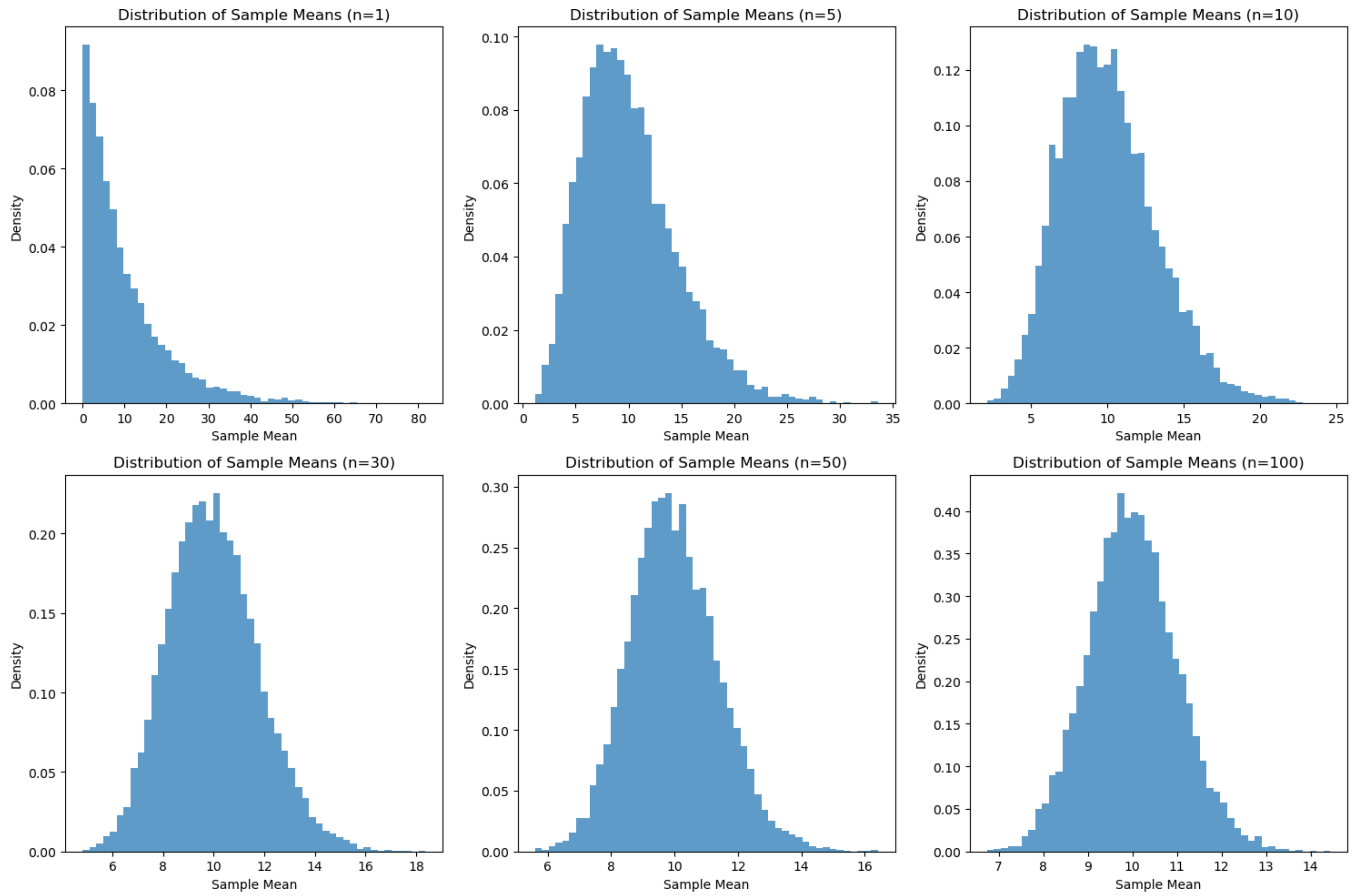
(10 pt.) Suppose the population distribution is highly skewed (e.g., exponential distribution with mean $\mu = 10$).

- According to the CLT, what happens to the shape of the distribution of the sample mean M_n as n increases? Simulate this scenario by taking multiple samples and computing the sample means.

Problem 3 Solution:

To illustrate this, let's simulate using an exponential distribution (highly skewed):

In [5]:
```
# Parameters
mu = 10  # mean of exponential distribution
sample_sizes = [1, 5, 10, 30, 50, 100]  # different sample sizes n
num_samples = 10000

# Plotting setup
fig, axes = plt.subplots(2, 3, figsize=(15, 10))

# Generate and plot sample means for each sample size
for i, n in enumerate(sample_sizes):
    sample_means = [np.mean(np.random.exponential(scale=mu, size=n)) for _ in range(num_
    axes = axes = plt.subplot(2, 3, sample_sizes.index(n) + 1)
    plt.hist(sample_means, bins=50, density=True, alpha=0.7)
    plt.title(f'Distribution of Sample Means (n={n})')
    plt.xlabel('Sample Mean')
    plt.ylabel('Density')

plt.tight_layout()
plt.show()
```



- For small n, the distribution of sample means closely resembles the skewed exponential distribution.
- As the sample size n increases, the distribution becomes increasingly symmetric and bell-shaped, converging towards a normal distribution, as predicted by the CLT.
- As the sample size n increase, the variance of M_n is reduced monotonically.

Problem 4:

(total 20 points, 5 point each)

Consider the following samples x shown in the code block.

determine the unbiased estimates of

a) the true mean μ_X;

b) the true variance σ_X^2;

c) Find the 90% and 95% confidence intervals of the true mean μ_X.

d) Assume the variance is 4. Find the 90% and 95% confidence intervals of the true mean μ_X.

In [6]:
```
x = np.array([ 5.13149548,  5.93772493,  9.06697128,  5.23739937, 10.97571492,
        6.57455483, 16.98124387,  6.43814608, 10.96175814, 12.99997309,
        6.35771001, 10.32057521, 14.2755244 , 14.67332882, 12.01342886,
        9.42476482,  5.83938407, 14.00531047,  5.5066388 , 16.9627389 ,
```

```
       11.2425588 ,  9.22283116,  8.81756564,  7.4542541 , 13.5276926 ,
        8.9838017 ,  6.17270784,  6.11628502, 12.73676266, 12.10245976,
        6.61158708, 11.63275555,  7.37901878, 10.89610414, 11.22716216,
       10.53632239,  6.28180412,  0.85423536,  7.25049042,  6.49677655,
       13.16411068, 19.76880339,  9.97978585,  8.54956202,  3.02158038,
       16.49559522,  5.35853099,  8.25208242, 11.12447038, 14.06371398])
```

Problem 4 Solution:

In [7]:
```python
# (a) Unbiased estimate of the true mean
mean_x = np.mean(x)
print(mean_x)
```

```
9.7001159498
```

In [8]:
```python
# (b) Unbiased estimate of the true variance
var_x = np.var(x, ddof=1)
print(var_x)
```

```
15.307503304153016
```

In [9]:
```python
# alternatively
var_x2 = x.var(ddof=1)
print(var_x2)
```

```
15.307503304153016
```

In [10]:
```python
# (c) Confidence intervals with unknown variance using t-distribution
# We will skip this problem because it is not covered yet.
n = len(x)

# Sample Standard Error of the Mean (SSEM)
ssem_x = stats.sem(x) # calculate estimated_sigma / sqrt(n) using ddof=1

# Significance levels
alpha_90 = 1 - 0.9
alpha_95 = 1 - 0.95

# Critical t-values
t_val_90 = stats.t.ppf(1 - alpha_90/2, df=n-1)
t_val_95 = stats.t.ppf(1 - alpha_95/2, df=n-1)

# Margin of errors
moe_90 = t_val_90 * ssem_x
moe_95 = t_val_95 * ssem_x

# Confidence Intervals (CI)
CI_t_90 = (mean_x - moe_90, mean_x + moe_90)
CI_t_95 = (mean_x - moe_95, mean_x + moe_95)

print("Confidence Intervals with unknown variance:")
print("90% CI:", CI_t_90)
print("95% CI:", CI_t_95)
```

```
Confidence Intervals with unknown variance:
90% CI: (8.77246643921188, 10.62776546038812)
95% CI: (8.588201309001102, 10.8120305905989)
```

In [13]:
```python
# (d) Confidence intervals with known variance (sigma^2 = 4, so sigma = 2) using z-distr
sigma = 2
# Standard Error of the Mean (SEM) or the variance of the mean estimator.
sem = sigma / np.sqrt(n)
```

```python
# Critical z-values
z_critical_90 = stats.norm.isf( alpha_90/2)
z_critical_95 = stats.norm.isf(alpha_95/2)

# Margin/distance d
d_z_90 = z_critical_90 * sem
d_z_95 = z_critical_95 * sem

# Confidence Intervals (CI)
CI_z_90 = (mean_x - d_z_90, mean_x + d_z_90)
CI_z_95 = (mean_x - d_z_95, mean_x + d_z_95)

print("\nConfidence Intervals with known variance:")
print("90% CI:", CI_z_90)
print("95% CI:", CI_z_95)
```

```
Confidence Intervals with known variance:
90% CI: (9.234881088329331, 10.16535081127067)
95% CI: (9.145754420060129, 10.254477479539872)
```

Problem 5 - Biased Estimator

(Total 10 points. 5 points each)

Consider a set of i.i.d. data $X=\{X_i\}_{i=1}^N$, with mean μ and varaince σ^2. Define the following estimator for the mean:

\begin{align*} \hat{\mu}_c &= \frac{1}{N} \sum_{i=1}^N (X_i + c), \qquad c \in \mathbb{R} \end{align*}
1 (5 pt). Compute the bias of this estimator, $b_{\mu}(\hat{\mu}_c)$.

2 (5 pt). Compute $\operatorname{Var}[\hat{\mu}_c]$.

Problem 5 Solution:

(1) Bias of the Estimator

The bias is defined as: $b_{\mu}(\hat{\mu}_c) = \mathbb{E}[\hat{\mu}_c] - \mu$

1. Compute the expectation of $\hat{\mu}_c$:

   $ \mathbb{E}[\hat{\mu}_c] = \mathbb{E}\left[\frac{1}{N}\sum_{i=1}^N (X_i + c)\right] $

2. By linearity of expectation:

   $ \mathbb{E}[\hat{\mu}_c] = \frac{1}{N} \sum_{i=1}^N \mathbb{E}[X_i + c] = \frac{1}{N} \sum_{i=1}^N \left(\mathbb{E}[X_i] + c\right) $

3. Since $\mathbb{E}[X_i] = \mu$ for all i:

   $ \mathbb{E}[\hat{\mu}_c] = \frac{1}{N} \cdot N (\mu + c) = \mu + c $

4. Therefore, the bias is:

   $ b_{\mu}(\hat{\mu}_c) = (\mu + c) - \mu = c $

(2) Variance of the Estimator

To compute the variance: $ \operatorname{Var}[\hat{\mu}_c] $

1. Since the X_i's are i.i.d., the variance of their sum is:

   $ \operatorname{Var}[\hat{\mu}_c] = \operatorname{Var}\left[\frac{1}{N}\sum_{i=1}^N (X_i + c)\right] = \sum_{i=1}^N \operatorname{Var}\left[\frac{1}{N}(X_i + c)\right] $

2. Notice that adding a constant c does not affect the variance, scaling a random variable by $\frac{1}{N}$ reduces the variance by a factor of $\frac{1}{N^2}$:

   $ \operatorname{Var}\left[\frac{1}{N}(X_i + c)\right] = \frac{1}{N^2}\operatorname{Var}(X_i) = \frac{\sigma^2}{N^2} $

3. Finally, we get:

   $ \operatorname{Var}[\hat{\mu}_c] = \operatorname{Var}\left[\frac{1}{N}\sum_{i=1}^N (X_i + c)\right] = N \cdot \frac{\sigma^2}{N^2} = \frac{\sigma^2}{N}. $

Problem 6 - CI with known variance

(total 10 pt) A random sample $X_1,\ldots, X_{100}$ is given from a distribution with known variance $Var(X_i)=16$. For the observed sample, the sample mean is $\bar X=23.5$, Find an approximate 98% confidence interval for the mean of the underlying distribution X_i.

Problem 6 Solution:

In [14]:

```
n = 100
sigma = np.sqrt(16)
mean_x = 23.5

# Standard Error of the Mean (SEM)
sem = sigma / np.sqrt(n)

# Significance levels
alpha_98 = 1 - 0.98

# Critical z-values
z_critical_98 = stats.norm.isf(alpha_98/2)

# Margin of errors
moe_z_98 = z_critical_98 * sem

# Confidence Intervals (CI)
CI_z_98 = (mean_x - moe_z_98, mean_x + moe_z_98)

print("\nConfidence Intervals with known variance:")
print("98% CI:", CI_z_98)
```

```
Confidence Intervals with known variance:
98% CI: (22.569460850383663, 24.430539149616337)
```

Problem 7

(30pt,)

In this problem you will be working with the Breast Cancer Data Set).

This data set contains 569 samples of digitized images of a fine needle aspirate (FNA) of a breast mass. Each sample describes the mass using 30 features, which include the average radius of the cell present in the FNA image. Each sample is labeled as benign (class = 1) or malignant (class = 0).

We will use the `scikit-learn` library to load it and write it as a pandas dataframe:

In [11]:
```
import pandas as pd
import numpy as np
from sklearn.datasets import load_breast_cancer
data = load_breast_cancer(return_X_y = False)
# print(data.DESCR) # uncomment this to learn more about this dataset

df = pd.DataFrame(data = np.hstack((data.target[:,np.newaxis], data.data)),
                      columns = np.concatenate((['Class'],data.feature_names)))
df
```

Out[11]:

	Class	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry
0	0.0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.30010	0.14710	0.2419
1	0.0	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.08690	0.07017	0.1812
2	0.0	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.19740	0.12790	0.2069
3	0.0	11.42	20.38	77.58	386.1	0.14250	0.28390	0.24140	0.10520	0.2597
4	0.0	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.19800	0.10430	0.1809
...	...	...	...	...	...	...	...	...	...	...
564	0.0	21.56	22.39	142.00	1479.0	0.11100	0.11590	0.24390	0.13890	0.1726
565	0.0	20.13	28.25	131.20	1261.0	0.09780	0.10340	0.14400	0.09791	0.1752
566	0.0	16.60	28.08	108.30	858.1	0.08455	0.10230	0.09251	0.05302	0.1590
567	0.0	20.60	29.33	140.10	1265.0	0.11780	0.27700	0.35140	0.15200	0.2397
568	1.0	7.76	24.54	47.92	181.0	0.05263	0.04362	0.00000	0.00000	0.1587

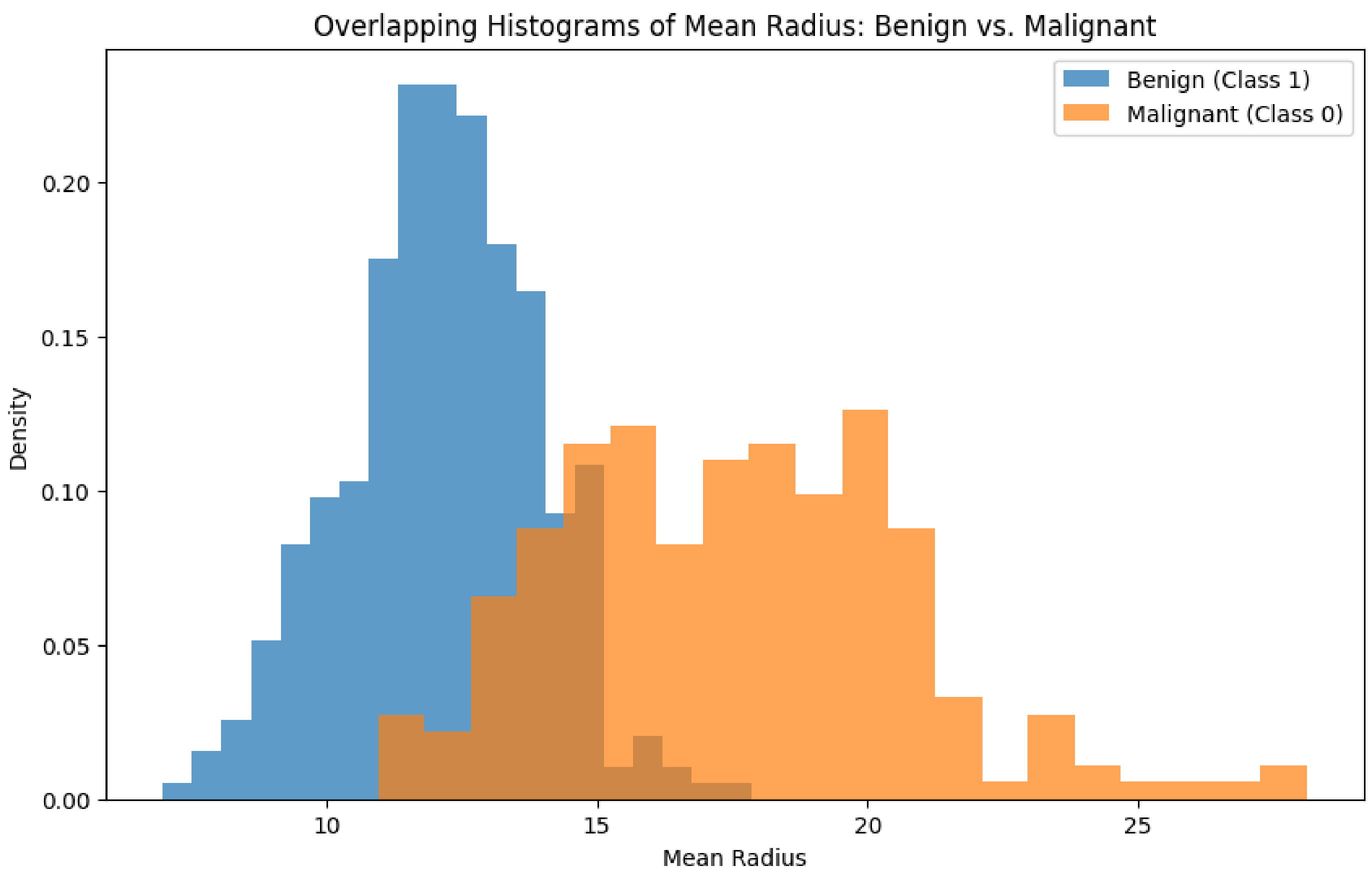
569 rows × 31 columns

For each class (benign and malignant), consider the mean radius column. Answer the following questions:

Consider the mean radius feature (second column in dataframe) for both benign (class=1) and malignant (class=0) samples. Answer the following questions:

1.(5pt) **Plot overlapping histograms of the two types of samples (malignant and benign).**

In [12]:
```
# Extract the mean radius column for benign and malignant samples.
benign = df[df['Class'] == 1]['mean radius']
malignant = df[df['Class'] == 0]['mean radius']

# Plot overlapping histograms
plt.figure(figsize=(10, 6))
plt.hist(benign, bins=20, alpha=0.7, label='Benign (Class 1)', density=True)
plt.hist(malignant, bins=20, alpha=0.7, label='Malignant (Class 0)', density=True)
plt.xlabel('Mean Radius')
plt.ylabel('Density')
plt.title('Overlapping Histograms of Mean Radius: Benign vs. Malignant')
plt.legend()
plt.show()
```



2.(20pt)**Assume that the two groups follow a Gaussian distribution. Estimate the parameters of each distribution using unbiased estimators from the sample data.**

In [13]:
```
# Estimate parameters for the benign group
benign_mean = benign.mean()                         # Unbiased estimator of the mean
benign_variance = benign.var(ddof=1)                 # Unbiased estimator of the variance

# Estimate parameters for the malignant group
malignant_mean = malignant.mean()                   # Unbiased estimator of the mean
malignant_variance = malignant.var(ddof=1)           # Unbiased estimator of the variance

print("Benign Samples (Class = 1):")
print("Estimated Mean:", benign_mean)
```

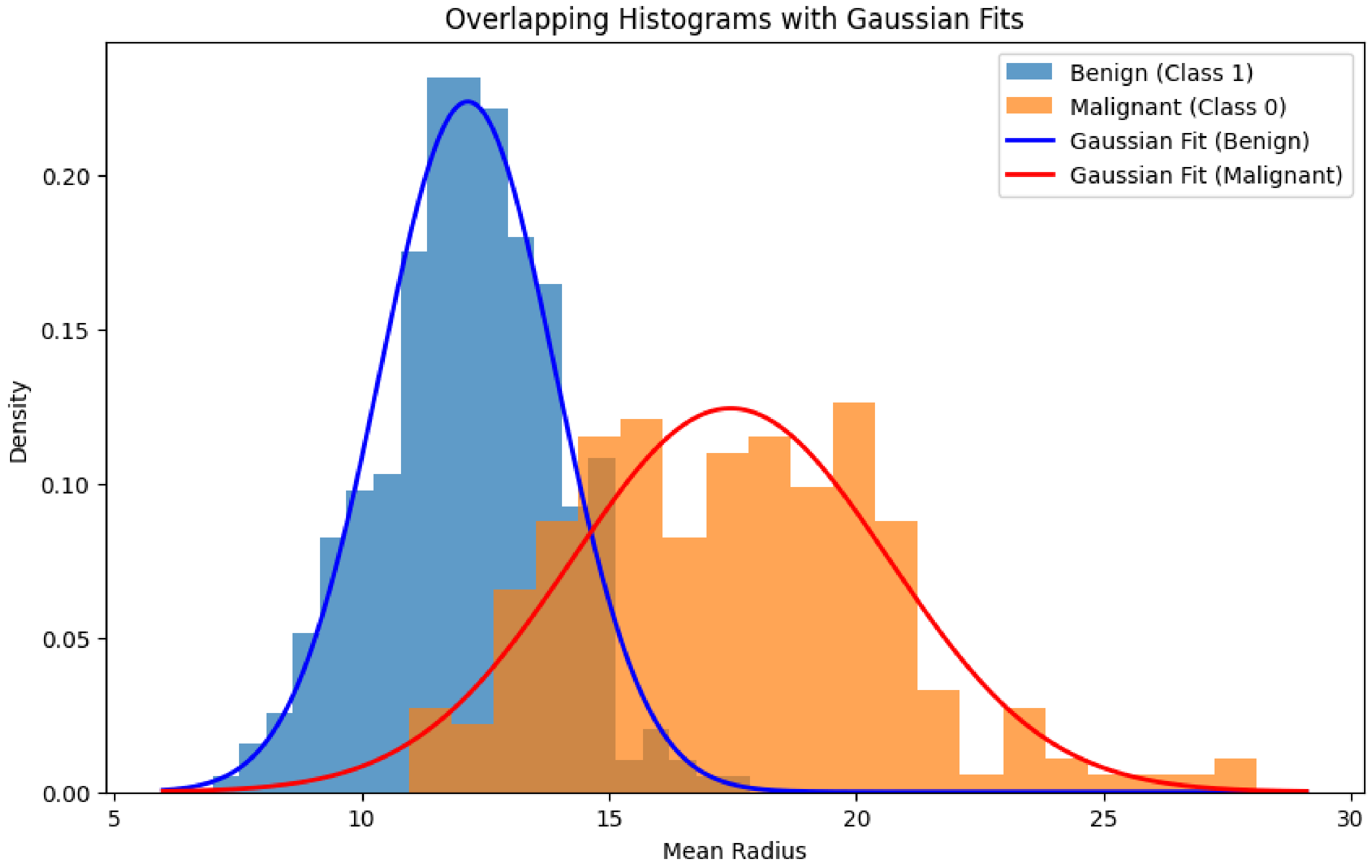
```
print("Estimated Variance:", benign_variance)
print("\nMalignant Samples (Class = 0):")
print("Estimated Mean:", malignant_mean)
print("Estimated Variance:", malignant_variance)
```

```
Benign Samples (Class = 1):
Estimated Mean: 12.146523809523808
Estimated Variance: 3.170221722043872

Malignant Samples (Class = 0):
Estimated Mean: 17.462830188679245
Estimated Variance: 10.265430814629346
```

3.(5pt) **Plot the resulting Gaussian distributions overlapping with the previous histogram plot and comment the results.**

In [14]:

```
benign_std = np.sqrt(benign_variance)
malignant_std = np.sqrt(malignant_variance)

# Create a range of x values covering the data
x_values = np.linspace(min(df['mean radius']) - 1, max(df['mean radius']) + 1, 300)

# Calculate the PDFs for the benign and malignant groups
pdf_benign = stats.norm.pdf(x_values, loc=benign_mean, scale=benign_std)
pdf_malignant = stats.norm.pdf(x_values, loc=malignant_mean, scale=malignant_std)

# Plot overlapping histograms of the two groups
plt.figure(figsize=(10, 6))
plt.hist(benign, bins=20, alpha=0.7, density=True, label='Benign (Class 1)')
plt.hist(malignant, bins=20, alpha=0.7, density=True, label='Malignant (Class 0)')

# Overlay the Gaussian PDFs
plt.plot(x_values, pdf_benign, color='blue', lw=2, label='Gaussian Fit (Benign)')
plt.plot(x_values, pdf_malignant, color='red', lw=2, label='Gaussian Fit (Malignant)')

plt.xlabel('Mean Radius')
plt.ylabel('Density')
plt.title('Overlapping Histograms with Gaussian Fits')
plt.legend()
plt.show()
```


Overlapping Histograms with Gaussian Fits
Benign (Class 1)
Malignant (Class 0)
Gaussian Fit (Benign)
Gaussian Fit (Malignant)
Density
0.00
0.05
0.10
0.15
0.20
5
10
15
20
25
30
Mean Radius