Probability & Statistics Project Report

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Probability & Statistics Project Report

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REPORT SUBMITTED TO THE FACULTY OF COMPUTING, KARACHI INSTITUTE OF ECONOMICS AND TECHNOLOGY, IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE OF BACHELOR OF SCIENCE IN COMPUTER SCIENCE

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➢ Topics

1. Confidence Interval for Population Mean

1.1. Description:

A confidence interval for a population mean is a method that offers a span of values where the actual population mean is probable to be found derived from sample data. It considers the fluctuations inherent, in sampling. Provides an evaluation of the uncertainty surrounding the sample mean. The range is determined by the sample average, the error (which is influenced by the sample size and variability) and a critical value from the z- or t-distribution based on whether the population standard deviation is known. The confidence level, like 95% or 99% reflects our certainty that the interval includes the true population mean. For example, a 95% confidence interval implies that if we repeated the sampling process many times, approximately 95% of the intervals calculated would include the true mean. Thus, confidence intervals provide a useful way to express the reliability of an estimate rather than just giving a single point value.

1.2. Code:

```python
# Confidence Interval for Population Mean
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from scipy.stats import norm, t
from IPython.display import display, Markdown
from google.colab import files
# ------------------ INPUT ------------------
print("Choose input method:")
print("1: Enter data manually")
print("2: Upload Excel file with sample data (single column)")
print(" ")
choice = input("Enter your choice (1 or 2): ")
if choice == "1":
    n = int(input("Enter sample size (n): "))
    sample_mean = float(input("Enter sample mean: "))
    sample_std = float(input("Enter sample standard deviation: "))
    confidence_level = float(input("Enter confidence level (e.g., 0.95):
"))
elif choice == "2":
    uploaded = files.upload()
    file_name = list(uploaded.keys())[0]
    df = pd.read_excel(file_name)
    display(df)
    sample_data = df.iloc[:, 0].dropna().values
    n = len(sample_data)
```

```
    sample_mean = np.mean(sample_data)
    sample_std = np.std(sample_data, ddof=1)
    confidence_level = float(input("Enter confidence level (e.g., 0.95):
"))
else:
    print("Invalid choice")
    exit()
# ------------------ CALCULATIONS ------------------
alpha = 1 - confidence_level
if n < 30:
    critical_value = t.ppf(1 - alpha/2, n-1)
    distribution = "t-distribution"
else:
    critical_value = norm.ppf(1 - alpha/2)
    distribution = "z-distribution"
margin_of_error = critical_value * (sample_std / np.sqrt(n))
lower_bound = sample_mean - margin_of_error
upper_bound = sample_mean + margin_of_error
# ------------------ OUTPUT ------------------
display(Markdown("## Confidence Interval for Population Mean"))
display(Markdown(f"**Sample Size (n): {n}**"))
display(Markdown(f"**Distribution Used: {distribution}**"))
display(Markdown(f"**Sample Mean: {sample_mean:.2f}**"))
display(Markdown(
    f"**{int(confidence_level*100)}% Confidence Interval: "
    f"({lower_bound:.2f}, {upper_bound:.2f})**"
))
# ------------------ GRAPH ------------------
x = np.linspace(sample_mean - 4*sample_std, sample_mean + 4*sample_std,
1000)
if distribution == "t-distribution":
    y = t.pdf(x, df=n-1, loc=sample_mean, scale=sample_std/np.sqrt(n))
else:
    y = norm.pdf(x, loc=sample_mean, scale=sample_std/np.sqrt(n))
plt.figure()
plt.plot(x, y)
# Shade confidence interval
x_fill = np.linspace(lower_bound, upper_bound, 500)
if distribution == "t-distribution":
    y_fill = t.pdf(x_fill, df=n-1, loc=sample_mean,
scale=sample_std/np.sqrt(n))
else:
    y_fill = norm.pdf(x_fill, loc=sample_mean,
scale=sample_std/np.sqrt(n))
plt.fill_between(x_fill, y_fill, alpha=0.4)
# Mean line
plt.axvline(sample_mean, linestyle='--')
plt.title("Confidence Interval for Population Mean Graph")
```

```
plt.xlabel("Value")
plt.ylabel("Probability Density")
plt.show()
```

1.3. Output:

```
Choose input method:
1: Enter data manually
2: Upload Excel file with sample data (single column)

Enter your choice (1 or 2): 1
Enter sample size (n): 25
Enter sample mean: 72
Enter sample standard deviation: 8
Enter confidence level (e.g., 0.95): 0.95
```

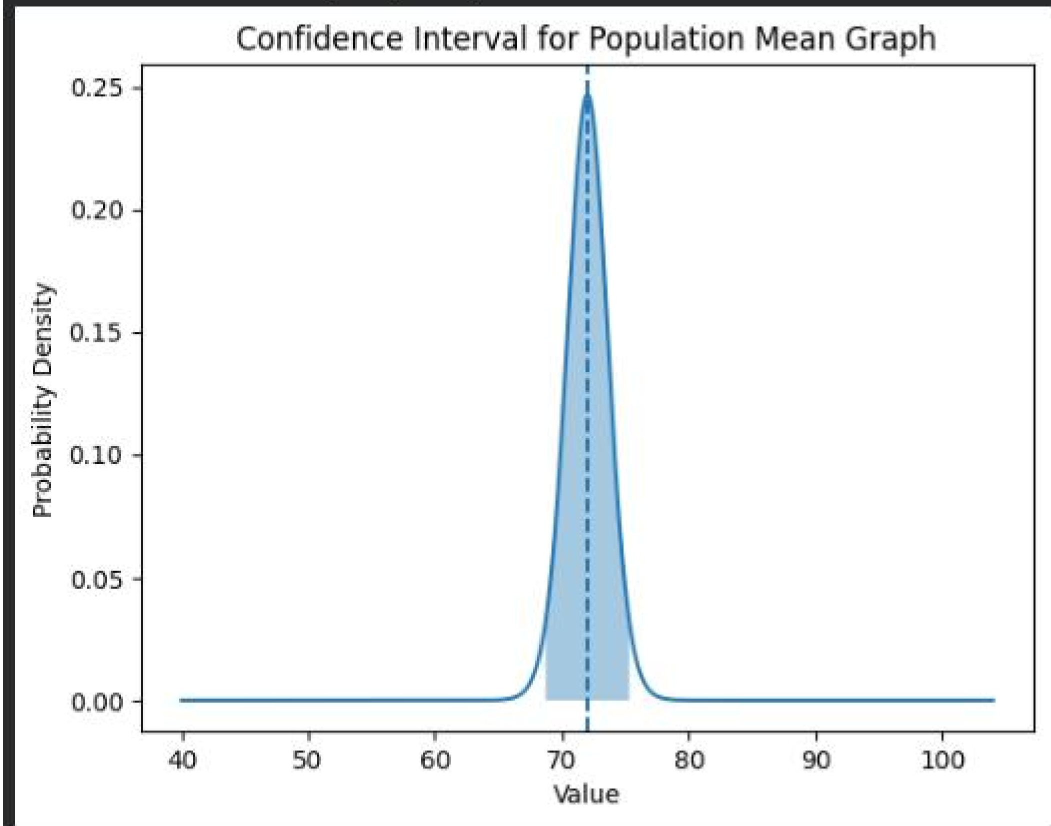
Confidence Interval for Population Mean

Sample Size (n): 25

Distribution Used: t-distribution

Sample Mean: 72.00

95% Confidence Interval: (68.70, 75.30)



2. Confidence Interval for Population Variance

2.1. Description:

A confidence interval for a population variance is a range of values that is likely to contain the true variance (σ2\sigma^2σ2) of a population, based on a sample. It provides a measure of how much the data in the population are spread out and quantifies the uncertainty in estimating the variance from sample data. To calculate it, we use the sample variance and the chi-square (χ2\chi^2χ2) distribution, because the distribution of the sample variance (scaled appropriately) follows a chi-square distribution. The confidence level, such as 95% or 99%, indicates the probability that the interval contains the true population variance. Specifically, a 95% confidence interval means that if we repeatedly took samples and computed the interval each time, about 95% of those intervals would include the actual population variance. This interval is particularly useful in quality control, risk assessment, and any field where understanding variability is important.

2.2. Code:

```
# Confidence Interval for Population Variance
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from scipy.stats import chi2
from IPython.display import display, Markdown
from google.colab import files
# ------------------ INPUT ------------------
print("Choose input method:")
print("1: Enter data manually")
print("2: Upload Excel file with sample data (single column)")
print(" ")
choice = input("Enter choice (1 or 2): ")
if choice == "1":
    n = int(input("Enter sample size (n): "))
    sample_variance = float(input("Enter sample variance (s^2): "))
    confidence_level = float(input("Enter confidence level (e.g., 0.95):
"))
elif choice == "2":
    uploaded = files.upload()
    file_name = list(uploaded.keys())[0]
    df = pd.read_excel(file_name)
    display(df)
    sample_data = df.iloc[:, 0].dropna().values
    n = len(sample_data)
    sample_variance = np.var(sample_data, ddof=1)
    confidence_level = float(input("Enter confidence level (e.g., 0.95):
"))
else:
    print("Invalid choice")
    exit()
# ------------------ CALCULATIONS ------------------
```

```
alpha = 1 - confidence_level
dfree = n - 1
chi2_lower = chi2.ppf(alpha / 2, dfree)
chi2_upper = chi2.ppf(1 - alpha / 2, dfree)
lower_bound = (dfree * sample_variance) / chi2_upper
upper_bound = (dfree * sample_variance) / chi2_lower
# ------------------ OUTPUT ------------------
display(Markdown("## Confidence Interval for Population Variance"))
display(Markdown(f"**Sample Size (n): {n}**"))
display(Markdown(f"**Sample Variance (s²): {sample_variance:.2f}**"))
display(Markdown(
    f"**{int(confidence_level*100)}% Confidence Interval: "
    f"({lower_bound:.2f}, {upper_bound:.2f})**"
))
# ------------------ GRAPH ------------------
x = np.linspace(0, chi2.ppf(0.999, dfree), 1000)
y = chi2.pdf(x, dfree)
plt.figure()
plt.plot(x, y)
# Shade confidence interval region
x_fill = np.linspace(chi2_lower, chi2_upper, 500)
y_fill = chi2.pdf(x_fill, dfree)
plt.fill_between(x_fill, y_fill, alpha=0.4)
# Critical lines
plt.axvline(chi2_lower, linestyle='--')
plt.axvline(chi2_upper, linestyle='--')
plt.title("Confidence Interval for Population Variance Graph")
plt.xlabel("Chi-Square Value")
plt.ylabel("Probability Density")
plt.show()
```

2.3. Output:

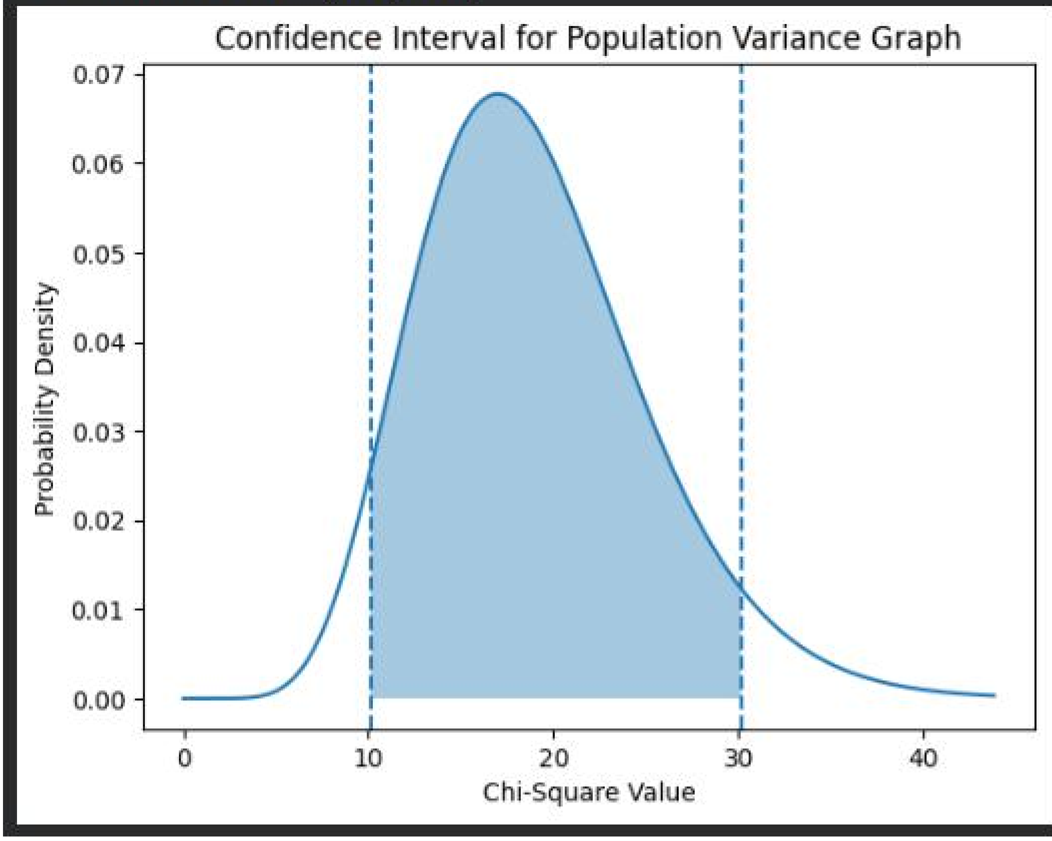
```
Choose input method:
1: Enter data manually
2: Upload Excel file with sample data (single column)

Enter choice (1 or 2): 1
Enter sample size (n): 20
Enter sample variance (s^2): 16
Enter confidence level (e.g., 0.95): 0.90
```

Confidence Interval for Population Variance

Sample Size (n): 20

Sample Variance (s²): 16.00

90% Confidence Interval: (10.09, 30.05)



3. Confidence Interval for Population Standard Deviation

3.1. Description:

A confidence interval for a population standard deviation is a range of values that is likely to contain the true standard deviation (σ\sigmaσ) of a population, based on sample data. Since the standard deviation measures the spread of data around the mean, the interval helps quantify the uncertainty in estimating this spread from a sample. It is calculated using the sample variance and the chi-square (χ2\chi^2χ2) distribution, because the distribution of the sample variance (scaled appropriately) follows a chi-square distribution. The confidence level, such as 95% or 99%, indicates how confident we are that the interval includes the true population standard deviation. For example, a 95% confidence interval means that if we repeatedly took samples and computed intervals, approximately 95% of those intervals would contain the actual population standard deviation. This is useful in fields like quality control, finance, and research, where understanding variability is important.

3.2. Code:

```
# Confidence Interval for Population Standard Deviation
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from scipy.stats import chi2
from IPython.display import display, Markdown
from google.colab import files
# ------------------ INPUT ------------------
print("Choose input method:")
print("1: Enter data manually")
print("2: Upload Excel file with sample data (single column)")
print(" ")
choice = input("Enter choice (1 or 2): ")
if choice == "1":
    n = int(input("Enter sample size (n): "))
    sample_std = float(input("Enter sample standard deviation: "))
    confidence_level = float(input("Enter confidence level (e.g., 0.95): "))
elif choice == "2":
    uploaded = files.upload()
    file_name = list(uploaded.keys())[0]
    df = pd.read_excel(file_name)
    display(df)
    sample_data = df.iloc[:, 0].dropna().values
    n = len(sample_data)
    sample_std = np.std(sample_data, ddof=1)
    confidence_level = float(input("Enter confidence level (e.g., 0.95): "))
else:
    print("Invalid choice")
    exit()
# ------------------ CALCULATIONS ------------------
alpha = 1 - confidence_level
dfree = n - 1
chi2_lower = chi2.ppf(alpha / 2, dfree)
chi2_upper = chi2.ppf(1 - alpha / 2, dfree)
lower_std = np.sqrt((dfree * sample_std**2) / chi2_upper)
```

```
upper_std = np.sqrt((dfree * sample_std**2) / chi2_lower)
# ------------------ OUTPUT ------------------
display(Markdown("## Confidence Interval for Population Standard
Deviation"))
display(Markdown(f"**Sample Size (n): {n}**"))
display(Markdown(f"**Sample Standard Deviation (s):
{sample_std:.2f}**"))
display(Markdown(
    f"**{int(confidence_level*100)}% Confidence Interval: "
    f"({lower_std:.2f}, {upper_std:.2f})**"
))
# ------------------ GRAPH ------------------
x = np.linspace(0, chi2.ppf(0.999, dfree), 1000)
y = chi2.pdf(x, dfree)
plt.figure()
plt.plot(x, y)
# Shade confidence interval region
x_fill = np.linspace(chi2_lower, chi2_upper, 500)
y_fill = chi2.pdf(x_fill, dfree)
plt.fill_between(x_fill, y_fill, alpha=0.4)
# Critical lines
plt.axvline(chi2_lower, linestyle='--', color='red')
plt.axvline(chi2_upper, linestyle='--', color='red')
plt.title("Confidence Interval for Population Standard Deviation Graph")
plt.xlabel("Chi-Square Value")
plt.ylabel("Probability Density")
plt.show()
```

3.3. Output:

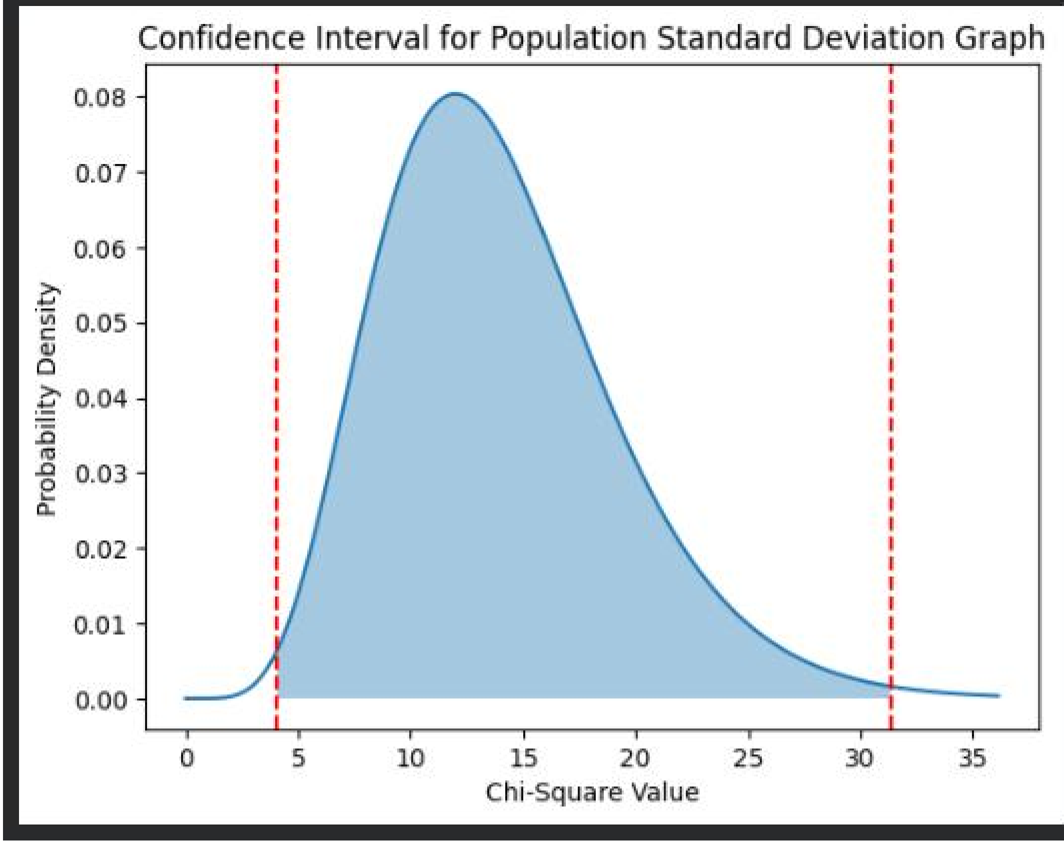
```
Choose input method:
1: Enter data manually
2: Upload Excel file with sample data (single column)

Enter choice (1 or 2): 1
Enter sample size (n): 15
Enter sample standard deviation: 4
Enter confidence level (e.g., 0.95): 0.99
```

Confidence Interval for Population Standard Deviation

Sample Size (n): 15

Sample Standard Deviation (s): 4.00

99% Confidence Interval: (2.67, 7.41)



4. Hypothesis Testing for Population Mean

4.1. Description:

Hypothesis testing for the population mean is used to determine whether sample data provides sufficient evidence to conclude that the population mean (μ\muμ) is equal to, greater than, or less than a specified value. Depending on the situation, a Z-test is used when the population variance is known or the sample size is large, while a T-test is applied when the population variance is unknown and the sample size is small. Tests can be one-tailed, checking a specific direction, or two-tailed, checking for any difference from the hypothesized mean.

4.2. Code:

```
# Hypothesis Testing for Population Mean
import numpy as np
import pandas as pd
from scipy.stats import t
import matplotlib.pyplot as plt
from google.colab import files
from IPython.display import display, Markdown
# Functions
def one_sample_t_test(sample_mean, sample_std, n, pop_mean, tail='two',
direction='>'):
    t_stat = (sample_mean - pop_mean) / (sample_std / np.sqrt(n))
    if tail.lower() == 'two':
        p_value = 2 * (1 - t.cdf(abs(t_stat), df=n-1))
    elif tail.lower() == 'one':
        if direction == '>':
            p_value = 1 - t.cdf(t_stat, df=n-1)
        elif direction == '<':
            p_value = t.cdf(t_stat, df=n-1)
        else:
            raise ValueError("Invalid direction for one-tailed test")
    else:
        raise ValueError("Invalid tail option")
    return t_stat, p_value, n-1
def two_sample_t_test(mean1, std1, n1, mean2, std2, n2, tail='two',
direction='>'):
    se = np.sqrt(std1**2/n1 + std2**2/n2)
    t_stat = (mean1 - mean2) / se
    df = ((std1**2/n1 + std2**2/n2)**2) / (((std1**2/n1)**2)/(n1-1) +
((std2**2/n2)**2)/(n2-1))
    if tail.lower() == 'two':
        p_value = 2 * (1 - t.cdf(abs(t_stat), df=df))
    elif tail.lower() == 'one':
        if direction == '>':
            p_value = 1 - t.cdf(t_stat, df=df)
        elif direction == '<':
            p_value = t.cdf(t_stat, df=df)
        else:
            raise ValueError("Invalid direction for one-tailed test")
    else:
        raise ValueError("Invalid tail option")
    return t_stat, p_value, df
def plot_t_distribution(t_stat, df, tail='two', direction='>',
p_value=None):
    # Dynamic x-range
    x_min = min(-5, t_stat - 3)
```

```
    x_max = max(5, t_stat + 3)
    x = np.linspace(x_min, x_max, 1000)
    y = t.pdf(x, df)
    plt.figure(figsize=(10,5))
    plt.plot(x, y, label=f't-distribution df={df}')
    # Shade p-value area
    if tail.lower() == 'two':
        plt.fill_between(x, 0, y, where=(x <= -abs(t_stat)) | (x >=
abs(t_stat)), color='red', alpha=0.3, label='P-value region')
    elif tail.lower() == 'one':
        if direction == '>':
            plt.fill_between(x, 0, y, where=(x >= t_stat), color='red',
alpha=0.3, label='P-value region')
        else:
            plt.fill_between(x, 0, y, where=(x <= t_stat), color='red',
alpha=0.3, label='P-value region')
    plt.axvline(t_stat, color='blue', linestyle='--', linewidth=2,
label=f'T-statistic = {t_stat:.2f}')
    plt.title("Hypothesis Testing for Population Mean")
    plt.xlabel("t-value")
    plt.ylabel("Density")
    plt.legend()
    plt.show()
# Main Program
choice = input("Input method: 1=Manual, 2=Excel file: ")
if choice == '1':
    test_type = input("One-sample or Two-sample? (1 or 2): ")
    if test_type == '1':
        n = int(input("Sample size (n): "))
        sample_mean = float(input("Sample mean: "))
        sample_std = float(input("Sample std dev: "))
        pop_mean = float(input("Population mean (H0): "))
        tail = input("Tail type (one/two): ").lower()
        direction = '>'
        if tail == 'one':
            direction = input("Direction for one-tailed test ('>' or
'<'): ")
        t_stat, p_value, df = one_sample_t_test(sample_mean, sample_std,
n, pop_mean, tail, direction)
    elif test_type == '2':
        n1 = int(input("Sample 1 size: "))
        mean1 = float(input("Sample 1 mean: "))
        std1 = float(input("Sample 1 std dev: "))
        n2 = int(input("Sample 2 size: "))
        mean2 = float(input("Sample 2 mean: "))
        std2 = float(input("Sample 2 std dev: "))
        tail = input("Tail type (one/two): ").lower()
        direction = '>'
```

```
        if tail == 'one':
            direction = input("Direction for one-tailed test ('>' or
'<'): ")
        t_stat, p_value, df = two_sample_t_test(mean1, std1, n1, mean2,
std2, n2, tail, direction)
elif choice == '2':
    uploaded = files.upload()
    file_name = list(uploaded.keys())[0]
    df_excel = pd.read_excel(file_name)
    display(df_excel)
    if df_excel.shape[1] == 1:
        sample_data = df_excel.iloc[:,0].dropna().values
        n = len(sample_data)
        sample_mean = np.mean(sample_data)
        sample_std = np.std(sample_data, ddof=1)
        pop_mean = float(input("Population mean (H0): "))
        tail = input("Tail type (one/two): ").lower()
        direction = '>'
        if tail == 'one':
            direction = input("Direction for one-tailed test ('>' or
'<'): ")
        t_stat, p_value, df = one_sample_t_test(sample_mean, sample_std,
n, pop_mean, tail, direction)
    elif df_excel.shape[1] == 2:
        sample1 = df_excel.iloc[:,0].dropna().values
        sample2 = df_excel.iloc[:,1].dropna().values
        n1, n2 = len(sample1), len(sample2)
        mean1, mean2 = np.mean(sample1), np.mean(sample2)
        std1, std2 = np.std(sample1, ddof=1), np.std(sample2, ddof=1)
        tail = input("Tail type (one/two): ").lower()
        direction = '>'
        if tail == 'one':
            direction = input("Direction for one-tailed test ('>' or
'<'): ")
        t_stat, p_value, df = two_sample_t_test(mean1, std1, n1, mean2,
std2, n2, tail, direction)
    else:
        print("Excel must have 1 or 2 columns")
        exit()
else:
    print("Invalid choice")
    exit()
# Display Results
display(Markdown("## Hypothesis Testing for Population Mean"))
display(Markdown(f"**T-statistic:** {t_stat:.4f}"))
display(Markdown(f"**P-value:** {p_value:.4f}"))
alpha = 0.05
if p_value < alpha:
```

```
    display(Markdown(f"**Result: Reject H0 at α={alpha}**"))
else:
    display(Markdown(f"**Result: Fail to Reject H0 at α={alpha}**"))
# Plot t-distribution with shaded p-value region
plot_t_distribution(t_stat, df, tail, direction, p_value)
```

4.3. Output:

```
Input method: 1=Manual, 2=Excel file: 2
Choose Files one_sample.xlsx
one_sample.xlsx(application/vnd.openxmlformats-officedocument.spreadsheetml.sheet) - 8971 bytes, last modified: 12/17/2025 - 100% done
Saving one_sample.xlsx to one_sample (1).xlsx
```

	SampleData
0	72
1	75
2	70
3	68
4	74
5	73
6	69
7	71
8	70
9	72

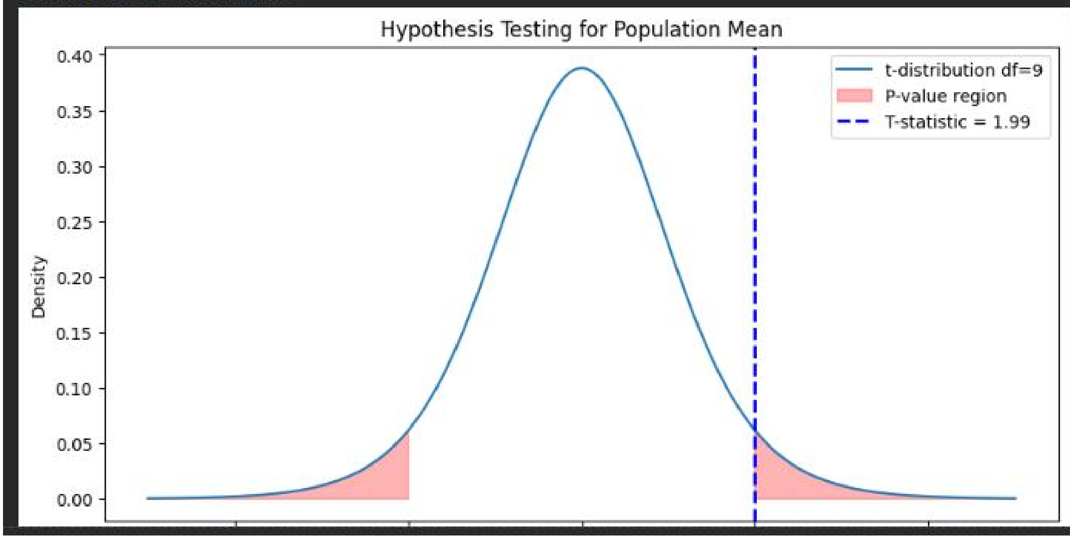
```
Population mean (H0): 70
Tail type (one/two): two
```

Hypothesis Testing for Population Mean

T-statistic: 1.9932

P-value: 0.0774

Result: Fail to Reject H0 at α=0.05



5. Hypothesis Testing for Population Variance

5.1. Description:

Hypothesis testing for the population variance evaluates whether the variability in the population matches a hypothesized variance (σ2\sigma^2σ2). The chi-square (χ2\chi^2χ2) test is commonly used for this purpose. This test is particularly important in fields like quality control and reliability studies, where maintaining consistent variability is critical.

5.2. Code:

```
# Hypothesis Testing for Population Variance
import numpy as np
import pandas as pd
from scipy.stats import chi2
import matplotlib.pyplot as plt
from google.colab import files
from IPython.display import display, Markdown
# Functions
def one_sample_variance_test(sample_var, n, pop_var, tail='two',
direction='>'):
    chi_stat = (n - 1) * sample_var / pop_var
    df = n - 1
    if tail.lower() == 'two':
        p_value = 2 * min(chi2.cdf(chi_stat, df), 1 - chi2.cdf(chi_stat,
df))
    elif tail.lower() == 'one':
        if direction == '>':
            p_value = 1 - chi2.cdf(chi_stat, df)
        elif direction == '<':
            p_value = chi2.cdf(chi_stat, df)
        else:
            raise ValueError("Invalid direction for one-tailed test")
    else:
        raise ValueError("Invalid tail option")
    return chi_stat, p_value, df
def plot_chi2_distribution(chi_stat, df, tail='two', direction='>'):
    x_min = 0
    x_max = max(chi_stat + df, df * 3)
    x = np.linspace(x_min, x_max, 1000)
    y = chi2.pdf(x, df)
    plt.figure(figsize=(10,5))
    plt.plot(x, y, label=f'Chi-square distribution df={df}')
    # Shade p-value area
    if tail.lower() == 'two':
        plt.fill_between(x, 0, y, where=(x <= chi_stat) | (x >=
chi2.ppf(1 - chi2.cdf(chi_stat, df), df)),
                         color='red', alpha=0.3, label='P-value region')
    elif tail.lower() == 'one':
        if direction == '>':
            plt.fill_between(x, 0, y, where=(x >= chi_stat),
color='red', alpha=0.3, label='P-value region')
        else:
```

```
            plt.fill_between(x, 0, y, where=(x <= chi_stat),
color='red', alpha=0.3, label='P-value region')
    plt.axvline(chi_stat, color='blue', linestyle='--', linewidth=2,
label=f'Chi-statistic = {chi_stat:.2f}')
    plt.title("Hypothesis Testing for Population Variance")
    plt.xlabel("Chi-square value")
    plt.ylabel("Density")
    plt.legend()
    plt.show()
# Main Program
choice = input("Input method: 1=Manual, 2=Excel file: ")
if choice == '1':
    n = int(input("Sample size (n): "))
    sample_var = float(input("Sample variance: "))
    pop_var = float(input("Population variance (H0): "))
    tail = input("Tail type (one/two): ").lower()
    direction = '>'
    if tail == 'one':
        direction = input("Direction for one-tailed test ('>' or '<'):
")
    chi_stat, p_value, df = one_sample_variance_test(sample_var, n,
pop_var, tail, direction)
elif choice == '2':
    uploaded = files.upload()
    file_name = list(uploaded.keys())[0]
    df_excel = pd.read_excel(file_name)
    display(df_excel)
    sample_data = df_excel.iloc[:,0].dropna().values
    n = len(sample_data)
    sample_var = np.var(sample_data, ddof=1)
    pop_var = float(input("Population variance (H0): "))
    tail = input("Tail type (one/two): ").lower()
    direction = '>'
    if tail == 'one':
        direction = input("Direction for one-tailed test ('>' or '<'):
")
    chi_stat, p_value, df = one_sample_variance_test(sample_var, n,
pop_var, tail, direction)
else:
    print("Invalid choice")
    exit()
# Display Results
display(Markdown("## Hypothesis Testing for Population Variance"))
display(Markdown(f"**Chi-square statistic:** {chi_stat:.4f}"))
display(Markdown(f"**P-value:** {p_value:.4f}"))
alpha = 0.05
if p_value < alpha:
    display(Markdown(f"**Result: Reject H0 at α={alpha}**"))
```

```
else:
    display(Markdown(f"**Result: Fail to Reject H0 at α={alpha}**"))
# Plot chi-square distribution with shaded p-value
plot_chi2_distribution(chi_stat, df, tail, direction)
```

5.3. Output:

```
Input method: 1=Manual, 2=Excel file: 2
Choose Files one_sample.xlsx
one_sample.xlsx(application/vnd.openxmlformats-officedocument.spreadsheetml.sheet) - 8971 bytes, last modified: 12/17/2025 - 100% done
Saving one_sample.xlsx to one_sample (2).xlsx
```

1 to 10 of 10 entries Filter

index	SampleData
0	72
1	75
2	70
3	68
4	74
5	73
6	69
7	71
8	70
9	72

Show 25 per page

Like what you see? Visit the data table notebook to learn more about interactive tables.

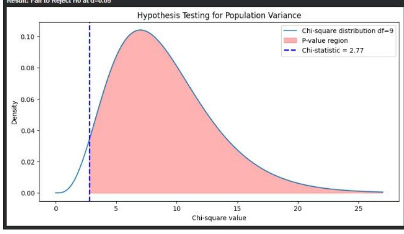
```
Population variance (H0): 16
Tail type (one/two): one
Direction for one-tailed test ('>' or '<'): >
```

Hypothesis Testing for Population Variance

Chi-square statistic: 2.7750

P-value: 0.9726

Result: Fail to Reject H0 at α=0.05



6. Hypothesis Testing for Population Standard Deviation

6.1. Description:

Testing for the population standard deviation is similar to testing for variance, as the standard deviation is the square root of variance. The chi-square statistic is used to determine whether the population's spread or dispersion differs from a specified value. This test helps in assessing the consistency and reliability of measurements in a population.

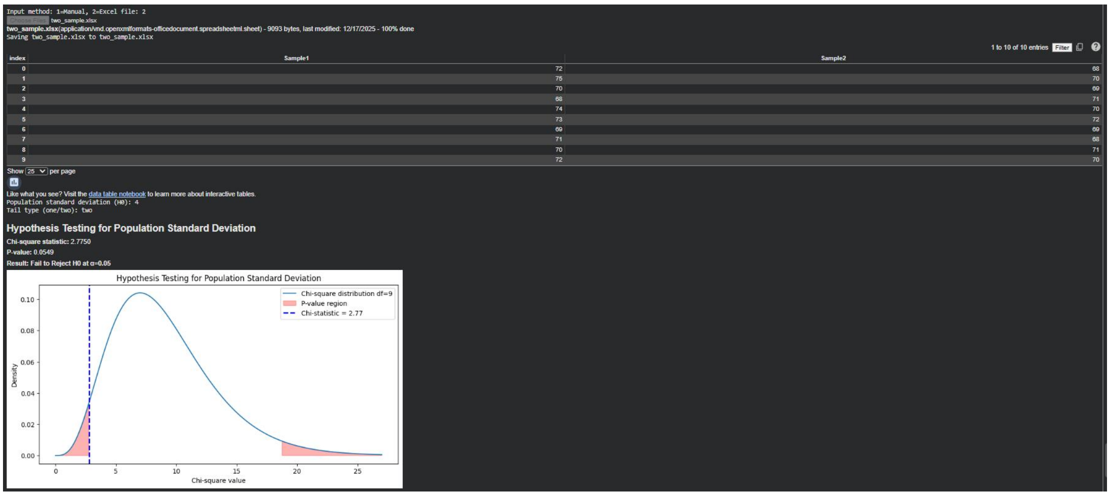
6.2. Code:

```
# Hypothesis Testing for Population Standard Deviation
import numpy as np
import pandas as pd
from scipy.stats import chi2
import matplotlib.pyplot as plt
from google.colab import files
from IPython.display import display, Markdown
# Functions
def one_sample_std_test(sample_std, n, pop_std, tail='two', 
direction='>'):
    # Convert standard deviations to variances
    sample_var = sample_std ** 2
    pop_var = pop_std ** 2
    chi_stat = (n - 1) * sample_var / pop_var
```

```
    df = n - 1
    if tail.lower() == 'two':
        p_value = 2 * min(chi2.cdf(chi_stat, df), 1 - chi2.cdf(chi_stat,
df))
    elif tail.lower() == 'one':
        if direction == '>':
            p_value = 1 - chi2.cdf(chi_stat, df)
        elif direction == '<':
            p_value = chi2.cdf(chi_stat, df)
        else:
            raise ValueError("Invalid direction for one-tailed test")
    else:
        raise ValueError("Invalid tail option")
    return chi_stat, p_value, df
def plot_chi2_distribution_std(chi_stat, df, tail='two', direction='>'):
    x_min = 0
    x_max = max(chi_stat + df, df * 3)
    x = np.linspace(x_min, x_max, 1000)
    y = chi2.pdf(x, df)
    plt.figure(figsize=(10,5))
    plt.plot(x, y, label=f'Chi-square distribution df={df}')
    # Shade p-value area
    if tail.lower() == 'two':
        plt.fill_between(x, 0, y, where=(x <= chi_stat) | (x >=
chi2.ppf(1 - chi2.cdf(chi_stat, df), df)),
                         color='red', alpha=0.3, label='P-value region')
    elif tail.lower() == 'one':
        if direction == '>':
            plt.fill_between(x, 0, y, where=(x >= chi_stat),
color='red', alpha=0.3, label='P-value region')
        else:
            plt.fill_between(x, 0, y, where=(x <= chi_stat),
color='red', alpha=0.3, label='P-value region')
    plt.axvline(chi_stat, color='blue', linestyle='--', linewidth=2,
label=f'Chi-statistic = {chi_stat:.2f}')
    plt.title("Hypothesis Testing for Population Standard Deviation")
    plt.xlabel("Chi-square value")
    plt.ylabel("Density")
    plt.legend()
    plt.show()
# Main Program
choice = input("Input method: 1=Manual, 2=Excel file: ")
if choice == '1':
    n = int(input("Sample size (n): "))
    sample_std = float(input("Sample standard deviation: "))
    pop_std = float(input("Population standard deviation (H0): "))
    tail = input("Tail type (one/two): ").lower()
    direction = '>'
```

```
    if tail == 'one':
        direction = input("Direction for one-tailed test ('>' or '<'): ")
    chi_stat, p_value, df = one_sample_std_test(sample_std, n, pop_std, tail, direction)
elif choice == '2':
    uploaded = files.upload()
    file_name = list(uploaded.keys())[0]
    df_excel = pd.read_excel(file_name)
    display(df_excel)
    sample_data = df_excel.iloc[:,0].dropna().values
    n = len(sample_data)
    sample_std = np.std(sample_data, ddof=1)
    pop_std = float(input("Population standard deviation (H0): "))
    tail = input("Tail type (one/two): ").lower()
    direction = '>'
    if tail == 'one':
        direction = input("Direction for one-tailed test ('>' or '<'): ")
    chi_stat, p_value, df = one_sample_std_test(sample_std, n, pop_std, tail, direction)
else:
    print("Invalid choice")
    exit()
# Display Results
display(Markdown("## Hypothesis Testing for Population Standard Deviation"))
display(Markdown(f"**Chi-square statistic:** {chi_stat:.4f}"))
display(Markdown(f"**P-value:** {p_value:.4f}"))
alpha = 0.05
if p_value < alpha:
    display(Markdown(f"**Result: Reject H0 at α={alpha}**"))
else:
    display(Markdown(f"**Result: Fail to Reject H0 at α={alpha}**"))
# Plot chi-square distribution with shaded p-value
plot_chi2_distribution_std(chi_stat, df, tail, direction)
```

6.3. Output:



➢ Inputs Method

All the codes accept data either through manual user input or by uploading an Excel file; in the examples above, both methods were used to demonstrate their functionality.