In [1]:

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

In [2]:

```
iris_df = sns.load_dataset('iris')
```

In [3]:

```
population = iris_df['sepal_width']
population
```

Out[3]:

```
0      3.5
1      3.0
2      3.2
3      3.1
4      3.6
      ...
145    3.0
146    2.5
147    3.0
148    3.4
149    3.0
Name: sepal_width, Length: 150, dtype: float64
```

In [4]:

```
sample = population.sample(n=30)
```

In [5]:

```
sample.count()
```

Out[5]:

```
30
```

In [6]:

```
# the measure which describes sample data called statistic
# the measure which describes population data called parameter
```

In [7]:

```
sample.mean()# statistic
```

Out[7]:

```
3.0999999999999996
```

In [8]:

```
population.mean() #called parameter
```

Out[8]:

```
3.0573333333333337
```

In [9]:

```
# our sample size is small and not contains all information about population so this leads to standard error
```

In [10]:

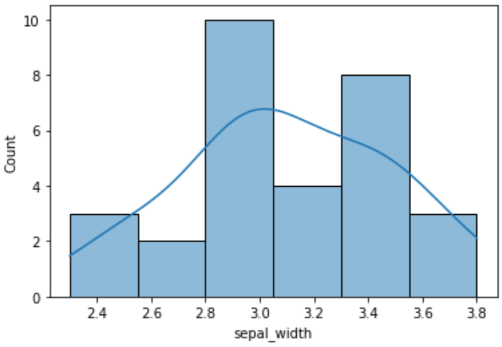
```
# Point estimation - The value of statistics which estimate the value of parameter
# our sample mean can estimate population mean
```

In [11]:

```
sns.histplot(sample,kde=True)
```

Out[11]:

```
<AxesSubplot: xlabel='sepal_width', ylabel='Count'>
```

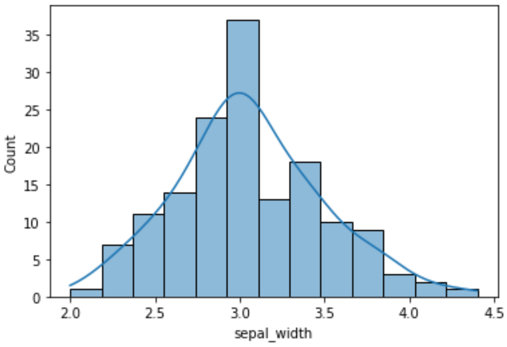


In [12]:

```
sns.histplot(population,kde=True)
```

Out[12]:

```
<AxesSubplot: xlabel='sepal_width', ylabel='Count'>
```



In [13]:

```
# Confidence interval = (point estimate) + or - (margin error)
# lower bound  =(point estimate) - (margin error)
# upper bound  =(point estimate) + (margin error)
```

In [14]:

```
# assuming
alpha = 0.05
alpha_by_2 = 0.025 # always rembember we need to check z table for 1-0.025 (for ztest)
# we check z value for 0.975
z_value = 1.906
standard_error = population.std()/np.sqrt(sample.count())
lower_bound = sample.mean()-z_value*standard_error
upper_bound = sample.mean()+z_value*standard_error
```

In [15]:

```
lower_bound
```

Out[15]:

```
2.948324461407359
```

In [16]:

```
upper_bound
```

Out[16]:

```
3.2516755385926404
```

In [17]:

```
# Z-TEST
# we are supposing that we have population std and also we have n>=30
```

In [18]:

```
from statsmodels.stats.weightstats import ztest as ztest
```

In [19]:

```
ztest(sample,value=population.mean()) # returned first value is ztest value and second value is p value
```

Out[19]:

```
(0.604092545376455, 0.545782115437665)
```

In [20]:

```
if alpha>0.037396284157051:
    print("Reject the null hypothesis")
else:
    print('Failed to reject null hypothesis')
```

```
Reject the null hypothesis
```

In [21]:

```
# Another way as per theory
# our alpha value is 0.05
# z table value for 1-0.05 is 1.6
if np.abs(-2.0814112026040994)>np.abs(1.6):
    print("Reject the null hypothesis")
else:
    print('Failed to reject null hypothesis')
```

```
Reject the null hypothesis
```

In [22]:

```
# Now if we do not have standard deviation of population data then we have perform t-test
sample1 = sample
sample2 = population.sample(30)
```

In [23]:

```
# T-TEST
from scipy import stats
# two sample t test
t_value,p_value = stats.ttest_ind(sample1,sample2)
```

In [24]:

```
t_value
```

Out[24]:

```
-1.1405158984122017
```

In [25]:

```
p_value
```

Out[25]:

```
0.2587591390429018
```

In [26]:

```
# 1.
if alpha>p_value:
    print("Reject the null hypothesis")
else:
    print('Failed to reject null hypothesis')
```

```
Failed to reject null hypothesis
```

In [27]:

```
# 2.
# alpha = 0.05,degree of freedom = n-1 = 29
# from t table ,tscore = 0.683
tscore = 0.683 # this is decision rule boundation
if t_value<-0.683 or t_value>0.683:
    print("Reject the null hypothesis")
else:
    print('Failed to reject null hypothesis')
```

```
Reject the null hypothesis
```

In [ ]:

```

```

CHI SQUARE TEST

In [28]:

```
# Chi square test
# non parametric,perform on categorical data
```

In [29]:

```
chi_population = iris_df['species']
```

In [30]:

```
chi_sample = chi_population.sample(30)
chi_sample
```

Out[30]:

```
66     versicolor
56     versicolor
114     virginica
132     virginica
146     virginica
147     virginica
134     virginica
73     versicolor
105     virginica
62     versicolor
75     versicolor
148     virginica
69     versicolor
113     virginica
55     versicolor
144     virginica
149     virginica
14         setosa
93     versicolor
76     versicolor
123     virginica
48         setosa
84     versicolor
8          setosa
57     versicolor
67     versicolor
29         setosa
63     versicolor
53     versicolor
109     virginica
Name: species, dtype: object
```

In [31]:

```
chi_population.value_counts()
```

Out[31]:

```
setosa        50
versicolor    50
virginica     50
Name: species, dtype: int64
```

In [32]:

```
chi_sample.value_counts()
```

Out[32]:

```
versicolor    14
virginica     12
setosa         4
Name: species, dtype: int64
```

In [33]:

```
# VERY VERY IMPORTANT CODE !!!!!!!!

chi_data = pd.concat((chi_population.value_counts(),chi_population.value_counts()/chi_population.count(),chi_sample.value_counts(),chi_sam
```

In [34]:

```
chi_data.columns = ['population','population_relative','sample','sample_relative']
chi_data
```

Out[34]:

	population	population_relative	sample	sample_relative
setosa	50	0.333333	4	0.133333
versicolor	50	0.333333	14	0.466667
virginica	50	0.333333	12	0.400000

In [35]:

```
chi_data['sample_expected'] = chi_data['population_relative']*chi_data['sample'].sum()
chi_data
```

Out[35]:

	population	population_relative	sample	sample_relative	sample_expected
setosa	50	0.333333	4	0.133333	10.0
versicolor	50	0.333333	14	0.466667	10.0
virginica	50	0.333333	12	0.400000	10.0

In [36]:

```
# Now we have our sample values and expected sample values
```

In [37]:

```
chi_data['test'] = (chi_data['sample']-chi_data['sample_expected'])**2/chi_data['sample']
chi_data
```

Out[37]:

	population	population_relative	sample	sample_relative	sample_expected	test
setosa	50	0.333333	4	0.133333	10.0	9.000000
versicolor	50	0.333333	14	0.466667	10.0	1.142857
virginica	50	0.333333	12	0.400000	10.0	0.333333

In [38]:

```
chi_value = chi_data['test'].sum()
chi_value
```

Out[38]:

```
10.476190476190476
```

In [39]:

```
# alpha = 0.05,n = 3-1=2(degree of freedom)
# so from chi squre table
chi_decision_value = 5.991
if chi_decision_value < -5.991 or chi_value>5.991:
    print('Reject the null hypothesis')
else:
    print('Fail to reject null hypothesis')
```

```
Reject the null hypothesis
```

In [ ]:

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In [ ]: