

# Understanding the Hypothesis Testing using t value method

**Wait!** You might be wondering what is hypothesis testing in the first place?

No worries, I will walk you through the formal definition and then emphasise some examples to make the concept clear.

## What does hypothesis mean?

When we perform an analysis on a sample from a population let the analysis could be descriptive, inferential, or exploratory in nature. We get certain information from which we can make claims about the entire population. This basically known as making an inference on the population by observing the characteristics of a sample. But, these are just the claims; we can't be sure if they're actually true. This kind of claim or assumption is called a **hypothesis**.

**Example 1:** *The average zomato rating of chicken biriyani from pista house restaurant is 4.8*

Well that might still be ambiguous to some of you,

**Example 2** *let us suppose that you wanted to know the average time it takes for each day scholar in your college to reach the campus from home*

Assume that you just have 20 minutes to come up with the report, in these scenarios we would not attempt to find the average commute time of the complete population which is both time and resource consuming. Rather we use samples to collect the average. i.e.,

1. you ask say 5 students
2. collect 10 such sample
3. calculate the mean commute time of the sample
4. Approximate sample's mean to the total population's average commute time.

This is called making an inference on the population. But we are not sure upto what extent we can trust this claim or whether it is true for all the cases or not, So these kind of claims or assumptions made is called hypothesis.

Before diving deep into the hypothesis testing, let us understand the differences between inferential statistics and hypothesis testing.

**Inferential statistics** is used to find the mean of a population parameter when you have no initial number to start with. So, you start with the sampling activity and find out the sample mean. Then, you estimate the population mean from the sample mean using the confidence interval.

**Hypothesis testing** on the other hand is used to confirm your conclusion (or hypothesis) about the population mean (which you know from EDA or your intuition). Through hypothesis testing, you can determine whether there is enough evidence to conclude if the hypothesis about a population parameter is true or not.

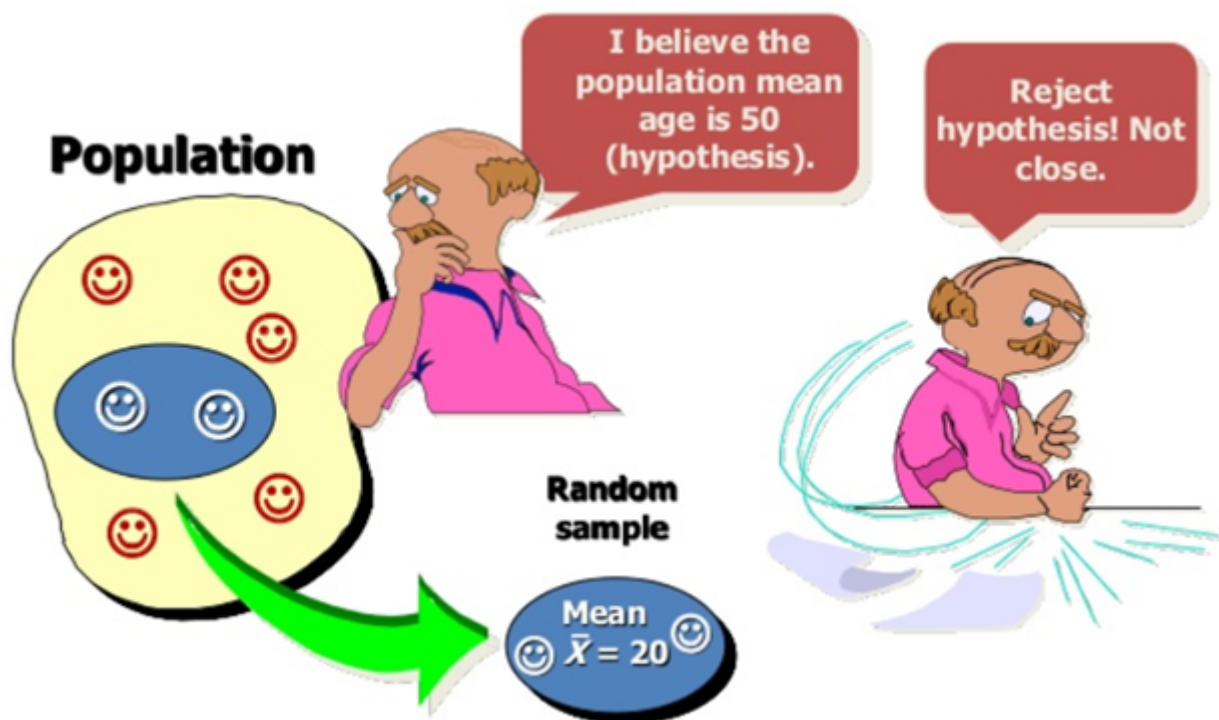
## What is Hypothesis testing?

So far, we have learnt about what is hypothesis and we realised that there is a need for validating our hypothesis or claims. The this process of validating our claims is called hypothesis testing.

The goal is to determine whether there is enough evidence to infer that the hypothesis about the population parameter is true. In hypothesis testing, we confirm our assumptions about the population based on sample data. There are ways to check if your hypothesis has any truth to it, and if the hypothesis is true then apply it to the population parameters. This is called hypothesis testing.

Hypothesis Testing starts with the formulation of these two hypotheses:

- **Null hypothesis ( $H_0$ ):** The status quo
- **Alternate hypothesis ( $H_1$ ):** The challenge to the status quo (**The BOLD claim**)



**Example:** \_Suppose that there are two friends who are looking at a group of people in the park, one of the friends said that the average age of this population is 50 years. Where as the second friend did not agreed with this hypothesis and said that the mean age of this population of this population is not 50.

- **The null hypothesis** is the prevailing belief about a population; it states that there is no change or no difference in the situation. In our example, the mean age of the population was considered 50. So, the null hypothesis claims that it is equal to 50, it is denoted by  **$H_0$**

• **The alternate hypothesis** or research hypothesis as it is also called, is the Bold claim that opposes the null hypothesis. In our example the second friend did not agree it to be 50, his claim would be that the age is not 50, and you would try to prove this. So, the alternate hypothesis is an assumption that competes with the null hypothesis. Alternate Hypothesis is denoted by **H1**.

## Outcome of the hypothesis testing:

In our example, we can see that friend 1 collected a sample of 2 people and calculated their mean age which found to be 20!!.

**In this case, What would be the outcome in terms of hypothesis testing?**

- If the calculated sample mean is not equal to the assumption made, it means that the test rejects the null hypothesis in favour of the alternate hypothesis. So, we can decide that there is enough evidence to support the alternate hypothesis, and to conclude that the population mean age is not 50.

- On the other hand, if suppose the mean of the sample turns out to be 50, it means that there is not enough evidence to support the alternate hypothesis. Note that this does not mean that the population mean age is 50, it just means that there is not enough evidence to conclude that it is not 50. In other words, we cannot accept the null hypothesis; we can only fail to reject it.

Therefore, in hypothesis testing, if there is sufficient evidence to support the alternate hypothesis, you **reject the null hypothesis**;  
if there is not sufficient evidence to support the alternate hypothesis, you **fail to reject the null hypothesis**.

So, you should never say that you “accept” the null hypothesis

So far, we have understood about what is hypothesis testing, null and alternate hypothesis.

It is now important to understand how we are going to formulate null hypothesis and alternate hypothesis from the given scenario.

## Formulating Null and Alternate hypothesis

If your claim statement has words like “*at least*”, “*at most*”, “*less than*”, or “*greater than*”, you cannot formulate the null hypothesis just from the claim statement (because it’s not necessary that the claim is always about the status quo).

You can use the following rule to formulate the null and alternate hypotheses:

- The null hypothesis **H0** always has the following signs: **= OR  $\leq$  OR  $\geq$**
- The alternate hypothesis **H1** always has the following signs:  **$\neq$  OR  $>$  OR  $<$**

Finally, let us see two scenarios to understand how to formulate null and alternate hypothesis from the claim.

**Scenario 1** : Amazon claimed that its total valuation in December 2020 was atleast \$14 billion. Here, the claim contains  $\geq$  sign (i.e. the at least sign), so the **null hypothesis is the original claim**.

The hypothesis in this case can be calculated as,



**Scenario 2** : Amazon claimed that its total valuation in December 2020 was greater than \$14 billion. Here, the claim contains  $>$  sign (i.e. greater than sign),

So the **null hypothesis is the complement of the original claim**

The hypothesis in this case can be calculated as,



Well.. That is a lot of information, to make sure that the understanding of the hypothesis testing is made right, we will solve few examples.

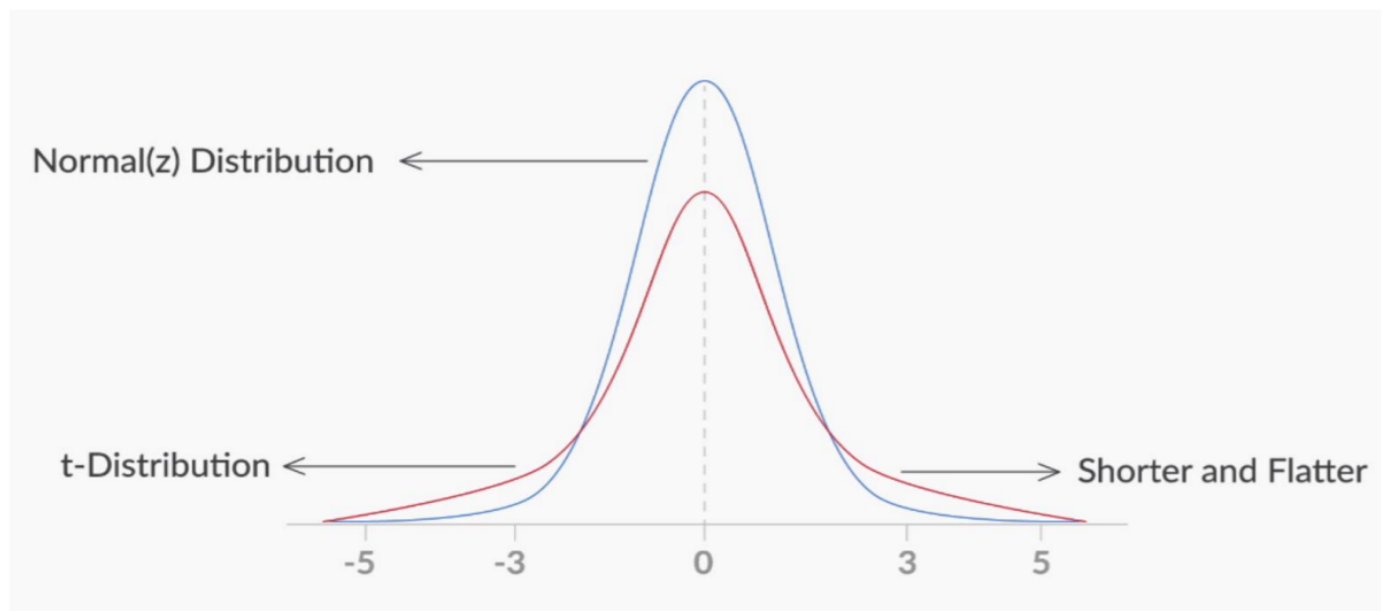
There are many methods to validate the hypothesis. Namely,

- Z test
- p value test
- t test
- chi square testing etc .., Z test usually used when the sample size is larger and the population's parameter like standard deviation is known.

Many a times in the industry, it is not possible to know the standard deviation of the population in advance, So, we come up with widely used method which is **T-distribution**.

**T-distribution (or Student T distribution)**: It is similar to the normal distribution in many cases. For example, it is symmetrical about its central tendency. However, it is usually shorter than the normal distribution and has a flatter tail, which would eventually mean that it has a larger standard deviation.

The following graph shows t-distribution vs normal distribution



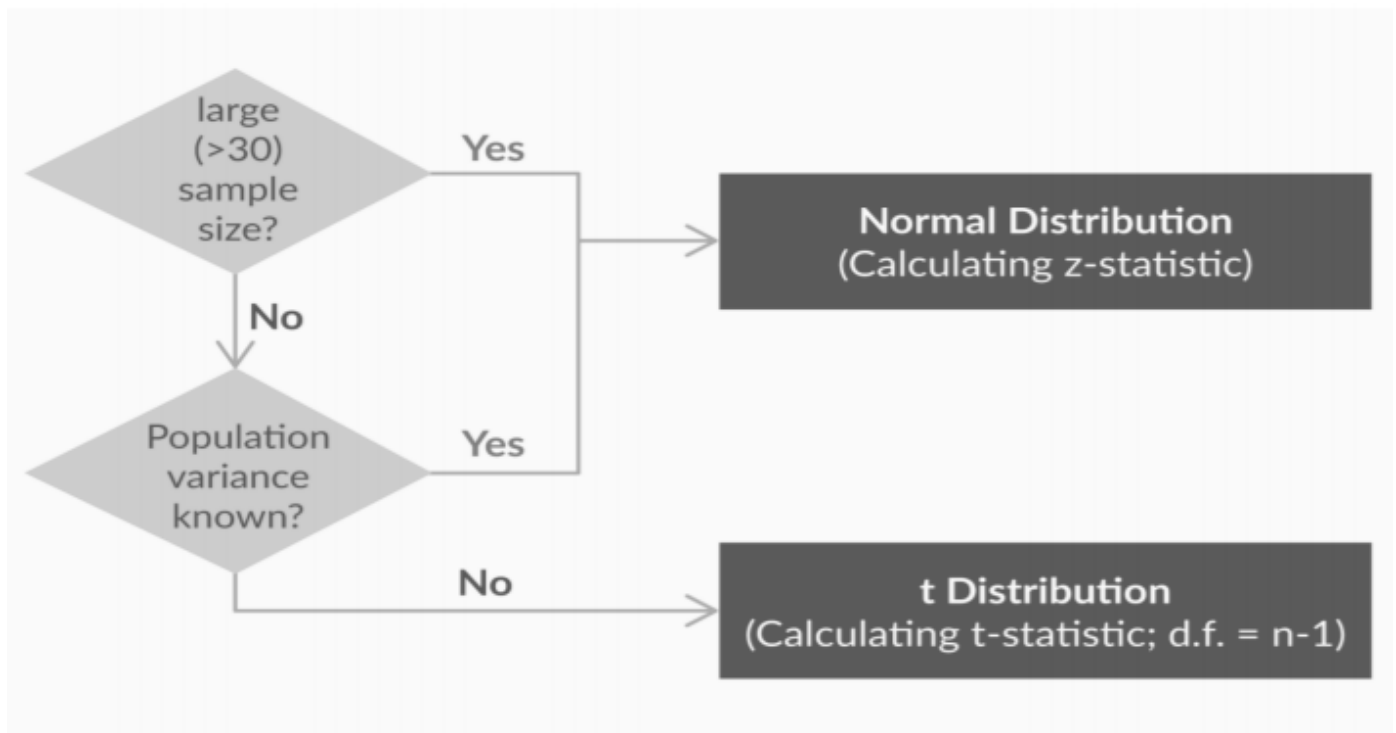
### T-Distribution characteristics:

- At a sample size beyond 30, the t-distribution becomes approximately equal to the normal distribution.
- Each t-distribution is distinguished by its degrees of freedom, which are related to the sample size of the data set.
- If your sample size is  $n$ , the degrees of freedom for the corresponding t-distribution is  $n - 1$ . (For example, if your sample size is 10, you use a t-distribution with  $10 - 1$  or 9 degrees of freedom, denoted  $t_9$ .)
- Smaller sample sizes have flatter t-distributions than larger sample sizes.
- The larger the sample size becomes, the larger will be the degree of freedom, So more the t-distribution looks like a standard normal distribution or the Z-distribution.

### When to use a T-distribution?

The most important use of the t-distribution is that you can approximate the value of the **standard deviation of the population ( $\sigma$ )** from the **sample standard deviation ( $s$ )**. However, as the sample size increases more than 30, the t-value tends to be equal to the z-value.

The following flowchart summarises the decision making process.



Now that we have covered a lot of theoretical concepts understanding the hypothesis testing process and the reasons to choose t-value method, we shall emphasize more on reinforcing the understanding by solving few case studies.

## Case 1:

*Pista House selling Hyderabad Chicken Dum biryani claims that each parcel packet has 500 grams of biryani (also mentioned on the label of packet). You are sceptic of their claims and believe that on average each packet does not contain 500 grams of biryani. How do you prove your claim?*

**Solution:** Let us follow a step by step approach to solve these type of problems.

**Step 1:** Understanding the scenario and plot the Null hypothesis and Alternate hypothesis. For our case 1,

Null Hypothesis  $H_0$  (Status Quo) is that the weight of the biriyani packet is 500 gms.

$$H_0 : \bar{X} = 500$$

Alternate Hypothesis  $H_1$  (Bold Claim) is that the average weight of biriyani packet is not 500 gms.

$$H_1 : \bar{X} \neq 500$$

**Step 2:** Collecting a sample of size N and computing its mean.

In our example, let us collect 10 biriyani packets to form a sample.

Sample size  $N = 10$

Let the sample be,

[490, 420, 470, 500, 495, 496, 496, 498, 508, 480]

Now, in order to compute the mean of this sample  $\bar{X}$  we shall dive into programming.

In [75]:

```
# Let us import some useful modules into the environment.
import matplotlib.pyplot as plt
import numpy as np
import math
from scipy.stats import t
```

In [76]:

```
pop_mean = 500 #Given
sample = [490,420,470,500,495,496,496,498,508,480]
N = len(sample)
sample_mean = sum(sample)/N
print("The mean of the sample is {}".format(sample_mean))
```

The mean of the sample is 485.3

**Step 3:** Calculate the test statistic value t.

The formula for calculating t is given as,

$$t = \frac{\bar{X} - \mu}{\frac{s}{\sqrt{N}}}$$

Where,

- t = Test value
- $\bar{X}$  = Mean of the sample
- $\mu$  = Mean of the population
- s = standard deviation of the sample
- N = Sample size

In [77]:

```
# Let us define a function for calculating t value
def t_value(sample_size, sample_mean, pop_mean, sample_std):
    numerator = sample_mean - pop_mean
    denominator = sample_std / sample_size**0.5
    return numerator / denominator
```

In [78]:

```
# Let us find the standard deviation of the sample s.
sample_std = np.std(sample)
print("The standard deviation s of the sample of size N is {}".format(sample_std))
```

The standard deviation s of the sample of size N is 24.008540147205952

In [79]:

```
t_val = t_value(N,sample_mean,pop_mean,sample_std)
print("The t static value for the given case is {}".format(t_val))
```

The t static value for the given case is -1.9362060883108294

**Step 4:** We should define the significance level of our hypothesis which is denoted by  $\alpha$  refer to the likelihood that the random sample you choose is not representative of the population. The lower the significance level, the more confident you can be in replicating your results.

Lwt us assume the confidence level is 95% i.e. 0.95  
 $\alpha = 1 - \text{confidence level}$   
Therefore  $\alpha = 0.05$

In [80]:

```
confidence_interval = 0.95  
alpha = 1 - confidence_interval
```

**Step 5:** Deciding the type of test.

We have to decide the type of test depending on the context of hypothesis. The tests are,

- Two-tailed test
- One-tailed test

*You can tell the type of the test and the position of the critical region on the basis of the 'sign' in the alternate hypothesis.*

- $\neq$  in  $H_1 \rightarrow$  Two-tailed test  $\rightarrow$  Rejection region on both sides of distribution
- $<$  in  $H_1 \rightarrow$  Lower-tailed test  $\rightarrow$  Rejection region on left side of distribution
- $>$  in  $H_1 \rightarrow$  Upper-tailed test  $\rightarrow$  Rejection region on right side of distribution

From step 1, the alternate hypothesis  $H_1$  has a  $\neq$  and we should perform a two tailed test.

In [81]:

```
# To find the t value of a two tailed test,  
t_critical = t.ppf(1-alpha/2,df = N-1)  
print("The t critical value for the given data is {}".format(t_critical))
```

The t critical value for the given data is 2.2621571627409915

In [82]:

```
# interpret via critical value  
if abs(t_val) >= t_critical:  
    print("Reject the null hypothesis.")  
else:  
    print('Fail to Reject the null hypothesis.')
```

Fail to Reject the null hypothesis.

Let us plot the distribution with the t critical value and the obtained t static value to visualise the hypothesis output.



In [83]:

```
# Plotting the sampling distribution with rejection regions

# Defining the x minimum and x maximum
x_min = 400
x_max = 600
df = N-1
# Defining the sampling distribution mean and sampling distribution std
mean = pop_mean
std = sample_std

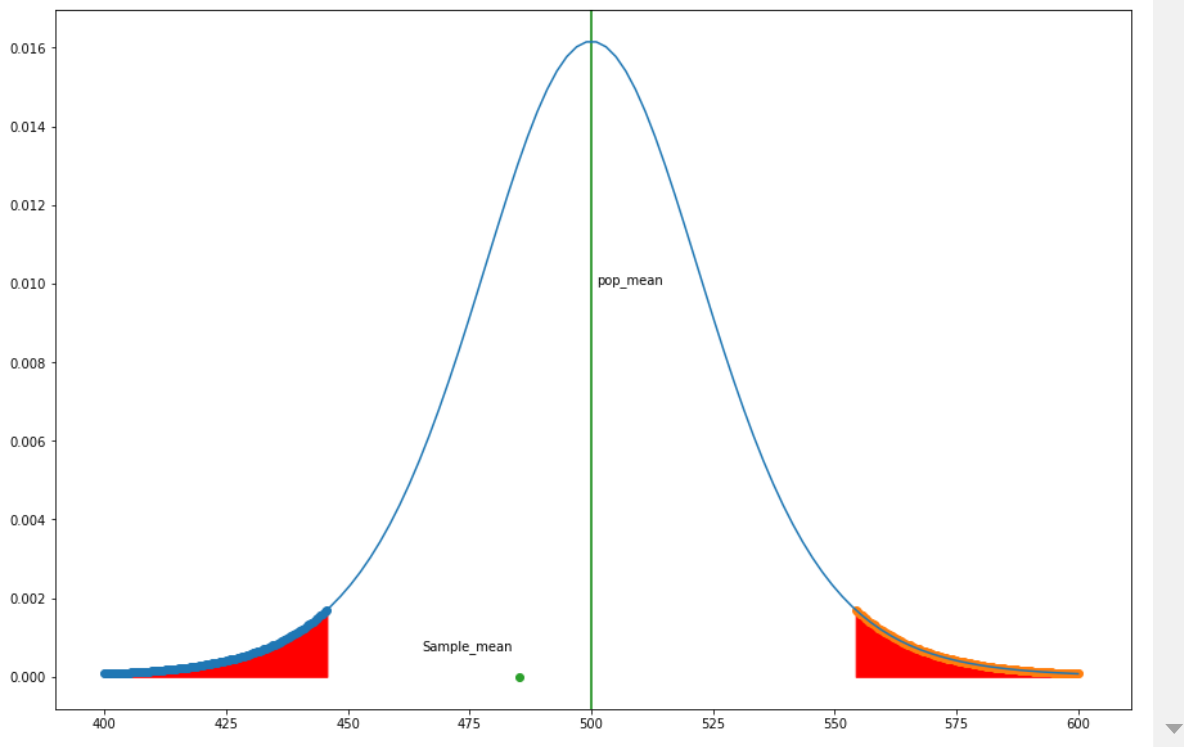
# Plotting the graph and setting the x limits
x = np.linspace(x_min, x_max, 100)
y = t.pdf(x, df, mean, std)
plt.figure(figsize = (15,10))

# Computing the left and right critical values (Two tailed Test)
t_critical_left = pop_mean - (t_critical * std)
t_critical_right = pop_mean + (t_critical * std)

# Shading the left rejection region
x1 = np.linspace(x_min, t_critical_left, 100)
y1 = t.pdf(x1, df, mean, std)
plt.fill_between(x1, y1, color='red')
plt.scatter(x1, y1)

# Shading the right rejection region
x2 = np.linspace(t_critical_right, x_max, 100)
y2 = t.pdf(x2, df, mean, std)
plt.fill_between(x2, y2, color='red')
plt.scatter(x2, y2)
plt.scatter(sample_mean, 0)
plt.annotate("Sample_mean", (sample_mean-20, 0.0007))
plt.axvline(mean, color='green')
plt.annotate("pop_mean", (mean+1, 0.01))

plt.plot(x, y)
plt.show()
# Plotting the sample mean and concluding the results
```



So, to conclude in our case 1, we failed to gather enough evidence to reject the null hypothesis.

## Case 2:

You have developed a new Natural Language Processing Algorithms and done a user study. You claim that the average rating given by the users is greater than 4 on a scale of 1 to 5. How do you prove this to your client?

**Solution:** Let us follow a step by step approach to solve these type of problems.

**Step 1:** Understanding the scenario and plot the Null hypothesis and Alternate hypothesis. For our case 1,

Null Hypothesis  $H_0$  (Status Quo) is that opposite to the claim so it becomes.

$$H_0 : \bar{X} \leq 4$$

Alternate Hypothesis  $H_1$  (Bold Claim) is that the average rating of the algorithm is greater than 4.

$$H_1 : \bar{X} > 4$$

**Step 2:** Collecting a sample of size N and computing its mean.

In our example, let us consider a sample of 20 user ratings.

Sample size N = 20

Let the sample be,

[4, 3, 5, 4, 5, 3, 5, 5, 4, 2, 4, 5, 5, 4, 4, 5, 4, 5, 4, 5]

Now, in order to compute the mean of this sample  $\bar{X}$  we shall dive into programming.

In [84]:

```
pop_mean = 4 #Given
sample = [4, 3, 5, 4, 5, 3, 5, 5, 4, 2, 4, 5, 5, 4, 4, 5, 4, 5, 4, 5]
N = len(sample)
sample_mean = sum(sample)/N
print("The mean of the sample is {}".format(sample_mean))
```

The mean of the sample is 4.25

**Step 3:** Calculate the test statistic value t.

The formula for calculating t is given as,

$$t = \frac{\bar{X} - \mu}{\frac{s}{\sqrt{N}}}$$

Where,

- t = Test value
- $\bar{X}$  = Mean of the sample
- $\mu$  = Mean of the population
- s = standard deviation of the sample
- N = Sample size

In [85]:

```
# Let us define a function for calculating t value
def t_value(sample_size, sample_mean, pop_mean, sample_std):
    numerator = sample_mean - pop_mean
    denominator = sample_std / sample_size**0.5
    return numerator / denominator
```

In [86]:

```
# Let us find the standard deviation of the sample s.
sample_std = np.std(sample)
print("The standard deviation s of the sample of size N is {}".format(sample_std))
```

The standard deviation s of the sample of size N is 0.82915619758885

In [87]:

```
t_val = t_value(N, sample_mean, pop_mean, sample_std)
print("The t static value for the given case is {}".format(t_val))
```

The t static value for the given case is 1.3483997249264843

**Step 4:** We should define the significance level of our hypothesis which is denoted by  $\alpha$  refer to the likelihood that the random sample you choose is not representative of the population. The lower the significance level, the more confident you can be in replicating your results.

Lwt us assume the confidence level is 95% i.e. 0.95  
 $\alpha = 1 - \text{confidence level}$

Therefore  $\alpha = 0.05$

In [88]:

```
confidence_interval = 0.95
alpha = 1 - confidence_interval
```

**Step 5:** Deciding the type of test.

We have to decide the type of test depending on the context of hypothesis. The tests are,

- Two-tailed test
- One-tailed test

*You can tell the type of the test and the position of the critical region on the basis of the '**sign**' in the alternate hypothesis.*

- $\neq$  in  $H_1 \rightarrow$  Two-tailed test  $\rightarrow$  Rejection region on both sides of distribution
- $<$  in  $H_1 \rightarrow$  Lower-tailed test  $\rightarrow$  Rejection region on left side of distribution
- $>$  in  $H_1 \rightarrow$  Upper-tailed test  $\rightarrow$  Rejection region on right side of distribution

From step 1, the alternate hypothesis  $H_1$  has a  $>$  and we should perform a one tailed test.

In [89]:

```
# To find the t value of
t_critical = t.ppf(1-alpha,df = N-1)
print("The t critical value for the given data is {}".format(t_critical))
```

The t critical value for the given data is 1.729132811521367

In [90]:

```
# interpret via critical value
if abs(t_val) > t_critical:
    print("Reject the null hypothesis.")
else:
    print('Fail to Reject the null hypothesis.')
```

Fail to Reject the null hypothesis.

Let us plot the distribution with the t critical value and the obtained t static value to visualise the hypothesis output.

In [91]:

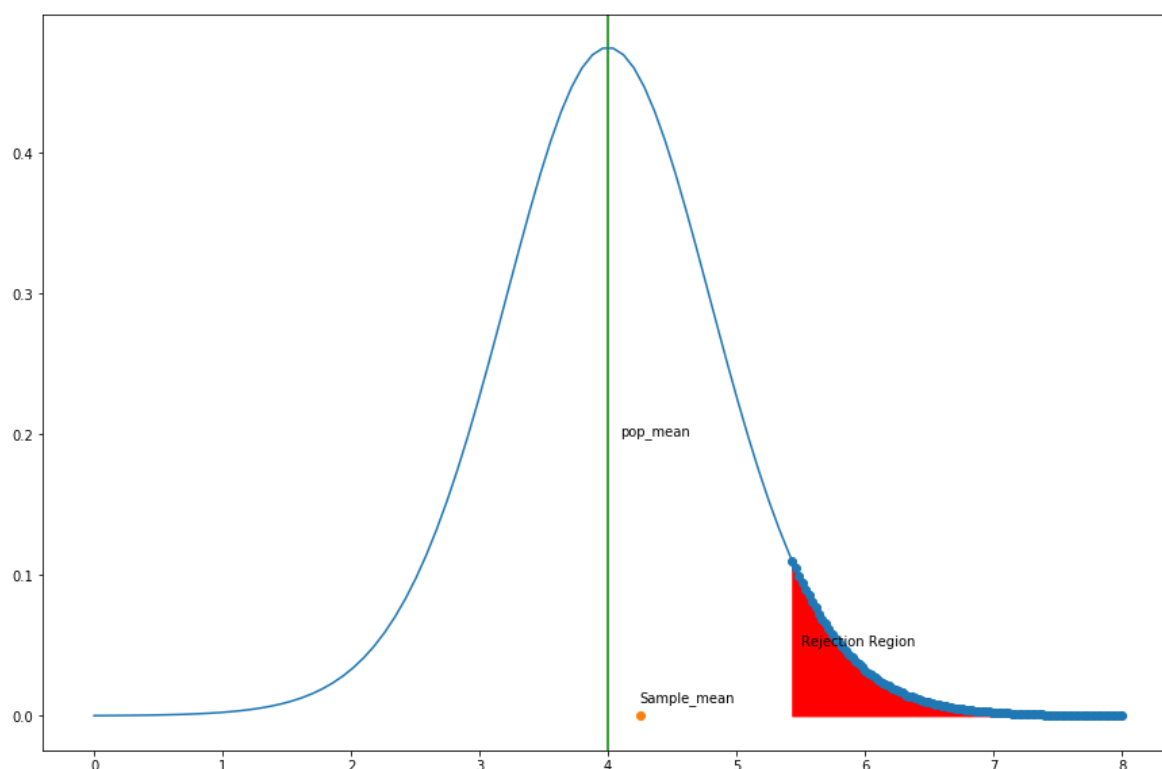
```
# Plotting the sampling distribution with rejection regions

# Defining the x minimum and x maximum
x_min = 0
x_max = 8
df = N-1
# Defining the sampling distribution mean and sampling distribution std
mean = pop_mean
std = sample_std

# Plotting the graph and setting the x Limits
x = np.linspace(x_min, x_max, 100)
y = t.pdf(x,df, mean, std)
plt.figure(figsize = (15,10))
# calculating right critical value for the one tailed test
t_critical_right = pop_mean + (t_critical * std)
# Shading the right rejection region
x2 = np.linspace(t_critical_right, x_max, 100)
y2 = t.pdf(x2,df, mean, std)
plt.fill_between(x2, y2, color='red')

plt.annotate("Rejection Region", (5.5, 0.05))
plt.scatter(x2, y2)
plt.scatter(sample_mean, 0)
plt.annotate("Sample_mean", (sample_mean, 0.01))
plt.axvline(mean, color='green')
plt.annotate("pop_mean", (mean+0.1, 0.2))

plt.plot(x, y)
plt.show()
# Plotting the sample mean and concluding the results
```



So, to conclude in our case 2, we failed to gather enough evidence to reject the null hypothesis.

### Case 3:

*TATA has developed a better fuel management system for the SUV segment. They claim that with this system, on average the SUV's mileage is at least 15 km/litre?*

**Solution:** Let us follow a step by step approach to solve these type of problems.

**Step 1:** Understanding the scenario and plot the Null hypothesis and Alternate hypothesis. For our case 1,

Null Hypothesis  $H_0$  (Status Quo) is something against to the bold claim by tata which mean that its average milage will be less than or equal to 15.

$$H_0 : \bar{X} \leq 15$$

Alternate Hypothesis  $H_1$  (Bold Claim) is that the average milage of the new SUV is greater than 15.

$$H_1 : \bar{X} > 15$$

**Step 2:** Collecting a sample of size N and computing its mean.

In our example, let us collect a sample of milage values.

Sample size N = 20

Let the sample be,

[14.08, 14.13, 15.65, 13.78, 16.26, 14.97, 15.36, 15.81, 14.53, 16.79, 15.78, 16.98, 13.23, 15.43, 15.38]

Now, in order to compute the mean of this sample  $\bar{X}$  we shall dive into programming.

In [92]:

```
pop_mean = 15 #Given
sample = [14.08,14.13,15.65,13.78,16.26,14.97,15.36,15.81,14.53,16.79,15.78,16.98,13.23,15.43,15.38]
sample_mean = sum(sample)/N
print("The mean of the sample is {}".format(sample_mean))
```

The mean of the sample is 15.098999999999998

**Step 3:** Calculate the test statistic value t.

The formula for calculating t is given as,

$$t = \frac{\bar{X} - \mu}{\frac{s}{\sqrt{N}}}$$

Where,

- t = Test value
- $\bar{X}$  = Mean of the sample
- $\mu$  = Mean of the population
- s = standard deviation of the sample
- N = Sample size

In [93]:

```
# Let us define a function for calculating t value
def t_value(sample_size, sample_mean, pop_mean, sample_std):
    numerator = sample_mean - pop_mean
    denominator = sample_std / sample_size**0.5
    return numerator / denominator
```

In [94]:

```
# Let us find the standard deviation of the sample s.
sample_std = np.std(sample)
print("The standard deviation s of the sample of size N is {}".format(sample_std))
```

The standard deviation s of the sample of size N is 0.9994043225842081

In [95]:

```
t_val = t_value(N,sample_mean,pop_mean,sample_std)
print("The t static value for the given case is {}".format(t_val))
```

The t static value for the given case is 0.44300534782572615

**Step 4:** We should define the significance level of our hypothesis which is denoted by  $\alpha$  refer to the likelihood that the random sample you choose is not representative of the population. The lower the significance level, the more confident you can be in replicating your results.

Lwt us assume the confidence level is 95% i.e. 0.95  
 $\alpha$  = 1 - confidence level  
Therefore  $\alpha$  = 0.05

In [96]:

```
confidence_interval = 0.95
alpha = 1 - confidence_interval
```

**Step 5:** Deciding the type of test.

We have to decide the type of test depending on the context of hypothesis. The tests are,

- Two-tailed test
- One-tailed test

*You can tell the type of the test and the position of the critical region on the basis of the ‘**sign**’ in the alternate hypothesis.*

- $\neq$  in  $H_1 \rightarrow$  Two-tailed test  $\rightarrow$  Rejection region on both sides of distribution
- $<$  in  $H_1 \rightarrow$  Lower-tailed test  $\rightarrow$  Rejection region on left side of distribution
- $>$  in  $H_1 \rightarrow$  Upper-tailed test  $\rightarrow$  Rejection region on right side of distribution

From step 1, the alternate hypothesis  $H_1$  has a  $\neq$  and we should perform a two tailed test.

In [97]:

```
# To find the t value of a two tailed test,
t_critical = t.ppf(1-alpha,df = N-1)
print("The t critical value for the given data is {}".format(t_critical))
```

The t critical value for the given data is 1.729132811521367

In [98]:

```
# interpret via critical value
if abs(t_val) >= t_critical:
    print("Reject the null hypothesis.")
else:
    print('Fail to Reject the null hypothesis.')
```

Fail to Reject the null hypothesis.

Let us plot the distribution with the t critical value and the obtained t static value to visualise the hypothesis output.



In [99]:

```
# Plotting the sampling distribution with rejection regions

# Defining the x minimum and x maximum
x_min = 10
x_max = 20
df = N-1
# Defining the sampling distribution mean and sampling distribution std
mean = pop_mean
std = sample_std

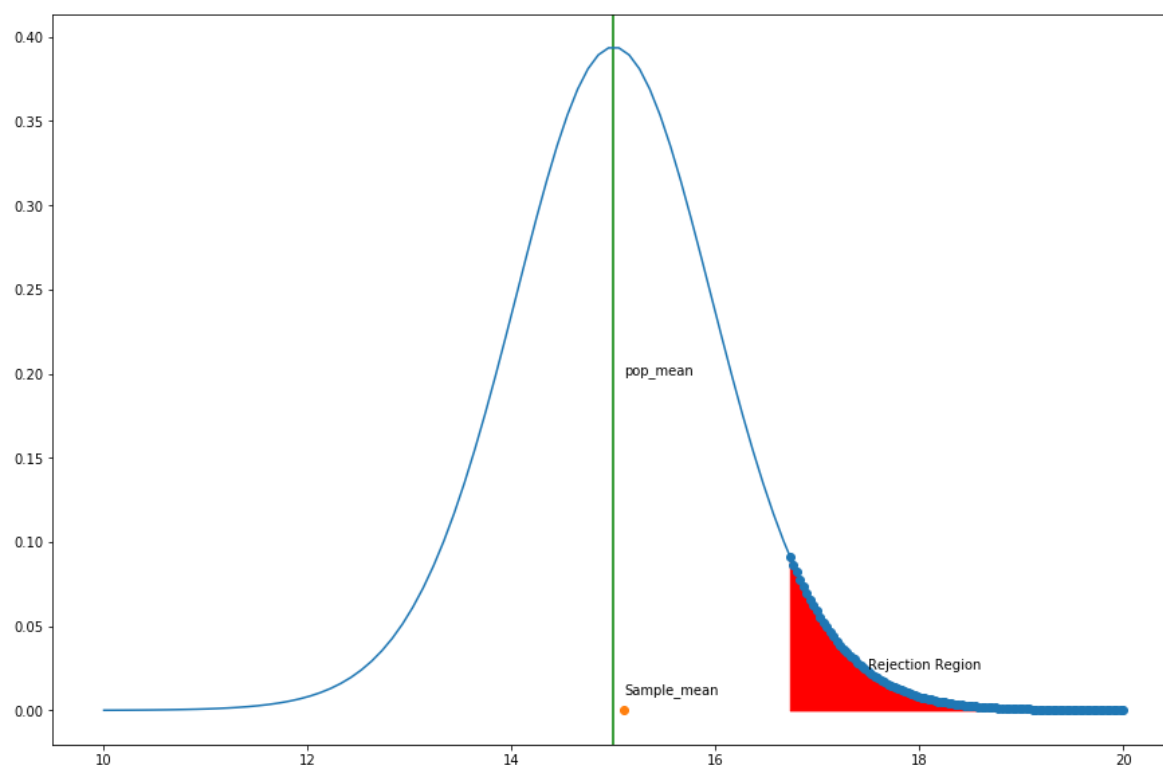
# Plotting the graph and setting the x Limits
x = np.linspace(x_min, x_max, 100)
y = t.pdf(x,df, mean, std)
plt.figure(figsize = (15,10))

# calculating right critical value for the one tailed test
t_critical_right = pop_mean + (t_critical * std)

# Shading the right rejection region
x2 = np.linspace(t_critical_right, x_max, 100)
y2 = t.pdf(x2,df, mean, std)
plt.fill_between(x2, y2, color='red')
plt.scatter(x2,y2)
plt.annotate("Rejection Region", (17.5,0.025))
plt.scatter(sample_mean, 0)
plt.annotate("Sample_mean", (sample_mean, 0.01))
plt.axvline(mean, color='green')
plt.annotate("pop_mean", (mean+0.1, 0.2))

plt.plot(x, y)
plt.show()
```

```
# Plotting the sample mean and concluding the results
```



Since the sample mean is out of rejection region. we fail to reject the null hypothesis.

Since the sample mean is not in rejection region, we fail to reject the null hypothesis.

## Case 4:

You have developed a new Machine Learning Application and claim that on average it takes less than 100 ms to predict for any future datapoint. How do you convince your client about this claim?

**Solution:** Let us follow a step by step approach to solve these type of problems.

**Step 1:** Understanding the scenario and plot the Null hypothesis and Alternate hypothesis. For our case 1,

Null Hypothesis  $H_0$  (Status Quo) is that it takes more than 100 ms.

$$H_0 : \bar{X} \geq 100$$

Alternate Hypothesis  $H_1$  (Bold Claim) is that the average time that my application takes to predict new data point is less than 100 ms.

$$H_1 : \bar{X} < 100$$

**Step 2:** Collecting a sample of size N and computing its mean.

In our example, let us test the application for 100 times.

Sample size N = 100

Let the sample be,

[112, 85, 99, 91, 103, 96, 114, 100, 102, 109]

Now, in order to compute the mean of this sample  $\bar{X}$  we shall dive into programming.

In [100]:

```
pop_mean = 100 #Given
sample = [112,85,95,91,103,96,104,100,102,90]
N = len(sample)
sample_mean = sum(sample)/N
print("The mean of the sample is {}".format(sample_mean))
```

The mean of the sample is 97.8

**Step 3:** Calculate the test statistic value t.

The formula for calculating t is given as,

$$t = \frac{\bar{X} - \mu}{\frac{s}{\sqrt{N}}}$$

Where,

- t = Test value
- $\bar{X}$  = Mean of the sample
- $\mu$  = Mean of the population
- s = standard deviation of the sample
- N = Sample size

In [101]:

```
# Let us define a function for calculating t value
def t_value(sample_size, sample_mean, pop_mean, sample_std):
    numerator = sample_mean - pop_mean
    denominator = sample_std / sample_size**0.5
    return numerator / denominator
```

In [102]:

```
# Let us find the standard deviation of the sample s.
sample_std = np.std(sample)
print("The standard deviation s of the sample of size N is {}".format(sample_std))
```

The standard deviation s of the sample of size N is 7.56042326857432

In [103]:

```
t_val = t_value(N, sample_mean, pop_mean, sample_std)
print("The t static value for the given case is {}".format(t_val))
```

The t static value for the given case is -0.9201880113363464

**Step 4:** We should define the significance level of our hypothesis which is denoted by  $\alpha$  refer to the likelihood that the random sample you choose is not representative of the population. The lower the significance level, the more confident you can be in replicating your results.

Lwt us assume the confidence level is 95% i.e. 0.95  
 $\alpha = 1 - \text{confidence level}$   
Therefore  $\alpha = 0.05$

In [104]:

```
confidence_interval = 0.95
alpha = 1 - confidence_interval
```

**Step 5:** Deciding the type of test.

We have to decide the type of test depending on the context of hypothesis. The tests are,

- Two-tailed test
- One-tailed test

*You can tell the type of the test and the position of the critical region on the basis of the 'sign' in the alternate hypothesis.*

- $\neq$  in  $H_1 \rightarrow$  Two-tailed test  $\rightarrow$  Rejection region on both sides of distribution
- $<$  in  $H_1 \rightarrow$  Lower-tailed test  $\rightarrow$  Rejection region on left side of distribution
- $>$  in  $H_1 \rightarrow$  Upper-tailed test  $\rightarrow$  Rejection region on right side of distribution

From step 1, the alternate hypothesis  $H_1$  has a  $\neq$  and we should perform a two tailed test.

In [105]:

```
# To find the t value of a one tailed test,  
t_critical = t.ppf(1-alpha,df = N-1)  
print("The t critical value for the given data is {}".format(t_critical))
```

The t critical value for the given data is 1.8331129326536335

In [106]:

```
# interpret via critical value  
if abs(t_val) < t_critical:  
    print("Reject the null hypothesis.")  
else:  
    print('Fail to Reject the null hypothesis.')
```

Reject the null hypothesis.

Let us plot the distribution with the t critical value and the obtained t static value to visualise the hypothesis output.

In [107]:

```
# Plotting the sampling distribution with rejection regions

# Defining the x minimum and x maximum
x_min = 75
x_max = 125
df = N-1
# Defining the sampling distribution mean and sampling distribution std
mean = pop_mean
std = sample_std

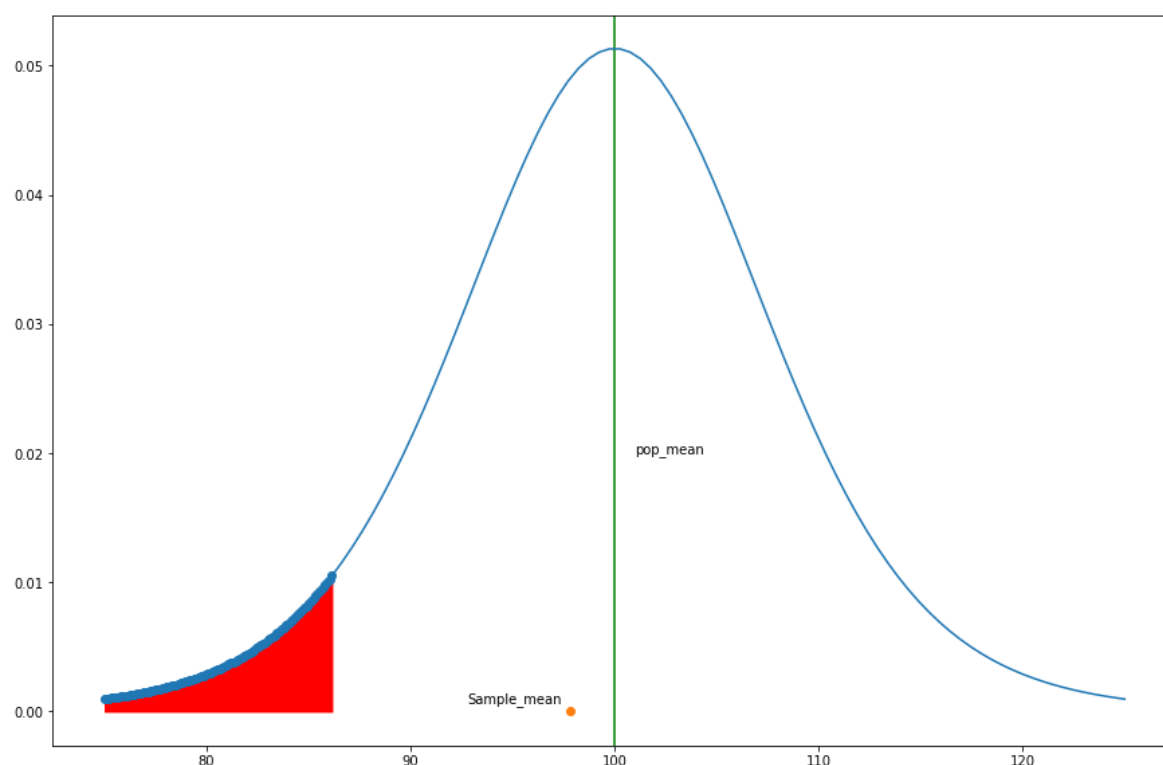
# Plotting the graph and setting the x Limits
x = np.linspace(x_min, x_max, 100)
y = t.pdf(x, df, mean, std)
plt.figure(figsize = (15,10))

# Computing the left critical value (one tailed Test)
t_critical_left = pop_mean - (t_critical * std)

# Shading the left rejection region
x1 = np.linspace(x_min, t_critical_left, 100)
y1 = t.pdf(x1, df, mean, std)
plt.fill_between(x1, y1, color='red')
plt.scatter(x1, y1)

plt.scatter(sample_mean, 0)
plt.annotate("Sample_mean", (sample_mean-5, 0.0007))
plt.axvline(mean, color='green')
plt.annotate("pop_mean", (mean+1, 0.02))

plt.plot(x, y)
plt.show()
# Plotting the sample mean and concluding the results
```



So, to conclude in our case 4, we reject the null hypothesis statement that the mean prediction time of application is greater than 100.