# conf_interval

November 18, 2022

Python 3.8.10 (default, Jun 22 2022, 20:18:18)
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IPython 8.4.0 – An enhanced Interactive Python. Type '?' for help.

# Confidence Intervals + Quick Reference to my fantastic CI tutorial + This code is based on this blog post We are taking the data from Uniform distribution. According to the Central Limit Theorem (CLT). Means of any distribution will follow a normal distribution. with std of $\frac{\sigma}{\sqrt{n}}$ where n is the sample size and $\sigma$ is the global std which usually is estimated by sample std. If we can say (based on CLT) that the sample means center around the global mean with std $\frac{\sigma}{\sqrt{n}}$ then based on the characteristics of normal distribution we can also say that that 66 % percent of the means are +/- 1 std away from the global mean. ~95 % is ~2 std away from the global mean and ~99% means is 2.3 std away from global mean. Thus if we have the sample mean and based on the sample size and sample std, the std for the sample means, we can now say the interval where (66%,95%,99%) of the means should be located.

[ ]:
```
import numpy as np
from scipy.stats import t,norm
import math
import matplotlib.pyplot as plt
from dataclasses import dataclass
```

[ ]:
```
@dataclass
class ConfidenceInterval:
    mean:float
    lower_bound:float
    upper_bound:float
    test_type:str
    extremum_val:float
    def get_size(self)->float:
        return self.upper_bound-self.lower_bound
    def print_statistics(self):
        print(f"Test type: {self.test_type}")
        print(f"Median: {self.mean}")
        print(f"Min boundary {self.lower_bound}")
        print(f"Max boundary {self.upper_bound}")
        print(f"{self.test_type} val: {self.extremum_val}")
        print(f"Width is {self.get_size()}" )
```

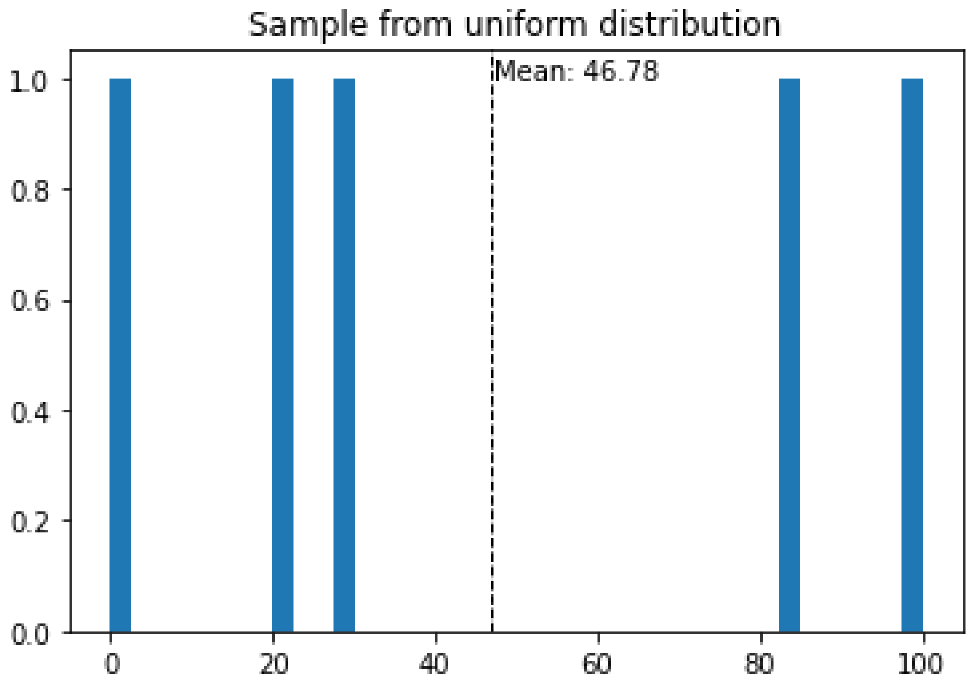
```
def␣
↪calculate_confidence_interval(sample_mean,sample_std,sample_size,confidence,test_type)->Con
↪
    alpha=1-confidence
    # Only thing that is different for t and z confidence intervale is the␣
↪extremum value
    if test_type == "t":
        degrees_of_freedom=sample_size-1
        extremum_val=float(np.abs(t.ppf(alpha/2,degrees_of_freedom))) # t_val -␣
↪based on confidence we have chosen, how many standard distributions is the␣
↪ci width. If Confidence is 95%, then std is  ~2
    elif test_type == "z":
        extremum_val=float(np.abs(norm.ppf(alpha/2))) # z_val - based on␣
↪confidence we have chosen, how many standard distributions is the ci width.␣
↪If Confidence is 95%, then std is ~2.
    else:
        raise Exception("Wrong test type provided")

    clt_based_std = sample_std / math.sqrt(sample_size) # The std for sample␣
↪means. Calculated based on CLT
    max_expected_difference = extremum_val *  clt_based_std # std * (how many␣
↪stds based on chosen confidence interval size)
    return␣
↪ConfidenceInterval(mean=sample_mean,lower_bound=sample_mean-max_expected_difference,upper_b



def perform_comparison(sample_size:int, confidence:float):
    # Generate sample data from uniform distritubution on the range 0..100
    x = np.random.uniform(size=sample_size)
    x_positive = x-min(x)
    x_scaled = x_positive/max(x_positive)*100
    x = x_scaled
    # Calculate confidence intervals based on both Normal distribution (Z val)␣
↪and t distribution (t val)
    ci_z=calculate_confidence_interval(sample_mean=x.mean(),sample_std=x.
↪std(),sample_size=sample_size,confidence=confidence,test_type='z')
    ci_t=calculate_confidence_interval(sample_mean=x.mean(),sample_std=x.
↪std(),sample_size=sample_size,confidence=confidence,test_type='t')
    return x, ci_z, ci_t
```

Lets take 1 sample with size SAMPLE_SIZE from the Uniform distribution and plot this sample

[ ]:
```
SAMPLE_SIZE=5
CONFIDENCE=0.99
x, ci_z, ci_t = perform_comparison(sample_size=SAMPLE_SIZE,confidence=0.95)
```

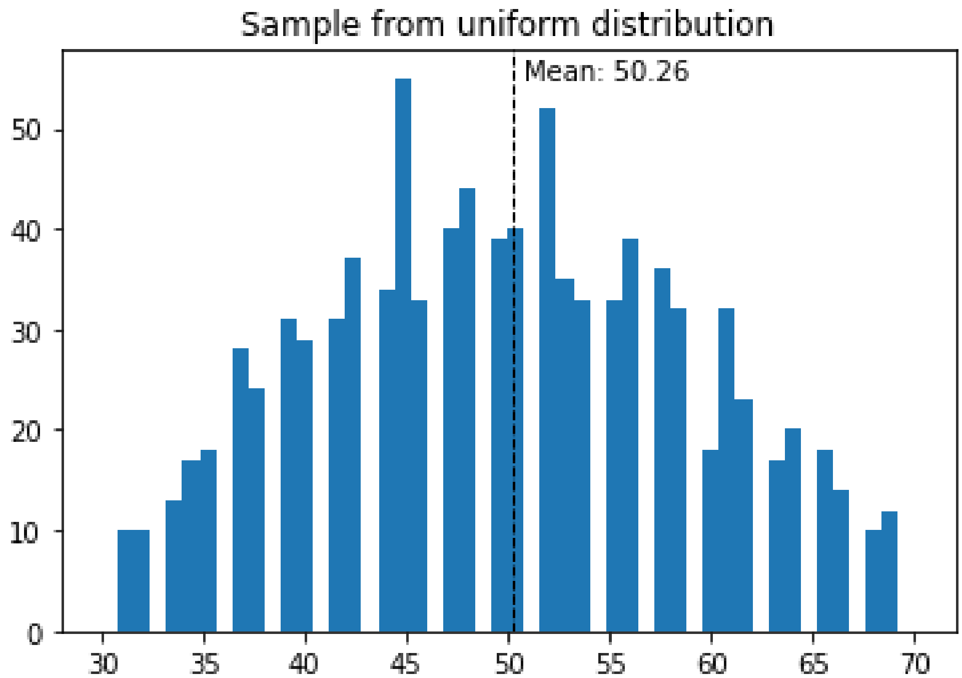
```python
print(f"Sample size: {SAMPLE_SIZE}, Sample std: {x.std()}, Confidence␣
    ↪{CONFIDENCE}, Max value {max(x)}, Min value: {min(x)}")
ci_z.print_statistics()
ci_t.print_statistics()
print(f"Differences in CI size ci_t-ci_z {ci_t.get_size()-ci_z.get_size()}")

# PLOT THE GENERATED DISTRIBUTION X

def plot_default_histogram(x,bins=40,start=0,end=100):
    counts, bins = np.histogram(x,bins=bins)
    plt.hist(bins[:-1],len(bins)-1,weights=counts,range=(start,end))
    plt.axvline(x.mean(), color='k', linestyle='dashed', linewidth=1)
    # plt.axvline(m+s, color='r', linestyle='dashed', linewidth=1)
    # plt.axvline(m-s, color='r', linestyle='dashed', linewidth=1)
    min_ylim, max_ylim = plt.ylim()
    plt.text(x.mean()*1.01, max_ylim*0.95, 'Mean: {:.2f}'.format(x.mean()))
    plt.title("Sample from uniform distribution")

plot_default_histogram(x)
```

```
Sample size: 5, Sample std: 38.76123002449158, Confidence 0.99, Max value 100.0,
Min value: 0.0
Test type: z
Median: 46.78444042832694
Min boundary 12.809348611386305
Max boundary 80.75953224526756
z val: 1.959963984540054
Width is 67.95018363388127
Test type: t
Median: 46.78444042832694
Min boundary -1.3439834191791533
Max boundary 94.91286427583303
t val: 2.7764451051977987
Width is 96.25684769501218
Differences in CI size ci_t-ci_z 28.306664061130917
```




Now we perform this experiment 1000 times and see how the distribution of means will look like. E.g. we take the sample with size sample_size (set above) and we do this 1000 times. Then we plot the means of these 1000 samples. Based on the Central Limit Theorem (CLT) this distribution should now be a normal distribution with ~ global mean and the standard distribution $\frac{\sigma}{\sqrt{n}}$ where $\sigma$= Global STD (Can be estimated by sample std/Bootstrapping) and n is sample size for 1 sample. **PS! In reality we almost always limit our experiment with taking 1 sample only. The 1000 sample setup only aims to showcase how Central Limit Theorem turns any distribution (in this case Uniform) into Normal Distribution (With smaller samples t distribution) with sample mean as the global mean and std $\frac{\sigma}{\sqrt{n}}$**

[ ]:
```
means = []
for i in range(1000):
    x, ci_z, ci_t = perform_comparison(sample_size=SAMPLE_SIZE,confidence=0.95)
    means.append(x.mean())

means = np.asarray(means)
plot_default_histogram(means,bins=50,start=30,end=70)
```



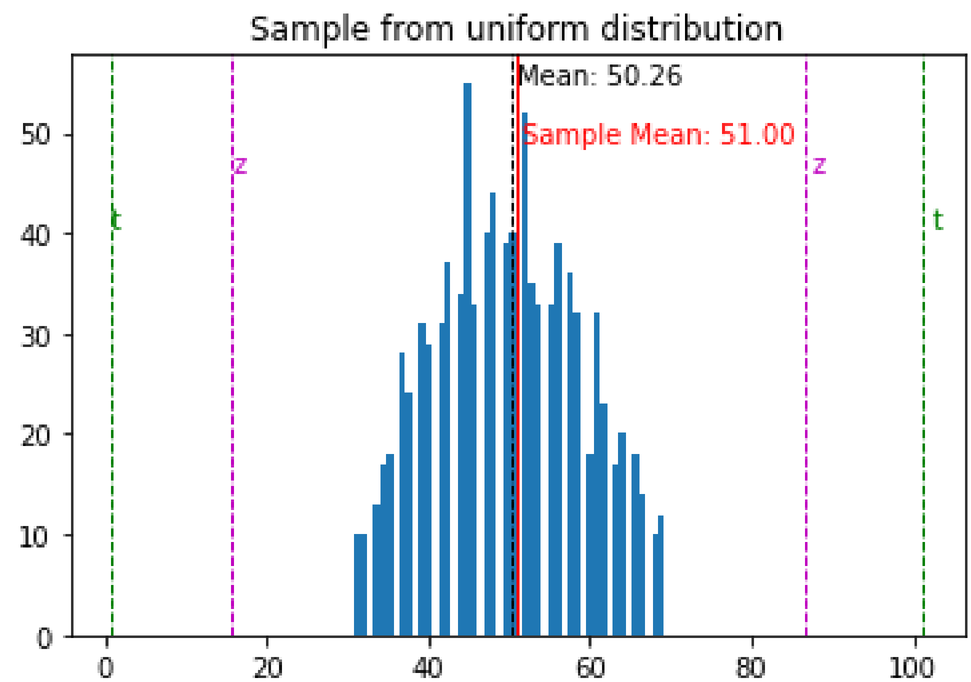

Lets now take a few additional samples to show how we derive the confidence interval from 1 sample. **Run the cells below at least 5 times to see how the confidence intervals are generated for each sample**

**ADDITIONAL SAMPLE 1 COMPARED TO MEAN**

[ ]:
```
def take_sample_and_show(means):
    x_sample, sample_ci_z, sample_ci_t =␣
 ↪perform_comparison(sample_size=SAMPLE_SIZE,confidence=0.95)
    plot_default_histogram(means,bins=50,start=30,end=70)

    # ADD THE SAMPLE
    plt.axvline(x_sample.mean(), color='r', linewidth=1)
    min_ylim, max_ylim = plt.ylim()
    plt.text(x_sample.mean()*1.01,max_ylim*0.85, 'Sample Mean: {:.2f}'.
 ↪format(x_sample.mean()),color='r')

    print(f"Sample size: {len(x_sample)}, Sample std: {x_sample.std()},␣
 ↪Confidence {CONFIDENCE}, Max value {max(x_sample)}, Min value:␣
 ↪{min(x_sample)}")

    # PLOT CI INFOR FOR Z TESTS
    z_color='m'
    plt.axvline(sample_ci_z.upper_bound, color=z_color, linestyle='dashed',␣
 ↪linewidth=1)
```

```
    plt.axvline(sample_ci_z.lower_bound, color=z_color, linestyle='dashed',␣
↪linewidth=1)
    plt.text(sample_ci_z.upper_bound*1.01, max_ylim*0.8, 'z',color=z_color)
    plt.text(sample_ci_z.lower_bound*1.01, max_ylim*0.8, 'z',color=z_color)
    sample_ci_z.print_statistics()

    # PLOT CI INFO FOR T TESTS
    t_color='g'
    plt.axvline(sample_ci_t.upper_bound, color=t_color, linestyle='dashed',␣
↪linewidth=1)
    plt.axvline(sample_ci_t.lower_bound, color=t_color, linestyle='dashed',␣
↪linewidth=1)
    plt.text(sample_ci_t.upper_bound*1.01, max_ylim*0.7, 't',color=t_color)
    plt.text(sample_ci_t.lower_bound*1.01, max_ylim*0.7, 't',color=t_color)
    sample_ci_t.print_statistics()
    print("t distribution has wider confidence intervals compared to z␣
↪distribution")
    print(f"t.width-z.width {sample_ci_t.get_size()-sample_ci_z.get_size()} ")


take_sample_and_show(means)
```

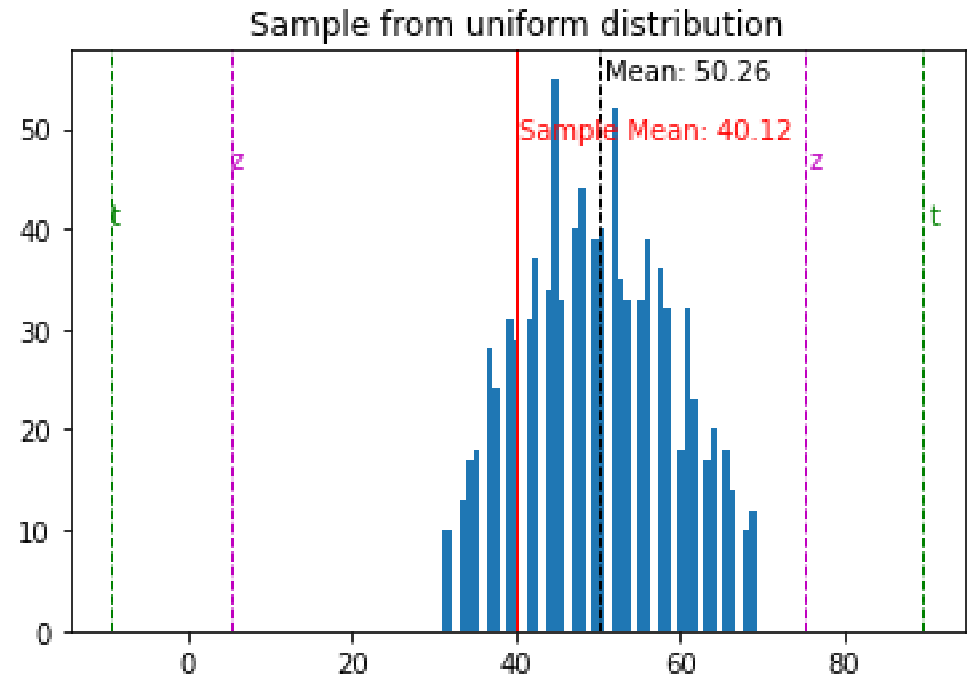
```
Sample size: 5, Sample std: 40.469748600294565, Confidence 0.99, Max value
100.0, Min value: 0.0
Test type: z
Median: 50.998294526494774
Min boundary 15.525647666869034
Max boundary 86.47094138612051
z val: 1.959963984540054
Width is 70.94529371925148
Test type: t
Median: 50.998294526494774
Min boundary 0.7484646731517444
Max boundary 101.2481243798378
t val: 2.7764451051977987
Width is 100.49965970668606
t distribution has wider confidence intervals compared to z distribution
t.width-z.width 29.55436598743458
```




**ADDITIONAL SAMPLE 2 COMPARED TO MEAN**

```
[ ]: take_sample_and_show(means)
```

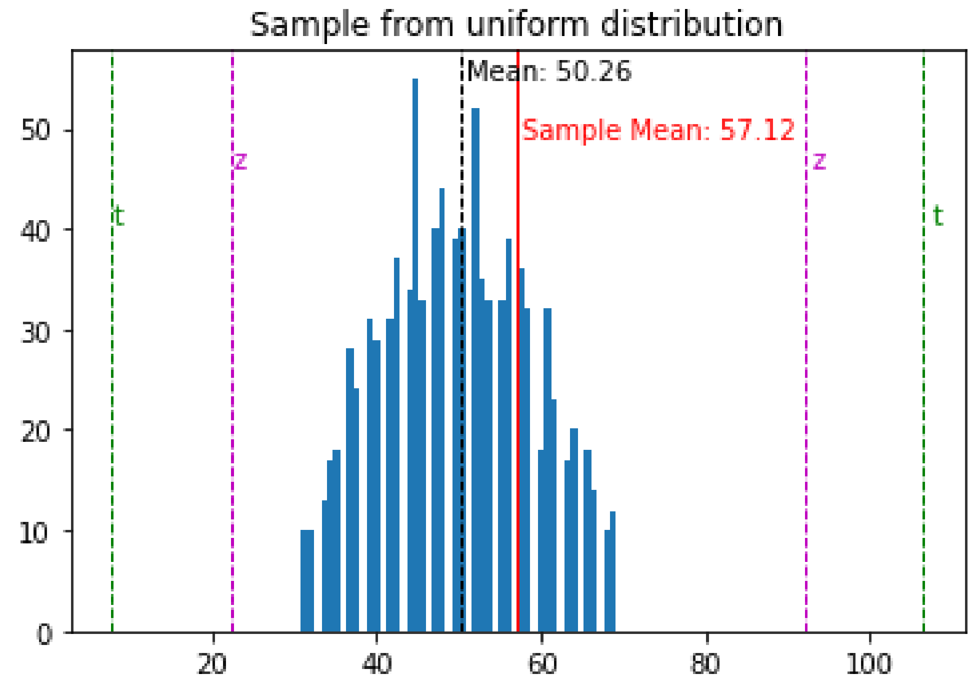
```
Sample size: 5, Sample std: 39.80587930116279, Confidence 0.99, Max value 100.0,
Min value: 0.0
Test type: z
Median: 40.12342337075145
Min boundary 5.2326729158114915
Max boundary 75.01417382569142
z val: 1.959963984540054
Width is 69.78150090987992
Test type: t
Median: 40.12342337075145
Min boundary -9.302103874346884
Max boundary 89.54895061584979
t val: 2.7764451051977987
Width is 98.85105449019667
t distribution has wider confidence intervals compared to z distribution
t.width-z.width 29.06955358031675
```




**ADDITIONAL SAMPLE 3 COMPARED TO MEAN**

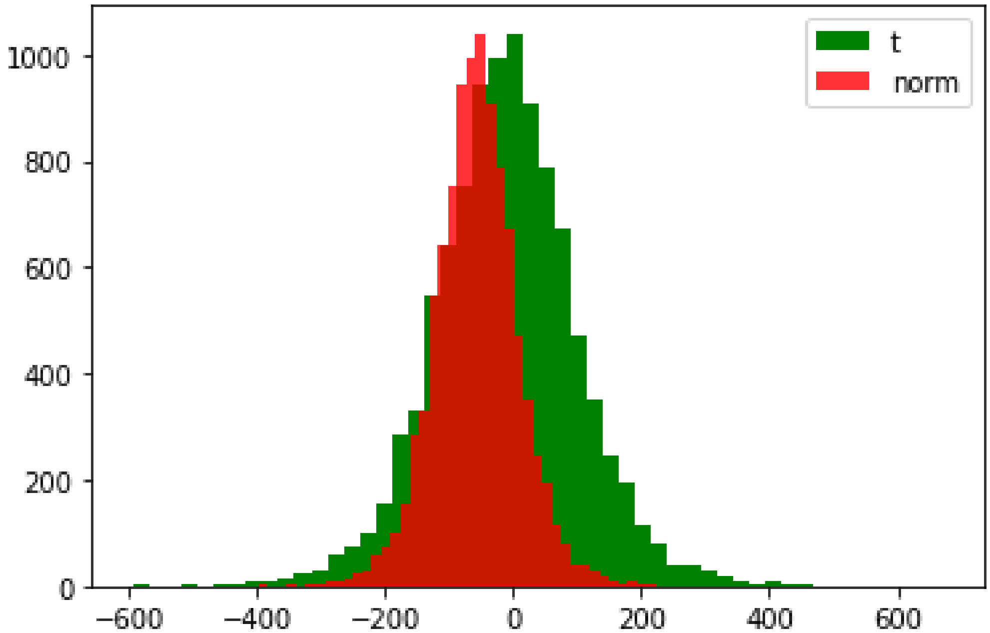
[ ]:
```
take_sample_and_show(means)
```

```
Sample size: 5, Sample std: 39.77701233420924, Confidence 0.99, Max value 100.0,
Min value: 0.0
Test type: z
Median: 57.124977437069234
Min boundary 22.25952952934213
Max boundary 91.99042534479634
z val: 1.959963984540054
Width is 69.7308958154542
Test type: t
Median: 57.124977437069234
Min boundary 7.735293265574455
Max boundary 106.51466160856401
t val: 2.7764451051977987
Width is 98.77936834298956
t distribution has wider confidence intervals compared to z distribution
t.width-z.width 29.048472527535353
```



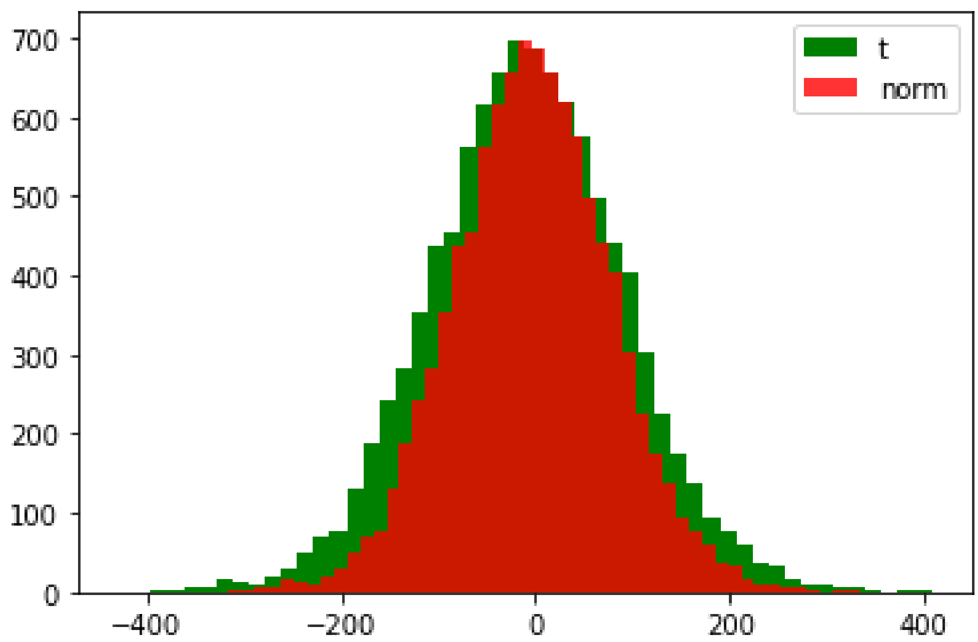

# Theory - Shape Difference between t-distribution and normal distribution Additional note. In this experiment we are showcasing Normal Distribution based confidence intervals and T-Distribution based confidence intervals. Based on CLT we are assuming in general a normal distribution to the means of data, however when the sample sizes are small, it is better to assume a variant of normal distribution that has wider tails/proportionally less data in the middle (t-distribution). the t-distribution has wider tails with smaller sample sizes. With sample sizes 30 t-distribution starts to follow the normal distribution. The distribution assumption for the mean data is important because based on that we calculate the extremum values (t or z). For Normal distribution we assume the 66% of data to be within 1 std from mean, 95 % data to be wtihin ~2 std from mean, 99% of data to be within ~2.3 std from the mean. For t-distribution the amount of standard distributions we need for any of (66%,95%,99%) are wider based on the sample size. In t-distribution we call this “degrees of freedom”

[ ]:
```
sample_size = 10
t_dist = np.random.standard_t(sample_size-1, 10000,)*100
n_dist = np.random.normal(0,1,10000)*100

t_counts, t_bins = np.histogram(t_dist,50)
n_counts, n_bins = np.histogram(n_dist,50)
plot1=plt.hist(t_bins[:-1],len(t_bins)-1,weights=t_counts,color="g",label="t")
plot2=plt.hist(n_bins[:-1],len(n_bins)-1,weights=t_counts,color="r",alpha=0.
 ↪8,label="norm")
legend=plt.legend(('t','norm'))
```




When t-distribution sample size grows however, we can see that the normal distribution and t-distribution difference is not so big anymore

[ ]:
```
sample_size = 30
t_dist = np.random.standard_t(sample_size-1, 10000,)*100
n_dist = np.random.normal(0,1,10000)*100

t_counts, t_bins = np.histogram(t_dist,50)
n_counts, n_bins = np.histogram(n_dist,50)
plot1=plt.hist(t_bins[:-1],len(t_bins)-1,weights=t_counts,color="g",label="t")
plot2=plt.hist(n_bins[:-1],len(n_bins)-1,weights=t_counts,color="r",alpha=0.
  ↪8,label="norm")
legend=plt.legend(('t','norm'))
```




# T-TEST with T distribution https://numpy.org/doc/stable/reference/random/generated/numpy.random.standa

We have a sample called "intake". From previous results we have knowledge that that the global mean is 7725. Based on this we form hypotheses + H0 - "intake" mean is not significantly larger. + H1 - "intake" mean is significantly larger. We set the significance standard level to 5%. Because we are looking at differences both smaller and larger, this is going to be a two sided t-test. E.g we will look if the mean extracted from this sample does not fall into the 95% Confidence interval of the samples(size=11) from distribution with mean 7725 E.g on both sides only roughly 2.5 percent of values are larger/smaller than it.

[ ]:
```
intake = np.array([5260., 5470, 5640, 6180, 6390, 6515, 6805, 7515, \
                   7515, 8230, 8770])
assumed_global_mean = 7725
```

To get "intake" means t-value compared with the "assumed_global_mean" we are standardizing it. The formula for this is $\frac{X-\mu}{\sigma}$. 'As we are looking at the distribution over means, based on CLT the $\sigma = \frac{\sigma}{\sqrt{n}}$. CLT assumes $\sigma$ to be the global STD but in our case we have taken the sample std as the estimate. To make it a bit larger, we have taken the std to be with only degrees of freedom=1. This reduces the t-value as it makes the element below the fraction to be larger.

[ ]:
```
t_val =  (np.mean(intake) - assumed_global_mean) / (intake.std(ddof=1)/np.
 ↪sqrt(len(intake)))
```

In this case we are taking 1000000 samples from **standard** t distribution with 10 degrees of freedom. Then we are a just comparing our calculated t-value for the "intake" mean with all the samples and finding the fraction our t_value is smaller than the sample element. Basically, if our calculated t-value is very large, this should happen very few times. Infact less than 0.025 time

```
[ ]: degrees_of_freedom=len(intake)-1
alpha=1-0.95
extremum_val=float(np.abs(t.ppf(alpha/2,degrees_of_freedom))) # PPF Percent␣
 ↪Point Function. The percent point function (ppf) is the inverse of the␣
 ↪cumulative distribution function. https://www.itl.nist.gov/div898/handbook/
 ↪eda/section3/eda362.htm

s = np.random.standard_t(df=degrees_of_freedom,size=1000000)
h = plt.hist(s, bins=100, density=True)
probability=np.sum(np.abs(t_val) < np.abs(s)) / float(len(s))
print(f"Probability of having a more extreme value than t_val:{t_val} is␣
 ↪{probability} < 0.025")
plt.axvline(t_val, color='k', linestyle='dashed', linewidth=1)
plt.axvline(-extremum_val, color='r', linestyle='dashed', linewidth=1)
plt.axvline(extremum_val, color='r', linestyle='dashed', linewidth=1)
min_ylim, max_ylim = plt.ylim()
plt.text(t_val*1.7, max_ylim*0.95, 't_val')
plt.text(-extremum_val*0.9, max_ylim*0.95, 'ci-')
plt.text(extremum_val*1.1, max_ylim*0.95, 'ci+')
```

```
Probability of having a more extreme value than t_val:-2.8207540608310198 is
0.018409 < 0.025
```

```
[ ]: Text(2.450952737161433, 0.38774181274783137, 'ci+')
```