# Hypothesis Testing

**Null Hypothesis (H0):** A statement of no change and is 0 assumed true until evidence indicates otherwise

**Alternate Hypothesis (Ha)**: A statement that the researcher is trying to find evidence to support

**Type I Error:** Reject the null hypothesis when the null hypothesis is true

**Type II Error:** Do not reject the null hypothesis when the alternative hypothesis is true

**Test Statistics (t):** A single number that summarizes the sample data used to conduct the test hypothesis

**Standard Error:** How far sample statistics (e.g., mean) deviates from the actual population mean

**p-value:** Probability of observing a test statistics

**Significance level (α):** Probability of making Type I error

**Test Statistics**

## Binomial Distribution

```
n = number of iterations
p = probablity of success
(1-p) = probablity of failure
```

Expirement of 100 coin flips and getting 57 right

---

**Null** I'm not special, my true rate of flip prediction is 0.5. **Alternative:** My true rate of flip prediction is greater than 0.5

```
from scipy.stats import binom
prob = 1 - binom.cdf(56, 100, 0.5)
prob
# Hence the prob of getting 57 or more correct is 9.6% which is more than 0.5 so we fail to reject null hypothesis
```

```
0.09667395224782138
```

# Hypothesis testing for insurance dataset

```
import skillsnetwork
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import scipy.stats as stats
import scipy.stats as chi2_contingency

from statsmodels.formula.api import ols
from statsmodels.stats.anova import anova_lm
```

```
URL = 'https://cf-courses-data.s3.us.cloud-object-storage.appdomain.cloud/IBM-ML0232EN-SkillsNetwork/asset/insurance.csv'
await skillsnetwork.download(URL, 'insurance.csv')
data = pd.read_csv('insurance.csv')
data.head()
```

```
Saved as 'insurance.csv'
```

| | age | sex | bmi | children | smoker | region | charges |
|---|---|---|---|---|---|---|---|
| **0** | 19 | female | 27.900 | 0 | yes | southwest | 16884.92400 |
| **1** | 18 | male | 33.770 | 1 | no | southeast | 1725.55230 |
| **2** | 28 | male | 33.000 | 3 | no | southeast | 4449.46200 |
| **3** | 33 | male | 22.705 | 0 | no | northwest | 21984.47061 |
| **4** | 32 | male | 28.880 | 0 | no | northwest | 3866.85520 |

Next steps: Generate code with data | View recommended plots

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1338 entries, 0 to 1337
Data columns (total 7 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       1338 non-null   int64  
 1   sex       1338 non-null   object 
 2   bmi       1338 non-null   float64
 3   children  1338 non-null   int64  
 4   smoker    1338 non-null   object 
 5   region    1338 non-null   object 
 6   charges   1338 non-null   float64
dtypes: float64(2), int64(2), object(3)
memory usage: 73.3+ KB
```

```
data.describe()
```

| | age | bmi | children | charges |
|---|---|---|---|---|
| **count** | 1338.000000 | 1338.000000 | 1338.000000 | 1338.000000 |
| **mean** | 39.207025 | 30.663397 | 1.094918 | 13270.422265 |
| **std** | 14.049960 | 6.098187 | 1.205493 | 12110.011237 |
| **min** | 18.000000 | 15.960000 | 0.000000 | 1121.873900 |
| **25%** | 27.000000 | 26.296250 | 0.000000 | 4740.287150 |
| **50%** | 39.000000 | 30.400000 | 1.000000 | 9382.033000 |
| **75%** | 51.000000 | 34.693750 | 2.000000 | 16639.912515 |
| **max** | 64.000000 | 53.130000 | 5.000000 | 63770.428010 |

Response variable: Charges

Predictor variable: age, sex, bmi, children, smoker and region

## Steps of Hypothesis testing

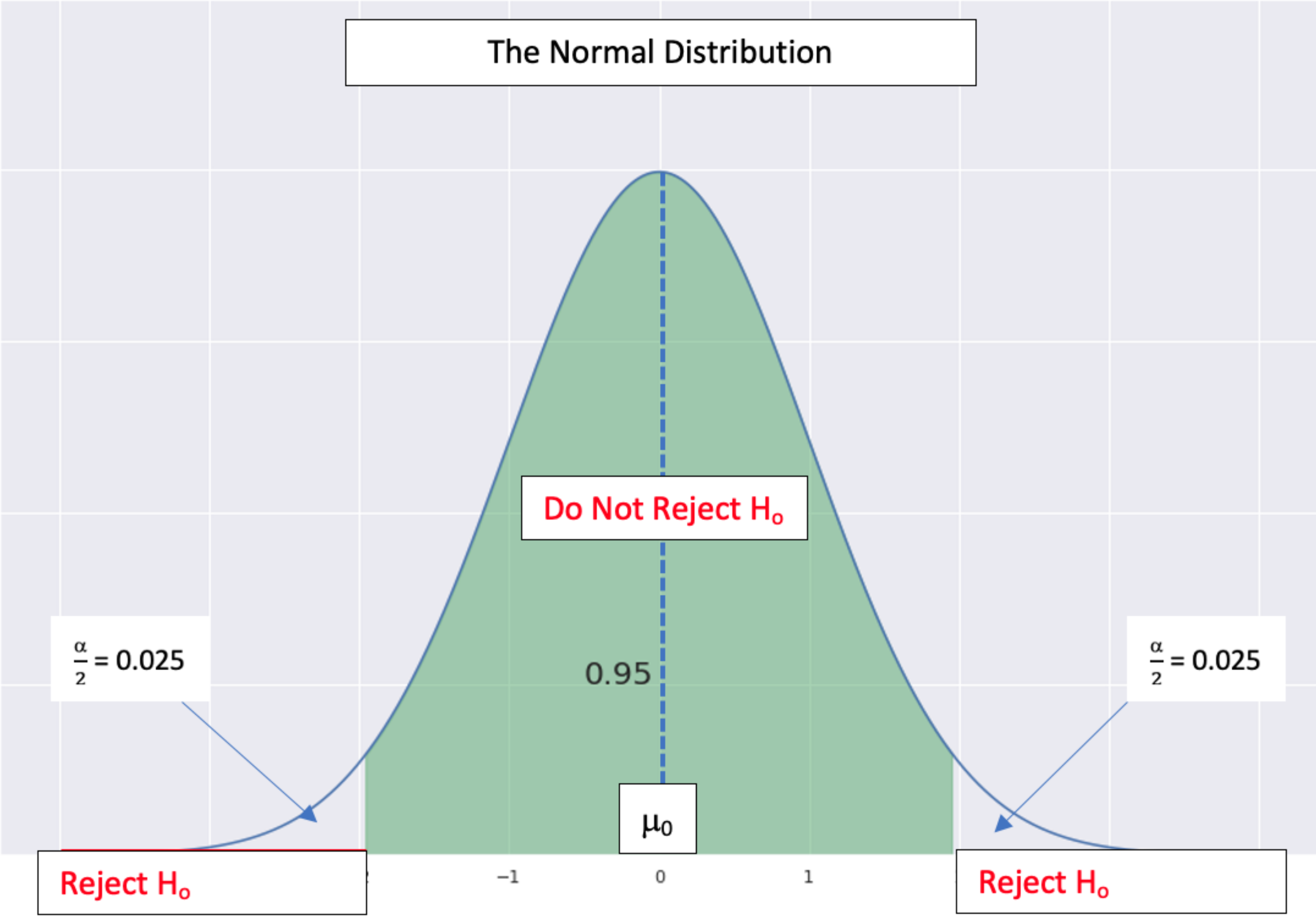
First, we will prove or disprove with statistical evidence that the BMI of females is different from males

**Step 1:** Choose a sample statistic Let u1: population mean for BMI of males
u2: population mean for BMI of females

**Step 2:** Define null and alternate hypothesis

H0: u1-u2 = 0 (No difference in BMI of male and female)
H1: u1-u2 != 0

**Step 3:* *Set the decision criteria




## Type of tests

A t-test is used for testing the mean of one population against a standard or comparing the means of two populations if you do not know standard deviation of the the population and when you have a limited sample ($n < 30$). If you know the standard deviation of the populations , you may use a z-test.

A z-test is used for testing the mean of a population versus a standard, or comparing the means of two populations, with large ($n \geq 30$) samples, whether you know the population standard deviation or not. It is also used for testing the proportion of some characteristic versus a standard proportion, or comparing the proportions of two populations.

An f-test is used to compare variances between 2 populations. The samples can be any size. It is the basis of ANOVA.

chi-squared test is used to determine whether there is a statistically significant difference between the expected and the observed frequencies in one or more categories of a contingency table. A contingency table is a tabular representation of categorical data. It shows the frequency distribution of the variables.

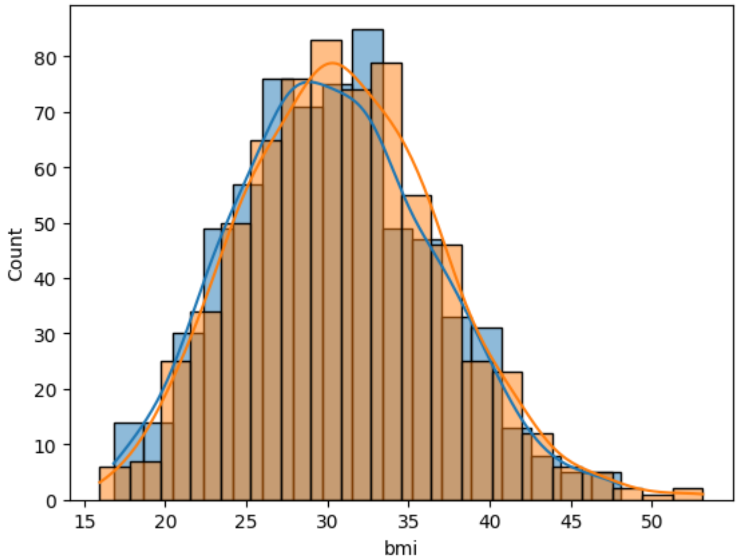
## Step 4: Evaluate and interpret the result

```
female = data.loc[data.sex=='female']
male = data.loc[data.sex=='male']


f_bmi = female.bmi
m_bmi = male.bmi


# Plotting distribution of 'bmi' values for females and males
sns.histplot(f_bmi, kde=True)
sns.histplot(m_bmi, kde=True)
```

```
<Axes: xlabel='bmi', ylabel='Count'>
```




We can see the two distribution are very similar

```
female.bmi.mean()
```

```
30.37774924471299
```

```
male.bmi.mean()
```

```
30.943128698224854
```

Calculating t-value and p-value

```
alpha=0.05
t_value1, p_value1 = stats.ttest_ind(m_bmi, f_bmi)
print(t_value1, p_value1)
```

```
1.696752635752224 0.08997637178984932
```

```
if p_value1 < alpha:
    print('Reject null hypothesis that there is no difference between bmi of femals and males')
else:
    print('Fail to reject null hypothesis')
```

```
Fail to reject null hypothesis
```

Start coding or generate with AI.

## Prove that medical claims made by the people who smoke are greater than those who don't

```
smoker = data.loc[data.smoker=='yes']
smoker_char = smoker.charges
smoker_mean = smoker_char.mean()
smoker_mean
```

```
32050.23183153284
```

```
nonsmoker = data.loc[data.smoker=='no']
nonsmoker_char = nonsmoker.charges
nonsmoker_mean = nonsmoker_char.mean()
nonsmoker_mean
```

```
8434.268297856204
```

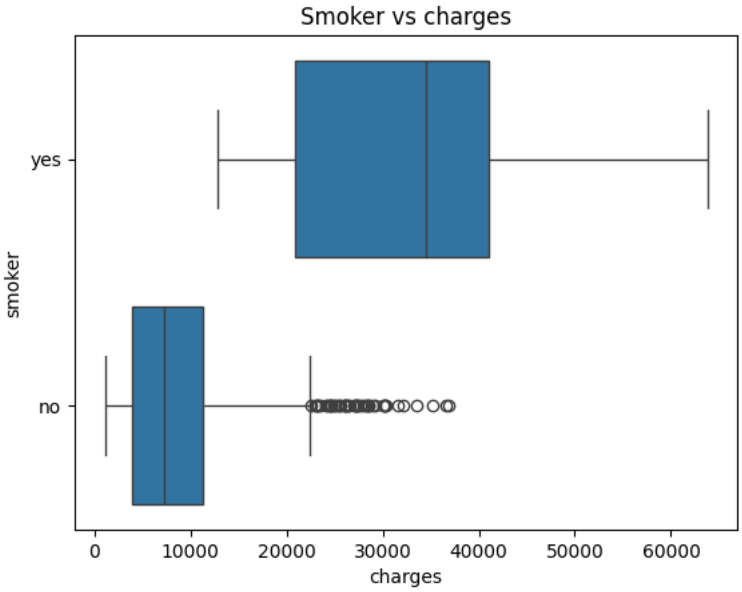
Defining null and alternate hypothesis

H0: u1 <= u2 (Average charges of smoker is less than or equal to non smoker)

H1: u1 > u2 (Average charges of smoker is greater)

```
sns.boxplot(x=data.charges, y=data.smoker, data=data).set(title='Smoker vs charges')
```

```
[Text(0.5, 1.0, 'Smoker vs charges')]
```




```
alpha=0.05
t_val2, p_value2 = stats.ttest_ind(smoker_char, nonsmoker_char)
p_value_onetail = p_value2/2
print(t_val2, p_value_onetail, p_value2)
```

```
46.66492117272371 4.135717921089551e-283 8.271435842179102e-283
```

```
if p_value2 < alpha:
    print('Reject null hypothesis that the charges for smoker are less than or equal to nonsmoker')
else:
    print('Fail to reject null hypothesis')
```

```
Reject null hypothesis that the charges for smoker are less than or equal to nonsmoker
```

## Determine if the proportion of smokers is significantly different accross the different regions

H0: Smokers proportions are not significantly different accross different regions

H1: Smokers proportions are different accross different regions

```
# Here we are comparing two different cateogrical variables. For this type of analysis we will perform chi-square test
contingency = pd.crosstab(data.smoker, data.region)
contingency
```

| region | northeast | northwest | southeast | southwest |
|---|---|---|---|---|
| smoker | | | | |
| no | 257 | 267 | 273 | 267 |
| yes | 67 | 58 | 91 | 58 |

Next steps: Generate code with contingency View recommended plots

```
contingency.plot(kind='bar')
```

```
<Axes: xlabel='smoker'>
```