# Python for Data 24: Hypothesis Testing

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Point estimates and confidence intervals are basic inference tools that act as the foundation for another inference technique: statistical hypothesis testing. Statistical hypothesis testing is a framework for determining whether observed data deviates from what is expected. Python's scipy.stats library contains an array of functions that make it easy to carry out hypothesis tests.

## Hypothesis Testing Basics

Statistical hypothesis tests are based a statement called the null hypothesis that assumes nothing interesting is going on between whatever variables you are testing. The exact form of the null hypothesis varies from one type test to another: if you are testing whether groups differ, the null hypothesis states that the groups are the same. For instance, if you wanted to test whether the average age of voters in your home state differs from the national average, the null hypothesis would be that there is no difference between the average ages.

The purpose of a hypothesis test is to determine whether the null hypothesis is likely to be true given sample data. If there is little evidence against the null hypothesis given the data, you accept the null hypothesis. If the null hypothesis is unlikely given the data, you might reject the null in favor of the alternative hypothesis: that something interesting is going on. The exact form of the alternative hypothesis will depend on the specific test you are carrying out. Continuing with the example above, the alternative hypothesis would be that the average age of voters in your state does in fact differ from the national average.

Once you have the null and alternative hypothesis in hand, you choose a significance level (often denoted by the Greek letter $\alpha$.). The significance level is a probability threshold that determines when you reject the null hypothesis. After carrying out a test, if the probability of getting a result as extreme as the one you observe due to chance is lower than the significance level, you reject the null hypothesis in favor of the alternative. This probability of seeing a result as extreme or more extreme than the one observed is known as the p-value.

The T-test is a statistical test used to determine whether a numeric data sample of differs significantly from the population or whether two samples differ from one another.

## One-Sample T-Test

A one-sample t-test checks whether a sample mean differs from the population mean. Let's create some dummy age data for the population of voters in the entire country and a

sample of voters in Minnesota and test the whether the average age of voters Minnesota differs from the population:

```
%matplotlib inline

import numpy as np
import pandas as pd
import scipy.stats as stats
import matplotlib.pyplot as plt
import math

np.random.seed(6)

population_ages1 = stats.poisson.rvs(loc=18, mu=35, size=150000)
population_ages2 = stats.poisson.rvs(loc=18, mu=10, size=100000)
population_ages = np.concatenate((population_ages1, population_ages2))

minnesota_ages1 = stats.poisson.rvs(loc=18, mu=30, size=30)
minnesota_ages2 = stats.poisson.rvs(loc=18, mu=10, size=20)
minnesota_ages = np.concatenate((minnesota_ages1, minnesota_ages2))

print( population_ages.mean() )
print( minnesota_ages.mean() )
```

```
43.000112
39.26
```

Notice that we used a slightly different combination of distributions to generate the sample data for Minnesota, so we know that the two means are different. Let's conduct a t-test at a 95% confidence level and see if it correctly rejects the null hypothesis that the sample comes from the same distribution as the population. To conduct a one sample t-test, we can the stats.ttest_1samp() function:

```
stats.ttest_1samp(a = minnesota_ages,                # Sample data
                  popmean = population_ages.mean())  # Pop mean
```

```
Ttest_1sampResult(statistic=-2.5742714883655027,
pvalue=0.013118685425061678)
```

The test result shows the test statistic "t" is equal to -2.574. This test statistic tells us how much the sample mean deviates from the null hypothesis. If the t-statistic lies outside the quantiles of the t-distribution corresponding to our confidence level and degrees of freedom, we reject the null hypothesis. We can check the quantiles with stats.t.ppf():

```
stats.t.ppf(q=0.025,  # Quantile to check
            df=49)  # Degrees of freedom
```

```
-2.0095752344892093
```

```
stats.t.ppf(q=0.975,  # Quantile to check
            df=49)  # Degrees of freedom
```

```
2.009575234489209
```

We can calculate the chances of seeing a result as extreme as the one we observed (known as the p-value) by passing the t-statistic in as the quantile to the stats.t.cdf() function:

```
stats.t.cdf(x= -2.5742,      # T-test statistic
               df= 49) * 2   # Multiply by two for two tailed test *
```

```
0.013121066545690117
```

*Note: The alternative hypothesis we are checking is whether the sample mean differs (is not equal to) the population mean. Since the sample could differ in either the positive or negative direction we multiply the by two.*

Notice this value is the same as the p-value listed in the original t-test output. A p-value of 0.01311 means we'd expect to see data as extreme as our sample due to chance about 1.3% of the time if the null hypothesis was true. In this case, the p-value is lower than our significance level α (equal to 1-conf.level or 0.05) so we should reject the null hypothesis. If we were to construct a 95% confidence interval for the sample it would not capture population mean of 43:

```
sigma = minnesota_ages.std()/math.sqrt(50)  # Sample stdev/sample size

stats.t.interval(0.95,                      # Confidence level
                 df = 49,                   # Degrees of freedom
                 loc = minnesota_ages.mean(), # Sample mean
                 scale= sigma)              # Standard dev estimate
```

```
(36.369669080722176, 42.15033091927782)
```

On the other hand, since there is a 1.3% chance of seeing a result this extreme due to chance, it is not significant at the 99% confidence level. This means if we were to construct a 99% confidence interval, it would capture the population mean:

```
stats.t.interval(alpha = 0.99,              # Confidence level
                 df = 49,                   # Degrees of freedom
                 loc = minnesota_ages.mean(), # Sample mean
                 scale= sigma)              # Standard dev estimate
```

```
(35.40547994092107, 43.11452005907893)
```

With a higher confidence level, we construct a wider confidence interval and increase the chances that it captures to true mean, thus making it less likely that we'll reject the null hypothesis. In this case, the p-value of 0.013 is greater than our significance level of 0.01 and we fail to reject the null hypothesis.

## Two-Sample T-Test

A two-sample t-test investigates whether the means of two independent data samples differ from one another. In a two-sample test, the null hypothesis is that the means of both

groups are the same. Unlike the one sample-test where we test against a known population parameter, the two sample test only involves sample means. You can conduct a two-sample t-test by passing with the stats.ttest_ind() function. Let's generate a sample of voter age data for Wisconsin and test it against the sample we made earlier:

```
np.random.seed(12)
wisconsin_ages1 = stats.poisson.rvs(loc=18, mu=33, size=30)
wisconsin_ages2 = stats.poisson.rvs(loc=18, mu=13, size=20)
wisconsin_ages = np.concatenate((wisconsin_ages1, wisconsin_ages2))

print( wisconsin_ages.mean() )
```

```
42.8
```

```
stats.ttest_ind(a= minnesota_ages,
                b= wisconsin_ages,
                equal_var=False)    # Assume samples have equal
variance?
```

```
Ttest_indResult(statistic=-1.7083870793286842,
pvalue=0.09073104343957748)
```

The test yields a p-value of 0.0907, which means there is a 9% chance we'd see sample data this far apart if the two groups tested are actually identical. If we were using a 95% confidence level we would fail to reject the null hypothesis, since the p-value is greater than the corresponding significance level of 5%.

## Paired T-Test

The basic two sample t-test is designed for testing differences between independent groups. In some cases, you might be interested in testing differences between samples of the same group at different points in time. For instance, a hospital might want to test whether a weight-loss drug works by checking the weights of the same group patients before and after treatment. A paired t-test lets you check whether the means of samples from the same group differ.

We can conduct a paired t-test using the scipy function stats.ttest_rel(). Let's generate some dummy patient weight data and do a paired t-test:

```
np.random.seed(11)

before= stats.norm.rvs(scale=30, loc=250, size=100)

after = before + stats.norm.rvs(scale=5, loc=-1.25, size=100)

weight_df = pd.DataFrame({"weight_before":before,
                          "weight_after":after,
                          "weight_change":after-before})
```

```
weight_df.describe()              # Check a summary of the data
```

```
       weight_before  weight_after  weight_change
count     100.000000    100.000000     100.000000
mean      250.345546    249.115171      -1.230375
std        28.132539     28.422183       4.783696
min       170.400443    165.913930     -11.495286
25%       230.421042    229.148236      -4.046211
50%       250.830805    251.134089      -1.413463
75%       270.637145    268.927258       1.738673
max       314.700233    316.720357       9.759282
```

The summary shows that patients lost about 1.23 pounds on average after treatment. Let's conduct a paired t-test to see whether this difference is significant at a 95% confidence level:

```
stats.ttest_rel(a = before,
                b = after)
```

```
Ttest_relResult(statistic=2.5720175998568284,
pvalue=0.011596444318439857)
```

## Type I and Type II Error

The result of a statistical hypothesis test and the corresponding decision of whether to reject or accept the null hypothesis is not infallible. A test provides evidence for or against the null hypothesis and then you decide whether to accept or reject it based on that evidence, but the evidence may lack the strength to arrive at the correct conclusion. Incorrect conclusions made from hypothesis tests fall in one of two categories: type I error and type II error.

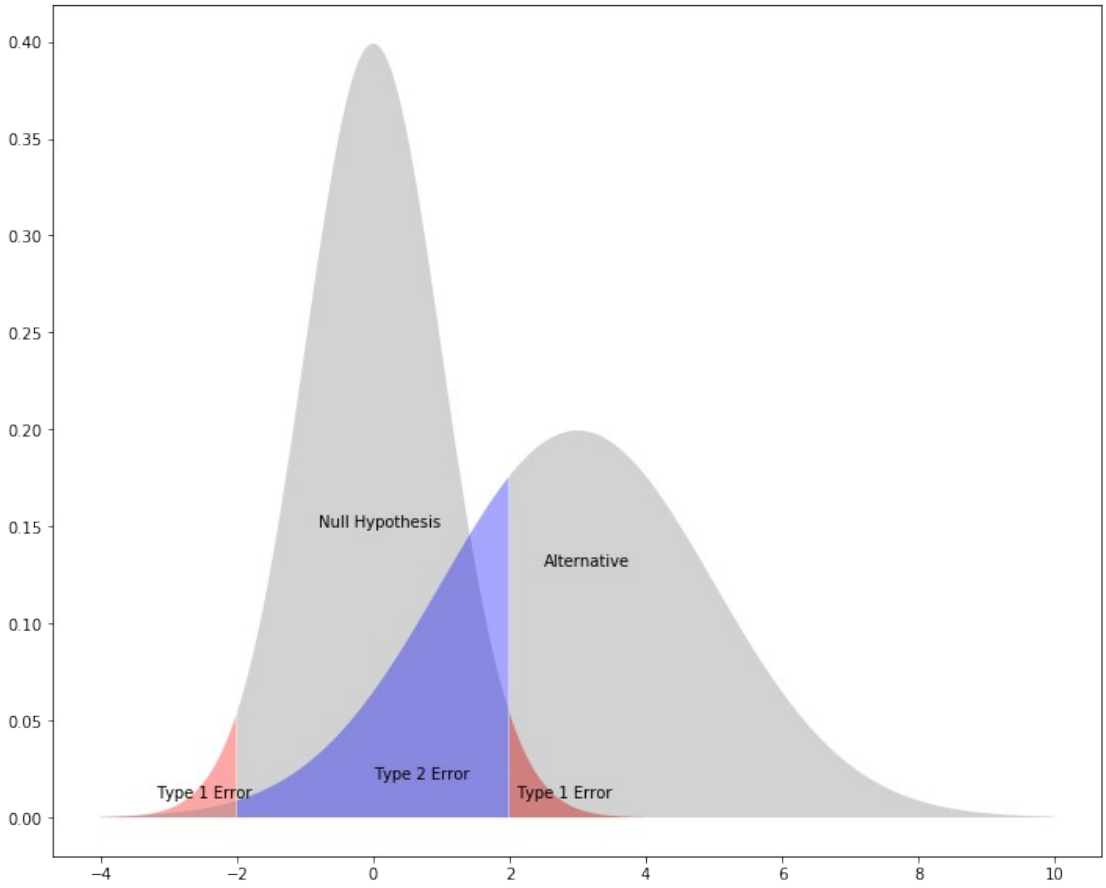
Type I error describes a situation where you reject the null hypothesis when it is actually true. This type of error is also known as a "false positive" or "false hit". The type 1 error rate is equal to the significance level $\alpha$, so setting a higher confidence level (and therefore lower alpha) reduces the chances of getting a false positive.

Type II error describes a situation where you fail to reject the null hypothesis when it is actually false. Type II error is also known as a "false negative" or "miss". The higher your confidence level, the more likely you are to make a type II error.

Let's investigate these errors with a plot:

```
plt.figure(figsize=(12,10))


plt.fill_between(x=np.arange(-4,-2,0.01),
                 y1= stats.norm.pdf(np.arange(-4,-2,0.01)) ,
                 facecolor='red',
```

```
                  alpha=0.35)

plt.fill_between(x=np.arange(-2,2,0.01),
                  y1= stats.norm.pdf(np.arange(-2,2,0.01)) ,
                  facecolor='grey',
                  alpha=0.35)

plt.fill_between(x=np.arange(2,4,0.01),
                  y1= stats.norm.pdf(np.arange(2,4,0.01)) ,
                  facecolor='red',
                  alpha=0.5)

plt.fill_between(x=np.arange(-4,-2,0.01),
                  y1= stats.norm.pdf(np.arange(-4,-2,0.01),loc=3,
scale=2) ,
                  facecolor='grey',
                  alpha=0.35)

plt.fill_between(x=np.arange(-2,2,0.01),
                  y1= stats.norm.pdf(np.arange(-2,2,0.01),loc=3,
scale=2) ,
                  facecolor='blue',
                  alpha=0.35)

plt.fill_between(x=np.arange(2,10,0.01),
                  y1= stats.norm.pdf(np.arange(2,10,0.01),loc=3,
scale=2),
                  facecolor='grey',
                  alpha=0.35)

plt.text(x=-0.8, y=0.15, s= "Null Hypothesis")
plt.text(x=2.5, y=0.13, s= "Alternative")
plt.text(x=2.1, y=0.01, s= "Type 1 Error")
plt.text(x=-3.2, y=0.01, s= "Type 1 Error")
plt.text(x=0, y=0.02, s= "Type 2 Error");
```




In the plot above, the red areas indicate type I errors assuming the alternative hypothesis is not different from the null for a two-sided test with a 95% confidence level.

The blue area represents type II errors that occur when the alternative hypothesis is different from the null, as shown by the distribution on the right. Note that the Type II error rate is the area under the alternative distribution within the quantiles determined by the null distribution and the confidence level. We can calculate the type II error rate for the distributions above as follows:

```
lower_quantile = stats.norm.ppf(0.025)  # Lower cutoff value
upper_quantile = stats.norm.ppf(0.975)  # Upper cutoff value

# Area under alternative, to the left the lower cutoff value
low = stats.norm.cdf(lower_quantile,
                     loc=3,
                     scale=2)

# Area under alternative, to the left the upper cutoff value
high = stats.norm.cdf(upper_quantile,
                      loc=3,
                      scale=2)
```

```
# Area under the alternative, between the cutoffs (Type II error)
high-low
```

```
0.294956061112323
```

With the normal distributions above, we'd fail to reject the null hypothesis about 30% of the time because the distributions are close enough together that they have significant overlap.

## Statistical Power

The power of a statistical test is the probability that the test rejects the null hypothesis when the alternative is actually different from the null. In other words, power is the probability that the test detects that there is something interesting going on when there actually *is* something interesting going on. Power is equal to one minus the type II error rate. The power of a statistical test is influenced by:

1. The significance level chosen for the test.
2. The sample size.
3. The effect size of the test.

When choosing a significance level for a test, there is a trade-off between type I and type II error. A low significance level, such as 0.01 makes a test unlikely to have type I errors (false positives), but more likely to have type II errors (false negatives) than a test with larger value of the significance level $\alpha$. A common convention is that a statistical tests should have a power of at least 0.8.

A larger sample size reduces the uncertainty of the point estimate, causing the sample distribution to narrow, resulting in lower type II error rates and increased power.

Effect size is a general term that describes a numeric measure of the size of some phenomenon. There are many different effect size measurements that arise in different contexts. In the context of the T-test, a simple effect size is the difference between the means of the samples. This number can be standardized by dividing by the standard deviation of the population or the pooled standard deviation of the samples. This puts the size of the effect in terms of standard deviations, so a standardized effect size of 0.5 would be interpreted as one sample mean being 0.5 standard deviations from another (in general 0.5 is considered a "large" effect size).

Since statistical power, the significance level, the effect size and the sample size are related, it is possible to calculate any one of them for given values of the other three. This can be an important part of the process of designing a hypothesis test and analyzing results. For instance, if you want to conduct a test with a given significance level (say the standard 0.05) and power (say the standard 0.8) and you are interested in a given effect size (say 0.5 for standardized difference between sample means), you could use that information to determine how large of a sample size you need.

In python, the statsmodels library contains functions to solve for any one parameter of the power of T-tests. Use statsmodels.stats.power.tt_solve_power for one sample t-tests and statsmodels.stats.power.tt_ind_solve_power for a two sample t-test. Let's check the sample size we should use need to use given the standard parameter values above for a one sample t-test:

```
from statsmodels.stats.power import tt_solve_power

tt_solve_power(effect_size = 0.5,
               alpha = 0.05,
               power = 0.8)
```

```
33.3671314275208
```

In this case, we would want a sample size of at least 34 to make a study with the desired power and signifiance level capable of detecting a large effect size.

## Wrap Up

The t-test is a powerful tool for investigating the differences between sample and population means. T-tests operate on numeric variables; in the next lesson, we'll discuss statistical tests for categorical variables.

## Next Lesson: Python for Data 25: Chi-Squared Tests

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1) What is Null hypothesis ?

-> In statistics, a null hypothesis is a statement that assumes there is no significant difference between two populations or variables being compared. It is a type of hypothesis that is assumed to be true until there is enough evidence to reject it.

For example, if we are comparing the mean weight of two groups of people, the null hypothesis would state that there is no difference in the mean weight between the two groups. The alternative hypothesis, in contrast, would be that there is a significant difference in the mean weight between the two groups.

The null hypothesis is typically tested using statistical hypothesis testing, which involves calculating a test statistic and comparing it to a critical value or p-value. If the test statistic falls within the rejection region (i.e., has a low p-value), the null hypothesis is rejected, and the alternative hypothesis is accepted.

It is important to note that while the null hypothesis is assumed to be true until proven otherwise, it does not necessarily mean that it is always true. Instead, it is a way of setting a baseline assumption for statistical testing and allows us to make conclusions based on evidence and data.

2) What is alternate hypothesis?

-> In statistics, an alternative hypothesis (also known as research hypothesis) is a statement that contradicts the null hypothesis. It is a claim that suggests that there is a significant difference between two populations or variables being compared.

For example, if we are comparing the mean weight of two groups of people, the alternative hypothesis would state that there is a significant difference in the mean weight between the two groups. The null hypothesis, in contrast, would be that there is no difference in the mean weight between the two groups.

The alternative hypothesis is typically what the researcher is trying to prove or find evidence for. In statistical hypothesis testing, the alternative hypothesis is accepted when the null hypothesis is rejected based on the statistical evidence.

It is important to note that the alternative hypothesis is not always the opposite of the null hypothesis. Instead, it can take various forms depending on the research question and the hypothesis being tested.

3) Define Type 1 and Type 2 errors.

-> In statistical hypothesis testing, there are two types of errors that can occur: type I errors and type II errors.

Type I error, also known as a false positive, occurs when the null hypothesis is rejected even though it is actually true. In other words, type I error occurs when we conclude that there is a significant effect or difference between two groups, when in fact there is no such effect or difference. This error is denoted by the symbol alpha ($\alpha$) and is typically set at a predetermined level (e.g., 0.05 or 0.01) by the researcher.

Type II error, also known as a false negative, occurs when the null hypothesis is not rejected even though it is actually false. In other words, type II error occurs when we fail to detect a significant effect or difference between two groups, when in fact there is such an effect or difference. This error is denoted by the symbol beta ($\beta$) and is dependent on the sample size, the effect size, and the level of alpha.

Both type I and type II errors are undesirable in statistical hypothesis testing, and researchers must balance between the two errors based on the research question and the consequences of each type of error. For example, in medical testing, type I errors (false positives) are often considered more serious than type II errors (false negatives) as they can result in unnecessary treatments and interventions.

# Python for Data 26: ANOVA

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In lesson 24 we introduced the t-test for checking whether the means of two groups differ. The t-test works well when dealing with two groups, but sometimes we want to compare more than two groups at the same time. For example, if we wanted to test whether voter age differs based on some categorical variable like race, we have to compare the means of each level or group the variable. We could carry out a separate t-test for each pair of groups, but when you conduct many tests you increase the chances of false positives. The analysis of variance or ANOVA is a statistical inference test that lets you compare multiple groups at the same time.

## One-Way ANOVA

The one-way ANOVA tests whether the mean of some numeric variable differs across the levels of one categorical variable. It essentially answers the question: do any of the group means differ from one another? We won't get into the details of carrying out an ANOVA by hand as it involves more calculations than the t-test, but the process is similar: you go through several calculations to arrive at a test statistic and then you compare the test statistic to a critical value based on a probability distribution. In the case of the ANOVA, you use the "f-distribution".

The scipy library has a function for carrying out one-way ANOVA tests called scipy.stats.f_oneway(). Let's generate some fake voter age and demographic data and use the ANOVA to compare average ages across the groups:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import scipy.stats as stats

np.random.seed(12)

races =   ["asian","black","hispanic","other","white"]

# Generate random data
voter_race = np.random.choice(a= races,
                              p = [0.05, 0.15 ,0.25, 0.05, 0.5],
                              size=1000)

voter_age = stats.poisson.rvs(loc=18,
                              mu=30,
                              size=1000)

# Group age data by race
```

```
voter_frame = pd.DataFrame({"race":voter_race,"age":voter_age})
groups = voter_frame.groupby("race").groups

# Etract individual groups
asian = voter_age[groups["asian"]]
black = voter_age[groups["black"]]
hispanic = voter_age[groups["hispanic"]]
other = voter_age[groups["other"]]
white = voter_age[groups["white"]]

# Perform the ANOVA
stats.f_oneway(asian, black, hispanic, other, white)
```

The test output yields an F-statistic of 1.774 and a p-value of 0.1317, indicating that there is no significant difference between the means of each group.

Another way to carry out an ANOVA test is to use the statsmodels library, which allows you to specify a model with a formula syntax that mirrors that used by the R programming language. R users may find this method more familiar:

```
import statsmodels.api as sm
from statsmodels.formula.api import ols

model = ols('age ~ race',                  # Model formula
            data = voter_frame).fit()

anova_result = sm.stats.anova_lm(model, typ=2)
print (anova_result)
```

As you can see, the statsmodels method produced the same F statistic and P-value (listed as PR(<F)) as the stats.f_oneway method.

Now let's make new age data where the group means do differ and run a second ANOVA:

```
np.random.seed(12)

# Generate random data
voter_race = np.random.choice(a= races,
                              p = [0.05, 0.15 ,0.25, 0.05, 0.5],
                              size=1000)

# Use a different distribution for white ages
white_ages = stats.poisson.rvs(loc=18,
                               mu=32,
                               size=1000)

voter_age = stats.poisson.rvs(loc=18,
                              mu=30,
                              size=1000)
```

```
voter_age = np.where(voter_race=="white", white_ages, voter_age)

# Group age data by race
voter_frame = pd.DataFrame({"race":voter_race,"age":voter_age})
groups = voter_frame.groupby("race").groups

# Extract individual groups
asian = voter_age[groups["asian"]]
black = voter_age[groups["black"]]
hispanic = voter_age[groups["hispanic"]]
other = voter_age[groups["other"]]
white = voter_age[groups["white"]]

# Perform the ANOVA
stats.f_oneway(asian, black, hispanic, other, white)

# Alternate method
model = ols('age ~ race',                 # Model formula
            data = voter_frame).fit()

anova_result = sm.stats.anova_lm(model, typ=2)
print (anova_result)
```

The test result suggests the groups don't have the same sample means in this case, since the p-value is significant at a 99% confidence level. We know that it is the white voters who differ because we set it up that way in the code, but when testing real data, you may not know which group(s) caused the test to throw a positive result. To check which groups differ after getting a positive ANOVA result, you can perform a follow up test or "post-hoc test".

One post-hoc test is to perform a separate t-test for each pair of groups. You can perform a t-test between all pairs using by running each pair through the stats.ttest_ind() we covered in the lesson on t-tests:

```
# Get all race pairs
race_pairs = []

for race1 in range(4):
    for race2  in range(race1+1,5):
        race_pairs.append((races[race1], races[race2]))

# Conduct t-test on each pair
for race1, race2 in race_pairs:
    print(race1, race2)
    print(stats.ttest_ind(voter_age[groups[race1]],
                          voter_age[groups[race2]]))
```

The p-values for each pairwise t-test suggest mean of white voters is likely different from the other groups, since the p-values for each t-test involving the white group is below 0.05. Using unadjusted pairwise t-tests can overestimate significance, however, because the

more comparisons you make, the more likely you are to come across an unlikely result due to chance. We can adjust for this multiple comparison problem by dividing the statistical significance level by the number of comparisons made. In this case, if we were looking for a significance level of 5%, we'd be looking for p-values of 0.05/10 = 0.005 or less. This simple adjustment for multiple comparisons is known as the Bonferroni correction.

The Bonferroni correction is a conservative approach to account for the multiple comparisons problem that may end up rejecting results that are actually significant. Another common post hoc-test is Tukey's test. You can carry out Tukey's test using the pairwise_tukeyhsd() function in the statsmodels.stats.multicomp library:

```
from statsmodels.stats.multicomp import pairwise_tukeyhsd

tukey = pairwise_tukeyhsd(endog=voter_age,     # Data
                          groups=voter_race,   # Groups
                          alpha=0.05)          # Significance level

tukey.plot_simultaneous()    # Plot group confidence intervals
plt.vlines(x=49.57,ymin=-0.5,ymax=4.5, color="red")

tukey.summary()              # See test summary
```

The output of the Tukey test shows the average difference, a confidence interval as well as whether you should reject the null hypothesis for each pair of groups at the given significance level. In this case, the test suggests we reject the null hypothesis for 3 pairs, with each pair including the "white" category. This suggests the white group is likely different from the others. The 95% confidence interval plot reinforces the results visually: only 1 other group's confidence interval overlaps the white group's confidence interval.

## Wrap Up

The ANOVA test lets us check whether a numeric response variable varies according to the levels of a categorical variable. Python's scipy library makes it easy to perform an ANOVA without diving too deep into the details of the procedure.

Next time, we'll move on from statistical inference to the final topic of this guide: predictive modeling.

## Next Lesson: Python for Data 27: Linear Regression

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4) When to go for Anova instead of t-test or chi square test ?

-> ANOVA (Analysis of Variance) is a statistical test used to determine if there are any significant differences between the means of two or more groups. T-tests and Chi-square

tests are also used to compare means and frequencies, respectively, but ANOVA is generally preferred over these tests in the following situations:

Multiple groups: If you have more than two groups to compare, ANOVA is the appropriate choice. T-tests can only compare two groups at a time, and performing multiple t-tests can increase the likelihood of type I errors.

Continuous data: ANOVA is used when the outcome variable is continuous, while t-tests are used when comparing the means of two groups with continuous data.

Equal variance: When comparing means of two groups, t-tests assume that the variances are equal between the two groups. If the variances are not equal, ANOVA should be used instead.

Categorical independent variables: When the independent variable is categorical with more than two categories, chi-square tests can be used to test for differences in frequency counts. However, if the independent variable has more than two categories and the dependent variable is continuous, ANOVA is appropriate.

In summary, ANOVA is used when there are more than two groups to compare, the outcome variable is continuous, and the independent variable is either continuous or categorical with more than two categories.

5) What role does Anova play in a ML Project ppipeline ?

-> ANOVA (Analysis of Variance) can play a role in a machine learning project pipeline in the following ways:

Feature selection: ANOVA can be used to determine which features are most important in predicting the target variable. By measuring the variation between groups, ANOVA can identify which features have the greatest impact on the outcome variable.

Model selection: ANOVA can also be used to compare the performance of different models. By comparing the variation in performance between models, ANOVA can identify which models are better at predicting the target variable.

Hyperparameter tuning: ANOVA can be used to optimize hyperparameters of machine learning models. By measuring the variation in performance across different hyperparameter settings, ANOVA can identify the optimal combination of hyperparameters that produces the best performance.

Overall, ANOVA can help in optimizing the performance of machine learning models by identifying important features, selecting the best model, and tuning hyperparameters.