Experimental Design in Python

Lawal's Note

2025-03-02

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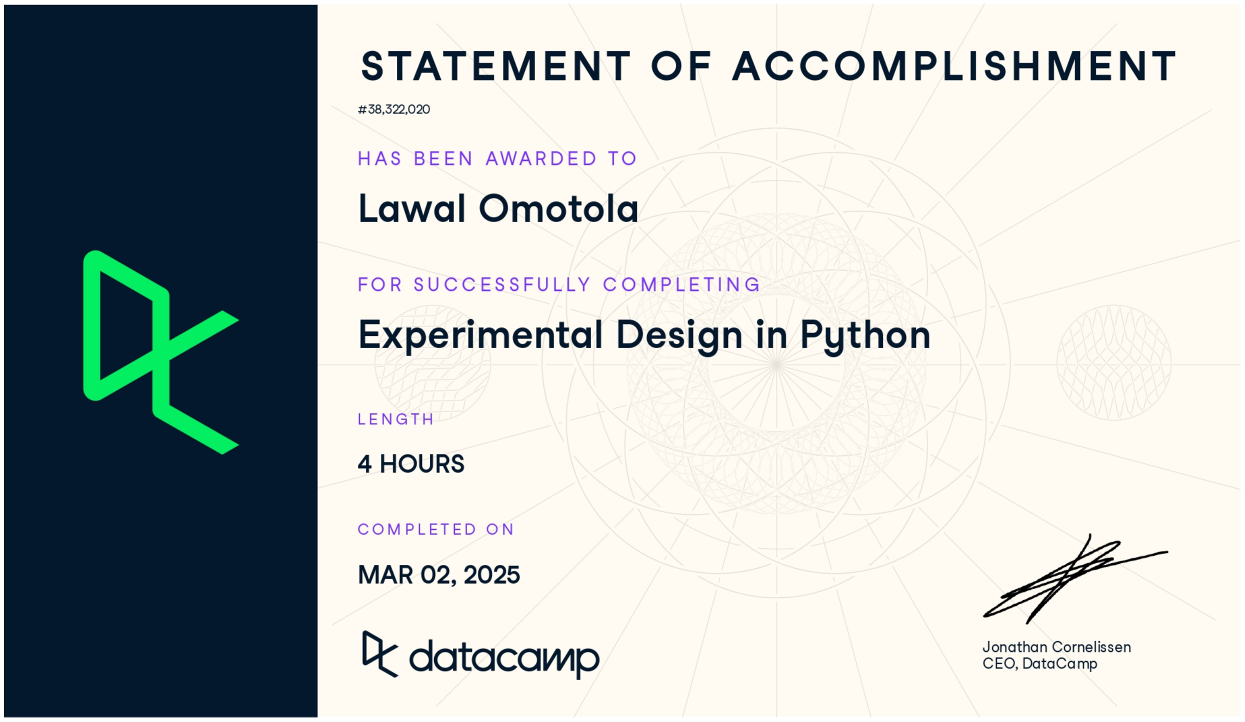

STATEMENT OF ACCOMPLISHMENT

#38,322,020

HAS BEEN AWARDED TO

Lawal Omotola

FOR SUCCESSFULLY COMPLETING

Experimental Design in Python

LENGTH

4 HOURS

COMPLETED ON

MAR 02, 2025

datacamp

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CEO, DataCamp

1 Experimental Design in Python

1.1 Chapter 1: Experimental Design Preliminaries

Building knowledge in experimental design allows you to test hypotheses with best-practice analytical tools and quantify the risk of your work. You'll begin your journey by setting the foundations of what experimental design is and different experimental design setups such as blocking and stratification. You'll then learn and apply visual and analytical tests for normality in experimental data.

1.1.1 Chapter 1.1: Setting up experiments

Hi! Welcome to this course on experimental design in Python.

Experimental Design definition

Experimental design is the process in which we carry out research in an objective and controlled fashion. The purpose of this is to ensure we can make specific conclusions in reference to a hypothesis we have.

1 https://www.sciencedirect.com/topics/earth-and-planetary-sciences/experimental-design

Forming robust statements

Because we use objective tools, we need to use quantified language. Instead of using words like 'probably', 'likely', and 'small' when noting our conclusions, we should use precise and quantified language. This often takes the form of noting the percentage risk on a Type I error in the conclusion. Recall that Type I errors occur when we incorrectly reject the null hypothesis when it is actually true. In this course, you'll learn to design experiments and conduct statistical analyses such that you begin making precise statements about observed results and take informed actions as a result.

Why experimental design?

Experimental design is useful in many fields. Naturally, it is used in academia such as in medical research. It is also useful in many corporate contexts such as marketing and product analytics, which conduct lots of A/B tests. It is also used in agriculture and increasingly in government policy through the use of behavioral psychology experiments.

Some terminology...

Before we begin our first topic, let's define some important terminology. Subjects are what we are experimenting on. It could be people, employees, or users on a website.

A treatment is some change given to one group of subjects. We could call that group the treatment group. The control group is not given any change. This could be a placebo group, for example.

Assigning subjects to groups

An important concept in experimental design is how to assign subjects to test groups. There are two ways we could do this. We could just split the dataset non-randomly into chunks and assign each chunk to a group. Or we could use random assignment to sample into our desired groups. Let's look at each option using a DataFrame of 200 subjects' heights where we want to split into two groups of 100 each.

Non-random assignment

Let's try non-random assignment first. We can use `.iloc[]` to slice the first 100 rows from heights and assign to group1 and the next 100 rows into group2. We can use pandas' describe method to check descriptive statistics of our groups. Concatenating the two results with `pd.concat()` and `axis=1` will allow for easier comparison. These groups appear very different! Looking at the mean row, we can see there's a 9cm difference. Because of the differences in these groups, it will be harder to confidently determine if any changes are due to the treatment intervention.

Random assignment

Let's now try random assignment. We can use pandas' sample method to create a sample of size n, or use the frac argument and specify a proportion of the dataset, between 0 and 1, to sample. We want two equally-sized groups, so we specify `frac=0.5`. Using `n=100` would also work here. We also set the replace argument to False, so samples aren't selected twice. The random_state argument allows the splits to be consistently reproduced. group2 can be made by dropping the ids in group1 from the overall DataFrame. Using the same comparison method we see much closer means.

Assignment summary

This demonstrates the importance of randomly assigning subjects to groups. It means we can attribute observed changes to treatment interventions rather than natural differences between the group. We can use pandas' sample method to select randomly from a DataFrame, and then use pandas' describe method to check differences in group assignment.

1.1.2 Exercise 1.1.1

Non-random assignment of subjects

An agricultural firm is conducting an experiment to measure how feeding sheep different types of grass affects their weight. They have asked for your help to properly set up the experiment. One of their managers has said you can perform the subject assignment by taking the top 250 rows from the DataFrame and that should be fine.

Your task is to use your analytical skills to demonstrate why this might not be a good idea. Assign the subjects to two groups using non-random assignment (the first 250 rows) and observe the differences in descriptive statistics.

You have received the DataFrame, `weights` which has a column containing the `weight` of the sheep and a unique `id` column.

1.1.3 Instructions

- Use DataFrame slicing to put the first 250 rows of `weights` into `group1_non_rand` and the remaining into `group2_non_rand`.
- Generate descriptive statistics of the two groups and concatenate them into a single DataFrame.
- Print out to observe the differences.

Note: Due to non-availability of weights DataFrame, I had to generates mine myself, the proper code should have been this below.

```
# Non-random assignment
group1_non_rand = weights.iloc[0:250, :]
group2_non_rand = weights.iloc[250:, :]

# Compare descriptive statistics of groups
compare_df_non_rand = pd.concat([group1_non_rand['weight'].describe(), group2_non_rand['weight'].
compare_df_non_rand.columns = ['group1', 'group2']

# Print to assess
print(compare_df_non_rand)
```

```python
import pandas as pd
import numpy as np

# Generate 250 random weights for group1 between 39.07 and 65.10
weights_group1 = np.random.uniform(39.07, 65.10, 250)

# Generate 250 random weights for group2 between 65.10 and 95.82
```

```
weights_group2 = np.random.uniform(65.10, 95.82, 250)

# Create DataFrames for each group
group1_non_rand = pd.DataFrame({
    'id': range(1, 251),
    'weight': weights_group1
})

group2_non_rand = pd.DataFrame({
    'id': range(251, 501),
    'weight': weights_group2
})

# Combine the two groups into one DataFrame
weights = pd.concat([group1_non_rand, group2_non_rand]).reset_index(drop=True)

# Compare descriptive statistics of groups
compare_df_non_rand = pd.concat([group1_non_rand['weight'].describe(), group2_non_rand['weight'].
compare_df_non_rand.columns = ['group1', 'group2']

# Print to assess
print(compare_df_non_rand)
```

```
           group1      group2
count  250.000000  250.000000
mean    52.572795   80.144596
std      7.656688    9.088120
min     39.399457   65.198783
25%     46.407699   71.750618
50%     53.064179   80.017700
75%     59.125692   87.407890
max     64.861309   95.772082
```

Note

Wow! Those two datasets have a much greater difference in means. It may be that the dataset was sorted before you received it. Presenting these results to the firm will help them understand best-practice group assignment. Hopefully you can now work with them to set up the experiment properly.

1.1.4 Exercise 1.1.2

Random assignment of subjects

Having built trust from your last work with the agricultural firm, you have been given the task of properly setting up the experiment.

Use your knowledge of best practice experimental design set up to assign the sheep to two even groups of 250 each.

1.1.5 Instructions

- Randomly select 250 subjects from the `weights` DataFrame into a new DataFrame `group1` without replacement.
- Put the remaining 250 subjects into `group2`.
- Concatenate the descriptive statistics of your two newly created DataFrames.

```python
import pandas as pd
import numpy as np

# Generate 250 random weights for group1 between 39.07 and 65.10
weights_group1 = np.random.uniform(39.07, 65.10, 250)

# Generate 250 random weights for group2 between 65.10 and 95.82
weights_group2 = np.random.uniform(65.10, 95.82, 250)

# Create DataFrames for each group
group1_rand = pd.DataFrame({
    'id': range(1, 251),
    'weight': weights_group1
})

group2_rand = pd.DataFrame({
    'id': range(251, 501),
    'weight': weights_group2
})

# Combine the two groups into one DataFrame
weights = pd.concat([group1_rand, group2_rand]).reset_index(drop=True)

# Randomly assign half
group1_random = weights.sample(frac=0.5, random_state=42, replace=False)

# Create second assignment
group2_random = weights.drop(group1_random.index)

# Compare assignments
compare_df_random = pd.concat([group1_random['weight'].describe(), group2_random['weight'].descri
compare_df_random.columns = ['group1', 'group2']
print(compare_df_random)
```

```
           group1      group2
count  250.000000  250.000000
mean    65.209091   67.254563
std     16.890399   16.190219
min     39.321838   39.190141
25%     49.092715   53.396443
50%     63.260020   66.777355
75%     79.986397   80.826429
max     95.796744   95.749981
```

Note

While there are some differences in these datasets, you can clearly see the mean of the two sets are very close. This best-practice setup will ensure the experiment is on the right path from the beginning. Let's continue building foundational experimental design skills by learning about experimental design setup.

1.1.6 Chapter 1.2: Experimental data setup

We've seen that randomization is often the best technique for setting up experimental data, but it isn't always.

The problem with randomization

There are several scenarios where pure randomization can lead to undesirable outcomes. Firstly, when it results in uneven numbers of subjects in different groups, often seen more in smaller experiment sizes.

Covariates are variables that potentially affect experiment results but aren't the primary focus. If covariates are highly variable or not equally distributed among groups, randomization might not produce balanced groups. This imbalance can lead to biased results. Overall these make it harder to see an effect from a treatment, as these issues may be driving an observed change.

Block randomization

A solution to our uneven problem is block randomization. This involves splitting into a block of size n first, then randomly splitting. This is what it looks like. Subjects are split into two groups, then randomly assigned to be Treatment (orange) or control (white). This fixes the uneven issue, and the smaller blocks give us more control over the allocation.

Our dataset

Let's give block randomization a go on a dataset of 1000 members from an e-commerce site that contains variables for their average basket size in dollars, the average time spent on the website each day, and whether they are a power user. Power users spend an average of 40+ minutes on the website each day. There are 100 power users in these 1000 subjects.

Block randomization in Python

We can use pandas' sample method to randomly assign subjects into two blocks. A block column has also been added to both DataFrames for convenience. This produces even block sizes, fixing the uneven issue, but let's check for covariates.

Visualizing splits

A nice way of checking for potential covariate issues is with visualizations. We can use seaborn's displot function to produce a kde (or kernal density) plot to visualize the distribution of the basket size, split by whether the user is a power user. There is quite a difference in the group distributions. It seems like the power_user variable could have an effect on basket size. When an effect could be because of a variable rather than the treatment, this is often called confounding. The covariate issue can be solved with stratified randomization.

Stratified randomization

Stratified randomization involves splitting based on a potentially confounding variable first, followed by randomization. This is what it may look like. Firstly, we split into two blocks (sometimes called strata) of power users, in green, and non-power users, in yellow. Then, inside the groups, randomly allocating to treatment or control. This fixes the uneven covariate issue, and can even be done for multiple covariates, but managing more strata does increase complexity.

Our first strata

Let's stratify our power users. We separate them out first and label the block. We then sample half the power users to be in Treatment. The `T_C`Let's stratify our power users. We separate them out first and label the block. We then sample half the power users to be in Treatment. The `T_C` column notes this status. We then place the remaining into control by dropping the subjects in the treatment group. column notes this status. We then place the remaining into control by dropping the subjects in the treatment group.

The second strata

For our other strata, we separate out non-power users first and label the block differently. The rest of the code is the same as before. We allocate half to treatment and control using the same column headers.

Confirming stratification

Let's bring our work together by firstly concatenating the strata and groups. We can confirm our work using groupby and chaining the `.size()` method. This will show the number of power users in each block by their treatment or control status. We can see two blocks: one with all 100 power users and another with the other 900 users, split evenly into treatment and control groups.

1.1.7 Exercise 1.2.1

Blocking experimental data

You are working with a manufacturing firm that wants to conduct some experiments on worker productivity. Their dataset only contains 100 rows, so it's important that experimental groups are balanced.

This sounds like a great opportunity to use your knowledge of blocking to assist them. They have provided a `productivity_subjects` DataFrame. Split the provided dataset into two even groups of 50 entries each.

Instructions

- Randomly select 50 subjects from the `productivity_subjects` DataFrame into a new DataFrame `block_1` without replacement.
- Set a new column, `block` to 1 for the `block_1` DataFrame.
- Assign the remaining subjects to a DataFrame called `block_2` and set the `block` column to 2 for this DataFrame.
- Concatenate the blocks together into a single DataFrame, and print the count of each value in the `block` column to confirm the blocking worked.

```python
import pandas as pd
import numpy as np

# Create DataFrame with 100 rows and subject_id ranging from 1 to 100
productivity_subjects = pd.DataFrame({'subject_id': range(1, 101)})

# Randomly assign half
block_1 = productivity_subjects.sample(frac=0.5, random_state=42, replace=False)

# Set the block column
block_1['block'] = 1

# Create second assignment and label
block_2 = productivity_subjects.drop(block_1.index)
block_2['block'] = 2
```

```
# Concatenate and print
productivity_combined = pd.concat([block_1, block_2], axis=0)
print(productivity_combined['block'].value_counts())
```

```
block
1    50
2    50
Name: count, dtype: int64
```

1.1.8 Exercise 1.2.2

Stratifying an experiment

You are working with a government organization that wants to undertake an experiment around how some particular government policies impact the net wealth of individuals in a number of areas.

They have approached you to help set up the experimental design. They have warned you that there is likely to be a small group of users who already have high net wealth and are concerned that this group might overshadow any experimental outcome observed. You know just what to do!

Use your knowledge of experimental design to undertake block randomization, stratifying by the `high_wealth` column in the provided `wealth_data` DataFrame. There are 2000 rows in the DataFrame with 200 high net wealth subjects (`high_wealth` is 1).

Instructions 1/3

1. Create the first block which contains all the `high_wealth` subjects and set the `Block` column to 1.

- Create two groups from this block randomly assigning the `high_wealth` subjects to the Treatment (T) or control (C) group.

2. Repeat for the second block (all the not `high_wealth` subjects), setting the `Block` column to 2, and perform the group assignment (randomly assigning to Treatment (T) or control (C) group).
3. Concatenate the four groups created into `wealth_data_stratified` in order of creation (strata 1 group 1, strata 1 group 2, etc.)

```
import pandas as pd
import numpy as np

# Set random seed for reproducibility
```

```
np.random.seed(42)

# Number of rows
n_rows = 2000

# Number of high net wealth subjects
n_high_wealth = 200

# Create the 'high_wealth' column
high_wealth = np.zeros(n_rows, dtype=int)
high_wealth[:n_high_wealth] = 1

# Shuffle the 'high_wealth' column
np.random.shuffle(high_wealth)

# Create the DataFrame
wealth_data = pd.DataFrame({'high_wealth': high_wealth})

# Create the first block
strata_1 = wealth_data[wealth_data['high_wealth'] == 1]
strata_1['Block'] = 1

# Create two groups assigning to Treatment or Control
strata_1_g1 = strata_1.sample(frac=0.5, replace=False)
strata_1_g1['T_C'] = 'T'
strata_1_g2 = strata_1.drop(strata_1_g1.index)
strata_1_g2['T_C'] = 'C'

# Create the second block and assign groups
strata_2 = wealth_data[wealth_data['high_wealth'] == 0]
strata_2['Block'] = 2

strata_2_g1 = strata_2.sample(frac=0.5, replace=False)
strata_2_g1['T_C'] = 'T'
strata_2_g2 = strata_2.drop(strata_2_g1.index)
strata_2_g2['T_C'] = 'C'

# Concatenate the grouping work
wealth_data_stratified = pd.concat([strata_1_g1, strata_1_g2, strata_2_g1, strata_2_g2])
print(wealth_data_stratified.groupby(['Block','T_C', 'high_wealth']).size())
```

```
Block  T_C  high_wealth
1      C    1              100
       T    1              100
2      C    0              900
```

```
       T    0               900
dtype: int64
```

Caution

You were able to split your data into different blocks and then randomly assign to treatment and control. You can clearly see two blocks, where the first block has half the ***`high_wealth`*** *subjects split into treatment and control. The same is seen in the second block for the other subjects*

1.1.9 Chapter 1.3: Normal data

Let's review the concept of normal data and how it relates to experimental analysis.

The normal distribution

Normal data is drawn from a normal distribution, which has the familiar bell curve shape. The normal distribution is intrinsically linked to z-scores, which recall, is a standardized measure of how many standard deviations a value is from the population mean. The most common normal distribution used for z-scores has a mean of zero and a standard deviation of one. This answers questions such as 'How many standard deviations is this point from the mean?' and 'What is the probability of obtaining this score?'.

Normal data and statistical tests

Normal data is an underlying assumption for many statistical tests, called parametric tests. There are also nonparametric tests that don't assume normal data.

Normal, Z, and alpha

In hypothesis testing, alpha, or the significance level, is often closely linked to the normal distribution. For normal data, we can visually see the risk of error for a given significance level and compare that result to the p-value, which is related to the z-score. An `alpha` of 0.05 on a standard two-tailed test represents a small region in the tails. It means there is a 5% risk of rejecting the null hypothesis when it is actually true - a so-called Type I error.

Visualizing normal data

We can visually check data for normality using a kde (or kernel density) plot, available via Seaborn's `displot()` function. On this salaries dataset, the data appears approximately normal.

QQ plots

A more statistically robust visual tool is a quantile-quantile, or QQ, plot. It plots the quantiles or sections of two distributions against each other. The qqplot function from statsmodels plots our data. Setting the dist argument to the normal distribution from scipy.stats compares our data against a standard normal distribution. If the distributions are similar, the dots in the QQ plot hug the line tightly. Our data again seems quite normal. Here is another example. The dots bow out at the ends, which means that the data is not very normal.

Tests for normality

There are also various numerical hypothesis tests for normality. The Shapiro-Wilk test is known to be good for small datasets. The D'Agostino K-squared test uses kurtosis and skewness to determine normality. These terms relate to the symmetry and size of a distribution's tails, respectively. Anderson-Darling is another common test which returns a list of values, rather than just one so we can see normality at different levels of alpha. Each of these tests has a null hypothesis that the provided dataset is drawn from a normal distribution.

A Shapiro-Wilk test

Let's run one of these tests, the Shapiro-Wilk test. We import it from `scipy.stats`, and set our `alpha` at 0.05. The function takes a series of values and returns a test statistic and `p-value`. The `p-value` is greater than `alpha`, so we have evidence our data that looked quite normal is normal. We fail to reject the null hypothesis and have evidence that the data sample is normal at the `alpha` level of 0.05.

An Anderson-Darling test

To implement an Anderson-Darling test, we provide data and set the dist argument to norm to test for normality. The result object contains a test statistic and a range of critical values and significance levels. To interpret, we check the test statistic against each critical value. If the test statistic is higher than the critical value, the null hypothesis is rejected at that particular significance level, and the data is not normal. 0.2748 is less than all the critical values, so we fail to reject the null hypothesis and suspect that the data is normal.

1.1.10 Exercise 1.3.1

Visual normality in an agricultural experiment

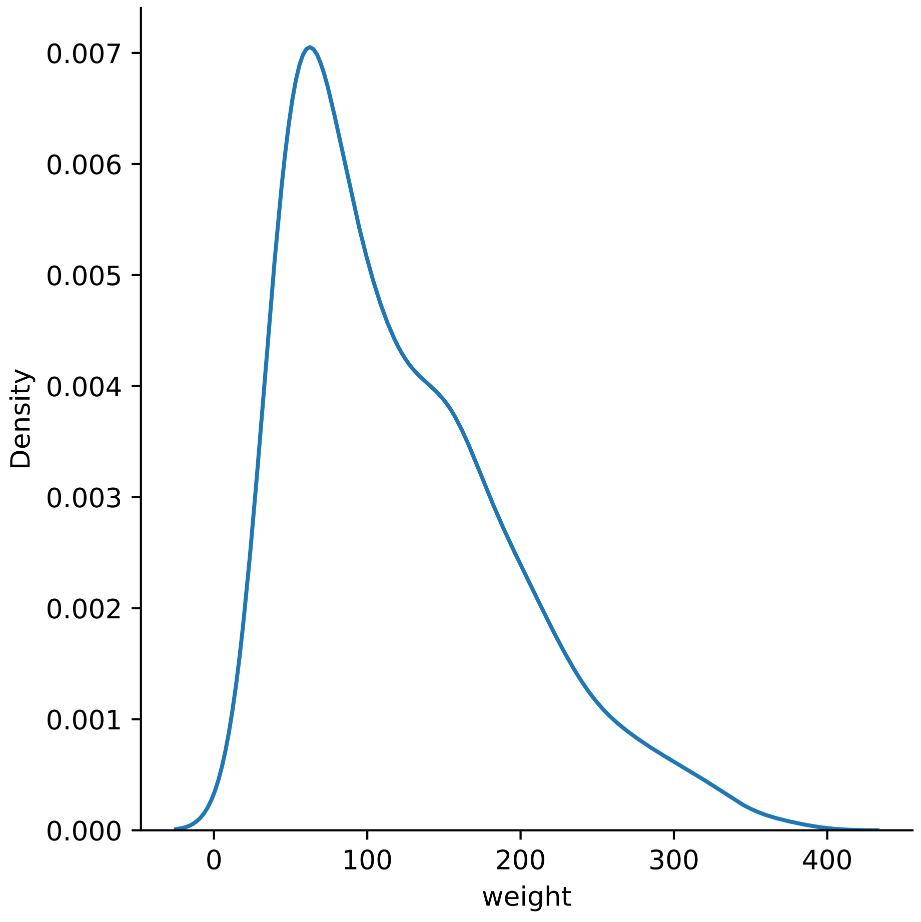
You have been contracted by an agricultural firm conducting an experiment on 50 chickens, divided into four groups, each fed a different diet. Weight measurements were taken every second day for 20 days.

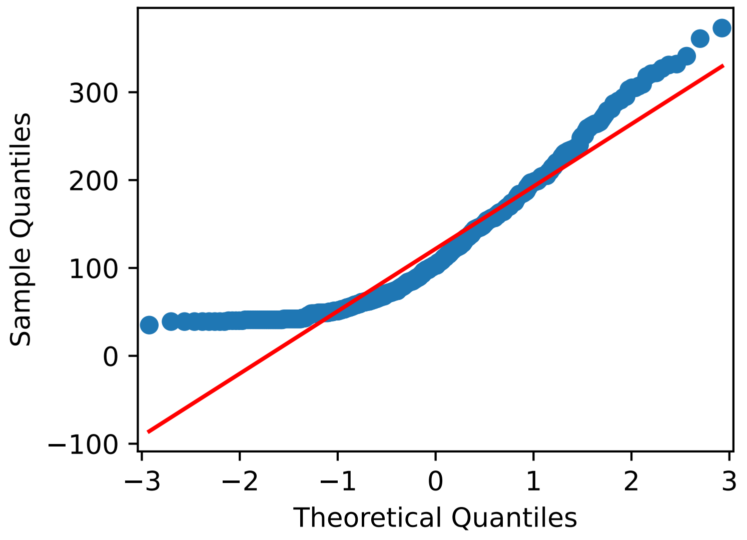
You'll analyze chicken_data to assess normality, which will determine the suitability of parametric statistical tests, beginning with a visual examination of the data distribution.

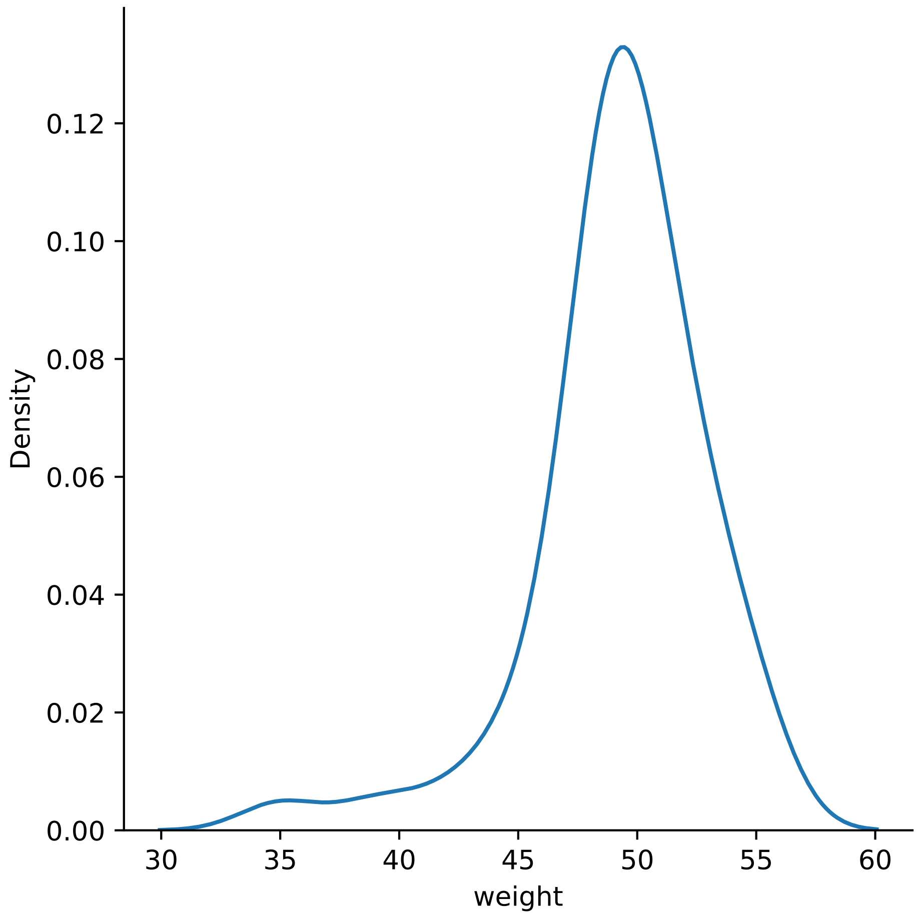
1.1.10.1 Instructions

1. Plot the distribution of the chickens' `weight` using the kernel density estimation (KDE) to visualize normality.
2. Create a qq plot with a standard line of the chickens' `weight` to assess normality visually.
3. Subset `chicken_data` for a `'Time'` of 2, and plot the KDE of `'weight'` from `subset_data` to check if data is normal across time.

```python
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from statsmodels.graphics.gofplots import qqplot

chicken_data = pd.read_csv('datasets/chick_weight.csv')

# Plot the distribution of the chickens' weight
sns.displot(data=chicken_data, x='weight', kind="kde")
plt.show()

# Plot the qq plot of the chickens' weight
qqplot(data=chicken_data['weight'], line='s')
plt.show()

# Subset the data and plot the weight of the subset
subset_data = chicken_data[chicken_data['Time'] == 2]

sns.displot(data=subset_data, x='weight', kind="kde")
plt.show()
```


0.007
0.006
0.005
0.004
0.003
0.002
0.001
0.000
Density
0
100
200
300
400
weight


300
200
100
0
−100
Sample Quantiles
−3
−2
−1
0
1
2
3
Theoretical Quantiles



1.1.11 Exercise 1.3.2

Analytical normality in an agricultural experiment

Carrying on from your previous work, your visual inspections of the data indicate it may not be a normal dataset overall, but that the initial time point may be.

Build on your previous work by using analytical methods to determine the normality of the dataset.

Instructions

1. Run a Shapiro-Wilk test of normality on the `'weight'` column and print the test statistic and p-value.
2. Run an Anderson-Darling test for normality and print out the test statistic, significance levels, and critical values from the returned object.

```
import pandas as pd
from scipy.stats import shapiro
from scipy.stats import anderson
import numpy as np

chicken_data = pd.read_csv('datasets/chick_weight.csv')

# Run a Shapiro-Wilk normality test on the weight column
test_statistic, p_value = shapiro(chicken_data['weight'])

print(f"p: {round(p_value, 4)} test stat: {round(test_statistic, 4)}")

# Run the Anderson-Darling test
result = anderson(x= chicken_data['weight'], dist='norm')

print(f"Test statistic: {round(result.statistic, 4)}")
print(f"Significance Levels: {result.significance_level}")
print(f"Critical Values: {result.critical_values}")
```

```
p: 0.0 test stat: 0.9087
Test statistic: 14.6868
Significance Levels: [15.  10.   5.   2.5  1. ]
Critical Values: [0.572 0.652 0.782 0.912 1.085]
```

1.1.11.1 Question 2

At a significance level of 0.05, does the Shapiro-Wilk test indicate the data is normally distributed? *No*

1.1.11.2 Question 4

Given the returned Anderson-Darling test result, what could you conclude at the 5% significance level

- *The critical value which matches the significance level of 5 is 0.781. When compared to the Anderson-Darling test statistic (12.5451), the critical value is much smaller and so we reject the null hypothesis and can conclude the data is unlikely to have been drawn from a normal distribution.*

1.2 Chapter 2: Experimental Design Techniques

You'll delve into sophisticated experimental design techniques, focusing on factorial designs, randomized block designs, and covariate adjustments. These methodologies are instrumental in enhancing the accuracy, efficiency, and interpretability of experimental results. Through a combination of theoretical insights and practical applications, you'll acquire the skills needed to design, implement, and analyze complex experiments in various fields of research.

1.2.1 Chapter 2.1: Factorial designs: principles and applications

Welcome back! In this lesson, we'll explore factorial designs.

Understanding factorial design

Factorial designs allow for the simultaneous examination of multiple variables. In this setup, every possible combination of factor levels is tested, which not only measures the direct effects of each factor but also the interactions between them. In the example shown of plant growth in different conditions, implementing a factorial design will mean that we can test the effect of different factors on plant growth, including light conditions and fertilizer type, simultaneously, and identify interactions between them. These interactions can illuminate complex dynamics that might be overlooked in simpler experimental setups.

1 Image Generated with DALL · E 3

Factorial design data example

To explain this concept further, we'll work with this plant growth DataFrame. It has 120 rows and four columns: an identifier column, two factors, and one response/dependent variable. Both factors have two levels: `Light_Condition` can be Full Sunlight or Partial Shade, and `Fertilizer_Type` can be either Synthetic or Organic. The `Growth_cm` column is the numeric response, or dependent variable in the experiment.

Organizing data to visualize interactions

We next create a pivot table from the DataFrame using pandas' `pivot_table` function. It aggregates the `Growth_cm` values by taking their mean for each combination of `Light_Condition` and `Fertilizer_Type`. The resulting table displays these average outcomes, with light values as rows and fertilizer values as columns, illustrating how the growth varies across different levels of the two factors. For example, the value 19.869 represents the average growth for the combination of Full Sunlight from `Light_Condition` and Synthetic from `Fertilizer_Type`.

Visualize interactions with heatmap

The Seaborn heatmap function paints a picture of how these factors interact, with the color intensity revealing the strength and direction of their interactions. Setting annot to True displays the numerical value of the cell, and 'coolwarm' is a color map that ranges from cooler, or bluer colors, to warmer or redder colors. Lastly, the format argument fmt is set to 'g' to avoid scientific notation.

Interpreting interactions

The variation in outcomes when changing levels within a factor indicates an interaction. For instance, the decrease from Organic to Synthetic fertilizer within Full Sunlight (from 20.602 to 19.869) contrasts with the modest change within Partial Shade, illustrating how outcomes differ based on factor levels. The differing changes in outcomes between Full Sunlight and Partial Shade across `Fertilizer_Type` suggest the factors interact, underscoring the need for nuanced strategies considering the interaction of factors.

Factorial designs vs. randomized block designs

Let's conclude by comparing factorial designs to the randomized block design we saw earlier in the course, and that we'll dive deeper into in the next video. Factorial designs investigate multiple treatments and their interactions to understand their combined effects on outcomes. They aim to unravel the effects and interactions of various factors, crucial for complex scenarios with multiple influencing variables. In factorial designs, units experience all treatment combinations, offering thorough exploration but requiring more subjects as treatments grow. Randomized block designs utilize blocks to group similar subjects, minimizing confounding impacts and clearer treatment effects. The focus of randomized block designs is on enhancing experimental precision by managing within-block variability, aiding in the detection of treatment differences. Randomized block designs assign one treatment per unit within blocks, ensuring each treatment's presence in every block to control for block-related variance and bolster treatment effect assessments.

1.2.2 Exercise 2.1.1

Understanding marketing campaign effectiveness

Imagine you're a digital marketer analyzing data from a recent campaign to understand what messaging style and time of day yield the highest conversions. This analysis is crucial for guiding future marketing strategies, ensuring that your messages reach potential customers when they're most likely to engage. In this exercise, you're working with a dataset giving the outcomes of different messaging styles (`'Casual'` versus `'Formal'`) and times of day (`'Morning'` versus `'Evening'`) on conversion rates, a common scenario in marketing data analysis.

Instructions

- Create a pivot table with `'Messaging_Style'` as the index and `'Time_of_Day'` as the columns, computing the mean of Conversions.
- Print this pivot table.

```python
import pandas as pd
import numpy as np

marketing_data = pd.read_feather('datasets/marketing_data.feather')
```

```python
# Create a pivot table for marketing campaign data
marketing_pivot = marketing_data.pivot_table(
  values='Conversions',
  index='Messaging_Style',
  columns='Time_of_Day',
  aggfunc='mean')

# View the pivoted results
print(marketing_pivot)
```

```
Time_of_Day         Evening     Morning
Messaging_Style
Casual           402.329004  401.133891
Formal           432.913043  411.096000
```

Note

!Notice that the mean conversion is highest for the `'Formal'` messaging style in the `'Evening'` time of day.

1.2.3 Exercise 2.1.2

Heatmap of campaign interactions

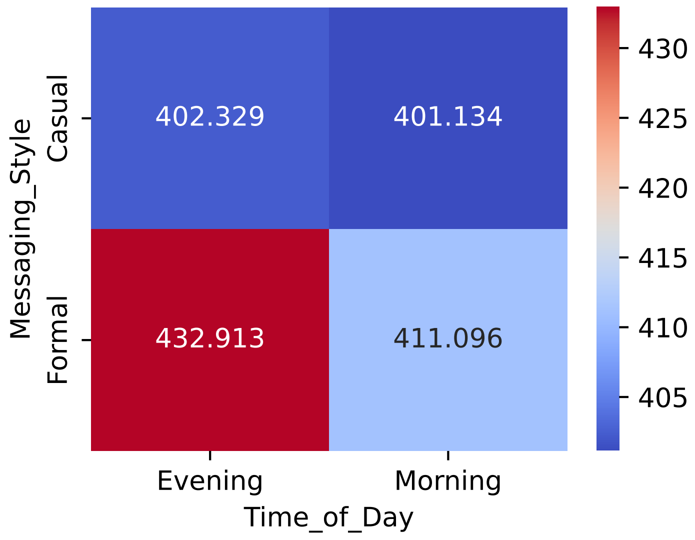
Visualizing data can often reveal patterns that are not immediately obvious. In the context of marketing, understanding how different factors interact and affect the success of a campaign is vital. By creating a heatmap of conversions based on messaging style and time of day, you can quickly identify which combinations perform best and which ones need reevaluation. This visual tool is invaluable for marketing teams looking to optimize their strategies for maximum impact.

Instructions

- Visualize interactions between `Messaging_Style` and `Time_of_Day` with respect to conversions by creating an annotated cool-warm heatmap of `marketing_pivot`.

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

marketing_data = pd.read_feather('datasets/marketing_data.feather')

# Create a pivot table for marketing campaign data
marketing_pivot = marketing_data.pivot_table(
    values='Conversions',
    index='Messaging_Style',
    columns='Time_of_Day',
    aggfunc='mean')

# View the pivoted results
print(marketing_pivot)

# Visualize interactions with a heatmap
sns.heatmap(marketing_pivot,
         annot=True,
         cmap='coolwarm',
         fmt='g')

plt.show()
```

```
Time_of_Day          Evening     Morning
Messaging_Style
Casual            402.329004  401.133891
Formal            432.913043  411.096000
```



1.2.4 Chapter 2.2: Randomized block design: controlling variance

Next, we'll delve further into the concept of blocking in experimental design.

Understanding blocking

Blocking involves grouping experimental units, often with similar characteristics, to minimize variance within these groups. This ensures that each block, representing a specific level of the blocking factor, receives every treatment. This approach allows us to concentrate on the treatment effects while controlling for variance attributable to the blocking factor, thus improving the precision of our results.

Block design data example

For this athlete performance DataFrame of 200 rows, blocking is represented by `Initial_Fitness_Level` with categories of `Beginner`, `Intermediate`, and `Advanced`. `Muscle_Gain_kg` is a numeric response variable measured on participants for the year prior to blocks being assigned.

Implementing randomized block design

To implement a randomized block design, we'll group the rows into blocks based on the `Initial_Fitness_Level` in this case, shuffle the rows within these blocks, and randomly assign a treatment. To shuffle the rows in each `Initial_Fitness_Level` block, we start with `.groupby()` on `Initial_Fitness_Level`. To shuffle each row in that block, we chain the `.apply()` method to the `groupby`, and pass it a `lambda` function that reads: `for each group`, denoted by x, we sample all rows with `frac=1`, effectively shuffling them. We reset the index to not have both an index and column called Block. The grouped data is ordered alphabetically by fitness level.

Implemented randomized blocks

Then, within each block, we assign exercise program treatments randomly using `numpy.random.choice()`. This method allows us to control for block effects while focusing on the differences caused by the treatments. Here is a sample of the implemented randomized block DataFrame with the treatment randomly applied within each block.

Visualizing treatment effects within blocks

A boxplot is an effective tool for visualizing the distribution of treatment effects across different blocks. By plotting the `Muscle_Gain_kg` variable versus the `Initial_Fitness_Level`, coloring by `Treatment`, we observe the central tendencies and variabilities within each block. Scanning this boxplot, we see similar median values throughout the blocks and treatments. The variability is a bit wider for some, though, such as Cardio for Advanced and Beginner.

ANOVA within blocks

We can use ANOVA to statistically check for these differences. Let's set a significance level at 5% prior to reviewing our results. We group the DataFrame by the blocking column and then apply a `lambda` function to each group. Within the lambda function, we perform a one-way ANOVA test between the `Muscle_Gain_kg` values for each treatment within each block using `f_oneway` from `scipy.stats`. Finally, it returns the `F-statistic` and `p-value` for each block's ANOVA test. Each of the p-values are above the alpha significance level of 5%. This gives evidence that significant differences don't exist across treatments within blocks. This is an ideal goal when setting up randomized block design experiments.

Visualizing effects across blocks

We can also look for differences in the outcome across randomized blocks. Here, we do not break down further by treatment. These boxplots look similar, so we might guess that none of the blocks has a significantly different mean outcome compared to the others.

ANOVA between blocks

Next we compute the one-way ANOVA test across the blocks. It compares the `Muscle_Gain_kg` values for each block separately to assess whether there are significant differences in means among the blocks. The function `f_oneway` calculates the `F-statistic` and associated `p-value`, indicating the likelihood of observing the data if the null hypothesis of equal means across all blocks is true. A p-value greater than 0.05 supports what we saw with the boxplot - that there is no significant difference.

1.2.5 Exercise 2.2.1

Implementing a randomized block design

The manufacturing firm you worked with earlier is still interested in conducting some experiments on worker productivity. Previously, the two blocks were set randomly. While this can work, it can be better to group subjects based on similar characteristics.

The same employees are again loaded but this time in a DataFrame called `productivity` including 1200 other colleagues. It also includes a worker `'productivity_score'` column based on units produced per hour. This column was binned into three groups to generate blocks based on similar productivity values. The firm would like to apply a new incentive program with three options (`'Bonus'`, `'Profit Sharing'` and `'Work from Home'`) throughout the firm with treatment applied randomly.

Instructions

- Shuffle the blocks to create a new DataFrame called `prod_df`.
- Reset the index so that `block` is not both an index and a column.
- Randomly assign the three treatment values in the `'Treatment'` column.

1.2.6 Exercise 2.2.2

Visualizing productivity within blocks by incentive

Continuing with the worker productivity example, you'll explore if the productivity scores are distributed throughout the data as one would expect with random assignment of treatment. Note that this is a precautionary step, and the treatment and follow-up results on the impact of the three treatments is not done yet!

seaborn and matplotlib.pyplot as sns and plt respectively are loaded.

1.2.6.1 Instructions

- Visualize the productivity scores within blocks by treatment using a boxplot with `'block'` for `x`, `'productivity_score'` for `y`, and `'Treatment'` for `hue`.

1.2.7 Exercise 2.2.3

ANOVA within blocks of employees

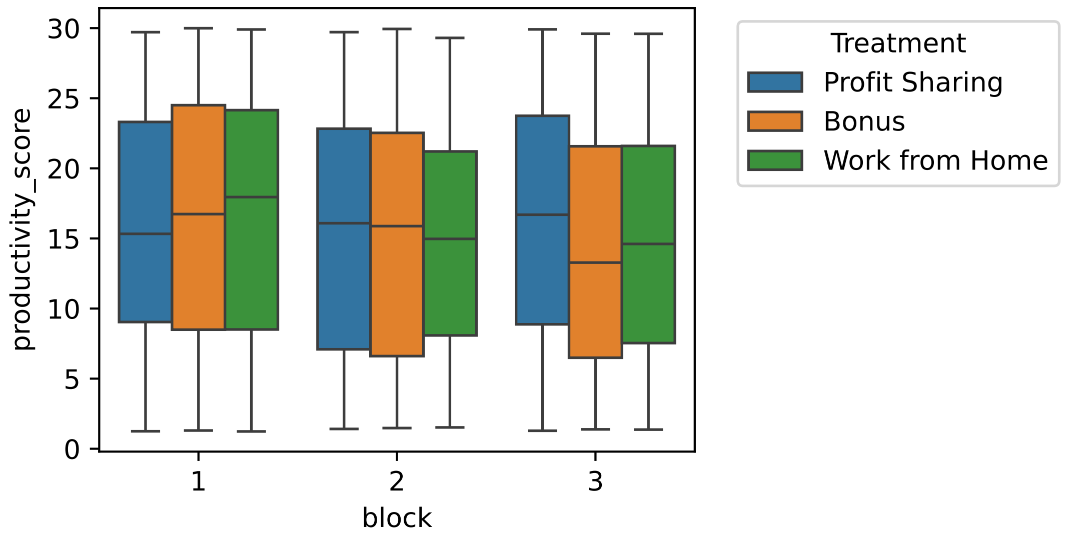
Building on your previous analyses with the manufacturing firm, where worker productivity was examined across different blocks and an incentive program was introduced, you're now delving deeper into the data. The firm, equipped with a more comprehensive dataset in the productivity DataFrame, including 1200 additional employees and their productivity_score, has structured the workforce into three blocks based on productivity levels. Each employee has been randomly assigned one of three incentive options: 'Bonus', 'Profit Sharing', or 'Work from Home'.

Before assessing the full impact of these incentive treatments on productivity, it's crucial to verify that the initial treatment assignment was indeed random and equitable across the different productivity blocks. This step ensures that any observed differences in productivity post-treatment can be confidently attributed to the incentive programs themselves, rather than pre-existing disparities in the blocks.

Instructions

- Group `prod_df` by the appropriate column that represents different blocks in your data.
- Use a lambda function to apply the ANOVA test within each `block`, specifying the `lambda` function's argument.
- For each treatment group within the blocks, filter `prod_df` based on the `'Treatment'` column values and select the `'productivity_score'` column.

```python
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from scipy.stats import f_oneway

# Set random seed for reproducibility
np.random.seed(42)

# Create the DataFrame
subject_id = np.arange(1, 1301)
productivity_score = np.random.uniform(1.1, 30.0, 1300)
block = np.random.randint(1, 4, 1300)

productivity = pd.DataFrame({
    'subject_id': subject_id,
    'productivity_score': productivity_score,
    'block': block
})

# Randomly assign workers to blocks
prod_df = productivity.groupby('block').apply(
  lambda x: x.sample(frac=1)
)

# Reset the index
prod_df = prod_df.reset_index(drop=True)

# Assign treatment randomly
prod_df['Treatment'] = np.random.choice(
  ['Bonus', 'Profit Sharing', 'Work from Home'],
  size=len(prod_df)
)

# Sample Boxplot
sns.boxplot(x='block',
            y='productivity_score',
            hue='Treatment',
            data=prod_df)

# Move the legend outside the plot
plt.legend(title='Treatment', bbox_to_anchor=(1.05, 1), loc='upper left')

# Show plot
plt.show()

# Perform the within blocks ANOVA, first grouping by block
within_block_anova = prod_df.groupby('block').apply(
  # Set function
  lambda x: f_oneway(
    # Filter Treatment values based on outcome
    x[x['Treatment'] == 'Bonus']['productivity_score'],
    x[x['Treatment'] == 'Profit Sharing']['productivity_score'],
    x[x['Treatment'] == 'Work from Home']['productivity_score'])
)
print(within_block_anova)
```



```
block
1     (0.8437999669869772, 0.4307774592046686)
2    (0.33640460765350616, 0.7145131123685446)
3    (1.5967688826774828, 0.20381926296045258)
dtype: object
```

Note

An ANOVA analysis was performed to compare productivity scores across different blocks for the three treatment groups. The results show that all three p-values exceed the alpha threshold of 0.05, indicating no significant differences in productivity scores among the treatment groups within the blocks.

1.2.8 Chapter 2.3: Covariate adjustment in experimental design

Let's now explore covariates in experimental design and analysis, and how they can be used to minimize confounding. We'll also learn about ANCOVA, or analysis of covariance, for evaluating treatment effects while controlling for covariates.

Introduction to covariates

Recall that covariates are variables that are not of primary interest but are related to the outcome variable and can influence its analysis. Including covariates in statistical analyses is crucial for reducing confounding, which occurs when an external variable influences both the dependent variable and independent variable(s). By adjusting for covariates, researchers can isolate the effect of the independent variable on the outcome, minimizing the influence of confounders. Accounting for covariates in experimental design and analysis controls for variability that is not attributable to the primary variables being studied. This leads to more valid conclusions about the relationship between the independent and dependent variables, as the analysis better reflects the true effect by isolating it from the influence of covariates. Consider the investigation of a new teaching method's effectiveness on student test scores. Here, the primary variables of interest are the teaching method (independent variable) and the student test scores (dependent variable). However, students' prior subject knowledge serves as a crucial covariate because prior knowledge can significantly impact learning outcomes, yet it's not the main focus of the study.

Experimental data example

Let's bring back our plant growth data and set it to experimental data as the `exp_data` DataFrame, keeping `Fertilizer_Type` as treatment and `Growth_cm` as response.

Covariate data example

The covariate_data DataFrame also includes `Plant_ID` identifiers for each subject, again ranging from 1 to 120, ensuring each subject's covariate data is matched with their experimental data. `Watering_Days_Per_Week` is another variable measured for each plant. Recall that covariates are additional variables potentially influencing the outcome and are included in analyses to control for their effects.

Combining experimental data with covariates

Combining the experimental with covariate data is a crucial step in adjusting for covariates. We use `pandas`' `merge` function to combine DataFrames; we do this on the `Plant_ID` to ensure each that subject's experimental and covariate data are aligned.

Adjusting for covariates

To adjust for covariates in our analysis, we employ ANCOVA, or analysis of covariance, using the ols model from statsmodels. This `ols()` function takes a formula that specifies the dependent and independent variables. `Growth_cm` is the dependent variable we're interested in, which we want to model using the `Fertilizer_Type`, the categorical independent variable representing different groups in the experiment, and the potential covariate, `Watering_Days_Per_Week`, to control for its effects. The first portion of summary output provides details on the significance of the model; it show a large p-value here of 0.531, which implies a lack of support for covariates affecting the model.

Further exploring ANCOVA results

Looking at the second and third rows of this second portion of output from summary, we see that the factors and covariate each have large p-values of 0.760 and 0.275, concluding that each of them alone are not significant predictors of growth for this model.

Visualizing treatment effects with covariate adjustment

This seaborn lmplot shows treatment effects adjusted for the covariate. The regression lines for each treatment category offer a visual representation of how treatment effects trend across different levels of the covariate. We see that `Organic` remains relatively constant going from 1 watering to 7 `Watering_Days_Per_Week`. Synthetic shows an increase. The crossing regression lines suggest we may want to add an interaction term of `Watering_Days_Per_Week` by `Fertilizer_Type` in another model. Parallel lines would suggest a lack of interaction.

1.2.9 Exercise 2.3.1

Covariate adjustment with chick growth

Imagine studying in agricultural science the growth patterns of chicks under various dietary regimens. The data from this study sheds light on the intricate relationship between their respective diets and the consequent impact on their weight. This data includes weight measurements of chicks at different ages, allowing for an exploration of covariate adjustment. `age` serves as a covariate, potentially influencing the outcome variable: the `weight` of the chicks.

Instructions

1. Join the experimental and covariate data based on common column(s), and print this merged data.
2. Produce an ANCOVA predicting `'weight'` based on `'Diet'` and `'Time'`.

- Print a summary of the ANCOVA model.

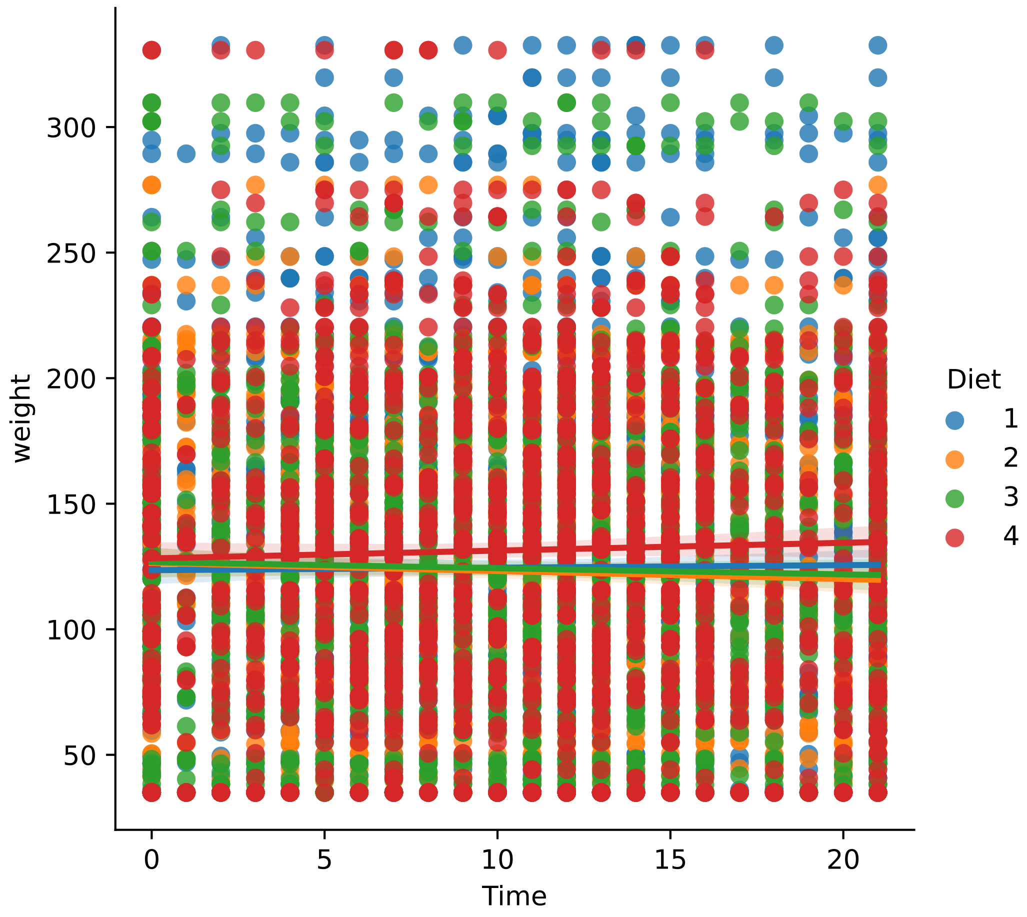
3. Design an `lmplot` to see `hue='Diet'` effects on `y='weight'` adjusted for `x='Time'`.

```python
import pandas as pd
import numpy as np
from statsmodels.formula.api import ols
import seaborn as sns
import matplotlib.pyplot as plt

# Set random seed for reproducibility
np.random.seed(42)

# Generate 578 values for Chick (randomly sampled from 1 to 50)
chick_values = np.random.randint(1, 51, size=578)

# Generate 578 values for Diet (randomly sampled from 1 to 4)
diet_values = np.random.randint(1, 5, size=578)

# Generate 578 values for weight with approximate mean and std
weight_values = np.random.normal(loc=121.818, scale=71.072, size=578)

# Ensure weights are within the specified range
weight_values = np.clip(weight_values, 35, 373)

# Create DataFrame
exp_chick_data = pd.DataFrame({
    "Chick": chick_values,
    "Diet": diet_values,
    "weight": weight_values
})

# Generate 578 values for Chick (randomly sampled from 1 to 50)
chick_values = np.random.randint(1, 51, size=578)

# Generate 578 values for Time (normally distributed around mean 10.718 with std 6.758)
time_values = np.random.normal(loc=10.718, scale=6.758, size=578)

# Ensure Time values are within the specified range (0 to 21)
time_values = np.clip(time_values, 0, 21).astype(int)
```

```python
# Create DataFrame
cov_chick_data = pd.DataFrame({
    "Chick": chick_values,
    "Time": time_values
})

# Join experimental and covariate data
merged_chick_data = pd.merge(exp_chick_data,
                            cov_chick_data, on='Chick')

# Print the merged data
print(merged_chick_data)

# Join experimental and covariate data
merged_chick_data = pd.merge(exp_chick_data,
                             cov_chick_data, on='Chick')

# Perform ANCOVA with Diet and Time as predictors
model = ols('weight ~ Diet + Time', data=merged_chick_data).fit()

# Print a summary of the model
print(model.summary())

# Visualize Diet effects with Time adjustment
sns.lmplot(x='Time', y='weight',
         hue='Diet',
         data=merged_chick_data)

plt.show()
```

```
      Chick  Diet      weight  Time
0        39     1  138.685119    11
1        39     1  138.685119    20
2        39     1  138.685119     7
3        39     1  138.685119     7
4        39     1  138.685119    14
...     ...   ...         ...   ...
6727     35     3  150.487736    16
6728     35     3  150.487736     0
6729     35     3  150.487736    21
6730     35     3  150.487736     0
6731     35     3  150.487736     2

[6732 rows x 4 columns]
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:                 weight   R-squared:                       0.001
Model:                            OLS   Adj. R-squared:                  0.001
Method:                 Least Squares   F-statistic:                     4.288
Date:                Thu, 20 Mar 2025   Prob (F-statistic):             0.0138
Time:                        11:13:07   Log-Likelihood:                -37536.
No. Observations:                6732   AIC:                         7.508e+04
Df Residuals:                    6729   BIC:                         7.510e+04
Df Model:                           2
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------
Intercept    121.2380      2.310     52.486      0.000     116.710     125.766
Diet           2.0087      0.691      2.906      0.004       0.654       3.364
Time          -0.0400      0.130     -0.308      0.758      -0.295       0.215
==============================================================================
Omnibus:                      234.618   Durbin-Watson:                   0.188
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              258.758
Skew:                           0.478   Prob(JB):                     6.48e-57
Kurtosis:                       2.904   Cond. No.                         37.2
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
```



1.3 Chapter 3: Analyzing Experimental Data: Statistical Tests and Power

Master statistical tests like t-tests, ANOVA, and Chi-Square, and dive deep into post-hoc analyses and power analysis essentials. Learn to select the right test, interpret p-values and errors, and skillfully conduct power analysis to determine sample and effect sizes, all while leveraging Python's powerful libraries to bring your data insights to life.

1.3.1 Chapter 3.1. Choosing the right statistical test

We'll now look into choosing the right statistical test for analyzing experimental data.

Selecting the right test

Just as choosing the right book or the right measurement tool for is vital to research, choosing the right statistical test is foundational to any data analysis. Understanding our dataset's features and the hypotheses under examination is vital. It necessitates assessing the data types—categorical or continuous—their distributions, often assumed to be normal by many statistical tests, and the number of variables in the study. It's essential to align the chosen statistical method with the dataset's properties and the study's goals to ensure accurate and dependable outcomes. In this chapter, we'll explore how to apply t-tests, ANOVA, and Chi-Square tests, focusing on analyzing experimental data.

The dataset: athletic performance

We'll work with a DataFrame called `athletic_perf` containing athletes' performance data, focusing on the effects of different training programs and diets on athletic performance. Key variables are the type of training program, assigned diet, initial fitness level, and the observed performance increase as a percentage.

Independent samples t-test

An independent samples t-test is used to compare the means of two distinct groups to determine if there is a statistically significant difference between them. This test relies on the assumptions that the response data for both groups are normally distributed and have equal variances, ensuring the validity and reliability of the test results. We'll use an `alpha` of `0.5` and compare the mean athletic performance improvements between two groups undergoing High-Intensity Interval Training (HIIT) and Endurance training by assigning their performance increases to group1 and group2. Next we call `ttest_ind` on `group1` and `group2` and retrieve the test statistics and p-value. A large p-value here leads us to conclude that there is no significant difference in the mean performance increase between the HIIT and Endurance groups.

One-way ANOVA

A one-way ANOVA test is employed to determine if there are statistically significant differences among the means of more than two groups. The one-way corresponds to ANOVA with a single independent variable, and it assumes that the variances among the groups are equal. For our example, we gather the athletic performance increase data for each training program type into a list of groups using a list comprehension. The `f_oneway` function from `scipy.stats` is then used to conduct the ANOVA test across these groups by unpacking the groups list using an asterisk. The relatively high P-value implies that, based on the provided data, we cannot confidently assert that different training programs lead to different mean increases in athletic performance.

Chi-square test of association

The Chi-square test of association is a statistical method used to assess whether there is a significant association between two categorical variables. Unlike many other statistical tests, the chi-square test does not require assumptions about the distribution of the data. To prepare for the test, we start by creating a contingency table using `crosstab` from `pandas`, which cross-tabulates athletes by their `Training_Program` and `Diet_Type`.

Chi-square test of association

The `chi2_contingency` function from `scipy.stats` is then employed to conduct the chi-square test on the contingency table. The large P-value suggests that any observed association between training programs and diet types is not statistically significant.

1.3.2 Exercise 3.1.1

Choosing the right test: petrochemicals

In a chemistry research lab, scientists are examining the efficiency of three well-known catalysts—Palladium (Pd), Platinum (Pt), and Nickel (Ni)—in facilitating a particular reaction. Each catalyst is used in a set of identical reactions under controlled conditions, and the time taken for each reaction to reach completion is meticulously recorded. Your goal is to compare the mean reaction times across the three catalyst groups to identify which catalyst, if any, has a significantly different reaction time.

Instructions

- Use a list comprehension to filter into `groups` iterating over the `catalyst_types` and each of their `'Reaction_Time'`s.

```python
import numpy as np
import pandas as pd
from scipy.stats import f_oneway

chemical_reactions = pd.read_csv('datasets/chemical_reactions.csv')

catalyst_types = ['Palladium', 'Platinum', 'Nickel']

# Collect reaction times for each catalyst into a list
groups = [chemical_reactions[chemical_reactions['Catalyst'] == catalyst]['Reaction_Time'] for cat

# Perform the one-way ANOVA across the three groups
f_stat, p_val = f_oneway(*groups)
print(f"F-Statistic: {f_stat}, P-value: {p_val}")
```

```
F-Statistic: 478.7412625615453, P-value: 4.710677600047866e-151
```

Question

Assume a significance level of $\alpha = 0.01$. What is the appropriate conclusion to glean from the P-value in comparison with this α value?

The P-value is substantially smaller than the α value, indicating a significant difference in reaction times across the catalysts.

1.3.3 Exercise 3.1.2

Choosing the right test: human resources

In human resources, it's essential to understand the relationships between different variables that might influence employee satisfaction or turnover. Consider a scenario where an HR department is interested in understanding the association between the department in which employees work and their participation in a new workplace wellness program. The HR team has compiled this data over the past two years and has asked you if there's any significant association between an employee's department and their enrolling in the wellness program.

Instructions

- Create a contingency table comparing `'Department'` and `'Wellness_Program_Status'`.
- Perform a chi-square test of association on the contingency table and print the p-value.

```python
import pandas as pd
import numpy as np
from scipy.stats import chi2_contingency

hr_wellness = pd.read_csv('datasets/hr_wellness.csv')

# Create a contingency table
contingency_table = pd.crosstab(
  hr_wellness['Department'],
  hr_wellness['Wellness_Program_Status']
)

# Perform the chi-square test of association
chi2_stat, p_val, dof, expected = chi2_contingency(contingency_table)
print(f"F-Statistic: {chi2_stat}, P-value: {p_val}")
```

```
F-Statistic: 3.4775739037369617, P-value: 0.17573344450112738
```

Question

- Assume a significance level of 0.05. Given the P-value, what is the appropriate conclusion?

There's no significant association between department and enrollment in the wellness program, as the P-value is larger than `0.05`.

1.3.4 Exercise 3.1.3

Choosing the right test: finance

In the realm of finance, investment strategists are continually evaluating different approaches to maximize returns. Consider a scenario where a financial firm wishes to assess the effectiveness of two investment strategies: "Quantitative Analysis" and "Fundamental Analysis". The firm has applied each strategy to a separate set of investment portfolios for a year and now asks you to compare the annual returns to determine if there is any difference in strategy returns by comparing the mean returns of the two groups.

Instructions

1. What type of hypothesis test should be performed in this scenario?

- Possible answer: Independent samples t-test

2. Filter `'Strategy_Type'` on `'Quantitative'` to retrieve their `'Annual_Return'` and do the same for `'Fundamental'` strategies.
3. Complete for the two groups an independent samples t-test and print the p-value.

```python
import pandas as pd
import numpy as np
from scipy.stats import ttest_ind

investment_returns = pd.read_csv('datasets/investment_returns.csv')

# Separate the annual returns by strategy type
quantitative_returns = investment_returns[investment_returns['Strategy_Type'] == 'Quantitative'][
fundamental_returns = investment_returns[investment_returns['Strategy_Type'] == 'Fundamental']['A

# Perform the independent samples t-test between the two groups
t_stat, p_val = ttest_ind(quantitative_returns, fundamental_returns)
print(f"T-statistic : {t_stat}, P-value: {p_val}")
```

```
T-statistic : 7.784788496693728, P-value: 2.0567003424807146e-14
```

4. Assume a significance level of 0.1. What is the appropriate conclusion to glean from the P-value in comparison with this α value?

The P-value is much smaller than α, suggesting a significant difference in returns between the two strategies.

1.3.5 Chapter 3.2: Post-hoc analysis following ANOVA

After conducting ANOVA, we often need to understand specific differences between groups. This is where post-hoc analysis comes in, providing detailed insights into pairwise comparisons.

When to use post-hoc tests

Post-hoc tests are pivotal when ANOVA reveals significant differences among groups. They allow us to pinpoint which specific pairs of groups differ, allowing us to peek behind the curtain to explore the inner workings of pairwise differences.

Key post-hoc methods

There are two common post-hoc methods: Tukey's HSD, named after statistician John Tukey, which is known for its robustness in multiple comparisons. There's also the Bonferroni correction, named after mathematician Carlo Bonferroni, which adjusts p-values to control for Type I errors. For broader comparisons, use Tukey's HSD; Bonferroni is better for reducing false positives in more focused tests.

1 https://www.amphilsoc.org/item-detail/photograph-john-wilder-tukey

2 https://en.wikipedia.org/wiki/Carlo_Emilio_Bonferroni

The dataset: marketing ad campaigns

We'll work with a dataset of marketing campaigns, examining the `Click_Through_Rate` for different `Ad` campaigns to identify differences and which strategy is most effective.

Data organization with pivot tables

Pivot tables in pandas can be extremely helpful for organizing data, especially before conducting post-hoc analysis. It provides a clear comparison of the mean `Click_Through_Rates` for each campaign type.

Performing ANOVA

We start with ANOVA to assess if there's a significant difference in these `Click_Through_Rates` among the campaigns. This sets the stage for further analysis if significant differences are found. First, we specify the different campaign types. Then we create the groups using a list comprehension to extract the `Click_Through_Rate` for each `Ad_Campaign`. Next, we perform the ANOVA across the three campaign types, unpacking the groups using an asterisk, to compare their mean click-through rates. The very small P-value here indicates significant differences in these means.

Tukey's HSD test

If ANOVA indicates significant differences, Tukey's HSD test helps us understand exactly which campaigns differ. The `pairwise_tukeyhsd` function from `statsmodels.stats` takes arguments for the continuous response variable, `Click_Through_Rate` in this case, the categorical variable with more than two groups, `Ad_Campaign`, and α. To interpret the results of this table, we focus on the meandiff, p-adj (adjusted P-value), and reject columns. For the first row, Loyalty Reward versus New Arrival, the mean difference is 0.2211, with a p-value less than 0.05, indicating that the `Loyalty Reward` group has a significantly higher mean than the `New Arrival group`. For `Loyalty Reward` versus Seasonal Discount, on row 2, the mean difference is -0.2738. With a p-value less than 0.05, it suggests that the Loyalty Reward group has a significantly lower mean than the Seasonal Discount group. Lastly, for New Arrival versus Seasonal Discount, the mean difference is -0.4949, with a p-value less than 0.05, indicating that the New Arrival group has a significantly lower mean than the Seasonal Discount group.

Bonferroni correction set-up

The Bonferroni correction is a stringent method to adjust p-values when conducting multiple pairwise comparisons, effectively reducing the chances of a Type I error. A little more data preparation is required before applying the Bonferroni correction. We begin by creating an empty P-values list. Then, we lay out a list of tuples containing the pairwise comparisons that we will iterate over. Next, we iterate over the tuples in comparisons, using the tuple elements to extract the `Click_Through_Rate` for both groups. We run `ttest_ind` on the click through rates in a pairwise fashion, and append the p-values to our list.

Performing Bonferroni correction

Now we apply the Bonferroni correction using the multipletests function. The resulting p-values for the three comparisons are all extremely small. This again provides evidence that each of the three groups have significant click through rate differences.

1.3.6 Exercise 3.2.1

Anxiety treatments ANOVA

Psychologists conducted a study to compare the effectiveness of three types of therapy on reducing anxiety levels: Cognitive Behavioral Therapy (CBT), Dialectical Behavior Therapy (DBT), and Acceptance and Commitment Therapy (ACT). Participants were randomly assigned to one of the three therapy groups, and their anxiety levels were measured before and after the therapy sessions. The psychologists have asked you to determine if there are any significant differences in the effectiveness of these therapies.

Instructions

1. Create a pivot table to calculate the mean 'Anxiety_Reduction' value across groups of 'Therapy_Type' in this data.
2. Filter groups of therapy types and their 'Anxiety_Reduction' values by first creating a list of the three therapy types: 'CBT', 'DBT', and 'ACT'.

```
import numpy as np
import pandas as pd
from scipy.stats import f_oneway

# Set random seed for reproducibility
np.random.seed(4)

# Define therapy types
therapy_types = ['CBT', 'DBT', 'ACT']

# Generate random therapy assignments
therapy_assignments = np.random.choice(therapy_types, size=1422, p=[0.34, 0.33, 0.33])

# Generate Anxiety Reduction values following a normal distribution with given mean and std
danxiety_reduction = np.random.normal(loc=15.201, scale=4.938, size=1422)

# Ensure min and max are within expected range
danxiety_reduction = np.clip(danxiety_reduction, -1.206, 34.264)

# Create DataFrame
therapy_outcomes = pd.DataFrame({
    'Therapy_Type': therapy_assignments,
    'Anxiety_Reduction': danxiety_reduction
})

# Print summary statistics
print(therapy_outcomes.describe())

# Create pivot table
pivot_table = therapy_outcomes.pivot_table(
    values='Anxiety_Reduction',
    index='Therapy_Type',
    aggfunc='mean'
)

# Pivot to view the mean anxiety reduction for each therapy
print(pivot_table)

# Create groups to prepare the data for ANOVA
```

```
therapy_types = ['CBT', 'DBT', 'ACT']
groups = [therapy_outcomes[therapy_outcomes['Therapy_Type'] == therapy]['Anxiety_Reduction'] for

# Conduct ANOVA
f_stat, p_val = f_oneway(*groups)
print(p_val)
```

```
       Anxiety_Reduction
count        1422.000000
mean           15.224009
std             4.781342
min             0.723195
25%            11.855642
50%            15.360508
75%            18.602824
max            34.264000
              Anxiety_Reduction
Therapy_Type
ACT                   15.653751
CBT                   14.701516
DBT                   15.310404
0.007803856353541549
```

Caution

By analyzing the data with ANOVA, you've taken an important step in comparing the effectiveness of different therapies. Assuming an α of 0.05, the P-value indicates significant differences in therapy effectiveness.

1.3.7 Exercise 3.2.2

Applying Tukey's HSD

Following the ANOVA analysis which suggested significant differences in the effectiveness of the three types of therapy, the psychologists are keen to delve deeper. They wish for you to explain exactly which therapy types differ from each other in terms of reducing anxiety levels. This is where Tukey's Honest Significant Difference (HSD) test comes into play. It's a post-hoc test used to make pairwise comparisons between group means after an ANOVA has shown a significant difference. Tukey's HSD test helps in identifying specific pairs of groups that have significant differences in their means.

Instructions

- At a significance level of 0.05, perform Tukey's HSD test to compare the mean anxiety reduction across the three therapy groups.

```python
import numpy as np
import pandas as pd
from scipy.stats import f_oneway
from statsmodels.stats.multicomp import pairwise_tukeyhsd

# Set random seed for reproducibility
np.random.seed(4)

# Define therapy types
therapy_types = ['CBT', 'DBT', 'ACT']

# Generate random therapy assignments
therapy_assignments = np.random.choice(therapy_types, size=1422, p=[0.34, 0.33, 0.33])

# Generate Anxiety Reduction values following a normal distribution with given mean and std
danxiety_reduction = np.random.normal(loc=15.201, scale=4.938, size=1422)

# Ensure min and max are within expected range
danxiety_reduction = np.clip(danxiety_reduction, -1.206, 34.264)

# Create DataFrame
therapy_outcomes = pd.DataFrame({
    'Therapy_Type': therapy_assignments,
    'Anxiety_Reduction': danxiety_reduction
})

# Create pivot table
pivot_table = therapy_outcomes.pivot_table(
    values='Anxiety_Reduction',
    index='Therapy_Type',
    aggfunc='mean'
)

# Pivot to view the mean anxiety reduction for each therapy
print(pivot_table)

# Create groups to prepare the data for ANOVA
therapy_types = ['CBT', 'DBT', 'ACT']
groups = [therapy_outcomes[therapy_outcomes['Therapy_Type'] == therapy]['Anxiety_Reduction'] for

# Conduct ANOVA
```

```
f_stat, p_val = f_oneway(*groups)
print(p_val)

# Perform Tukey's HSD test
tukey_results = pairwise_tukeyhsd(
    therapy_outcomes['Anxiety_Reduction'],
    therapy_outcomes['Therapy_Type'],
    alpha= 0.05
)

print(tukey_results)
```

```
              Anxiety_Reduction
Therapy_Type
ACT                   15.653751
CBT                   14.701516
DBT                   15.310404
0.007803856353541549
Multiple Comparison of Means - Tukey HSD, FWER=0.05
====================================================
group1 group2 meandiff p-adj   lower   upper  reject
----------------------------------------------------
   ACT    CBT  -0.9522 0.0059 -1.6767 -0.2278   True
   ACT    DBT  -0.3433 0.5087 -1.0697   0.383  False
   CBT    DBT   0.6089  0.123 -0.1205  1.3383  False
----------------------------------------------------
```

Note

The Tukey HSD test provided clear insights into which therapy types significantly differ in reducing anxiety. These findings can guide psychologists in refining treatment approaches. Did you catch that (ACT and DBT) and (CBT and DBT)don't differ significantly from this experiment?

1.3.8 Exercise 3.2.3

Applying Bonferoni correction

After identifying significant differences between therapy groups with Tukey's HSD, we want to confirm our findings with the Bonferroni correction. The Bonferroni correction is a conservative statistical adjustment used to counteract the problem of multiple comparisons. It reduces the chance of obtaining false-positive results by adjusting the significance level. In the context of your study on the effectiveness of CBT, DBT, and ACT, applying the Bonferroni correction will help ensure that the significant differences you observe between therapy groups are not due to chance.

Instructions

- Conduct independent t-tests between all pairs of therapy groups in `therapy_pairs` and append the p-values (`p_val`) to the `p_values` list.
- Apply the Bonferroni correction to adjust the `p-values` from the multiple tests and print them.

```python
import numpy as np
import pandas as pd
from scipy.stats import ttest_ind
from statsmodels.sandbox.stats.multicomp import multipletests

# Set random seed for reproducibility
np.random.seed(4)

# Define therapy types
therapy_types = ['CBT', 'DBT', 'ACT']

# Generate random therapy assignments
therapy_assignments = np.random.choice(therapy_types, size=1422, p=[0.34, 0.33, 0.33])

# Generate Anxiety Reduction values following a normal distribution with given mean and std
danxiety_reduction = np.random.normal(loc=15.201, scale=4.938, size=1422)

# Ensure min and max are within expected range
danxiety_reduction = np.clip(danxiety_reduction, -1.206, 34.264)

# Create DataFrame
therapy_outcomes = pd.DataFrame({
    'Therapy_Type': therapy_assignments,
    'Anxiety_Reduction': danxiety_reduction
})

p_values = []

therapy_pairs = [('CBT', 'DBT'), ('CBT', 'ACT'), ('DBT', 'ACT')]

# Conduct t-tests and collect P-values
for pair in therapy_pairs:
    group1 = therapy_outcomes[therapy_outcomes['Therapy_Type'] == pair[0]]['Anxiety_Reduction']
    group2 = therapy_outcomes[therapy_outcomes['Therapy_Type'] == pair[1]]['Anxiety_Reduction']
    t_stat, p_val = ttest_ind(group1, group2)
    p_values.append(p_val)

# Apply Bonferroni correction
print(multipletests(p_values, alpha=0.05, method='bonferroni')[1])
```

```
[0.15515276 0.00483525 0.83050552]
```

Note

The Bonferroni correction applied to adjust for the P-values for multiple comparisons. This step is critical to control for Type I error, ensuring the reliability of my findings. Here again it is obvious that (ACT and DBT) and (CBT and DBT) don't differ significantly from this experiment due to the corrected P-value of 1.

1.3.9 Chapter 3.3: P-values, alpha, and errors

In this lesson, we'll deepen our understanding of p-values, alpha levels, and experimental errors. This will prepare us for the next video, where we'll tackle a key concept in experimental design called power analysis!

P-values and alpha

P-values and alpha can be viewed as a game. Think of conducting a scientific experiment where we are trying to determine whether a certain strategy (our hypothesis) leads to winning (or a significant result) more often than just by chance. P-values help us understand the likelihood of observing our data if the null hypothesis was true. That is they serve as the scoreboard of the game. Setting an α level, often 0.05, allows us to determine the threshold at which we consider our results statistically significant, akin to setting the rules of a game before playing. Alpha is like establishing a rule for what counts as a "remarkable" win in this game. If your P-value is below this alpha level, it's as if we've achieved a high score or a remarkable performance in the game, leading us to conclude that our strategy (the alternative hypothesis) might indeed be effective, and it's not just the luck of the draw.

The dataset: crop yields

We'll work with a dataset of crop yields from different fields, where each field was treated with either organic or synthetic fertilizer. Our goal is to analyze this data to determine if there's a significant difference in crop yields between the two fertilizer types.

Visualizing the data

It's helpful to visualize the crop yields for each fertilizer type. By plotting the kernel density estimates (kde), we get a sense of how the two fertilizers might differ in terms of their effect on crop yields and whether there's an overlap between their effects. It appears that Organic tends to produce a higher yield than Synthetic with some overlap.

Conducting an independent samples t-test

We set our alpha to the standard five-percent level. To compare the effectiveness of organic versus synthetic fertilizers, we perform a t-test on the crop yields from the two groups. The p-value is smaller than alpha suggesting that fertilizer type has a statistically significant impact on crop yield.

Exploring experimental errors

In experimental design, we encounter two main types of errors. Type I errors occur when we incorrectly reject a true null hypothesis, akin to a false alarm. Type II errors happen when we fail to reject a false null hypothesis, similar to a missed detection.

More on alpha

Alpha, or the significance level, is crucial in hypothesis testing; it indicates the probability of a Type I error—rejecting a true null hypothesis. Common α levels include 0.05, 0.01, and 0.10, representing risks of 5%, 1%, and 10%, respectively, for such errors. Selecting an alpha hinges on the study's context and a balance between tolerating a Type I error and the risk of overlooking a true effect, known as a Type II error. The choice should align with the study's goals and the implications of potential errors. Conventionally, 0.05 is the standard for statistical significance across many disciplines. For more rigorous scrutiny, particularly where the cost of a Type I error is high, an α of 0.01 is preferred. In preliminary studies, where a higher error tolerance is permissible, an α of 0.10 may be utilized, allowing for a broader exploration of potential effects with subsequent validation through more stringent testing.

1.3.10 Exercise 3.3.1

Analyzing toy durability

In product development within the toy industry, it's crucial to understand the durability of toys, particularly when comparing educational toys to recreational ones. Durability can significantly impact customer satisfaction and repeat business. Researchers in a toy manufacturing company have asked you to conduct the analysis of a study comparing the durability of educational toys versus recreational toys. The `toy_durability` DataFrame contains the results of these tests, with durability scores assigned based on rigorous testing protocols.

Instructions

- Calculate the mean `'Durability_Score'` for both `'Educational'` and `'Recreational'` toys using a pivot table.
- Perform an independent samples t-test to compare the durability of `'Educational'` and 'Recreational' toys by first separating durability scores by `Toy_Type`.

```python
import numpy as np
import pandas as pd
from scipy.stats import ttest_ind

# Set random seed for reproducibility
np.random.seed(36)

# Generate Toy_Type column with approximately equal distribution
toy_types = np.random.choice(['Educational', 'Recreational'], size=1900)

# Generate Durability_Score based on the means for each Toy_Type
durability_scores = np.where(
    toy_types == 'Educational',
    np.random.normal(loc=80.101, scale=6.0, size=1900),
    np.random.normal(loc=79.461, scale=6.0, size=1900)
)

# Create the DataFrame
toy_durability = pd.DataFrame({'Toy_Type': toy_types, 'Durability_Score': durability_scores})

# Compute the pivot table
mean_durability = toy_durability.pivot_table(values='Durability_Score', index='Toy_Type', aggfunc
print(mean_durability)

# Perform t-test
educational_durability_scores = toy_durability[toy_durability['Toy_Type'] == 'Educational']['Dura
recreational_durability_scores = toy_durability[toy_durability['Toy_Type'] == 'Recreational']['Du
t_stat, p_val = ttest_ind(educational_durability_scores, recreational_durability_scores)

print("P-value:", p_val)
```

```
              Durability_Score
Toy_Type
Educational          80.060756
Recreational         79.430888
P-value: 0.025042366796540375
```

Note

The P-value suggests that there's a statistically significant difference in durability between `'Educational'` *and* `'Recreational'` *toys, assuming an alpha of 0.05. This insight could be crucial for product development and marketing strategies.*

1.3.11 Exercise 3.3.2

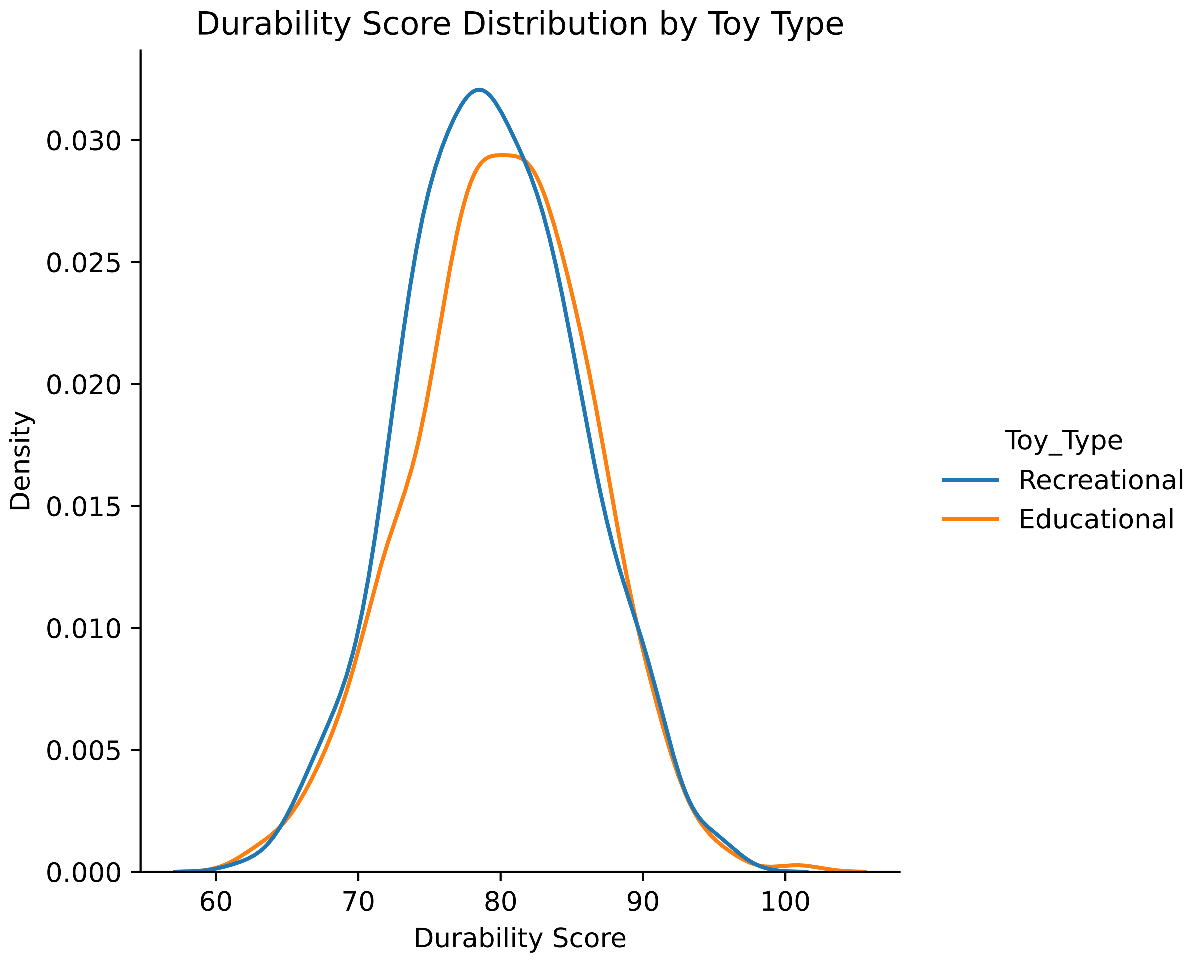
Visualizing durability differences

Following the analysis of toy durability, the research team is interested in you visualizing the distribution of durability scores for both Educational and Recreational toys. Such visualizations can offer intuitive insights into the data, potentially highlighting the range and variability of scores within each category. This step is essential for presenting findings to non-technical stakeholders and guiding further product development decisions.

Instructions

- Visualize the distribution of `'Durability_Score'` for Educational and Recreational toys using a Kernel Density Estimate (KDE) plot, highlighting differences by using the `'Toy_Type'` column to color the distributions differently.

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

# Set random seed for reproducibility
np.random.seed(36)

# Generate Toy_Type column with approximately equal distribution
toy_types = np.random.choice(['Educational', 'Recreational'], size=1900)

# Generate Durability_Score based on the means for each Toy_Type
durability_scores = np.where(
    toy_types == 'Educational',
    np.random.normal(loc=80.101, scale=6.0, size=1900),
    np.random.normal(loc=79.461, scale=6.0, size=1900)
)

# Create the DataFrame
toy_durability = pd.DataFrame({'Toy_Type': toy_types, 'Durability_Score': durability_scores})

# Visualize the distribution of Durability_Score for each Toy_Type
sns.displot(data=toy_durability, x="Durability_Score",
         hue="Toy_Type", kind="kde")
plt.title('Durability Score Distribution by Toy Type')
plt.xlabel('Durability Score')
plt.ylabel('Density')

plt.show()
```



1.3.12 Chapter 3.4: Power analysis: sample and effect size

We now dive into the intricacies of power analysis, focusing on understanding effect size and how it influences sample size.

A primer on effect size

Effect size quantifies the magnitude of the difference between groups, beyond just noting if the difference is statistically significant. Cohen's d is a commonly used measure, calculated as the difference in means divided by a pooled standard deviation.

The dataset: video game engagement

A video game company conducted an experiment with sixty participants to understand player engagement across two game genres: Action and Puzzle. They recorded the average number of hours players spent engaged to assess which type tends to captivate players more effectively.

Calculating power overview

Power analysis revolves around the probability that our test will correctly reject a false null hypothesis. This corresponds to identifying a true effect, avoiding a Type II error. A type II error is denoted as beta, so power is one minus beta and it ranges from zero to one, where one is certainty in our ability to detect a true effect. To calculate power, we first assume an effect size. Here we choose a value of 1, derived from historical data comparing the engagement scores of video game genres. We can also use our sample data to make an estimate of the effect size, but traditionally power analysis is done prior to the data collection. This can also help us determine how big of a sample size we should use in our study. We initialize the power object and call the `.solve_power()` method, using a sample size for how many video game players were assessed in either group (30), our assumed effect size, and our alpha of 0.05. This high power tells us the likelihood that our test will detect a significant result, given our effect size and sample size.

Cohen's d formulation

To calculate Cohen's d as an effect size, we define a function. Its two inputs are numeric data corresponding to the two groups from our sample data. We calculate the difference in the means of the two groups, their sample sizes, and their variances. Next, we determine a pooled standard deviation using this information. Lastly, Cohen's d is the difference in means divided by the pooled standard deviation.

Cohen's d for video game data

To apply this to the video game data, we first split the data into two groups based on the genre. Then we apply our function to get the effect size. The result here is near the theoretical result of 1 we assumed earlier.

Understanding sample size and power

Balancing the need for sufficient power with practical constraints on sample size is a fundamental aspect of planning a study, such as comparing engagement times across different video game genres. A larger sample size can enhance an experiment's power, improving the likelihood of detecting a true effect.

1 https://grabngoinfo.com/power-analysis-for-sample-size-using-python/

Sample size calculation in context

Let's contextualize this within our video game study. Assuming our calculated value for Cohen's d engagement time between game genres, we calculate the sample size needed for each group to achieve 99% power with an alpha of 0.05 and equally-sized groups with a ratio of 1. This calculation is pivotal in ensuring our study is adequately powered to detect meaningful differences in player engagement across genres. Assuming we have an effect size of around 1.2, we would need at least 28 participants in each group to achieve a power of 99%. Recall we collected 30 participants, so we can feel confident about our experiment's power.

Visualizing sample size requirements

We next build a visualization illustrating the relationship between effect size measured as Cohen's d and required sample size for our video game study, by plotting varying effect sizes against required sample sizes. As effect size increases, the required sample size for each group decreases, highlighting the importance of understanding the expected magnitude of differences when planning a study.

1.3.13 Exercise 3.4.1

Estimating required sample size for energy study

In the energy sector, researchers are often tasked with evaluating the effectiveness of new technologies or initiatives to enhance energy efficiency or reduce consumption. A study is being designed to compare the impact of two energy-saving measures: "Smart Thermostats" and "LED Lighting". To ensure the study has sufficient power to detect a meaningful difference in energy savings between these two measures, you'll conduct a power analysis.

Instructions

- Instantiate a `TTestIndPower` object.
- Conduct the power analysis to estimate the required sample size for each group (Smart Thermostats and LED Lighting) to achieve a power of 0.9, assuming a moderate effect size (Cohen's d = 0.5) and an alpha of 0.05 with an equal sized groups.

```
import numpy as np
import pandas as pd
from statsmodels.stats.power import TTestIndPower

# Instantiate a TTestIndPower object
power_analysis = TTestIndPower()

# Conduct a power analysis to determine the required sample size
required_n = power_analysis.solve_power(
    effect_size=0.5,
    alpha=0.05,
    power=0.9,
    ratio=1)

print(required_n)
```

```
<script.py> output:
    85.03128688801092
```

By conducting a power analysis, you've determined that approximately `85` participants are required in each group to achieve a power of `0.9`, assuming an Cohen's d effect size of `0.5`. This information is crucial for planning a sufficiently powered study to compare the energy-saving effectiveness of Smart Thermostats versus LED Lighting.

1.4 Chapter 4: Advanced Insights from Experimental Complexity

Hop into the complexities of experimental data analysis. Learn to synthesize insights using pandas, address data issues like heteroscedasticity with `scipy.stats`, and apply nonparametric tests like Mann-Whitney U. Learn additional techniques for transforming, visualizing, and interpreting complex data, enhancing your ability to conduct robust analyses in various experimental settings.

1.4.1 Chapter 4.1: Synthesizing insights from complex experiments

We'll next explore how to synthesize insights from complex experiments, focusing on integrating data across different experimental factors to derive meaningful conclusions.

Manufacturing yield data

We'll work with `manufacturing_yield` dataset, which captures how factors like `material` type, `production speed`, and `temperature` settings impact the `yield` in our experiment. The `BatchID` column stores a unique identifier for each item in the data. Determining whether these factors have an impact on the yield strength can be used to optimize manufacturing outcomes.

```
manufacturing_yield
```

```
BatchID MaterialType ProductionSpeed TemperatureSetting YieldStrength
39           Polymer          Medium            Optimal         58.83
195            Metal            High               High         51.29
462          Polymer            High             Optimal         55.15
696        Composite          Medium                Low         50.27
142        Composite            High                Low         57.62
```

Manufacturing quality data

A separate experiment was also done on the same items exploring the impact of production speed on the quality of the product as the response. This data is stored in the `manufacturing_quality` DataFrame.

```
manufacturing_quality

BatchID ProductionSpeed ProductQuality
149                 Low         93.87
739                  High        93.35
617               Medium        90.45
131                  High        90.26
684                   Low        91.62
```

Merging strategy

We can use the pandas merge method to seamlessly integrate the `manufacturing_yield` and `manufacturing_quality` datasets, joining on the `BatchID` and `ProductionSpeed` columns so associated data is connected together. We can now explore this data in a variety of ways, looking for relationships in the data with the two response columns of yield and quality.

```
merged_manufacturing = pd.merge(manufacturing_yield, manufacturing_quality, on=['BatchID', 'Produ

print(merged_manufacturing)

BatchID MaterialType ProductionSpeed TemperatureSetting YieldStrength ProductQuality
1               Metal             Low               High         57.32          91.19
5           Composite          Medium            Optimal         51.82          90.20
7             Polymer             Low               High         56.12          91.66
8           Composite            High            Optimal         50.91          93.05
11            Polymer             Low               High          50.13          92.31
```

Side-by-side bar graph

We can showcase potential interactions between `MaterialType` and `ProductionSpeed` on `YieldStrength` using Seaborn's catplot function. `Yield` is on the vertical axis broken down by `material` on the horizontal, and the bars are colored by `ProductionSpeed`. It seems that Polymer tends to have the highest yield followed by Composite and then by Metal. Production speed has a negative impact on yield across each of the materials as well with slower production leading to better yield than faster production.

```
import seaborn as sns
sns.catplot(x='MaterialType', y='YieldStrength', hue='ProductionSpeed', kind='bar',
data=merged_manufacturing)
```

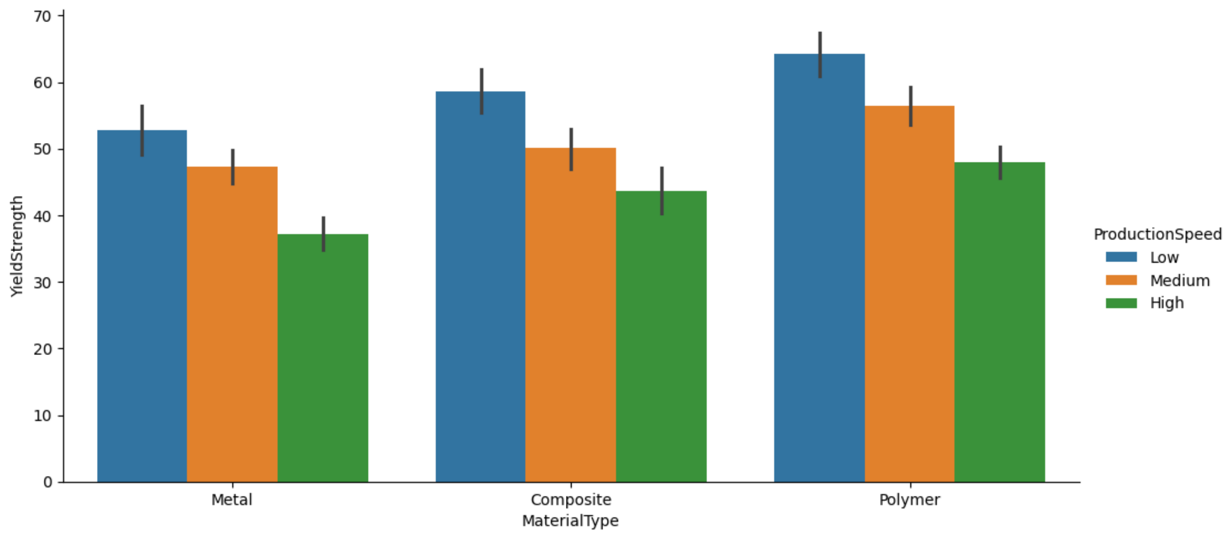
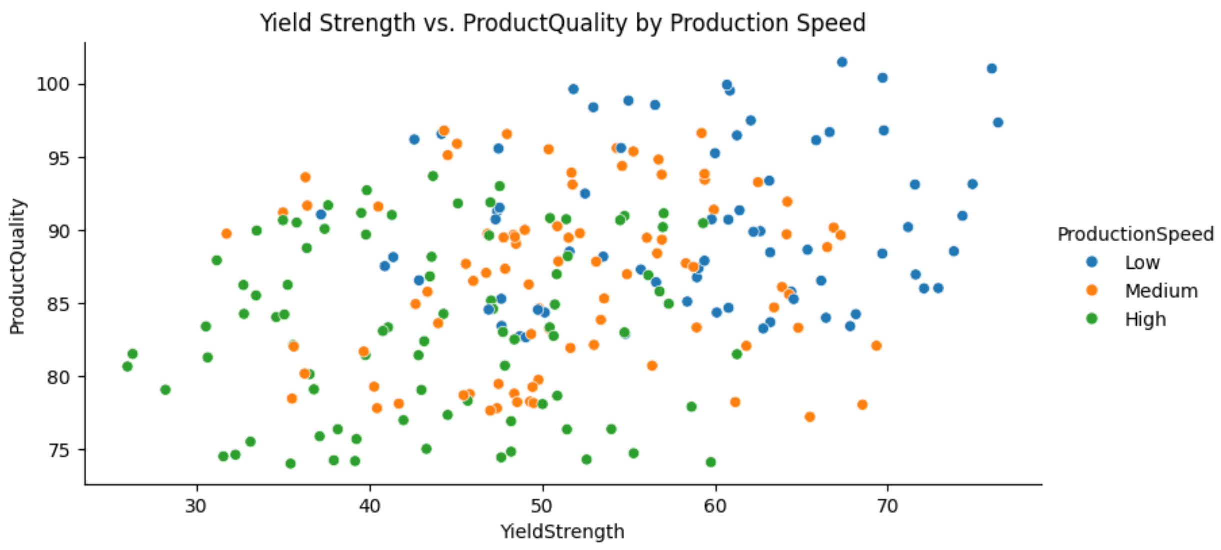


Figure 1: image

Three variable scatterplot

To further explore relationships in the data, we can look to see how both of the response variables relate conditioned on ProductionSpeed. We use a scatterplot with each of the response variables on the axes colored by speed. The green High values tend to be lower in each, with the orange Medium values more near the center of the plot, and the low ProductionSpeed points tending to be near the upper right of the plot.

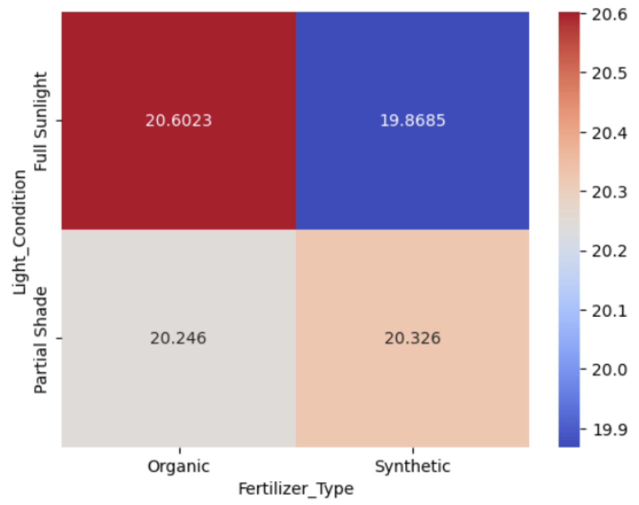
```
sns.relplot(x='YieldStrength', y='ProductQuality', hue='ProductionSpeed',
kind='scatter', data=merged_manufacturing)
plt.title('Yield Strength vs. Product Quality by Production Speed')
```



Communicating data to technical audiences

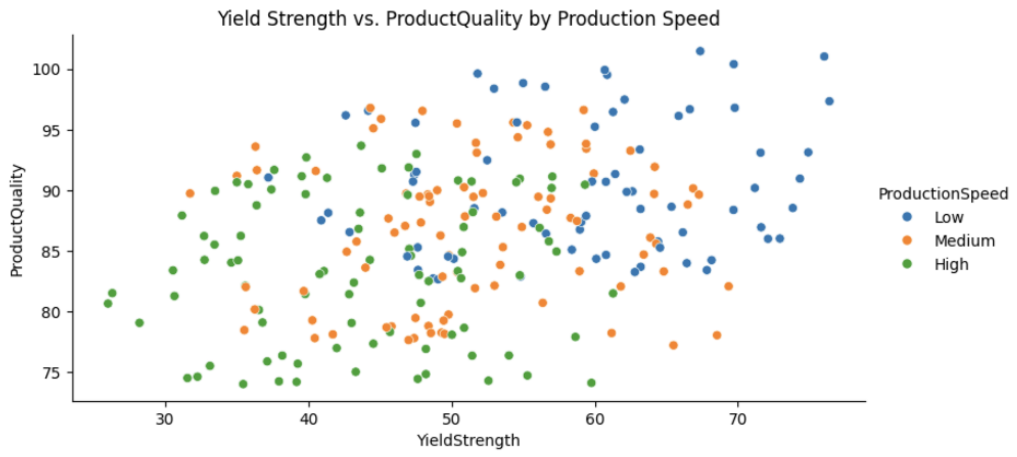
Now that we've seen some visualizations on complex experimental data, let's focus on how we can tailor our approach when presenting to technical audiences. Crafting data narratives for this group involves integrating detailed statistical analysis, such as p-values, test statistics, and significance levels, into our stories. This not only enriches the narrative but also supports the validity of our findings with concrete evidence. Additionally, visualizing complex data for technical stakeholders should go beyond basic charts and include advanced visualizations like heat maps, scatter plots using multiple colors, and projection lines. These types of visuals can more precisely demonstrate relationships and trends within the data, catering to an audience that values depth and detail in data exploration.

“The test statistic was **7.78**”



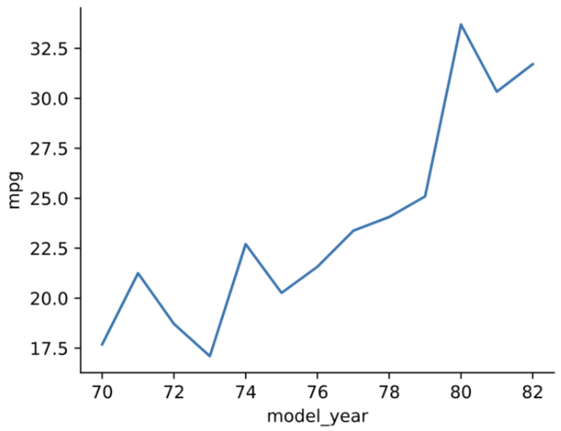
“The p-value is **0.023**”

“We opted for a **5%** significance level”



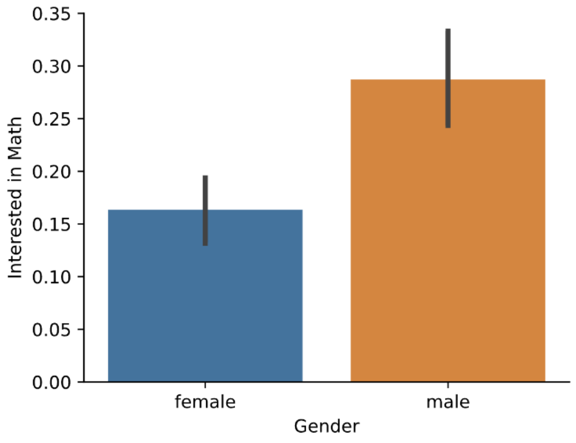
Engaging non-technical audiences with data

Moving on to non-technical audiences, our focus shifts towards simplifying the insights derived from our data. It’s crucial to distill complex information into its essence, presenting it in a clear and straightforward manner. Use foundational visualizations like bar graphs and line charts, which are easier to interpret and highlight key points without the need for statistical jargon. When preparing presentations for a non-technical crowd, ensure that the content is audience-centric by highlighting why the data matters to them in practical terms. Connect the data insights to real-world applications and outcomes that resonate with their interests and professional challenges. This approach not only maintains relevance but also enhances engagement by aligning the presentation contents with their level of expertise and need for application rather than detailed analysis.



"The Ceramic catalyst **significantly increases** rate of reaction"

"The mobile app converts **50% more** customers than the web browser"



1.4.2 Exercise 4.1.1

Visualizing loan approval yield

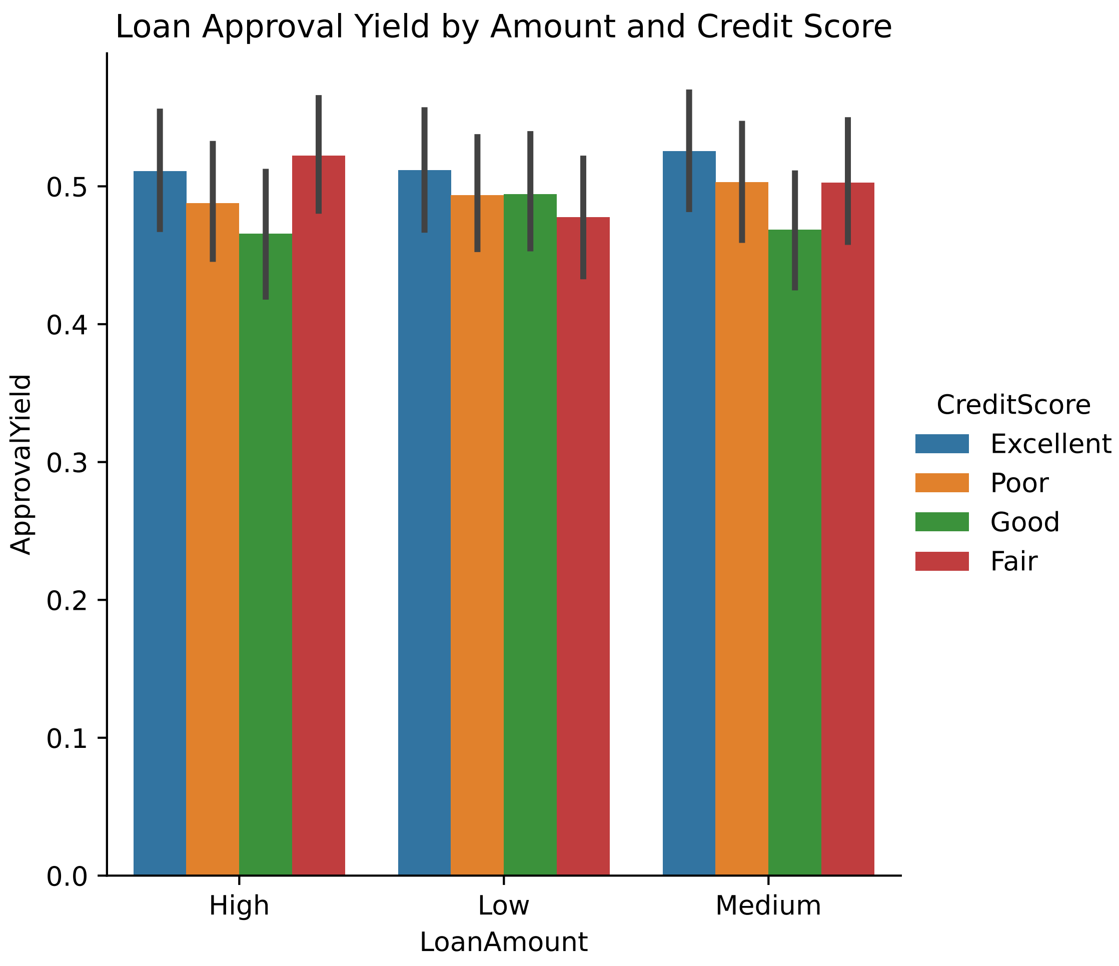
In the realm of financial services, understanding the factors that influence loan approval rates is crucial for both lenders and borrowers. A financial institution has conducted a study and collected data on loan applications, detailing the amount requested, the applicant's credit score, employment status, and the ultimate yield of the approval process. This rich dataset offers a window into the nuanced dynamics at play in loan decision-making. You have been asked to dive into the `loan_approval_yield` dataset to understand how loan amounts and credit scores influence approval yields.

Instructions

1. Create a side-by-side bar graph, setting the x-axis to `'LoanAmount'`, the y-axis to `'ApprovalYield'`, and differentiating the bars with hues for `'CreditScore'`.
2. Question: What does the analysis of approval yields across different credit scores and loan amounts reveal?

The data shows that Poor credit scores tend to have similar approval yields across various loan amounts, while Good credit scores exhibit more variability, reflecting different lending criteria based on the loan size.

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

loan_approval_yield = pd.read_csv('datasets/loan_approval_yield.csv')

# Use Seaborn to create the bar graph
sns.catplot(x="LoanAmount",
            y="ApprovalYield",
            hue="CreditScore",
            kind="bar",
            data=loan_approval_yield)
plt.title("Loan Approval Yield by Amount and Credit Score")
plt.show()
```



1.4.3 Exercise 4.1.2

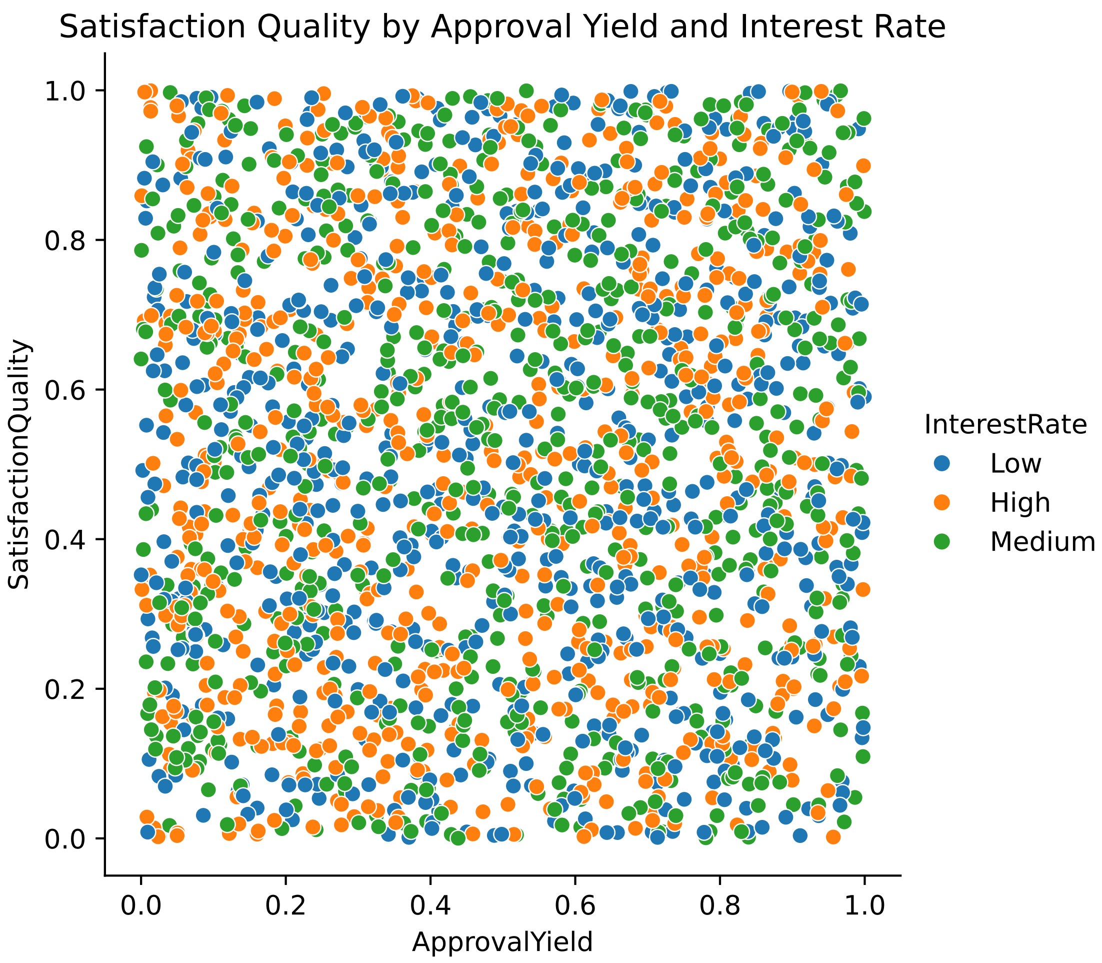
Exploring customer satisfaction

Merging datasets is a crucial skill in data analysis, especially when dealing with related data from different sources. You're working on a project for a financial institution to understand the relationship between loan approval rates and customer satisfaction. Two separate studies have been conducted: one focusing on loan approval yield based on various factors, and another on customer satisfaction under different conditions. Your task is to analyze how approval yield correlates with customer satisfaction, considering another variable such as interest rates.

Instructions

1. Merge `loan_approval_yield` with `customer_satisfaction`.
2. Create a scatter plot to compare `'SatisfactionQuality'` versus `'ApprovalYield'`, coloring the points by `'InterestRate'`.

```python
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt

loan_approval_yield = pd.read_csv('datasets/loan_approval_yield.csv')

customer_satisfaction = pd.read_csv('datasets/customer_satisfaction.csv')

# Merge the two datasets
merged_data = pd.merge(loan_approval_yield,
                      customer_satisfaction,
                      on='ApplicationID')

# Use Seaborn to create the scatter plot
sns.relplot(x="ApprovalYield",
            y="SatisfactionQuality",
            hue="InterestRate",
            kind="scatter",
            data=merged_data)
plt.title("Satisfaction Quality by Approval Yield and Interest Rate")
plt.show()
```



3. Question: What does the scatterplot of Customer Satisfaction versus Approval Yield, including Interest Rate as a variable, indicate about their relationship in the experimental data?

There isn't a strong relationship between Customer Satisfaction and Approval Yield in this experimental data. The resulting scatterplot looks similar to white noise scattered all about even when including Interest Rate

1.4.4 Chapter 4.2: Addressing complexities in experimental data

Next, we will look into addressing complexities in experimental data, focusing on identifying and mitigating issues like interactions, confounding variables, and heteroscedasticity.

Geological data

The `mineral_rocks` dataset encompasses 300 rock samples, detailing attributes like rock type, geographical location, mineral hardness, and rock porosity. Each entry in the dataset represents a unique sample, identified by its `SampleID`, and characterized by varying levels of `MineralHardness` and `RockPorosity` across different rock types and locations. Understanding the distribution and interactions within this data is critical for selecting the right statistical tests for our analysis.

```
mineral_rocks
```

```
SampleID     RockType Location MineralHardness RockPorosity
       1  Metamorphic     West             5.9         12.3
       2      Igneous    North             5.3          1.6
       3  Metamorphic     East             5.6         11.0
       4  Metamorphic    South             3.2         12.2
       5  Sedimentary    South             2.0         29.8
```

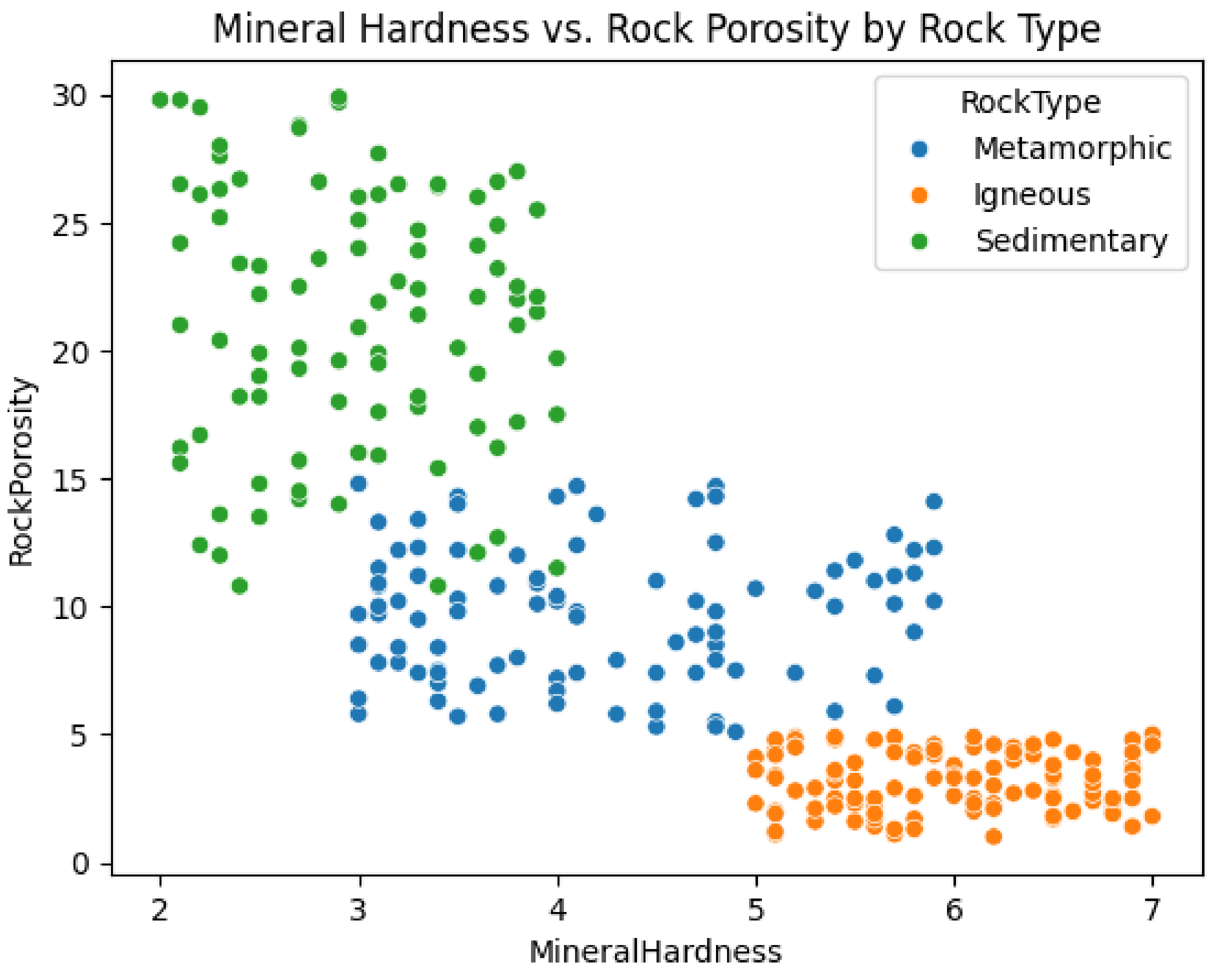
Understanding data complexities

Our exploration begins by identifying potential complexities within our `mineral_rocks` dataset: Interactions between rock types and their mineral hardness might influence the observed mineral properties. The variance in rock porosity, a key feature of our dataset, might not be consistent across all samples, indicating potential heteroscedasticity. There could be confounding variables that affect both mineral hardness and rock porosity. This is often the hardest problem to solve as it likely means that further data gathering is necessary to retrieve that extra variable information. Understanding these issues helps us decide whether parametric tests, which assume normality and homoscedasticity, can be employed or if we should rely on non-parametric tests, not assuming a specific distribution.

Addressing interactions

With the `mineral_rocks` dataset, we begin by visualizing the relationship between `MineralHardness` and `RockPorosity`, colored by `RockType`. This initial exploration helps identify potential complexities, such as interactions between variables. We seem to have an interaction between rock type and mineral hardness on rock porosity from the plot, since there are distinct groupings by `RockType`. Addressing interactions helps us understand whether more robust non-parametric methods are necessary for accurate analysis.

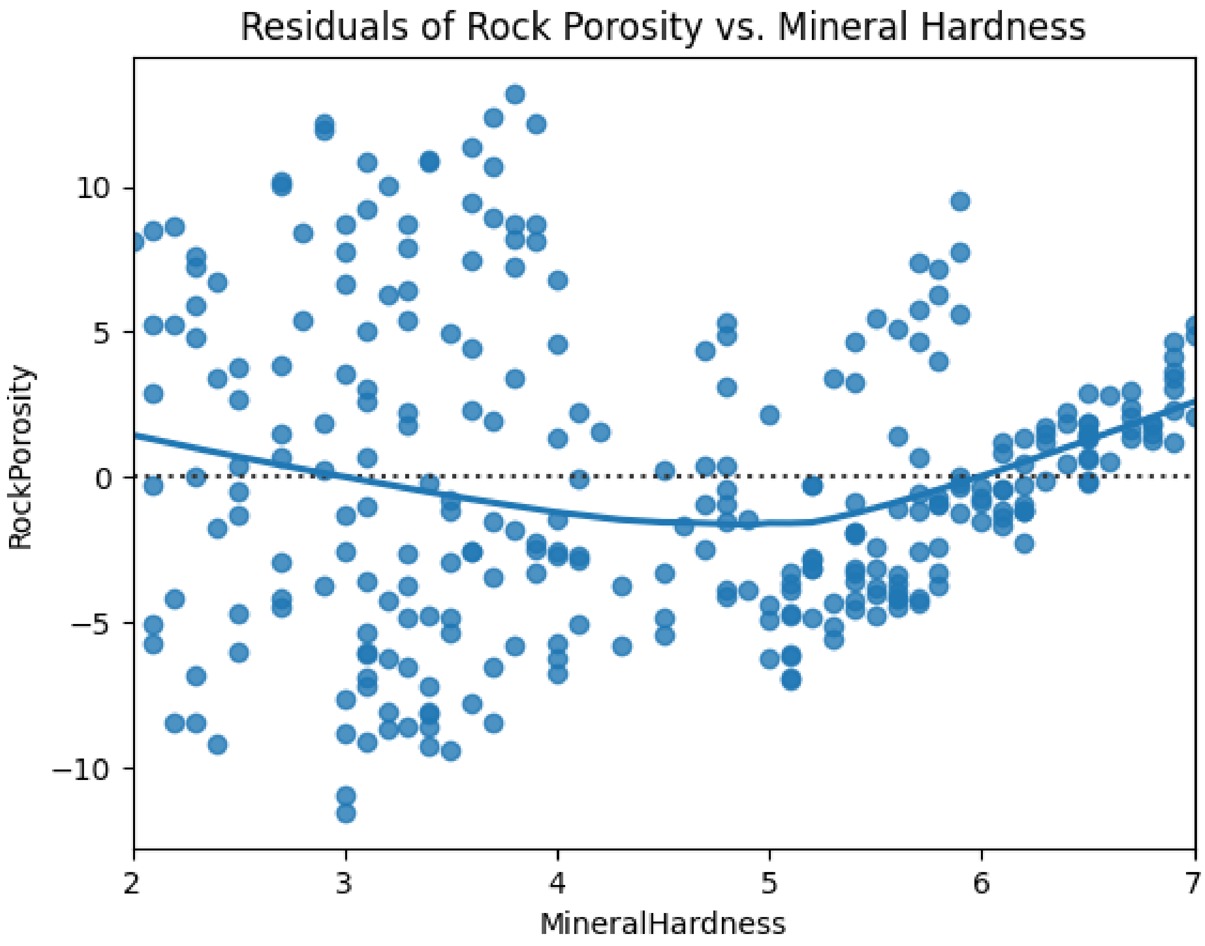
```
sns.scatterplot(x='MineralHardness', y='RockPorosity',
hue='RockType', data=mineral_rocks)
```



Addressing heteroscedasticity

Heteroscedasticity refers to the changing variability of a variable across the range of another variable. We use Seaborn's `residplot` to check for heteroscedasticity in our data, plotting residuals of `RockPorosity` against `MineralHardness`. We include the `lowess` smoothing option to show the trend in the data going from left to right. We see that, overall, the `lowess` line remains somewhat close to 0 and relatively flat, but the curve does lead us to be a little cautious since it highlights the spread being different in some areas of our data.

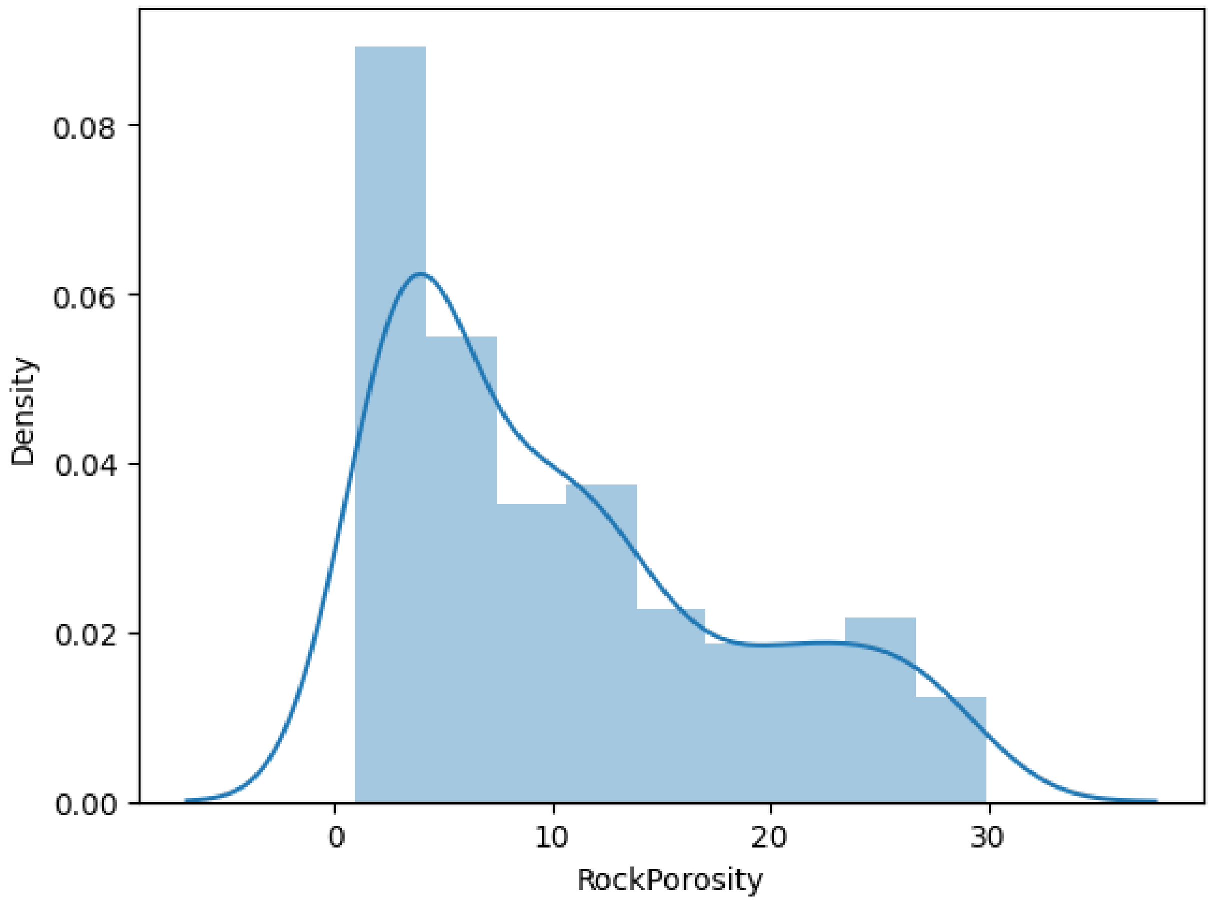
```
sns.residplot(x='MineralHardness', y='RockPorosity',
data=mineral_rocks, lowess=True)
```



Non-normal data

When the residual plot deviates from expectations, it can be useful to explore the distribution of the variables used. Here, we investigate `RockPorosity` with a histogram using Seaborn's `displot` function. We see that the data is skewed and of a non-normal shape.

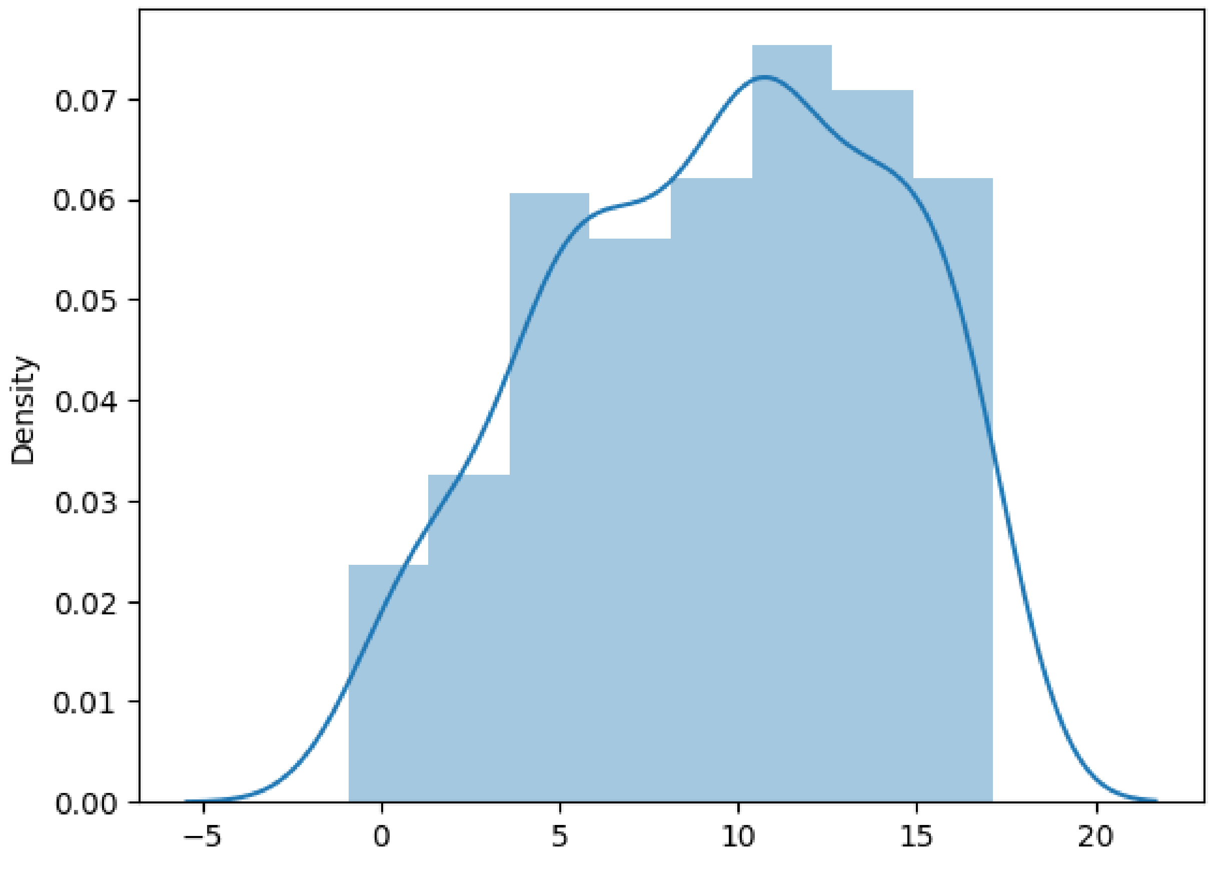
```
sns.displot(mineral_rocks['RockPorosity'])
```



Data transformation with Box-Cox

To address issues like skewness and heteroscedasticity, we can apply data transformations. Here, we use the `Box-Cox` transformation from `scipy.stats` on `RockPorosity` to stabilize variance and make the data more closely resemble a normal distribution. We add the transformed data as a column to our DataFrame. The `Box-Cox` transformation requires non-zero entries, which we have for all `RockPorosity` values. Note that this transformed data isn't perfectly normal, but does have much more of that bell shape than it did originally.

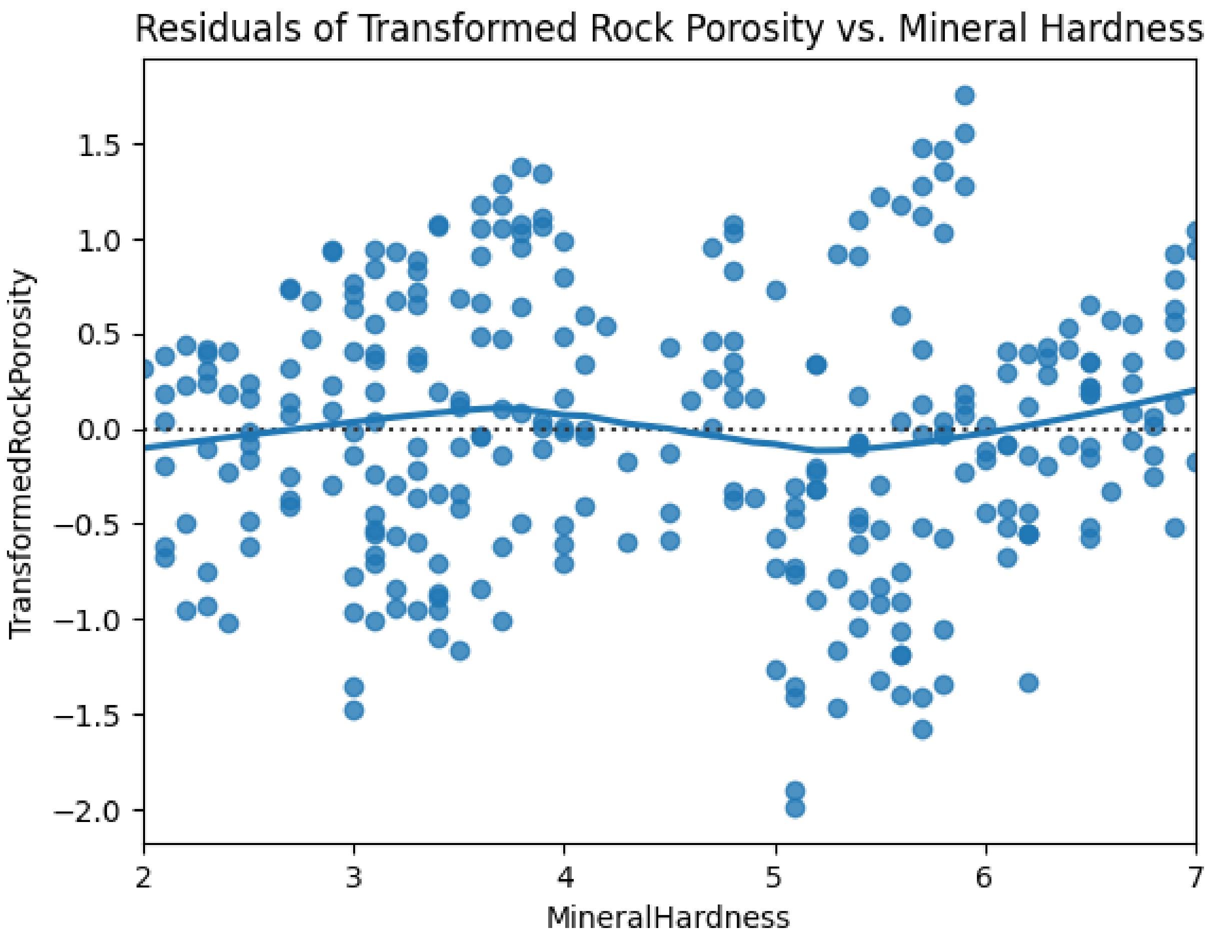
```
from scipy.stats import boxcox

mineral_rocks['TransformedRockPorosity'], _ = boxcox(mineral_rocks['RockPorosity'])

sns.displot(mineral_rocks['TransformedRockPorosity'])
```



Post-transformation analysis

To verify that we've better addressed the heteroscedasticity with the Box-Cox transformation, we can repeat our `residplot` with the `TransformedRockPorosity`. This visualization helps us understand whether the Box-Cox transformation has successfully stabilized the variance across the range of `MineralHardness`, an important assumption for many statistical tests. The `lowess` line is now much flatter, going from left to right across the plot. We can now feel more confident that this transformed data has better addressed heteroscedasticity than the non-transformed data.

```
sns.residplot(x='MineralHardness', y='TransformedRockPorosity',
data=mineral_rocks, lowess=True)
```



1.4.5 Exercise 4.2.1

Check for heteroscedasticity in shelf life

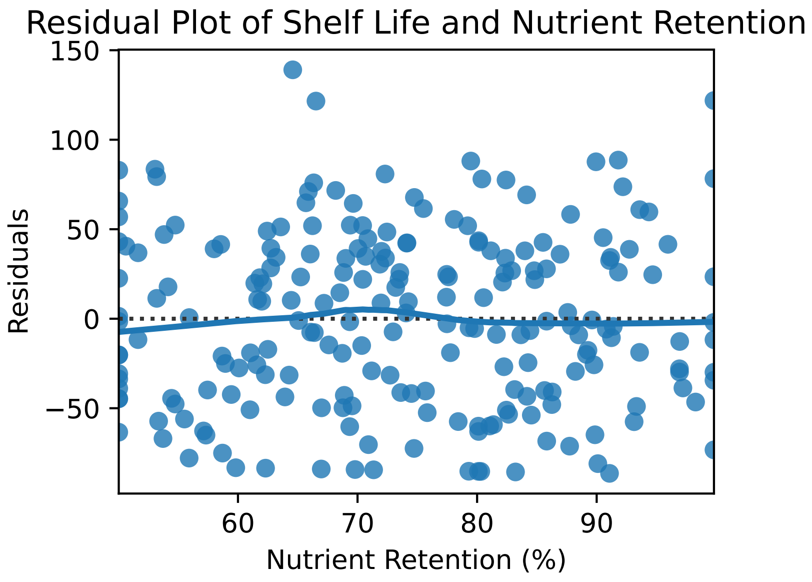
When examining food preservation methods, it's crucial to understand how the variance of one variable, such as shelf life, might change across the range of another variable like nutrient retention. Identifying such patterns, known as heteroscedasticity, can provide insights into the consistency of preservation effects. The `food_preservation` dataset encapsulates the outcomes of various preservation methods on different food types, specifically highlighting the balance between nutrient retention and resultant shelf life.

Instructions

- Use an appropriate plot to check for heteroscedasticity between `'NutrientRetention'` and `'ShelfLife'`.

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

# Set random seed for reproducibility
np.random.seed(242)

# Define number of rows
num_rows = 215

# Generate ProductID from 1 to 215
product_id = np.arange(1, num_rows + 1)

# Generate NutrientRetention with the given summary statistics
nutrient_retention = np.random.normal(loc=73.481, scale=14.838, size=num_rows)
nutrient_retention = np.clip(nutrient_retention, 50.030, 99.810)  # Ensuring within min-max range

# Generate ShelfLife with the given summary statistics
shelf_life = np.random.normal(loc=105.210, scale=54.661, size=num_rows)
shelf_life = np.clip(shelf_life, 27.860, 267.500)  # Ensuring within min-max range

# Create FoodType and PreservationMethod categories
food_types = ['Fruit', 'Meat', 'Vegetable']
preservation_methods = ['Canning', 'Drying', 'Freezing']
counts = [22, 32, 26, 21, 22, 23, 23, 21, 25]

# Generate categorical data for FoodType and PreservationMethod based on given counts
food_preservation_data = []
for (food, method), count in zip([(f, p) for f in food_types for p in preservation_methods], coun
    food_preservation_data.extend([(food, method)] * count)

# Convert to DataFrame and ensure it has the required 215 rows
food_preservation_categorical = pd.DataFrame(food_preservation_data[:num_rows], columns=['FoodTyp

# Create final DataFrame
food_preservation = pd.DataFrame({
    'ProductID': product_id,
    'NutrientRetention': nutrient_retention,
    'ShelfLife': shelf_life
})

# Add categorical data
food_preservation = pd.concat([food_preservation, food_preservation_categorical], axis=1)
```

```
# Check for heteroscedasticity with a residual plot
sns.residplot(x='NutrientRetention', y='ShelfLife',
         data=food_preservation, lowess=True)
plt.title('Residual Plot of Shelf Life and Nutrient Retention')
plt.xlabel('Nutrient Retention (%)')
plt.ylabel('Residuals')

plt.show()
```



1.4.6 Exercise 4.2.3

Exploring and transforming shelf life data

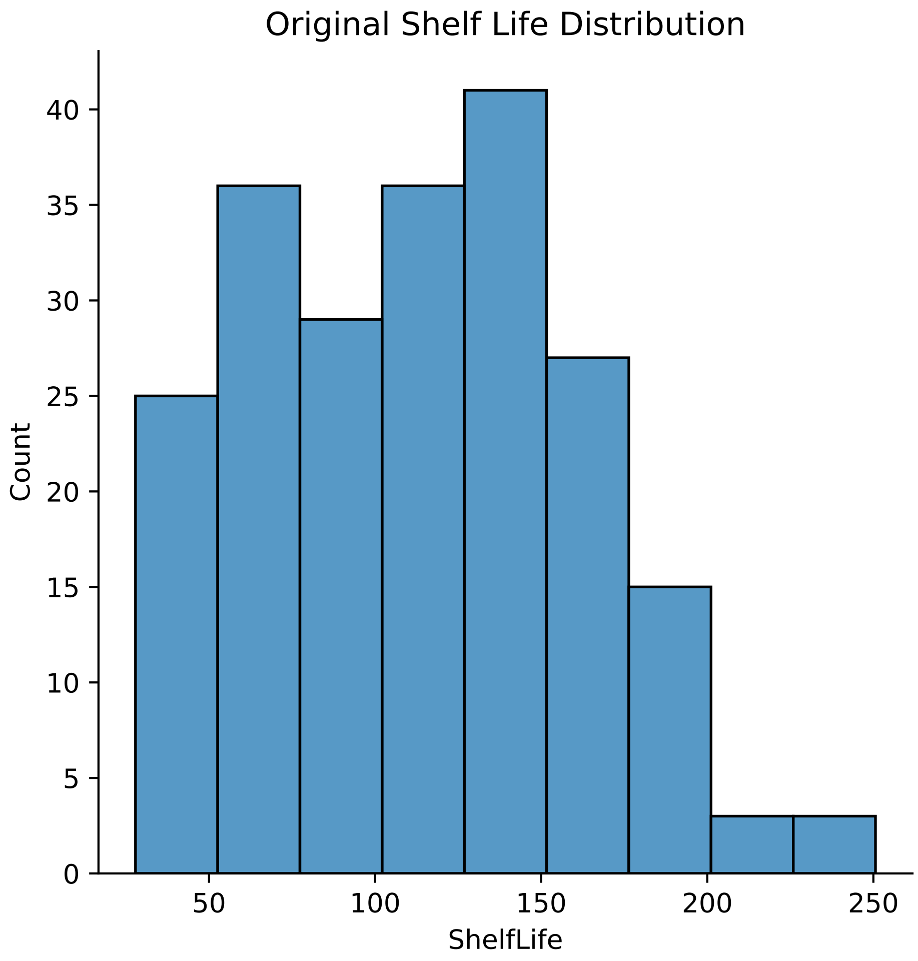
Understanding the distribution of different variables in our data is a key aspect of any data work including experimental analysis. The `food_preservation` dataset captures various food preservation methods and their impact on nutrient retention and shelf life. A crucial aspect of this data involves the shelf life of preserved foods, which can vary significantly across different preservation methods and food types.

Instructions

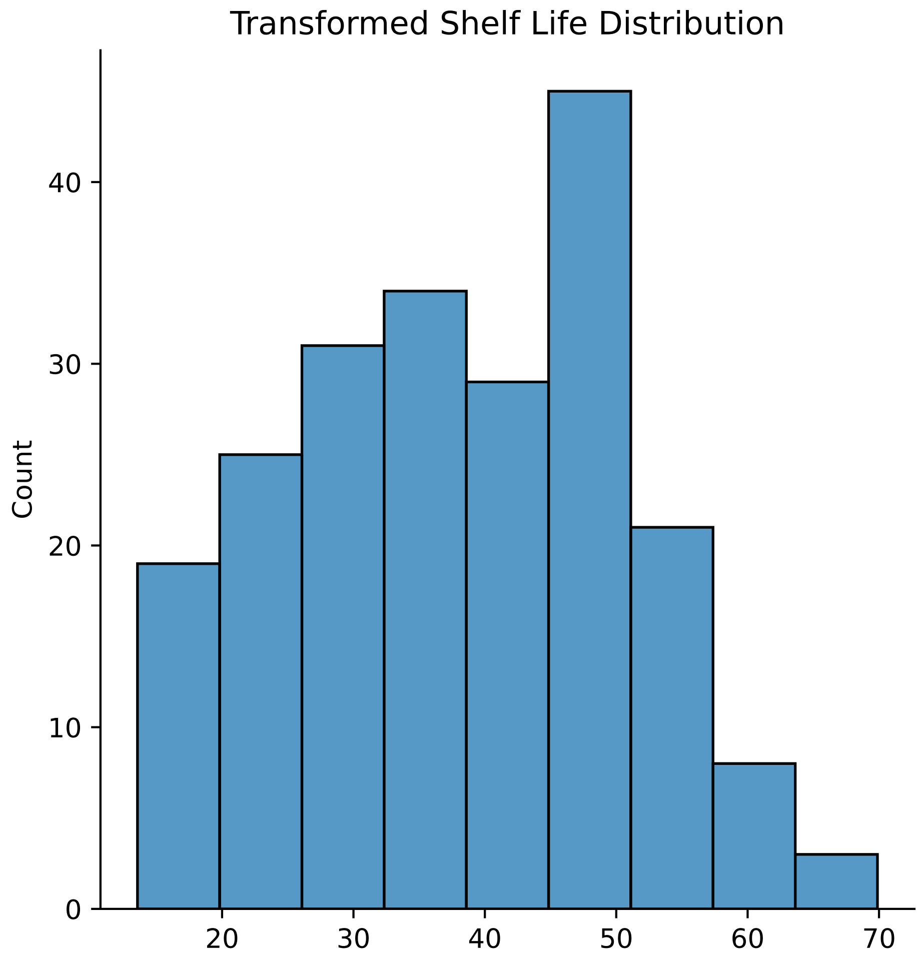
1. Visualize the original distribution of the `'ShelfLife'` column.
2. Visualize the distribution of the `'ShelfLifeTransformed'`.

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from scipy.stats import boxcox

# Set random seed for reproducibility
np.random.seed(242)

# Define number of rows
num_rows = 215

# Generate ProductID from 1 to 215
product_id = np.arange(1, num_rows + 1)

# Generate NutrientRetention with the given summary statistics
nutrient_retention = np.random.normal(loc=73.481, scale=14.838, size=num_rows)
nutrient_retention = np.clip(nutrient_retention, 50.030, 99.810)  # Ensuring within min-max range

# Generate ShelfLife with the given summary statistics
shelf_life = np.random.normal(loc=105.210, scale=54.661, size=num_rows)
shelf_life = np.clip(shelf_life, 27.860, 267.500)  # Ensuring within min-max range

# Create FoodType and PreservationMethod categories
food_types = ['Fruit', 'Meat', 'Vegetable']
preservation_methods = ['Canning', 'Drying', 'Freezing']
counts = [22, 32, 26, 21, 22, 23, 23, 21, 25]

# Generate categorical data for FoodType and PreservationMethod based on given counts
food_preservation_data = []
for (food, method), count in zip([(f, p) for f in food_types for p in preservation_methods], coun
    food_preservation_data.extend([(food, method)] * count)

# Convert to DataFrame and ensure it has the required 215 rows
food_preservation_categorical = pd.DataFrame(food_preservation_data[:num_rows], columns=['FoodTyp

# Create final DataFrame
food_preservation = pd.DataFrame({
    'ProductID': product_id,
    'NutrientRetention': nutrient_retention,
    'ShelfLife': shelf_life
})

# Add categorical data
food_preservation = pd.concat([food_preservation, food_preservation_categorical], axis=1)

# Visualize the original ShelfLife distribution
sns.displot(food_preservation['ShelfLife'])
```

```
plt.title('Original Shelf Life Distribution')

plt.show()

# Create a Box-Cox transformation
ShelfLifeTransformed, _ = boxcox(food_preservation['ShelfLife'])

# Visualize the transformed ShelfLife distribution
plt.clf()
sns.displot(ShelfLifeTransformed)
plt.title('Transformed Shelf Life Distribution')
plt.show()
```



```
<Figure size 1200x900 with 0 Axes>
```



1.4.7 Chapter 4.3: Applying nonparametric tests in experimental analysis

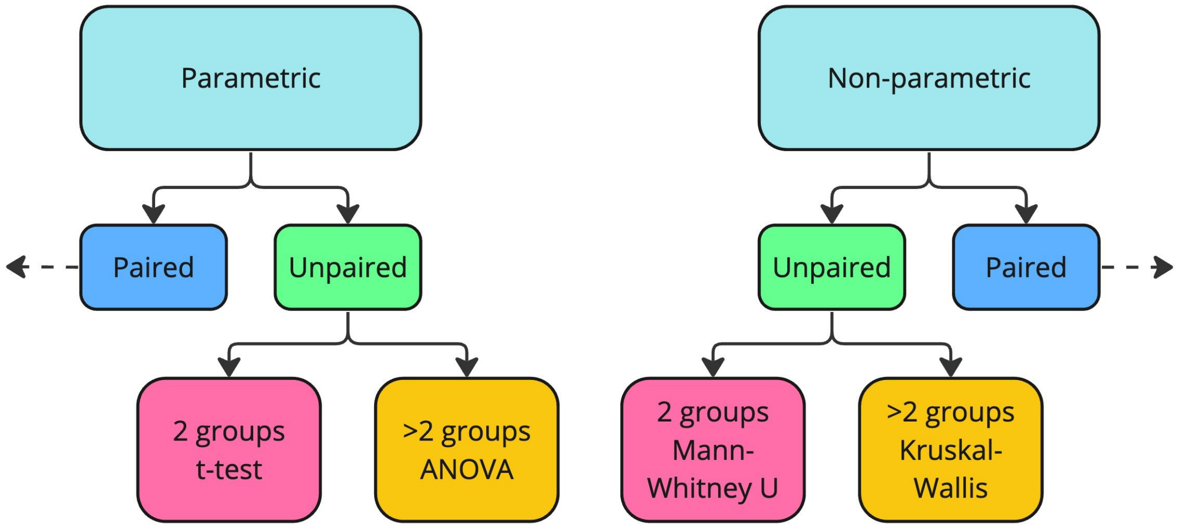
We'll now explore the world of nonparametric tests, which are vital tools in situations where parametric test assumptions don't hold.

When to use nonparametric tests

Nonparametric tests come into play when data challenges the usual assumptions of parametric tests. For example, they serve as an alternative to needing to transform data in order for normality assumptions to hold. They're ideal for ordinal data or distributions far from normality, offering resilience against outliers and accommodating a wider range of data behaviors.

Exploring nonparametric methods

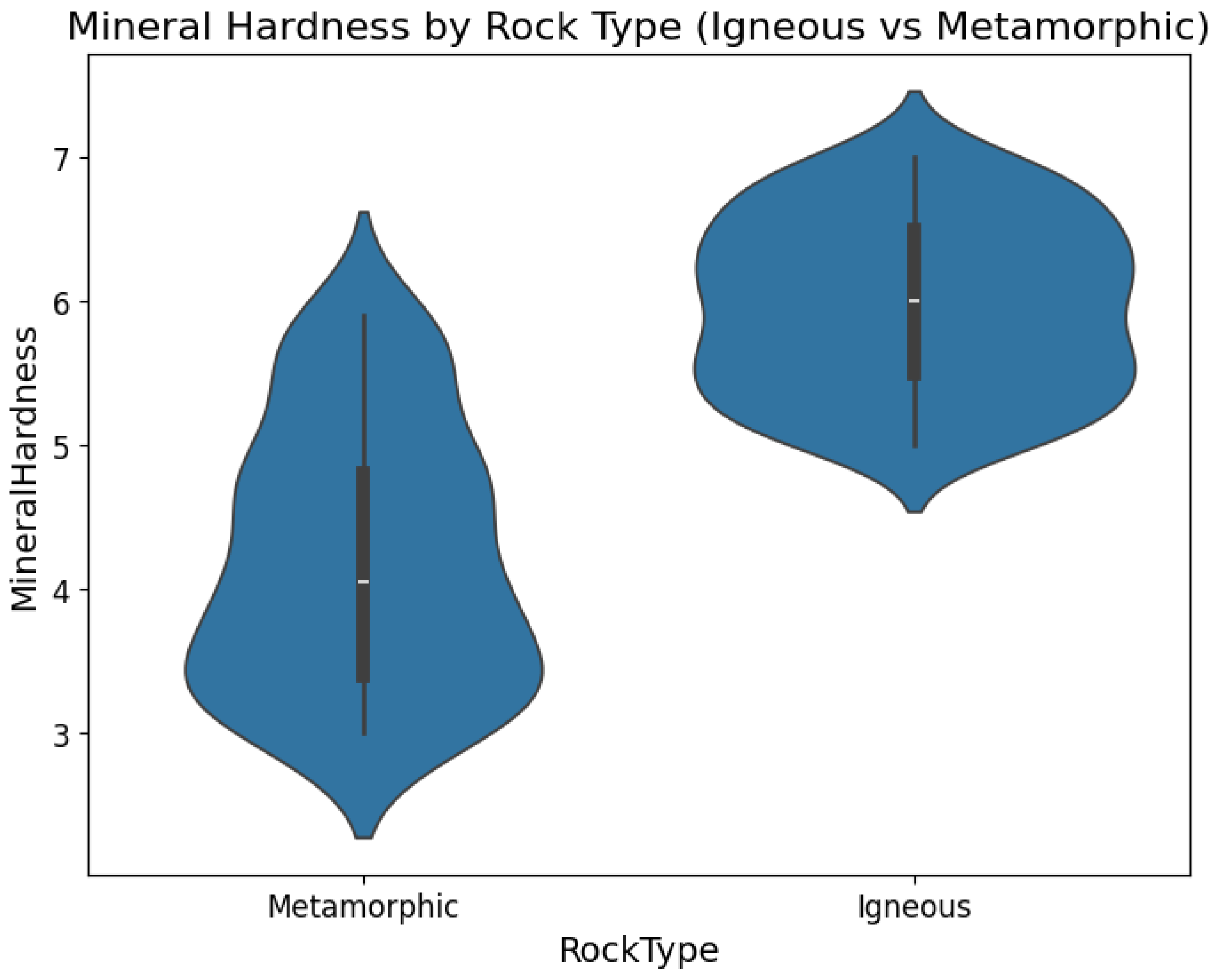
When data doesn't meet parametric assumptions, nonparametric methods offer a solution. The `Mann-Whitney U` Test is our go-to for comparing two independent groups - the non-parametric alternative to the independent two-sample `t-test`. When our experiment involves more than two groups with a numeric response, we turn to the `Kruskal-Wallis` Test - the non-parametric version of the one-way ANOVA test.



Visualizing nonparametric data

Visualizing nonparametric data effectively can reveal underlying patterns. Violin plots offer a comprehensive view of our data's distribution across multiple groups. Let's compare `MineralHardness` for Igneous and Metamorphic rocks from our data. We begin by using the `.isin()` method to extract these two groups of data into a DataFrame called `condensed_data`. Next, we use Seaborn's `violinplot` function on the two variables of interest. This violin plot contrasts `MineralHardness` between metamorphic and igneous rocks. Notice that the violins for each do not have a normal shape mirrored vertically, but instead exhibit some skew. Metamorphic rocks show a greater hardness range and lower median than igneous rocks (denoted by the white line in the center of each "violin"). Igneous rocks display smaller hardness variability and higher median values.

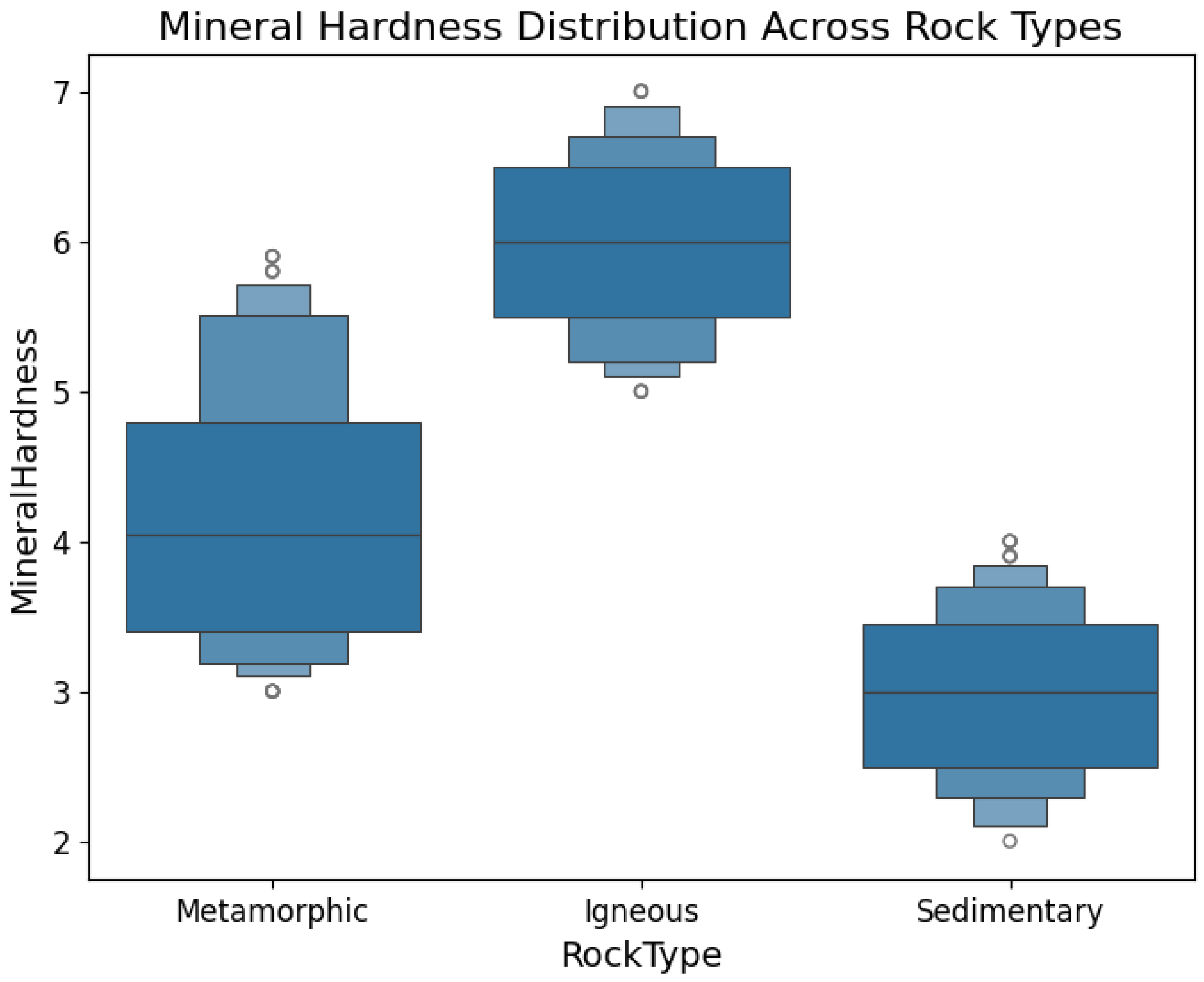
```
condensed_data = mineral_rocks[mineral_rocks['RockType'].isin(['Igneous', 'Metamorphic'])]

sns.violinplot(x='RockType', y='MineralHardness', data=condensed_data)
```



Visualizing nonparametric data

Boxen plots are an extended version of box plots that provide more information about the shape of the distribution. We use Seaborn's `boxenplot` function to display the distribution of `MineralHardness` across three rock types: metamorphic, igneous, and sedimentary. Sedimentary rocks show the smallest median hardness value, with outliers indicating some extreme values. Metamorphic rocks show the most skew of the three rock types and have a median hardness between that of sedimentary and igneous. They also have a wider interquartile range, indicating significant variability. Igneous rocks exhibit the highest median hardness and a narrower interquartile range, suggesting less variability.

```
sns.boxenplot(x=
'RockType'
, y=
'MineralHardness'
, data=mineral_rocks)
```



Applying nonparametric tests - Mann Whitney U

We perform the `Mann-Whitney U` test to compare the distributions of `MineralHardness` between igneous and sedimentary rocks using data from the `mineral_rocks` DataFrame. We select the hardness values corresponding to each rock type and apply the test to determine if there's a statistically significant difference in their medians. The test returns a p-value of `0.9724`. The high p-value indicates that there is no significant difference in the median mineral hardness between igneous and sedimentary rocks at the common significance levels.

```
from scipy.stats import mannwhitneyu, kruskal

u_stat, u_pval = mannwhitneyu(
mineral_rocks[mineral_rocks['RockType'] == 'Igneous']['MineralHardness'],
mineral_rocks[mineral_rocks['RockType'] == 'Sedimentary']['MineralHardness']
)
```

```
print(f"Mann-Whitney U test p-value: {u_pval:.4f}")
```

```
Mann-Whitney U test p-value: 0.9724
```

Applying nonparametric tests - Kruskal-Wallis

We apply the `Kruskal-Wallis` test, a nonparametric method, to determine if there are statistically significant differences in mineral hardness distributions across igneous, sedimentary, and metamorphic rock types from the `mineral_rocks` dataset. It computes the p-value for the hypothesis that the medians of all groups are equal. This test returns a p-value of `0.0630`, which indicates that there's a suggestion of a difference in medians, but it does not reach the conventional significance threshold of `0.05`. Therefore, while there may be differences in mineral hardness by rock type, they are not statistically significant at the 5% level.

```
k_stat, k_pval = kruskal(
mineral_rocks[mineral_rocks['RockType'] == 'Igneous']['MineralHardness'],
mineral_rocks[mineral_rocks['RockType'] == 'Sedimentary']['MineralHardness'],
mineral_rocks[mineral_rocks['RockType'] == 'Metamorphic']['MineralHardness']
)

print(f"Kruskal-Wallis test p-value: {k_pval:.4f}")
```

```
Kruskal-Wallis test p-value: 0.0630
```

1.4.8 Exercise 4.3.1

Visualizing and testing preservation methods

As a food scientist, you're tasked with evaluating the effectiveness of different preservation methods on nutrient retention and how these methods impact shelf life. You have been provided with a dataset, food_preservation, that includes various types of food preserved by methods such as freezing and canning. Each entry in the dataset captures the nutrient retention and calculated shelf life for these foods, providing a unique opportunity to analyze the impacts of preservation techniques on food quality.

Instructions

1. Filter the DataFrame to include only Freezing and Canning rows.

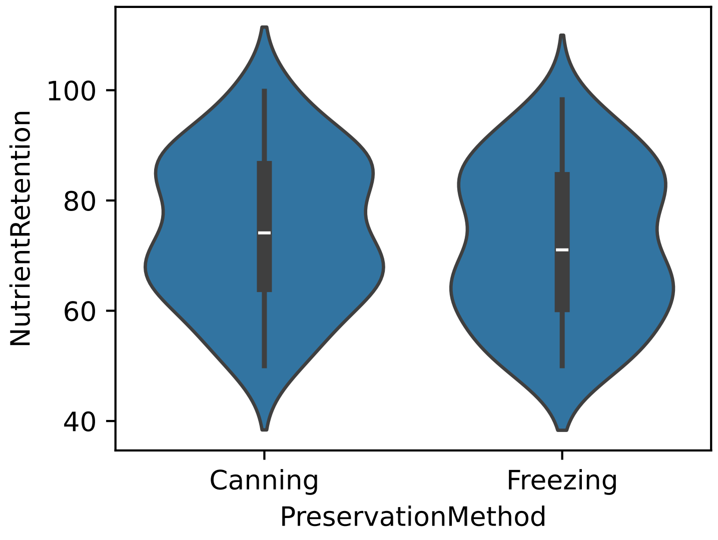
- Create a violin plot to visualize the distribution of nutrient retention for different preservation methods.

2. Extract the nutrient retention values for both Freezing and Canning entries.

- Perform a Mann Whitney U test to compare nutrient retention between Freezing and Canning methods.

```python
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from scipy.stats import mannwhitneyu

# Set random seed for reproducibility
np.random.seed(242)

# Define number of rows
num_rows = 215

# Generate ProductID from 1 to 215
product_id = np.arange(1, num_rows + 1)

# Generate NutrientRetention with the given summary statistics
nutrient_retention = np.random.normal(loc=73.481, scale=14.838, size=num_rows)
nutrient_retention = np.clip(nutrient_retention, 50.030, 99.810)  # Ensuring within min-max range

# Generate ShelfLife with the given summary statistics
shelf_life = np.random.normal(loc=105.210, scale=54.661, size=num_rows)
shelf_life = np.clip(shelf_life, 27.860, 267.500)  # Ensuring within min-max range

# Create FoodType and PreservationMethod categories
food_types = ['Fruit', 'Meat', 'Vegetable']
preservation_methods = ['Canning', 'Drying', 'Freezing']
counts = [22, 32, 26, 21, 22, 23, 23, 21, 25]

# Generate categorical data for FoodType and PreservationMethod based on given counts
food_preservation_data = []
for (food, method), count in zip([(f, p) for f in food_types for p in preservation_methods], coun
    food_preservation_data.extend([(food, method)] * count)

# Convert to DataFrame and ensure it has the required 215 rows
food_preservation_categorical = pd.DataFrame(food_preservation_data[:num_rows], columns=['FoodTyp

# Create final DataFrame
food_preservation = pd.DataFrame({
    'ProductID': product_id,
    'NutrientRetention': nutrient_retention,
    'ShelfLife': shelf_life
})
```

```
# Add categorical data
food_preservation = pd.concat([food_preservation, food_preservation_categorical], axis=1)

# Filter to Freezing and Canning data
condensed_food_data = food_preservation[food_preservation['PreservationMethod'].isin(['Freezing',

# Create a violin plot for nutrient retention by preservation method
sns.violinplot(data=condensed_food_data,
     x="PreservationMethod",
     y="NutrientRetention")

plt.show()

# Separate nutrient retention for Freezing and Canning methods
freezing = food_preservation[food_preservation['PreservationMethod'] == 'Freezing']['NutrientRete
canning = food_preservation[food_preservation['PreservationMethod'] == 'Canning']['NutrientRetent

# Perform Mann Whitney U test
u_stat, p_val = mannwhitneyu(freezing, canning)

# Print the p-value
print("Mann Whitney U test p-value:", p_val)
```



```
Mann Whitney U test p-value: 0.2333133474790744
```

Note

The violin plot shows that the distribution and median values are similar across Freezing and Canning. The large p-value leads us to suspect that a statistical difference does not exist in the medians of nutrient retention for freezing versus canning preservation methods.

1.4.9 Exercise 4.3.2

Further analyzing food preservation techniques

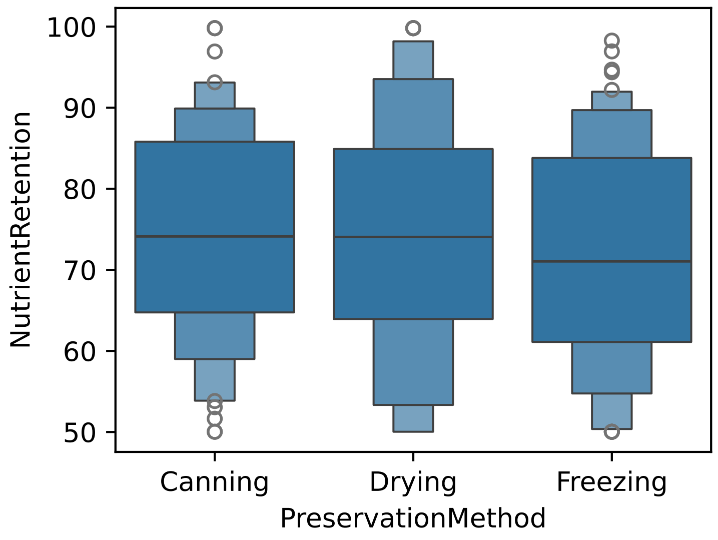
In your role as a food scientist, you're exploring into the comparative effects of various food preservation methods on nutrient retention, utilizing a `food_preservation` dataset that includes measurements from freezing, canning, and drying methods. This dataset has been crafted to incorporate variations in shelf life that depend on the nutrient retention values, reflecting real-world scenarios where preservation efficacy varies significantly. Your analysis will involve visually exploring these differences using advanced plotting techniques and nonparametric tests.

Instructions

1. Create a boxen plot to explore the distribution of nutrient retention across the three different preservation methods.

```python
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from scipy.stats import kruskal

# Set random seed for reproducibility
np.random.seed(242)

# Define number of rows
num_rows = 215

# Generate ProductID from 1 to 215
product_id = np.arange(1, num_rows + 1)

# Generate NutrientRetention with the given summary statistics
nutrient_retention = np.random.normal(loc=73.481, scale=14.838, size=num_rows)
nutrient_retention = np.clip(nutrient_retention, 50.030, 99.810)  # Ensuring within min-max range

# Generate ShelfLife with the given summary statistics
shelf_life = np.random.normal(loc=105.210, scale=54.661, size=num_rows)
shelf_life = np.clip(shelf_life, 27.860, 267.500)  # Ensuring within min-max range
```

```
# Generate ShelfLife with the given summary statistics
shelf_life = np.random.normal(loc=105.210, scale=54.661, size=num_rows)
shelf_life = np.clip(shelf_life, 27.860, 267.500)  # Ensuring within min-max range

# Create FoodType and PreservationMethod categories
food_types = ['Fruit', 'Meat', 'Vegetable']
preservation_methods = ['Canning', 'Drying', 'Freezing']
counts = [22, 32, 26, 21, 22, 23, 23, 21, 25]

# Generate categorical data for FoodType and PreservationMethod based on given counts
food_preservation_data = []
for (food, method), count in zip([(f, p) for f in food_types for p in preservation_methods], coun
    food_preservation_data.extend([(food, method)] * count)

# Convert to DataFrame and ensure it has the required 215 rows
food_preservation_categorical = pd.DataFrame(food_preservation_data[:num_rows], columns=['FoodTyp

# Create final DataFrame
food_preservation = pd.DataFrame({
    'ProductID': product_id,
    'NutrientRetention': nutrient_retention,
    'ShelfLife': shelf_life
})

# Add categorical data
food_preservation = pd.concat([food_preservation, food_preservation_categorical], axis=1)

# Create a boxen plot for nutrient retention by preservation
sns.boxenplot(data=food_preservation,
      x="PreservationMethod",
     y="NutrientRetention")
plt.show()

# Separate nutrient retention for each preservation method
freezing = food_preservation[food_preservation['PreservationMethod'] == 'Freezing']['NutrientRete
canning = food_preservation[food_preservation['PreservationMethod'] == 'Canning']['NutrientRetent
drying = food_preservation[food_preservation['PreservationMethod'] == 'Drying']['NutrientRetentio

# Perform Kruskal-Wallis test
k_stat, k_pval = kruskal(freezing, canning, drying)
print("Kruskal-Wallis test p-value:", k_pval)
```



```
Kruskal-Wallis test p-value: 0.4070541794831697
```

Note

By effectively visualizing and statistically analyzing the nutrient retention across different preservation methods, I've gained insights into how these methods impact food quality. The boxen plot provided a deeper understanding of the data's distribution, and the Kruskal-Wallis test helped me assess the statistical differences between groups. The large p-value leads us to fail to conclude that a difference in the median values across the three groups of preservation methods exists for nutrient retention.