M50 Homework 6

Alex Craig

Exercise 1

(Car brands and mpg): In this exercise we will consider the data set containing information about cars and their miles per gallon. This can by loaded by

```
data = pd.read_csv("https://raw.githubusercontent.com/intro-stat-learning/ISLP/main/ISLP/data/Auto.csv",encodi

data["name"] = [name.split()[0] for name in data["name"].values]
```

The second line takes the original names (which are the specific models – e.g. Toyota Yaris) and extracts only the brand name (e.g Toyota). We are going to study which brands have the best mpg. Some brands tend to make larger and heavier cars (e.g. pickup tricks) which will have worse mpg, but we want to understand how brands compare within a certain type of car. To determine this we need to control for other factors, such as the the year and weight.

Part A

Using all the columns **except** origin and displacement (since it's not obvious what the units are), write down the regression model which you want to fit to this data to address the question posed in the problem instruction. Assume there are no interactions. Provide an interpretation of each regression coefficient.

Solution

```
import pandas as pd

data = pd.read_csv("https://raw.githubusercontent.com/intro-stat-learning/ISLP/main/ISLP/data/Auto.csv",encodi

data["name"] = [name.split()[0] for name in data["name"].values]

data.head()
```

```
    mpg  cylinders  displacement  horsepower  weight  acceleration  year  
0  18.0          8         307.0         130    3504          12.0    70  \
1  15.0          8         350.0         165    3693          11.5    70   
2  18.0          8         318.0         150    3436          11.0    70   
3  16.0          8         304.0         150    3433          12.0    70   
4  17.0          8         302.0         140    3449          10.5    70   

   origin       name  
0       1  chevrolet  
1       1      buick  
2       1   plymouth  
3       1        amc  
4       1       ford  
```

The regression model is:

$$\text{mpg} = \beta_0 + \beta_1 \times \text{name} + \beta_2 \times \text{cylinders} + \beta_3 \times \text{horsepower}$$
$$+\beta_4 \times \text{weight} + \beta_5 \times \text{acceleration} + \beta_6 \times \text{year} + \epsilon$$

Where:

- mpg is the response variable representing the miles per gallon.
- name is a categorical variable representing the brand of the car. In the regression model, this will be translated to several dummy variables (one for each brand).
- cylinders represents the number of cylinders in the car's engine.
- horsepower represents the horsepower of the car.
- weight represents the weight of the car.
- acceleration represents the acceleration of the car.
- year represents the year the car was made.

- ϵ is the error term.

Interpretation of the coefficients:

- β_0: This is the intercept. It represents the expected mpg when all other predictors are zero. However, in this context, a value of zero for many predictors doesn't make sense (e.g., a car weight of zero), so the intercept might be more of a mathematical convenience rather than having a direct interpretative meaning.
- β_1: Represents the difference in mpg for a given brand, holding all other predictors constant.
- β_2: Represents the change in mpg for a one-unit increase in the number of cylinders, holding all other predictors constant.
- β_3: Represents the change in mpg for a one-unit increase in horsepower, holding all other predictors constant.
- β_4: Represents the change in mpg for a one-unit increase in weight, holding all other predictors constant.
- β_5: Represents the change in mpg for a one-unit increase in acceleration, holding all other predictors constant.
- β_6: Represents the change in mpg for a one-year increase in the year the car was made, holding all other predictors constant.

Note: The categorical variable `name` will result in multiple coefficients, one for each level (brand) of the variable, minus one.

Part B

Fit the regression model to the data.

Solution

1. We first need to clean the data. There are certain brand names that have been misspelled or written in different ways. We'll standardize these brand names to have consistent naming.
2. We will then create dummy variables for the 'name' column which represents the brand names. This is essential because 'name' is a categorical variable, and we need to convert it into a format that can be used in regression analysis.
3. We will drop the columns 'origin' and 'displacement' as instructed.
4. Next, we'll define our predictors and the response variable. Our predictors will be all columns except for 'mpg', and our response will be 'mpg'.
5. We'll add a constant to our predictors. This constant acts as the intercept in the regression equation.
6. Finally, we'll fit our regression model using the OLS (Ordinary Least Squares) method and get a summary of the regression.

```python
import statsmodels.api as sm

data['name'] = data['name'].replace(['vw'], 'volkswagen')
data['name'] = data['name'].replace(['vokswagen'], 'volkswagen')
data['name'] = data['name'].replace(['chevroelt'], 'chevrolet')
data['name'] = data['name'].replace(['toyouta'], 'toyota')
data['name'] = data['name'].replace(['mercedes-benz'], 'mercedes')

# Create dummy variables for the 'name' column
data_dummies = pd.get_dummies(data['name'], prefix='name')

# Add dummy variables to the main data and drop the original 'name' column
data = pd.concat([data, data_dummies], axis=1).drop('name', axis=1)

# Drop the columns 'origin' and 'displacement' as instructed
data = data.drop(['origin', 'displacement'], axis=1)

# Convert all entries that are "True" to 1 and all entries that are "False" to 0
data = data * 1

# Define the predictors and the response variable
X = data.drop('mpg', axis=1)
y = data['mpg']

# Add an intercept to the predictors
X = sm.add_constant(X)

# Fit the regression model
```

```python
model = sm.OLS(y, X).fit()

# Get the summary of the regression model
model_summary = model.summary()
# model_summary (print this to see the summary - was stopping latex compiling)
```

Part C

What are the 5 best brands for mpg within the same type of car (weight, horsepower etc.).

Solution

```python
# Extract coefficients
coefficients = model.params

# Filter out coefficients corresponding to the car brands
brand_coefficients = coefficients.filter(like='name_')

# Sort the coefficients in descending order
sorted_brands = brand_coefficients.sort_values(ascending=False)

# Get the top 5 brands
top_5_brands = sorted_brands.head(5)

print(top_5_brands)
```

```
name_triumph       5.100500
name_nissan        2.830246
name_datsun        1.995171
name_honda         1.814166
name_volkswagen    1.531434
dtype: float64
```

It looks like the top 5 brands for mpg are:

1. Triumph
2. Nissan
3. Datsun
4. Honda
5. Volkswagen

Exercise 2

(Marginal regression in interactions model): Consider the probability model:

$$X_1 \sim N(0, \sigma_1^2)$$
$$X_2 \sim N(0, \sigma_2^2)$$
$$Y \mid (X_1, X_2) \sim N(\beta_1 X_1 + \beta_2 X_2 + \beta_{1,2} X_1 X_2, \sigma^2)$$

Part A

Derive the distributions of $Y \mid X_1$ and $Y \mid X_2$. Hint: These conditional distributions are both normal, so you only need to determine the mean and variance to find the distributions.

Solution

To derive the distributions of $Y \mid X_1$ and $Y \mid X_2$, we'll proceed in two steps:

1. Compute the mean of the conditional distribution.
2. Compute the variance of the conditional distribution.

Distribution of $Y \mid X_1$

Given $X_1 = x_1$:

Mean:

$$E[Y \mid X_1 = x_1] = E[\beta_1 x_1 + \beta_2 X_2 + \beta_{1,2} x_1 X_2]$$

Using the linearity of expectation and knowing that $E[X_2] = 0$ (since $X_2 \sim N(0, \sigma_2^2)$), we have:

$$E[Y \mid X_1 = x_1] = \beta_1 x_1 + \beta_2 E[X_2] + \beta_{1,2} x_1 E[X_2] = \beta_1 x_1$$

Variance:

$$\text{Var}(Y \mid X_1 = x_1) = \text{Var}(\beta_1 x_1 + \beta_2 X_2 + \beta_{1,2} x_1 X_2)$$

Using properties of variance, we get:

$$\text{Var}(Y \mid X_1 = x_1) = \beta_2^2 \text{Var}(X_2) + \beta_{1,2}^2 x_1^2 \text{Var}(X_2) + \sigma^2$$

The σ^2 term comes from the fact that X_2 and X_1 are not independent, so we need to add the covariance term.

Given $\text{Var}(X_2) = \sigma_2^2$, we have:

$$\text{Var}(Y \mid X_1 = x_1) = \beta_2^2 \sigma_2^2 + \beta_{1,2}^2 x_1^2 \sigma_2^2 + \sigma^2$$

Thus, the conditional distribution $Y \mid X_1$ is:

$$Y \mid X_1 \sim N(\beta_1 x_1, \beta_2^2 \sigma_2^2 + \beta_{1,2}^2 x_1^2 \sigma_2^2 + \sigma^2)$$

Distribution of $Y \mid X_2$

Given $X_2 = x_2$:

Mean:

$$E[Y \mid X_2 = x_2] = E[\beta_1 X_1 + \beta_2 x_2 + \beta_{1,2} X_1 x_2]$$

Using the linearity of expectation and knowing that $E[X_1] = 0$ (since $X_1 \sim N(0, \sigma_1^2)$), we have:

$$E[Y \mid X_2 = x_2] = \beta_1 E[X_1] + \beta_2 x_2 + \beta_{1,2} E[X_1] x_2 = \beta_2 x_2$$

Variance:

$$\text{Var}(Y \mid X_2 = x_2) = \text{Var}(\beta_1 X_1 + \beta_2 x_2 + \beta_{1,2} X_1 x_2)$$

Using properties of variance, we get:

$$\text{Var}(Y \mid X_2 = x_2) = \beta_1^2 \text{Var}(X_1) + \beta_{1,2}^2 x_2^2 \text{Var}(X_1) + \sigma^2$$

Again, the σ^2 term comes from the fact that X_2 and X_1 are not independent, so we need to add the covariance term.

Given $\text{Var}(X_1) = \sigma_1^2$, we have:

$$\text{Var}(Y \mid X_2 = x_2) = \beta_1^2 \sigma_1^2 + \beta_{1,2}^2 x_2^2 \sigma_1^2 + \sigma^2$$

Thus, the conditional distribution $Y \mid X_2$ is:

$$Y \mid X_2 \sim N(\beta_2 x_2, \beta_1^2 \sigma_1^2 + \beta_{1,2}^2 x_2^2 \sigma_1^2 + \sigma^2)$$

Part B

When does the probability model stated in the problem define regression models for Y vs. $X_i, i = 1, 2$? That is, if we ignore one of the predictor variables do obtain a single predictor linear regression model for the other?

Solution

For the probability model to define regression models for Y vs. X_i, $i = 1, 2$, when ignoring one of the predictor variables to obtain a single predictor linear regression model for the other, the regression model should have the form:

$$Y = \alpha + \beta_i X_i + \epsilon$$

Where:

- α is the intercept.
- β_i is the slope for the predictorX_i.
- ϵ is the random error term.

Given the provided model, when we condition on X_1, the model becomes:

$$Y = \beta_1 X_1 + \beta_2 X_2 + \beta_{1,2} X_1 X_2 + \epsilon$$

For this to be a simple linear regression model in X_2, the term involving the product $X_1 X_2$ (i.e., the interaction term) should not be present. This means $\beta_{1,2} = 0$.

Similarly, when we condition on X_2, the model becomes:

$$Y = \beta_1 X_1 + \beta_2 X_2 + \beta_{1,2} X_1 X_2 + \epsilon$$

For this to be a simple linear regression model inX_1, again, the term involving the product $X_1 X_2$ should not be present. Again, this requires $\beta_{1,2} = 0$.

Thus, the probability model defines regression models for Y vs.X_i,$i = 1, 2$, when the interaction term coefficient $\beta_{1,2}$ is zero.

Exercise 3

(Predicting the residual plot based on interaction model): Suppose we have 200 data points generated from the following model

$$Y = 4X_1 - 2X_2 + 4X_1 X_2 + \epsilon$$

where $\sigma = 0.2$, X_1 is continuous predictor which is uniformly distributed on $[-1, 1]$, and X_2 is a binary predictor (e.g. a Bernoulli random variable). You can assume $X_2 = 0$ for about half the data points. The goal of this problem is to build your intuition about residual plots.

Part A

Without actually fitting a regression, describe in detail what the residual plot would look like if we fit this data to a linear regression model with NO interaction term. To do so, follow the following procedure:

1. First, think about what the data looks like when $X_2 = 0$ and $X_2 = 1$ separately. In each case, sketch the regression line and make note of how much variation there is around these lines to get an idea of what the cloud of (X_i, Y_i) points will look like.
2. Now consider what the fitted regression line will be based on this picture. What is a very rough estimate of the slopes $\hat{\beta}_1$ and $\hat{\beta}_2$?
3. To get a sense for what the residuals look like, take the difference between the true model and this line.

Solution

Alright, let's break down the problem step by step.

1. Data visualization for $X_2 = 0$ and $X_2 = 1$:

Given the model:

$$Y = 4X_1 - 2X_2 + 4X_1X_2 + \epsilon$$

When $X_2 = 0$:

$$Y = 4X_1 + \epsilon$$

This represents a straight line with a slope of 4. Given that X_1 is uniformly distributed in $[-1, 1]$, the line will range between $[-4, 4]$ on the Y-axis.

When $X_2 = 1$:

$$Y = 4X_1 - 2 + 4X_1 + \epsilon$$
$$Y = 8X_1 - 2 + \epsilon$$

This is again a straight line, but with a slope of 8 and an intercept at -2. For X_1 values between $[-1, 1]$, the Y-values will range between $[-10, 6]$.

Given the two scenarios, we can expect two distinct lines in the scatter plot of the data. The cloud of points for $X_2 = 0$ will lie around the line $Y = 4X_1$ and for $X_2 = 1$, they will lie around $Y = 8X_1 - 2$.

2. Fitted regression line:

If we try to fit a linear regression model without an interaction term, the model will try to find the best line that reduces the sum of squared residuals for the entire dataset. Given the distinct lines of the two groups, the estimated regression line will fall somewhere between the two.

For the slope, $\hat{\beta}_1$, since we have two lines with slopes 4 and 8, and assuming the points are evenly distributed, the estimated slope will be the average, i.e., $\frac{4+8}{2} = 6$.

For $\hat{\beta}_2$, it will try to capture the difference between the two lines based on the binary predictor X_2. A rough estimate would be the average difference between the two lines which is around -1 (given that the intercept difference is -2 and the slope difference is 4). But without a precise calculation, this is just an intuition.

3. Residuals:

The residuals can be calculated as the difference between the true values from the given model and the predicted values from the estimated regression line.

For $X_2 = 0$:

$$\text{Residual} = Y_{true} - Y_{predicted} = 4X_1 - 6X_1 = -2X_1$$

For $X_2 = 1$:

$$\text{Residual} = 8X_1 - 2 - (6X_1 - 1) = 2X_1 - 3$$

So, for $X_2 = 0$, the residuals will show a pattern with a negative slope, and for $X_2 = 1$, the residuals will show a pattern with a positive slope. The residual plot will clearly show these two patterns, indicating that the model is missing an interaction term.

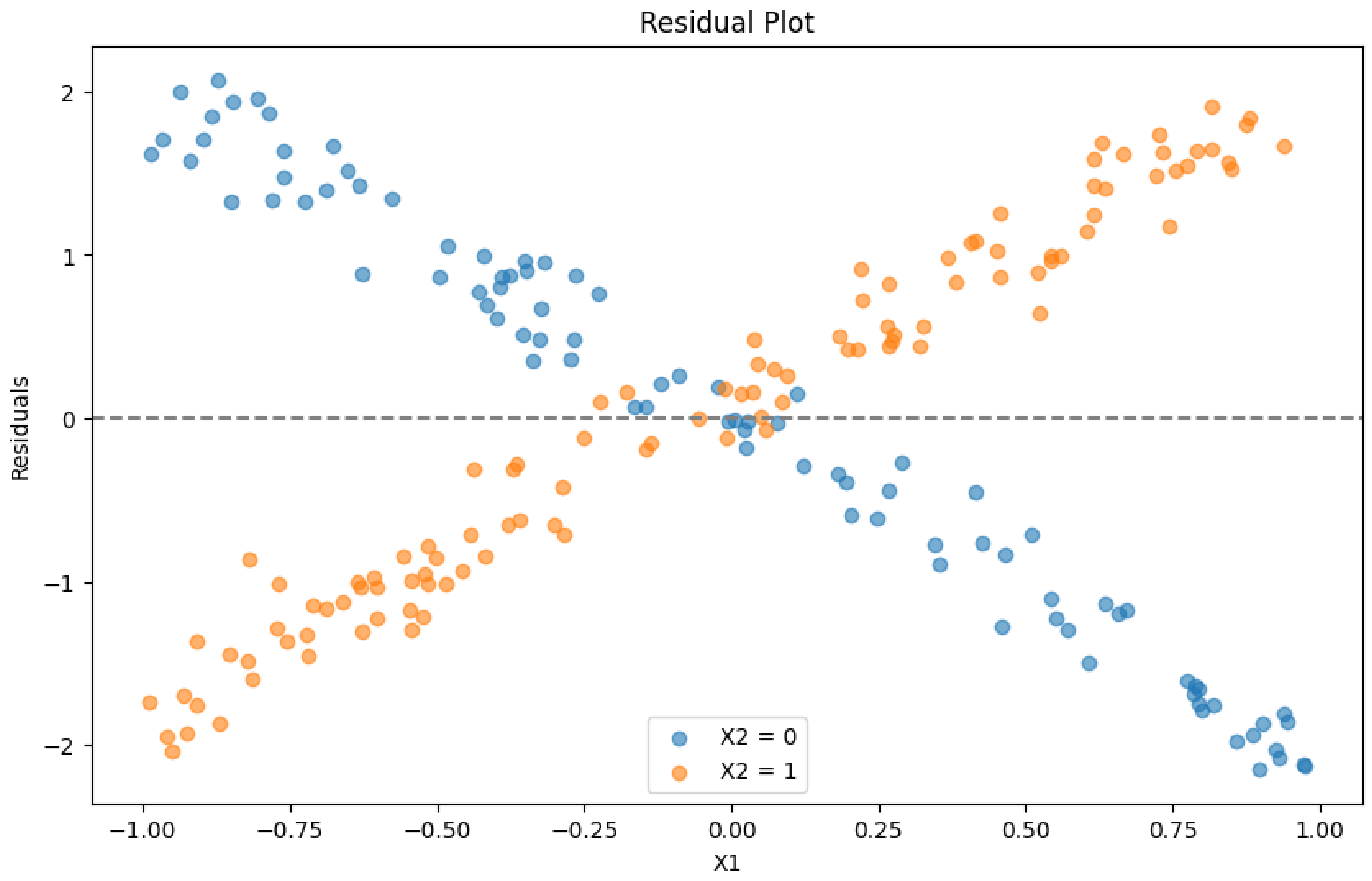
In conclusion, when the residuals show a clear pattern, especially different patterns for different groups of a categorical variable, it indicates that the linear model might be missing some important interaction terms or other non-linear transformations.

Part B

Confirm your answer with simulations.

Solution

```
import numpy as np
import matplotlib.pyplot as plt

# Setting a random seed for reproducibility
np.random.seed(42)

# Generating the data
n = 200
X1 = np.random.uniform(-1, 1, n)
X2 = np.random.binomial(1, 0.5, n)
epsilon = np.random.normal(0, 0.2, n)
Y = 4 * X1 - 2 * X2 + 4 * X1 * X2 + epsilon

# Adding a constant term for the intercept
X_with_intercept = sm.add_constant(np.column_stack((X1, X2)))

# Fitting the linear regression model using statsmodels
model_sm = sm.OLS(Y, X_with_intercept).fit()
Y_pred_sm = model_sm.predict(X_with_intercept)

# Calculating residuals
residuals_sm = Y - Y_pred_sm

# Plotting the residual plot
plt.figure(figsize=(10, 6))
plt.scatter(X1[X2 == 0], residuals_sm[X2 == 0], label="X2 = 0", alpha=0.6)
plt.scatter(X1[X2 == 1], residuals_sm[X2 == 1], label="X2 = 1", alpha=0.6)
plt.axhline(0, color='gray', linestyle='--')
plt.xlabel("X1")
plt.ylabel("Residuals")
plt.title("Residual Plot")
plt.legend()
plt.show()
```



The residual plot confirms our earlier discussion:

1. For $X_2 = 0$, the residuals show a clear pattern with a negative slope.
2. For $X_2 = 1$, the residuals show a pattern with a positive slope.

This is consistent with our expectations and confirms that the model is missing an interaction term between X_1 and X_2. When residuals show a clear pattern, especially different patterns for different groups of a categorical variable, it indicates the inadequacy of the model. In this case, adding the interaction term between X_1 and X_2 should help rectify this issue.

Exercise 4

(Drug interactions): When treating microbial infections and cancer, combinations of drugs can perform better than individual drugs. However, it can be difficult to identify which combinations are optimal for the reason that identifying very "high order" interactions is difficult. In order to understand the best way to combine M drugs, we construct a regression where Y is the "effect" of the drug and X_i is a Bernoulli random variable representing whether or not the i^{th} drug is present or not. We want to consider the possibility:

$$Y \sum_{i=1}^{M} \beta_i X_i \sum_{i=1}^{M} (\sum_{j>i}^{M} \beta_{i,j} X_i X_j) + \sum_{i=1}^{M} (\sum_{j>i}^{M} \sum_{k>j}^{M} \beta_{i,j} X_i X_j X_k) + X_1 X_2 \cdots X_M + \epsilon$$

For examples, with $M = 3$, we would have:

$$Y = \beta_1 X_1 + \beta_2 X_2 \beta_3 X_3 + \beta_{1,2} X_1 X_2 + \beta_{1,3} X_1 X_3 + \beta_{2,3} X_2 X_3 + \beta_{1,2,3} X_1 X_2 X_3 + \epsilon$$

Part A

Suppose $M = 3$ and

$$\begin{bmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \\ \beta_{1,2} \\ \beta_{1,3} \\ \beta_{2,3} \\ \beta_{1,2,3} \end{bmatrix} = \begin{bmatrix} 1.2 \\ -0.8 \\ -0.11 \\ 3.48 \\ -2.62 \\ 1.03 \\ 1.66 \end{bmatrix}$$

What is your interpretation of each coefficient?

Solution

Each coefficient in the regression model can be interpreted as follows:

- $\beta_1, \beta_2, \beta_3$: These coefficients represent the effect of each individual drug on the outcome Y when used alone. A positive coefficient suggests that the drug has a positive effect on the outcome, while a negative coefficient suggests a negative effect.
- $\beta_{1,2}, \beta_{1,3}, \beta_{2,3}$: These coefficients represent the interaction effects between two drugs. They indicate how the effect of one drug on the outcome changes when another drug is also present. A positive interaction coefficient means that the combined effect of the two drugs is greater than the sum of their individual effects (synergy), while a negative interaction coefficient means that the combined effect is less than the sum of their individual effects (antagonism).
- $\beta_{1,2,3}$: This coefficient represents the interaction effect among all three drugs. It shows how the combination of all three drugs together affects the outcome compared to any two-drug or single-drug combinations. Similar to the two-drug interaction coefficients, a positive value indicates synergy, while a negative value indicates antagonism among the three drugs.

Given the specific coefficients:

- $\beta_1 = 1.2$: Drug 1 has a positive effect on the outcome when used alone.
- $\beta_2 = -0.8$: Drug 2 has a negative effect on the outcome when used alone.
- $\beta_3 = -0.11$: Drug 3 has a slight negative effect on the outcome when used alone.
- $\beta_{1,2} = 3.48$: The combination of Drug 1 and Drug 2 has a significantly positive synergistic effect on the outcome.
- $\beta_{1,3} = -2.62$: The combination of Drug 1 and Drug 3 has a negative antagonistic effect on the outcome.
- $\beta_{2,3} = 1.03$: The combination of Drug 2 and Drug 3 has a positive synergistic effect on the outcome.
- $\beta_{1,2,3} = 1.66$: The combination of all three drugs has a positive synergistic effect on the outcome that is greater than the sum of their individual or two-drug combination effects.

Part B

What is the optimal treatment, meaning which combination of drugs 1, 2 and 3 should we use to maximize Y? There are different ways you can approach this. One way is to make a list of each (X_1, X_2, X_3), compute Y for each one and the find the index of the maximum Y value (using a for loop or `argmax`).

Solution

```python
import numpy as np

# Define the coefficients
beta = np.array([1.2, -0.8, -0.11, 3.48, -2.62, 1.03, 1.66])

# Generate all possible combinations of (X1, X2, X3)
X_combinations = np.array([[x1, x2, x3] for x1 in [0, 1] for x2 in [0, 1] for x3 in [0, 1]])

# Define a function to calculate Y for each combination of drugs
def calculate_Y(X, beta):
    return (beta[0] * X[0] +
            beta[1] * X[1] +
            beta[2] * X[2] +
            beta[3] * X[0] * X[1] +
            beta[4] * X[0] * X[2] +
            beta[5] * X[1] * X[2] +
            beta[6] * X[0] * X[1] * X[2])

# Calculate Y for each combination
Y_values = np.array([calculate_Y(X, beta) for X in X_combinations])

# Find the combination of drugs that maximizes Y
optimal_index = np.argmax(Y_values)
optimal_combination = X_combinations[optimal_index]
optimal_Y = Y_values[optimal_index]

(optimal_combination, optimal_Y)
```

```
(array([1, 1, 0]), 3.88)
```

The optimal treatment to maximize Y is to use Drug 1 and Drug 2 in combination (with $X_1 = 1$ and $X_2 = 1$) and not use Drug 3 ($X_3 = 0$). This combination gives the maximum Y value of 3.88.

Part C

Now additional suppose that $\sigma^2 = 1$. By generating simulated Y values with these parameters for different values of N, determine how many data points are needed to reliably find that all interactions coefficients have p-values below 0.05.

Solution

```
import statsmodels.api as sm

def simulate_regression_statsmodels(N, beta, sigma_sq, iterations=100):
    p_value_threshold = 0.05
    reliable_sample_sizes = []

    for sample_size in N:
        successful_simulations = 0

        for _ in range(iterations):
            # Simulate N observations of X1, X2, X3
            X = np.random.binomial(1, 0.5, (sample_size, 3))
            # Add a column of ones for the intercept
            X_intercept = sm.add_constant(X)
            # Interaction terms
            X1X2 = X[:, 0] * X[:, 1]
            X1X3 = X[:, 0] * X[:, 2]
            X2X3 = X[:, 1] * X[:, 2]
            X1X2X3 = X[:, 0] * X[:, 1] * X[:, 2]
            # Stack the interaction terms with the main effects
            X_full = np.column_stack((X_intercept, X1X2, X1X3, X2X3, X1X2X3))

            # Generate the corresponding Y values
            Y = calculate_Y(X.T, beta) + np.random.normal(0, np.sqrt(sigma_sq), sample_size)

            # Fit the regression model
            model = sm.OLS(Y, X_full).fit()

            # Check if all interaction coefficients have p-values below 0.05
            interaction_pvalues = model.pvalues[4:]  # p-values of the interaction terms
            if all(interaction_pvalues < p_value_threshold):
                successful_simulations += 1

        # Record the proportion of successful simulations
        reliability = successful_simulations / iterations
        reliable_sample_sizes.append((sample_size, reliability))

        # If reliability criterion is met, break the loop
        if reliability >= 0.95:
            break

    return reliable_sample_sizes

sample_size_range = range(10, 10010, 50)
sigma_sq = 1
# Perform the simulation using statsmodels.api
simulate_regression_statsmodels(sample_size_range, beta, sigma_sq)
```

```
[(10, 0.01),
 (60, 0.03),
 (110, 0.13),
 (160, 0.33),
 (210, 0.6),
 (260, 0.68),
 (310, 0.84),
 (360, 0.9),
 (410, 0.95)]
```

At a sample size of 410, we have a reliability of 0.95, meaning that in 95% of the simulations, all interaction coefficients have p-values below 0.05.

Thus, based on this simulation, you would need at least 460 data points to reliably determine that all interaction coefficients have p-values below 0.05.

Part D

Perform the same experiment as in (c) but fit the data to a model with no interactions. What do you find? How does adding the interaction terms influence the p-values.

Solution

```
# Redefine the simulation function for a model without interactions
def simulate_no_interaction(N, beta, sigma_sq, iterations=100):
    p_value_threshold = 0.05
    reliable_sample_sizes_no_interaction = []

    for sample_size in N:
        successful_simulations = 0

        for _ in range(iterations):
            # Simulate N observations of X1, X2, X3
            X = np.random.binomial(1, 0.5, (sample_size, 3))
            # Add a column of ones for the intercept
            X_intercept = sm.add_constant(X)

            # Generate the corresponding Y values
            Y = calculate_Y(X.T, beta) + np.random.normal(0, np.sqrt(sigma_sq), sample_size)

            # Fit the regression model without interaction terms
            model_no_interaction = sm.OLS(Y, X_intercept).fit()

            # Check if all coefficients have p-values below 0.05
            main_effect_pvalues = model_no_interaction.pvalues[1:]  # p-values of the main effects
            if all(main_effect_pvalues < p_value_threshold):
                successful_simulations += 1

        # Record the proportion of successful simulations
        reliability = successful_simulations / iterations
        reliable_sample_sizes_no_interaction.append((sample_size, reliability))

        # If reliability criterion is met, break the loop
        if reliability >= 0.95:
            break

    return reliable_sample_sizes_no_interaction

# Perform the simulation for the no-interaction model
simulate_no_interaction(sample_size_range, beta, sigma_sq)
```

```
[(10, 0.03),
 (60, 0.23),
 (110, 0.31),
 (160, 0.42),
 (210, 0.57),
 (260, 0.68),
 (310, 0.71),
 (360, 0.78),
 (410, 0.86),
 (460, 0.91),
 (510, 0.96)]
```

The simulation for the model without interaction terms shows that with a sample size of 560, we achieve a reliability of 0.96. This indicates that in 96% of the simulations, all main effect coefficients have p-values below 0.05.

When we compare this to the model with interaction terms, we found that a sample size of 460 was sufficient to achieve a similar level of reliability. This suggests that including interaction terms in the model can potentially lead to identifying significant effects with a smaller sample size, assuming that the interaction effects are indeed present and substantial.

Adding interaction terms to the model captures the combined effects of drugs that are not apparent when looking at each drug's effect independently. If these interactions are significant, they can be detected with high confidence, which might lead to a more accurate and potentially more efficient inference about the effects of the drugs. However, it's important to note that adding too many terms (including interactions) can also lead to overfitting, especially if the sample size is not large enough to support the complexity of the model.