Data Science & ML

Case Study 2

Unsupported Cell Type. Double-Click to inspect/edit the content.

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

```
from google.colab import drive
drive.mount('/content/drive')
```

```
# Load the dataset cereal.csv.
#data = pd.read_csv('cereal.csv')
data = pd.read_csv('/content/drive/My Drive/Colab_Data/cereal.csv')
```

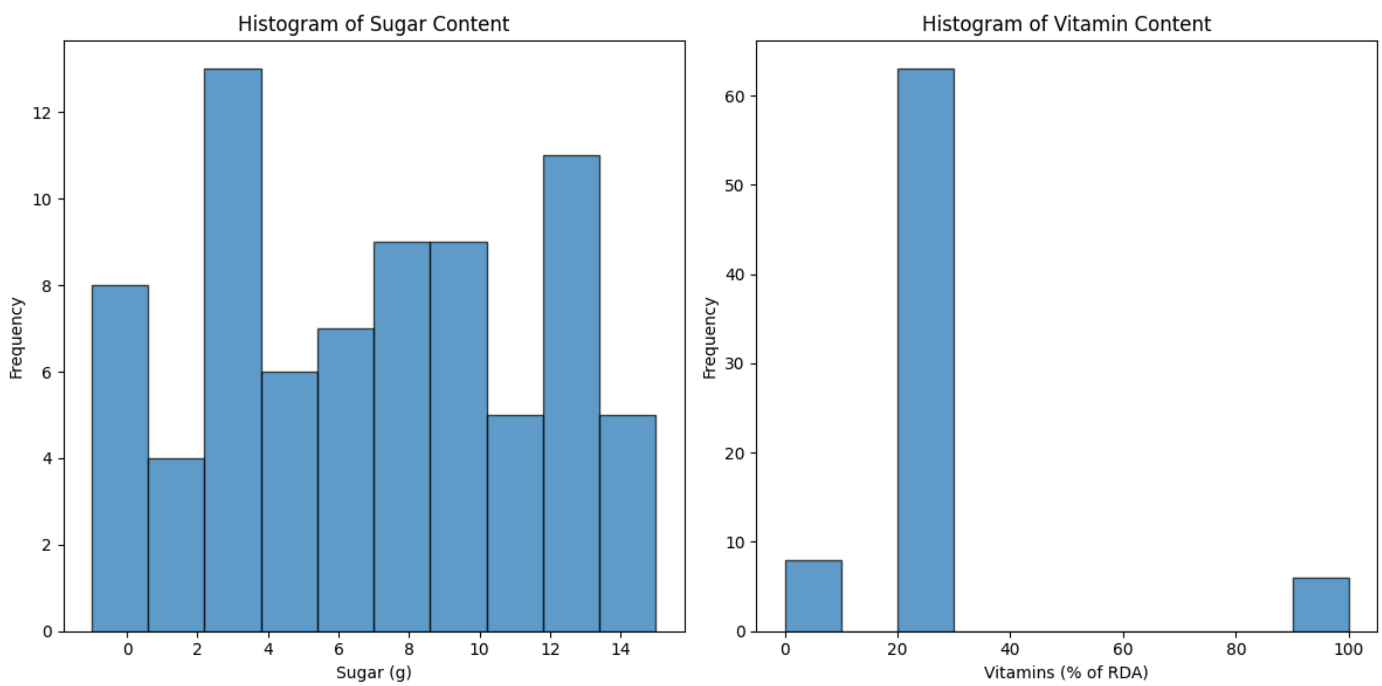
```
print("Info of the dataset:")
print(data.info())
print("-"*50)
print("Check for null values in the dataset:")
print(data.isnull().sum())
print("-"*50)
print("Print the first rows from the dataset:")
print(data.head())
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 77 entries, 0 to 76
Data columns (total 16 columns):
 #   Column    Non-Null Count  Dtype
---  ------    --------------  -----
 0   name      77 non-null     object
 1   mfr       77 non-null     object
 2   type      77 non-null     object
 3   calories  77 non-null     int64
 4   protein   77 non-null     int64
 5   fat       77 non-null     int64
 6   sodium    77 non-null     int64
 7   fiber     77 non-null     float64
 8   carbo     77 non-null     float64
 9   sugars    77 non-null     int64
 10  potass    77 non-null     int64
 11  vitamins  77 non-null     int64
 12  shelf     77 non-null     int64
 13  weight    77 non-null     float64
 14  cups      77 non-null     float64
 15  rating    77 non-null     float64
dtypes: float64(5), int64(8), object(3)
memory usage: 9.8+ KB
None
--------------------------------------------------
Check for null values in the dataset:
name        0
mfr         0
type        0
calories    0
protein     0
fat         0
sodium      0
fiber       0
carbo       0
sugars      0
potass      0
vitamins    0
shelf       0
weight      0
cups        0
rating      0
```

```
                        name mfr type  calories  protein  fat  sodium  fiber  \
0                  100% Bran   N    C        70        4    1     130   10.0
1          100% Natural Bran   Q    C       120        3    5      15    2.0
2                   All-Bran   K    C        70        4    1     260    9.0
3  All-Bran with Extra Fiber   K    C        50        4    0     140   14.0
4             Almond Delight   R    C       110        2    2     200    1.0

   carbo  sugars  potass  vitamins  shelf  weight  cups     rating
0    5.0       6     280        25      3     1.0  0.33  68.402973
1    8.0       8     135         0      3     1.0  1.00  33.983679
2    7.0       5     320        25      3     1.0  0.33  59.425505
3    8.0       0     330        25      3     1.0  0.50  93.704912
4   14.0       8      -1        25      3     1.0  0.75  34.384843
```

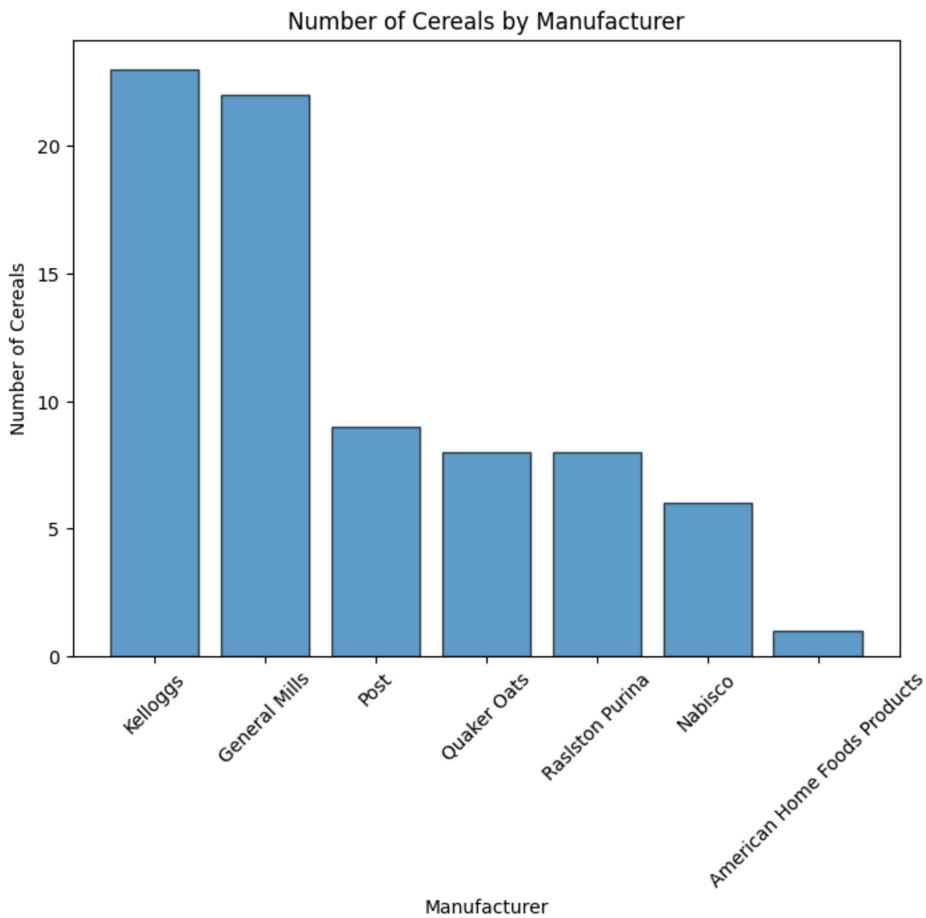
Unsupported Cell Type. Double-Click to inspect/edit the content.

```
#1
# Plot histograms
plt.figure(figsize=(12, 6))

# Histogram for sugar content
plt.subplot(1, 2, 1)
plt.hist(data['sugars'], bins=10, edgecolor='black', alpha=0.7)
plt.title('Histogram of Sugar Content')
plt.xlabel('Sugar (g)')
plt.ylabel('Frequency')

# Histogram for vitamin content
plt.subplot(1, 2, 2)
plt.hist(data['vitamins'], bins=10, edgecolor='black', alpha=0.7)
plt.title('Histogram of Vitamin Content')
plt.xlabel('Vitamins (% of RDA)')
plt.ylabel('Frequency')

plt.tight_layout()
plt.show()
```




```
# 2. Create a new column with full manufacturer names and plot a bar chart

# Mapping manufacturer codes to full names
manufacturer_mapping = {
    'N': 'Nabisco',
    'Q': 'Quaker Oats',
    'K': 'Kelloggs',
    'R': 'Raslston Purina',
    'G': 'General Mills',
```

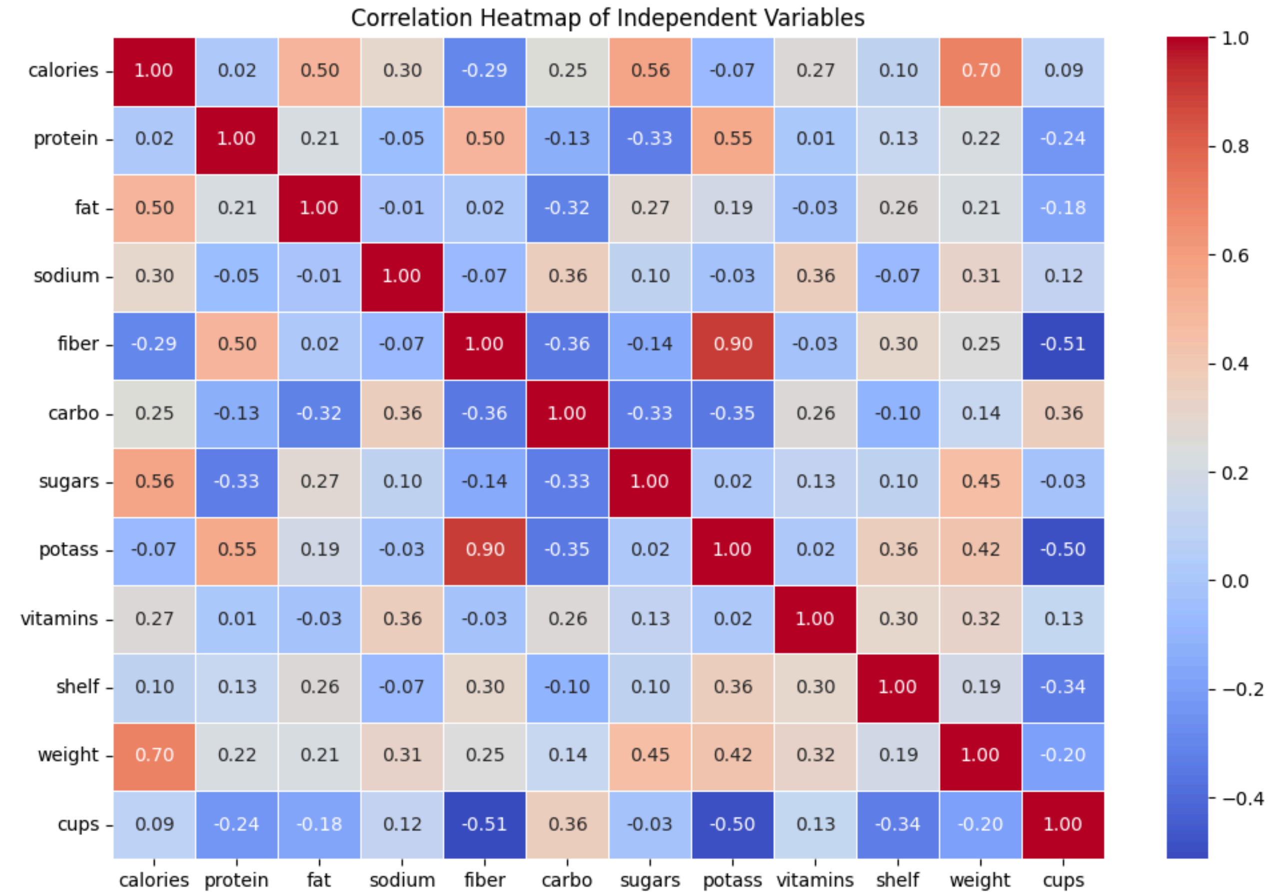
```
    'P': 'Post',
    'A': 'American Home Foods Products'
}

# Add a new column with full manufacturer names
data['manufacturer_full'] = data['mfr'].map(manufacturer_mapping)

# Count the number of cereals by manufacturer
manufacturer_counts = data['manufacturer_full'].value_counts()

# Plot the bar chart
plt.figure(figsize=(8, 6))
plt.bar(manufacturer_counts.index, manufacturer_counts.values, alpha=0.7, edgecolor='black')
plt.title('Number of Cereals by Manufacturer')
plt.xlabel('Manufacturer')
plt.ylabel('Number of Cereals')
plt.xticks(rotation=45)
plt.show()

print(manufacturer_counts)
```




```
manufacturer_full
Kelloggs                        23
General Mills                   22
Post                             9
Quaker Oats                      8
Raslston Purina                  8
Nabisco                          6
American Home Foods Products     1
```

```
# 3. Extract target and predictors, split the data

# Import necessary libraries
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.linear_model import LinearRegression
from sklearn.metrics import mean_squared_error
import seaborn as sns
import matplotlib.pyplot as plt
```

```
# Step 1. Define the target variable (y) and predictors (x)
# The 'rating' column is the target, and the predictors are all numeric columns except 'rating'.
y = data['rating']
x = data.select_dtypes(include=['int64', 'float64']).drop(columns=['rating'])

# Step 2. Compute the correlation matrix for feature selection
correlation_matrix = x.corr()

# Function to drop highly correlated features
def drop_highly_correlated(corr_matrix, threshold=0.9):
    """
    Identifies and returns features to drop based on a correlation threshold.
    Only the lower triangle of the correlation matrix is scanned to avoid redundancy.
    """
    to_drop = set()  # Set to keep track of features to drop
    cols = corr_matrix.columns

    # Iterate over the lower triangle of the matrix
    for i in range(len(cols)):
        for j in range(i):  # Only check lower triangle (j < i)
            if abs(corr_matrix.iloc[i, j]) > threshold:  # Check if correlation exceeds the threshold
                print(f"Highly correlated pair: {cols[i]} and {cols[j]} with correlation {abs(corr_matrix.iloc[i, j])}")
                to_drop.add(cols[i])  # Add one of the features to the set

    return list(to_drop)

# Step 3. Visualize the correlation matrix as a heatmap
plt.figure(figsize=(12, 8))
sns.heatmap(correlation_matrix, annot=True, cmap="coolwarm", fmt=".2f", linewidths=0.5)
plt.title("Correlation Heatmap of Independent Variables")
plt.show()

# Identify redundant features with a threshold of 0.68
redundant_features = drop_highly_correlated(correlation_matrix, threshold=0.68)
print(f"Features to drop: {redundant_features}")

# Drop redundant features from the dataset
x_reduced = x.drop(columns=redundant_features)

#Step  4. Split the data into training and testing sets
# 75% of the data is used for training, and 25% for testing
x_train, x_test, y_train, y_test = train_test_split(x_reduced, y, test_size=0.25, random_state=42)

print("Training data shape:", x_train.shape)
print("Test data shape:", x_test.shape)

# Display a preview of the training data
print(x_train.head())
```




```
Highly correlated pair: potass and fiber with correlation 0.9033736685942043
Highly correlated pair: weight and calories with correlation 0.6960910769169041
Features to drop: ['potass', 'weight']
Training data shape: (57, 10)
Test data shape: (20, 10)
    calories  protein  fat  sodium  fiber  carbo  sugars  vitamins  shelf  \
30       100        2    0      45    0.0   11.0      15        25      1
40       110        2    1     260    0.0   21.0       3        25      2
39       140        3    1     170    2.0   20.0       9       100      3
16       100        2    0     290    1.0   21.0       2        25      1
65        90        3    0       0    3.0   20.0       0         0      1

    cups
30  0.88
40  1.50
39  0.75
16  1.00
```

```
# 4. Fit a linear regression model and evaluate mean squared error

from sklearn.linear_model import LinearRegression
from sklearn.metrics import mean_squared_error
from sklearn.model_selection import cross_val_score

# Step 1: Fit a linear regression model and evaluate performance
# Initialize the linear regression model
model = LinearRegression()

# Train the model on the training data
model.fit(x_train, y_train)

# Display the coefficients of the linear regression model
print("Coefficients: ", model.coef_)

# Make predictions on the test data
y_pred = model.predict(x_test)

# Calculate the Mean Squared Error (MSE) on the test data
mse = mean_squared_error(y_test, y_pred)
print(f"Mean Squared Error on Test Data: {mse:.2f}")
```

```
# Step 2: Perform Cross-Validation
# Evaluate the model using 5-fold cross-validation
cv_scores = cross_val_score(model, x_reduced, y, cv=5, scoring='r2')
print(f"Cross-Validation R² Scores: {cv_scores}")
print(f"Mean CV R²: {cv_scores.mean():.4f}")
```

```
Coefficients:  [-0.22140948  2.98332938 -2.07671607 -0.05408762  2.61721877  1.05226752
 -0.80333669 -0.05374602 -0.13755986  0.63127598]
Mean Squared Error on Test Data: 1.15
Cross-Validation R² Scores: [0.99545177 0.99201605 0.9913534  0.98657617 0.99529792]
Mean CV R²: 0.9921
```

1. Mean Squared Error (MSE)

$$MSE = \frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{y}_i)^2$$

Where:

- n: Number of data points.
- y_i : Actual value of the target variable for the ith observation.
- $\hat{y}_i$ Predicted value by the model for the ith observation.

Meaning:

- MSE is the average squared difference between the actual and predicted values.
- It penalizes larger errors more heavily due to squaring.
- A lower MSE indicates better model performance, with 0 being the ideal (perfect predictions).

Interpretation:

- MSE is in the same units as the square of the target variable.
- For example, if rating is measured in points, MSE is in points squared.
- While useful for comparison, it lacks intuitive interpretability since it doesn't represent actual error magnitude.

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2. Coefficient of Determination (R^2)

$$R^2 = 1 - \frac{\text{SS}_{\text{res}}}{\text{SS}_{\text{tot}}}$$

Where:

- $SS_{\text{res}} = \sum_{i=1}^{n}(y_i - \hat{y}_i)^2$: Residual sum of squares (unexplained variance).
- $SS_{\text{tot}} = \sum_{i=1}^{n}(y_i - \bar{y})^2$ Total sum of squares (variance in the target variable).
- $\bar{y}$: Mean of the actual target values.

Meaning:

- R^2 measures the proportion of variance in the target variable explained by the model.
- Values range from 0 to 1:
- $R^2 = 1$: Perfect fit; the model explains all variance.
- $R^2 = 0$: The model explains no variance (equivalent to predicting the mean of y).
- Negative R^2: The model performs worse than simply predicting the mean.

Interpretation:

- $R^2 = 0.99$: The model explains 99% of the variance in the target variable.
- While R^2 is useful, it does not penalize overfitting and may appear high for overly complex models.