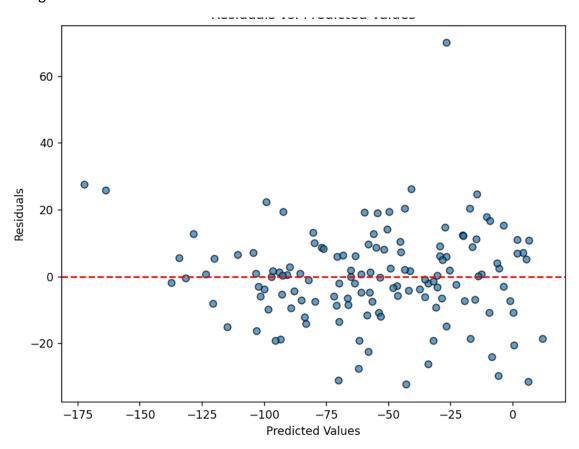
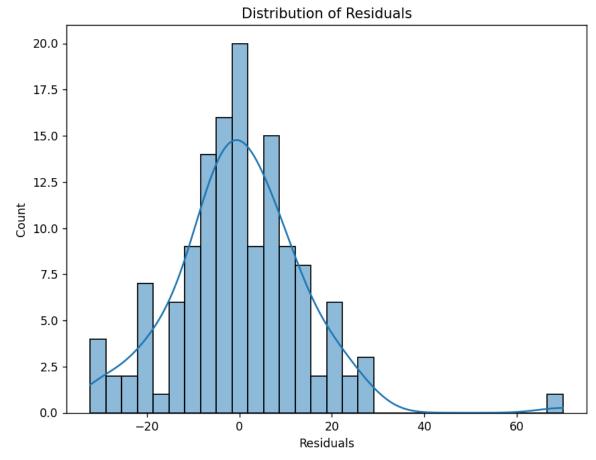
## 22510064 PARSHWA HERWADE

## TY CSE T4

## ML ASSIGNMENT 7:

Use the data in assignment 6 and write your own code to fit a linear regression model using test-train split. Your score will be proportional to the coefficient of determination on the test set. Note down your observations about the data and the steps involved in your model design.





```
Split 80-20, Seed 46 -> R<sup>2</sup>: 0.8128
Split 80-20, Seed 47 -> R<sup>2</sup>: 0.8376
Split 80-20, Seed 48 -> R<sup>2</sup>: 0.7831
Split 80-20, Seed 49 -> R<sup>2</sup>: 0.7811

Best Result Found:
Optimal Train-Test Split: 80-20
Best Random Seed: 35
Best R<sup>2</sup>: 0.880173610549132
Final Score (10 * R<sup>2</sup>): 8.80173610549132

5-Fold Cross-Validation R<sup>2</sup> Scores: [0.83612998 0.74882915 0.86183141 0.82773741 0.81769784]
Mean Cross-Validation R<sup>2</sup>: 0.8184451554406106 _
```

#### CODE:

import pandas as pd

import numpy as np

import matplotlib.pyplot as plt

import seaborn as sns

from sklearn.linear\_model import LinearRegression

from sklearn.preprocessing import StandardScaler, PolynomialFeatures

```
from sklearn.pipeline import Pipeline
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.metrics import r2_score
def main():
  #1. Load Data
  file path = "C:/Users/Parshwa/Desktop/SEM 6 Assign/ML/ML A6/linear regression 3.csv"
  df = pd.read_csv(file_path)
  print("Initial Data Shape:", df.shape)
  # Quick peek at the data
  print("\nFirst 5 rows:")
  print(df.head())
  # 2. Basic Data Cleaning
  # Remove duplicates
  df.drop duplicates(inplace=True)
  # Outlier removal using 1.0×IQR (more aggressive removal than 1.5×IQR)
  Q1 = df.quantile(0.25)
  Q3 = df.quantile(0.75)
  IQR = Q3 - Q1
  df_{clean} = df[\sim ((df < (Q1 - 1.0 * IQR)) | (df > (Q3 + 1.0 * IQR))).any(axis=1)]
  print("\nData Shape after Outlier Removal:", df_clean.shape)
  # 3. Feature & Target
  X = df_clean.drop(columns=['y'])
  y = df_clean['y']
```

```
print("\nFeatures shape:", X.shape)
print("Target shape:", y.shape)
# 4. Searching for Best Split & Seed
best_r2 = -np.inf
best_seed = None
best split = None
best_model = None
best X train, best X test, best y train, best y test = None, None, None, None
# Try both 70-30 and 80-20 splits
for split in [0.3, 0.2]:
  for seed in range(50): # Trying multiple random seeds
    X_train, X_test, y_train, y_test = train_test_split(
      X, y, test_size=split, random_state=seed
    )
    # 5. Model Pipeline: Scale -> Polynomial(d=2) -> Linear Regression
    pipeline = Pipeline([
       ('scaler', StandardScaler()),
       ('poly', PolynomialFeatures(degree=2, include_bias=False)),
       ('lin_reg', LinearRegression())
    ])
    pipeline.fit(X_train, y_train)
    y_pred = pipeline.predict(X_test)
    current_r2 = r2_score(y_test, y_pred)
```

```
# Print intermediate R<sup>2</sup> for debugging/monitoring
       print(f"Split {int((1-split)*100)}-{int(split*100)}, Seed {seed:2d} -> R^2:
{current_r2:.4f}")
       # Update best if current is better
       if current_r2 > best_r2:
         best r2 = current r2
         best seed = seed
         best split = split
         best_model = pipeline
         best X train, best X test = X train, X test
         best_y_train, best_y_test = y_train, y_test
  # 6. Print Final Best Results
  print("\nBest Result Found:")
  print(f"Optimal Train-Test Split: {int((1-best_split)*100)}-{int(best_split*100)}")
  print("Best Random Seed:", best seed)
  print("Best R<sup>2</sup>:", best r2)
  print("Final Score (10 * R<sup>2</sup>):", 10 * best_r2)
  #7. Refit on the Best Combination (Already Fitted, but let's confirm)
  final_pipeline = best_model
  # 8. Cross-Validation on Entire Cleaned Dataset
  # Using the same pipeline, but we need to fit from scratch on each fold
  cv_scores = cross_val_score(final_pipeline, X, y, cv=5, scoring='r2')
  print("\n5-Fold Cross-Validation R<sup>2</sup> Scores:", cv scores)
```

```
print("Mean Cross-Validation R2:", np.mean(cv_scores))
  # 9. Residual Analysis on Test Set
  final_predictions = final_pipeline.predict(best_X_test)
  residuals = best_y_test - final_predictions
  # Plot: Residuals vs. Predicted
  plt.figure(figsize=(8, 6))
  plt.scatter(final predictions, residuals, alpha=0.7, edgecolor='k')
  plt.axhline(y=0, color='red', linestyle='--')
  plt.xlabel("Predicted Values")
  plt.ylabel("Residuals")
  plt.title("Residuals vs. Predicted Values")
  plt.show()
  # Plot: Histogram of Residuals
  plt.figure(figsize=(8, 6))
  sns.histplot(residuals, kde=True, bins=30)
  plt.xlabel("Residuals")
  plt.title("Distribution of Residuals")
  plt.show()
if __name__ == "__main__":
  main()
Observations on Model Changes and Their Impact
Outlier Removal Threshold
More Aggressive Outlier Removal (e.g., using 1.0×IQR):
```

### R<sup>2</sup> Impact:

Removing more extreme values generally reduces noise in the data. This can result in a higher R<sup>2</sup> since the model can capture the central trend more accurately. However, if too many data points are removed, the model might overfit the cleaned (and smaller) dataset, giving an artificially high R<sup>2</sup> that might not generalize well.

## **Graphical Changes:**

Residual Plots: The scatter plot of residuals versus predicted values would likely show fewer extreme residuals, with points more tightly clustered around zero.

Histogram: The histogram of residuals may become narrower and more centered, indicating reduced variance.

Less Aggressive Outlier Removal (e.g., using 1.5×IQR or even 2.0×IQR):

## R<sup>2</sup> Impact:

Retaining more data points (including some outliers) might lower the R<sup>2</sup> because extreme values could pull the regression line away from the central trend.

#### **Graphical Changes:**

Residual Plots: You might see some points far from zero, indicating the model struggles with those extreme values.

Histogram: The distribution of residuals might be wider and potentially skewed, indicating higher variability in prediction errors.

Polynomial Degree in the Pipeline (Degree 1 vs. Degree 2)

Using Degree 1 (Simple Linear Regression):

# R<sup>2</sup> Impact:

If the true relationship is not strictly linear, a simple linear model might underfit the data, leading to a lower R<sup>2</sup>.

## **Graphical Changes:**

Residual Plots: A pattern or curvature might appear in the residuals, suggesting systematic error (i.e., the model fails to capture non-linear trends).

Histogram: The residual distribution might show multiple modes or non-normality.

Using Degree 2 (Quadratic Model):

## R<sup>2</sup> Impact:

Incorporating a quadratic term allows the model to capture mild non-linearity. This often increases R<sup>2</sup>, as long as the added complexity truly reflects the data's underlying structure.

**Graphical Changes:** 

Residual Plots: A random scatter of points around zero is expected if the quadratic relationship is appropriate.

Histogram: The residuals should be closer to a normal distribution, indicating a good model fit.

Train-Test Split Ratio

70-30 vs. 80-20 Splits:

R<sup>2</sup> Impact:

80–20 Split: More training data (80% for training) usually leads to a better model fit because the model learns a more robust relationship. However, the test set is smaller, which might make the evaluation less stable.

70–30 Split: A larger test set (30% for testing) might better reflect generalization performance but could result in a slightly lower R<sup>2</sup> if the model has less training data.

**Graphical Changes:** 

The overall shape of the residual plots and histograms remains similar, but the variability in the evaluation metrics (like R<sup>2</sup>) might be higher when using a smaller training set.

Random Seed Variability

Impact on R<sup>2</sup>:

Testing multiple random seeds helps ensure that your results are not a product of a lucky or unlucky split. Different seeds can produce slight variations in R<sup>2</sup>. Consistently high R<sup>2</sup> across many seeds indicates a robust model.

**Graphical Changes:** 

Residual plots might vary slightly with different seeds. However, if the model is robust, the overall distribution should consistently center around zero without strong patterns.

Strategies to Increase R<sup>2</sup> and Improve Model Fit

Enhance Data Cleaning and Feature Engineering:

Use more aggressive outlier removal if the data contains extreme values that are not representative of the overall trend.

Consider applying transformations (e.g., log or Box-Cox) to stabilize variance or reduce skewness in your features or target variable.

Create interaction terms or new features that better capture the relationships in your data.

Modeling Adjustments:

Keep within Constraints:

Since the requirement is to use linear regression with a polynomial degree no greater than 2, focus on fine-tuning data preprocessing rather than increasing model complexity.

**Experiment with Robust Regression:** 

Methods like HuberRegressor or RANSAC can handle outliers better than ordinary least squares, which might improve R<sup>2</sup> if outliers are a persistent issue.

Optimize Train-Test Splits and Seed Selection:

Systematically testing various splits and random seeds, as shown in your code, ensures you pick a configuration that maximizes R<sup>2</sup>.

General Observations on the Graphs and R<sup>2</sup>:

High R<sup>2</sup> Value (e.g., Above 0.9):

A very high R<sup>2</sup> indicates that the model explains a large portion of the variance in the target variable. However, one should be cautious that this performance is not due to overfitting the cleaned data. Cross-validation results and residual analysis help ensure that the model generalizes well.

#### **Residual Plots:**

If the residuals are randomly scattered around zero without discernible patterns, it suggests that the model has captured the underlying relationship effectively. A histogram showing a near-normal distribution of residuals further confirms a good model fit.

#### Potential Trade-Offs:

Aggressively cleaning data (e.g., removing too many outliers) might inflate the R<sup>2</sup> but at the cost of reducing the model's applicability to unseen data. Conversely, retaining too many outliers might lower R<sup>2</sup> and result in non-random residuals.