CSCI485HW2

February 23, 2026

```
[1]: from sklearn.datasets import load_diabetes
     import matplotlib
     import pandas as pd
     import numpy as np
     import altair as alt
     import pandas as pd
     from sklearn.linear_model import LinearRegression
     from sklearn.metrics import mean_squared_error
     from sklearn import set_config
     from sklearn.metrics import r2_score
     from sklearn.feature_selection import RFE
     from sklearn.model_selection import cross_val_score, train_test_split
     import matplotlib.pyplot as plt
     from sklearn.datasets import make_regression
```

1 Task 1: Dataset Exploration

```
[2]: # Load data

     diabetes = load_diabetes()

     df = pd.DataFrame(data=diabetes.data, columns=diabetes.feature_names)
     y = diabetes.target

     df.head()
```

```
[2]:         age       sex       bmi        bp        s1        s2        s3  \
     0  0.038076  0.050680  0.061696  0.021872 -0.044223 -0.034821 -0.043401
     1 -0.001882 -0.044642 -0.051474 -0.026328 -0.008449 -0.019163  0.074412
     2  0.085299  0.050680  0.044451 -0.005670 -0.045599 -0.034194 -0.032356
     3 -0.089063 -0.044642 -0.011595 -0.036656  0.012191  0.024991 -0.036038
     4  0.005383 -0.044642 -0.036385  0.021872  0.003935  0.015596  0.008142

              s4        s5        s6
     0 -0.002592  0.019907 -0.017646
     1 -0.039493 -0.068332 -0.092204
```

```
2 -0.002592  0.002861 -0.025930
3  0.034309  0.022688 -0.009362
4 -0.002592 -0.031988 -0.046641
```

[ ]:
```python
# Explore the dataset and describe features and target variables

print(df.info())
```

[ ]:
```python
print(df.describe())
```

We have 10 features that will be used to predict our target:

Features:

```
age: Age of the patient.
sex: Gender of the patient.
bmi: Body mass index.
bp: Average blood pressure.
Six other quantitative variables derived from blood samples.
```

Target: A continuous variable measuring the disease progression within a one-year period. Larger values generally correspond to more severe progression of diabetes.

All our values are floats, with no nulls.

442 observations (diabetes patients).

[3]:
```python
# split the dataset into testing and training using an 80-20 split.

X = pd.DataFrame(data=diabetes.data, columns=diabetes.feature_names)
y = diabetes.target

# seperating by X and y values will help calculate Adjusted R squared later
X_train, X_test, y_train, y_test = train_test_split(
    X, y, train_size=0.80, random_state = 42
)
```

2 Task 2: Linear Regression Model

[4]:
```python
# Full Model
full_model = LinearRegression()
full_model.fit(X_train, y_train)
full_pred = full_model.predict(X_test)

# Metrics for Full Model
full_mse = mean_squared_error(y_test, full_pred)
full_r2 = r2_score(y_test, full_pred)
print("Full Model Metrics:")
print(f"MSE: {full_mse:.10f}, R²: {full_r2:.10f}")
```

```
Full Model Metrics:
MSE: 2900.1936284935, R²: 0.4526027630
```

45.26% of the variation in our target is accounted for by our model.

3 Tasks 3/4: Implement Recursive Feature Elimination (RFE) & Analyze Feature Importance

[5]:
```python
def rfe_starting_with_all_features():
    rfe_results = []
    feature_names = diabetes.feature_names
    threshold = 0.01

    for k in range(len(feature_names), 0, -1):
        rfe = RFE(estimator=full_model, n_features_to_select=k)
        rfe.fit(X_train, y_train)

        current_r2 = r2_score(y_test, rfe.predict(X_test))

        # put 0 if the feature isn't selected
        coef_map = {name: 0.0 for name in feature_names}
        selected_features = [feature_names[i] for i in␣
 ↪range(len(feature_names)) if rfe.support_[i]]

        for name, coef in zip(selected_features, rfe.estimator_.coef_):
            coef_map[name] = coef

        # Store results
        coef_map['n_features'] = k
        coef_map['R2_Score'] = current_r2
        rfe_results.append(coef_map)

    table_df = pd.DataFrame(rfe_results).set_index('n_features').sort_index()

    # getting the largest count where the improvement is above the defined␣
 ↪threshold 0.01
    optimal_n = 1
    for i in range(2, len(feature_names), 1):
        improvement = table_df.loc[i, 'R2_Score'] - table_df.loc[i-1,␣
 ↪'R2_Score']
        if improvement > threshold:
            optimal_n = i
    print(f"Optimal number of features given threshold {threshold}:␣
 ↪{optimal_n}")
    return table_df, optimal_n
```

```
results_table, optimal_n = rfe_starting_with_all_features()
display(results_table)

plt.figure(figsize=(10, 6))
plt.plot(results_table.index, results_table['R2_Score'], marker='o', label='R²')
plt.axvline(optimal_n, color='red', linestyle='--', label=f'Optimal Features␣
  ↪({optimal_n})')
plt.title("R² Scores vs Number of Features")
plt.xlabel("Number of Features")
plt.ylabel("R²")
plt.legend()
plt.grid()
plt.show()
```

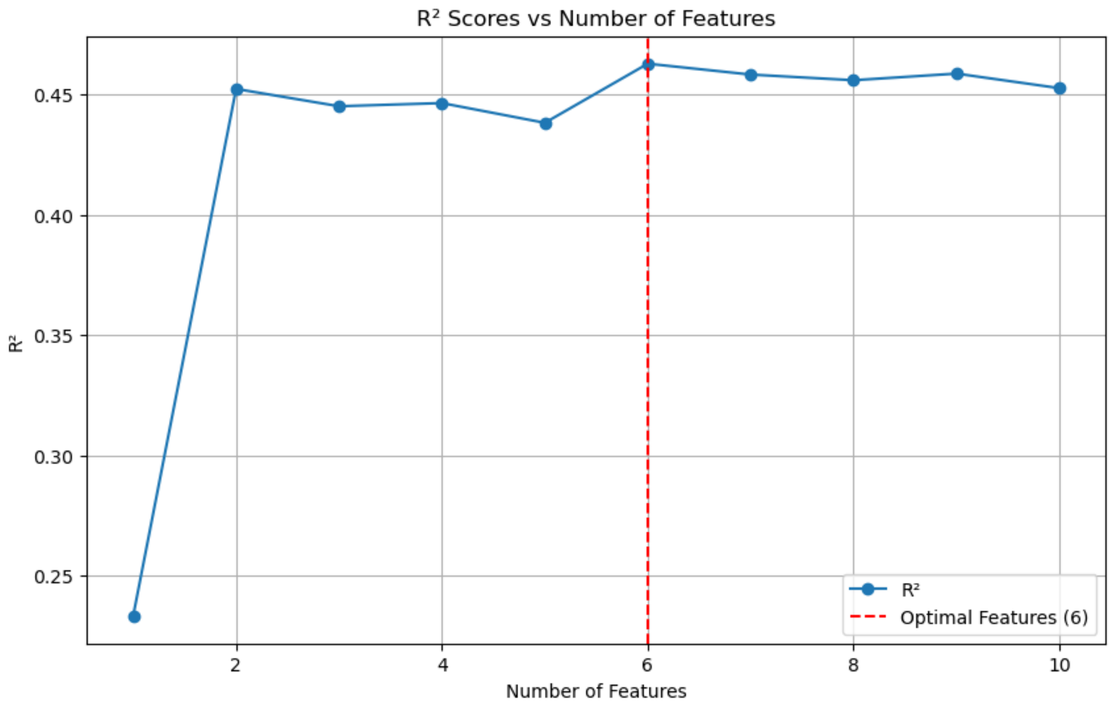
```
Optimal number of features given threshold 0.01: 6

                  age         sex         bmi          bp          s1  \
n_features
1            0.000000    0.000000  998.577689    0.000000    0.000000
2            0.000000    0.000000  732.109021    0.000000    0.000000
3            0.000000    0.000000  737.685594    0.000000 -228.339889
4            0.000000    0.000000  691.460102    0.000000 -592.977874
5            0.000000    0.000000  597.892739  306.647913 -655.560612
6            0.000000 -215.267423  557.314167  350.178667 -851.515734
7            0.000000 -235.364224  551.866448  362.356114 -660.643160
8            0.000000 -233.754686  550.744365  363.791753 -947.823133
9            0.000000 -236.649588  542.799508  354.211438 -936.350589
10          37.904021 -241.964362  542.428759  347.703844 -931.488846

                   s2          s3          s4          s5          s6  \
n_features
1            0.000000    0.000000    0.000000    0.000000    0.000000
2            0.000000    0.000000    0.000000  562.226535    0.000000
3            0.000000    0.000000    0.000000  680.224653    0.000000
4          362.950323    0.000000    0.000000  783.168538    0.000000
5          409.622184    0.000000    0.000000  728.643647    0.000000
6          591.093315    0.000000    0.000000  803.121285    0.000000
7          343.348089    0.000000  185.140764  664.774591    0.000000
8          541.585796  172.250588  277.741072  761.921177    0.000000
9          528.796592  167.800414  270.396514  744.447429   53.350483
10         518.062277  163.419983  275.317902  736.198859   48.670657

            R2_Score
n_features
1           0.233350
2           0.452293
3           0.445095
4           0.446404
```

```
5               0.438201
6               0.462777
7               0.458255
8               0.455901
9               0.458659
10              0.452603
```



My code above starts with 10 features and decreases by 1 feature incrementally, tracking each R^2 value and coefficents in a table. Then to find the optimal amount of features, it checks each R^2, and if it improves by at least the desired threshold I defined to be 0.01, then it is considered the optimal model. This method allowed me to find the optimal number of features as 6 (sex, bmi, s1, s2, , s5, and s6) given a threshold of 0.01. Finally, I graphed my results.

2. The three most important features are bmi, s1, and s5 because their coefficients are furthest from 0 during each iteration, shown by my table. Those 3 features alone are able to explain 44.51% of the variance in the target. This is not far from the 46.27% of variance explained from the optimal 6-feature model. Choosing these 3 features, given they have similar R^2, would give us a less complex model for similar model results. Changing our threshold value based on how much accuracy we're willing to give up for less complexity is the clear goal of RFE.

3. Our baseline model, with all 10 features, has R^2 of 0.4526, meaning 45.26% of the variation in our target is accounted for by our model. The RFE process removed the least important feature, or the feature with coefficient closest to 0, one at a time. My results showed that removing age, s6, s3, then s4, left us with the best r^2 given our threshold. Therefore, our optimal model explains 46.28% of the variation in the target using the 6 remaining features

sex, bmi, s1, s2, , s5, and s6.

4 Task 5: Reflection

1. I learned that the way RFE works is by iteratively elimating the least important features to find the model that gives us the best R^2. I learned that it's important to choose a good threshold for how much accuracy you're willing to part with in exchange for model simplicity. The difference in R^2 from a 2-feature model to our optimal model (6 features) is very small, so it may be worth using just 2 features depending on the circumstance.
2. RFE removes the coefficents with the smallest absolute value, whereas Lasso's methodology involves minimizing the sum of the absolute values of the coefficients by penalizing large coefficients. They both aim to improve model performance by reducing the number of features.
3. Age of the patient is the worst predictor (out of our 10 features) for predicting our target, followed by s6 and s3. The best predictors we have are bmi of the patient, then s5 and s1.