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Q1. Gradient Descent Implementation

1. Batch Gradient Descent

In [99]:
```
# a) Load the employee_salary.csv dataset. Display the first 10 rows a

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt

df = pd.read_csv('emplyee_salary.csv')

df.head(10)
```

Out[99]:

	Unnamed: 0	YearsExperience	Salary
0	0	1.2	39344.0
1	1	1.4	46206.0
2	2	1.6	37732.0
3	3	2.1	43526.0
4	4	2.3	39892.0
5	5	3.0	56643.0
6	6	3.1	60151.0
7	7	3.3	54446.0
8	8	3.3	64446.0
9	9	3.8	57190.0

In [100]:
```
df.describe()
```

Out[100]:

	Unnamed: 0	YearsExperience	Salary
count	30.000000	30.000000	30.000000
mean	14.500000	5.413333	76004.000000
std	8.803408	2.837888	27414.429785
min	0.000000	1.200000	37732.000000
25%	7.250000	3.300000	56721.750000
50%	14.500000	4.800000	65238.000000
75%	21.750000	7.800000	100545.750000
max	29.000000	10.600000	122392.000000

Explanation

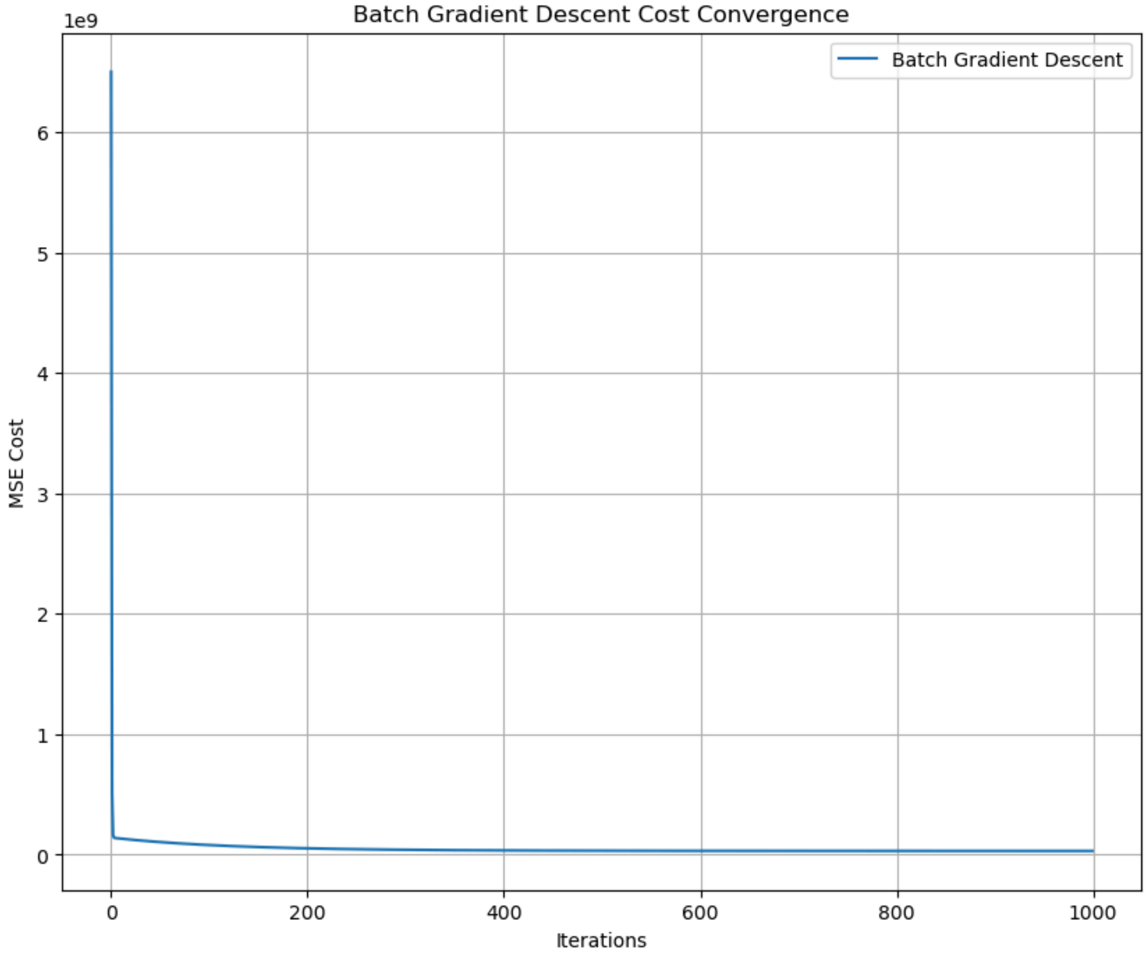
The dataset 'employee_salary.csv' consist of 30 rows and 3 columns. The first 10 rows display two columns: 'Experience' (in years) and 'Salary' (in currency).
The basic statistics show the mean, standard deviation, minimum, and maximum for both columns, offering a summary of the data's distribution.

In [101]:
```
'''
b) Implement Batch Gradient Descent from scratch to fit a linear regre
(Salary = m * Experience + b):
Initialize: m = 0, b = 0
Learning rate α = 0.01
Iterations = 1000
'''

X = df['YearsExperience'].values
y = df['Salary'].values

m, b = 0, 0
alpha = 0.01
epochs = 1000
n = len(X)
cost_history = []

for i in range(epochs):
    y_pred = m * X + b
    error = y_pred - y
    cost = (1/n) * np.sum(error**2)
    cost_history.append(cost)
    dm = (2/n) * np.sum(error * X)
    db = (2/n) * np.sum(error)
    m = m - alpha * dm
    b = b - alpha * db
```

In [102]:
```
# c) Print the final slope and intercept

print("\nFinal Batch GD slope (m):", m)
print("Final Batch GD intercept (b):", b)
```

```
Final Batch GD slope (m): 9504.801321957242
Final Batch GD intercept (b): 24474.557566113308
```

In [134]:
```
# d) Plot cost vs iterations

plt.figure(figsize=(10, 8))
plt.plot(range(epochs), cost_history, label='Batch Gradient Descent')
plt.xlabel('Iterations')
plt.ylabel('MSE Cost')
plt.title('Batch Gradient Descent Cost Convergence')
plt.legend()
plt.grid()
plt.show()
```



Explanation

The final slope (m) and intercept (b) values found by Batch Gradient Descent algorithm after 1000 iterations are 9504.80 and 24474.55.
This plot shows the Mean Squared Error (MSE) at each iteration. As the algorithm runs, the cost steadily decreases, which means the model's predictions are getting progressively better.
At the end the curve becomes flat which is a sign that the model has reached an optimal solution.

2. Stochastic Gradient Descent

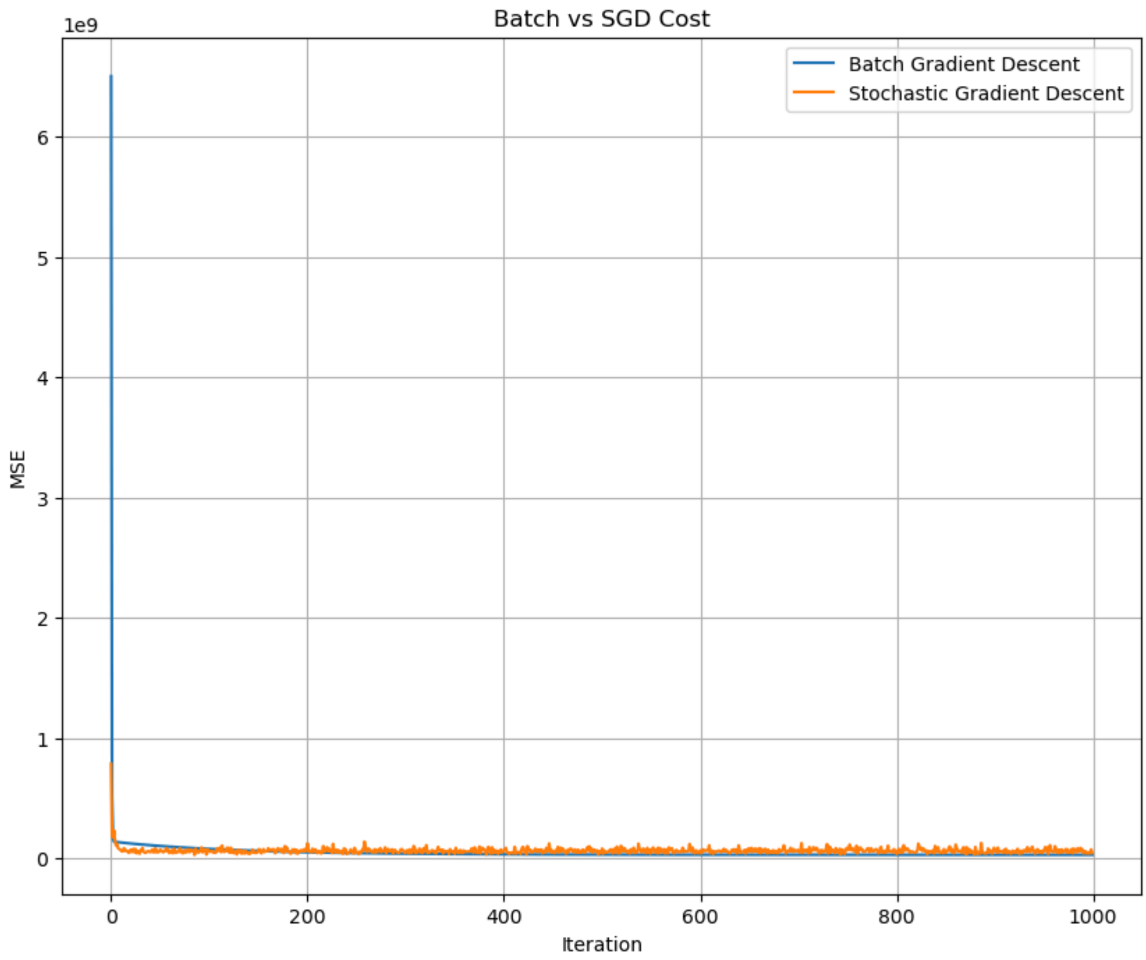
In [104]:
```
'''
a) Implement Stochastic Gradient Descent for the same problem:
Use learning rate α = 0.01
Update parameters using one sample at a time
Run for 1000 epochs
Set random_state = 42
'''

m_sgd = 0
b_sgd = 0
costs_sgd = []
np.random.seed(42)
alpha = 0.01
epochs = 1000

for _ in range(epochs):
    total_cost = 0
    for i in np.random.permutation(n):
        x_i = X[i]
        y_i = y[i]
        y_pred_i = m_sgd * x_i + b_sgd
        error_i = y_pred_i - y_i

        m_sgd -= alpha * 2 * error_i * x_i
        b_sgd -= alpha * 2 * error_i
        total_cost += error_i**2

    costs_sgd.append(total_cost / n)

print("SGD: m =", round(m_sgd, 2), "b =", round(b_sgd, 2))
```

```
SGD: m = 9108.01 b = 24789.13
```

In [105]:
```
# b) Print the final slope and intercept

print("\nFinal SGD slope (m):", m_sgd)
print("Final SGD intercept (b):", b_sgd)
```

```

Final SGD slope (m): 9108.011768134738
Final SGD intercept (b): 24789.134700500756
```

In [135]:
```
# c) Plot both cost curves (Batch GD and SGD) on the same graph.

plt.figure(figsize=(10, 8))
plt.plot(cost_history, label="Batch Gradient Descent")
plt.plot(costs_sgd, label="Stochastic Gradient Descent")
plt.title("Batch vs SGD Cost")
plt.xlabel("Iteration")
plt.ylabel("MSE")
plt.legend()
plt.grid(True)
plt.show()
```



d) Compare the convergence behavior of both methods. Which converges faster? Which is more stable?

Ans: SGD converges faster initially because it updates parameters more frequently.This is because SGD make many small updates while BGD makes only one large update per epoch.

```
BGD is more stable because its cost curve is a smooth, predic
table decline.
This is because it uses the entire dataset to compute the gra
dient,ensuring it always moves in the direction of the true m
inimum.
```

3. Matrix Operations

In [107]:
```
# a) Create a matrix A with shape (4, 3) containing random values betw

A = np.random.rand(4, 3) * 10
print("\nMatrix A:\n", A)
```

```
Matrix A:
 [[5.81038324 2.86636853 7.34115301]
 [5.89139816 0.12727282 9.01644178]
 [5.45643618 8.68627265 8.82736839]
 [4.44966657 5.07659996 4.15754388]]
```

In [108]:
```
'''
b) Perform the following matrix operations and display results:
Transpose of A (A)
Compute A * AT(matrix multiplication)
Compute AT * A (matrix multiplication)
Explain the shapes of the resulting matrices and why they differ.
'''

A_T = A.T
print("\nA Transpose:\n", A_T)
print("\nA * A_T:\n", A @ A_T)
print("\nA_T * A:\n", A_T @ A)
```

```
A Transpose:
 [[5.81038324 5.89139816 5.45643618 4.44966657]
 [2.86636853 0.12727282 8.68627265 5.07659996]
 [7.34115301 9.01644178 8.82736839 4.15754388]]

A * A_T:
 [[ 95.86914948 100.78717063 121.40510596  70.92684017]
 [100.78717063 116.02099297 112.84301761  64.3471229 ]
 [121.40510596 112.84301761 183.14646114 105.07622451]
 [ 70.92684017  64.3471229  105.07622451  62.85657085]]

A_T * A:
 [[118.04135406  87.38978405 162.44001719]
 [ 87.38978405 109.45546674 119.97311365]
 [162.44001719 119.97311365 230.39635363]]
```

A : shape (4, 3) means 4 samples, 3 features

AT : transpose ofA, shape (3, 4)

1. A.AT : Shape: (4, 3) × (3, 4) = (4, 4)
2. AT.A : Shape: (3, 4) × (4, 3) = (3, 3)

Why They Differ

The order of multiplication matters in matrix algebra. A.AT and AT.A are not the same shape and represent different relationships.
Think of it like this:
A.AT : compares rows (samples)
AT.A : compares columns (features)

In [109]:
```
'''
c) Create a square matrix B (3x3) with random values. Compute:(4 Point
Inverse of B (B-1)
Verify that B *B-1 = Identity matrix
Print both matrices and explain what the inverse represents.
'''

B = np.random.rand(3, 3)
B_inv = np.linalg.inv(B)
print("\nMatrix B:\n", B)
print("\nInverse of B:\n", B_inv)
print("\nB * B_inv:\n", B @ B_inv)
```

```
Matrix B:
 [[0.44943678 0.89514716 0.78814401]
 [0.12652568 0.61030778 0.99590664]
 [0.5955507  0.78587163 0.76906147]]

Inverse of B:
 [[-3.30067252 -0.72740432  4.32453346]
 [ 5.22357291 -1.30361222 -3.66505377]
 [-2.78175409  1.89539855  1.69659107]]

B * B_inv:
 [[ 1.00000000e+00 -5.08897375e-17  6.66253461e-17]
 [ 2.76623050e-16  1.00000000e+00  7.77862507e-17]
 [ 5.80220616e-16 -1.15440567e-17  1.00000000e+00]]
```

Q2. Singular Value Decomposition (SVD) for Movie Recommendations

In [110]:
```
'''
a) Load the movies.csv and ratings.csv datasets. Display the first 5 r
dataset to understand the structure. How many unique movies and users
ratings data?
'''

import pandas as pd
movies = pd.read_csv("movies.dat", sep="::", engine="python",
                     header=None, names=["Movie ID", "Title", "Genres"

ratings = pd.read_csv("ratings.dat", sep="::", engine="python",
                      header=None, names=["User ID", "Movie ID", "Rat:
```

In [111]:
```
movies.head()
```

Out[111]:

	Movie ID	Title	Genres
0	1	Toy Story (1995)	Animation|Children's|Comedy
1	2	Jumanji (1995)	Adventure|Children's|Fantasy
2	3	Grumpier Old Men (1995)	Comedy|Romance
3	4	Waiting to Exhale (1995)	Comedy|Drama
4	5	Father of the Bride Part II (1995)	Comedy

In [112]:
```
ratings.head()
```

Out[112]:

	User ID	Movie ID	Rating	Timestamp
0	1	1193	5	978300760
1	1	661	3	978302109
2	1	914	3	978301968
3	1	3408	4	978300275
4	1	2355	5	978824291

In [113]:
```
# Count unique movies and users

num_movies = ratings["Movie ID"].nunique()
num_users = ratings["User ID"].nunique()

print("\nUnique Movies:", num_movies)

print("Unique Users:", num_users)
```

```

Unique Movies: 3706
Unique Users: 6040
```

In [114]:
```
'''
b) Create a user-movie ratings matrix where:
Rows represent Movie IDs
Columns represent User IDs
Values are the ratings
'''

ratings_matrix = ratings.pivot_table(index="Movie ID", columns="User I
```

In [115]:
```
'''
c) Fill missing values with 0 (indicating no rating)
You can use: ratings_df.pivot_table(index='Movie ID', columns='User ID
values='Rating', fill_value=0) Apply Min-Max normalization to scale a
between 0 and 1. Print the shape of the normalized matrix. The expecte
(3706, 6040)
'''

from sklearn.preprocessing import MinMaxScaler

scaler = MinMaxScaler()
normalized = scaler.fit_transform(ratings_matrix)
print("Normalized Matrix Shape:", normalized.shape)
```

```
Normalized Matrix Shape: (3706, 6040)
```

In [116]:
```
'''
d) Perform Singular Value Decomposition (SVD) on the normalized rating
to obtain:
U matrix (movie feature vectors)
S matrix (singular values representing importance of each component)
V matrix (user feature vectors)
Print the shapes of U, S, and V. Explain what these matrices represent
of movie recommendations.
'''

import numpy as np
from numpy.linalg import inv, eig, svd

print("\nU = Movie feature vectors")
print("S = Importance of each latent feature")
print("Vt = User feature vectors\n")

U, S, Vt = np.linalg.svd(normalized, full_matrices=False)
print("U shape:", U.shape)
print("S shape:", S.shape)
print("Vt shape:", Vt.shape)
```

```

U = Movie feature vectors
S = Importance of each latent feature
Vt = User feature vectors

U shape: (3706, 3706)
S shape: (3706,)
Vt shape: (3706, 6040)
```

In [117]:
```
'''
e) The singular values in S are ordered by importance. Select the top
(largest 25 singular values) to reduce dimensionality while retaining
important patterns. This reduces computational cost and removes noise.
sum of the top 25 singular values compared to the sum of all singular
What percentage of information do these 25 components capture?
'''

top_k = 25
S_total = np.sum(S)
S_top = np.sum(S[:top_k])
info_retained = (S_top / S_total) * 100

print("\nTop 25 Singular Values Sum:", S_top)
print("Total Singular Values Sum:", S_total)
print("Information Retained (%):", round(info_retained, 2))
```

```
Top 25 Singular Values Sum: 1874.698200659423
Total Singular Values Sum: 25779.77205659257
Information Retained (%): 7.27
```

In [118]:
```
'''
f) Extract the top 25 eigenvectors (principal components) from the rec
These represent the 25 most important latent features in your movie-us
preference space. Verify the shape of your reduced movie representatio
'''

U_reduced = U[:, :top_k]
S_reduced = np.diag(S[:top_k])
movie_features = np.dot(U_reduced, S_reduced)

print("Reduced Movie Feature Matrix Shape:", movie_features.shape)
```

```
Reduced Movie Feature Matrix Shape: (3706, 25)
```

In [119]:
```
'''
g) Using the reduced 25-component representation, find the 5 most sim
to Movie ID 2025 by (hint : Computing cosine similarity between Movie
and all other movies using the reduced feature vectors)
i. Selecting the top 5 movies with highest similarity scores (excludi
movie itself)
ii. Print the Movie IDs and their similarity scores
'''

from sklearn.metrics.pairwise import cosine_similarity

target_vector = movie_features[2025].reshape(1, -1)
similarities = cosine_similarity(target_vector, movie_features)[0]

similarities[2025] = -1
top_5 = np.argsort(similarities)[-5:][::-1]

print("\nTop 5 Similar Movies to Movie ID 2025:")
for idx in top_5:
    print("Movie ID:", idx, "Similarity Score:", round(similarities[i
```

```
Top 5 Similar Movies to Movie ID 2025:
Movie ID: 2037 Similarity Score: 0.9216
Movie ID: 3289 Similarity Score: 0.9151
Movie ID: 901 Similarity Score: 0.9028
Movie ID: 3574 Similarity Score: 0.902
Movie ID: 3284 Similarity Score: 0.9003
```

h) Why Cosine Similarity?

Cosine similarity measures the angle between two vectors, not their magnitude.

It’s ideal for comparing patterns of preferences, even if users rate on different scales.

It focuses on directional similarity, which is perfect for identifying similar taste profiles.

Q3. Life Expectancy Prediction

In [120]:
```python
# a. Load the dataset and present the statistics of data.

import pandas as pd

df = pd.read_csv("LifeExpectancy.csv")

df.head()
```

Out[120]:

	Country	Year	Status	Life expectancy	Adult Mortality	infant deaths	Alcohol	percentage expenditure	Hepatitis B
0	Afghanistan	2015	Developing	65.0	263.0	62	0.01	71.279624	65.(
1	Afghanistan	2014	Developing	59.9	271.0	64	0.01	73.523582	62.(
2	Afghanistan	2013	Developing	59.9	268.0	66	0.01	73.219243	64.(
3	Afghanistan	2012	Developing	59.5	272.0	69	0.01	78.184215	67.(
4	Afghanistan	2011	Developing	59.2	275.0	71	0.01	7.097109	68.(

5 rows × 22 columns

In [121]:
```python
df.describe()
```

Out[121]:

	Year	Life expectancy	Adult Mortality	infant deaths	Alcohol	percentage expenditure	Hepa
count	2938.000000	2938.000000	2938.000000	2938.000000	2938.000000	2938.000000	2938.0
mean	2007.518720	69.234717	164.725664	30.303948	4.546875	738.251295	83.0
std	4.613841	9.509115	124.086215	117.926501	3.921946	1987.914858	22.9
min	2000.000000	36.300000	1.000000	0.000000	0.010000	0.000000	1.0
25%	2004.000000	63.200000	74.000000	0.000000	1.092500	4.685343	82.0
50%	2008.000000	72.100000	144.000000	3.000000	3.755000	64.912906	92.0
75%	2012.000000	75.600000	227.000000	22.000000	7.390000	441.534144	96.0
max	2015.000000	89.000000	723.000000	1800.000000	17.870000	19479.911610	99.0

In [122]:
```
# b. Categorize the columns into categorical and continuous.

categorical = df.select_dtypes(include='object').columns.tolist()
continuous = df.select_dtypes(include=['int64', 'float64']).columns.to

print("\nCategorical Columns:", categorical)
print("\nContinuous Columns:", continuous)
```

```
Categorical Columns: ['Country', 'Status']

Continuous Columns: ['Year', 'Life expectancy', 'Adult Mortality',
'infant deaths', 'Alcohol', 'percentage expenditure', 'Hepatitis B',
'Measles', 'BMI', 'under-five deaths ', 'Polio', 'Total expenditur
e', 'Diphtheria', ' HIV/AIDS', 'GDP', 'Population', 'thinness  1-19
years', 'thinness 5-9 years', 'Income composition of resources', 'Sc
hooling']
```

In [123]:
```
# c. Are there any missing values in the dataset? Mention the approach

df.isnull().sum()
```

Out[123]:
```
Country                            0
Year                               0
Status                             0
Life expectancy                    0
Adult Mortality                    0
infant deaths                      0
Alcohol                            0
percentage expenditure             0
Hepatitis B                        0
Measles                            0
BMI                                0
under-five deaths                  0
Polio                              0
Total expenditure                  0
Diphtheria                         0
 HIV/AIDS                          0
GDP                                0
Population                         0
thinness  1-19 years               0
thinness 5-9 years                 0
Income composition of resources    0
Schooling                          0
dtype: int64
```

There are no missing values in the dataset.

Approaches to Deal With Missing Data:

1. Deletion Methods:

- Remove rows with missing values
- Remove entire columns

2. Filling Missing Data

- Missing values can be filled using central tendencies such as mean, median, mode and standard deviation.

Role of EDA:

- EDA helps by visualizing distributions, correlations, and spotting patterns to guide imputation.
- Identifies the patterns of missing values.
- Reveals data distribution

In [124]:
```
# d. Explain what is label encoding and how it changes the dataset. Pe

from sklearn.preprocessing import LabelEncoder

le = LabelEncoder()
for col in categorical:
    if col != "Year":
        df[col] = le.fit_transform(df[col])
```

Label Encoding is a technique used to convert categorical (text) data into numerical values.

How Does Label Encoding Change the Dataset?

When you apply label encoding:

```
Text columns become numeric
- All string categories are replaced by integers.

The dataset becomes ready for machine learning algorithms
- Algorithms such as Linear Regression, SVM, KNN, etc., requi
re numeric inputs.
```

Year is already numeric and represents a real measurable quantity, so it should be left as-is.

In [125]:
```
# e. Perform data normalization on 'Population', 'Total expenditure',

from sklearn.preprocessing import StandardScaler

scaler = StandardScaler()
cols_to_scale = ['Population', 'Total expenditure', 'Income compositic
df[cols_to_scale] = scaler.fit_transform(df[cols_to_scale])
print("Standard Scaler applied to:", cols_to_scale)
```

```
Standard Scaler applied to: ['Population', 'Total expenditure', 'Inc
ome composition of resources']
```

f. Explain the difference between Min-Max Scaling, Z-Score Normalization, and Robust Scaling.

1. **Min-Max Scaling:** Min–Max Scaling is a normalization technique that transforms all feature values into a fixed range, usually 0 to 1. It does this by subtracting the minimum value of the feature and dividing by the range (max – min). It is very sensitive to outliers.
2. **Z-Score Normalization:** Z-Score Normalization transforms data so that it has a mean of 0 and a standard deviation of 1. It subtracts the mean of the feature and divides by its standard deviation. Since mean and standard deviation are affected by outliers, Z-score is still influenced by extreme values.

3. **Robust Scaling:** Robust Scaling uses the median and interquartile range (IQR) instead of mean and standard deviation. Because medians and IQR are resistant to the effects of outliers, this scaling method minimizes their influence.

In [126]:
```
# g. Drop the column 'country' and 'status' from the dataset and split

from sklearn.model_selection import train_test_split

df.drop(['Country', 'Status'], axis=1, inplace=True)
X = df.drop('Life expectancy', axis=1)
y = df['Life expectancy']

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.
```

In [127]:
```
X_train.head()
```

Out[127]:

	Year	Adult Mortality	infant deaths	Alcohol	percentage expenditure	Hepatitis B	Measles	BMI	under-five deaths	Polio	e
456	2007	126.0	0	5.28	345.463714	96.0	0	25.5	0	98.0	
462	2001	152.0	0	3.81	150.743486	92.0	0	22.1	0	91.0	
2172	2011	143.0	0	10.43	0.000000	99.0	0	44.5	0	99.0	
2667	2013	13.0	3	1.29	594.645310	98.0	16	59.3	3	98.0	
381	2002	95.0	0	0.13	941.703687	99.0	0	28.0	0	99.0	

In [128]:
```
# h. Build a linear regression model using the training and testing da

from sklearn.linear_model import LinearRegression
from sklearn.metrics import mean_absolute_error

lr_model = LinearRegression()
lr_model.fit(X_train, y_train)
y_pred_lr = lr_model.predict(X_test)

mae_lr = mean_absolute_error(y_test, y_pred_lr)
print("Linear Regression MAE:", round(mae_lr, 2))
```

```
Linear Regression MAE: 2.86
```

In [129]:
```
'''
i. Build a linear regression model using stochastic gradient descent v
alpha = 0.001
learning rate = 'invscaling'
maximum iterations = 500
batch-size = 32
Compute mean absolute error. (Use sklearn)
'''

from sklearn.linear_model import SGDRegressor

sgd_model = SGDRegressor(alpha=0.001, learning_rate='invscaling', max_
sgd_model.fit(X_train, y_train)
y_pred_sgd = sgd_model.predict(X_test)

mae_sgd = mean_absolute_error(y_test, y_pred_sgd)
print("\nSGD Regression MAE:", round(mae_sgd, 2))
```

```
SGD Regression MAE: 3.337724810096441e+16
```

In [130]:
```
'''
j. Discuss the above performed methods by applying different learning
(constant, invscaling, adaptive). Which is the best learning rate for
why?
'''

rates = ['constant', 'invscaling', 'adaptive']
for rate in rates:
    model = SGDRegressor(alpha=0.001, learning_rate=rate, max_iter=50(
    model.fit(X_train, y_train)
    y_pred = model.predict(X_test)
    mae = mean_absolute_error(y_test, y_pred)
    print(f"Learning Rate: {rate} -> MAE: {round(mae, 2)}")
```

```
Learning Rate: constant -> MAE: 4.717323434682044e+17
Learning Rate: invscaling -> MAE: 1.5184851647330342e+17
Learning Rate: adaptive -> MAE: 262426249415502.53
```

Q4. Low-Rank Adaptation (LoRA) Concepts

a. Research and explain the concept of Low-Rank Adaptation (LoRA) in machine learning model fine-tuning. How does it relate to SVD?

Low-Rank Adaptation (LoRA) is a modern technique to efficiently fine-tune massive models (like ChatGPT).

- **The Idea:** Instead of re-training all 175 billion weights of a model (which is slow and expensive), LoRA freezes the original model. It then trains two very small "adapter" matrices (A and B) that represent the change to the weights.
- **The Relation to SVD:** SVD is the mathematical theory that proves any large matrix can be approximated by multiplying two smaller, "low-rank" matrices. LoRA uses this exact principle, assuming the "change" needed to fine-tune a model is "low-rank" and can be captured by the small A and B matrices.

b. Explain one advantage of using low-rank decomposition for model adaptation.

One primary advantage of LoRA is that it significantly reduces computational cost.

- **How it works:** Instead of updating all the massive weight matrices in a large model (which requires huge amounts of memory), low-rank decomposition approximates these changes using two much smaller matrices.
- **Why it matters:** This compression allows you to fine-tune very large models on smaller hardware (like a single GPU) because you are training far fewer parameters, effectively preserving the most important patterns while discarding noise

In [ ]: