# lgdwtqjkx

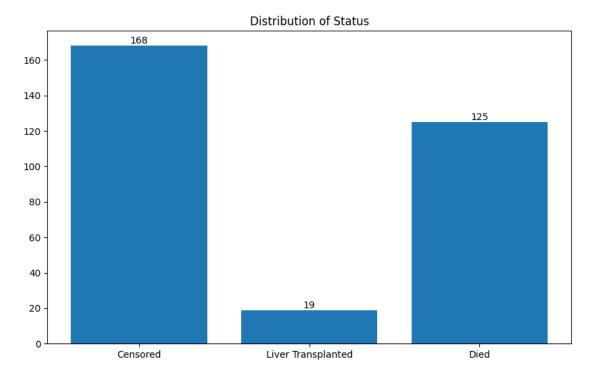
## September 16, 2024

```
[103]: import pandas as pd
       import numpy as np
       import matplotlib.pyplot as plt
       import seaborn as sns
       np.random.seed(42)
[104]: #Load the data
       data=pd.read_csv('Cirrhosis.csv')
[105]: #check column names
       data.shape
[105]: (312, 20)
[106]: #First rows of dataset
       data.head()
[106]:
          index duration status
                                                                                spiders \
                                     drug
                                                       ascites
                                                                 hepatomology
                                             age
                                                  sex
              1
                       400
                                 2
                                        1
                                           21464
                                                     1
              2
                                           20617
       1
                      4500
                                 0
                                        1
                                                     1
                                                              0
                                                                             1
                                                                                       1
       2
              3
                      1012
                                 2
                                           25594
                                                              0
                                                                             0
                                                                                       0
       3
              4
                      1925
                                 2
                                           19994
                                                              0
                                                                             1
                                                                                       1
                      1504
                                          13918
              5
                                 1
                                                              0
                 bilirubin
                             cholesterol
                                           albumin
                                                     copper
                                                             phosphatase
                                                                             SGOT \
          edema
       0
            1.0
                       14.5
                                    261.0
                                              2.60
                                                      156.0
                                                                          137.95
                                                                  1718.0
            0.0
                                    302.0
                                              4.14
                                                       54.0
       1
                        1.1
                                                                  7394.8
                                                                           113.52
       2
            0.5
                        1.4
                                    176.0
                                              3.48
                                                      210.0
                                                                   516.0
                                                                            96.10
       3
            0.5
                        1.8
                                    244.0
                                              2.54
                                                       64.0
                                                                  6121.8
                                                                            60.63
            0.0
                        3.4
                                    279.0
                                              3.53
                                                      143.0
                                                                   671.0 113.15
          triglicerides platelets prothrombin stage
       0
                   172.0
                              190.0
                                             12.2
                                                        4
       1
                    88.0
                              221.0
                                             10.6
                                                        3
       2
                    55.0
                              151.0
                                             12.0
                                                        4
                    92.0
       3
                              183.0
                                             10.3
                                                        4
       4
                    72.0
                              136.0
                                             10.9
```

```
[148]: #Status distribution
status_counts = data['status'].value_counts().sort_index()

plt.figure(figsize=(10, 6))
plt.bar(status_counts.index, status_counts.values)
map = {0: 'Censored', 1: 'Liver Transplanted', 2: 'Died'}
plt.xticks(status_counts.index, [map[i] for i in status_counts.index])
plt.title('Distribution of Status')
for i, v in enumerate(status_counts.values):
    plt.text(i, v, str(v), ha='center', va='bottom')

plt.show()
```



```
status count
0 0 83
1 1 1
2 2 65
```

```
status count
0 0 85
1 1 9
2 2 60
```

```
[110]: #checking duplicates in dataset data.duplicated ().sum()
```

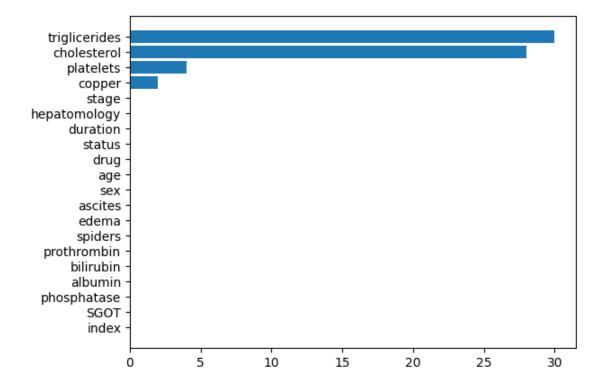
### [110]: 0

```
[111]: #hecking missing values

plt.barh(data.isnull().sum().sort_values(ascending=True).index, data.isnull().

sum().sort_values(ascending=True).values)
```

### [111]: <BarContainer object of 20 artists>



```
[]: data.isnull().sum().sort_values (ascending=False)
```

```
[]: #checking data distribution of variables with missing values to determine which
        \hookrightarrow imputaion method (mean and median) to be used
       plt.figure(figsize=(12, 8))
       plt.subplot(2, 2, 1)
       sns.histplot(data['triglicerides'], kde=True, bins=30, color='blue')
       plt.title('Triglycerides')
       plt.subplot(2, 2, 2)
       sns.histplot(data['cholesterol'], kde=True, bins=30, color='green')
       plt.title('Cholesterol')
       plt.subplot(2, 2, 3)
       sns.histplot(data['platelets'], kde=True, bins=30, color='red')
       plt.title('Platelets')
       plt.subplot(2, 2, 4)
       sns.histplot(data['copper'], kde=True, bins=30, color='purple')
       plt.title('Copper')
       plt.tight_layout()
       plt.show()
[114]: # Missing values imputation
       data['triglicerides'].fillna(data['triglicerides'].median(), inplace=True)
       data['cholesterol'].fillna(data['cholesterol'].median(), inplace=True)
       data['platelets'].fillna(data['platelets'].mean(), inplace=True)
       data['copper'].fillna(data['copper'].median(), inplace=True)
[115]: #recheck missing values after imputation
       data.isnull().sum().sort_values (ascending=False)
[115]: index
                        0
                        0
       duration
       prothrombin
                        0
      platelets
                        0
       triglicerides
       SGOT
      phosphatase
                        0
                        0
       copper
                        0
       albumin
       cholesterol
                        0
       bilirubin
                        0
       edema
                        0
```

spiders 0 hepatomology 0 ascites 0 0 sex age 0 drug 0 status 0 stage 0 dtype: int64

## [116]: #checking data type

data.dtypes

[116]: index int64 int64 duration status int64 drug int64 int64 age sex int64 ascites int64 int64 hepatomology spiders int64 edema float64 bilirubin float64 cholesterol float64 albumin float64 float64 copper float64 phosphatase SGOT float64 triglicerides float64 platelets float64 prothrombin float64 stage int64

dtype: object

# [117]: #Summary Statistics

data.describe ()

[117]:		index	duration	status	drug	age	\
	count	312.000000	312.000000	312.000000	312.000000	312.000000	
	mean	156.500000	2006.362179	0.862179	1.493590	18269.442308	
	std	90.210864	1123.280843	0.960764	0.500762	3864.805407	
	min	1.000000	41.000000	0.000000	1.000000	9598.000000	
	25%	78.750000	1191.000000	0.000000	1.000000	15427.750000	
	50%	156.500000	1839.500000	0.000000	1.000000	18187.500000	
	75%	234.250000	2697.250000	2.000000	2.000000	20715.000000	
	max	312.000000	4556.000000	2.000000	2.000000	28650.000000	

```
count
              312.000000
                           312.000000
                                          312.000000
                                                       312.000000
                                                                   312.000000
                                                         0.288462
                                                                      0.110577
       mean
                0.884615
                             0.076923
                                            0.512821
       std
                0.319999
                             0.266897
                                            0.500639
                                                         0.453775
                                                                      0.274507
       min
                                                                      0.00000
                0.000000
                             0.000000
                                            0.000000
                                                         0.000000
       25%
                1.000000
                             0.00000
                                                         0.000000
                                                                      0.000000
                                            0.000000
       50%
                1.000000
                             0.000000
                                            1.000000
                                                         0.000000
                                                                      0.000000
       75%
                1.000000
                             0.000000
                                            1.000000
                                                         1.000000
                                                                      0.000000
       max
                1.000000
                             1.000000
                                            1.000000
                                                         1.000000
                                                                      1.000000
                           cholesterol
                                                                   phosphatase
               bilirubin
                                            albumin
                                                          copper
              312.000000
                            312.000000
                                         312.000000
                                                     312.000000
                                                                    312.000000
       count
                            364.125000
                3.256090
                                           3.520000
                                                       97.490385
                                                                   1982.655769
       mean
                            221.923027
                                                       85.360932
                                                                   2140.388824
       std
                4.530315
                                           0.419892
       min
                0.300000
                            120.000000
                                           1.960000
                                                       4.000000
                                                                    289.000000
       25%
                            255.750000
                0.800000
                                           3.310000
                                                       41.750000
                                                                    871.500000
       50%
                1.350000
                            309.500000
                                           3.550000
                                                       73.000000
                                                                   1259.000000
       75%
                3.425000
                            392.250000
                                           3.800000
                                                      123.000000
                                                                   1980.000000
                                                                  13862.400000
                           1775.000000
       max
               28.000000
                                           4.640000
                                                      588.000000
                           triglicerides
                                            platelets
                                                       prothrombin
                    SGOT
                                                                           stage
                              312.000000
                                           312.000000
                                                         312.000000
              312.000000
                                                                     312.000000
       count
                              123.096154
       mean
              122.556346
                                           261.935065
                                                          10.725641
                                                                        3.032051
       std
               56.699525
                               62.122820
                                            94.991905
                                                           1.004323
                                                                        0.877880
       min
               26.350000
                               33.000000
                                            62.000000
                                                           9.000000
                                                                        1.000000
       25%
               80.600000
                               87.000000
                                           200.000000
                                                          10.000000
                                                                        2.000000
       50%
              114.700000
                              108.000000
                                           258.500000
                                                          10.600000
                                                                        3.000000
       75%
              151.900000
                              145.250000
                                           322.000000
                                                          11.100000
                                                                        4.000000
              457.250000
                              598.000000
                                           563.000000
                                                          17.100000
                                                                        4.000000
       max
[118]: # #droping the 'index' (identifier)
       data = data.drop(columns='index', axis=1)
[119]: #Class balance
       # Status counts
       status_counts = data['status'].value_counts()
       print(f"Class distribution before handling imbalance:\n{status_counts}\n")
       # Separate the classes
       status_0 = data[data['status'] == 0]
                                               # Majority class
       status_2 = data[data['status'] == 2]
                                               # Second largest class
       status_1 = data[data['status'] == 1]
                                               # Minority class
       # Determine the target size for oversampling (match the size of status_0)
       target_size = len(status_0)
```

hepatomology

spiders

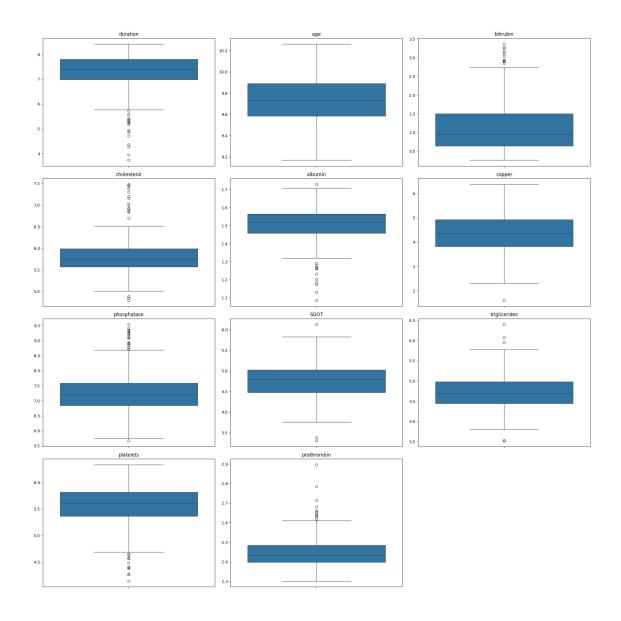
edema

ascites

sex

```
# Perform oversampling of the minority class (status_1)
     status_1_oversampled = status_1.sample(n=target_size, replace=True,_
      →random_state=42)
     # Combine the original majority class and the oversampled minority class
     balanced_data = pd.concat([status_0, status_2, status_1_oversampled])
     # Shuffle the dataset to mix the samples
     balanced_data = balanced_data.sample(frac=1, random_state=42).
     →reset_index(drop=True)
     # Verify the new class distribution
     new_status_counts = balanced_data['status'].value_counts()
     print(f"Class distribution after handling imbalance:\n{new_status_counts}\n")
    Class distribution before handling imbalance:
    status
         168
    2
         125
          19
    1
    Name: count, dtype: int64
    Class distribution after handling imbalance:
    status
         168
    1
         168
         125
    Name: count, dtype: int64
[]: #Data transformation by log
     selected_features = ['duration', 'age', 'bilirubin', 'cholesterol', 'albumin', |
     'phosphatase', 'SGOT', 'triglicerides', 'platelets', 'prothrombin']
     # Check for the presence of negative values
     for feature in selected_features:
         if balanced_data[feature].min() < 0:</pre>
            print(f"Feature {feature} contains negative values; log1pu
     ⇔transformation may not be appropriate.")
     # Apply log1p transformation to the DataFrame
     data_transformed = balanced_data.copy()
     for feature in selected_features:
        if balanced_data[feature].min() >= 0: # Only to non-negative values
```

```
data_transformed[feature] = np.log1p(balanced_data[feature])
          else:
              print(f"Skipping log1p transformation for feature {feature} due to⊔
        ⇔negative values.")
       # Check the result
       data transformed.head()
[121]: print(data_transformed['status'].value_counts())
      status
           168
      1
           168
      2
           125
      Name: count, dtype: int64
[122]: import matplotlib.pyplot as plt
       import seaborn as sns
       def plot_boxplots(data_transformed, figsize=(20, 20)):
           # List of continuous columns
          numeric_columns = ['duration', 'age', 'bilirubin', 'cholesterol', 'albumin',
                              'copper', 'phosphatase', 'SGOT', 'triglicerides', u
        'prothrombin']
          n = len(numeric_columns)
          ncols = 3
          nrows = (n // ncols) + (n % ncols > 0)
          fig, axes = plt.subplots(nrows=nrows, ncols=ncols, figsize=figsize)
          axes = axes.flatten()
          for i, column in enumerate(numeric_columns):
               sns.boxplot(y=data_transformed[column], ax=axes[i])
               axes[i].set_title(column)
               axes[i].set_xlabel('')
               axes[i].set_ylabel('')
          for i in range(n, len(axes)):
               fig.delaxes(axes[i])
          plt.tight_layout()
          plt.show()
       plot_boxplots(data_transformed)
```



```
[]: # Function to detect outliers using IQR method
def detect_outliers_iqr(df, features):
    outliers = {}
    for feature in features:
        Q1 = df[feature].quantile(0.25)
        Q3 = df[feature].quantile(0.75)
        IQR = Q3 - Q1

# Define outlier bounds
    lower_bound = Q1 - 1.5 * IQR
        upper_bound = Q3 + 1.5 * IQR

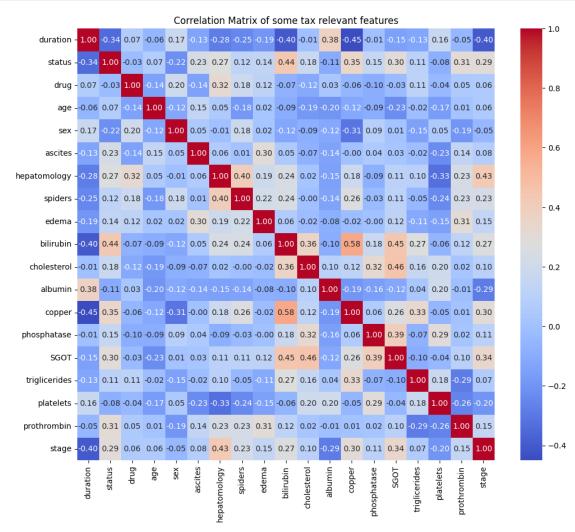
# Identify outliers
```

```
→upper_bound)].index
               outliers[feature] = outlier_indices
          return outliers
       # Function to display outliers
      def display_outliers(df, outliers):
           # Combine all outlier indices into a single set to avoid duplicates
          all_outlier_indices = set()
          for indices in outliers.values():
               all_outlier_indices.update(indices)
          # Display rows corresponding to the outliers
          outlier_rows = df.loc[list(all_outlier_indices)]
          return outlier_rows
      # Define numeric columns to check for outliers
      numeric_columns = ['duration', 'age', 'bilirubin', 'cholesterol', 'albumin',
                         'copper', 'phosphatase', 'SGOT', 'triglicerides',
       'prothrombin']
       # Detect outliers
      outliers = detect_outliers_iqr(data_transformed, numeric_columns)
       # Display outliers
      outlier_rows = display_outliers(data_transformed, outliers)
      print(f"Rows corresponding to outliers:{outlier_rows}")
      print(outlier rows)
      print(f"Number of outlier rows: {outlier_rows.shape}")
[124]: def remove_outliers(df, outliers):
           # Combine all outlier indices into a single set to avoid duplicates
          all_outlier_indices = set()
          for indices in outliers.values():
              all_outlier_indices.update(indices)
          # Remove outliers from the DataFrame
          df cleaned = data transformed.drop(index=all outlier indices,
        ⇔errors='ignore')
          return df_cleaned
       # Handle outliers by removing them
      data_cleaned = remove_outliers(data_transformed, outliers)
       # Verify the result
```

outlier\_indices = df[(df[feature] < lower\_bound) | (df[feature] > \_\_

```
print("Data before removing outliers:")
      print(data_transformed.shape)
      print("Data after removing outliers:")
      print(data_cleaned.shape)
      Data before removing outliers:
      (461, 19)
      Data after removing outliers:
      (365, 19)
 []: data_cleaned.head()
 []: def normalization(df, features):
          df_normalized = df.copy() # Use the provided DataFrame, not `data_cleaned`
          for feature in features:
              min value = df[feature].min()
              max_value = df[feature].max()
               # Check if min and max are the same (to avoid division by zero)
              if min value == max value:
                   df_normalized[feature] = 0 # or 1, or any other value that makes_
        ⇔sense for your data
              else:
                   # Normalization formula
                   df_normalized[feature] = (df[feature] - min_value) / (max_value -__
        →min_value)
          return df_normalized
       # Define numeric columns to normalize
      numeric_columns = ['duration', 'age', 'bilirubin', 'cholesterol', 'albumin',
                          'copper', 'phosphatase', 'SGOT', 'triglicerides',
        'prothrombin']
       # Apply normalization
      df_cleaned = normalization(data_cleaned, numeric_columns)
      # Display the first few rows of the normalized dataset
      print("Normalized dataset:")
      df_cleaned.head()
[127]: # Compute correlation matrix
      correlation_matrix = df_cleaned.corr()
       # Plot heatmap of correlation matrix
      plt.figure(figsize=(12, 10))
```

```
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', fmt='.2f')
plt.title('Correlation Matrix of some tax relevant features')
plt.show()
```



#### #Survival Prediction

##Multi-Class Logistic Regression

```
[128]: #Data Spliting
    #Split predictors and response
X = df_cleaned.drop('status', axis=1).values
y = df_cleaned['status'].values

# Ensure y is numeric and integer type
y = y.astype(int)
```

```
#Split train and test
      limit = int(len(df_cleaned) * 0.8)
      X_train, X_test = X[:limit], X[limit:]
      y_train, y_test = y[:limit], y[limit:]
[129]: #Important function
      # Softmax function to normalize output
      def softmax(H):
          return (np.exp(H.T) / np.sum(np.exp(H), axis=1)).T
      # Categorical cross-entropy loss function
      def cat_cross_entropy(Y, P_hat):
          return -(1/len(Y)) * np.sum(np.sum(Y * np.log(P_hat), axis=1), axis=0)
      # Convert indices to one-hot encoding
      def indices_to_one_hot(data, nb_classes):
          targets = np.array(data).reshape(-1)
          return np.eye(nb_classes)[targets]
       # Accuracy function to calculate prediction accuracy
      def accuracy(y, y_hat):
          return np.mean(y == y_hat)
[130]: # Multi-Class Logistic Regression class
      class MVLLogisticRegression():
          def fit(self, X, y, eta=1e-3, epochs=1e3, show_curve=False):
               epochs = int(epochs)
              N, D = X.shape
              K = len(np.unique(y)) # Number of classes
              Y = indices_to_one_hot(y, K) # One-hot encode labels
               # Initialize weights and biases
              self.W = np.random.randn(D, K) # Weights
              self.b = np.random.randn(K) # Biases
              J = np.zeros(epochs)
               # SGD Training
               for epoch in range(epochs):
                   P_hat = self.__forward__(X) # Compute predicted probabilities
                   J[epoch] = cat_cross_entropy(Y, P_hat) # Compute loss
                   # Weight updates using gradient descent
                   self.W = eta * (1/N) * X.T @ (P_hat - Y)
                   self.b -= eta * (1/N) * np.sum(P_hat - Y, axis=0)
               if show_curve:
                   plt.figure()
```

```
plt.plot(J)
    plt.xlabel('Epochs')
    plt.ylabel('Loss')
    plt.title('Training Curve')
    plt.show()

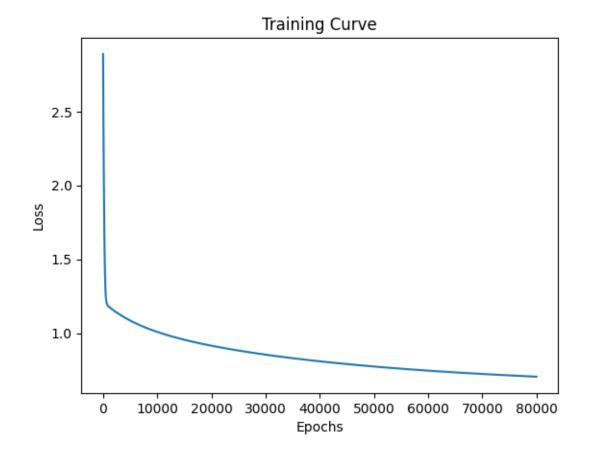
# Define the forward method (linear transformation + softmax)

def __forward__(self, X):
    return softmax(X @ self.W + self.b)

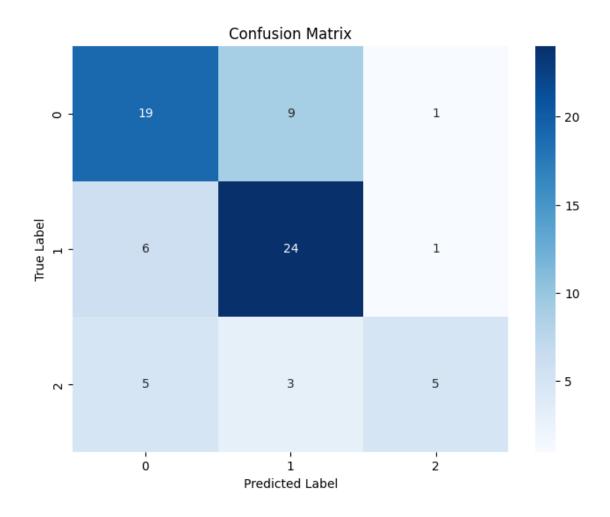
# Predict classes

def predict(self, X):
    P_hat = self.__forward__(X)
    return np.argmax(P_hat, axis=1) # Return class with max probability
```

```
[131]: # Train the model
mv_logreg = MVLLogisticRegression()
mv_logreg.fit(X_train, y_train, epochs=8e4, show_curve=True)
```



```
[132]: # Predict on the test set
       y_hat = mv_logreg.predict(X_test)
 []: # Evaluate accuracy on the test set
       # np.random.seed(42)
       test_accuracy = accuracy(y_test, y_hat)
       print(f"Test Accuracy: {test_accuracy * 100:.2f}%")
       #mv_logreg.W
       #mv_logreg.b
[134]: # Compute confusion matrix
       def confusion_matrix(y_true, y_pred, num_classes):
           matrix = np.zeros((num_classes, num_classes), dtype=int)
           for true, pred in zip(y_true, y_pred):
               matrix[true, pred] += 1
           return matrix
       # Define the function to plot the confusion matrix
       def plot_confusion_matrix(conf_matrix, class_names):
           plt.figure(figsize=(8, 6))
           sns.heatmap(conf_matrix, annot=True, fmt='d', cmap='Blues',
                       xticklabels=class_names, yticklabels=class_names)
           plt.xlabel('Predicted Label')
           plt.ylabel('True Label')
           plt.title('Confusion Matrix')
           plt.show()
       num_classes = len(np.unique(y))
       conf_matrix = confusion_matrix(y_test, y_hat, num_classes)
       # Class names
       class_names = [str(i) for i in range(num_classes)]
       # Plot confusion matrix
       plot_confusion_matrix(conf_matrix, class_names)
```



## 0.1 Optimized MV Logistic regression

```
[]: # Set random seed for reproducibility
np.random.seed(42)

# Softmax function to normalize output
def softmax(H):
    H_exp = np.exp(H - np.max(H, axis=1, keepdims=True))
    return H_exp / np.sum(H_exp, axis=1, keepdims=True)

# Categorical cross-entropy loss function
def cat_cross_entropy(Y, P_hat):
    return -np.mean(np.sum(Y * np.log(np.clip(P_hat, 1e-10, 1-1e-10)), axis=1))

# Convert indices to one-hot encoding
def indices_to_one_hot(data, nb_classes):
    return np.eye(nb_classes)[data]
```

```
# Accuracy function to calculate prediction accuracy
def accuracy(y, y_hat):
    return np.mean(y == y_hat)
# Multi-Class Logistic Regression class with Early Stopping
class MVLLogisticRegression:
    def __init__(self, learning_rate=0.01, 12_lambda=0.01):
        self.learning_rate = learning_rate
        self.12 lambda = 12 lambda
        self.best W = None
        self.best_b = None
        self.best val loss = float('inf')
        self.patience_counter = 0
    def fit(self, X, y, epochs=1000, batch_size=32, validation_split=0.2,_
 →patience=20, show_curve=False):
        # Store parameters for printing
        self.epochs = epochs
        self.batch_size = batch_size
        self.validation split = validation split
        self.patience = patience
        # Split the data into training and validation sets
        split_index = int(len(X) * (1 - validation_split))
        X_train, X_val = X[:split_index], X[split_index:]
        y_train, y_val = y[:split_index], y[split_index:]
        N, D = X_train.shape
        K = len(np.unique(y))
        Y_train = indices_to_one_hot(y_train, K)
        Y_val = indices_to_one_hot(y_val, K)
        # Initialize weights and biases
        self.W = np.random.randn(D, K) / np.sqrt(D)
        self.b = np.zeros(K)
        train_losses = []
        val losses = []
        for epoch in range(epochs):
            # Mini-batch gradient descent
            for i in range(0, N, batch_size):
                X_batch = X_train[i:i+batch_size]
                Y_batch = Y_train[i:i+batch_size] # Ensure Y_batch is one-hot_
 \rightarrow encoded
```

```
P_hat = self.forward(X_batch)
               grad_W = (1/batch_size) * X_batch.T @ (P_hat - Y_batch) + self.
→12_lambda * self.W
               grad_b = (1/batch_size) * np.sum(P_hat - Y_batch, axis=0)
               self.W -= self.learning rate * grad W
               self.b -= self.learning_rate * grad_b
           # Compute training and validation loss
           train_loss = cat_cross_entropy(Y_train, self.forward(X_train))
           val_loss = cat_cross_entropy(Y_val, self.forward(X_val)) #__
\hookrightarrow Corrected variable name
           train_losses.append(train_loss)
           val_losses.append(val_loss)
           # Early stopping
           if val_loss < self.best_val_loss:</pre>
               self.best_val_loss = val_loss
               self.patience_counter = 0
               self.best_W = self.W.copy()
               self.best_b = self.b.copy()
           else:
               self.patience_counter += 1
           if self.patience_counter >= patience:
               print(f"Early stopping at epoch {epoch}")
               self.W = self.best W
               self.b = self.best_b
               break
       if show_curve:
           plt.figure(figsize=(10, 5))
           plt.plot(train_losses, label='Training Loss')
           plt.plot(val_losses, label='Validation Loss')
           plt.xlabel('Epochs')
           plt.ylabel('Loss')
           plt.title('Training and Validation Loss Curves')
          plt.legend()
           plt.show()
  def forward(self, X):
      return softmax(X @ self.W + self.b)
  def predict(self, X):
      P_hat = self.forward(X)
      return np.argmax(P_hat, axis=1)
```

```
std = np.std(X_train, axis=0)
           std[std == 0] = 1  # Avoid division by zero
           X_train_scaled = (X_train - mean) / std
           X_test_scaled = (X_test - mean) / std
           return X_train_scaled, X_test_scaled, mean, std
       # Apply scaling
       X train scaled, X test scaled, mean, std = manual scaling(X train, X test)
       # Train the model
       mv_logreg1 = MVLLogisticRegression(learning_rate=0.01, 12 lambda=0.01)
       mv_logreg1.fit(X_train_scaled, y_train, epochs=1000, batch_size=32,_
        →validation_split=0.2, patience=20, show_curve=True)
       # Predict on the test set
       y hat1 = mv logreg1.predict(X test scaled)
       # Evaluate accuracy on the entire dataset
       overall_accuracy = accuracy(y_test, y_hat1)
       print(f"Overall Accuracy: {overall_accuracy * 100:.2f}%")
       # Print optimized parameters and training details
       print("Optimized Parameters:")
       print("Weights (W):")
       print(mv_logreg1.W)
       print("Biases (b):")
       print(mv_logreg1.b)
       print("Learning Rate:", mv_logreg1.learning_rate)
       print("Epochs:", mv_logreg1.epochs)
       print("Batch Size:", mv_logreg1.batch_size)
       print("Validation Split:", mv_logreg1.validation_split)
       print("Patience:", mv_logreg1.patience)
[154]: # Compute confusion matrix
       def confusion_matrix(y_true, y_pred, num_classes):
           matrix = np.zeros((num_classes, num_classes), dtype=int)
           for true, pred in zip(y_true, y_pred):
              matrix[true, pred] += 1
           return matrix
       # Function to plot the confusion matrix
       def plot confusion matrix(conf matrix, class names):
           plt.figure(figsize=(8, 6))
           sns.heatmap(conf_matrix, annot=True, fmt='d', cmap='Blues',
```

# Scaling

def manual\_scaling(X\_train, X\_test):
 mean = np.mean(X\_train, axis=0)

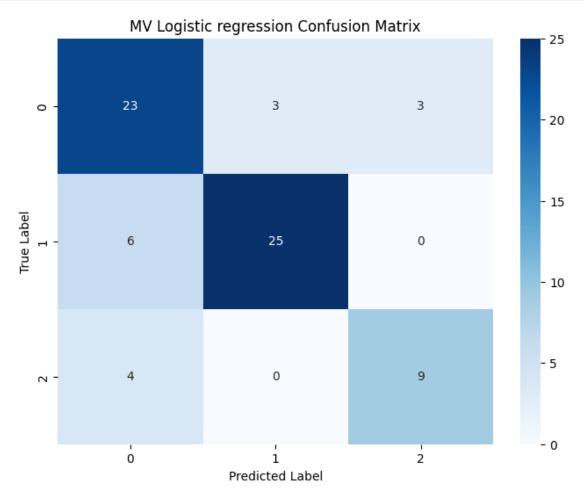
```
xticklabels=class_names, yticklabels=class_names)
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('MV Logistic regression Confusion Matrix')
plt.show()

# Number of classes from the true labels
num_classes = len(np.unique(y_test))

# Predict on the test set
y_hat = mv_logreg1.predict(X_test_scaled)

# Compute confusion matrix
conf_matrix = confusion_matrix(y_test, y_hat1, num_classes)
class_names = [str(i) for i in range(num_classes)]

# Plot confusion matrix
plot_confusion_matrix(conf_matrix, class_names)
```



```
[]: # Softmax function to normalize output
     def softmax(H):
         H_exp = np.exp(H - np.max(H, axis=1, keepdims=True))
         return H_exp / np.sum(H_exp, axis=1, keepdims=True)
     # Categorical cross-entropy loss function
     def cat_cross_entropy(Y, P_hat):
         return -np.mean(np.sum(Y * np.log(np.clip(P_hat, 1e-10, 1-1e-10)), axis=1))
     # Convert indices to one-hot encoding
     def indices to one hot(data, nb classes):
         return np.eye(nb_classes)[data]
     # Accuracy function to calculate prediction accuracy
     def accuracy(y, y_hat):
         return np.mean(y == y_hat)
     # Multi-Class Logistic Regression class with Early Stopping
     class MVLLogisticRegression:
         def __init__(self, learning_rate=0.01, 12_lambda=0.01):
             self.learning_rate = learning_rate
             self.12_lambda = 12_lambda
             self.best W = None
             self.best_b = None
             self.best_val_loss = float('inf')
             self.patience_counter = 0
         def fit(self, X, y, epochs=1000, batch_size=32, validation_split=0.2,_
      →patience=20, show_curve=False):
             # Store parameters for printing
             self.epochs = epochs
             self.batch_size = batch_size
             self.validation_split = validation_split
             self.patience = patience
             # Split the data into training and validation sets
             split_index = int(len(X) * (1 - validation_split))
             X_train, X_val = X[:split_index], X[split_index:]
             y_train, y_val = y[:split_index], y[split_index:]
             N, D = X_train.shape
             K = len(np.unique(y))
             Y_train = indices_to_one_hot(y_train, K)
             Y_val = indices_to_one_hot(y_val, K)
             # Initialize weights and biases
```

```
self.W = np.random.randn(D, K) / np.sqrt(D)
      self.b = np.zeros(K)
      train_losses = []
      val_losses = []
      for epoch in range(epochs):
           # Mini-batch gradient descent
           for i in range(0, N, batch_size):
               X_batch = X_train[i:i+batch_size]
              Y_batch = Y_train[i:i+batch_size]
              P_hat = self.forward(X_batch)
               grad_W = (1/batch_size) * X_batch.T @ (P_hat - Y_batch) + self.
→12_lambda * self.W
               grad_b = (1/batch_size) * np.sum(P_hat - Y_batch, axis=0)
               self.W -= self.learning_rate * grad_W
               self.b -= self.learning_rate * grad_b
           # Compute training and validation loss
           train_loss = cat_cross_entropy(Y_train, self.forward(X_train))
           val_loss = cat_cross_entropy(Y_val, self.forward(X_val)) #__
→ Corrected variable name
          train_losses.append(train_loss)
           val_losses.append(val_loss)
           # Early stopping
           if val_loss < self.best_val_loss:</pre>
               self.best_val_loss = val_loss
               self.patience_counter = 0
               self.best_W = self.W.copy()
               self.best_b = self.b.copy()
           else:
               self.patience_counter += 1
           if self.patience_counter >= patience:
              print(f"Early stopping at epoch {epoch}")
               self.W = self.best_W
               self.b = self.best_b
              break
      if show_curve:
           plt.figure(figsize=(10, 5))
          plt.plot(train_losses, label='Training Loss')
           plt.plot(val_losses, label='Validation Loss')
          plt.xlabel('Epochs')
```

```
plt.ylabel('Loss')
            plt.title('Training and Validation Loss Curves')
            plt.legend()
            plt.show()
   def forward(self, X):
        return softmax(X @ self.W + self.b)
   def predict(self, X):
       P hat = self.forward(X)
       return np.argmax(P_hat, axis=1)
# Scaling
def manual_scaling(X_train, X_test):
   mean = np.mean(X_train, axis=0)
   std = np.std(X_train, axis=0)
   std[std == 0] = 1  # Avoid division by zero
   X_train_scaled = (X_train - mean) / std
   X_test_scaled = (X_test - mean) / std
   return X_train_scaled, X_test_scaled, mean, std
# Function to print class probabilities
def print_class_probabilities(model, X):
   P hat = model.forward(X)
   print("Class Probabilities for Each Sample:")
   print(P_hat)
# Function to print feature importance
def print_feature_importance(model, feature_names):
   print("Feature Importance (magnitude of weights):")
   feature_importance = np.abs(model.W)
   for i, feature_name in enumerate(feature_names):
        importance = np.mean(feature_importance[i])
        print(f"{feature_name}: Importance {importance:.4f}")
# Apply scaling
X_train_scaled, X_test_scaled, mean, std = manual_scaling(X_train, X_test)
# Train the model
mv_logreg1 = MVLLogisticRegression(learning_rate=0.01, 12_lambda=0.01)
mv_logreg1.fit(X_train_scaled, y_train, epochs=1000, batch_size=32,_
 ovalidation_split=0.2, patience=20, show_curve=True)
# Predict on the test set
y_hat1 = mv_logreg1.predict(X_test_scaled)
# Evaluate accuracy on the entire dataset
```

```
overall_accuracy = accuracy(y_test, y_hat1)
print(f"Overall Accuracy: {overall_accuracy * 100:.2f}%")
# Print optimized parameters and training details
print("Optimized Parameters:")
print("Weights (W):")
print(mv_logreg1.W)
print("Biases (b):")
print(mv logreg1.b)
print("Learning Rate:", mv_logreg1.learning_rate)
print("Epochs:", mv_logreg1.epochs)
print("Batch Size:", mv_logreg1.batch_size)
print("Validation Split:", mv_logreg1.validation_split)
print("Patience:", mv_logreg1.patience)
# Print class probabilities for the test set
print_class_probabilities(mv_logreg1, X_test_scaled)
# Print feature importance
feature_names = X_train_scaled.columns if hasattr(X_train_scaled, 'columns')__
 ⇔else [f'Feature {i}' for i in range(X_train_scaled.shape[1])]
print_feature_importance(mv_logreg1, feature_names)
```

##ANN

```
[141]: # Activation functions and their derivatives
def ReLU(Z):
    return np.maximum(0, Z)

def sigmoid(Z):
    return 1 / (1 + np.exp(-Z))

def linear(Z):
    return Z

def softmax(Z):
    expZ = np.exp(Z - np.max(Z, axis=1, keepdims=True)) # Stability improvement
    return expZ / expZ.sum(axis=1, keepdims=True)
```

```
[142]: # Derivatives of Activation Functions

def derivative (Z, a):
    if a == linear:
        return 1
    elif a==sigmoid:
        return Z*(1-Z)
    elif a==np.tanh:
```

```
return 1-Z**2
        elif a==ReLU:
          return (Z>0).astype(int)
          ValueError('Unknown activation function')
[143]: # One-hot encoding
      def one_hot(y):
          nb_classes = len(np.unique(y))
          return np.eye(nb_classes)[y.reshape(-1)]
      # Loss functions
      def cross_entropy(Y, P_hat):
          return -(1/len(Y)) * np.sum(np.sum(Y * np.log(P_hat), axis=1), axis=0)
      def OLS(Y, P_hat): # Ordinary Least Squares for regression
          return np.mean((Y - P_hat)**2)
[144]: # ANN class
      class ANN():
          def __init__(self, architecture, activations=None, mode=0):
              self.mode = mode
              self.architecture = architecture
              self.activations = activations
              self.L = len(architecture) + 1
          def fit(self, X, y, eta=1e-3, epochs=1e3, show_curve=False):
              epochs = int(epochs)
              if self.mode:
                  Y = y
                  K = 1
              else:
                  Y = one_hot(y)
                  K = Y.shape[1]
              N, D = X.shape
              # Initialize Weights and Biases
              self.W = {1: np.random.randn(M[0], M[1]) for 1, M in enumerate(zip([D]__
        self.B = {1: np.random.randn(M) for 1, M in enumerate(self.architecture_
        \hookrightarrow+ [K], 1)}
              # Activation setup
              if self.activations is None:
                  self.a = {1: ReLU for 1 in range(1, self.L)}
```

```
else:
           self.a = {1: act for 1, act in enumerate(self.activations, 1)}
       # Output activation function
       if self.mode:
           self.a[self.L] = linear
       else:
           self.a[self.L] = softmax
       # Loss Function
       J = np.zeros(epochs)
       # Training loop
       for epoch in range(epochs):
           self.__forward__(X) # Forward pass
           if self.mode:
               J[epoch] = OLS(Y, self.Z[self.L])
           else:
               J[epoch] = cross_entropy(Y, self.Z[self.L]) # Cross-entropy_
\hookrightarrow loss for classification
           # Backpropagation
           dH = (1/N) * (self.Z[self.L] - Y)
           for 1 in sorted(self.W.keys(), reverse=True):
               dw = self.Z[1 - 1].T @ dH
               dB = dH.sum(axis=0)
               # Weight update rules
               self.W[l] -= eta * dw
               self.B[1] -= eta * dB
               if 1 > 1:
                   dZ = dH @ self.W[1].T
                   dH = dZ * derivative(self.Z[1 - 1], self.a[1 - 1])
       # Plotting loss curve
       if show_curve:
           plt.figure()
           plt.plot(J)
           plt.xlabel('Epochs')
           plt.ylabel('Loss')
           plt.title('ANN Training Curve')
           plt.show()
  def __forward__(self, X):
       self.Z = \{0: X\}
```

```
for 1 in sorted(self.W.keys()):
    self.Z[1] = self.a[1](self.Z[1 - 1] @ self.W[1] + self.B[1])

def predict(self, X):
    self.__forward__(X)
    if self.mode:
        return self.Z[self.L]
    else:
        return self.Z[self.L].argmax(axis=1)
```

```
[]: # 2 hidden layers with 64 and 32 neurons
architecture = [64, 32]
activations = [ReLU, np.tanh]

# Instantiate and train ANN for classification
ann = ANN(architecture, activations=activations, mode=0)
ann.fit(X_train_scaled, y_train, eta=1e-3, epochs=3000, show_curve=True)

# Predictions on test set
y_hat = ann.predict(X_test_scaled)

# Accuracy calculation
test_accuracy = np.mean(y_hat == y_test)
print(f"Test Accuracy: {test_accuracy * 100:.2f}%")
```

```
[]: # Activation functions and their derivatives
     def ReLU(Z):
         return np.maximum(0, Z)
     def sigmoid(Z):
         return 1 / (1 + np.exp(-Z))
     def linear(Z):
         return Z
     def softmax(Z):
         expZ = np.exp(Z - np.max(Z, axis=1, keepdims=True)) # Stability improvement
         return expZ / expZ.sum(axis=1, keepdims=True)
     # Derivatives of Activation Functions
     def derivative (Z, a):
         if a == linear:
             return 1
         elif a == sigmoid:
            return Z*(1-Z)
         elif a == np.tanh:
             return 1-Z**2
```

```
elif a == ReLU:
        return (Z>0).astype(int)
    else:
        raise ValueError('Unknown activation function')
# One-hot encoding
def one_hot(y):
    nb_classes = len(np.unique(y))
    return np.eye(nb_classes)[y.reshape(-1)]
# Loss functions
def cross_entropy(Y, P_hat):
    return -(1/len(Y)) * np.sum(np.sum(Y * np.log(P_hat + 1e-8), axis=1), ___
 ⇒axis=0)
def OLS(Y, P_hat):
    return np.mean((Y - P_hat)**2)
# Xavier weight initialization
def xavier_init(fan_in, fan_out):
    return np.random.randn(fan_in, fan_out) * np.sqrt(2 / (fan_in + fan_out))
# ANN class
class ANN():
    def __init__(self, architecture, activations=None, mode=0, dropout_prob=0.
 ⇒5):
        self.mode = mode
        self.architecture = architecture
        self.activations = activations
        self.L = len(architecture) + 1
        self.dropout_prob = dropout_prob
    def fit(self, X, y, eta=1e-3, epochs=1e3, show_curve=False, batch_size=64):
        epochs = int(epochs)
        if self.mode:
            Y = v
            K = 1
        else:
            Y = one_hot(y) # One-hot encode labels for classification
            K = Y.shape[1]
        N, D = X.shape
        # Initialize Weights and Biases using Xavier initialization
        self.W = {1: xavier_init(M[0], M[1]) for 1, M in enumerate(zip([D] +
 →self.architecture, self.architecture + [K]), 1)}
```

```
self.B = {1: np.zeros(M) for 1, M in enumerate(self.architecture + [K], u
→1)}
       # Activation setup
      if self.activations is None:
           self.a = {1: ReLU for 1 in range(1, self.L)}
       else:
           self.a = {1: act for 1, act in enumerate(self.activations, 1)}
       # Output activation function
      if self.mode:
           self.a[self.L] = linear
      else:
           self.a[self.L] = softmax
       # Loss Function
      J = np.zeros(epochs)
       # Training loop
      for epoch in range(epochs):
           idx = np.random.permutation(N)
           X_shuffled, Y_shuffled = X[idx], Y[idx]
          for i in range(0, N, batch_size):
               X_batch = X_shuffled[i:i + batch_size]
               Y_batch = Y_shuffled[i:i + batch_size]
               self.__forward__(X_batch) # Forward pass
               if self.mode:
                   J[epoch] = OLS(Y_batch, self.Z[self.L])
               else:
                   J[epoch] = cross_entropy(Y_batch, self.Z[self.L]) #_
→Cross-entropy loss for classification
               # Backpropagation
               dH = (1 / batch_size) * (self.Z[self.L] - Y_batch)
               for l in sorted(self.W.keys(), reverse=True):
                   dw = self.Z[l - 1].T @ dH # Gradient of weights
                   dB = dH.sum(axis=0) # Gradient of biases
                   # Weight update rules with momentum
                   self.W[l] -= eta * dw
                   self.B[1] -= eta * dB
                   if 1 > 1:
                       dZ = dH @ self.W[1].T
```

```
dH = dZ * derivative(self.Z[1 - 1], self.a[1 - 1]) #_{\square}
 → Chain rule for backpropagation
            # Decay learning rate
            if epoch \% 100 == 0 and epoch > 0:
                eta *= 0.95 # Learning rate decay
        # Plotting loss curve
        if show_curve:
            plt.figure()
            plt.plot(J)
            plt.xlabel('Epochs')
            plt.ylabel('Loss')
            plt.title('Training Curve')
            plt.show()
    def __forward__(self, X):
        self.Z = {0: X} # Input layer
        for 1 in sorted(self.W.keys()):
            self.Z[1] = self.a[1](self.Z[1 - 1] @ self.W[1] + self.B[1]) #__
 → Compute activations for each layer
    def predict(self, X):
        self.__forward__(X)
        if self.mode:
            return self.Z[self.L]
        else:
            return self.Z[self.L].argmax(axis=1)
# 2 hidden layers with 64 and 32 neurons
architecture = [64, 32]
activations = [ReLU, np.tanh] # Activation functions for each layer
# Instantiate and train ANN for classification
ann1 = ANN(architecture, activations=activations, mode=0)
ann1.fit(X_train_scaled, y_train, eta=1e-3, epochs=3000, show_curve=True, __
 ⇔batch_size=64)
# Predictions on test set
y_hat = ann1.predict(X_test_scaled)
# Accuracy calculation
test_accuracy = np.mean(y_hat == y_test)
print(f"Test Accuracy: {test_accuracy * 100:.2f}%")
```

```
[147]: # Function to compute confusion matrix
       def confusion_matrix(y_true, y_pred):
           classes = np.unique(y_true) # Identify unique classes
           num_classes = len(classes)
           # Create a zero matrix to hold the confusion matrix values
           cm = np.zeros((num_classes, num_classes), dtype=int)
           # Populate the confusion matrix
           for i in range(len(y_true)):
               true label = np.where(classes == y true[i])[0][0]
               predicted_label = np.where(classes == y_pred[i])[0][0]
               cm[true_label, predicted_label] += 1
           return cm, classes
       # Predict values
       y_hat = ann1.predict(X_test_scaled)
       # Calculate confusion matrix
       cm, classes = confusion_matrix(y_test, y_hat)
       # Display confusion matrix
       print("ANN Confusion Matrix:")
       print(cm)
       plt.figure(figsize=(8, 6))
       sns.heatmap(cm, annot=True, fmt="d", cmap="Blues", xticklabels=classes, __
        ⇔yticklabels=classes)
       plt.xlabel("Predicted Labels")
       plt.ylabel("True Labels")
       plt.title("ANN Confusion Matrix")
       plt.show()
      ANN Confusion Matrix:
```

[[24 2 3] [ 3 28 0] [ 5 0 8]]

