



#### Problem Description

- Detecting and classifying thyroid diseases accurately from clinical data
- Addressing the challenge of subtle and varied symptoms associated with thyroid disorders
- Improving early detection and diagnosis to enhance patient care and treatment outcomes
- Leveraging machine learning techniques to augment traditional diagnostic methods









#### Dataset

```
[38] # Load the dataset
     data_path = 'sample_data/thyroidDF.csv'
     df = pd.read csv(data path)
[39] # Print the initial shape of the dataset
     print("Initial dataset shape:", df.shape)
    Initial dataset shape: (9172, 31)
[40] print(df.iloc[:, :4], df['target'])
          age sex on_thyroxine query_on_thyroxine
     [9172 rows x 4 columns] 0
           target, Length: 9172, dtype: object
```

Dataset Description: Sourced from Kaggle, the dataset features a multiclass target variable representing various types of thyroid diseases diagnosed clinically.





#### Dataset

#### **Data Preprocessing**

```
# Handling missing values
       for column in df.columns:
           if df[column].dtype in ['float64', 'int64']:
               df[column].fillna(df[column].median(), inplace=True)
           elif df[column].dtype == 'object':
               df[column].fillna(df[column].mode()[0], inplace=True)
[25] # Encode categorical variables using Label Encoder
       for column in df.columns:
           if df[column].dtype == 'object':
               encoder = LabelEncoder()
               df[column] = encoder.fit_transform(df[column])
\frac{\checkmark}{0s} [26] # Balancing skewed dataset
       # Separate majority and minority classes
       df_majority = df[df.target == df.target.mode()[0]]
       df_minority = df[df.target != df.target.mode()[0]]
       # Upsample minority class
       df_minority_upsampled = resample(df_minority,
                                         replace=True,
                                                           # sample with replacement
                                         n_samples=len(df_majority), # to match majority class
                                         random_state=123) # reproducible results
       # Combine majority class with upsampled minority class
       df = pd.concat([df_majority, df_minority_upsampled])
       # Shuffle the dataset to avoid any order bias
       df = df.sample(frac=1, random_state=42).reset_index(drop=True)
       print("New dataset shape:", df.shape) # Print the new shape of the dataset
       New dataset shape: (13542, 31)
```

```
[27] # Separate features and target variable
features = df.drop(['target', 'patient_id'], axis=1)
labels = df['target']

[28] # Scale the features
scaler = StandardScaler()
features_scaled = scaler.fit_transform(features)

[29] # Split the data into training and testing sets
trainX, testX, trainY, testY = train_test_split(features_scaled, labels, test_size=0.2, random_state=42)
```



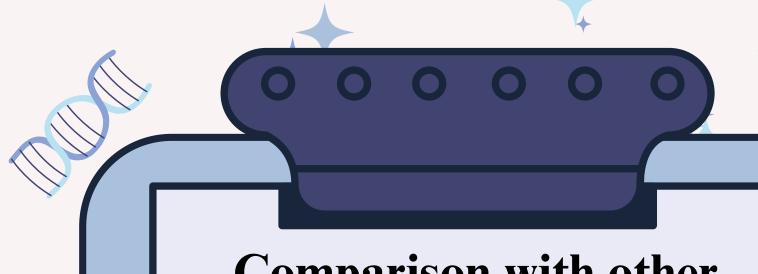


#### Model selection

# 00000

#### Why neural network?

- Chosen for its effectiveness in handling multiclass classification tasks.
- Demonstrated capability to capture complex patterns in the dataset.
- Evidenced superior performance metrics compared to other models in the research paper.



### Comparison with other models:

- Demonstrated efficacy in prior studies for similar classification tasks.
- Neural network architecture deemed suitable for the problem's complexity and dataset characteristics.

# Training and Evaluation

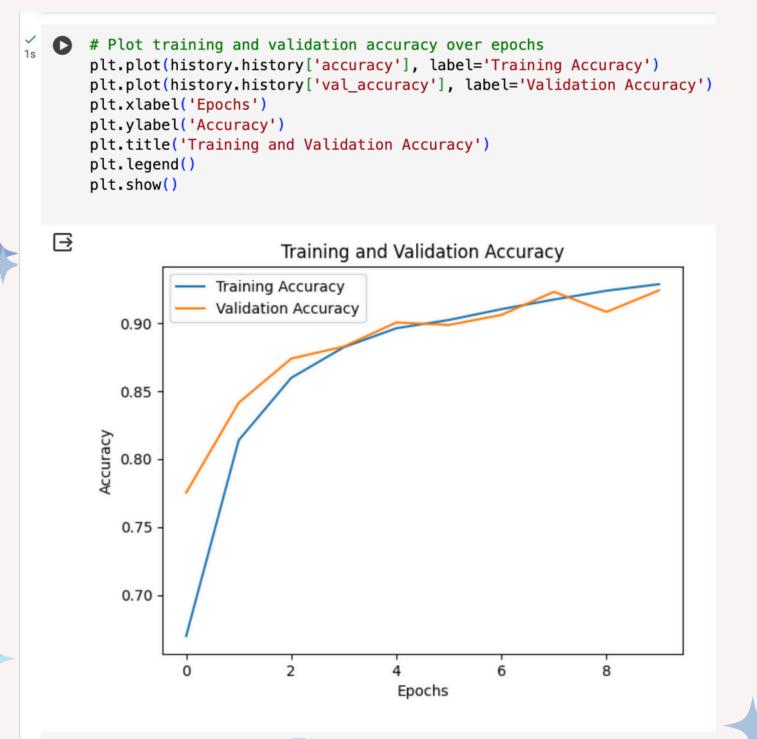
#### Model

```
[46] # Define the neural network
     model = Sequential([
         Dense(128, activation='relu', input_shape=(trainX.shape[1],)),
         Dense(128, activation='relu'),
         Dense(64, activation='relu'),
         Dense(len(labels.unique()), activation='softmax')
     1)
[47] model.compile(optimizer='adam',
                   loss='sparse_categorical_crossentropy',
                   metrics=['accuracy'])
[48] # Train the model
     history = model.fit(trainX, trainY, epochs=10, validation_data=(testX, testY))
```

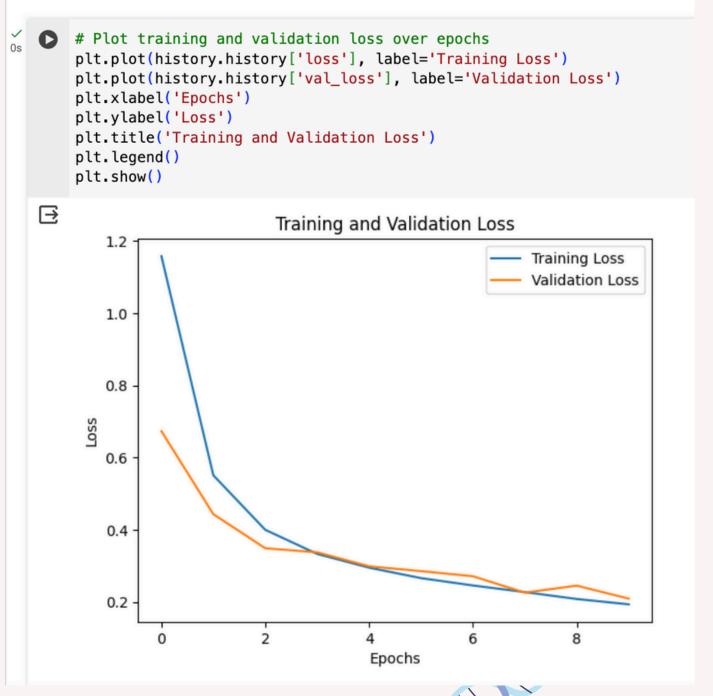


# Training and Evaluation

#### Plot Training



#### Plotting Training and Validation Metrics



## Training and Evaluation

Confusion Metrics and Model summary

```
predictions = model.predict(testX)
    predicted_classes = np.argmax(predictions, axis=1)
    accuracy = accuracy_score(testY, predicted_classes)
    precision = precision_score(testY, predicted_classes, average='weighted')
    recall = recall_score(testY, predicted_classes, average='weighted')
    f1 = f1_score(testY, predicted_classes, average='weighted')
    print("Accuracy:", accuracy)
    print("Precision:", precision)
    print("Recall:", recall)
    print("F1-score:", f1)
    85/85 [========== ] - 0s 2ms/step
    Accuracy: 0.9239571797711332
    Precision: 0.9267401822828139
    Recall: 0.9239571797711332
    F1-score: 0.9233015582302116
[36] model.summary()
    Model: "sequential_1"
     Layer (type)
                                 Output Shape
                                                           Param #
     dense_4 (Dense)
                                 (None, 128)
                                                           3840
                                 (None, 128)
     dense_5 (Dense)
                                                           16512
     dense 6 (Dense)
                                 (None, 64)
                                                           8256
     dense 7 (Dense)
                                 (None, 32)
                                                           2080
    Total params: 30688 (119.88 KB)
    Trainable params: 30688 (119.88 KB)
    Non-trainable params: 0 (0.00 Byte)
```



### Interpretation of Results

Our study demonstrates the effectiveness of neural networks for thyroid disease classification while highlighting the need for future work to explore the impact of additional features on model performance.

# Thank you for your attention ...

