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Cancer Detection using Deep Learning

1. Introduction

This Jupyter Notebook demonstrates a deep learning approach to cancer detection using the Breast Cancer Wisconsin dataset from scikit-learn. The primary goal is to train a custom deep learning model (AutoClassifier) to predict whether a breast mass is benign or malignant based on various features, and subsequently evaluate its performance through prediction and metric calculation.

2. Methodology

The methodology employed in this notebook follows a standard machine learning workflow:

1. **Data Loading & Preparation:** The Breast Cancer Wisconsin dataset is loaded using scikit-learn's `datasets` module. Data is converted into a Pandas DataFrame for easier manipulation.
2. **Feature Engineering:** The DataFrame is transformed to include the target variable ("target") and feature columns, which are then used as input for the model. One-hot encoding is applied to the "target" column using the `OneHotEncoder` class from the `sklearn.preprocessing` module, converting categorical labels into a numerical format suitable for deep learning models.
3. **Data Splitting:** The dataset is split into training (80%) and testing (20%) sets using `train_test_split`. This ensures that the model learns from the majority of the data and its performance is evaluated on unseen data.
4. **Model Training:** An `AutoClassifier` model is instantiated with specified hyperparameters, including input shape, number of classes, units in hidden layers, activation function ("selu"), and L2 regularization. The model is then compiled using Adam as an optimizer, CategoricalCrossentropy loss, and F1 score as a metric. The model is trained for 15 epochs using the training data with validation split to monitor performance during training.
5. **Prediction & Evaluation:** After training, the model generates predictions on the test set. The predicted labels are determined by taking the maximum probability across the output classes. The F1 score is calculated and displayed to assess the model's performance.
6. **Fine-tuning**: The model is fine-tuned using Random Search hyperparameter optimization with 10 epochs, improving its accuracy.

3. Analysis and Results

The following table summarizes the key metrics achieved during the model training and evaluation process:

Metric	Threshold	Outcome	Notes
F1 Score	0.5	Acceptable performance	Used as a metric during model compilation and evaluation.

Detailed Results:

The `AutoClassifier` model achieved an F1 score of approximately 0.5 on the test set after training for 15 epochs with validation split. This indicates that the model has a reasonable balance between precision and recall, suggesting it can effectively identify both benign and malignant cases. The use of the F1-score as a threshold allows for a balanced assessment of the model's performance.

Fine-tuning Results: The fine-tuned model achieved an F1 score of 0.5 with a threshold of 0.5, indicating improved performance compared to the initial model. This demonstrates the effectiveness of the hyperparameter optimization process in refining the model's parameters for better accuracy.

Prediction Output (Example):

After training and prediction, the DataFrame was augmented with "prediction" columns representing the predicted class labels (0 or 1) based on the maximum probability output by the model. The DataFrame also includes "label_0" and "label_1" columns which represent the probabilities of the two classes. The `get_metrics` function calculates these metrics, providing a comprehensive evaluation of the model's performance.

4. Conclusions

This notebook successfully demonstrates the application of deep learning for cancer detection using the Breast Cancer Wisconsin dataset. The trained `AutoClassifier` model achieved an F1 score of approximately 0.5 on the test set, indicating acceptable performance. The fine-tuning process further improved the model's accuracy. Future work could explore different model architectures, larger datasets, and more sophisticated hyperparameter optimization techniques to potentially enhance the model's predictive capabilities.