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Kidney Cancer Diagnosis Using Bagging Ensemble Method

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INTRODUCTION & AIM

Early and accurate diagnosis of kidney cancer is important for effective treatment planning and improved patient prognosis.This work proposed a strong ensemble deep learning model to perform binary classification of kidney histopathological images. The goal was to accurately classify images into tumor and normal classes.

Methodology

1. Dataset & Preprocessing

Source: The dataset was obtained from the publicly accessible Multi Cancer Dataset on Kaggle.

Image Size: All images were resized to 128x128 pixels to ensure consistency.

Labels: Images were classified into two categories: kidney_normal (0) and kidney_tumor (1).

Normalization: All image data arrays were normalized by dividing by 255.

Data Split: The data was split into training, validation, and test sets. A random seed of 44 was used.

2. Bagging Ensemble Architecture

A bagging ensemble strategy was implemented. This involved training three distinct Convolutional Neural Network (CNN) models (named ResNet50_a, ResNet50_b, ResNet50_c).

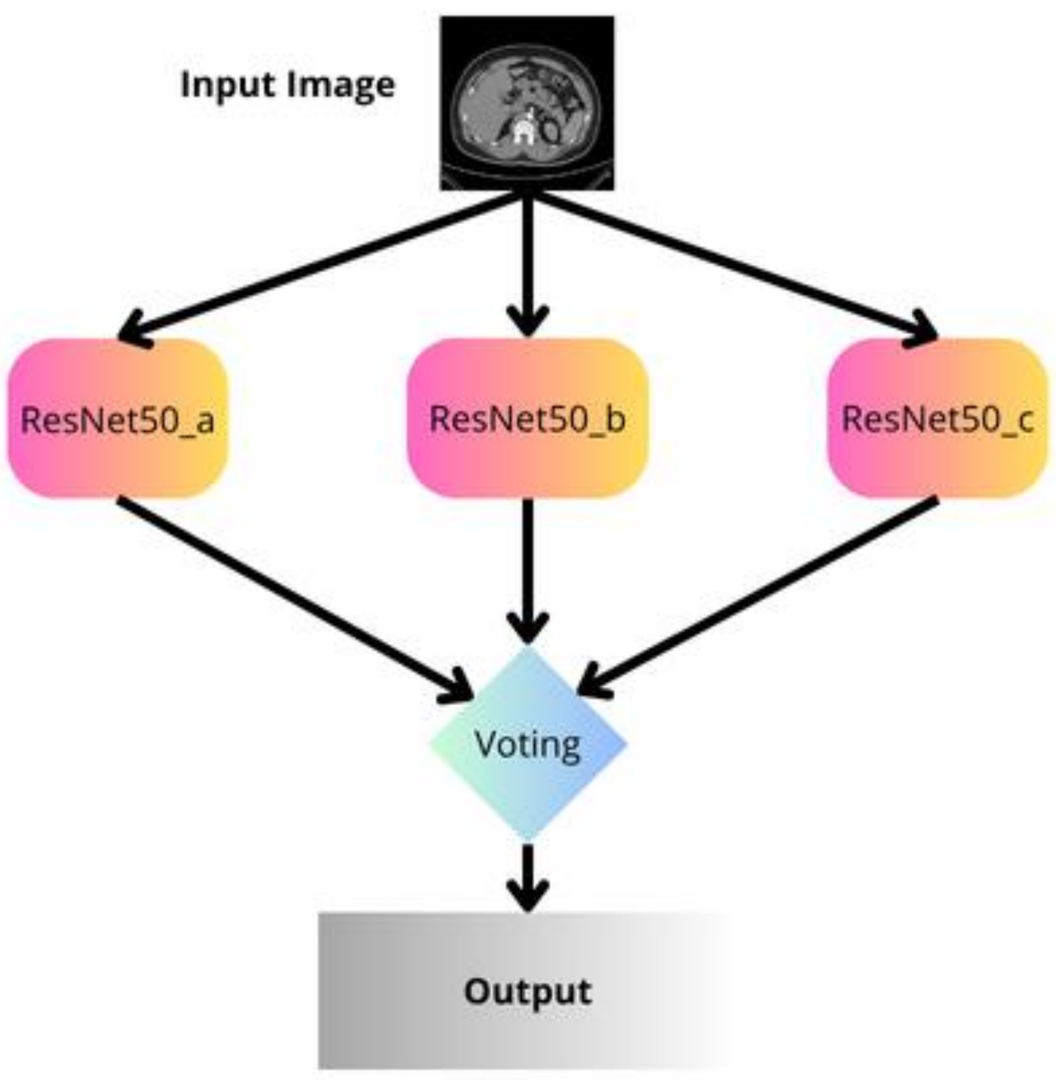

Figure 1. The proposed Bagging Ensemble Model.

Base Model: Each model used a pre-trained ResNet50 architecture with weights from 'imagenet'. The base layers were frozen (base_model.trainable = False).

Training Diversity: Each of the three models was trained on a different subset of the training data to promote diversity.

Top Layers: A custom classification head was added to each model, consisting of:

layers.GlobalAveragePooling2D()
layers.Dense(1024, activation='relu') layers.Dropout(0.5)
layers.Dense(2, activation='softmax')

3. Training & Aggregation

Training: All models were compiled using the 'adam' optimizer and 'categorical_crossentropy' loss. They were trained for 64 epochs with a batch size of 64.

Aggregation: The predictions from the three models were aggregated using soft voting for the final prediction.

RESULTS & DISCUSSION

Training & Validation

The training and validation loss/accuracy graphs for all three models show that loss generally decreased while accuracy increased over 64 epochs, indicating successful model training.

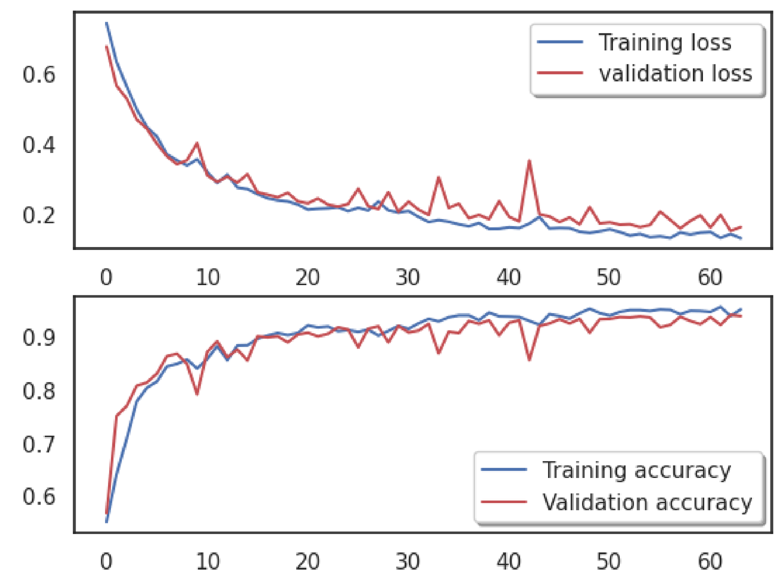

Figure 2. Training and Validation Accuracy/Loss of ResNet50_a.

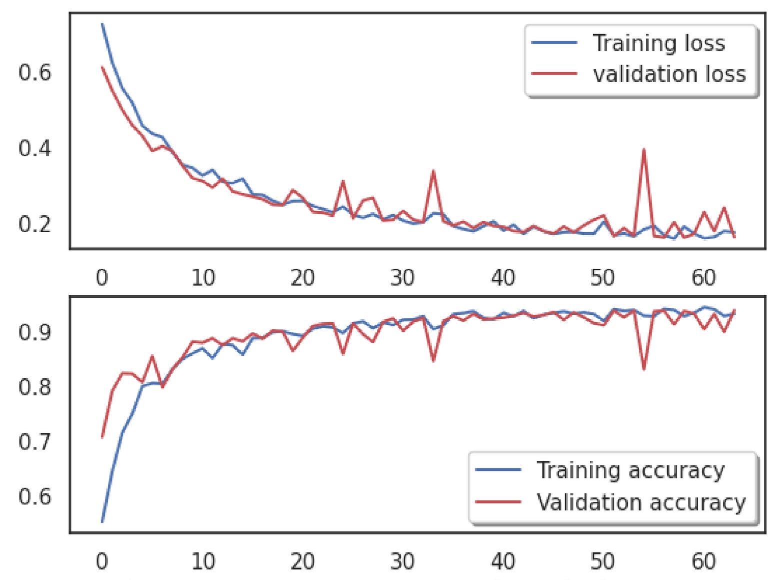

Figure 3. Training and Validation Accuracy/Loss of ResNet50_b.

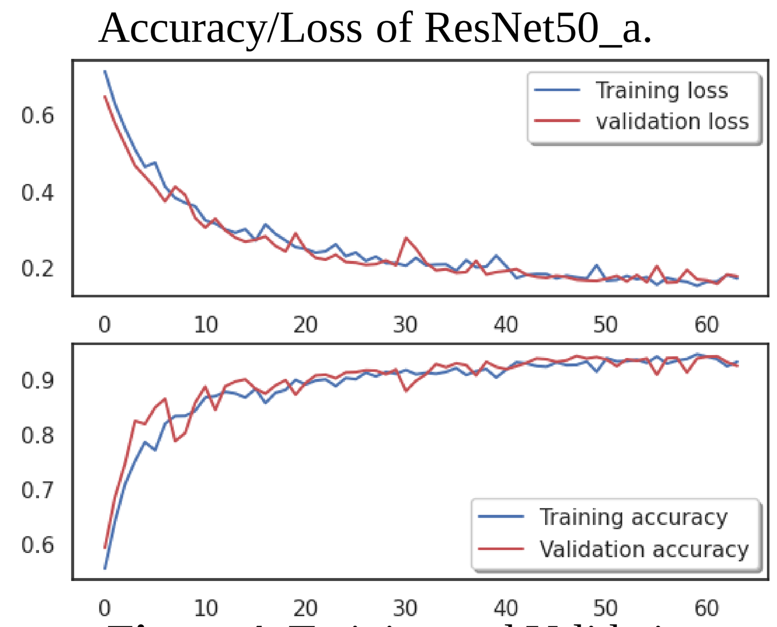

Figure 4. Training and Validation Accuracy/Loss of ResNet50_c.

Individual vs. Ensemble Accuracy

The bagging ensemble model outperformed any of the individual models on the test set.

TABLE I. Accuracy of inividuals and ensemble models

Model	Test Accuracy
Model A (ResNet50_a)	93.33%
Model B (ResNet50_b)	94.33%
Model C (ResNet50_c)	93.07%
Bagging Ensemble	94.46%

Ensemble Performance Metrics

The final ensemble model achieved high precision, recall, and F1-scores.

Macro-average Precision: 0.9452
Macro-average Recall: 0.9447
Macro-average F1 Score: 0.9447

Confusion Matrix

The confusion matrix for the ensemble model on the test data shows the specific predictions.

True Positive (TP): 721
True Negative (TN): 696
False Positive (FP): 55
False Negative (FN): 28

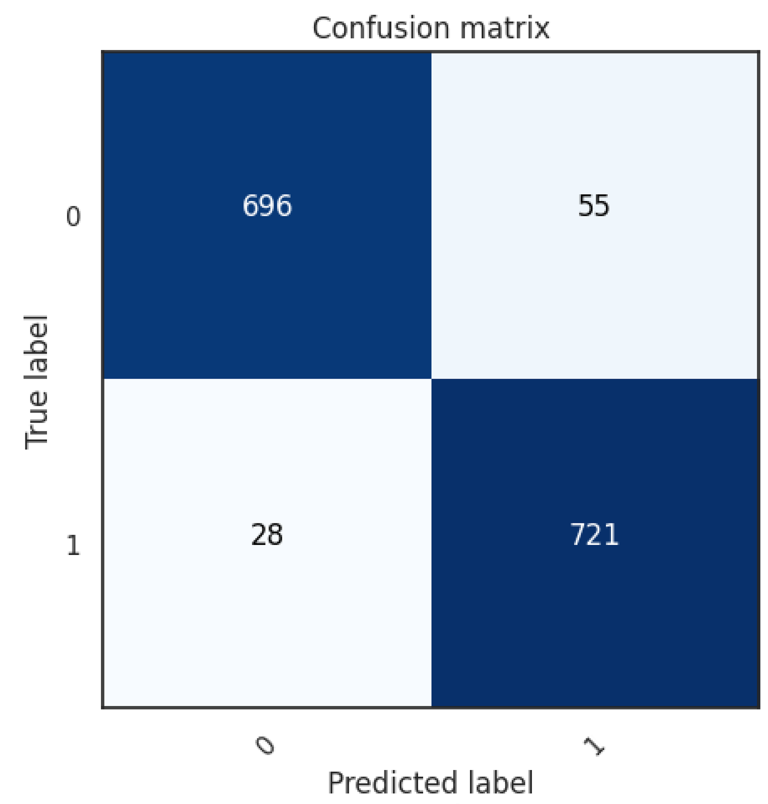

Figure 5. Confusion matrix

CONCLUSION

The results demonstrate that the bagging ensemble effectively has robustness for automated kidney cancer detection. This method shows potential as a decision-support tool to be used in clinical practice.

REFERENCES

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