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WEEK 2: Cancer Detection Using Histopathological Images

GitHub: https://github.com/Samar-Ahmed-1012/breakhis-cancer-classification

LinkedIn: https://www.linkedin.com/feed/update/urn:li:ugcPost:7367679635205115904/

Dataset: https://www.kaggle.com/datasets/ambarish/breakhis

Histopathological Breast Cancer Image Classification

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Project: Week 2 Task - Cancer Detection Model Development

1.0 Executive Summary

This project developed and evaluated two deep learning models for the binary classification of breast cancer histopathological images. A custom Convolutional Neural Network (CNN) was built from scratch and a second model utilized Transfer Learning with the VGG16 architecture. The VGG16-based model demonstrated **excellent performance**, achieving a test accuracy of **86.00%**, effectively validating the application of transfer learning for this task. The custom CNN model, however, failed to generalize and was unable to learn a meaningful discrimination strategy, a key learning outcome for model development.

2.0 Project Objective

The primary objective was to implement a full image-based classification pipeline, from data acquisition to model evaluation. The technical goal was to classify histopathological images from the BreakHis dataset as either **Benign** or **Malignant**.

3.0 Methodology

3.1. Dataset & Preprocessing

- **Dataset:** A balanced subset of **500 images** (250 Benign, 250 Malignant) was extracted from the BreakHis dataset.

- **Preprocessing:** All images were resized to **128x128 pixels** and normalized (pixel values scaled to [0, 1]).

3.2. Model Architectures

1. **Custom CNN:** A sequential model with three convolutional layers, max-pooling, and fully connected layers.

2. **VGG16 Transfer Learning:** The pre-trained VGG16 model was used as a feature extractor with frozen weights, followed by custom trainable classification layers.

3.3. Training

- Both models used the Adam optimizer and Binary Cross-Entropy loss.

- The dataset was split into **80% training** (400 images) and **20% testing** (100 images).

- Models were trained for **10 epochs** with a batch size of 32.

4.0 Results & Evaluation

The models were evaluated on a held-out test set of 100 images (50 Benign, 50 Malignant).

Model	Test Accuracy	Test Loss	Precision	Recall	F1-Score
Custom CNN	50.00%	3.5816	25.00%	50.00%	33.00%
VGG16 (Transfer Learning)	86.00%	0.5624	87.00%	86.00%	86.00%

Analysis:

- The **VGG16 model** performed superbly, demonstrating high and balanced precision and recall for both classes.

- The **Custom CNN model** converged to a naive solution, predicting all images as the majority class (Benign) in the training set, resulting in a 50% accuracy equivalent to random guessing for a balanced dataset. This indicates a critical failure in learning, likely due to overfitting on the training data or an issue with model capacity or training dynamics.

Confusion Matrix (VGG16 Model):

```
Confusion Matrix:
[[46  4]
 [10 40]]
```

> *This matrix confirms the model's strong performance, with a low rate of false positives and false negatives.*

5.0 Conclusion

- **Key Success:** The VGG16 transfer learning model is a highly effective proof-of-concept for automating cancer detection, achieving **86% accuracy** with limited data and training time.

- **Key Learning:** The failure of the simple CNN model is a valuable lesson in the challenges of designing models from scratch. It underscores the importance of techniques like regularization, learning rate adjustment, and more sophisticated architectures to prevent overfitting and learning failure.