DEEP LEARNING BASED COLORECTAL CANCER CLASSIFICATION

[1]Khadakkar Poonam Ravindra, [2]Dr. Rahul M. Patil, [3]Chandrashekhar V. Patil
Department of Electronics and Telecommunication Engineering,
NES'S Ganagamai College Of Engineering, Nagaon
poonamnikume39@gmail.com

ABSTRACT

Colorectal cancer (CRC) remains a leading cause of cancer-related morbidity and mortality worldwide. Conventional histopathological diagnosis, while effective, is labor-intensive, subjective, and prone to inter-observer variability. Recent advances in artificial intelligence, particularly deep learning, offer the potential to augment diagnostic workflows with automated, accurate, and interpretable image classification systems. This study develops and evaluates a deep learning-based framework for binary classification of CRC using histopathological images from the LC25000 dataset. Three convolutional neural network architectures—MobileNet, DenseNet, and EfficientNet—were implemented with transfer learning, data augmentation, and Grad-CAM interpretability tools. Among these, MobileNet demonstrated a balance of high accuracy (99.37%) and computational efficiency, highlighting its suitability for real-time clinical deployment. This work underscores the promise of lightweight deep learning models in supporting early CRC detection and provides a foundation for scalable AI-assisted pathology solutions.

Keywords: Colorectal cancer, deep learning, CNN, MobileNet, DenseNet, EfficientNet, LC25000.

INTRODUCTION

One of the most prevalent types of cancer, colorectal cancer (CRC) affects both men and women globally. Usually starting in the colon or rectum, it develops into malignant tumors that, if not discovered in time, could spread to other areas of the body. Colorectal cancer has been a crucial area of emphasis for clinical research and public health activities due to its increasing incidence and fatality rates. Global health data show that colorectal cancer (CRC) is one of the top three causes of cancer-related fatalities, hence early detection and efficient treatment are essential[1].

The manual examination of histopathological slides by pathologists is time-consuming and prone to interpretational variability. Conventional diagnostic procedures for colorectal cancer (CRC) involve invasive methods like colonoscopy and biopsy, which are effective but labor-intensive, expensive, and prone to human error. As the amount of medical imaging data increases, there is an increasing need for automated, accurate, and scalable diagnostic tools that can help medical professionals deliver timely and precise diagnoses [2].

Medical image analysis has been transformed by the introduction of artificial intelligence (AI), especially deep learning (DL). Convolutional Neural Networks (CNNs), in particular, are deep learning models that have shown impressive performance in tasks including image detection, segmentation, and classification. By learning complex patterns and features straight from unprocessed picture data, these models can increase diagnosis accuracy and lessen the need for manually created features [3].

In colorectal cancer, deep learning methods can evaluate histopathological images to differentiate between benign and malignant tissue samples. This ability is especially crucial due to the subtle variations in tissue structure that

might not be readily identified using conventional techniques. Utilizing extensive datasets like LC25000, deep learning models can be developed to attain high precision and generalization, thus aiding the clinical workflow with objective and uniform evaluations [4-6].

A potential remedy for the drawbacks of conventional diagnostic techniques is the incorporation of deep learning into the diagnosis of colorectal cancer. In addition to providing the automated CRC classification is feasible, this initiative lays the groundwork for further study and advancement in AI-assisted medical diagnostics [7-8].

MATERIALS AND RESOURCES USED

Dataset:

The study used the LC25000 dataset, comprising 25,000 histopathological image patches. For this work, only colorectal samples were selected, with 5,000 benign and 5,000 malignant images (224×224 pixels). These images have been extracted from digital pathology slides and are stained using **Hematoxylin and Eosin (H&E)**, which is the most commonly, used staining protocol in histopathology. H&E staining highlights nuclei in blue-purple (hematoxylin) and cytoplasmic components in pink (eosin), providing essential contrast for visual interpretation of tissue morphology and cellular structures.

Deep Learning Architectures:

- MobileNet: Lightweight model for real-time, resource-constrained deployment.
- DenseNet: For deep feature extraction and hierarchical learning.
- EfficientNet: For parameter efficiency and scalable accuracy.

Software / Frameworks:

- Python
- TensorFlow and Keras for model implementation.
- OpenCV for image processing.
- NumPy, Matplotlib, Pandas for data handling and visualization.

Hardware:

- GPU-enabled workstation (e.g., NVIDIA Tesla T4 / GTX 1080 Ti).
- Minimum 16GB RAM.
- Windows or Linux OS.

Data Preprocessing Tools & Techniques:

- Image Resizing
- Normalization (pixel values scaled to [0,1])
- Contrast Enhancement (CLAHE)
- Data Augmentation (rotation, flipping, zoom, brightness adjustment)

Training Configuration:

- Optimizer: Adam
- Learning Rate: 0.0001
- Loss Function: Binary Cross entropy
- Batch Size: 32 or 128
- Epochs: 10–20 (with Early Stopping)
- Grad-CAM for visual interpretability

Evaluation Metrics:

- Accuracy
- Precision
- Recall
- F1-Score
- AUC (Area Under ROC Curve)

METHODOLOGY:

Convolutional Neural Networks (CNNs) are deep learning models designed to process data with a grid-like topology such as images. They are the foundation for most modern computer vision applications to detect features within visual data Key Components of a Convolutional Neural Network

Convolutional Layers: These layers apply convolutional operations to input images using filters or kernels to detect features such as edges, textures and more complex patterns. Convolutional operations help preserve the spatial relationships between pixels.

Pooling Layers: They down sample the spatial dimensions of the input, reducing the computational complexity and the number of parameters in the network. Max pooling is a common pooling operation where we select a maximum value from a group of neighbouring pixels.

Activation Functions: They introduce non-linearity to the model by allowing it to learn more complex relationships in the data.

Fully Connected Layers: These layers are responsible for making predictions based on the high-level features learned by the previous layers. They connect every neuron in one layer to every neuron in the next

Several CNN architectures have been developed, each with its own strengths and weaknesses. Some popular examples include LeNet, AlexNet, MobileNet, EfficientNet, DenseNet, VGGNet, GoogLeNet, and ResNet. These architectures differ in their layer organization, number of parameters, and training requirements.

LeNet: Early CNN with 5 layers designed for handwritten digit recognition (MNIST), pioneering convolution and pooling.

AlexNet: Deeper CNN with ReLU activations and dropout that won ImageNet 2012, sparking the deep learning boom.

VGGNet: Very deep network using stacks of small 3×33 times 33×3 convolutions to improve accuracy and simplicity.

GoogLeNet (Inception): Introduced Inception modules combining multiple filter sizes in parallel to make deeper networks efficient.

ResNet: Added skip (residual) connections to train very deep networks by mitigating vanishing gradients.

DenseNet: Connected each layer to every other layer to improve feature reuse and strengthen gradient flow.

MobileNet: Lightweight CNN using depth wise separable convolutions for efficient inference on mobile devices.

EfficientNet: Scales depth, width, and resolution in a balanced way using a compound scaling method to maximize accuracy and efficiency.

MODEL WORKFLOW

Dataset Selection

- Use the **LC25000 dataset**, which contains histopathological images of colon tissue labelled as benign or malignant.
- Focus only on the colorectal subset of the dataset.

Data Preprocessing

I Image Resizing to 224×224 pixels for compatibility with pre-trained CNN architectures.

Pixel Normalization to scale intensity values between 0 and 1.

Data Augmentation including:

1. Random rotation
2. Zooming
3. Horizontal and vertical flipping
4. Width and height shifting
5. Shearing
6. Brightness adjustment

Dataset Splitting into training (80%) and validation (20%) sets.

Model Selection and Configuration

- Select **three CNN architectures**:
  1. **MobileNet**: Lightweight and efficient for real-time deployment.
  2. **DenseNet**: For deeper feature extraction.
  3. **EfficientNet**: For balanced accuracy and computational cost.
- Customize each model for binary classification:
  1. Remove the original top layers.
  2. Add Global Average Pooling, Dense layers, Dropout, and a final Sigmoid output layer.

Transfer Learning

- Load ImageNet pre-trained weights for each architecture.
- Freeze base layers initially to retain learned features.
- Fine-tune selected layers after initial training to adapt to histopathology data.

Model Training

- Use Adam optimizer with a learning rate of 0.0001.
- Apply Binary Cross entropy loss function.
- Configure early stopping and learning rate scheduling to prevent overfitting.
- Monitor:
  1. Accuracy
  2. Precision
  3. Recall
  4. F1-score
  5. AUC

Evaluation and Visualization

- Assess performance using the validation set.
- Generate:
  1. Confusion Matrix

2. Grad-CAM heatmaps to interpret model predictions.

- Compare performance across models to determine the best trade-off between accuracy and efficiency.

Analysis of Results

- Document validation accuracy, precision, recall, and F1-score for each model.
- Analyze model size, training time, and suitability for deployment in resource-limited environments.

5. Result:

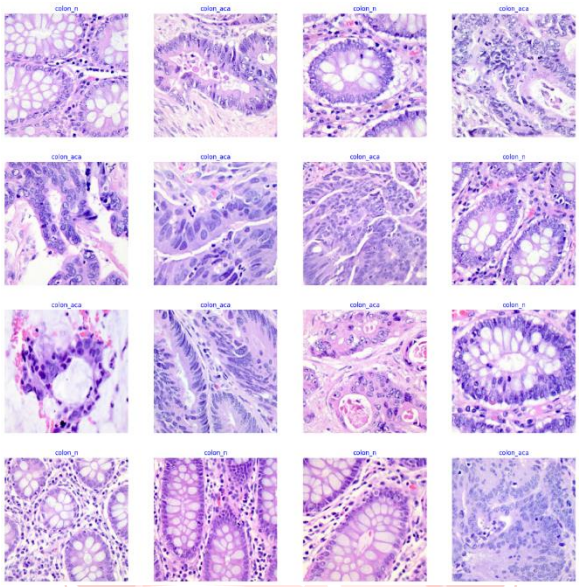

Figure 1: Sample Histopathological Images of Colorectal Tissue

This illustration (Figure 1) presents a set of histopathological image segments depicting two categories of colorectal tissue: healthy colon tissue (colon_n) and colon adenocarcinoma (colon_aca). The images are taken from high-resolution histology slides and dyed with Hematoxylin and Eosin (H&E) to emphasize cellular structures.

The images of normal tissue show consistent glandular structures with distinctly outlined epithelial cells and lumen, characteristic of healthy colon morphology. On the other hand, the adenocarcinoma specimens exhibit abnormal gland structures, varying nuclear shapes, darkly stained nuclei, and altered tissue organization, all of which signal malignant change.

These images form the basis for training deep learning models by allowing the network to identify distinguishing features between healthy and cancerous tissues. Their presence aids in confirming the visual diversity within the dataset and the significance of feature learning for precise classification.

Model Summary

Total params: 6,380,741 (24.34 MB)

Trainable params: 1,050,625 (4.01 MB)

Non-trainable params: 3,228,864 (12.32 MB)

Optimizer params: 2,101,252 (8.02 MB)

Following the resizing of the image to 224 x 224 pixels with the Mobile Net architecture, several data augmentation methods were utilized through Image Data Generator to improve the model's durability and minimize overfitting, which consist of

- Adjusting pixel values to fit within a [0,1] range.
- Arbitrary rotations (upto 20 degrees).
- Cropping and enlarging.
- Flipping horizontally.
- Moving across both width and height.

The model was built using the Adam optimizer with a learning rate of 1e-4, along with the binary cross-entropy loss function, appropriate for binary classification problems. Accuracy served as the measurement criterion.

Epoch	Training accuracy	Training loss	Validation Accuracy	Validation loss
Epoch 1/8	0.8112	0.3555	0.9750	0.1187
Epoch 2/8	0.9960	0.0170	0.9875	0.0542
Epoch 3/8	0.9947	0.0170	0.9875	0.0237
Epoch 4/8	0.9952	0.0102	1.0000	0.0325
Epoch 5/8	0.9991	0.0046	1.0000	0.0064
Epoch 6/8	0.9996	0.0024	1.0000	0.0.0030
Epoch 7/8	1.0000	0.0011	1.0000	6.0952e-04
Epoch 8/8	0.9987	0.0042	1.0000	0.0016

The table displays the training and validation results of the Mobile Net model across 8 epochs, with each epoch consisting of 25 steps. The training utilized an expanded dataset and was fine-tuned with the Adam optimizer.

During Epoch 1, the model starts with a training accuracy of 81.12% and a validation accuracy of 97.50%, suggesting that it begins to generalize effectively from the outset, even with a higher training loss of 0.3555 and a validation loss of 0.1187.

By Epoch 3, training accuracy rises notably to 99.47%, with a decreased loss of 0.0142 and validation accuracy hitting 100%, demonstrating rapid convergence.

From Epochs 4 to 8, the model consistently achieves remarkably high accuracy, almost reaching 100% in both training and validation. The validation loss continues to decrease steadily, hitting a low of 0.0006 in Epoch 7

These findings bolster the efficacy of the Mobile Net framework for classifying histopathological colorectal cancer, demonstrating solid convergence, substantial predictive ability, and low overfitting

CONCLUSION

This model effectively investigated the use of deep learning methods to classify colorectal cancer (CRC) utilizing histopathological images from the LC25000 dataset. The research focused on utilizing transfer learning

and assessing three well-known convolutional neural network (CNN) architectures—Mobile Net, Dense Net, and Efficient Net—to discover a model that strikes a balance between classification accuracy, computational efficiency, and practical deployability.

Among the assessed models, Mobile Net stood out as a notably strong option, attaining high accuracy, minimal validation loss, and great generalization while maintaining its lightweight design. This renders it particularly appropriate for use in resource-limited settings, such as rural health centers or mobile testing units, where computational resources are scarce.

The research further confirmed the significance of:

•Enhancing data to boost generalization,

•Utilize transfer learning to address limitations of dataset size,

• Additionally, standard evaluation metrics (accuracy, precision, recall, F1-score, AUC) offer a comprehensive view of model performance.

The results validate that models based on deep learning can function as efficient and scalable diagnostic instruments for the early identification of colorectal cancer, providing the opportunity to aid and improve decision-making in digital pathology.

REFERENCE

[1] Borkowski, A. A., Bui, M. M., Thomas, L. B., Wilson, C. P., DeLand, L. A., & Mastorides, S. M. (2019). Lung and Colon Cancer Histopathological Image Dataset (LC25000). *arXiv preprint arXiv:1912.12142*. https://arxiv.org/abs/1912.12142

[2] LeCun, Y., Bengio, Y., & Hinton, G. (2015). Deep learning. *Nature*, 521(7553), 436–444. https://doi.org/10.1038/nature14539

[3] Litjens, G., Kooi, T., Bejnordi, B. E., Setio, A. A. A., Ciompi, F., Ghafoorian, M., ... & Sánchez, C. I. (2017). A survey on deep learning in medical image analysis. *Medical Image Analysis*, 42, 60–88. https://doi.org/10.1016/j.media.2017.07.005

[4] Sung, H., Ferlay, J., Siegel, R. L., Laversanne, M., Soerjomataram, I., Jemal, A., & Bray, F. (2021). Global cancer statistics 2020: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. *CA: A Cancer Journal for Clinicians*, 71(3), 209–249. https://doi.org/10.3322/caac.21660

[5] American Cancer Society. (2023). *Colorectal Cancer Survival Rates by Stage*. Retrieved from https://www.cancer.org/cancer/colon-rectal-cancer/detection-diagnosis-staging/survival-rates.html

[6] Brenner, H., Kloor, M., & Pox, C. P. (2014). Colorectal cancer. *The Lancet*, 383(9927), 1490–1502. https://doi.org/10.1016/S0140-6736(13)61649-9

[7] Fearon, E. R., & Vogelstein, B. (1990). A genetic model for colorectal tumorigenesis. *Cell*, 61(5), 759–767. https://doi.org/10.1016/0092-8674(90)90186-I

[8] Issa, I., & Noureddine, M. (2017). Colorectal cancer screening: An updated review of the available options. *World Journal of Gastroenterology*, 23(28), 5086–5096. https://doi.org/10.3748/wjg.v23.i28.5086

[9] Litjens, G., Kooi, T., Bejnordi, B. E., Setio, A. A., Ciompi, F., Ghafoorian, M., ... & Sánchez, C. I. (2017). A survey on deep learning in medical image analysis. *Medical Image Analysis*, 42, 60–88. https://doi.org/10.1016/j.media.2017.07.005

[10] Siegel, R. L., Miller, K. D., Wagle, N. S., & Jemal, A. (2023). Cancer statistics, 2023. *CA: A Cancer Journal for Clinicians*, 73(1), 17–48. https://doi.org/10.3322/caac.21763

[11] Sung, H., Ferlay, J., Siegel, R. L., Laversanne, M., Soerjomataram, I., Jemal, A., & Bray, F. (2021). Global cancer statistics 2020: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. *CA: A Cancer Journal for Clinicians*, 71(3), 209–249. https://doi.org/10.3322/caac.21660

[12] Pacal, I., Karaboga, D., Basturk, A., Akay, B., & Nalbantoglu, U. A. (2020). A comprehensive review of deep learning in colon cancer. *Computers in Biology and Medicine*, 126, 104003. https://doi.org/10.1016/j.compbiomed.2020.104003

[13] Tummala, S., Kadry, S., Nadeem, A., Rauf, H. T., & Gul, N. (2023). An Explainable Classification Method Based on Complex Scaling in Histopathology Images for Lung and Colon Cancer. *Diagnostics*, 13(9), 1594. https://doi.org/10.3390/diagnostics13091594

[14] Hadiyoso, S., Aulia, S., & Irawati, I. D. (2023). Diagnosis of lung and colon cancer based on clinical pathology images using convolutional neural network and CLAHE framework. *International Journal of Applied Science and Engineering*, 20(1), 1–7. https://doi.org/10.6703/IJASE.202303_20(1).006

[15] Al-Jabbar, M., Alshahrani, M., Senan, E. M., & Ahmed, I. A. (2023). Histopathological Analysis for Detecting Lung and Colon Cancer Malignancies Using Hybrid Systems with Fused Features. *Bioengineering*, 10(3), 383. https://doi.org/10.3390/bioengineering10030383

[16] Singh, O., & Singh, K. K. (2023). An approach to classify lung and colon cancer of histopathology images using deep feature extraction and an ensemble method. *International Journal of Information Technology*, 15(8), 4149–4160. https://doi.org/10.1007/s41870-023-01487-1

[17] Provath, M. A. M., Deb, K., & Jo, K. H. (2023). Classification of Lung and Colon Cancer Using Deep Learning Method. *Communications in Computer and Information Science*, 1857, 56–70. https://doi.org/10.1007/978-981-99-4914-4_5

[18] Tan, M., & Le, Q. (2021). EfficientNetV2: Smaller models and faster training. *Proceedings of the 38th International Conference on Machine Learning*, PMLR 139, 10096–10106. https://arxiv.org/abs/2104.00298

[19] Iandola, F. N., et al. (2016). SqueezeNet: AlexNet-level accuracy with 50x fewer parameters and <0.5MB model size. *arXiv preprint*, arXiv:1602.07360.

[20] Sakr, A. S., et al. (2022). An Efficient Deep Learning Approach for Colon Cancer Detection. *Applied Sciences*, 12(17), 8450. https://doi.org/10.3390/app12178450