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Attention-Driven Lightweight Network For Colorectal Cancer Classification

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Abstract
Colorectal cancer (CRC) is a major cause of cancer-related deaths worldwide, making early and accurate diagnosis essential for improving patient outcomes. Although histopathological analysis remains the standard method for CRC diagnosis, manual examination of tissue images can be time-consuming, labor-intensive, and susceptible to variations in human interpretation. To address these limitations, this study presents an efficient attention-based deep learning framework built on the MobileNetV2 architecture for the automated classification of colorectal cancer histopathology images. The proposed model combines the lightweight nature of MobileNetV2 with attention refinement mechanisms to effectively identify and emphasize diagnostically important regions while learning both local and global discriminative features. A comparative evaluation is also conducted using the Xception model as a baseline architecture. Experimental findings indicate that the proposed attention-enhanced MobileNetV2 model delivers competitive, and in some cases improved, classification performance with lower computational requirements. Its lightweight design makes the framework particularly suitable for efficient and potentially real-time clinical implementation. The proposed approach can support pathologists in analyzing histopathological images, reduce diagnostic workload, and improve the consistency and reliability of colorectal cancer detection.

Keywords: *Colorectal Cancer, Histopathology Images, Deep Learning, MobileNetV2, Attention Mechanism, Xception, Image Classification, Automated Diagnosis, Cancer Detection, Lightweight Neural Network.*

1. Introduction

Colorectal cancer (CRC) remains a significant global health concern and continues to contribute substantially to cancer-related morbidity and mortality. The increasing burden of colorectal cancer has created a strong requirement for effective approaches that can support timely detection and accurate diagnosis. Epidemiological investigations have reported substantial variation in colorectal cancer incidence across populations and have also highlighted changes in disease occurrence among younger individuals. These developments have increased the importance of improving diagnostic pathways and developing technologies that can assist healthcare professionals in recognizing colorectal abnormalities at an earlier stage [1], [2].

The occurrence of colorectal cancer is influenced by a combination of demographic, lifestyle, dietary, environmental, and genetic factors. Changes in dietary habits, physical activity, obesity, smoking, alcohol consumption, and other environmental exposures have been associated with variations in colorectal cancer susceptibility. In addition, the increasing occurrence of colorectal cancer among younger populations has generated additional interest in understanding the factors associated with early-onset disease [3], [4]. These circumstances emphasize the need for diagnostic systems that can process medical information efficiently while providing consistent results.

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Histopathological examination remains an important component of colorectal cancer diagnosis because tissue morphology provides detailed information about cellular and structural abnormalities. However, the examination of large numbers of histopathology images can be demanding for pathologists. The interpretation process requires considerable expertise and concentration, and differences in visual judgment may result in variations between observers. As digital pathology continues to develop, computational analysis of tissue images has therefore emerged as an important research direction for assisting pathologists in identifying diagnostically relevant patterns.

Artificial intelligence has introduced new possibilities for automated histopathological image analysis. Machine learning algorithms can identify relationships within complex medical datasets, while deep learning models can automatically learn hierarchical visual representations from images. Wang et al. demonstrated the potential of artificial intelligence for colorectal cancer diagnosis using histopathological images, illustrating how learned image representations can support automated recognition of cancer-related tissue characteristics [5]. Such developments indicate that deep learning can potentially complement conventional pathological assessment by providing an additional computational interpretation of digitized tissue images.

The effectiveness of deep learning in medical image analysis is strongly influenced by the architecture used for feature extraction and classification. Conventional deep convolutional neural networks can learn detailed spatial patterns but may require substantial computational resources and memory. This can create difficulties when deploying sophisticated models in environments where computational resources are limited. Rana and Bhushan reviewed the application of machine learning and deep learning methods to medical image analysis and highlighted the growing role of deep neural architectures in automated diagnosis and detection tasks [6].

For colorectal histopathology, the ability to identify diagnostically meaningful regions is particularly important because tissue images contain large numbers of structures that may not contribute equally to classification. Background regions and visually similar tissue structures can introduce irrelevant information into the learning process. An attention mechanism can address this issue by assigning greater importance to informative image regions or feature channels while reducing the influence of less useful representations. Attention-driven feature refinement therefore provides an opportunity to improve the discriminative capability of a lightweight classification network.

MobileNetV2 provides a suitable foundation for developing such a lightweight system. Its inverted residual structure and linear bottleneck design enable efficient feature extraction with substantially lower computational requirements than many conventional deep architectures. Integrating an attention mechanism with MobileNetV2 can provide a balance between computational efficiency and discriminative feature learning. The attention component can refine the features generated by the backbone so that diagnostically relevant patterns receive greater emphasis during classification.

In addition to computational efficiency, model reliability is an important consideration in medical image classification. A useful automated system should not only achieve high overall classification accuracy but should also demonstrate balanced behavior across different classes. Metrics such as precision, recall, F1-score, and confusion matrices are therefore important for determining whether a model consistently recognizes the relevant diagnostic categories. Machine learning-based clinical decision systems have increasingly emphasized the need for appropriate evaluation and careful interpretation of automated predictions [7].

The present study proposes an **Attention-Driven Lightweight Network for Colorectal Cancer Classification** based on MobileNetV2. The proposed framework integrates a lightweight convolutional backbone with attention-based feature refinement to identify and emphasize diagnostically significant regions in colorectal histopathology images. The study also considers Xception as a comparative baseline to examine the trade-off between classification capability and computational requirements. By combining efficient feature extraction with attention-guided representation learning, the proposed framework aims to provide an effective approach for automated colorectal cancer image classification.

The principal objective of this research is to develop a computationally efficient classification framework that can learn discriminative local and global characteristics from colorectal histopathology images while maintaining a relatively lightweight architecture. The proposed approach is intended to support pathologists by reducing repetitive image-analysis workload and providing consistent computer-assisted classification. Such a system is not intended to replace pathological expertise but rather to provide an additional analytical mechanism that may contribute to efficient and reliable colorectal cancer assessment.

2. Literature Review

2.1 Colorectal Cancer Epidemiology and Diagnostic Challenges

C. Mattiuzzi, F. Sanchis-Gomar, and G. Lippi examined the epidemiological characteristics of colorectal cancer and provided an updated overview of disease occurrence and associated trends. Their study demonstrates the continuing importance of colorectal cancer as a major health problem and provides an epidemiological basis for research directed toward improving prevention, detection, and diagnosis. The changing distribution of colorectal cancer across populations reinforces the need for effective diagnostic approaches capable of supporting healthcare systems facing an increasing disease burden [1].

Y. Xi and P. Xu investigated the worldwide burden of colorectal cancer and projected future trends in disease incidence. Their analysis emphasized the substantial scale of colorectal cancer and the expected increase in the global disease burden. The findings provide strong motivation for developing efficient diagnostic technologies because growing patient numbers may increase the demand for pathological and imaging-based assessment. Automated image-analysis approaches may help address some of the workload associated with large-scale cancer diagnosis [2].

A. G. Russo et al. investigated the incidence of colon cancer among individuals younger than 50 years using long-term cancer registry data from Milan, Italy. Their analysis reported an increasing occurrence of colon cancer among younger individuals and highlighted the importance of understanding changes in disease patterns. The emergence of early-onset colorectal cancer further strengthens the need for diagnostic systems that can support timely recognition of pathological abnormalities across different age groups [3].

2.2 Risk Factors and Early-Onset Colorectal Cancer

N. Murphy et al. examined lifestyle, dietary, and environmental factors associated with colorectal cancer susceptibility. Their work demonstrates that colorectal cancer develops within a complex interaction of multiple contributing factors rather than through a single identifiable cause. Understanding these factors is important for prevention and risk assessment, while automated diagnostic systems can complement such approaches by focusing on the identification of pathological changes within tissue images [4].

A. O. Adigun et al. reviewed causes and prevention strategies associated with early-onset colorectal cancer. Their work draws attention to the changing epidemiological profile of colorectal cancer and the importance of identifying individuals at risk at earlier ages. The study also reinforces the need for improved awareness, preventive strategies, and diagnostic pathways capable of responding to the increasing occurrence of colorectal cancer in younger populations [8].

2.3 Artificial Intelligence in Histopathological Diagnosis

K. S. Wang et al. investigated artificial intelligence-based colorectal cancer diagnosis using histopathology images. Their research demonstrated the potential of computational image analysis to recognize cancer-related characteristics from tissue images. The study is particularly relevant to automated colorectal cancer classification because histopathological images contain complex cellular and tissue structures that can be difficult to characterize comprehensively using manually designed features. Deep learning provides an opportunity to learn these representations directly from image data [13].

M. Rana and M. Bhushan reviewed machine learning and deep learning techniques used for medical image analysis, covering applications ranging from disease detection to diagnosis. Their work illustrates the transition from conventional feature engineering toward deep representation learning. Deep neural networks can automatically construct hierarchical features from medical images, reducing the dependence on manually selected descriptors and enabling models to learn complex visual patterns from large image collections [14].

2.4 Machine Learning for Clinical Decision Support

L. Adlung, Y. Cohen, U. Mor, and E. Elinav examined the role of machine learning in clinical decision-making. Their study highlights both the opportunities and considerations associated with integrating machine learning into healthcare workflows. For medical image classification, this perspective is important because high predictive performance alone is not sufficient; models must also be evaluated carefully and integrated into clinical processes in a manner that supports rather than replaces professional judgment [24].

W. Hamilton and S. E. R. Bailey investigated diagnostic pathways for symptomatic patients with colorectal cancer and emphasized the importance of improving the process through which suspected cases

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are identified and investigated. Their work highlights the challenges associated with timely diagnosis and the potential value of approaches that can support healthcare professionals in handling diagnostic workloads more effectively. Automated histopathological image classification can potentially contribute to this broader diagnostic-support process [11].

2.5 Lightweight Deep Learning for Medical Image Analysis

The increasing complexity of medical image datasets has encouraged researchers to investigate architectures that provide strong feature-learning capability without requiring excessive computational resources. Lightweight networks are particularly attractive for applications where hardware resources, memory, or processing time are constrained. MobileNetV2 is designed around efficient convolutional operations, inverted residual connections, and linear bottlenecks, making it suitable as a backbone for computationally efficient image classification. In a colorectal histopathology setting, its lightweight structure can provide a practical foundation for developing systems intended for rapid inference.

The use of attention mechanisms can further improve a lightweight architecture by allowing the model to prioritize informative representations. Histopathology images contain regions with different levels of diagnostic relevance, and treating all feature responses equally may reduce classification efficiency. An attention module can selectively enhance important spatial or channel-level information and suppress less informative responses. Combining such refinement with MobileNetV2 provides the basis for the proposed attention-driven architecture.

2.6 Comparative Deep Learning Architecture

A comparison with a larger convolutional architecture can help determine whether the proposed lightweight approach provides an appropriate balance between predictive capability and computational efficiency. **Xception** provides a useful baseline because it employs depthwise separable convolution and has demonstrated strong feature-learning capability in image classification tasks. Comparing Xception with an attention-enhanced MobileNetV2 architecture allows the study to examine whether attention refinement can enable a lightweight model to achieve competitive performance while maintaining lower computational requirements.

Overall, the reviewed literature demonstrates a progression from epidemiological studies establishing the increasing burden of colorectal cancer toward artificial intelligence approaches capable of supporting automated diagnosis. Existing research confirms the potential of deep learning for histopathological image analysis, while machine learning literature emphasizes the importance of reliable evaluation and clinical integration. However, there remains a practical need for models that combine strong discriminative feature learning with computational efficiency. The proposed Attention-Driven Lightweight Network addresses this requirement by integrating MobileNetV2 with attention-based feature refinement and evaluating its performance against Xception as a comparative deep learning architecture.

Proposed System

The proposed system introduces an attention-driven lightweight deep learning framework for automated classification of colorectal cancer histopathology images. The primary objective is to develop a model that can learn discriminative tissue characteristics while maintaining lower computational requirements than relatively complex deep convolutional architectures. Histopathology images contain heterogeneous cellular structures, tissue patterns, nuclei distributions, and staining variations, and not all regions contribute equally to the classification decision. The proposed framework therefore combines the efficient feature extraction capability of MobileNetV2 with an attention mechanism that adaptively emphasizes diagnostically informative representations. Xception is employed as a baseline architecture to establish a comparative reference for evaluating the effectiveness of the proposed lightweight model.

The proposed framework begins with the acquisition of colorectal cancer histopathology images from a suitable dataset such as NCT-CRC-HE-100K or another appropriately authorized clinical dataset. The images are organized according to their corresponding tissue or diagnostic categories before model development. Since histopathology datasets may contain variations in staining, magnification, resolution, illumination, and tissue appearance, appropriate preprocessing is performed before the images are supplied to the neural networks. The dataset is also examined for corrupted, duplicated, or unsuitable samples to minimize the introduction of irrelevant information during model training. Where patient-level information is available, samples associated with the same patient are maintained within a single data partition to reduce the possibility of information leakage.

The preprocessing stage standardizes the histopathology images for deep learning analysis.

Images are resized to dimensions compatible with the selected network architectures, and pixel values are normalized to improve numerical stability during optimization. Because staining variations can occur between slides and acquisition environments, stain normalization is incorporated to reduce differences in color distribution while preserving diagnostically meaningful tissue structures. This step is particularly important for histopathological analysis because variations in staining intensity may otherwise become unintended features learned by the model. The preprocessing pipeline is designed to retain cellular morphology, tissue organization, and structural characteristics that are relevant to colorectal cancer classification.

Large histopathology images can contain substantially more visual information than can be processed directly by conventional CNN input layers. Therefore, the proposed framework employs image patch generation to divide large tissue images into smaller regions suitable for model processing. Patch extraction enables the networks to examine localized tissue structures at a consistent spatial scale. These patches may contain diagnostically relevant characteristics such as cellular arrangement, nuclear morphology, glandular organization, epithelial patterns, and local texture. Regions containing predominantly background information can be excluded where appropriate, thereby reducing unnecessary computational processing and allowing the learning process to concentrate on tissue-containing regions.

To improve generalization, data augmentation is applied to the training images. Controlled transformations such as rotation, horizontal and vertical flipping, translation, scaling, zooming, and contrast variation can be used to generate additional training representations. These transformations increase the diversity of the training data and reduce the likelihood that the proposed network will learn patterns that are specific to individual image orientations or acquisition conditions. Augmentation is restricted to the training subset, while validation and test images are retained independently to provide an unbiased evaluation of the final model.

The dataset is subsequently divided into training, validation, and testing subsets. A representative partition may be established according to the size and distribution of the available dataset, with stratification used to preserve the relative distribution of tissue categories across the subsets. The training data are used for model parameter optimization, the validation data are used for hyperparameter selection and monitoring of generalization, and the independent test set is used for final performance assessment. Where possible, patient-level separation is maintained between the subsets to ensure that the reported performance represents the ability of the model to classify previously unseen cases rather than previously observed tissue from the same patient.

The proposed architecture uses MobileNetV2 as its lightweight feature extraction backbone. MobileNetV2 is designed to provide efficient deep feature learning through inverted residual blocks and linear bottleneck structures. These architectural characteristics reduce computational requirements while retaining the ability to construct hierarchical representations from input images. In the proposed framework, the early layers of MobileNetV2 learn low-level characteristics such as edges, intensity transitions, color patterns, and local textures, whereas deeper layers progressively learn more abstract representations associated with tissue morphology and structural organization.

Although MobileNetV2 provides computational efficiency, conventional convolutional feature extraction does not explicitly distinguish between highly informative and less informative feature responses. To address this limitation, an attention mechanism is incorporated into the proposed architecture. The attention module learns feature importance from the intermediate representations generated by MobileNetV2 and selectively enhances features that contribute more strongly to the classification task. Depending on the experimental configuration, a channel-attention mechanism such as Squeeze-and-Excitation can be integrated into selected feature blocks, allowing the network to emphasize informative feature channels and suppress less useful responses.

Let F represent an intermediate feature map generated by the MobileNetV2 backbone. The attention mechanism generates an attention weighting function $A(F)$, which is applied to the original representation to obtain an enhanced feature map:

$$F_{att}=A(F)\odot F$$

where F_{att} represents the attention-refined feature representation and $\odot$ denotes element-wise multiplication. Through this process, feature responses associated with diagnostically relevant tissue characteristics can receive greater emphasis. The resulting representation is subsequently passed to the deeper layers of the network for further feature extraction and classification.

The attention mechanism is intended to improve the ability of the lightweight backbone to distinguish relevant tissue morphology from less informative

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image content. In colorectal histopathology, diagnostically meaningful patterns may occur at different spatial scales, ranging from cellular-level characteristics to broader tissue organization. Attention-based feature refinement can therefore help the network prioritize feature responses associated with cellular arrangement, nuclear distribution, glandular structures, tissue boundaries, and other morphological characteristics relevant to the classification task. This provides a mechanism for increasing the discriminative capability of a lightweight architecture without substantially increasing its computational complexity.

Following feature extraction and attention refinement, the resulting feature representation is converted into a compact vector using Global Average Pooling. This operation summarizes the spatial information within each feature channel and reduces the dimensionality of the representation. The resulting vector is passed through the classification head, which maps the learned representation to the target colorectal tissue categories. For multiclass classification, a Softmax activation function is employed to generate class probabilities, and the category associated with the highest probability is selected as the final prediction.

Transfer learning is incorporated to improve the effectiveness of model training when the available histopathology dataset is limited compared with the size of datasets typically required for training deep networks from random initialization. A pretrained MobileNetV2 model is initially used as the feature extraction backbone, after which its original classification layer is replaced by a task-specific classification head. During the initial training phase, selected backbone layers may be frozen while the newly introduced layers are optimized for the colorectal histopathology classification task. Subsequently, selected deeper layers are unfrozen and fine-tuned using a relatively low learning rate to adapt the learned visual representations to the characteristics of colorectal tissue images.

For comparative analysis, an Xception-based model is developed using the same dataset and preprocessing strategy. Xception provides a strong deep learning baseline because its depthwise separable convolution structure allows it to learn rich visual representations while maintaining greater efficiency than some conventional convolutional architectures. However, its overall model complexity can remain higher than that of MobileNetV2. Comparing the two architectures under similar experimental conditions enables the study to determine whether the proposed attention-enhanced lightweight architecture can achieve competitive classification performance with reduced computational requirements.

Both models are trained using the same training and validation framework to ensure a fair comparison. During training, batches of histopathology patches are passed through the network, and the predicted class probabilities are compared with the corresponding ground-truth labels. Categorical cross-entropy can be used as the classification loss for multiclass classification. The Adam optimizer is employed to update the trainable parameters based on the calculated gradients. Validation performance is monitored after each training epoch, and learning-rate adjustment and early stopping can be incorporated when validation performance reaches a plateau or begins to deteriorate.

Overfitting is controlled through a combination of data augmentation, transfer learning, validation monitoring, regularization, early stopping, and controlled fine-tuning. These strategies are particularly important because histopathology datasets may contain visually similar samples and correlated patches originating from the same tissue image. The model selection process is therefore based on validation performance rather than training accuracy alone. The final model is evaluated using an independent test dataset that is not involved in parameter optimization.

The performance of the proposed model is assessed using accuracy, precision, recall, F1-score, and Area Under the Curve (AUC), where applicable. Accuracy provides an overall measure of correctly classified samples, while precision indicates the reliability of the predictions assigned to each class. Recall measures the ability of the model to identify samples belonging to the relevant class, and the F1-score provides a combined measure of precision and recall. A confusion matrix is also generated to examine class-specific predictions and identify categories that are frequently confused by the model.

Because computational efficiency is a central objective of the proposed framework, the experimental evaluation also considers model complexity and inference efficiency. The number of trainable parameters, model size, computational requirements, and inference time are compared between the MobileNetV2-attention architecture and the Xception baseline. This comparison provides a more comprehensive assessment than accuracy alone because a clinically useful computational model should ideally provide reliable predictions without imposing excessive hardware or processing requirements.

International Journal of Artificial Intelligence and Communication Networks
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To further investigate the behavior of the proposed attention mechanism, visualization techniques such as Grad-CAM and attention heatmaps can be employed. These techniques provide visual information regarding the image regions or feature responses that contribute most strongly to the model's prediction. In the context of colorectal histopathology, such visualization can help determine whether the network is concentrating on tissue regions containing meaningful morphological characteristics rather than background areas or image artifacts. Interpretability analysis therefore provides an additional perspective for assessing the reliability of the learned representations.

The complete proposed framework can be summarized as a sequence of **histopathology image acquisition, image quality assessment, preprocessing, stain normalization, patch generation, data augmentation, dataset partitioning, MobileNetV2 feature extraction, attention-based feature refinement, global feature aggregation, classification, and performance evaluation**. In parallel, the Xception architecture is trained under comparable conditions and used as a baseline for performance comparison. The experimental results are analyzed in terms of both predictive performance and computational efficiency to determine whether the proposed attention-driven lightweight architecture provides an effective alternative to a comparatively larger deep learning model.

The proposed system is ultimately intended to provide an efficient computer-assisted approach for colorectal cancer histopathology image classification. By combining the lightweight structure of MobileNetV2 with attention-guided feature refinement, the framework aims to achieve an effective balance between discriminative capability and computational efficiency. The inclusion of Xception as a baseline enables objective evaluation of this trade-off, while attention visualization provides additional insight into the learned representations. The proposed framework is designed as a decision-support technology and is not intended to replace expert pathological examination or established clinical diagnostic procedures.

3. Design Engineering

Design Engineering deals with the various UML [Unified Modelling language] diagrams for the implementation of project. Design is a meaningful engineering representation of a thing that is to be built. Software design is a process through which the requirements are translated into representation of the software. Design is the place where quality is rendered in software engineering.

System Architecture

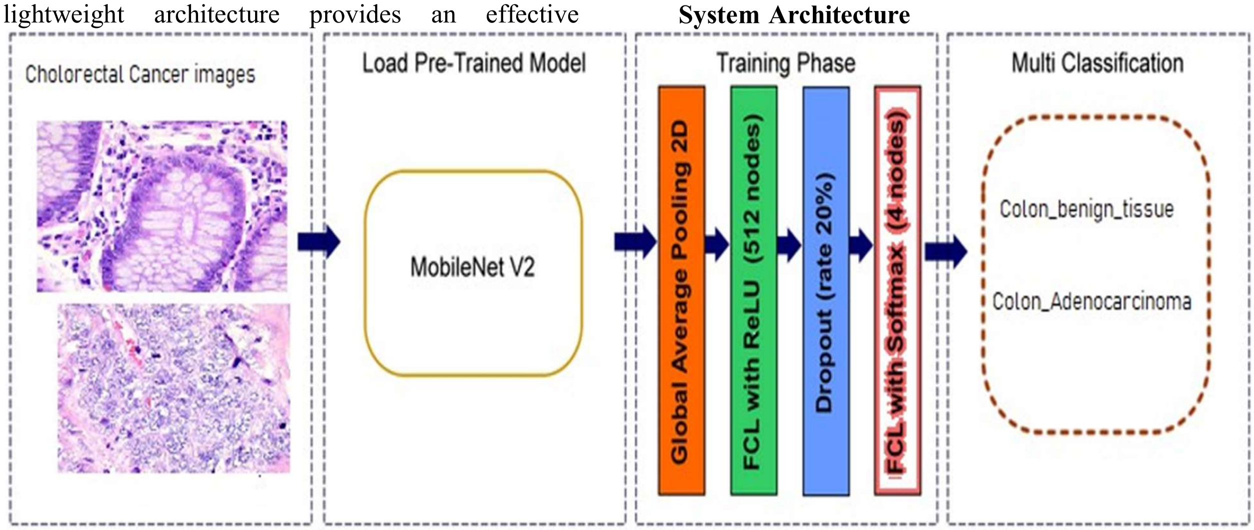

Fig 1: System Architecture

Python And Libraries Used

Python is a high-level, interpreted, interactive, and object-oriented programming language that is widely used in software development, data analysis, artificial intelligence, machine learning, and web applications. One of its major strengths is its simple and readable syntax, which makes programs easier to understand, develop, and maintain. Python uses clear English-like keywords and avoids unnecessary syntactic complexity, making it suitable for both beginners and experienced developers. Its flexibility and extensive ecosystem of libraries have made it one of the most commonly used programming languages for developing intelligent and data-driven applications.

History Of Python

Python was created by Guido van Rossum during the late 1980s and was introduced as a programming language in the early 1990s. Its development began at the Centrum Wiskunde & Informatica, a research institute for mathematics and computer science in the Netherlands. The language was influenced by several earlier programming languages, including ABC, Modula-3, C, C++, Algol-68, Smalltalk, and Unix-based scripting languages. Over time, Python evolved into a powerful general-purpose language supported by a large international development community. Being open source, Python can be freely used, modified, and improved according to its licensing terms. Although Guido van Rossum played a central role in the original development and growth of Python, the language is now continuously maintained and enhanced by a global community of developers.

Importance Of Python

Python is important in modern software development because of its simplicity, versatility, and support for multiple programming approaches. As an interpreted language, Python allows programs to be executed through an interpreter, making development and testing convenient. It also provides an interactive environment in which programmers can execute commands directly and observe the results immediately, which is particularly useful for experimentation and debugging. Python supports object-oriented programming through concepts such as classes, objects, inheritance, and encapsulation, allowing developers to organize complex applications effectively. Its simple syntax and easy-to-understand structure make it highly suitable for beginners, while its powerful libraries and frameworks enable the development of advanced applications involving artificial intelligence, machine learning, web development, scientific computing, and data processing.

Libraries Used In Python

Several Python libraries are used in the proposed colorectal cancer histopathology image classification system. NumPy is used for numerical computations and efficient handling of multidimensional arrays, particularly when converting and processing image data. Pandas is used for managing structured data and handling user information through DataFrames and Excel files. Matplotlib is useful for generating graphs, charts, and visual representations that can support data analysis and result presentation. Scikit-learn provides a collection of machine learning algorithms and utilities that are useful for data preprocessing, analysis, and evaluation.

The implementation also uses TensorFlow and Keras for loading and executing the trained deep learning model used for image classification. The Pillow library is employed to open, convert, resize, and process the uploaded histopathological images before prediction. Flask is used to develop the web-based application and manage functions such as routing, request handling, template rendering, file uploading, and session management. Werkzeug provides security functions for generating password hashes and verifying user credentials during authentication. In addition, OpenPyXL is used to read and write Excel files that store user-related information. Together, these libraries provide the required environment for implementing the web application and integrating the deep learning model for automated colorectal cancer image classification.

Figure: 2 NumPy, Pandas, Matplotlib, and Scikit-learn

4. Implementation

The proposed colorectal cancer histopathology image classification system is implemented using Python and the Flask web framework. The implementation combines web application functionality with a trained deep learning model to provide an automated image classification platform. The system allows users to register and log in securely before accessing the image prediction functionality. Once authenticated, a user can upload a histopathological image, which is processed and analyzed by the trained convolutional neural network model. The final prediction is then displayed through the web interface. The implementation uses several Python libraries, including Flask for web development, NumPy for numerical operations, Pandas for data management, Pillow for image processing, TensorFlow and Keras for deep learning inference, and Werkzeug for password security.

The Flask application is initialized as the central component of the web-based system. A secret key is configured to enable session management, allowing the application to maintain the authentication status of users while they navigate through different pages. Separate directories are also configured for storing user information and uploaded images. The user information is maintained in an Excel file, while the uploaded histopathological images are stored in a designated folder within the application. The required directories are created automatically when they are not already present, ensuring that the application has the necessary storage structure before processing user data and images.

The trained convolutional neural network model is loaded from the saved model file named best_model.h5. The system uses an input image size of 224 × 224 pixels, ensuring that every uploaded image has the same dimensions before it is passed to the model. The classification system is configured to identify two categories of colorectal tissue, namely colon_benign_tissue and colon_adenocarcinoma. The model receives the processed image as input and generates a prediction that is used to determine the corresponding tissue category.

Before classification, every uploaded image undergoes a preprocessing procedure. The image is first opened using the Pillow library and converted to RGB format to maintain consistency among the input samples. It is then resized to the required dimensions of 224 × 224 pixels. After resizing, the image is converted into a NumPy array, and its pixel values are normalized by dividing them by 255. This operation transforms the pixel values into a range between 0 and 1, which is suitable for processing by the trained neural network. Finally, an additional dimension is added to the image array to represent the batch dimension required by the model during prediction.

The home page acts as the main entry point to the web application and provides access to the available system functions. The registration module allows new users to create an account by entering a username, email address, password, and password confirmation. During registration, the application verifies that the entered password and confirmation password are identical. If the user information file already exists, the system checks whether the selected username is already registered. If the username is available, the password is converted into a secure hash using the password hashing functionality provided by Werkzeug. The new user information, including the username, email address, and hashed password, is then stored in the Excel file. After successful registration, the user is redirected to the login page.

The login module is responsible for verifying the credentials of registered users. When a user enters a username and password, the application reads the stored user information from the Excel file and searches for the corresponding username. If a matching user record is found, the stored password hash is compared with the password entered by the user. When the credentials are successfully verified, the application creates a session containing the username and redirects the user to the image prediction page. If the username or password is invalid, an appropriate error message is displayed. This authentication mechanism helps restrict access to the prediction functionality and provides a basic level of security for the web application.

The image prediction module is the main functional component of the proposed system. When an authenticated user uploads an image, the application first verifies that a valid file has been selected. The uploaded image is then saved in the configured upload directory. After saving the image, the preprocessing function converts the image into the required format and dimensions. The processed image is passed to the trained deep learning model, which produces a prediction value. Based on the defined classification threshold, the system determines whether the uploaded image belongs to the benign colon tissue category or the colon adenocarcinoma category. The predicted class and confidence value are then sent to the prediction page and displayed to the user along with the uploaded image.

The application also includes additional routes for the About page, an additional information page, and a chart page. The About pages provide information related to the application and its functionality. The chart page is protected through session verification, meaning that users must be logged in before accessing it. If a valid user session is not available, the application redirects the user to the login page. This approach ensures that certain application features remain accessible only to authenticated users.

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5. Results

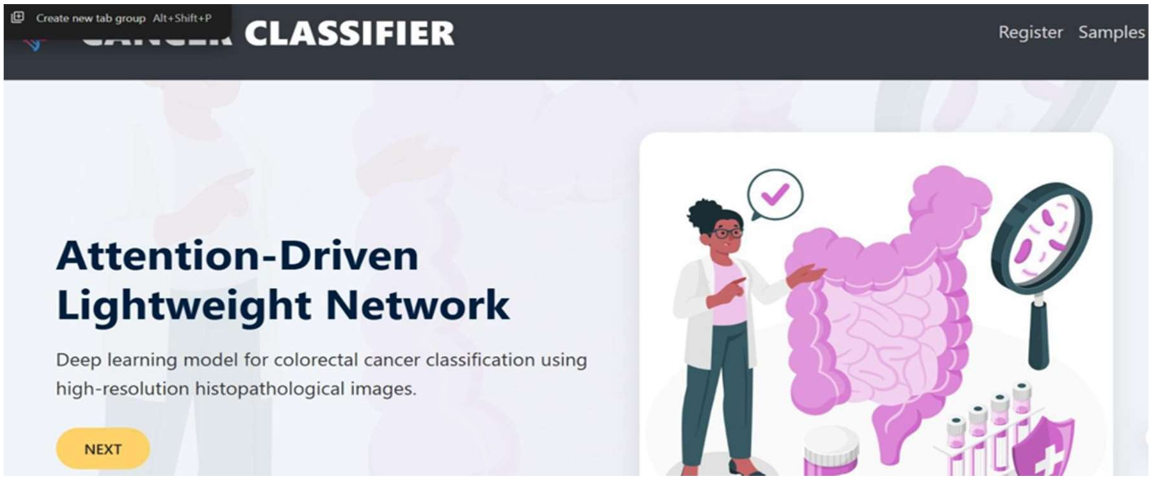

Fig 3

Fig 4

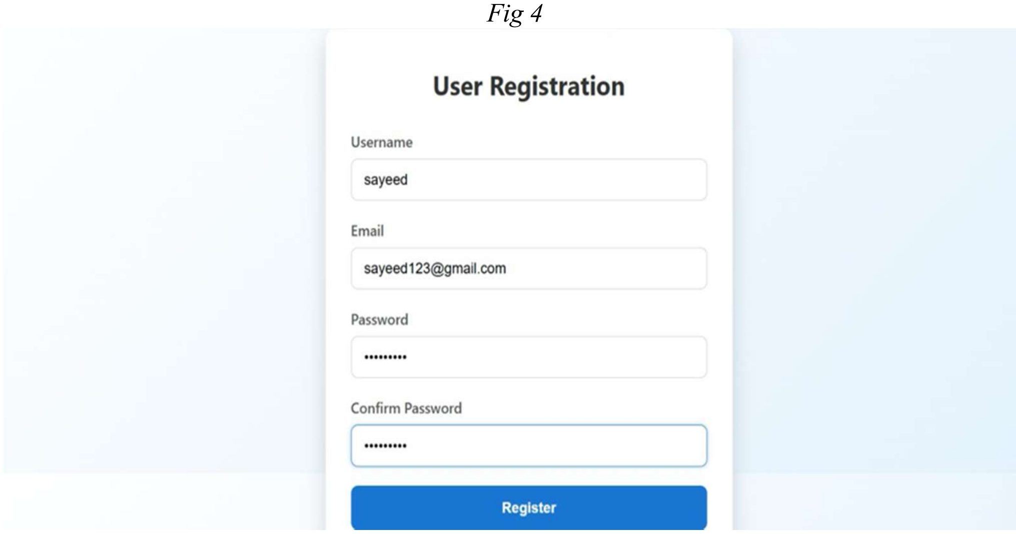

Fig 5

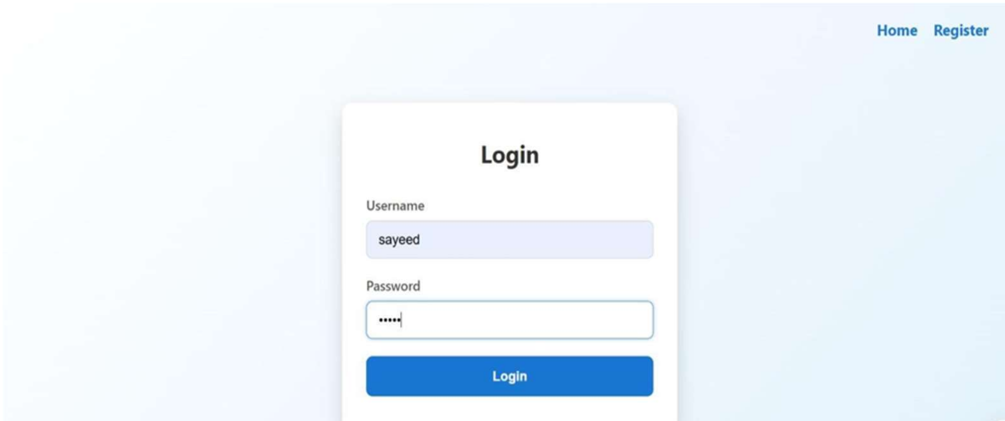

Fig 6

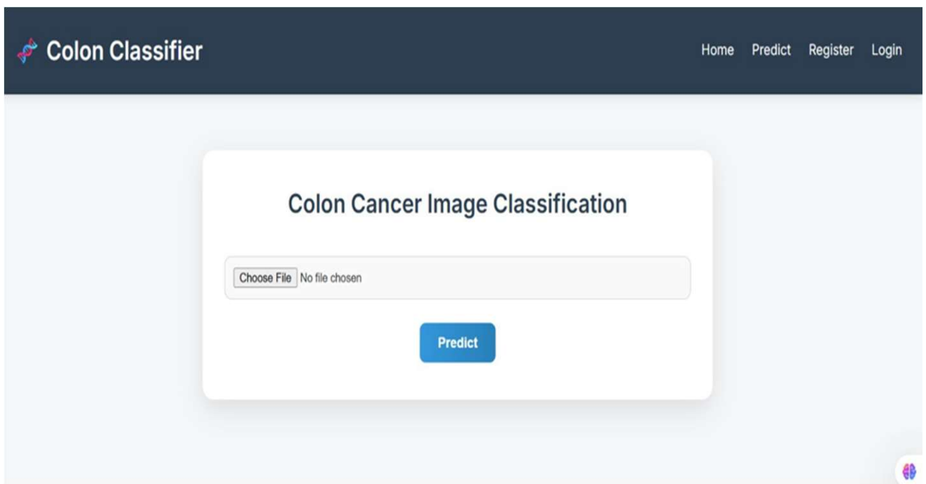

Fig 7

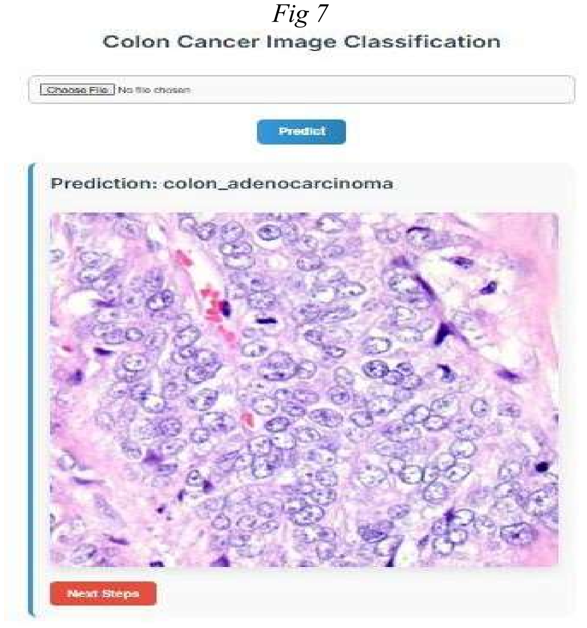

Fig 8

International Journal of Artificial Intelligence and Communication Networks
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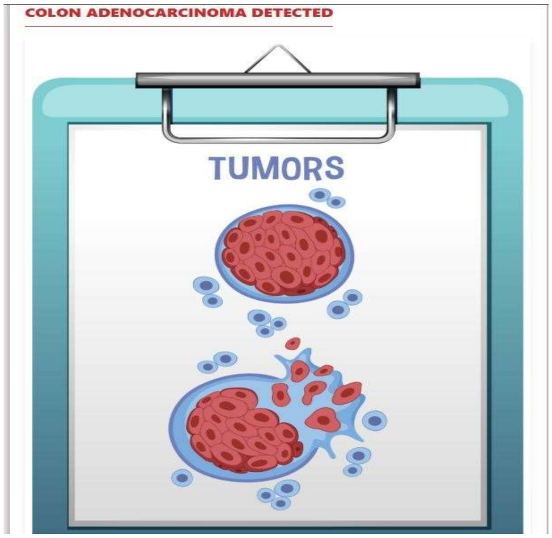

Fig 9

Fig 10

Software Testing

The purpose of testing is to discover errors. Testing is the process of trying to discover every conceivable fault or weakness in a work product. It provides a way to check the functionality of components, sub-assemblies, assemblies and/or a finished product it is the process of exercising software with the intent of ensuring that the Software system meets its requirements and user expectations and does not fail in an unacceptable manner. There are various types of test. Each test type addresses a specific testing requirement.

Developing Methodologies

The test process is initiated by developing a comprehensive plan to test the general functionality and special features on a variety of platform combinations. Strict quality control procedures are used. The process verifies that the application meets the requirements specified in the system requirements document and is bug free. The following are the considerations used to develop the framework from developing the testing methodologies.

has bugs can be identified and can be rectified from errors.

Future Enhancements

The proposed attention-driven lightweight deep learning model has shown promising results in the classification of colorectal cancer (CRC) using histopathological images. However, several enhancements can be implemented in future to further improve its performance, scalability, and clinical usability. Firstly, the current model is trained on static image patches; in the future, it can be extended to handle whole-slide images (WSIs) with region-based attention and tiling techniques to better mimic clinical diagnosis. Integration of multi-modal data, such as combining histopathological images with clinical records and genomic information, can provide a more holistic diagnostic system. Additionally, a self-supervised or semi-supervised learning approach can be introduced to leverage large volumes of unlabeled data, reducing dependency on costly manual annotations.Incorporating vision transformers (ViT) or hybrid CNN-transformer architectures could enhance the model's ability to learn global context more effectively. Furthermore, deploying the model as a web or mobile application for real-time diagnostics would increase accessibility in remote and resource-constrained areas. Explainability modules, such as Grad-CAM or attention heatmaps, can be improved to generate more intuitive and pathologist-friendly visual interpretations. The model can also be trained for multi-class classification to differentiate between various stages or types of colorectal abnormalities.To ensure adaptability, transfer learning can be explored for fine-tuning the model on related cancers like gastric or esophageal cancer. Model optimization techniques such as pruning, quantization, and edge AI deployment can make the solution more scalable for embedded systems. Future work may also involve collaboration with clinical institutions to validate the model on diverse, real-world datasets. Finally, active learning frameworks can be implemented, allowing the model to interactively query the pathologist for labeling difficult cases, thus continually improving its performance. These enhancements would collectively push this system closer to real-world clinical integration and broader impact in the field of AI-powered cancer diagnostics.

Conclusion

In this project, an efficient and attention-enhanced deep learning framework has been proposed for the classification of colorectal cancer (CRC) using histopathological images. By integrating the lightweight MobileNetV2 architecture with attention mechanisms, the model effectively captures both local and global tissue features while maintaining computational efficiency. This design not only improves classification accuracy but also enhances the interpretability of the results by highlighting diagnostically relevant regions. Compared to heavier models like Xception, the proposed model demonstrates a strong balance between performance and resource consumption, making it ideal for deployment in real-time, low-resource medical settings. The study reinforces the potential of AI-assisted diagnostic tools in reducing the workload of pathologists and improving early cancer detection. While the results are promising, this research also opens doors for future advancements in scalability, multi-modal integration, and clinical validation.

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