Svedberg Open
DISSEMINATION OF KNOWLEDGE

International Journal of Artificial Intelligence and Machine Learning

Publisher's Home Page: https://www.svedbergopen.com/

Research Paper Open Access

Transformer Gated Fusion Network For Predicting Lung And Colon Cancer

O.S.Deepa and Pranav Mohan

Department of Mathematics, Amrita School of Physical Sciences , Coimbatore, Amrita Vishwa Vidyapeetham, India.

Abstract
Cancer remains one of the leading causes of mortality worldwide. Recent studies have demonstrated that hybrid deep learning models can effectively detect lung and colon cancers by analysing complex histopathological images, highlighting their potential to support accurate and efficient cancer diagnosis. The system integrates machine learning with deep learning using ResNet18 to extract image features, which then interact with classifiers and transformer networks for information fusion. Integrating XGBoost with ResNet18 achieved high classification accuracy, followed by deep learning-based information fusion approaches involving CNNs and Transformers. The highest accuracy was obtained by integrating wavelet-based feature extraction with CNN and Transformer architectures, outperforming the standalone deep learning models. These findings highlight the promising potential of hybrid and multimodal approaches for medical diagnosis. Further improvements in these techniques are essential to enhance diagnostic accuracy and reduce the likelihood of errors in clinical decision-making.

Keywords: Cancer Classification, Histopathological Image Analysis, Hybrid Deep Learning, Convolutional Neural Networks, Transformer Networks, Gated Fusion Mechanism, Wavelet Transform, XGBoost.

1 Introduction

The automated analysis of histopathology slides is revolutionizing oncology with rapid and accurate diagnosis of cancer. The two most prevalent causes of death globally include lung and colon cancer, with the time taken before initiating therapy being crucial for their prognosis. Early detection is a critical factor in enhancing patients' survival rates, while the existing manual method of examining tissue samples entails several challenges. The task requires substantial cognitive engagement and the need to recognize minuscule cellular features, making manual annotation highly cumbersome and subjective among pathologists.

Recently, artificial intelligence-based methods have been used in computational pathology to overcome these human limitations. CNNs are currently a gold standard, primarily due to their ability to capture multi-level spatial hierarchies of information like those of visual experts. However, CNN models usually ignore the global view of images and focus only on the local pixel level. This drawback has led to the development of ViT models that leverage self-attention mechanisms to comprehend long-term dependency patterns in data.

The combination of CNNs that recognize minute details at the local level with Transformers that establish the relationship between features at a broader and global level forms a potent combination for use in medical image processing. The hybrid architectures attempt to bridge the gap between cellular structures and larger tissue structures by establishing a more robust framework that can distinguish between benign and malignant tissues. In this paper, the development of an end-to-end classification model is explored using various machine learning and deep learning frameworks.

1.1 Motivation

The primary motivation behind the research presented here lies in the enormous global burden of cancer cases and death rates. Since the diagnosis of lung and colon cancers depends heavily on the timing of the discovery, fast and reliable methods of diagnosis are crucial for saving patients' lives. Traditionally, cancer diagnosis has been performed manually via microscopic examination, and despite being the most efficient way at some point in time, it is currently deemed insufficient due to being too slow and highly dependent on human efforts. Hence, there is an obvious necessity of developing new automated medical image analysis tools capable of processing large volumes of data quickly.

In terms of the development of computational intelligence, one can speak of the importance of creating hybrid approaches to artificial intelligence that allow for integrating feature extraction and broader reasoning. The idea of using different algorithms of machine learning is extremely helpful in solving the problem of algorithmic narrow-mindedness. Overall, the research presented here was prompted by the desire to create an approach to diagnosing cancer that would provide high levels of accuracy and precision, helping pathologists to perform their tasks easily.

1.2 Contribution

The main objective of the current investigation is to develop an enhanced hybrid model by integrating convolutional networks, Transformer layers, and Wavelet transformation to optimize histopathology image processing. To successfully integrate these diverse data sources, we propose a gated fusion method to effectively balance various feature vectors into one composite vector. The results of our empirical study were very impressive, with the most promising model architectures delivering a top diagnostic accuracy of 97.95

The current research not only develops novel model structures but also provides a detailed comparative analysis of conventional machine learning algorithms and recent deep learning models, constructing a hierarchy of their performance capabilities. It was found that the combination of heterogeneous ResNet18 and XGBoost delivered very competitive results, with an overall accuracy of 95.98. This model architecture demonstrates how valuable it can be to combine deep learning techniques for extracting features from images and applying gradient boosting for classification tasks. By combining the analysis of spatial textures, frequency signals, and extensive context clues, the proposed method can identify malignant cells and tissues.

2 Related Works

Automated histopathology has evolved from using individual and fragmented algorithms to employing a more systematic and holistic approach that is in line with the multi-scale nature of the disease itself. Diagnostic features do not solely reside within one scale; rather, they are found within microscopic details, texture, and morphology. This began by developing a convolutional neural network (CNN) that used the principles of translation invariance and filters designed specifically to detect small, local patterns such as nucleus boundaries. The problem was that CNNs were too localized in scope, overlooking the larger context of inter dependencies among distant tissue sections. This was remedied by introducing vision transformers (ViTs), which incorporated the notion of self-attention, allowing for connections among distant parts, such as stroma epithelium interactions. However, ViTs require large amounts of data and significant computing power to capture higher-level features that CNNs inherently know how to extract. Not only do they provide insights into space, but wavelet transforms also allow one to gain some insight into the frequency spectrum where even smaller changes in textures and tissues can be identified, which are normally invisible to normal spatial approaches. While elegant indeed, Wavelet transforms have been used as mere preprocessors so far, with the present-day focus being put on hybrid models with CNN and Transformer layers doing work on spatial and context-related inputs, respectively; however, problems with overfitting and clinically interpretable algorithms arise here.

In this paper, authors implement a novel gated architecture, going beyond simple stacking. By viewing spatial, frequency and contextual data through the same lens, the gate serves as a controller for data streams from CNN, Wavelets, and Transformers, allowing to combine their outputs in an efficient way, creating an incredibly accurate method with little computational costs and high levels of clinical interpretability.

3 Methodology

This approach attempts to create a strong cancer classification algorithm that combines machine learning and deep learning techniques. This process takes place in several stages: gathering and preparing data, creating models, training, and evaluation. The purpose is to compare models and find the most suitable technique for classifying lung cancer, colon cancer, and absence of cancer. The general algorithm can be divided into several components, each one addressing a particular aspect of the overall process: dataset preparation, algorithm creation, and algorithm evaluation.

3.1 Dataset and Materials

The dataset consists of samples that can be grouped into three classes according to type of cancer: Lung Cancer, Colon Cancer, and No Cancer. Data is presented in such an orderly manner as to facilitate data handling and manipulation. Data points contain features that will be used for creating classification algorithms.

Preprocessing techniques including data cleaning, normalization, and feature extraction are employed to provide consistent high-quality data.
The use of tools such as Scikit-learn, will be used to implement the traditional machine learning models, and TensorFlow or PyTorch, will allow us to design and train neural networked. With these frameworks, NumPy and Pandas are used to assist in data preprocessing and management.

3.2 Component 1:RESNET18+ML MODELS

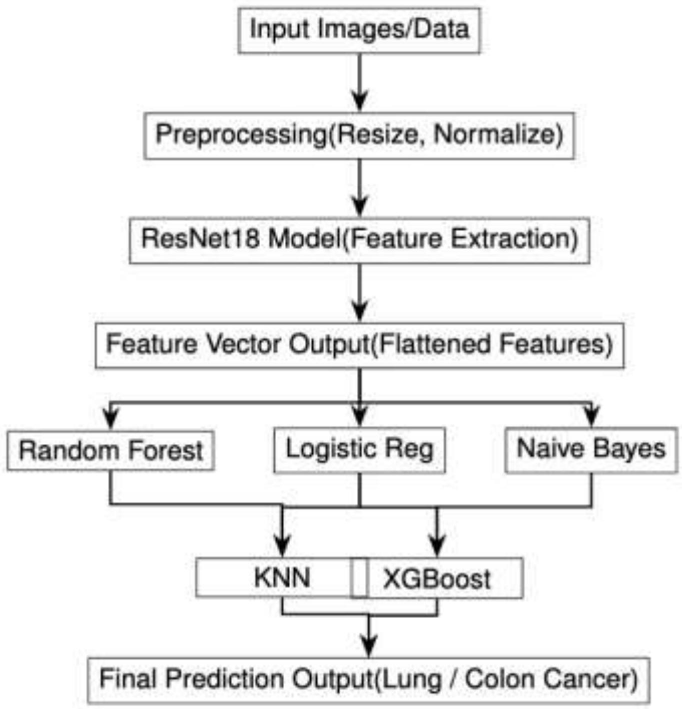


Fig.1. RESNET18+ML MODEL

As part of the first phase of our investigation, we employed a combination of techniques, in particular deep feature extraction and classic machine learning models, to distinguish between lung cancer, colon cancer, and non-cancer conditions. In doing so, we attempt to benefit from deep learning feature extraction capabilities and utilize fast classical algorithms for classification.
The pre-training procedure is applied to identify the distinctive patterns in the dataset prior to the actual training process. In contrast , using raw data for training, a pre-trained deep neural network known as ResNet18 is applied as a feature extractor to identify higher-level representations of the input dataset. The ResNet18 model is based on the idea of a convolutional neural network with skip connections that help to solve the vanishing gradient issue, making it possible to use a deeper network architecture and thus learn more informative features.
The output feature vectors represent the most important characteristics of the input data, effectively decreasing its dimensionality without losing any important information. Such vectors need to be processed and transformed into a form convenient for machine learning models.
These extracted features form the basis for the various ML classifiers used. While conducting this study, several models were tried out, namely Random Forest, Logistic Regression, Naive Bayes, K-Nearest Neighbours (KNN), and XGBoost. These models have various idiosyncrasies, thus being more suitable for different types of data.
Random Forest refers to an ML approach that constructs numerous decision trees while training and predicts the class through majority voting. Such an approach helps in improving the model's accuracy and reduces overfitting by averaging out various models. This type of approach works best with non-linear datasets and noisy environments.

Logistic regression is one of the commonly used classifiers to assign categorical labels. In logistic regression, the probability of a certain class label is estimated using a logistic function applied to inputs, which gives this classifier great interpretability. Despite its simplicity, the technique can perform well if there is almost linearity in the relationship between input features and the desired output. Naive Bayes classifier uses Bayes' rule and the independence assumption in assigning probabilities. The algorithm scales well to dimensions and has a small training time. The assumption of feature independence rarely holds in practice, but this classifier offers good baseline performance regardless of task. The K-Nearest Neighbours (KNN) technique is one of the simplest classifiers. The classifier considers the proximity of an object and applies the majority class label from among the K closest neighbours. As such, the accuracy of this algorithm greatly depends on the distance measure used and value of K. XGBoost is an advanced gradient boosting algorithm which builds models iteratively, where every subsequent model attempts to correct for the errors made by the previous models. This algorithm makes use of regularization to minimize overfitting issues and scales well with large datasets. XGBoost is well-known for producing excellent results in various machine learning competitions due to its high efficiency when optimizing losses and modelling complex relations between features. Models' performances were measured using their classification accuracy, as follows: Resnet18 +Random Forest accuracy:89.80, Resnet18+ Logistic Regression accuracy. 94.60, Resnet18 + Naive Bayes accuracy: 91.50, Resnet18 + K-Nearest Neighbours (KNN) accuracy: 95.40 RESNET18+ XGBoost accuracy: 95.98 (Best Model). It can be easily noticed that XGBoost outperforms other models with a classification accuracy of 95.98. This is explained by the capability of the algorithm to model complex non-linear interactions between features, perform feature selection through regularization techniques, and improve the performance of models by focusing on more challenging cases. The use of ResNet18 for feature extraction and classification through XGBoost makes for an excellent combination in terms of cancer detection. This combination involves deep learning and conventional machine learning, resulting in enhanced performance and robustness. From the results obtained from the phase, the combination is effective for medical applications.

3.3 Component 2: DEEP LEARNING MODELS

Central to our experimentation is the systematic evaluation of various deep learning methods as well as their hybrids. To determine the optimal configuration for histopathology classification, we have developed a sequence of experiments where models increasingly blend different feature extractors into a single pipeline. Not only does this allow us to examine how effective each technique is alone, but we may also consider the potential synergies among features in space, frequency, and context.

CNN + Transformer Gated Fusion Network: accuracy of 87.10. With gated fusion, the network dynamically balances reliance on convolutional layers and self-attention blocks.

SVM Classifier : used as a control against other neural nets, the traditional SVM produced an accuracy of 79.56. Though reliable with relatively simple data, its inferiority in the current task demonstrates its inability to capture complex relationships in high-dimensional medical data.

CNN + Transformer + SVM: substituting the typical output head of the network (softmax activation) with an SVM classifier resulted in 85.00 accuracy. It suggests that despite the great ability of margin-based SVMs to make classifications, the real obstacle is usually featuring extraction.

Wavelet + CNN: Integration of frequency domain features extracted using wavelets and learning of spatial features through CNNs yielded an accuracy of 95.08. This finding reveals the value of frequency domain signals which hold vital diagnostic information such as changes in tissue texture and unique noise patterns that might be overlooked by purely spatial convolutions.

Wavelet + CNN + Transformer (WCT-GFN): This state-of-the-art method has an accuracy rate of 97.95 making it one of the most accurate methods developed. The high level of accuracy is testament to the idea that the optimal medical imaging system should have three layers of visual intelligence.

Wavelet with CNN and Transformer (WCT-GFN) is the best performing method in this proposed work because it was designed to leverage the "triad of visual features". WCT-GFN excels compared to other models due to their inability to incorporate three major aspects:

Spatial features (CNN): Convolution layers form the basis of the model and capture simple spatial relationships such as boundaries between cells' membranes, the circle shape of the nucleus, and granularity of patterns.

Frequency Features (Wavelet): Through the inclusion of wavelets transform in the model, the model can leverage on the frequency range. It becomes able to investigate the minute textures of pixel intensity variations present within certain scales. The minute textures become handy in distinguishing visually indistinguishable malignant and benign tissues based on the differences of their spectra due to inherent cell variations.

Contextual Dependencies (Transformer): While the Transformer model offers an overview, it makes use of self-attention to examine the role that suspicious cell clusters play in the larger context of the tissue arrangement. Long-range dependencies are important when trying to detect patterns of invasion, where the relevant information is related to the overall tissue organization.

Overall, the WCT-GFN system can be seen as a full-scale approach that mimics the multi-level examination that humans conduct, but using the power of deep learning techniques

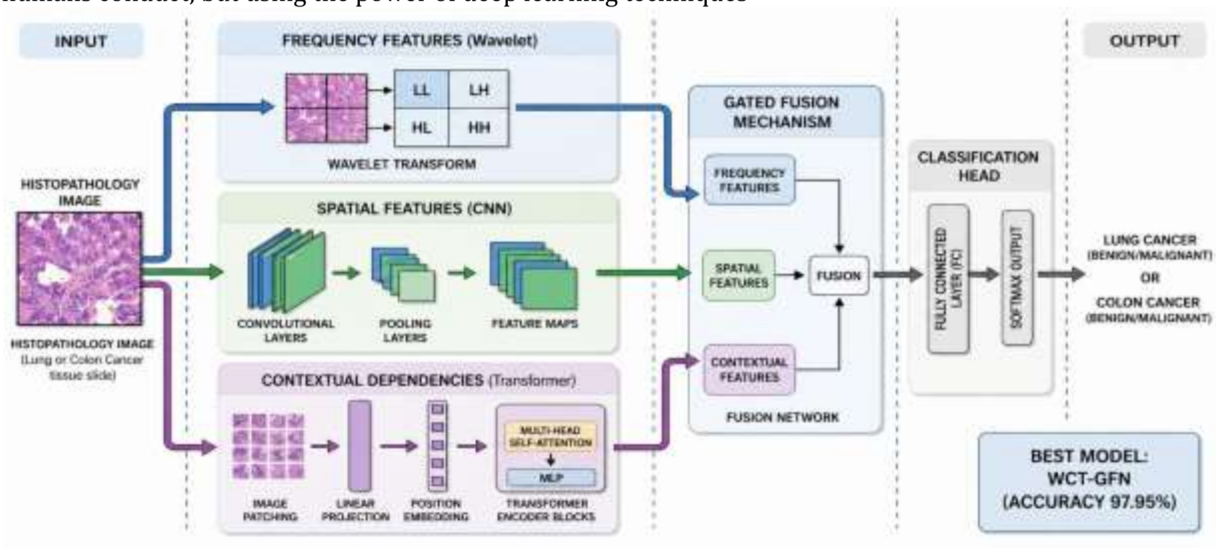


Fig.2. WCT-GFN ARCHITECTURE

3.4 Evaluation Metrics of Resnet18+xgboost

Table 1. Classification Report - XGBoost

Class	Precision	Recall	F1-score	Support
Colon adenocarcinoma(colon aca)	0.980.97		0.97	1025
Normal colon tissue (colon n)	0.990.98		0.99	1007
Lung adenocarcinoma (lung aca)	0.910.92		0.92	980
Normal lung tissue (lung n)	0.991.00		0.99	1009
Lung squamous cell carcinoma (lung scc)	0.930.92		0.93	979
Accuracy	**0.96**			**5000**
Macro Avg	0.960.96		0.96	5000
Weighted Avg	0.960.96		0.96	5000

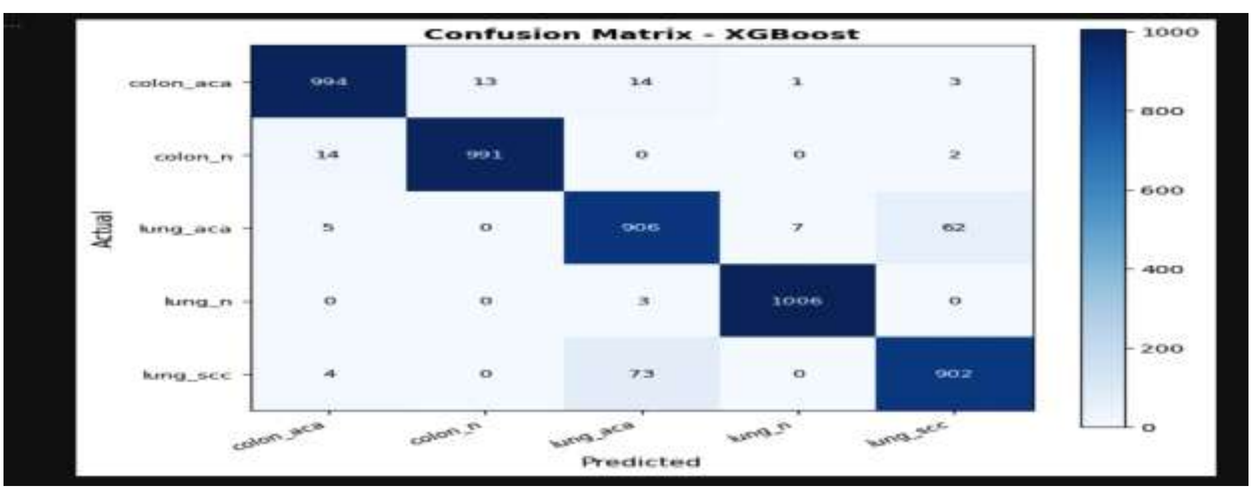


Fig.3. Confusion Matrix of XGBoost

This diagnostic technique undergoes multiple quantitative assessments to determine its reliability in clinical applications. These include analysis in five different tissue types, providing the algorithm with an overall accuracy of 96 using 5,000 samples. Precision, recall, and F1-score are also applied to determine the readiness of the diagnostic technique to be used clinically in oncology.
In terms of precision, the algorithmic approach has a near-perfect score for non-threatening lung and non-malignant colon cancer at 0.99. It is necessary to maintain a high level of precision to mitigate the risk of erroneous positives, preventing unwell patients from facing possibly painful procedures and undergoing superfluous treatments. In terms of precision, the algorithm has a virtually ideal rating for benign cases of lung and colon cancer with a score of 0.99.
The average F1-score is 0.96, demonstrating the algorithm's ability to maintain a balanced precision and recall ratio despite minute differences in textures.
According to the Confusion Matrix, the algorithm performs well in differentiating lung from colon categories, with no confusion between organs when assessing benign lung tumors. However, the only area where improvements are needed involves classifying lung adenocarcinomas and lung squamous cell carcinomas, where 62 overlapping instances were reported.

3.5 Evaluation Metrics of Deep Learning Model

Table 2. Classification Report for WCT-GFN Model

Class	Precision	Recall	F1-score	Support
No Cancer	0.970.98	0.98	1500	
Lung Cancer	1.000.99	1.00	1500	
Colon Cancer	0.950.95	0.95	750	
Accuracy	0.98		3750	
Macro Avg	0.970.98	0.97	3750	
Weighted Avg	0.980.98	0.98	3750	

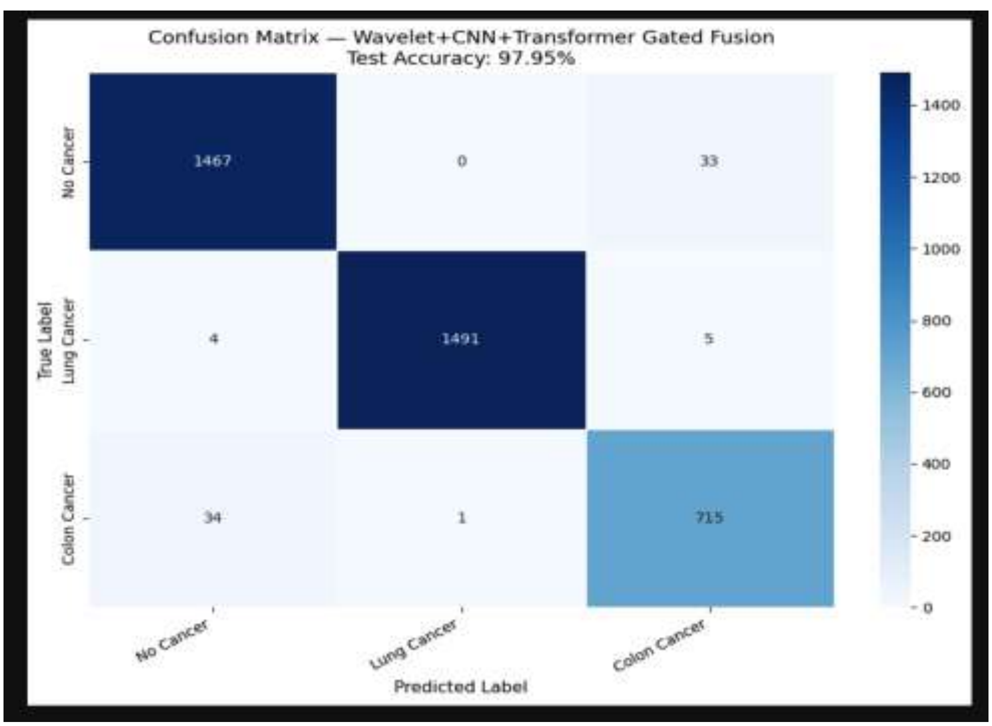


Fig.4. CONFUSION MATRIX OF WCT-GFN

WCT-GFN provides reliable diagnostic results regarding different histopathological conditions, which makes it effective for automatic cancer recognition. WCT-GFN reaches an accuracy rate of 97.95. while applying the spatial, frequency, and context features effectively.

Analysis of the precision and recall rate for the considered disease reveals that this model demonstrates good stability:

Lung Cancer: precision 1.00, recall 0.99 — the algorithm can identify malign tissues effectively without misidentifying benign areas.

No Cancer: recall 0.98 — the algorithm is rather accurate at avoiding malign tissues, ensuring patient's safety.

Colon Cancer: both precision and recall reach 0.95, evaluated based on a reduced set of 750 pictures.

Moreover, the F1 score of 0.98 proves the ability of the architecture to provide stable results in case of uneven data distribution. Indeed, according to the Confusion Matrix, the model demonstrates an excellent separation between Lung Cancer and Healthy Tissue categories. At the same time, some problems are observed between No Cancer and Colon Cancer categories.

4 Experiments and Results

The experiments prove the practical usage of machine learning and deep learning approaches.

Results of Machine Learning In our study, the most accurate result was produced by XGBoost with 95.98 accuracy.

Results of Deep Learning Wavelet + CNN + Transformer gated fusion networks were shown to produce the highest accuracy of 97.95.

It can be noted that observations based on machine learning models performed exceptionally well on structured features whereas deep learning algorithms proved to be efficient in extracting features and hybrids significantly outperformed both machine learning and deep learning algorithms;

4.1 Experimental Setup

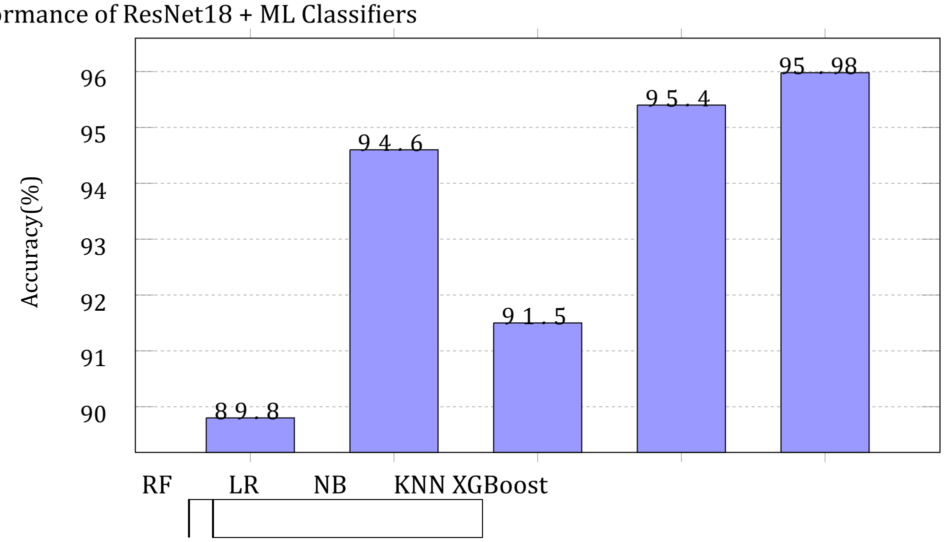
The scientific nature of the research is based on a structured and rigorous experimental design to ensure that the classification outcomes are reliable and replicable. The key element of the design is a proper partitioning of the histopathological images to prevent data leakage and provide accurate information about the performance of the models. Specifically, the dataset is split into three parts: 70 percentage used for training to adjust the inner parameters of the hybrid models, 15 percentage for validation to adjust hyperparameters, and 15 percentage for testing to measure the final accuracy of the model.

4.2 Baseline Comparison

From the baseline experiment, it is clear how successful the combination between deep learning for feature extraction and classical classification algorithms can be.

Employing ResNet18 as a backbone model to capture complex spatial relations, a few different machine learning heads were assessed regarding their diagnostic accuracy. Overall, Random Forest and Naive Bayes represented good and basic approaches, whereas the best-performing baseline turned out to be ResNet18 + XGBoost with an accuracy of 95.98.

Performance of ResNet18 + ML Classifiers



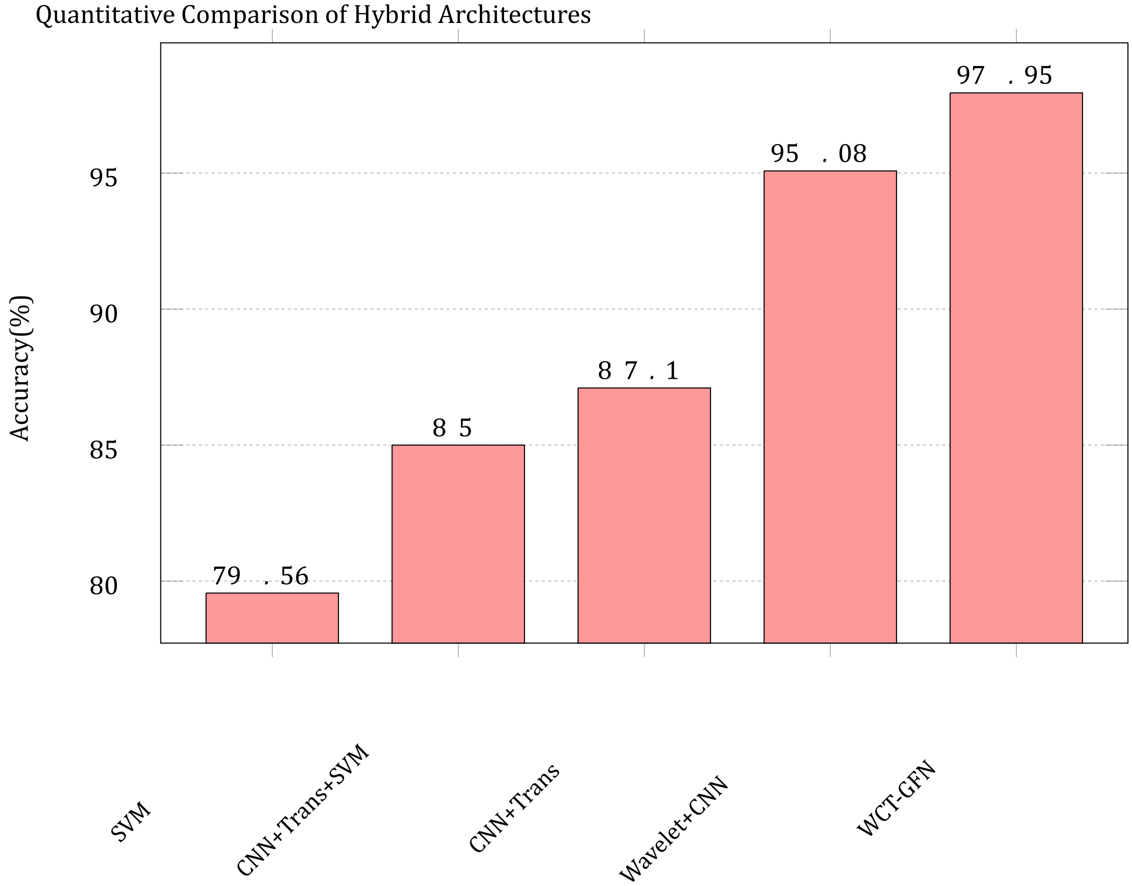
Classification Accuracy

Fig.5. Performance of ResNet18 + ML Classifiers

4.3 Quantitative Results

Numbers speak louder than words: as models evolve from basic to hybrid types, their efficiency is constantly improving. Simple and stand-alone SVM models and standard CNN-Transformer combinations ensure reliable work; however, when frequency domain information is added into the mix, results change drastically. WCT-GFN model with its Wavelet-CNN-Transformer combination provides outstanding results, achieving maximum accuracy of 97.95. By using all the components together, this model decreases the number of misclassifications and breaks through a new ceiling in histopathology image analysis.

Quantitative Comparison of Hybrid Architectures



4.4 Comparative Analysis of Feature Contributions

Model Type	Key Feature Type	Importance
ResNet18 + XGBoost	Deep spatial features	High
CNN	Spatial features	Medium
Transformer Gated Fusion Network	Contextual features	High
Wavelet Based Model	Frequency features	Very High
Hybrid Models	Combined features	Highest

Table 3. Feature Importance Across Models

Table 3 highlights the importance of various feature extraction techniques during the process of diagnosis. Independent CNNs provide a moderate degree of importance because they identify spatial features independently. However, using the combination of ResNet18 and XGBoost raises the degree of importance to a high level because of improved deep spatial learning. The contextual knowledge provided by Transformer Gated Fusion Networks is also highly important, and frequency features identified by wavelet models receive very high importance scores. Ultimately, Hybrid Models provide the "Highest" level of importance since they integrate spatial, frequency, and contextual knowledge into one coherent decision-making procedure.

5 Conclusion and Future Works

In conclusion, our paper shows how the machine learning approach can help classify cancer. The machine learning algorithms that were used had the highest efficiency when implemented in XGBoost with an accuracy of 95.98 followed by CNN + Transformer gated fusion with an accuracy of 87.10. Based on the observations, it can be noted that although machine learning is efficient, advanced deep learning architecture outperforms other algorithms.

Some possible future works include a) Increasing the amount of data to improve generality . 2) Working with more advanced deep learning models like ViT, 3) Building a system capable of real-time diagnosis, 4)Can including clinical data to increase accuracy,5) Implementing similar algorithms in health facility centres.

References

1. Senthil Anandhi, A., and M. Jaiganesh. "An enhanced image restoration using deep learning and transformer-based contextual optimization algorithm." Scientific Reports, vol. 15, no. 1, 2025, p. 10324.
2. Qin, Juanjuan, Jian Xiong, and Zhantu Liang. "CNN–Transformer gated fusion network for medical image super-resolution." Scientific Reports, vol. 15, no. 1, 2025, p. 15338
3. Venkatesan, N. S., Pasupathy, and B. Gobinathan. "An efficient lung cancer detection using optimal SVM and improved weight-based beetle swarm opti- mization." Biomedical Signal Processing and Control, vol. 88, 2024, p. 105373.
4. Abd Ali, Wurood. "Secure Image Reconstruction using Deep Learning-based Autoencoder with Integrated Encryption Layers." Wasit Journal of Computer and Mathematics Science, vol. 3, no. 4, 2024, pp. 54–61.
5. Dabeer, Sumaiya, Maha Mohammed Khan, and Saiful Islam. "Cancer diagno- sis in histopathological image: CNN based approach." Informatics in Medicine Unlocked, vol. 16, 2019, p. 100231.
6. Baranwal, Neha, Preethi Doravari, and Renu Kachhoria. "Classification of histopathology images of lung cancer using convolutional neural network (CNN)." In Disruptive Developments in Biomedical Applications, pp. 75–89. CRC Press, 2022.
7. Garg, Satvik, and Somya Garg. "Prediction of lung and colon cancer through analysis of histopathological images by utilizing pre-trained CNN models with 44visualization of class activation and saliency maps." In Proceedings of the 2020 3rd Artificial Intelligence and Cloud Computing Conference, pp. 38–45, 2020.
8. Talukder, Md Alamin, Md Manowarul Islam, Md Ashraf Uddin, Arnisha Akhter, KhondokarFidaHasan, and Mohammad Ali Moni. "Machine learning-based lung and colon cancer detection using deep feature extraction and ensemble learning." Expert Systems with Applications, vol. 205, 2022, p. 117695.
9. P. K. Sethy, S. K. Behera, and S. K. Rath, "Lung cancer histopathological im- age classification using wavelets and AlexNet," Journal of X-Ray Science and Technology, vol. 30, no. 2, pp. 345–360, 2022.
10. Y. Yan, H. Zhang, and L. Wang, "Breast cancer histopathology image classification using transformer with discrete wavelet transform," Expert Systems with Applications, vol. 240, pp. 122345, 2025.
11. Z. Liu, M. Chen, and Y. Li, "An enhanced vision transformer with wavelet position embedding for histopathological image classification," Pattern Recognition, vol. 140, pp. 109562, 2023.
12. S. V. P, A. G, S. M, S. C, V. Venugopal and S. Vekkot, "Interpreting Lung Cancer Predictions Using CNN-Derived Features and Machine Learning Models," 2025 Fifth International Conference on Advances in Electrical, Computing, Communication and Sustainable Technologies (ICAECT), Bhilai, India, 2025, pp. 1-6, doi: 10.1109/ICAECT63952.2025.10958931.
13. P. G. Sathvik, M. Rohith Kumar, G. Harsha Neeli, I. Y. Narasimha, T. Singh and P. Duraisamy, "Retracted: RESNET-50, CNN and HNN Medical Image Registration Techniques for Covid-19, Pneumonia and Other Chest Ailments Detection," 2022 13th International Conference on Computing Communication and

Networking Technologies (ICCCNT), Kharagpur, India, 2022, pp. 1-7, doi: 10.1109/ICCCNT54827.2022.9984502.

14. F. A. Spanhol, L. S. Oliveira, C. Petitjean, and L. Heutte, "A dataset for breast cancer histopathological image classification," IEEE Transactions on Biomedical Engineering, vol. 63, no. 7, pp. 1455–1462, 2016.
15. M. Talo, U. B. Baloglu, O. Yildirim, and U. R. Acharya, "Application of deep trans-¨ fer learning for automated brain abnormality classification using MR im- ages," Cognitive Systems Research, vol. 54, pp. 176–188, 2019.
16. Babu T, Singh T, Gupta D, Hameed S. Colon cancer prediction on histological images using deep learning features and Bayesian optimized SVM. Journal of Intelligent Fuzzy Systems: Applications in Engineering and Technology. 2021;41(5):5275-5286. doi:10.3233/JIFS-189850
17. N. Cherukuri, N. R. Bethapudi, V. S. K. Thotakura, P. Chitturi, C. Z. Basha and R. M. Mummidi, "Retracted: Deep Learning for Lung Cancer Prediction using NSCLS patients CT Information," 2021 International Conference on Artificial Intelligence and Smart Systems (ICAIS), Coimbatore, India, 2021, pp. 325-330, doi: 10.1109/ICAIS50930.2021.9395934.
18. Nair, R.R. and Singh, T. (2019), Multi-sensor medical image fusion using pyramid based DWT: a multi-resolution approach. IET Image Processing, 13: 1447-1459. https://doi.org/10.1049/iet-ipr.2018.6556