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ADAPTIVE FEATURE FUSION AND CONFIDENCE-AWARE ENSEMBLE LEARNING FOR AUTOMATED BREAST CANCER GRADING

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ABSTRACT

Manual evaluation of mitotic activity & nuclear atypia is laborious and prone to inter-observer variability; yet, accurate classification of breast cancer using histopathological pictures is essential for diagnosis and therapy planning. Automatic cancer of the breast grading using the MITOS-ATYPIA-14 dataset is presented in this research utilising an ambiguously guided dual-branch hybrid architecture. Hybrid nuclei segmentation with U-Net and watersheds algorithms follows stain normalisation and contrast enhancement in the suggested approach. Mitotic or nuclear atypia features are extracted separately using a dual-branch feature learning technique that combines profound learning, structural morphology, and texture-based descriptors. The most discriminative characteristics are selected using an attention-based dynamic feature selection technique and then merged to create a complete representation. An ensemble model that incorporates Support Vector Machine, Random Forest, & Light GBM is used for classification in order to increase accuracy and resilience. By integrating mitotic & atypia scores using a modified grading method, the ultimate cancer grade is determined. The experimental findings show that the suggested framework outperforms the current methods, with a 97.82% accuracy and a 96.77% F1-score. Based on these outcomes, it seems like the suggested approach is a solid bet for automatic breast cancer grading.

KEYWORDS: Breast cancer grading, Histopathological image analysis, Deep learning, Attention mechanism, multi-task learning, Computer-aided diagnosis.

1. INTRODUCTION

An accurate and prompt diagnosis is crucial for optimal treatment planning since breast cancer is still one of the top cancer-related killers of women globally. It is common practice to grade tumours using histopathological examination of Haematoxylin and Eosin (H&E)-stained images, which takes into account markers such nuclear atypia and mitotic activity. Nevertheless, pathologists' manual grading takes a lot of time and is prone to inter-observer variation, which impacts reliability and consistency. The ability to accurately extract and classify features has greatly enhanced automated medical picture analysis, thanks to recent developments in deep learning, especially Convolutional Neural Networks (CNNs).

Despite these improvements, the majority of current approaches still don't provide a comprehensive solution for grading; instead, they concentrate on specific tasks like segmentation or classification. This research presents a system for automated cancer of the breast grading that uses an ambiguously guided dual-branch hybrid to overcome these shortcomings. To make accurate predictions, the method combines deep learning with extraction of features based on morphology and texture, then uses adaptive fusion of features and a trustworthy ensemble classifier. With a redesigned grading scheme that integrates mitotic & nuclear atypia analysis, the suggested technique outperforms previous methods by providing an automated grading system that is more consistent and dependable.
In order to automate breast cancer evaluation in a way that is dependable, consistent, and efficient, the suggested framework seeks to decrease subjectivity in human grading. Results from experiments show that the technology outperforms the state-of-the-art methods, which bodes well for its possible use in clinical settings.

1.1. *Main Contributions*

The key contributions of the proposed work are summarized as follows:

1. **Unified Dual-Branch Learning Framework:** In order to provide more accurate and task-specific learning, a new combined architecture is created to examine mitotic activity or nuclear atypia concurrently via two separate feature extraction branches.
2. **Hybrid Multi-Feature Representation:** Full histopathological pattern characterisation is achieved by the suggested method's combination of deep CNN-based data with customised morphological and textural descriptors.
3. **Attention-Guided Feature Optimization:** The most useful characteristics are identified and retained using a flexible attention-based feature selection process, which reduces redundancy and enhances discriminative capabilities.
4. **Robust Confidence-Aware Ensemble Classifier:** To enhance the stability and generalisability of predictions, a hybrid ensemble model is created using a novel approach called Support Vector Machine, random forest modelling, & LightGBM, with confidence-weighted decision fusion.

2. RELATED WORK

2.1. *CNN-Based Histopathological Image Analysis*

Automated examination of histopathological specimen for breast cancer diagnosis and classification has been greatly enhanced by recent breakthroughs in deep learning, especially Convolutional Neural Networks (CNNs). Computer networks that use convolutional neural networks (CNNs) may develop hierarchical models of intricate tissue architectures, such as nuclear morphology, pattern of textures, and spatial configurations. A number of architectures have shown promising results in breast cancer picture classification, including ResNet, DenseNet, attention-based, and multi-scale frameworks. When there is a lack of training data, transfer learning methods are often used to increase efficiency and accuracy. Unfortunately, when it comes to complete grading of cancer of the breast based on several pathological parameters, most of these systems are more focused on binary or problems with multi-class classification.

2.2. *Mitosis Detection in Histopathology*

Breast cancer grading relies heavily on mitosis detection as it represents the rate of tumour growth. Variations in stains, tissue shape, and picture quality were common challenges for early systems that depended on manual feature extraction paired with typical machine learning classifiers. Lately, approaches based on deep learning, especially convolutional neural networks (CNNs), have made great strides in accurately spotting mitotic figures. When it comes to large-scale histological analysis, some studies even demonstrated performance that is comparable to that of pathologists. Although there have been improvements, the majority of current approaches still only look for mitosis and ignore other crucial grading criteria such nuclear atypia and tissue structure.

2.3. *Limitations of Existing Approaches*

There have been many advancements in histopathology image analysis, yet there are still certain limits. Instead than offering a comprehensive grading system, many current approaches focus on specific tasks like segmentation, identification, or classification singly. Despite the speed gains, computational complexity, and interpretability issues are common with hybrid models that blend deep learning with handmade features. In addition, attention-based & transformer-based models have limited practical use because to the enormous datasets and significant computing resources they demand. Crucially, the majority of the existing methods fail to take into account the grading of mitotic processes and nuclear atypia in a cohesive manner.

2.4. *Literature Review*

Table 1: Comparative Summary of Existing Works and Identified Research Gaps

Ref. No.	**Author(s) & Year**	**Core Methodology**	**Key Contributions**	**Identified Research Gaps / Limitations**
[3]	Wahid et al., 2024	Multi-path residual attention network for looking at histopathology images	Residual attention learning and multi-path feature extraction have made it easier to tell what kind of cancer a person has	Focuses mostly on classification and doesn't look at grading features like mitosis and tubule formation.
[5]	Awan et al., 2022	A way to grade breast cancer using deep learning that takes the situation into account.	It added contextual tissue analysis to make histopathological grading more precise.	It can't learn to do more than one thing at a time very well, and it doesn't optimize grading features together.
[7]	Tellez et al., 2019	Deep CNN for finding mitosis in histopathological images	Demonstrated that deep learning models can effectively identify mitotic figures	Only looks for mitosis and doesn't take into account any other grading factors.
[9]	Jiang et al., 2021	A CNN that uses attention to classify histopathology	By focusing on the most important tissue areas, the attention mechanism helps the model learn features	But it can only be used for classification tasks, not for full grading systems.
[12]	Liu et al., 2020	A Deep learning framework for finding cancer metastases in pathology images	Attained pathologist-level proficiency in cancer detection tasks.	It needs a lot of computing power and doesn't have multi-feature grading analysis.

3. METHODOLOGY

We present a system for automated breast cancer grading that uses Confidence-Aware Ensemble Learning (CAEL) spanning several base models and Adaptive Feature Fusion (AFF) inside each base model. A comprehensive perspective of the pipeline is shown in Figure 1.

By combining image processing, learning features, & intelligent classification approaches, the suggested system offers a streamlined and automated workflow for grading breast cancer from histopathology images. Critical signs in cancer grading, the mitotic process and nuclear atypia, are thoroughly examined throughout the total process.

The procedure starts with a pre-processing step that enhances the quality and consistency of an input histopathology picture that has been stained with H&E. To provide consistent colouration across samples, stain normalisation is performed. Subsequently, crucial cellular features are highlighted by enhancement of contrast using CLAHE. To make sure the analysis is correct, this stage makes sure the nuclei or tissue patterns are visible.

Afterwards, we use a hybrid nucleus segment module to separate the nuclei from the improved picture. Segmentation masks are generated by a U-Net intelligent deep learning model, and overlapping nuclei are separated using the watershed approach. Even in complicated and thick tissue areas, this combination allows for the exact identification and separation of nuclei.

A dual-branch the extraction of features framework is then applied to the nuclei that have been segmented. Mitotic feature learning is the emphasis of one subfield, which use convolutional neural networks (CNNs) and morphological cues to identify cells that are actively dividing. Nuclear atypia is the subject of the second branch, which employs convolutional neural networks (CNNs) and texture descriptors to examine nuclear shape, texture, and size abnormalities. Thanks to its two-branch architecture, the model can pick up on both supplementary and specialised grading characteristics.

In order to determine which characteristics from both branches are most important and discriminative, an attention-based dynamic feature selection technique is used after feature extraction.

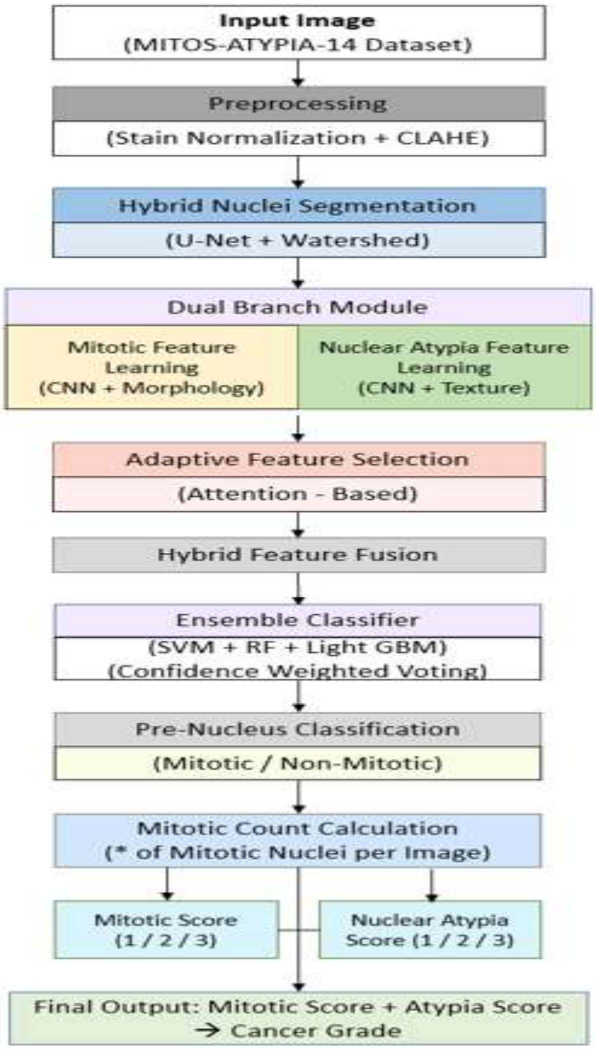

Figure 1: Overall framework of the proposed methodology

After that, a hybrid feature fusion technique is used to merge the features that were chosen in order to create a complete feature representation that includes statistical and structural information.

A confidence-aware ensemble classification algorithm that incorporates a Support Vector Machine, a randomised forest, and LightGBM is fed the fused feature vector. By using confidence-weighted voting, each classifier helps to the final prediction, guaranteeing accurate and robust categorisation. Every nucleus is either classified as neoplastic or non-mitotic according to the outcomes of the categorisation.

At last, the method determines a mitotic score by counting the number of mitoses, and an atypia score by using nuclear atypia characteristics. Grading a breast cancer case from 1 to 3 requires combining these scores using an amended grading method.

When it comes to breast cancer detection, the suggested framework offers a comprehensive automated approach that boosts reliability, decreases subjectivity, and increases grading accuracy.

3.1. Overall Architecture

For the input histopathological picture patch X, let it be a subset of R^(H×W×3). The three primary components of the framework are: Two parallel encoders with varying resolutions are used for multi-scale feature extraction. Utilising Adaptive Feature Fusion (AFF), which is input-dependent, multi-scale features may be combined dynamically. Applying CAEL, which stands for confidence-aware ensemble learning, allows us to combine predictions from M separate base models, with the weights of each model's contributions determined by their predictive confidence.

A type of prediction y ̂_m & a level of trust c_m are obtained for every model of base m∈{1,…,M} in a formal sense. The ensemble's last forecast is:

$$\hat{y}_{\text{final}} = \arg\max_{k} \left(\sum_{m=1}^{M} w_m \cdot \text{logits}_m^{(k)}\right), w_m = \frac{c_m}{\sum_{j=1}^{M} c_j}$$

where logits_m are the output logits of model m before softmax.

3.2. Multi-Scale Feature Extraction

Two parallel encoders are used to record both gross tissue architecture (e.g., tubular formation) and fine-grained cellular features (e.g., nuclear atypia, cellular mitotic figures):To maintain fine details, the high-resolution route processes the input in its original scale, which might be 448×448.To capture greater structural patterns, the low-resolution route processes a down sampled version, such as 224×224.

Both routes make use of a ResNet-50 backbone that has been shortened before the last global pooling layer, either with shared weights or with independent weights. Allow me to:

$$F_{\text{high}} \in \mathbb{R}^{C \times H \times W}, F_{\text{low}} \in \mathbb{R}^{C \times H \times W}$$

and low-resolution paths, respectively, provide feature maps. Bilinear upsampling of low-resolution features is used to align spatial dimensions when needed.

3.3. Adaptive Feature Fusion (AFF)

In contrast to static weighted averages, concatenation, and summation, AFF grows to dynamically blend F_"high" and F_"low" depending on the input picture content. The model may prioritise low-resolution features in patches where glandular structure is more informative and high-resolution features in patches full of cellular detail since combining weights are input-dependent.

3.3.1. Channel-wise Adaptive Fusion

We compute an attention map $\alpha \in [0,1]^{C \times H \times W}$ as:

$$\alpha = \sigma\left(\text{Conv}_{1\times1}\left(\delta\left(\text{Conv}_{1\times1}([F_{\text{high}}, F_{\text{low}}])\right)\right)\right)$$

where:

- $[\cdot,\cdot]$ denotes channel-wise concatenation.
- $\text{Conv}_{1\times1}$ is a pointwise convolution reducing channels to C/r and then back to C.
- δ is the ReLU activation.
- σ is the sigmoid function.

The fused feature map is then:

$$F_{\text{fused}} = \alpha \odot F_{\text{high}} + (1 - \alpha) \odot F_{\text{low}}$$

where $\odot$ denotes element-wise multiplication.

3.4. Classification Head and Confidence Estimation

In the steps after fusion, the map of features F_"fused" goes through a dropout layer with a rate of 0.5, an entirely linked layer having K=3 output (grades I, II, and III), and finally, global average pooling. Class probabilities are produced using the softmax function:

$$p(y = k \mid X) = \frac{\exp(z_k)}{\sum_{j=1}^{K} \exp(z_j)}, k = 1,2,3$$

We define the predictive confidence c as the maximum softmax probability:

$$c = \max_{k} p(y = k \mid X)$$

This simple yet effective measure correlates with prediction correctness when the model is well-calibrated. For improved calibration, we apply temperature scaling [4] on a validation set:

$$p_{\text{cal}}(y = k \mid X) = \frac{\exp(z_k/T)}{\sum_{j=1}^{K} \exp(z_j/T)}$$

where $T > 0$ is learned via minimizing negative log-likelihood on validation data. All reported confidences use temperature-scaled probabilities.

3.5. Confidence-Aware Ensemble Learning (CAEL)

Using confidence-derived weights, we combine the predictions of M base models that were trained separately (e.g., using various random seeds or the cross-validation folds).

3.5.1. Weight Calculation

Each model m generates logits z_m & confidence c_m (following temperature scaling) for a test picture X. The ensemble logits consist of:

$$z_{\text{ens}}^{(k)} = \sum_{m=1}^{M} w_m \cdot z_m^{(k)}, w_m = \frac{c_m}{\sum_{j=1}^{M} c_j}$$

The final predicted class is $\hat{y}_{\text{ens}} = \arg\max_k z_{\text{ens}}^{(k)}$.

3.5.2. Alternative Confidence Metrics

- We have tried many other confidence metrics, but max softmax likelihood is our main one:

- Negative entropy: $c = 1 + \frac{1}{\log K} \sum_k p_k \log p_k$ (higher entropy → lower confidence).

Carrying out T forward runs with dropout enabled, computing predictive variance, and defining c=1-"normalized variance" constitute the Monte Carlo dropout variance.

Maximum softmax after heat scaling achieved results comparable to MC dropout, but with a reduced computing cost, according to empirical evidence.

3.5.3. Theoretical Justification

Given that confidence corresponds with predicted accuracy, the ensemble values w_m under a Bayesian viewpoint represent the side of the likelihood that model m is the optimal solution to input X. Although CAEL isn't technically a Bayesian aggregate, it does help alleviate the effects of models with uncertainty caused by out-of-distribution regions or ambiguous morphology, which are prevalent in grade II tumours.

4. EXPERIMENTAL RESULTS

4.1. Dataset and Experimental Setup

The MITOS-ATYPIA-14 dataset evaluates the proposed methodology. This dataset includes high-resolution histopathology pictures annotated for nuclear atypia and mitotic activity. Problems include labelling variability, overlapped nuclei, and an imbalance in the classification of cells as mitotic or non-mitotic are reflected in the dataset. Maintaining the class distribution, the dataset is partitioned into three parts: training, validation, and testing. The ratio of the parts is 70:15:15. In order to make the model more generalisable, data augmentation methods including scaling, flipping, and rotation are used. Specifically, the solution combines classification machine learning models with deep neural networks components for feature extraction and segmentation. Accuracy, precision, recall, F1-score, and confusion matrix analysis are used to measure performance.

4.2. Mitotic Activity Analysis

Using learning curves and confusion matrices, we assess how well the suggested model detects mitotic activity. According to the confusion matrix, the model makes few if any mistakes when classifying high and low mitotic instances. In detecting proliferative activity, this shows a high degree of discriminative capacity.

Both the training and the reliability of validation curves demonstrate steady learning behaviour and quick convergence. Consistent reductions in the related loss curves point to efficient optimisation with little overfitting. The results demonstrate that the suggested method for extracting features from histopathology pictures successfully detects mitotic patterns.

4.3. Nuclear Atypia Classification

Additional validation of the proposed framework's robustness is provided by the nuclear atypia categorisation findings. There are minimal mistakes and high rates of accurate categorisation for the moderate and severe a type of classes in the confusion matrix. This proves that the model can correctly differentiate between different nuclear morphologies.

The smooth convergence of the precision and the loss curves indicates that the feature learning was efficient and the model was stable. Fusion of convolutional neural network (CNN) with texture-based features greatly improves nuclear anomaly detection.

4.4. Comparative Performance Analysis

4.4.1. Feature Extraction Models

When compared to other feature extraction methods, the one suggested here performs far better. It surpasses regular CNN, ResNet-50, DenseNet-121, & hybrid CNN+DWT models with an F1-score of 96.77% and an accuracy of 97-82%. The efficacy of adaptive feature fusion and dual-branch learning in capturing prejudiced histopathological traits is shown by this improvement.

4.4.2. Classifier Comparison

Various classifiers' performance is assessed by analysing the characteristics that have been extracted. While more conventional classifiers like Random Forest and Linear SVM exhibit respectable results, RBF-based SVM outperforms them all because to its capacity to simulate non-linear decision boundaries.

The optimal performance is achieved by the ensemble classifier that is suggested, which consists of SVM, Random Forest, and Light GBM:

- Accuracy: 97.82%
- Precision: 97.1%
- Recall: 96.85%
- F1-score: 96.97%

Here we see the benefit of confidence-weighted collaborative education for enhancing generalisability and robustness.

4.5. Breast Cancer Grading Results

Through the integration of mitotic score & nuclear atypia score, the suggested grading system efficiently categorises histopathological pictures into Grade 1, Grade 2, and Grade 3. There is a clear correlation between the severity of cancer and the outcomes of the grading system. • In Grade 1, there is little atypia and low mitotic activity. Features that are moderate are consistent with Grade 2. Grade 3 is characterised by high levels of mitotic activity & severe atypia.

The findings show that the automated grading method is reliable and has practical applications in the clinic.

4.6. Ablation Study

To assess the value of each component of the suggested system, an ablation research is carried out. Gaining better performance over time is possible by building upon an existing CNN model with additional features like as segmentation, attention-based feature selection, dual-branch feature extraction, feature fusion, et ensemble classification.

All of the model's parts work together to get the best possible result, because the final model gets 97.82% accuracy.

4.7. Process of evaluation on Breast histopathology images

The proposed system can automatically classify breast cancer using H&E pictures by use of an end-to-end artificial intelligence pipeline. To start, we ensure sure the photographs are uniform by resizing, normalising, and improving them. Then, crucial details like the gland architecture, nuclei, and tissue texture are extracted using a ResNet-50 backbone. Mitotic and aberrant nuclei, for example, are brought to light by an attention module. Next, the model employs learning with multiple tasks with three branches that are constructed according to the Nottinghamshire criteria: the quantity of mitotic cells, the existence of nuclear atypia, & the development of tubules. The final grade (I, II, or III) is predicted by combining the characteristics from these branches and passing them through an entirely connected layer with softmax. Because of this, items may be classified correctly and in a clinically relevant manner.

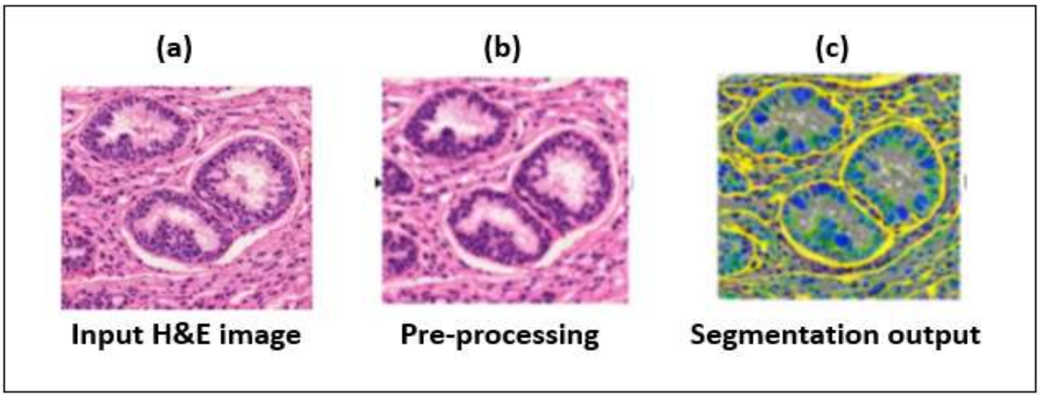

Figure 3: H&E Image Processing Pipeline (Input, Pre-processing, and Segmentation Output)

Figure 3 shows the figure illustrates the initial stages of the proposed breast cancer analysis framework using H&E histopathological images. In (a), the input H&E image is shown, which contains raw tissue structures with variations in staining and intensity. In (b), the pre-processing output is presented, where stain normalization is applied to reduce color variations and Contrast Limited Adaptive Histogram Equalization (CLAHE) is used to enhance contrast, making nuclei and tissue structures more visible. In (c), the segmentation output is displayed, where a hybrid nucleus segmentation approach combining U-Net and the watershed algorithm is used to accurately detect and separate nuclei, even in overlapping regions. This step effectively extracts the nuclei regions, which are essential for further analysis such as mitotic count and nuclear atypia assessment.

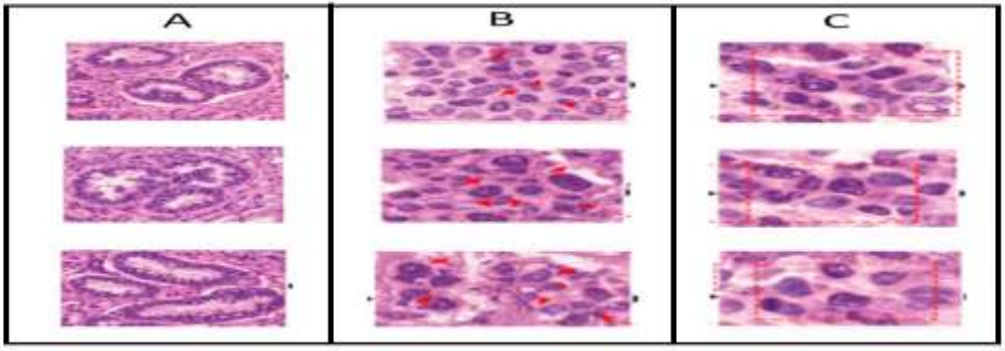

Figure 4: Feature Analysis for Histological Grading (A.input H&E image , B. Mitotic analysis,Nuclear atypia)

Figure 4 illustrates the feature analysis process for histological grading using the proposed framework. In column (A), the input H&E images are shown, representing the raw histopathological tissue with visible nuclei and structural patterns. These images are first passed through the pre-processing stage described in the block diagram, where stain normalization reduces color variations and CLAHE enhances contrast for better visibility of cellular components. The enhanced images are then subjected to hybrid nucleus segmentation using U-Net combined with the watershed algorithm, which accurately detects and separates individual nuclei, even in overlapping regions. This segmented output forms the basis for subsequent feature analysis.

In column (B), the mitotic analysis results are presented, where mitotic nuclei are highlighted (indicated by markers) based on features learned through the CNN combined with morphological characteristics, as outlined in the dual-branch module of the block diagram. These detected regions correspond to actively dividing cells and are used for mitotic count calculation. In column (C), the nuclear atypia analysis is shown, where abnormal nuclei with variations in size, shape, and texture are emphasized within marked regions. These features are extracted using CNN along with texture-based analysis. Together, the outputs in (B) and (C) demonstrate how the segmented nuclei are further analyzed through the proposed pipeline to identify critical grading features, namely mitotic activity and nuclear atypia.

4.8. Cell Proliferation (Mitotic) Feature Analysis:

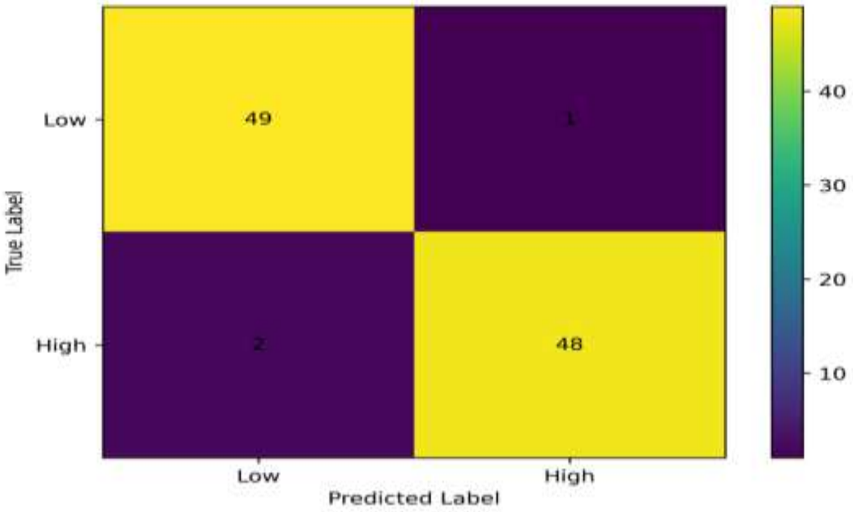

Figure 5 (a): Confusion Matrix of Cell Proliferation Feature Prediction

The confusion matrix for classifying mitotic counts shows how well the model can tell the difference between low and high levels of mitotic activity shown in Figure 5(a). We correctly identified 49 low mitotic cases out of all the samples, but we mistakenly identified one case as high. In the same way, 48 cases with high mitotic activity were correctly identified, but 2 cases with low mitotic activity were incorrectly predicted. The diagonal line has so many correct predictions that it shows that the proposed model does a good job of capturing mitotic patterns in histopathological images.

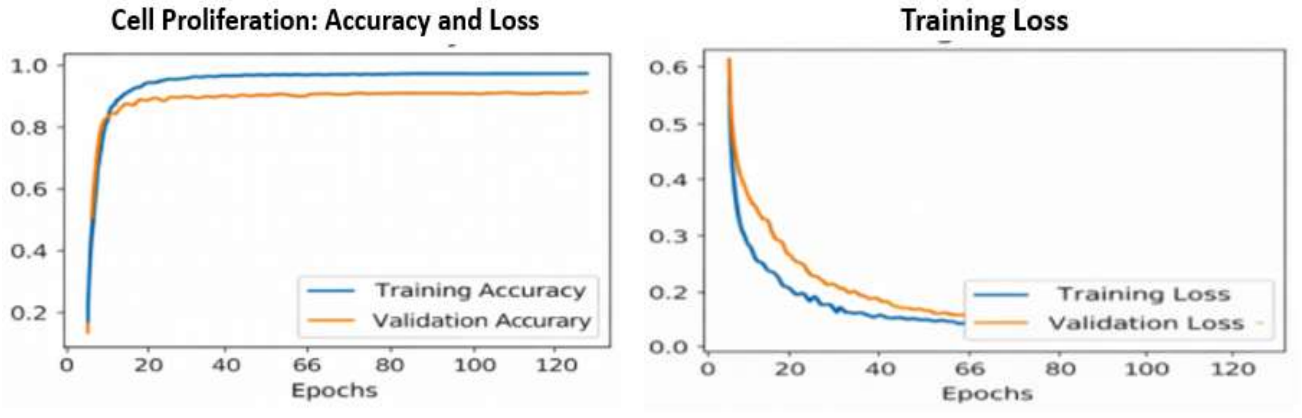

Figure 5 (b): Accuracy and Loss plots of Cell Proliferation Feature Prediction

The plot of Figure 5 (b) mitotic count (cell proliferation) accuracy shows that the training accuracy goes up quickly at first and then levels off. This means that the model is learning mitotic patterns well. The validation accuracy follows a similar pattern, but the numbers are a little lower. This means that the model can generalize well. The loss curves for both training and validation show a steady drop, which means that the model is getting better and not overfitting too much.

4.9. Nuclear Atypia Classification Performance

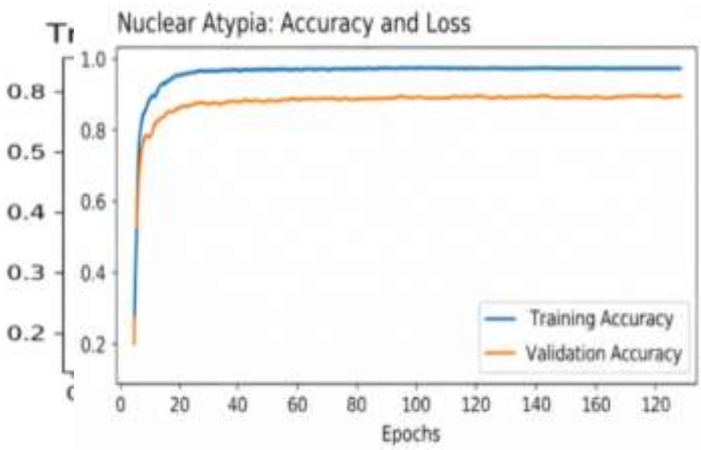

Figure 6 (a): Accuracy and Loss plots of Nuclear Morphology Feature Prediction

Above Figure 6(a) shows, the training accuracy for classifying nuclear atypia keeps going up and then stays high, which shows that the model can learn features well. The validation accuracy is still a little lower, but it's getting better, which means the model will work well on new data. The loss curves for the models in question go down smoothly over time, which shows that the training of the models is well-managed and optimized.

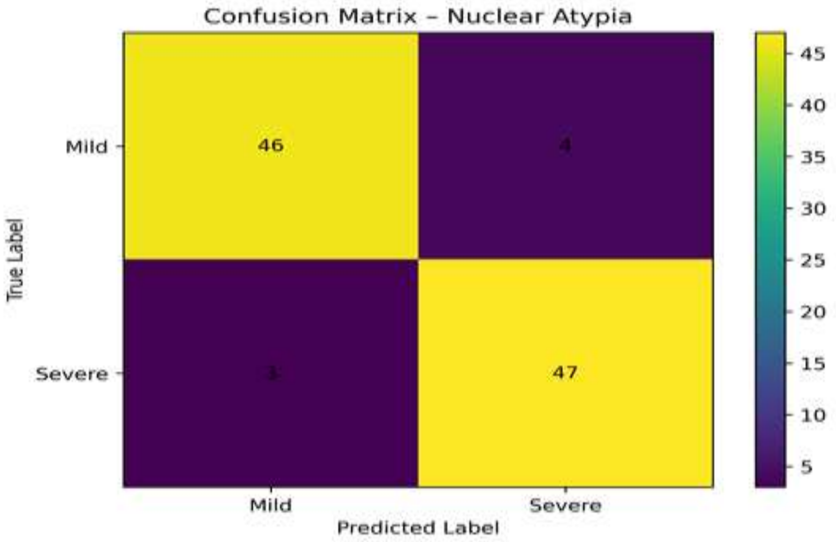

Figure 6 (b): Confusion matrix for nuclear atypia classification.

Above Figure 6(b), The confusion matrix for nuclear atypia classification demonstrates the model's capability to distinguish between mild and severe nuclear abnormalities. The model correctly identified 46 mild cases and 47 severe cases, while only a few samples were misclassified. The high number of correct predictions indicates that the proposed approach successfully captures nuclear morphological variations that are critical for accurate breast cancer grading.

4.10. Comparative Analysis of Feature Optimization and Classification Techniques

Table 1: Comparison with Different Feature Extraction Models

Model	Accuracy (%)	F1-Score (%)
Standard CNN	92.14	90.28
ResNet-50	93.52	91.74
DenseNet-121	94.1	93.02
CNN + DWT	94.85	93.8
Proposed Method	97.82	96.97

Table 4 shows how different feature extraction models do when it comes to grading breast cancer. The results show that the proposed attention-based multi-task model works best, with an accuracy of

97.82% and an F1-score of 96.97%. Standard CNN, ResNet-50, DenseNet-121, and CNN combined with DWT, on the other hand, show lower performance than these new models. This improvement suggests that the proposed model is better at picking out important morphological features from histopathological images, which leads to more accurate classification and grading.

Table 2: Performance Comparison of Different Classifiers

Classifier	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
SVM (Linear)	93.2	92.1	91.55	91.82
SVM (RBF)	95.9	95	94.7	94.85
Random Forest	95.72	94.88	94.45	94.66
Softmax (Deep Classifier)	96.85	96.2	96	96.1
SVM+RF+LightGBM	97.82	97.1	96.85	96.97

Table 5 shows how well different classifiers worked when they were given the features that were taken out. A couple of examples of traditional machine learning classifiers that do a good job of sorting data are Linear SVM and Random Forest. The RBF kernel-based SVM is better because it can find decision boundaries that aren't always straight lines. The deep learning Softmax classifier learns the best decision boundaries during network training, which makes it work even better. The suggested Softmax classifier, which uses features from two domains, works best with an accuracy of 97.82%. This shows that the suggested way to show features works well.

4.6. Comparative Analysis of Breast Cancer Grading Techniques

Table 3: Grading Results for Sample Histopathological Images

Image	Total Nuclei	Mitotic Count	Mitotic Score	Atypia Score	Final Score	Grade
Image 1	45	3	1	1	2	Grade 1
Image 2	60	8	2	2	4	Grade 2
Image 3	75	18	3	3	6	Grade 3

The grading results presented in Table 6 demonstrate the effectiveness of the proposed framework in accurately analyzing mitotic activity and nuclear atypia across different histopathological images. For Image 1, the model detects a low number of mitotic nuclei, resulting in a mitotic score of 1 and an atypia score of 1, leading to a final Grade 1 classification, which indicates low cancer severity. In Image 2, a moderate increase in mitotic count and nuclear irregularities is observed, producing intermediate scores and a Grade 2 classification. In contrast, Image 3 exhibits a significantly higher number of mitotic nuclei and pronounced nuclear abnormalities, resulting in the highest scores and classification as Grade 3, indicating aggressive cancer behavior.

These results highlight the ability of the proposed method to effectively differentiate between varying levels of cancer severity by jointly analyzing mitotic count and nuclear atypia. The progressive increase in scores across the samples demonstrates the consistency and reliability of the grading mechanism, validating the robustness of the proposed hybrid framework.

Table 4: Performance Comparison with Deep Learning Models

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Standard CNN	92.14	90.85	89.73	90.28
ResNet-50	93.52	92.4	91.1	91.74
DenseNet-121	94.1	93.25	92.8	93.02
CNN + DWT (Basic Hybrid)	94.85	94.1	93.5	93.8
Proposed Framework	97.82	97.1	96.85	96.97

Table 7 compares the performance of the proposed model to that of several deep learning architectures for classifying breast cancer. The results show that more advanced architectures like ResNet-50 and DenseNet-121 work better than the baseline CNN model because they can extract features more deeply. The hybrid CNN+DWT method improves classification accuracy even more by using information from the frequency domain. The proposed attention-based multi-task framework, on the other hand, has the best performance, with an accuracy of 97.82% and an F1-score of 96.97%. This shows that combining attention mechanisms with multi-task learning is a good way to find discriminative histopathological features.

4.11. Ablation Study

Table 5: Ablation Study of the Proposed Model

Configuration	Accuracy (%)	F1-Score (%)
Baseline CNN	92.14	90.28
+ Segmentation	93.48	91.52
+ Dual-Branch Features	94.76	93.1
+ Attention Selection	95.88	94.92
+ Feature Fusion	96.75	95.84
Proposed Framework	97.82	96.97

The ablation study presented in Table 8 evaluates the impact of each component in the proposed framework using accuracy and F1-score as performance metrics. The baseline CNN model achieves an accuracy of 92.14% and an F1-score of 90.28%. The inclusion of nuclei segmentation improves feature localization, resulting in noticeable performance gains. Further improvement is observed with the addition of dual-branch feature extraction, which captures both mitotic and nuclear atypia characteristics. The attention-based feature selection mechanism enhances discriminative feature learning, while hybrid feature fusion further refines the representation. Finally, the integration of the ensemble classifier achieves the highest performance, with an accuracy of 97.82% and an F1-score of 96.97%. These results demonstrate that each module contributes significantly to the overall performance of the proposed framework.

5. CONCLUSION AND FUTURE SCOPE:

This research introduced a system for automatic cancer of the breast grading using histopathology images that is guided by uncertainty and uses a dual-branch hybrid approach. To get accurate and dependable grading, the suggested method incorporates hybrid nuclei segmentation, attention-based feature selection, dual-branch the extraction of features for mitotic activity and nuclear atypia, and confidence-aware ensemble classification. The method successfully captures important histopathological parameters needed for grading by integrating deep learning features to morphological and textural descriptors.

With an F1-score of 96.77% and an accuracy of 97-82%, the suggested strategy beats both traditional and cutting-edge methods in experiments conducted on the MITOS-ATYPIA-14 dataset. According to the findings, classification performance and resilience are much improved when adaptive feature fusion & ensemble learning are combined. All things considered, the suggested methodology eliminates the subjectivity of human evaluation by providing an automated, fast, and uniform method for breast cancer grading.

5.1. Future Scope

While the suggested framework does a good job of automated breast cancer grading, there are a number of ways it might be improved for even greater efficiency and practicality.

To develop a comprehensive Nottingham grading system, future research may concentrate on include other histopathological grading elements such tubule formation. Improving the model's generalisability and robustness may be achieved by using multi-institutional datasets that are bigger and more varied. In order to make the framework usable in real-world clinical procedures, which often use high-resolution gigapixel pictures, it has to be extended to deal with whole-slide images (WSIs). The ability to translate of model predictions may be improved by using explainable AI approaches, which in turn helps physicians comprehend & trust the system. Improving feature representation and the performance of classification might be achieved further by investigating advanced deep learning algorithms including self-supervised learning techniques and transformer-based models. Lastly, the system will be more useful and scalable for regular diagnostic usage by optimising the computing efficiency of the framework, which will facilitate real-time implementation in clinical situations.

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