

MEDLIGHTNET: A LIGHTWEIGHT MULTI-COLOUR-SPACE CNN FOR CHILDHOOD MEDULLOBLASTOMA DIAGNOSIS FROM HISTOPATHOLOGICAL IMAGES

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Abstract: Early and accurate diagnosis of Childhood MedulloBlastoma (CMB) is essential for timely intervention and improved prognosis. Histopathological image analysis has greatly benefited from the integration of artificial intelligence. However, conventional models often rely solely on the RGB colour space, limiting the ability to capture diverse visual cues present in tumour tissues. This paper introduces a novel Multi-Colour-Space Decision Support System (MCSDSS) for CMB prediction using histopathological images, incorporating RGB, HSV, and LAB colour spaces to enhance feature representation. A custom-designed lightweight Convolutional Neural Network (CNN), MedLightNet, is designed to extract deep features from each colour space individually. The extracted features are fused to generate a comprehensive diagnostic biomarker for CMB prediction. Experimental validation demonstrates that the proposed MCSDSS powered by MedLightNet, achieves superior diagnostic performance compared to traditional single-space and conventional deep learning models, with high accuracy, sensitivity, and specificity.

Keywords: Childhood medulloblastoma, histopathological image analysis, multi-colour-space, lightweight convolutional neural network, medical image classification.

I. INTRODUCTION

CMB is one of the most common and aggressive brain tumours in paediatric patients, and early diagnosis is crucial for improving survival rates and guiding effective treatment strategies. Histopathological imaging plays a vital role in diagnosing medulloblastoma by providing detailed visual insights into tumour morphology. However, manual analysis of these images is often time-consuming, prone to inter-observer variability, and dependent on the expertise of pathologists. Recent advancements in machine learning, particularly deep learning techniques, have shown promise in automating the detection and classification of histopathological images, significantly improving diagnostic accuracy and reducing human error. Despite these advancements, many existing automated systems rely on traditional image representation techniques, such as the RGB colour space, which may not fully capture the complex morphological and textural patterns crucial for accurate diagnosis. Furthermore, RGB-based systems are often sensitive to variations in tissue colour and lighting conditions, which can affect their robustness and generalizability.

To address these challenges, this paper presents MedLightNet, a novel lightweight CNN for the early detection of CMB from histopathological images. MedLightNet leverages a multi-colour-space approach, incorporating RGB, HSV, and LAB colour spaces to extract complementary features that are crucial for accurate tumour detection. Each colour space offers distinct advantages. RGB provides raw colour information, HSV separates chromatic content from intensity, and LAB offers a perceptually uniform colour model, making it device independent. By integrating features from these diverse colour spaces, MedLightNet enhances the model's robustness and discriminative power, enabling more precise identification of medulloblastoma in paediatric patients. The major contributions of this work are as follows:

- A lightweight CNN architecture, MedLightNet, specifically designed for histopathological image analysis, ensuring computational efficiency while maintaining high classification performance.
- A multi-colour-space framework that fuses features from RGB, HSV, and LAB to enhance feature extraction and improve diagnostic accuracy.
- The evaluation of MCSDDS system on a publicly available dataset demonstrating superior performance compared to traditional single-space and conventional deep learning models.

This paper is organized as follows: Section 2 reviews related work in CMB classification using histopathology images and colour space analysis. Section 3 describes the proposed methodology and the design of MedLightNet. Section 4 outlines the experimental setup, including datasets and evaluation metrics. Section 5 presents the results and compares the performance of MedLightNet with existing approaches. Section 6 concludes the paper and discusses future directions for enhancing paediatric tumour diagnosis.

II. RELATED WORKS

A deep learning based histopathological image classification for CMB is discussed in [1]. A Ten-layer CNN is designed to examine stained tissue slides and predict tumour subtypes. It uses parametric ReLU and ReLU as activation function

in hidden layers. The automatic segmentation of histopathological tissue improves accuracy in identifying CMB cells [2]. It employs eight different approaches such as colour-based segmentation, local and global segmentation methods and clustering techniques. The contribution of computer-aided and biological features is studied in [3] for the classification of CMB. At first, K-means colour segmentation is employed to segment the CMB cells. Then colour, texture and morphological features are extracted from the segmented cells followed by feature reduction by Principal Component Analysis (PCA). Support Vector Machine (SVM) is used for binary and multiclass classification of CMB. Multivariate Analysis of Variance (MANOVA) based effective feature reduction technique is employed in [4] instead of PCA reduction in [3].

Textural feature classification analysis of CMB in WHO categories is shown in [5]. Five different texture features such as Grey-Level Co-occurrence Matrix (GLCM), Gray Level Run-length Matrix (GLRM), first-order histogram features, Local Binary Pattern (LBP) and Tamura features were extracted. Then features are reduced by PCA, and five-fold cross validation is employed for splitting dataset. Five classifiers such as Linear Discriminant Analysis (LDA), Quadratic Discriminant Analysis (QDA), SVM, k Nearest Neighbour (KNN) and Decision Tree (DT) are employed for the classification. Different automated diagnostic methods for CMB classification are reviewed in [6]. Automated classification of CMB is described in [7] using deep learning techniques with transfer learning. Different conventional architectures such as VGG-16, VGG-19, ResNet-50, Inception-V3 are applied for CMB classification. Deep transfer learning with multi scale EfficientNets is utilized in [8] for end-to-end CMB classification. EfficientNet-B0 to EfficientNet-B5 are utilized for different input image sizes and network dimensions.

Artificial Intelligence (AI)-based pipeline classification of CMB using histopathological images is defined in [9]. It uses texture features such as GLCM and GLRM along with features extracted from three CNN: the ResNet-101, Inception, and InceptionResNet models. Then, the fused features are classified using six different classifiers (LDA, QDA, SVM, Naïve Bayes (NB), KNN, and RF classifiers). A composite deep learning pipeline architecture for CMB classification is introduced in [10]. At first, spatial features are extracted using ten different CNNs. Discrete Wavelet Transform (DWT) is used for feature fusion and reducing the features also. Sequential forward and backward based algorithms are employed for feature selection and then Bi_Long Short-Term Memory (Bi_LSTM) is used for classification.

An AI based diagnosis is used for classification of CMB in [11]. Spatial DL features are extracted from three CNNs: DenseNet-201, MobileNet, and ResNet-50. DWT is also utilized to extract time-frequency features. These features are fused and then reduced by using PCA and discrete cosine transform. Fiva classifiers are used for the classification that includes linear and cubic SVM, ensemble subspace discriminant, LDA and k-NN. Shearlet based multiscale framework for CMB diagnosis is described in [12]. The improved sequential forward selection algorithm is described for selection of dominant feature subset. Then for melanoma classification, the Multi-Layer Perceptron (MLP) uses feed forward neural network with backpropagation for feed forward non-linearity with adaptive weights.

A multi-center Swedish cohort evaluation of state-of-the-art methods for CMB classification using digital histopathology and deep learning is described in [13]. Two feature extractors such as universal histopathology model and context-aware contrastive histopathology model are studied for the classification of CMB, and the performances are compared with ImageNet based pre-trained ResNet50. Two attention-based approaches such as multiple-instance learning and clustering-constrained-attention are evaluated. Advanced feature analysis is implemented in [14] for CMB classification. From the Whole Slide Image (WSI), perceptual features, Fourier LBP, Histogram, Gabor and GLCM features are extracted. Then the multidimensional feature set is classified using KNN, SVM, NB and logistic

regression. A transfer learning-based method for CMB classification is described in [15]. A large and deep VGG architecture with 16 layers and a 2-layer simple architecture are employed for anaplastic and non-anaplastic CMB classification from WSI.

Vision Transformer (ViT) and stain normalization-based classification system is described in [16]. It uses a pre-trained ViT B/16 model for feature extractor. PCA is implemented for reduction of trained features dimension. Then, SVM algorithm is used for classification of CMB tumours. A Reinhard stain normalization is used for classification accuracy of CMB tumour images using the ViT model. Vision Transformer (ViT) is adapted to transformer encoder architecture for classification of images. Also, it includes Layer Normalization, Multi-head Attention, and MLPs to capture dependencies within images. A multimodal data fusion approach is discussed in [17] for CMB classification. The ResNet-50 architecture with adam optimizer is connected to Cox Proportional Hazards (Cox-PH) for the classification brain tumour subtypes such as ependymoma and medulloblastoma. For classification of WSI's a locally supervised learning along with Random Feature Reconstruction (RFR) model is implemented in [18]. Different pretrained CNN architectures are combined for CMB classification in [19]. The CNN architectures such as ResNet-50, MobileNet, Xception model are ensembled to achieve CMB classification more accurately.

III. METHODS AND MATERIALS

The proposed MCSDDS architecture consists of four different layers to classify CMB. Figure 1 shows the block diagram of the proposed MCSDDS system.

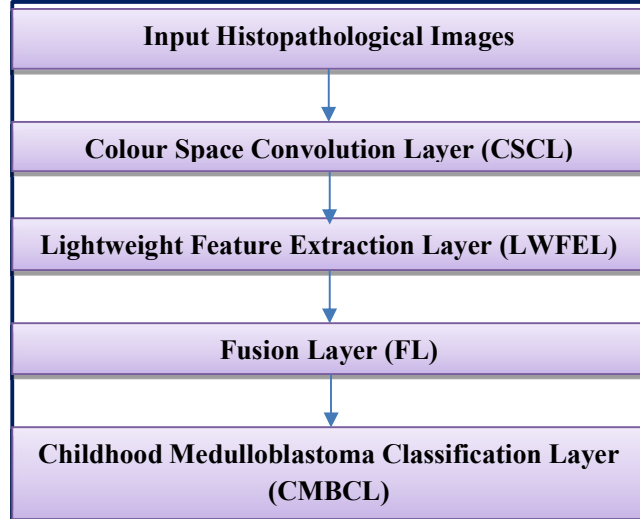


Fig. 1 Proposed MCSDDS system

The CSCL is designed to identify and extract discriminative features from multiple colour spaces. It processes the input image independently in RGB, HSV, and LAB channels, allowing the model to capture complementary colour and texture information relevant to the classification of CMB. The LWFEL is a computationally efficient CNN-based feature extractor that ensures low latency and minimal memory requirements. This layer employs depth-wise separable convolutions and reduced

filter sizes to extract high-quality spatial features while maintaining a light-weight design suitable for resource-constrained environments. The FL integrates the deep features extracted from the three colour space branches (RGB, HSV, and LAB). The final CMBCL maps the fused feature vector to the target output classes. These layers are discussed in the following sub-sections briefly.

A. Colour Space Convolution Layer (CSCL)

The primary objective of the CSCL is to improve the discriminative power of deep learning models by converting input images into a colour space that more successfully differentiates significant visual signals. Input images are often represented in the RGB (Red, Green, Blue) colour space, with each pixel denoted by three values that correspond to the intensities of red, green, and blue light. In RGB images, colour and intensity are closely linked, potentially masking minor variations in tissue staining, which is essential for distinguishing medulloblastoma subtypes. The CSCL resolves this by transforming the image into a colour space such as HSV, and LAB. HSV (Hue, Saturation, Value) accurately expresses colours in alignment with human perception, differentiating the colour type (hue), its intensity (saturation), and its luminance (value), hence facilitating the identification of staining patterns and colour intensities in tissue sections. The colour space conversion from RGB to HSV [20] is as follows:

The R, G, B values are divided by 255 to change the range from 0.255 to 0.1: $R' = \frac{R}{255}, G' = \frac{G}{255}, B' = \frac{B}{255}$. Equation 1 to 6 shows the conversion of RGB to HSV Formula.

$$C_{max} = \max(R') \quad (1)$$

$$C_{min} = \min(R') \quad (2)$$

$$\Delta = C_{max} - C_{min} \quad (3)$$

$$H = \begin{cases} 0, & \text{if } \Delta = 0 \\ 60^\circ \times \left(\frac{G-B}{\Delta} \bmod 6 \right) & \text{if } C_{max} = R \\ 60^\circ \times \left(\frac{B-R}{\Delta} + 2 \right) & \text{if } C_{max} = G \\ 60^\circ \times \left(\frac{R-G}{\Delta} + 4 \right) & \text{if } C_{max} = B \end{cases} \quad (4)$$

$$S = \begin{cases} 0 & \text{if } C_{max} = 0 \\ \frac{\Delta}{C_{max}} & , \text{otherwise} \end{cases} \quad (5)$$

$$V = C_{max} \quad (6)$$

where C_{max} is maximum channel value, C_{min} is minimum channel value, Δ is the channel difference. The CIELAB ($L^*a^*b^*$) is a perceptually uniform colour space in which L^* denotes brightness, a^* corresponds to the red-green axis, and b^* corresponds to the yellow-blue axis, making it very responsive to minor chromatic variations that are sometimes crucial for delineating tumour borders. The colour space conversion from RGB to LAB [21] happens in three main stages.

1. **Convert RGB to XYZ colour space:** The RGB values are normalized to [0, 1] before applying the gamma correction, and then transform using the XYZ matrix as shown below:

$$\begin{bmatrix} X \\ Y \\ Z \end{bmatrix} = \begin{bmatrix} 0.4124 & 0.3576 & 0.1805 \\ 0.2126 & 0.7152 & 0.0722 \\ 0.0193 & 0.1192 & 0.9505 \end{bmatrix} \begin{bmatrix} R \\ G \\ B \end{bmatrix} \quad (7)$$

2. **Normalize XYZ based on the reference white:** The obtained X, Y, Z values are normalized using the reference white X_n, Y_n, Z_n

$$x = \frac{X}{X_n}, \quad y = \frac{Y}{Y_n}, \quad z = \frac{Z}{Z_n} \quad (8)$$

3. **Convert XYZ to Lab using non-linear scaling:** Apply the following non-linear function to obtain Lab colour space.

$$f(t) = \begin{cases} t^{\frac{1}{3}}, & \text{if } t > 0.008856 \\ 7.787t + \frac{16}{116}, & \text{otherwise} \end{cases} \quad (9)$$

$$L^* = 116 f(y) - 16 \quad (10)$$

$$a^* = 500 [f(x) - f(y)] \quad (11)$$

$$b^* = 500 [f(y) - f(z)] \quad (12)$$

where L^* represents the brightness or lightness of the colour from 0 (black) to 100 (white) which does not carry any colour information, a^* represents the green-red axis, negative values (greenish tones), positive values (reddish tones), shows how much the colour leans toward red or green, b^* represents the blue-yellow axis, negative values (bluish tones), positive values (yellowish tones), shows how much the colour leans toward blue or yellow, $f(x)$, $f(y)$, $f(z)$ are non-linear transformations applied to the normalized XYZ colour space components. In CSCL, once the image is converted into the RGB, HSV and LAB colour spaces, they are processed independently for extracting features using LWFEL.

B. Lightweight Feature Extraction Layer (LWFEL)

The proposed LWFEL starts with a 3×3 Convolutional layer using 16 filters (Conv 1) in the first block, succeeded by a max pooling layer to diminish spatial dimensions. In the second block, two Convolutional layers (Conv 2) using 16 and 32 filters is implemented, then succeeded by pooling. In the third block, Conv 3 begins with 16 filters and thereafter employs 32 and 64 filters to extract more abstract information followed by max pooling layer. A 3×3 global average pooling layer ultimately condenses the acquired spatial data, facilitating classification. Figure 2 depicts a CNN architecture used for feature extraction from histopathological images of CMB, obtained at 10x and 100x magnification.

The standard Convolutional operation computes weighted sums over local areas by sliding 3×3 filter over all input channels, such as colour channels in an image. At each sliding location, the convolution calculates the dot product of filter weights and the overlapping 3×3 input patch, yielding a single result. A feature map that emphasises edges, corners, and textures is obtained by repeating this procedure over the image's height and breadth. With 16 filters in block 1, the layer creates 16 feature maps, each represents a distinct feature. It extracts low-level patterns from input and passes them to higher layers for processing. The standard convolution combines spatial (local) and cross-channel (depth) information for richer early feature learning. For an input image $F \in \mathbb{R}^{H \times W \times C_{in}}$ and output feature map $O \in \mathbb{R}^{H \times W \times C_{out}}$ the standard convolution operation is:

$$O_{h,w,out} = \sum_{i=1}^k \sum_{j=1}^k \sum_{C_{in}=1}^{C_{in}} W_{i,j,C_{in}} \cdot F_{h+i,w+j,C_{in}} \quad (13)$$

where W is the convolution kernel of size $k \times k \times C_{in} \times C_{out}$, C_{in} is number of input channels, C_{out} is number of output channels, h, w is spatial position.

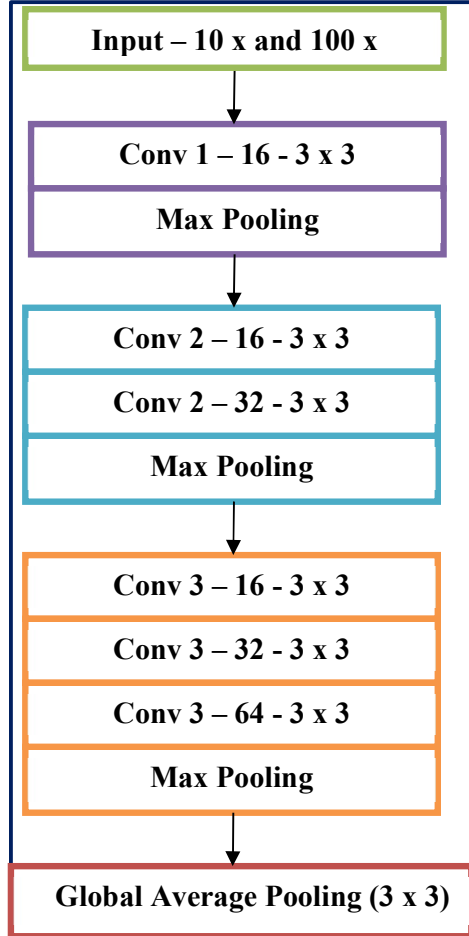


Fig. 2 LWFEL of the proposed MCSDDS architecture

Depthwise convolution employs an individual spatial filter (e.g., a 3×3 kernel) for each input channel separately. This indicates that each channel is handled independently, without any interaction or blending between them. This method is computationally efficient and optimises parameter use; nevertheless, it is limited to recognising spatial patterns within individual channels and fails to integrate or comprehend linkages across many channels. For Depthwise convolution, the input $F \in \mathbb{R}^{H \times W \times C}$ is convolved independently per channel:

$$O_{h,w,C} = \sum_{i=1}^k \sum_{j=1}^k W_{i,j,C} \cdot F_{h+i,w+j,C} \quad (14)$$

where W is now a set of channel-specific kernels of size $k \times k \times C$. Depthwise separable convolution is a bifurcated procedure that substitutes conventional convolution to enhance computing efficiency. During the Depthwise phase, an

individual spatial filter (e.g., a 3×3 kernel) is applied individually to each input channel, ensuring that each feature map is filtered without inter-channel mixing. This enables the model to identify localised patterns such as edges, textures, and distinct structural elements exclusive to each channel. By functioning on a channel-by-channel basis, it significantly decreases the necessary operations relative to conventional convolution, making it suitable for lightweight architectures such as LWFEL.

$$F_d(x, y, c) = \sum_{i=-k}^k \sum_{j=-k}^k K_d(i, j, c) \cdot F(x + i, y + j, c) \quad (15)$$

It performs spatial filtering channel-wise. This operation applies one separate filter per channel, each $K_d(i, j, c)$ is a spatial kernel (3×3) that operates only on the corresponding channel c of the input. It captures local spatial features (edges, textures, boundaries) in histopathology such as nuclei boundaries, tumor cell patterns, etc. Traditional convolutions operate over all channels together, which is computationally expensive. Depthwise convolution reduces this cost by operating channel-wise independently. Global Average Pooling (GAP) is a dimensionality reduction technique that calculates the average of all spatial components in each feature map, yielding a single scalar value for each channel. Instead of flattening feature maps or using thick layers, GAP generates a concise summary that encapsulates the general presence and intensity of learnt features over the whole image. It avoids overfitting and significantly decreases the number of parameters while preserving essential classification information. The result is a compact, fixed-dimension vector prepared for input into the final classifier. It is defined as

$$GAP_c = \frac{1}{H \cdot W} \sum_{x=1}^H \sum_{y=1}^W F_p(x, y, C) \Rightarrow GAP(F_p) \in \mathbb{R}^C \quad (16)$$

It essentially captures the presence of a feature (e.g., tumour region patterns) across the image, without focusing on exact location.

C. Fusion Layer (FL)

The FL is essential in CMB classification since it integrates feature representations acquired from several networks. In the Convolutional backbone, histopathological images are processed by many parallel pathways, each describing distinct spatial, textural, or chromatic attributes, including cell form, nuclear density, and tissue structure. The FL integrates these features by concatenation, stacking the feature maps along the channel dimension to form a cohesive, high-dimensional tensor while preserving signal integrity. This integrated representation enhances the model's comprehension by combining detailed cellular information with overarching spatial patterns, therefore maintaining both local and contextual diagnostic signals. It improves classification accuracy while preserving the system's lightweight and scalable architecture, making it ideal for real-time and clinical applications in paediatric brain tumour investigation.

The proposed MCSDDS model obtains three concurrent feature maps produced by CSCL functioning on RGB, HSV, and Lab inputs. These features are then combined by a concatenation procedure, which retains all extracted information by stacking feature maps along the channel dimension. The integrated output creates an extensive multi-channel representation that integrates luminance, chrominance, and structural information, allowing the classifier to provide precise judgements across tumour subtypes. The fused output is defined as

$$F_{fused}(x, y) = [F_{RGB}(x, y), F_{HSV}(x, y), F_{Lab}(x, y)] \quad (17)$$

where $F_{fused} \in \mathbb{R}^{H \times W \times (C_{RGB} + C_{HSV} + C_{Lab})}$, $F_{RGB}(x, y) \in \mathbb{R}^{H \times W \times C_{RGB}}$ is the feature map from RGB, $F_{HSV}(x, y) \in \mathbb{R}^{H \times W \times C_{HSV}}$ is the feature maps from HSV, and $F_{Lab}(x, y) \in \mathbb{R}^{H \times W \times C_{Lab}}$ is the feature maps from Lab. Figure 3 shows integration of features from three colour spaces in the FL.

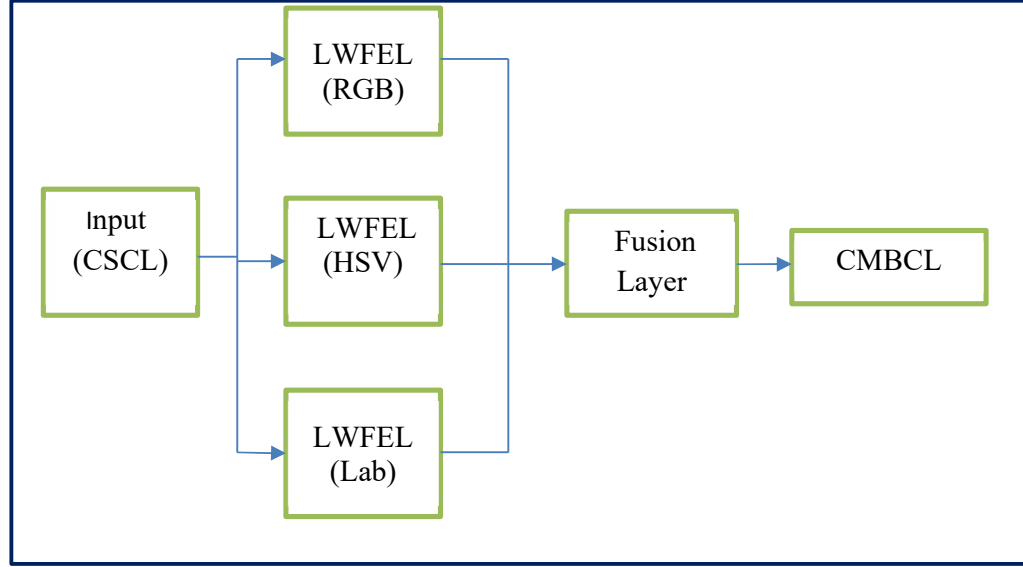


Fig. 3 Fusion Layer of the proposed MCSDDS architecture

D. Childhood Medulloblastoma Convolution Layer (CMBCL)

The CMBCL serves as the final decision-making component of the proposed MCSDDS framework. This layer is responsible for translating the high-level, discriminative features into five classes of CMB. It is composed of a fully connected neural network followed by a SoftMax activation function that outputs probabilistic scores corresponding to predefined CMB classes. The classification performance is optimized using the categorical cross-entropy loss function, which measures the divergence between the predicted class probabilities $\hat{p}$ and the ground truth labels p as:

$$L = -\sum_{k=1}^C p_k \log(\hat{p}_k) \quad (18)$$

where C is the number of CMB classes. The term corresponds to only true class contributes to the total loss. To update the model weights, the Adam optimizer is employed. Adam adaptively adjusts the learning rate using first and second moment estimates of gradients:

$$\theta_{t+1} = \theta_t - \alpha \cdot \frac{\hat{m}_t}{\sqrt{\hat{v}_t} + \epsilon} \quad \text{where } \epsilon = 10^{-8} \quad (19)$$

where, θ denotes model parameters, $\hat{m}$ is the mean of gradients, $\hat{v}$ is the average of the squared gradients and α the learning rate. The adaptive nature of Adam ensures efficient convergence and robustness, especially critical for training deep models on small histopathological datasets.

IV. RESULTS AND DISCUSSIONS

The performance of MedlightNet architecture is assessed using histopathological images obtained from [22]. This collection includes 204 images enlarged at 10x and 158 images magnified at 100x. These images are classified into five classifications: desmoplastic, classic, large cell, nodular, and normal. The resolution of the histopathological image amplified tenfold is 2048 by 1536 pixels, but the resolution of the image increased one hundredfold is just 800 by 600 pixels. Figures 4 and 5 show the sample images of 10x and 100x magnification, respectively.

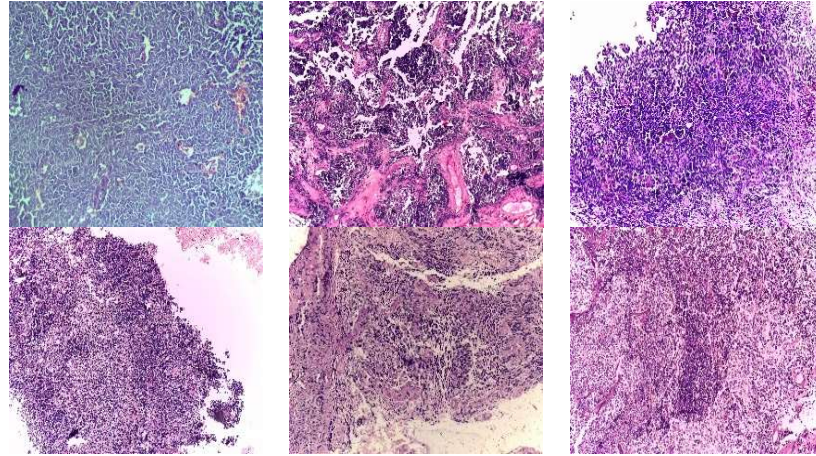


Fig. 4 Sample images magnified at 10x

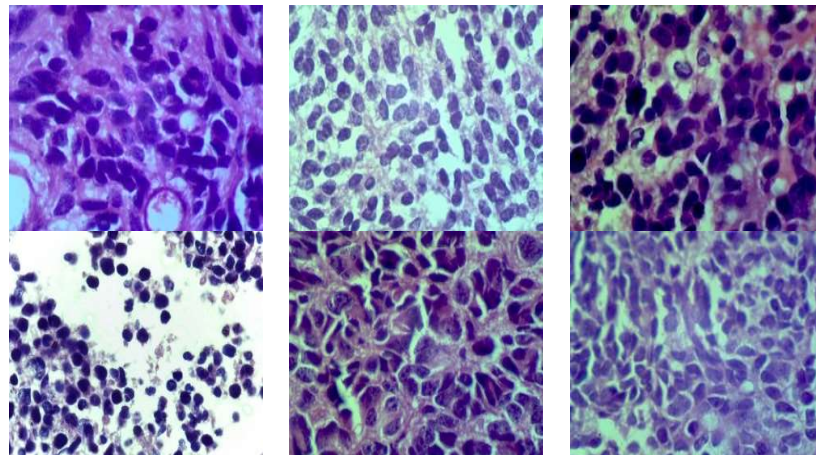


Fig. 5 Sample images magnified at 100x

To address the limited size of the dataset and achieve a balanced distribution of 500 images per class, extensive data augmentation is performed separately for each magnification level (10× and 100×) to preserve scale-dependent histological features. For both sets, label-preserving transformations are applied, including horizontal and vertical flips, and random rotations (0°–360°). Additionally, colour-based augmentations such as contrast adjustment, and brightness variation are employed to enhance visual diversity while maintaining diagnostic integrity. These augmentations are systematically applied to the original images to synthetically

expand the dataset and overcome overfitting, ensuring robust model generalization across both magnification conditions. Table 1 shows the mathematical formulae used to compute essential performance metrics such as accuracy, sensitivity, and specificity for the proposed system in the context of CMB classification at both 10× and 100× magnification. It uses the corresponding counts of true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN) from each magnification group. These metrics statistically evaluate the system's ability to differentiate between positive and negative situations, delivering a consistent and robust assessment across various image magnification levels.

TABLE. 1 Performance metrics of MedlightNet architecture

Metrics	Equation for 10× Magnification	Equation for 100× Magnification
Accuracy (%)	$\frac{TP_{10x} + TN_{10x}}{TP_{10x} + TN_{10x} + FP_{10x} + FN_{10x}} \times 100$	$\frac{TP_{100x} + TN_{100x}}{TP_{100x} + TN_{100x} + FP_{100x} + FN_{100x}} \times 100$
Sensitivity (%)	$\frac{TP_{10x}}{TP_{10x} + FN_{10x}} \times 100$	$\frac{TP_{100x}}{TP_{100x} + FN_{100x}} \times 100$
Specificity (%)	$\frac{TN_{10x}}{TN_{10x} + FP_{10x}} \times 100$	$\frac{TN_{100x}}{TN_{100x} + FP_{100x}} \times 100$
F1-Score	$F1_{10x} = 2x \frac{Precision_{10x} \times Recall_{10x}}{Precision_{10x} + Recall_{10x}}$	$F1_{100x} = 2x \frac{Precision_{100x} \times Recall_{100x}}{Precision_{100x} + Recall_{100x}}$

For training and evaluation of the proposed MCSDDS architecture for CMB classification, the augmented dataset is partitioned using a 60:20:20 split. Specifically, 60% of the images are used for training the model, 20% for validation to fine-tune hyperparameters and monitor overfitting, and the remaining 20% for testing to assess the final MCSDDS model performance on unseen data. This stratified split ensured balanced representation of all five classes across each subset. Figure 6 shows the confusion matrix obtained using RGB based feature maps for the classification of CMB among desmoplastic, classic, big cell, nodular, and normal classifications.

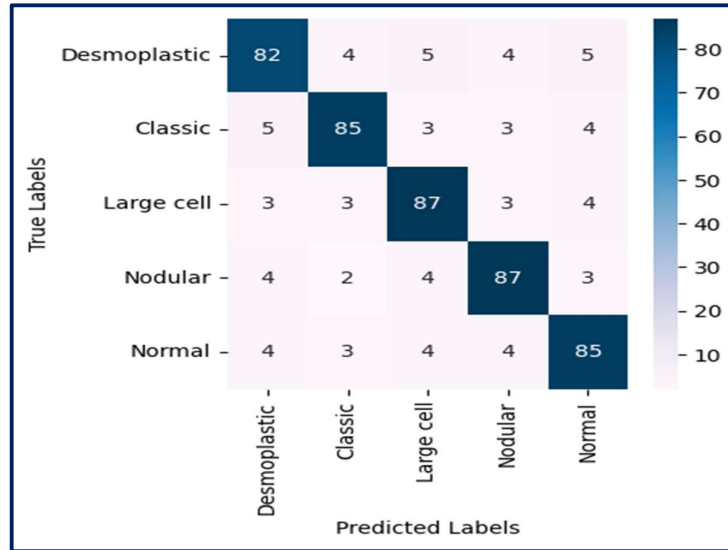


Fig. 6 RGB Confusion Matrix

It can be observed that the proposed MCSDDS architecture accurately classified many samples in each class, with correct predictions. While the classification performance is generally over 85%, misclassifications are observed primarily between visually similar subtypes. The overall performance indicates that RGB colour space provides sufficient discriminative features for reliable CMB subtype classification, although some inter-class visual similarities may limit absolute accuracy. Figures 7 and 8 show the confusion matrix obtained using HSV and Lab based feature maps respectively.

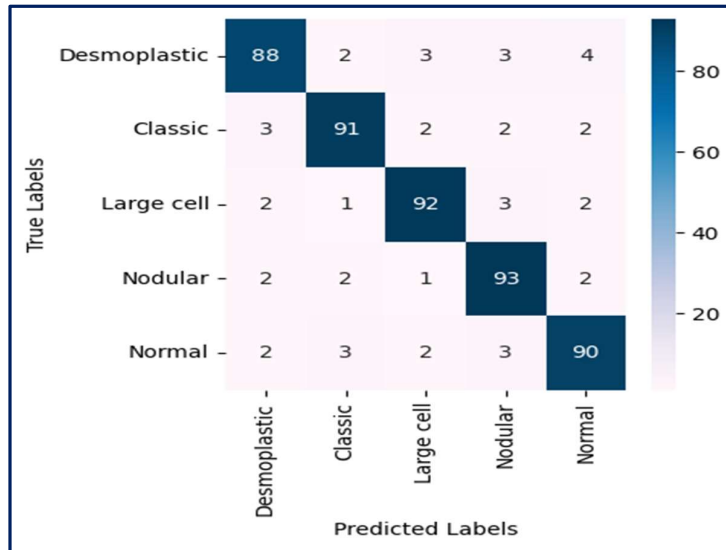


Fig. 7 HSV Confusion Matrix

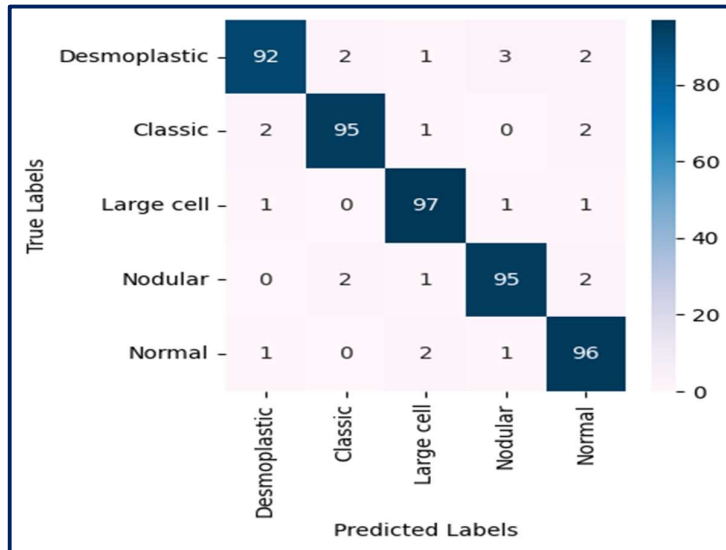


Fig. 8 Lab Confusion Matrix

When compared to the results obtained using the RGB colour space in Figure 6, with the HSV-based confusion matrix in Figure 7 demonstrates a clear

improvement in classification performance within the proposed MCSDDS architecture. Each class showing a gain of 3 to 6 correct classifications over the RGB-based results as the HSV colour space offers better inter-class discrimination. This enhancement can be also attributed to HSV's ability to decouple chromatic content (hue and saturation) from intensity, making it more effective in capturing histopathological variations.

It can be observed that a consistent improvement over both RGB and HSV, reflecting superior feature discrimination in the LAB space. Due to the LAB colour model's perceptual uniformity and its separation of luminance from chromatic components, it enables the MCSDDS system to more effectively distinguish between five classes of CMB. Figure 9 presents the confusion matrix obtained by integrating RGB, HSV, and LAB characteristics for the classification of CMB.

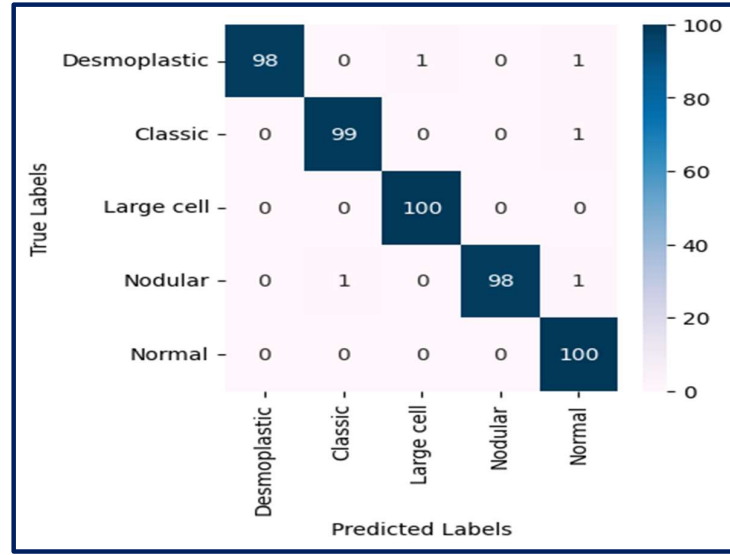


Fig. 9 Confusion Matrix- MCSDDS architecture

The final confusion matrix in Figure 9, obtained after fusing features from RGB, HSV, and LAB colour spaces, demonstrates better classification performance across all five CMB subtypes. The drastic reduction in off-diagonal values across all classes confirms that integrating features from multiple colour spaces allows the model to capture textural patterns more effectively than any single colour space alone. The RGB-based model achieved moderate accuracy, with correct classifications ranging from 82% to 87% per class, reflecting some inter-class confusion due to limited chromatic separation. The HSV colour space yielded improved results, increasing per-class accuracy to the range of 88%–93%, due to the hue and saturation differentiation. The LAB colour space further improved the system's performance, with 92%–97% correctly classified samples per class, leveraging its perceptual uniformity and effective luminance-chrominance separation to reduce misclassifications. Finally, the fusion of RGB, HSV, and LAB colour space features led to a substantial leap in classification performance, achieving near-perfect accuracy with 98%–100% correctly predicted instances per class. Figure 10 compares the proposed MCSDDS system with EfficientNet [8], and Bi-LSTM [10].

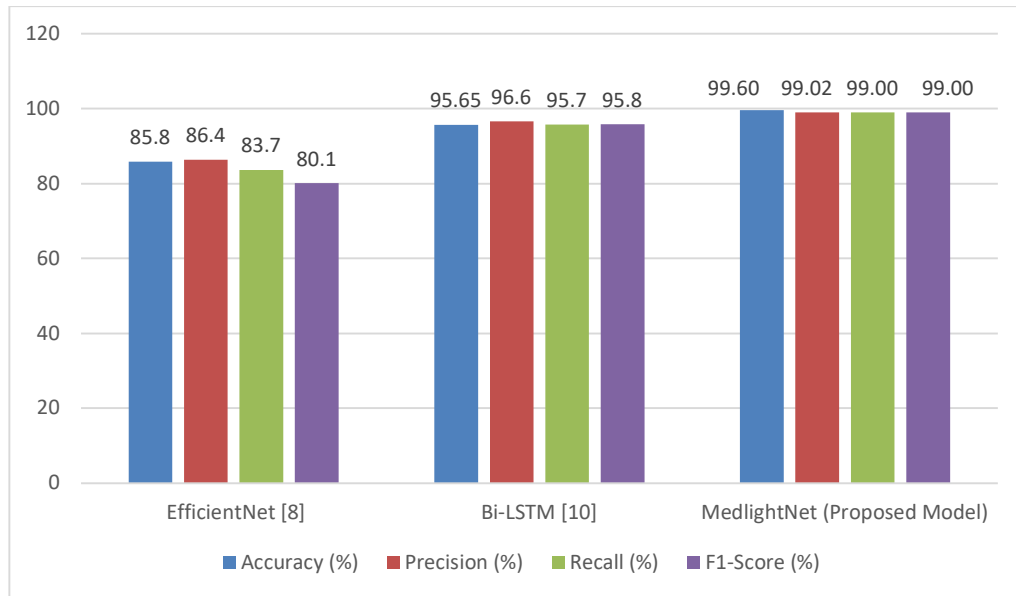


Fig. 10 MedLightNet Performance Comparison

It can be seen from Figure 10 that the proposed MedLightNet system performs better than SVM, EfficientNet, and Bi-LSTM, with classification accuracy of 99.36%, precision of 98.42%, recall of 98.4%, and F1-score of 98.4%. The lightweight architecture and multi-colour-space processing of MedLightNet improve texture and detail detection by incorporating RGB, HSV, and LAB characteristics.

V. CONCLUSIONS

In this study, a MCSDDS architecture is proposed for the accurate classification of CMB using histopathological images. It integrates the properties of RGB, HSV, and LAB colour spaces through CSCL, LWFEL, and a FL for multi-space feature integration. The MCSDDS system is trained and evaluated on an augmented dataset with a 60:20:20 split, ensuring balanced representation across five classes: desmoplastic, classic, large cell, nodular, and normal. Experimental results demonstrated that the classification performance progressively improved when the individual colour space features are fused to form multi-space representations. While RGB features provided a reasonable baseline, HSV and LAB colour spaces offered enhanced class separability, with LAB yielding superior discriminative power. The final fusion of RGB, HSV, and LAB feature maps significantly improved classification accuracy with 99.6% accuracy. The experimental results confirm that the fusion of colour feature maps enhances the model's ability to classify CMB for accurate diagnosis.

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