

# Fluorescence Microscopy And Histopathology Image Based Cancer Classification Using Graph Convolutional Network With Channel Splitting

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## ABSTRACT

Since the proliferation of deep learning, several convolutional neural networks (CNN) are developed to attain significant breakthroughs for automated cancer classification using histopathology and fluorescence microscopy images. This work enhances the performance of human breast and lung cancer classification further by exploring graph convolutional networks (GCN) upon a proposed light-weight deep convolutional backbone. A two-layer GCN is developed by splitting the features of graph nodes, called Channel-Splitting GCN (CS-GCN), for a holistic feature representation of image-based spatial structure. The significance of region-aware distinctness is explored for building a correlation among neighboring regions through the node-level mixed feature propagation of a graph. The experiments are carried out on three public datasets, representing the breast cancer (actin-labelled fluorescence microscopy image dataset (FMID), and BreakHis dataset), and lung cancer (LC25000) dataset. The top-1 accuracies attained on these datasets using the ResNet-50 backbones are: FMID 99.30%, BreakHis-40x 98.0%, BreakHis-100x 97.81%, BreakHis-200x 97.33%, BreakHis-400x 96.85%, and LC2500 100.0%. The CS-GCN improves the classification performances on these datasets, while built upon a proposed convolutional stem as well as standard backbones, ResNet-50 and DenseNet-201, implying the effectiveness of the proposed CS-GCN method.

## 1. Introduction

Advances in deep neural networks have broadened the pathways of profound signal processing applications in healthcare domain including cancer diagnosis, biomedical analysis, and many more AlQuraishi and Sorger (2021), Razmjoooy, Ramezani and Ghadimi (2017), Jabeen, Khan, Damaševičius, Alsenan, Baili, Zhang and Verma (2024a), Li, Daho, Conze, Zeghlache, Le Boité, Tadayoni, Cochener, Lamard and Quellec (2024c). Breast and lung cancers are two most widely diagnosed cancer types across the world. Diagnosis of cancer at early-stages leveraging machine learning (ML) increase survival rates Pan, Hua, Tong, Li, Luo, Yang and Ding (2025), Abbas, Le Vuong, Kim, Song and Kwak (2023), Talib, Amin, Sharif and Raza (2024). The histopathology and fluorescence microscopy images represent crucial phenotypic information, which is indispensable for accurate pathological diagnosis of breast cancer. The diagnosis by human experts requires domain knowledge Oei, Hou, Liu, Zhong, Zhang, An, Xu and Yang (2019). Also, proper treatment is a sensitive and labor-intensive task, and expensive for common people. The cost of cancer prognosis can be reduced using computer-aided diagnosis (CAD) tools Toğaçar, Özkurt, Ergen and Cömert (2020).

The rapid increase of biomedical and pathological images of breast and lung cancers have guided deep learning methods to attain significant breakthroughs in medical imaging Li, Mei, Li, Yu and Liu (2024a), Abdulaal, Valizadeh, Amirani and Shah (2024), Cai, Li, Razmjoooy and Ghadimi (2021), Fu, Chen, Wang and Huang (2025), Jabeen, Khan, Hameed, Alqahtani, Alouane and Masood (2024b). Beyond binary classification, sub-categorization of multi-class breast and lung cancer is a vital image recognition challenge due to subtle variations in cell structures, illumination, and external environment. In addition, normal and benign cells exhibit various mechanical properties. Also, cancer cells have irregular and abnormal growth. Thus, structural information and organization of cells is pivotal for determining the malignant cells and can be utilized as a diagnostic marker, which is beyond human inspection. Moreover, cell classification relying on the subcellular features and actin filaments (e.g., human breast epithelial cell lines, Fig. 4) is a complex image recognition problem that has not been explored widely in prior works Oei et al. (2019). Thus, cancer cell classification with high precision is considered to be a challenging job.

Convolutional neural networks (CNNs) and related deep learning (DL) techniques provide fast and accurate cancer classification results, leading to early detection of various types of cancers e.g., breast, skin, lung, etc. Zhang, Zhang, Gao, Bai, Li and Ghadimi (2024a), Razmjoooy, Sheykhammad and Ghadimi (2018), Xu, Sheykhammad,

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Ghadimi and Razmjoo (2020), Han, Zhao, Yin, Hu and Ghadimi (2024), Bera, Bhattacharjee and Nasipuri (2022a). Several works have addressed cancer classification using histopathology images, and especially, actin labeled fluorescence microscopy images. However, most of the available methods on breast cancers studied binary classification (i.e., malignant or benign) and achieved high performances, e.g., BreastNet Toğaçar et al. (2020), CSF transformer Huang, Yu, Huang and Cheng (2023), transfer learning methods Almaslukh (2024), Maurya, Pandey, Dutta and Karnati (2024), etc. A few ML/DL works experimented with multi-class categorization of breast cancers, providing more accurate insights for better diagnosis and treatment e.g., BHCNet Jiang, Chen, Zhang and Xiao (2019). Some studies explored transfer learning and fusion methods with pre-trained CNNs Jabeen, Khan, Alhaisoni, Tariq, Zhang, Hamza, Mickus and Damaševičius (2022).

Graph convolutional network (GCN), a popular variant of graph neural network (GNN), can be integrated with traditional CNN to build a graph structure comprising with nodes and edges Kipf and Welling (2017). Other variations of GNN include graph recurrent neural network, graph attention network, etc. GCN is suitable for solving classification of different types of human and plant diseases, human actions, etc. Berenguer, Kvasnytsia, Bossa, Mukherjee, Deligiannis and Sahli (2024), Bera, Bhattacharjee and Krejcar (2024a), Chen, Zhou, Ke, Huang, Xiong, Huang, Ma, Ning, Wu and Wu (2023), Liu and Ghadimi (2024), D’Souza, Wang, Giovannini, Foncubierta-Rodriguez, Beck, Boyko and Syeda-Mahmood (2024). Though diverse GCNs proved their efficacy in classifying histopathology, mammogram, MRI, and other categories of images, yet, more attention should be given for addressing challenges pertinent to medical image/signal processing. Existing works show pathways of GCNs in capturing relevant spatial descriptors for improving CAD performances Ding, Gao, Wang, Lu and Shi (2023), multi-level fusion of graphs for capturing topological relationships Peng, Peng, Zhou, Han, Xu, Lu and Lv (2024), etc. However, channel-wise feature calibration utilizing GCN that facilitates effective feature selection is not studied in existing works. This work adapts a multi-layer GCN devised by Kipf and Welling (2017), for learning region-aware semantics and enhancing feature summarization by channel-wise feature mixing. The GCN enables to recognize sub-classes of a variety of histopathology image datasets with enhanced performances.

Here, the importance of local contextual regions is integrated and propagated through the nodes of a spatial graph. A new feature aggregation scheme is developed by mixing node-level features, and then splitting them by down-sampling into a low dimension for selecting discriminative features through a GCN. The proposed method offers a lower computational cost by developing a base convolutional stem. The proposed method, named channel-splitting graph convolutional network (CS-GCN), demonstrates multi-classification of breast and lung-colon cancer sub-types. The contributions of this work are:

- A graph-based feature learning method using a two-layer GCN is integrated upon a CNN backbone for the classification of breast and lung-colon cancer histopathology images.
- The proposed method develops a low resource-intensive framework (i.e., light-weight deep learning model) by splitting and mixing node features of a spatial graph for precise feature representation.
- Performance improvement over existing methods on three public datasets, representing fluorescence microscopy images of breast, and histopathological images of breast and lung-colon cancers. The experimental evaluations evince superiority of proposed work.

The rest of this article is organized as follows: Section 2 summarizes related works. Section 3 describes the proposed methodology. The experimental results are showcased in Section 4, followed by the conclusion in Section 5.

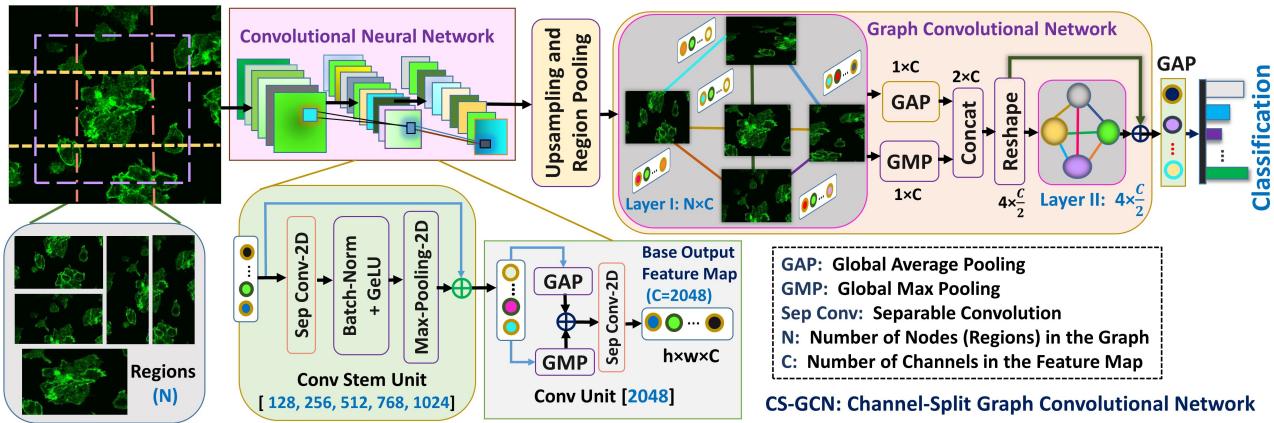
## 2. Related Works

Various cancer classification methods using artificial intelligence (AI) and machine learning (ML) techniques are summarized by Ramirez-Bautista, Chaparro-Cárdenas, Esmer and Huerta-Ruelas (2024). Handcrafted feature descriptors (e.g., Hu moment, Haralick textures, etc.) and CNNs were employed for breast cancer multi-classification using histopathology images of the BreakHis dataset Joseph, Abdullahi, Junaidu, Ibrahim and Chiroma (2022), Xiao, Li, Yan, Gao and Wang (2024).

### 2.1. Breast Cancer Classification Methods

A self-distilled supervised contrastive learning method was presented for automated diagnosis of breast cancers with limited histopathology training samples Gong, Wang, Wang, Ge, Yu and Shi (2022). The inception recurrent residual CNN was developed for histopathology image classification on the same dataset Alom, Yakopcic, Nasrin, Taha and Asari (2019). Pre-trained CNNs particularly the VGG-19, MobileNet, and DenseNet were ensembled for classifying breast histology images Kassani, Kassani, Wesolowski, Schneider and Deters (2019). A self-supervised federated learning framework enhanced the diagnostic accuracy and generalization ability Zhang, Li, Han, Ding, Li, Wang, Ying and Shi (2024b). An automated method of molecular subtyping of breast cancer was studied Niyas, Bygari, Naik, Viswanath, Ugwekar, Mathew, Kavya, Kini and Rajan (2023). Multi-stage transfer learning approach relying on domain adaptation tested for classifying histopathology images Mudeng, Farid, Ayana and Choe (2023). These works illustrate diverse learning strategies developed for cancer classification using CNNs and fusion.

Attention methods are developed for progressing state-of-the-art further in medical diagnosis, human action, object classification and many other tasks Bera, Krejcar and Bhattacharjee (2024b), Bera, Nasipuri, Krejcar and Bhattacharjee (2023). A multi-level fully convolutional attention network,



**Figure 1:** Proposed Channel-Splitting Graph Convolutional Network (CS-GCN) has been built upon a convolutional stem with pooled regions for constructing a region-aware spatial graph. The CS-GCN is a lightweight deep model developed for breast and lung cancer multi-class categorization using fluorescence and histopathology microscopy images.

called FCCS-Net, tested for breast cancer classification using transfer learning Maurya et al. (2024). A multi-scale dual-adaptive attention network relying on DenseNet was presented for breast cancer pathological image classification Li, Long, Zhan and Wu (2024b). A holistic attention network extended the bag-of-words model using Transformer for classifying breast biopsy images Mehta, Lu, Wu, Weaver, Hajishirzi, Elmore and Shapiro (2022). MbsCANet Cao, Pan, Ren, Lu and Zhang (2024) represented a multi-branch spectral channel attention network that combined the lowest frequency features with selected high frequency information from two-dimensional discrete cosine transform. DinNet exploited an attention mechanism underlying an improved DenseNet model Guo, Lin, Ji, Han, Liao, Shen, Feng and Tang (2024). These attention methods emphasize relevant features for discriminating various types of cancer images.

A study combined convolutional networks and vision transformers and tested on five histopathology datasets in addition to assessing the robustness using a generative adversarial network (GAN) Springenberg, Frommholz, Wenzel, Weicken, Ma and Strodthoff (2023). An ensemble of Swin transformers (i.e., tiny, small, base, and large) was developed for classifying the BreakHis samples Tummala, Kim and Kadry (2022). A dual-branch dual-task adaptive cross-weight feature fusion network integrated heterogeneous feature representations from CNN and transformers for cancer classification Bui, Song, Kim and Kwak (2024). A recent work has applied a Swin transformer for feature extraction to develop a two-fold feature fusion method Hao, Jia, Liu, Wang, Liu, Ji and Ganchev (2024). Notably, transformer models also evince their suitability for cancer classification.

### 2.1.1. GCN Based Approaches

Graph based message passing techniques through GCNs are used for medical diagnosis, generic object classification, and others Bera, Wharton, Liu, Bessis and Behera (2022b). A multi-cell type and multi-level graph aggregation network was developed for cancer grading Abbas et al. (2023). A MLP-mixer-based multi-path feature fusion combined

multi-level graph features with fractal structures from multiple paths for classifying histopathology images Ding et al. (2023). An automated breast cancer diagnosis method optimized with higher-order attribute enhancing heterogeneous GCN was presented using distributed nonlinear polynomial graph filter for quality enhancement and noise removal from mammogram images Kulandaivelu, Taluja, Gawas and Nath (2024). The PND-Net applied a two-layer GCN for classifying the BreakHis-40x and 100x samples Bera et al. (2024a). A label diffusion graph learning method was presented for breast cancer recognition in a semi-supervised framework Zeng and Xu (2023). An embedded fusion mutual learning was developed using an adaptive feature fusion classifier for breast and lung-colon cancer classification Li, Wu, Xu, Li, Zhu, Ye and Zhang (2023a). A cervical cell classification method applied worse-case boosting for learning from under-representative datasets Song, Zou, Choi, Lei and Qin (2024). Multi-modal fusion with a GCN has been studied for clinical analysis D’Souza et al. (2024). Delving into the depth of spatial graph structures, this work develops a GCN with channel interaction over a CNN backbone for classifying cancer samples.

### 2.1.2. Breast Cancer Fluorescence Microscopy Images

In another direction, CNNs were applied for cell classification based on actin-labeled fluorescence microscopy images, consisting of normal breast epithelial cell line, and two distinct types of breast cancer cell lines Oei et al. (2019). Following similar line of study, transfer learning-based multi-level ensemble technique was developed for classifying cell images captured by a immunofluorescence confocal microscopy and other imaging techniques for generalization Maurya, Pathak and Dutta (2021).

### 2.2. Methods on Lung-Colon Cancer

A lightweight deep model was developed for mobile-edge computing devices using microscopy images and attained superior performances for lung cancer classification Biswas and Barma (2024). An on-cloud decision support

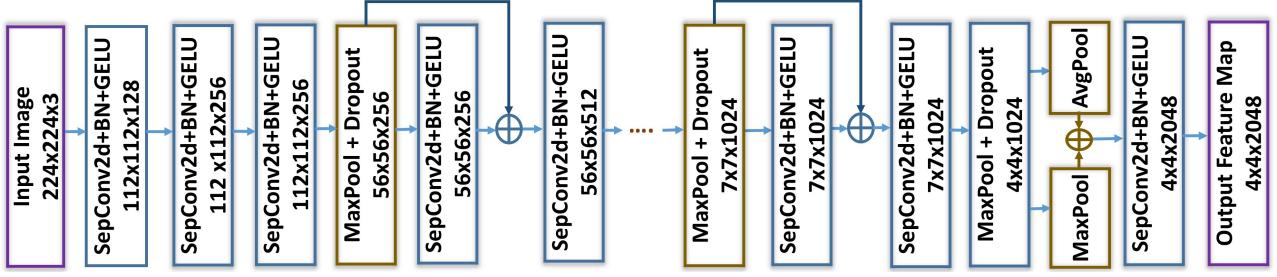


Figure 2: Model architecture of the proposed convolutional stem (CNN).

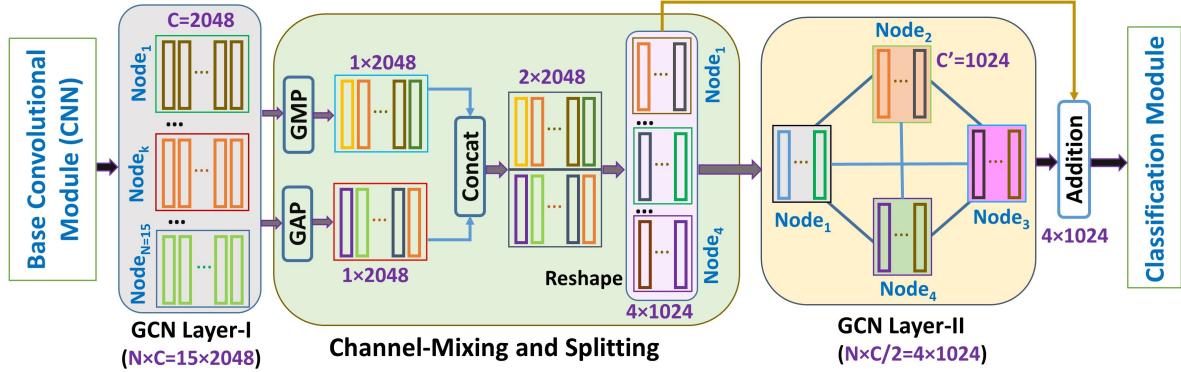


Figure 3: Proposed channel-mixing and splitting technique for GCN-based feature propagation

system for non-small cell lung cancer histology was developed by Tomassini, Falcionelli, Bruschi, Sbrollini, Marini, Sernani, Morettini, Müller, Dragoni and Burattini (2023). A multi-modal lung-colon cancer classification method using dense networks was described Uddin, Chen, Akter, Ku, Yang and Por (2024). Recently, HookEfficientNet has been developed for non-small cell lung cancer recognition Yuan, Kido, Hirata, Ueno, Imai, Chen, Ren, Yang, Chen, Qu et al. (2024).

Inspired with these decent progress, this work generalizes suitability of GCN by developing a convolutional stem attributed with low computational overhead for breast and lung-colon cancer multi-classification using fluorescence microscopy and histopathology images.

### 3. Proposed Methodology

The proposed method comprises two sub-networks: i) a base convolutional stem that can be alternatively replaced with a standard base CNN e.g., ResNet, DenseNet, etc. (ii) a two-layer GCN with channel-splitting (CS-GCN) to squeeze the feature space for aggregation. The proposed CS-GCN is added upon a base CNN, shown in Fig. 1.

#### 3.1. Base Convolutional Stem (CNN)

An input image, denoted with the class-label  $I_l \in \mathbb{R}^{h \times w \times 3}$ , is used to extract high-level deep features utilizing a CNN model. Among several CNN backbone families, residual, inception, and others have widely been used in the literature He, Zhang, Ren and Sun (2016). Besides, few works devised different CNN/stems using stacking

multiple convolutional blocks Truong, Philips and Veelaert (2024). A general convolution intrinsically requires more model parameters compared to the depth-wise separable convolution (*SepConv*) due to architectural design Chollet (2017). Also, *SepConv* offers better performances over other CNNs e.g., VGG family. Here, a convolutional stem is built using *SepConv* blocks, akin to a standard CNN backbone. The aim is to develop an efficient deep network for achieving competitive performance with respect to other backbones while trained with random initialization.

In depth-wise separable convolution, spatial convolution is applied to each channel independently, followed by point-wise convolution for transforming and projecting the channels into a new feature map. Clearly, this two-fold factoring technique decouples the feature map following spatial and channel-wise aspects for improving the learning performance. Yet, *SepConv* offers a low-rank factorization for spatial and channel-wise interactions. It is easy to use by replacing traditional convolution as *SepConv* requires lesser parameters Chollet (2017). Now, as the proposed stem is built with only a very less number of layers, aiming for a shallower architecture than existing deeper models, thus, it is lightweight. Details of the CNN/stem are provided below.

$$\mathbf{F}_{ConvBlock[k]}^{(l+1)} = BatchNorm(GELU(SepConv(\mathbf{F}^l)\mathcal{W}^l + b^l)) \quad (1)$$

The building block of proposed stem is *SepConv* with increasing channel size following residual convolutional blocks (*ConvBlock[k]*) of sizes  $[k] = [128, 256, 768, 1024]$ .

In addition, commonly used downsampling by max-pooling, the Gaussian Error Linear Unit (GELU) activation Hendrycks and Gimpel (2016), dropout, and *BatchNorm* layers are included in the network to improve the learning capacity. The convolutional stem (i.e., CNN) is shown block-wise in Fig. 2, and defined in eq. 1. Next, the output feature maps are mixed and aggregated along the channels using global average pooling (GAP) and global max pooling (GMP) layers. This feature-level aggregation is beneficial for selecting discriminatory information by mixing both max and average pooling strategies rather than using any one pooling. Subsequently, the last *SepConv* computes convolutional features with 2048 filters. The base output feature vector is denoted as  $\mathbf{F} \in \mathbb{R}^{h \times w \times C}$  where  $h$ ,  $w$ , and  $C$  imply the height, width, and channels, respectively. The weight is  $\mathcal{W}^{(l)}$  and the bias is  $b^l$  at  $l^{th}$  layer (eq. 1).

As deep layers represent high-level features, spatial references are squeezed into a reduced resolution, which might be enough to define an end-to-end network for solving generic image classification. However, in many complex visual recognition problems, such as the current one for addressing microscopy images, this type of generic CNN backbone having huge model parameters is not always beneficial for capturing discriminatory features from non-uniform cancer cell structures, resulting in underrepresented data. Also, standard pre-trained deep models (e.g., VGG, ResNet, etc.) are trained on generic object categories, which often ignore relevant information for learning structural details from biological cells. Hence, a sophisticated and lightweight backbone network is crucial for solving medical image recognition which is attempted here.

### 3.2. Region-Aware Feature Computation

Contextual information is crucial for aggregating structural content of image-level descriptions into a holistic feature map. It is observed that spatial layout of cell structure is inherently wider compared to generic object classes. The aim is to capture vital spatial structure from the cell characteristics by defining wider regions in conjunction with rectangular areas. The regions represent different slices/parts of an input image in horizontal and vertical directions, which are computed from the base feature map itself by means of a region based polling rather than slicing an input image. Following the same fashion, several hierarchical regions are selected at multi-scales from the same base feature map, geometrically implying around the centre of an image. In this way, a collection of  $N$  regions is formulated from base feature map indicating multiple spatial contexts having different aspect ratios.

For region construction, the output feature map of backbone network is upsampled to a higher spatial dimension ( $H \times W$ ) and intended to build a pair-wise spatiality mapping between actual input-image dimension and upscaled deep feature map. We establish an intrinsic relationship between image-parts with allied spatial dimensions of the feature map from which the regions are computed via bilinear pooling. The feature map dimension of each regions is uniform, given

as  $r_i \in F_i^{h \times w \times C}$ . Next, a global average pooling (GAP) is applied to select channel-wise features ( $1 \times 1 \times C$ ) from each region, resulting in a total of  $N$  regions, denoted as  $R \in F^{N \times C}$ . To this end, two different groups of non-overlapping regions representing holistic deep feature map are computed with different spatial window sizes. A bigger window-size generates  $N=5$  regions, and another group comprises  $N=15$  regions having smaller window-size. The number of regions is kept small, considering a low computational budget to formulate a graph with  $N$  regions as the nodes.

### 3.3. Graph Convolutional Network With Channel Splitting

Graph convolutional network (GCN), a sub-field of graph neural network (GNN), plays a vital role in modeling of graph structural data Li, Xie, Wan, Lv, Song and Lv (2023b). Graph convolution captures semantic correlation by building spatial relationship between the node features and propagates relevant features of different image-regions, maintaining the gradient flow as well as suppressing vanishing gradient problems. One of the most widely used layer-wise propagation rules for modeling graph-data was devised by Kipf and Welling (2017), which is apposite for semi-supervised node classification. This multi-layer GCN efficiently captures spatial structures while working with images. Herein, Kipf-Welling's formulation of normalized graph Laplacian for defining graph convolution diminishing overfitting problem is applied. Their renormalization method offers an efficient and fast layer-wise propagation of spectral convolutions on graph structures relying on the first-order approximation, called GCN. This GCN is scalable and suitable for graph-based data and broader classes of image classification including histopathology images.

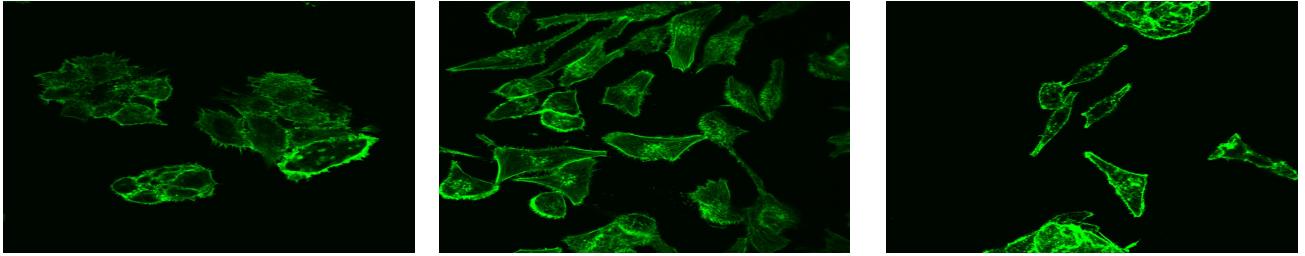
A graph  $\mathcal{G} = (\mathcal{N}, \mathcal{E})$  is constructed with  $\mathcal{N}$  nodes and  $\mathcal{E}$  edges, for deep feature propagation via semantic understanding among the local regions. A GCN is utilized to establish a spatial relation interpreting the features through a graph  $\mathcal{G}$ , where the nodes are defined with pooled channel-wise features ( $C$ ), as described in Sec. 3.2. The graph  $\mathcal{G}$  is constructed by an undirected adjacency matrix  $\mathbf{A} \in \mathbb{R}^{N \times N}$  to represent node-level interactions. The adjacency matrix  $\tilde{\mathbf{A}} = \mathbf{A} + \mathbf{I}_N$  denotes  $\mathbf{A}$  with added self-connections and  $\mathbf{I}_N$  is the identity matrix. The layer-wise feature propagation is computed as:

$$\mathcal{H}^{(l+1)} = \text{ReLU} \left( \hat{\mathbf{A}} \mathcal{H}^{(l)} \mathcal{W}^{(l)} \right); \mathcal{H}^{(0)} = \mathbf{F}; \quad \mathcal{H}^{(L)} = \mathcal{Y} \quad (2)$$

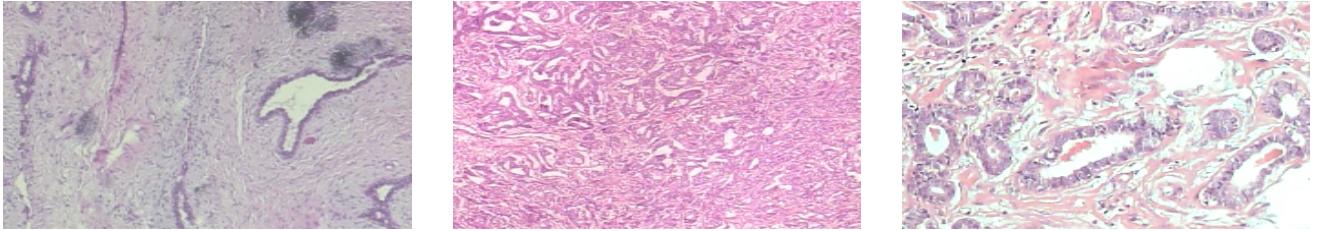
where  $l = 0, 1, \dots, L - 1$  is the number of layers,  $\tilde{\mathbf{D}}_{ii} = \sum_j \tilde{\mathbf{A}}_{ij}$ , and  $\mathcal{W}^{(l)}$  is a weight matrix of the  $l^{th}$  layer. ReLU activation function is denoted by  $\sigma(\cdot)$ . The symmetrically normalized adjacency matrix is  $\hat{\mathbf{A}} = Q \tilde{\mathbf{A}} Q$ ; and  $Q = \tilde{\mathbf{D}}^{-0.5}$  denotes the diagonal node-degree matrix of  $\tilde{\mathbf{A}}$ . The output  $\mathcal{Y}$  with the convoluted features per node.

Now, the region-aware feature vector, denoted as  $\mathbf{F}_{N \times C}$  is fed into the first layer of GCN, which captures local neighbourhood via aforesaid propagation rule, given as

$$\mathbf{F}^{(k+1)} = \mathcal{H}^{(k)} \left( \mathbf{F}_{N \times C}^{(k)}, \hat{\mathbf{A}}_{N \times N} \right) \quad (3)$$



**Figure 4:** Samples of cell images from the FMID dataset Oei et al. (2019)



**Figure 5:** Breast cancer images of the BreakHis dataset Spanhol et al. (2016)

where,  $\mathbf{F}^{(k)}$  is the output feature vector of graph convolution at  $k^{th}$  layer. Next, the feature maps are pooled along the channel dimension using global max-pooling (GMP) and global average-pooling (GAP) for selecting discriminative feature maps from these nodes (eq. 4).

$$\mathbf{F}^{(k+2)} = \text{Concat}[\text{MaxPool}(\mathbf{F}^{(k+1)}); \text{AvgPool}(\mathbf{F}^{(k+1)})] \quad (4)$$

Afterward, the channel-wise selected information, i.e., the output of layer  $(k+1)$  is  $\mathbf{F}^{(k+2)}$ , is mixed for determining an efficient feature descriptor, denoted as  $\mathbf{F}_{mix} \in \mathbb{R}^{2 \times C}$ . The mixed channel descriptors are downsampled for further feature selection and refinement,  $\mathbf{F}_{mix} \rightarrow \mathbf{F}_{m'} \in \mathbb{R}^{4 \times C/2}$ . This channel-splitting technique is suitable for reducing drastically the number of nodes of a spatial graph structure while preserving the salient features (eq. 5), shown in Fig. 3. As the number of regions could be scaled up, the node level interactions would become more complex, thereby increasing computation cost of applying more layer-wise propagation using GCN. Thus, considering a low computational cost of incurring additional layers in GCN, channel-wise feature splitting is effective for addressing cancer image classification problems.

A few methods built a GCN with comparatively more number of nodes, and then, selected discriminative nodes maintaining the same dimension of node-level features, i.e., channel dimension remains unaltered Bera et al. (2024a).

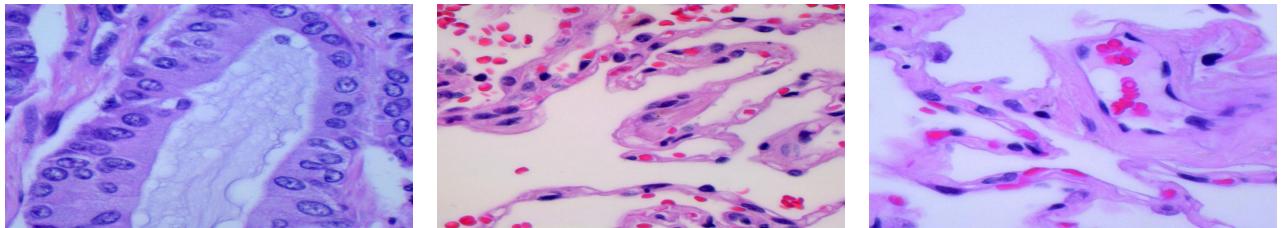
Those techniques overlook channel-wise feature interactions, and the nodes might propagate redundant features, which are addressed in this work. Essential features are selected via channel-splitting by ignoring less significant others, which in turn reduce model parameters maintaining a high performance. Thus, the CS-GCN offers an efficient feature aggregation.

$$\begin{aligned} \mathbf{F}_{m'} &= \text{Reshape}(\mathbf{F}_{mix}^{4 \times C/2}), \\ \mathbf{F}^{(k+3)} &= \mathcal{H}^{(k+2)}(\mathbf{F}_{m'}, \hat{\mathbf{A}}_{4 \times 4}) \end{aligned} \quad (5)$$

The output feature map of GCN layer-II (eq. 5) is denoted as  $\mathbf{F}^{(k+3)}$ . It represents a decreased feature space by mixing and reducing channel-wise features, obtained from GCN layer-I (eq. 3). Afterward, an average pooling layer is included to summarize GCN based feature maps. This readout layer aggregates blended and reduced node-level features into a fixed-dimensional feature vector  $\mathbf{F}_G$ .

$$\begin{aligned} Y_{pred} &= \text{Softmax}\left(\text{BatchNorm}(F_G)\right), \\ \text{where } F_G &= \text{AvgPool}(\mathbf{F}^{(k+3)}) \end{aligned} \quad (6)$$

The batch normalization (*BatchNorm*) and dropout layers are included in the network for handling the overfitting issues. The final feature vector is passed through a *softmax*



**Figure 6:** Samples of lung cancer images from the LC25000 dataset Borkowski et al. (2019).

**Table 1**

Dataset summary with the best Accuracy (%) of CS-GCN(+)

Dataset	Train: Test	No. Class	Accuracy (Proposed CNN)	Accuracy (ResNet-50)
FMID	402:150	3	97.22	99.30
BreakHis40x	1395:600	8	96.83	98.00
BreakHis100x	1460:621	8	97.43	97.81
BreakHis200x	1415:598	8	97.17	97.33
BreakHis400x	1270:550	8	96.11	96.85
LC25000	17500:7500	5	99.87	100.0

**Table 2**

Detailed specification of BreakHis Dataset Spanhol et al. (2016)

Subtype / Magnification	40x	100x	200x	400x	Total Images	No. Patients
Benign	652	644	623	588	2480	24
Malignant	1370	1437	1390	1232	5429	58
Adenosis (A)	114	113	111	106	444	4
Fibroadenoma (F)	253	260	264	237	1014	10
Phyllodes Tumor (PT)	109	121	108	115	453	3
Tubular Adenoma (TA)	149	150	140	130	569	7
Papillary Carcinoma (PC)	145	142	135	138	560	6
Ductal Carcinoma (DC)	864	903	896	788	3451	38
Lobular Carcinoma (LC)	156	170	163	137	626	5
Mucinous Carcinoma (MC)	205	222	196	169	792	9
Total	1995	2081	2013	1820	7909	82

layer for estimating probability of the output predicted class-label  $\bar{l} \in Y_{pred}$  corresponds to the true class-label  $l \in Y$  of object classes  $Y$ . The Stochastic Gradient Descent optimizer and categorical cross-entropy loss is applied to optimize the learning phase.

The GCN module can be plugged into state-of-the-art (SOTA) base CNNs such as pre-trained ResNet, MobileNet, and others, which are denoted as **CS-GCN+**. Whereas, **CS-GCN** symbolizes the proposed convolutional stem with the same GCN, trained from scratch. Here, both kinds of base CNNs are used alternatively to develop GCN module, denoted as **CS-GCN(+)**.

## 4. Results and Discussion

The characteristics of datasets are briefed in Table 1, followed by the implementation description and evaluation metrics. The performances are evaluated and compared with SOTA methods, the ablation studies are reported.

### 4.1. Dataset Description

Three different public datasets are evaluated using the CS-GCN(+). These are (a) human breast epithelial cell lines using actin-labeled fluorescence microscopy image dataset Oei et al. (2019), dubbed as FMID, illustrated in Fig. 4. This dataset consists of one non-cancerous human breast epithelial cell line (MCF-10A) and two cancerous human breast epithelial cell lines (MCF-7 and MDA-MB-231). The MCF-7 is less aggressive and MDA-MB-231 is more aggressive cancer cell lines, respectively.

(b) The BreakHis dataset consists of 7909 images representing four magnification types i.e., 40x, 100x, 200x, and 400x Spanhol et al. (2016). The sub-types are adenosis

(A), fibroadenoma (F), phyllodes tumor (PT), and tubular adenoma (TA); and four malignant tumors (breast cancer): ductal carcinoma (DC), lobular carcinoma (LC), mucinous carcinoma (MC) and papillary carcinoma (PC). This dataset has been widely studied in many works due to its higher clinical value. Detailed sub-class specifications are given in Table 2, and examples of two magnifications 40x and 100x are shown in Fig. 5.

(c) The LC25000 represents histology images of benign and cancerous lung and colon cancer, shown in Fig. 6 Borkowski et al. (2019). The dataset contains a total 25000 images of five classes with 5000 images per class. The classes are colon adenocarcinoma, benign colon tissue, lung adenocarcinoma, lung squamous cell carcinoma and benign lung tissue.

The experiments are conducted with a train-test ratio of 70:30 for multi-class categorization. Other splitting ratios of datasets and evaluation strategies (e.g., binary classification with 80:20 ratio) are avoided for a fair comparative study with SOTA methods. A summary of these datasets alongside the best results achieved by the proposed CNN stem (CS-GCN) and ResNet-50 (CS-GCN+) are given in Table 1.

### 4.2. Implementation Specification

The proposed CNN stem is trained from scratch (random initialization), whereas pre-trained *ImageNet* weights are used for initializing the standard base CNNs e.g., ResNet-50, DenseNet-201, etc. During pre-processing, affine transformations are applied. The input images are resized to 224×224 dimension. Image augmentation methods, particularly random rotation ( $\pm 25$  degrees), scaling ( $\pm 0.25$ ), and translation are applied on-the-fly for data diversity. The output feature map of a base CNN is 4×4 pixels and channels=2048, which is upsampled to 32×32. The size of each

**Table 3**

Performance evaluation of the CS-GCN with N=5 regions based on the proposed CNN Stem, and + GCN implies CS-GCN.

Dataset	Method	Top-1 Acc	Top-3 Acc	Precision	Recall	F1-Score
FMID	CNN Stem Baseline	84.02	96.0	86.0	84.0	85.0
	+ 5 Regions	94.02	99.0	94.0	94.0	94.0
	+ GCN	96.52	100.0	97.0	97.0	97.0
BreakHis 40x	CNN Stem Baseline	87.50	96.50	88.0	88.0	88.0
	+ 5 Regions	92.00	98.67	92.0	92.0	92.0
	+ GCN	96.16	99.70	96.0	96.0	96.0
BreakHis 100x	CNN Stem Baseline	85.73	94.50	90.0	86.0	88.0
	+ 5 Regions	92.23	99.20	94.0	94.0	94.0
	+ GCN	95.99	99.50	96.0	96.0	96.0
BreakHis 200x	CNN Stem Baseline	83.76	96.83	84.0	84.0	84.0
	+ 5 Regions	87.33	97.86	89.0	87.0	88.0
	+ GCN	92.33	98.75	93.0	93.0	93.0
BreakHis 400x	CNN Stem Baseline	84.44	95.30	84.0	84.0	84.0
	+ 5 Regions	89.25	95.66	89.0	89.0	89.0
	+ GCN	92.40	99.62	92.0	92.0	92.0
LC 25000	CNN Stem Baseline	64.50	95.0	83.0	75.0	79.0
	+ 5 Regions	92.78	96.0	93.0	93.0	93.0
	+ GCN	93.96	98.0	94.0	94.0	94.0

**Table 4**

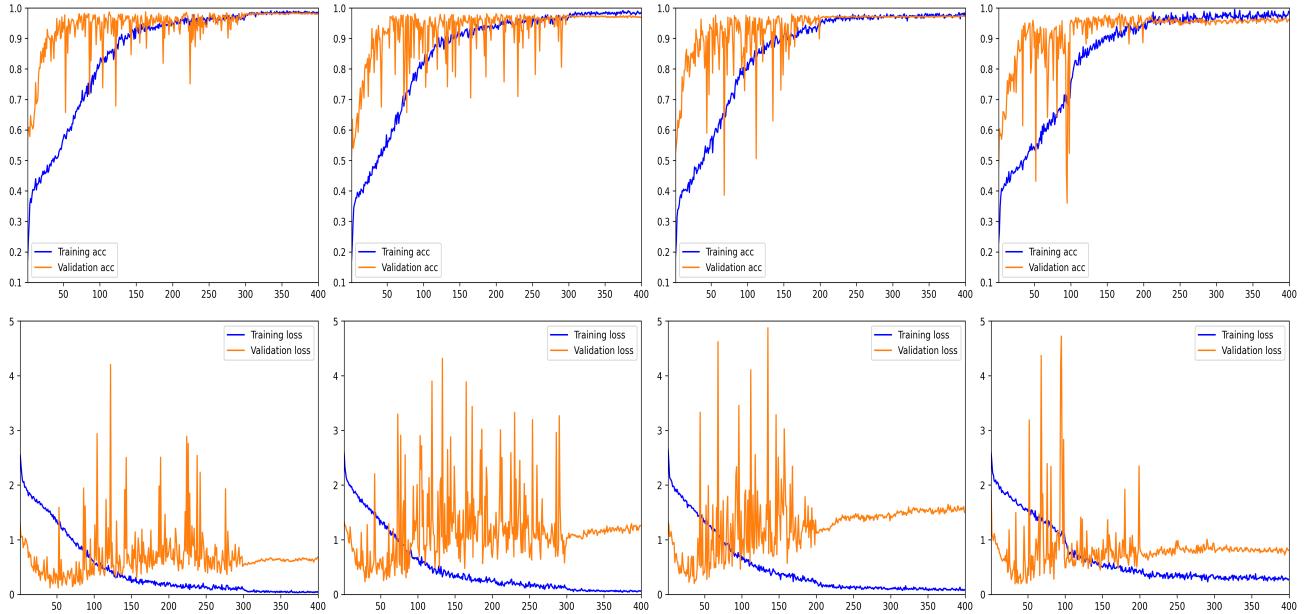
Performance of CS-GCN(+) using the CNN stem and base CNNs with 15 nodes (N). The best results are shown in bold font and second-best results are underlined.

Dataset	Method	Top-1 Acc	Top-3 Acc	Precision	Recall	F1-Score
FMID	Proposed CNN	<u>97.22</u>	100.0	97.0	97.0	97.0
	ResNet-50	99.30	100.0	99.0	99.0	99.0
	DenseNet-201	<b>100.0</b>	100.0	100.0	100.0	100.0
	MobileNet-v2	95.83	100.0	96.0	96.0	96.0
BreakHis 40x	Proposed CNN	<u>96.83</u>	99.83	96.0	96.0	96.0
	ResNet-50	<b>98.00</b>	99.83	98.0	98.0	98.0
	DenseNet-201	97.33	99.83	97.0	97.0	97.0
	MobileNet-v2	96.50	99.83	97.0	97.0	97.0
BreakHis 100x	Proposed CNN	<u>97.43</u>	99.48	97.0	97.0	97.0
	ResNet-50	<b>97.81</b>	99.70	98.0	98.0	98.0
	DenseNet-201	97.78	99.83	97.0	97.0	97.0
	MobileNet-v2	96.47	99.10	96.0	96.0	96.0
BreakHis 200x	Proposed CNN	<u>97.17</u>	99.50	97.0	97.0	97.0
	ResNet-50	<b>97.33</b>	99.83	97.0	97.0	97.0
	DenseNet-201	95.83	99.90	96.0	96.0	96.0
	MobileNet-v2	97.00	99.78	97.0	97.0	97.0
BreakHis 400x	Proposed CNN	<u>96.11</u>	99.44	96.0	96.0	96.0
	ResNet-50	<b>96.85</b>	100.0	97.0	97.0	97.0
	DenseNet-201	96.48	99.44	96.0	96.0	96.0
	MobileNet-v2	94.63	99.26	95.0	95.0	95.0
LC 25000	Proposed CNN	<u>99.87</u>	100.0	100.0	100.0	100.0
	ResNet-50	<b>100.0</b>	100.0	100.0	100.0	100.0
	DenseNet-201	<b>100.0</b>	100.0	100.0	100.0	100.0
	MobileNet-v2	99.67	100.0	100.0	100.0	100.0

region is set to 16×16 pixels for  $N = 5$  and 48×48 for  $N = 15$ . A dropout rate of 0.3 is applied to ease overfitting. The model is trained with a learning rate of 0.005 for 400 epochs and with a mini-batch size of 12. The model parameters are calculated in millions (M). The CS-GCN method is developed in Tensorflow 2.x and Keras 2.13.x using Python scripts. For experiments, a NVIDIA A100 40GB GPU and Intel Core Silver 4316 CPU x86\_64, 2.30 GHz 128 GB RAM computing system are used.

#### 4.3. Evaluation Metrics

The top-1 and top-3 accuracy, precision, recall, and F1-score (eq. 7) metrics are computed for performance evaluation and comparison. These metrics are widely used in prior works to tackle class imbalance problem. Also, patient-level metrics are used for evaluating the BreakHis dataset.



**Figure 7:** Accuracy (top-row) and loss (bottom-row) during training and testing of CS-GCN with 15 Rols built upon ResNet-50 on the BreakHis four magnifications are shown (left to right): 40x, 100x, 200x, and 400x, respectively.

$$\begin{aligned}
 \text{Accuracy} &= \frac{\mathcal{T}\mathcal{P} + \mathcal{T}\mathcal{N}}{\mathcal{T}\mathcal{P} + \mathcal{T}\mathcal{N} + \mathcal{F}\mathcal{P} + \mathcal{F}\mathcal{N}} \\
 \text{Precision} &= \frac{\mathcal{T}\mathcal{P}}{\mathcal{T}\mathcal{P} + \mathcal{F}\mathcal{P}} \\
 \text{Recall} &= \frac{\mathcal{T}\mathcal{P}}{\mathcal{T}\mathcal{P} + \mathcal{F}\mathcal{N}} \\
 \text{F1-Score} &= 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}
 \end{aligned} \tag{7}$$

where  $\mathcal{T}\mathcal{P}$  denotes the number of true positives,  $\mathcal{T}\mathcal{N}$  is the number of true negatives,  $\mathcal{F}\mathcal{P}$  is the number of false positives, and  $\mathcal{F}\mathcal{N}$  is the number of false negatives.

The image-level and patient-level performance metrics are evaluated for cancer classification as defined by Spanhol et al. (2016). The accuracy of patient-level is assessed as the patient recognition rate (PRR). Let the number of cancer images of a patient K is  $K_p$ , the number of images classified correctly is  $K_{rec}$ , and N be the number of total patients. The PRR is defined as

$$\text{PRR} = \frac{1}{N} \sum_{K=1}^N \frac{K_{rec}}{K_p} \tag{8}$$

The patient-level performance of CS-GCN is assessed on the BreakHis dataset following similar evaluation metrics Zou, Chen, Che, Zhang and Zhang (2022), given in Table 7. A fusion of inception and residual networks, called IRRCNN Alom et al. (2019), achieved a decent patient level average classification results ( $\approx 97.0\%$ ) on all four magnifications.

The image-level classification accuracy is mainly computed here due to its wider acceptability by the researchers. Let  $N_{total}$  be the number of all cancer images in the testing

set, and  $N_c$  defines the number of images correctly classified, then the image recognition rate (IRR) is given as

$$\text{IRR} = \frac{N_c}{N_{total}} \tag{9}$$

The performances are evaluated on different datasets according to aforesaid metrics, described next.

#### 4.4. Performance Analysis

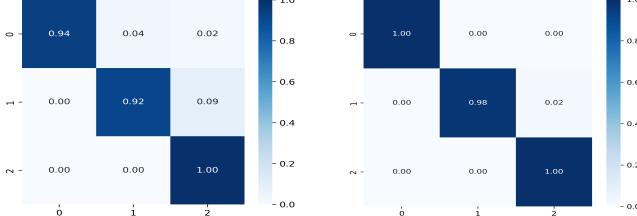
Firstly, baseline performance of the proposed CNN stem is computed. Then, the performance of five regions ( $N=5$ ) added on base CNN is evaluated. Lastly, the GCN module is integrated with the model to develop CS-GCN. Detailed performances showcasing baseline results on all datasets using proposed CNN and its integration with  $N=5$  nodes in GCN layer-I are provided in Table 3. It is evident that the performances are improved progressively with the added GCN module. Overall performances are satisfactory while evaluated using the proposed convolutional stem. To improve further, the number of regions is increased ( $N=15$ ) for enhancing local contextual representation and selecting more discriminatory information. The best performances are attained with  $N=15$  nodes in layer-I of GCN and overall results are showcased in Table 4.

Besides, many prior works utilized available backbone families, such as ResNet-50, DenseNet-201, and others. Here, experiments are conducted with three standard base CNNs upon which the GCN module is plugged-in. Particularly, more region-aware features with increased regions are learned through pre-trained backbones which have boosted the classification performances. The most significant results of CS-GCN(+) are demonstrated in Table 4. The top-1 accuracy (%) of CS-GCN for each dataset is underlined and the best top-1 accuracy of CS-GCN+ is denoted with boldface.

**Table 5**

Estimated model parameters (in millions) of the CS-GCN(+)

Model	Proposed CNN	ResNet-50	DenseNet-201	MobileNet-v2
Baseline	7.92	23.60	18.34	2.28
CS-GCN	13.15	28.85	25.10	5.94

**Figure 8:** Confusion matrix of the proposed method using (left) CNN stem and ResNet-50 (right) on the FMID dataset.

The results exhibit that performances of proposed base stem are very competitive with pre-trained CNNs, even having a lower parameter count than ResNet50 and DenseNet201.

The accuracy and loss graphs of training and testing phases of CS-GCN+ using ResNet-50 base on all four magnifications of BreakHis dataset are shown in Fig. 7. The graphs (top-row) exhibit very similar behaviors during evaluations and the estimated loss values are shown in bottom-row. Particularly, the training has stabilized after 300 epochs for all four scenarios. Similar behaviour has been observed in other datasets too.

Patient-level performances of CS-GCN+ with  $N=15$  nodes are computed on BreakHis (BH) dataset, and the results are provided with a comparative study in Table 7. The accuracy on the BH40x is  $97.40 \pm 0.4$  using ResNet-50, and similar accuracy on other magnifications are obtained accordingly. The accuracy of the proposed CNN is competitive with the pre-trained backbones. A patient-level performance comparison is presented in the next section.

The estimated model parameters are given in Table 5. Model parameters of the proposed stem is 7.92M and full CS-GCN is 13.15M, which is very low compared to ResNet and DenseNet models, and comparable with lightweight MobileNet base (2.28M). Hence, the proposed stem is considered to be a lightweight model having  $< 10$ M parameters. Notably, CS-GCN implemented using MobileNet-v2 backbone consists of 5.94M parameters, which is still a lightweight model.

The CS-GCN is a good choice while targeting a lower computational cost, yet powerful to attain SOTA results. The reason could be that standard CNNs are pre-trained on generic image classes, which always might not be a good choice for medical diagnostics, representing very complex patterns/textures and cell structures. To overcome this problem, many works ensembled multiple CNNs, ignoring computational cost. To avoid such a huge parametric overload of fusion-based models, CS-GCN is an effective alternative.

#### 4.4.1. Visualizations

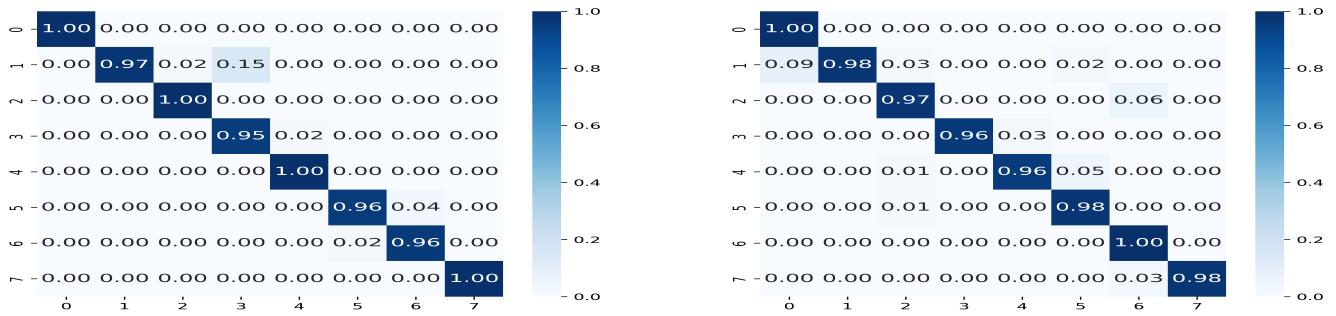
The confusion matrix of CS-GCN+ ( $N=15$ ) on each dataset is shown in Fig 8, 9, 10, and 11 for visual clarity of evaluation. The t-distributed stochastic neighbor embedding (t-SNE) Van der Maaten and Hinton (2008) visualizations exhibit data separability in different clusters of classes. Similar data points represent small pairwise distances, while different data points imply large pairwise distances using student-t distribution. Here, low-dimensional feature distributions reflect the discriminability of multiple classes using CS-GCN. The t-SNE plots show feature distributions of proposed method using ResNet-50 are given in Fig. 12.

The gradient weighted class activation mapping (Grad-CAM) visualizations Selvaraju, Cogswell, Das, Vedantam, Parikh and Batra (2017) reflect a deep model's capacity in coarse localizing crucial regions within input image for prediction without altering architectural design. Grad-CAM utilizes gradient information flowing into the last convolutional layer of a CNN to estimate the neuron-level importance for making a prediction. Grad-CAM is widely used for class-discriminative visual explanation with high resolution details and interpretability which are useful for decision making. These superimposed visual analyses, shown in Fig. 13, clearly showcase overall feature representations of multi-class cancer image classification using CS-GCN(+) .

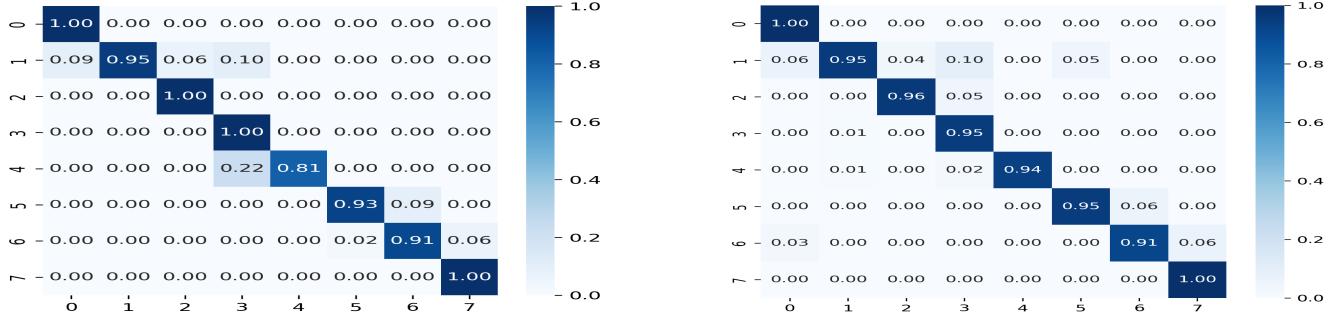
#### 4.5. Performance Comparison

The performances are compared with existing SOTA for multi-classification (Table 6), considering similar evaluation techniques like ours. A knowledge distillation based joint learning (student-teacher) framework achieved a classification accuracy of 97.23% and 96.92% on the BreakHis 40x and 100x magnifications, respectively Sepahvand and Abdali-Mohammadi (2023). A small squeeze-and-excitation block combined with a residual module, called BCHNet, trained with a Gaussian error scheduler (ERF), attained 94.43% accuracy on multi-classification on this dataset Jiang et al. (2019). In contrast, CS-GCN attains improved results on these magnifications. The best performances of CS-GCN+ are 98.0% and 97.81% using ResNet-50, on the BreakHis 40x and 100x, respectively, implying clear accuracy gain. Likewise, the accuracies of CS-GCN+ using ResNet-50 on BreakHis 200x (97.33%) and 400x (96.85%) are improved over EFML that reported 96.65% and 96.41% accuracies on BreakHis-200x and 400x, respectively Li et al. (2023a). DinNet has reported 97.62% accuracy on this dataset Guo et al. (2024). Also, the performance of using CNN stem outperforms several existing methods. The proposed stem (CS-GCN) is competitive with the methods

### Graph Convolutional Network With Channel Splitting for Cancer Classification



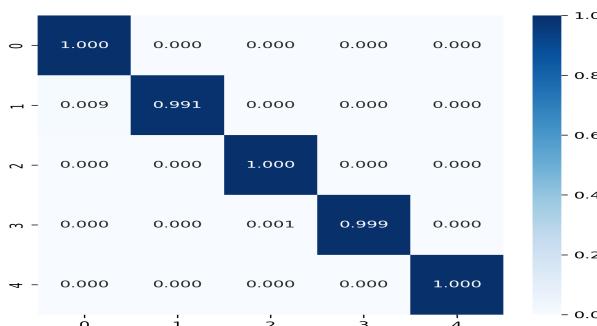
**Figure 9:** Confusion matrix evaluated using ResNet-50 on the BreakHis-40x (left) and BreakHis-100x (right) datasets.



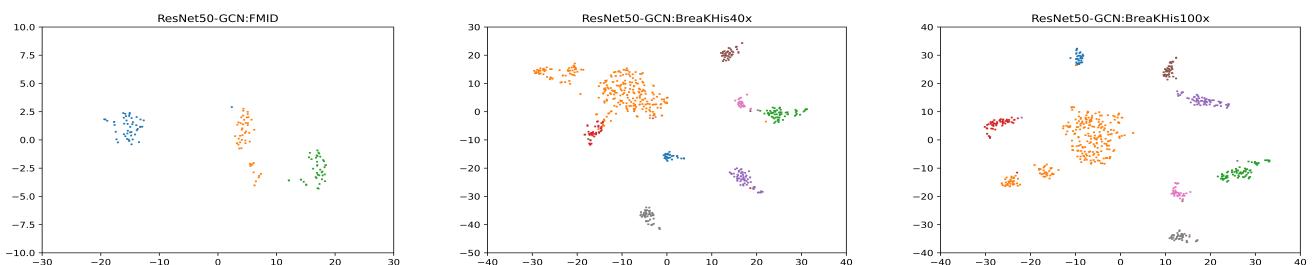
**Figure 10:** Confusion matrix evaluated using the proposed CNN on the BreakHis200x (left) and ResNet50 on the BreakHis400x (right) datasets.

based on ResNet-50. The CS-GCN attains better performances than MobileNetV2 (Table 4). VGGIN-Net used a modified VGG-16 with inception blocks, and reported an average accuracy of 95.81% on this dataset Saini and Susan (2023). The CTransNet achieved the best 98.21%

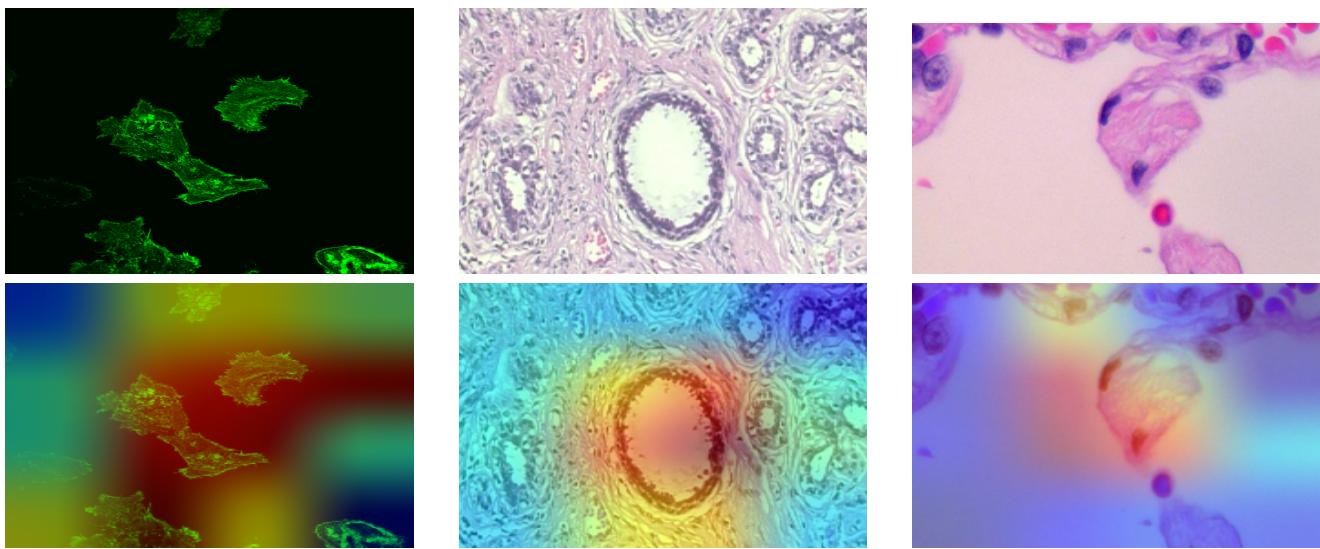
accuracy on BreakHis-40x magnification (BH40x) with 224×224 image size, whereas the average accuracy of all four magnifications is 97.39% Liu, Wang, Zhang, Qiao, Sun, Zhang, Xu and Shang (2024a). Recently, DinNet was tested with 80:20 train-test ratio, and achieved 97.62% average



**Figure 11:** Confusion matrix of CS-GCN(+) computed using the proposed CNN (left) and ResNet-50 (right) on the LC25000 dataset.



**Figure 12:** t-SNE plots of proposed CS-GCN(+) using ResNet-50 on the FMID (left), BreakHis 40x (mid) and BreakHis 100x (right) datasets.



**Figure 13:** Grad-CAM visualizations using the proposed method on the FMID (left), BreakHis 100x (mid) and LC25000 (right) datasets are shown in bottom row with the corresponding actual image given in top-row.

**Table 6**

Accuracy (%) comparison with SOTA on the BreakHis 40x and 100x, Average of all magnifications at image level datasets

Method	BH 40x	BH 100x	Avg
BHCNet +ERF Jiang et al. (2019)	$94.43 \pm 0.28$	$94.45 \pm 0.15$	
Hybrid harmonization Abdallah, Marion, Tauber, Carlier, Hatt and Chauvet (2023)	93.40	-	
CSDCNN Han, Wei, Zheng, Yin, Li and Li (2017)	$92.80 \pm 2.1$	$93.90 \pm 1.9$	
Semantic dual contrast Liu, Zhu, Gu, Pan, Li, Fan, Li and Zeng (2024b)	<b>95.70</b>	<b>94.50</b>	<b>95.40</b>
Ensemble of Swin Transformers Tummala et al. (2022)	96.00	92.60	
Embedded fusion mutual learning (EFML) Li et al. (2023a)	96.76	97.36	
VGGIN-Net Saini and Susan (2023)	<b>96.28</b>	<b>96.81</b>	<b>95.81</b>
DBLCNN Wang, Gong, Cheng and Qian (2022)	<b>96.58</b>	<b>95.65</b>	<b>96.00</b>
CS-GCN+ (GCN + ResNet-50)	<b><math>97.43 \pm 0.57</math></b>	<b><math>97.60 \pm 0.21</math></b>	97.50
CS-GCN (GCN + CNN stem)	<b>96.33</b>	<b>97.43</b>	96.88

accuracy Guo et al. (2024). However, CS-GCN has attained 97.50% average accuracy with 70:30 train-test ratio. Reasonably, this experimental setting is not directly comparable with those existing methods due to dissimilar experimental setup, yet CS-GCN achieves competitive performances.

The dependency-based lightweight convolutional neural network (DBLCNN) Wang et al. (2022), built upon MobileNetV2 with 12.19M parameters, achieved an average 96.00% accuracy of image-level classification on BreakHis. In contrast, CS-GCN based on MobileNet-V2, having 5.94M

parameters, has attained an average of 96.15% image-level classification accuracy.

The patient-level multi-classification performance of the proposed CS-GCN has been compared. The accuracy of CS-DCNN on augmented BreakHis 40x is  $94.1 \pm 2.1\%$  Han et al. (2017). A multi-level feature fusion (MLF2) method using pretrained CNN has gained  $95.2 \pm 2.4\%$  accuracy of patient-level assessment on the BreakHis 40x, and similar results on other magnifications are reported Taheri et al. (2024).

**Table 7**

Patient-level performance of CS-GCN+ using the BreakHis dataset.

method/CNN	BH 40x	BH 100x	BH 200x	BH 400x
CSDCNN Han et al. (2017)	$94.1 \pm 2.1$	$93.2 \pm 1.4$	$94.7 \pm 3.6$	$93.5 \pm 2.7$
MLF2-CNN Taheri, Golrizkhataami, Basabbrain and Hazzazi (2024)	$95.2 \pm 2.4$	$95.8 \pm 1.5$	$95.6 \pm 1.9$	$95.1 \pm 1.9$
RANet Zhou, Zhang and Gao (2022)	92.21	97.50	97.83	89.73
DSoPN Li, Zhang, Sun, Zhang, Dong, Che and Zhang (2020)	95.01	96.84	97.92	96.28
IRRCNN Alom et al. (2019)	$96.76 \pm 1.1$	$96.84 \pm 1.1$	$96.67 \pm 1.3$	$96.27 \pm 0.9$
CS-GCN ResNet-50	$97.40 \pm 0.4$	$97.46 \pm 0.3$	$97.81 \pm 1.4$	$96.74 \pm 1.1$
Proposed CNN	97.00	97.29	97.52	96.12
MobileNetV2	97.55	97.23	96.75	95.06

**Table 8**

The baseline accuracy of using base CNNs and added regions (N)

Method	FMID	BreakHis 40x	BreakHis 100x	BreakHis 200x	BreakHis 400x	LC25000
ResNet-50 Baseline +15 Regions	79.17	78.83	76.28	81.00	77.22	95.75
	90.26	92.16	91.02	94.00	92.40	97.93
DenseNet-201 Baseline +15 N	81.23	80.00	77.40	80.83	80.18	95.16
	92.36	85.50	83.33	93.66	87.40	97.80
MobileNet-v2 Baseline +15 Regions	78.47	68.50	65.38	73.50	76.48	94.68
	90.93	85.16	91.34	93.00	91.48	96.98

**Table 9**

Ablation study (c) with GCN Layer-I=2048 and Layer-II=1024 features in the CS-GCN(+); 512 denotes GCN Layer-II=512;  $5N^{(1L)}$  denotes 1 layer GCN with 5 nodes (1st row) while remaining all GCNs built with 2 layers; followed by the feature size of GCN Layer-II in 2nd column.

Method	Nodes; Feat.	FMID	BH40x	BH100x
Proposed	$5N^{(1L)}$ ; 1024	92.36	93.53	90.38
	5 N; 1024	96.52	96.16	95.99
CS-GCN	5 N; 1024	96.87	96.46	96.07
	5 N; 1024	96.44	94.33	94.91
CS-GCN	15 N; 512	97.00	97.10	96.15
ResNet50	15 N; 512	97.22	96.50	96.31
MobNetv2	15 N; 512	96.52	96.00	95.66
CS-GCN	15 N; 1024	97.22	96.50	96.47
ResNet50	15 N; 1024	97.91	95.16	97.11
MobNetv2	15 N; 1024	96.83	96.16	96.15

An ensemble of inception-residual model (IRRCNN) adapting data augmentation obtained  $96.76 \pm 1.1$  accuracy on BreakHis 40x Alom et al. (2019). In contrast, CS-GCN attains at least 97.0% patient-level accuracy in similar experiments on this sub-dataset. Clearly, CS-GCN performs the best compared to prior works. Though, several methods evaluated binary performances and attained more than 99% accuracy, which are avoided for comparison due to dissimilar experimental setup, as mentioned above.

An ensemble of CNNs reported 99% precision for classifying breast epithelial cell dataset (FMID) Maurya et al. (2021). A CNN following VGG-16 model achieved 97.20% accuracy using transfer learning Oei et al. (2019). In contrast, CS-GCN using DenseNet-201 has achieved 100% performance, given in Table 4. The top-1 accuracy is 99.30% of CS-GCN+ using ResNet-50. Also, CS-GCN built with CNN stem achieves 97.22% accuracy on FMID.

The MicrosMobiNet architecture developed for mobile-edge computing devices attained 96.52% accuracy and 91.30% F1-score on the LC25000 dataset Biswas and Barma (2024). Condorcet's Jury Theorem-based ensemble method attained 99.88% accuracy on the same dataset for multi-classification of lung and colon cancer Srivastava, Chauhan and Pradhan (2023). Also, the Pyramidal Deep-Broad Learning (PDBL) method achieved 99.91% using ResNet-50 on LC25000 dataset Lin, Han, Pan, Liu, Chen, Li, Jia, Shi, Wang, Cui et al. (2022). An embedded fusion mutual learning (EFML) achieved 99.89% average classification result and the best 100% on this dataset Li et al. (2023a).

Another work has attained 99.68% accuracy of lung-cancer classification by integrating the DenseNet-201, color histogram, and k-nearest neighbors (KNN) classifiers Noaman, Kanber, Smadi, Jiao and Alsmadi (2024). Likewise, CS-GCN attains 100% accuracy using both ResNet-50 and DenseNet-201 backbones (Table 4). Overall, a comparative study with recent SOTA works on three datasets implies that CS-GCN, having 13.15M parameters, has improved performances using proposed convolutional stem, which is built with only 7.92M parameters. The performances using ResNet-50 and other backbone CNNs have boosted the multi-class categorization of breast and lung-colon cancer datasets, and achieved SOTA results, indicating the benefits of CS-GCN+.

#### 4.6. Ablation Study

The ablation studies are conducted to explore the significance of the major components of CS-GCN.

(a) The baseline results of CNN stem are evaluated considering three different design variations. The results are comparatively shown in Fig. 14. The CNN stem configuration of [128, 256, 512, 1024] is considered using conventional convolutions and separable convolutions in two different experiments, denoted as *Conv2d*(1024) and *SepConv2d*(1024), respectively. Next, the stem-depth is increased with [128, 256, 512, 768, 1024, 2048] configuration using *SepConv2d*, denoted as ‘proposed (2048)’ in Fig. 14. Clearly, it is evident that the proposed stem with 2048 filter-sizes enhances baseline performances on all four magnifications of BreakHis with reasonable model parameters. The model parameters are 19.30M for *Conv2d*(1024), whereas it is 2.18M for *SepConv2d*(1024). Finally, the proposed stem i.e., *SepConv2d*(2048) is built with 7.92M, and performs better than the other two CNN stem architectures.

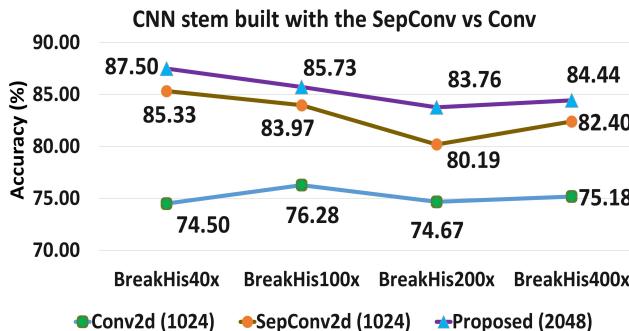
(b) Five complementary regions are integrated for region pooling. Finally, the GCN layers are included with  $N=5$  for performance improvement. The results of this study are given in Table 3. Likewise, the baseline performance of standard CNNs including 15 regions has been computed, and the results are given in Table 8. The baselines and regions progressively improve the performances which are obvious in network design.

(c) The effectiveness of feature propagation in GCN layers with  $C=1024$  features per node is studied, and the results are given in Table 9. It is observed that reducing node-level features aggressively discards relevant information, and results in performance degradation. **Output of base CNN**

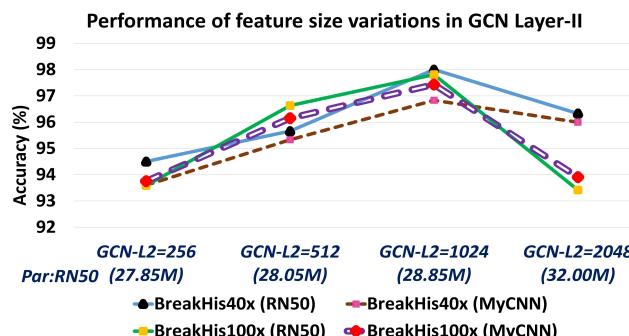
**Table 10**

Ablation study (d): Only max-pooling is applied in CS-GCN instead of concatenation of max and average pooling.

CNN	FMID	BreakHis 40x	BreakHis 100x	BreakHis 200x	BreakHis 400x
Proposed CNN	96.53	95.33	96.63	96.50	95.55
ResNet-50	97.22	96.33	95.91	96.66	94.62
DenseNet-201	97.22	97.17	96.63	94.50	95.41
MobileNet-V2	95.14	95.66	95.15	93.66	92.40



**Figure 14:** Comparative study on the base convolutional stem built with Separable convolutions (*SepConv2D*), and conventional convolutions (*Conv2D*).



**Figure 15:** Comparative study of performances using different feature sizes in the GCN Layer-II based on the ResNet-50 backbone. The estimated model parameters with respective feature spaces are also shown.

**Table 11**

Ablation study (e) with GCN Layer-I=2048 only followed by the classification avoiding the channel splitting.

Method/CNN	Nodes	FMID	BH40x	BH100x
CS-GCN	5	94.66	93.83	90.16
ResNet50	5	94.66	94.33	90.80
MobileNetv2	5	94.00	94.16	90.64
CS-GCN	15	96.00	95.66	93.38
ResNet50	15	96.66	95.83	93.54
MobileNetv2	15	96.00	95.50	93.06

stem is the same 1024 feature dimension in GCN layer-I for designing the network that provides satisfactory results, given in the first-row of Table 9. The performance of  $N=5$  region is studied which implies the need of more regional information for graph-based feature representation.

The performances with variations of feature dimension in GCN layer-II are studied, as shown in Fig. 15. In this

study, layer-I contains 2048 features, whereas, channel-splitting module is varied with 256, 512, 1024, and 2048 features using ResNet-50. The results on BreakHis 40x and 100x magnifications clearly show that SOTA performances are achieved with the feature size 1024 in GCN layer-II of CS-GCN(+). Hence, a two-layer GCN with  $N=15$  nodes, and  $C=2048$  features per node in layer-I and 1024 features in layer-II of GCN is the best performer in present context.

(d) An ablation study is conducted to justify the feature pooling using both GMP and GAP in the GCN module is beneficial than using standalone GMP. The results are provided in Table 10. An average accuracy of 96.0% is attained by CS-GCN using only GMP built upon proposed CNN on BreakHis dataset considering all magnifications. In contrast, using both GAP and GMP in similar experiments, an average accuracy of 96.88% has been achieved. Likewise, similar gains in performances are achieved using other CNNs on other dataset variations. It implies that feature mixing using both pooling enhances overall feature representation through the graph-nodes of CS-GCN.

(e) The experiments are carried out with only one layer GCN excluding the channel-splitting module (i.e., GCN layer-II) from the model. Both  $N=5$  nodes and  $N=15$  nodes in GCN-model are tested in different experiments, and the results are provided in Table 11. It is evident that 95.83% accuracy has been attained on BreakHis 40x using ResNet-50 in this experimental study, whereas the best 98.00% accuracy is achieved by CS-GCN+ full model with ResNet-50 (Table 4). It is evident that the accuracy has been degraded excluding channel-splitting module, indicating the module indeed boosts the performances.

#### 4.7. Clinical Applications and Limitations

In recent time, deep learning approaches has achieved remarkable success in various clinical applications including breast cancer diagnosis, classification of histopathological sub-types, lymph node metastasis, and others Zhao, Bai, Guo, Ren and Zhang (2023). Also, visualizations using Grad-CAM showcase qualitative explanations for better diagnostics which are suitable for early detection of cancer and prognosis. Automated methods leveraging machine/deep learning are inexpensive compared to manual time-consuming pathological lesion/biopsy sample collection, testing, and analysis. To mitigate errors in decision making of automated cancer sub-type determination, experts' diagnosis decisions could be combined. Recent integration of large language models (LLMs) in medical applications, multi-modal deep learning and data fusion approaches will improve the correctness in medical reasoning

and personalized treatment in rural areas. Thus, integration of vision-language models (i.e., pre-trained CNNs + GPT models) offers a huge potential in cancer patient-care and low-cost clinical applications. However, due to limited training data, advanced pre-processing techniques are yet to be developed for further progress. Nevertheless, generalized deep learning models should be developed for avoiding biases, and addressing data imbalance issues which are major challenges.

Currently, the proposed GCN requires a large number of model parameters (0.42M) per layer, which is computationally expensive in the context of lightweight design. To overcome this limitation, further improvement is essential for reducing the intrinsic model parameters of GCN for a real-world clinical application as well as lightweight model development. Other types of imaging modalities and data collection from various nations should be carried out for generalizing the model's performance, which is considered as an important future direction.

## 5. Conclusion

In this paper, a two-layer GCN integrated upon a CNN stem, called CS-GCN, is proposed for cancer multi-class categorization using histopathology and actin-labelled fluorescence microscopy images. The performances are evaluated using three standard backbone CNNs. A CNN stem is proposed considering a lower computational cost of the network architecture upon which the GCN layers are integrated. The CS-GCN is computationally light-weight compared to standard base CNNs including the ResNet, DenseNet, and other heavier backbone families. Yet, the performance of our shallower CNN is competitive with those standard backbones. The performances of CG-GCN on three public cancer datasets using both types of CNNs have been improved compared to existing works. A new fusion strategy using GCN-based deep models will be tested on other datasets on different types of cancers to boost the performance of CAD-based medical diagnosis.

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