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SUPERPIXEL BASED CLASSIFICATION FOR GRAPH NEURAL NETWORK(GNN) IN LEUKEMIA IMAGES

B. REVATHI[1], M. KALIAPPAN[2], P. CHANTHIYA[3], S.V. ANANDHI[4], CALLINS CHRISTIYANA.C[5], S.K. KEZIAL ELIZABETH[6]

[1]Assistant Professor, Ramco Institute of Technology, Department of Artificial Intelligence and Data Science, India.

[2]Professor, Ramco Institute of Technology, Department of Artificial Intelligence and Data Science, India.

[3]Associate Professor, Dr. Sivanthi Aditanar College of Engineering, Department of Artificial Intelligence and Data Science, India.

[4]Associate Professor, Ramco Institute of Technology, Department of Artificial Intelligence and Data Science, India.

[5] Professor, SRM Madurai College for Engineering and Technology, Department of Computer Science and Engineering, India

[6]Assistant Professor, Mangayarkarasi College of Engineering, Department of Computer Science and Engineering, India

E-mail: [1]revas85@gmail.com, [2]kalsrajan@yahoo.co.in, [3]chanthiyapuhal@gmail.com, [4]svanandhi2020@gmail.com, [5]callinschristiyanac@gmail.com, [6]kezialcse@gmail.com

ABSTRACT

Patient survival depends heavily on accurately and quickly detecting leukemia, but traditional diagnostic methods can be time-consuming and subjective. We present a innovative approach that utilizes Superpixel-based image segmentation and graph neural networks (GNN) to classify leukemia in microscopic cell images. The C-NMC dataset converts each image into a graph, with nodes representing meaningful regions (Superpixels) and edges capturing spatial relations. The accuracy of our model is 99.56%, and it performs well in Precision, Recall, and F1-score metrics. This method not only improves accuracy but also makes it easier to model spatial patterns in medical images.

Keywords: *Leukemia Detection, Graph Neural Networks, Superpixel Segmentation, Graph Attention Network, Image Classification, Medical Imaging*

1. INTRODUCTION

Leukemia is a cancer that can be life-threatening and occurs in the blood and bone marrow, characterized by the production of abnormal white blood cells. Effective treatment and improved survival rates require early detection, but traditional diagnostic methods are often manual and subjective and time-consuming. Deep learning models, specifically CNNs, have shown promise in medical image classification, they typically do not pay attention to the spatial and contextual relationships within images.

This work aims to overcome these limitations by combining superpixel segmentation with graph neural networks (GNN) of leukemia images. Using the C-NMC dataset, each microscopic image is segmented into superpixels, compact regions of similar pixels, that serve as nodes in a graph. The spatial relationships between regions are communicated through edges, and node features include color, texture, and positional data. The use of a graph attention network (GAT) is followed by the application of meaningful patterns to classify images as leukemic or non-leukemic.

This method not only enhances precision but also incorporates structural interpretability into the

classification process. The proposed system achieves high performance and has the potential to assist clinicians in obtaining early and reliable diagnosis of leukemia. Main objectives of our proposed work is as follows,

1.1. *Overcoming limitations of traditional CNN-based leukemia classification*

Earlier approaches relied heavily on convolutional neural networks (CNN), which struggle to effectively model spatial relationships between different regions of a medical image. This project introduces a graph-based representation to overcome this limitation, enabling more accurate and structured analysis of leukemia cell images.

1.2. Converting leukemia cell images into graph-structured data using superpixel segmentation

Traditional methods process images at the pixel level, treating each pixel independently. Instead, this project uses SLIC superpixel segmentation to transform images into graphs, where:

a. Each node represents a meaningful superpixel region.
b. Edges capture spatial connections between regions this approach enables structure-aware learning, preserving crucial biological patterns often missed by CNNs.

1.3. *Developing a GNN-based classification model using graph attention networks (GAT*)

Previous techniques lacked strong relational learning capabilities. This project leverages graph attention networks (GAT) to:

a. Classify leukemia images by analysing node features and their neighbourhood attention.
b. Improve accuracy by focusing on the most relevant cell regions.
c. Enhance interpretability through attention weighted visual explanations.

2. LITERATURE SURVEY

This section discusses several existing methodologies for classification of leukemia images using machine learning (ML), deep learning (DL), and graph-based methods. The comparison of various works highlights the need for an effective and interpretable model, such as the proposed superpixel-based graph neural network. [1] Bibi Et Al. (Mdpi, 2022) proposed a superpixel-based attention GNN for semantic segmentation in aerial images. While their work was not related to leukemia-specific, the method inspired spatial segmentation in medical image analysis. The key merit was the integration of CNN for feature extraction; however, the paper did not report exact classification accuracy, which limits reproducibility. [2] Sunita Chand and Virendra P. Vishwakarma (Icasiset, 2021) compared various segmentation algorithms for leukemia classification. Hey concluded that machine learning algorithms work well for segmentation tasks, but models showed signs of overfitting, and exact accuracy values were missing. [3] Bibi Et Al. (nih, 2020) proposed an iomt-based deep learning model for automated leukemia detection. CNN was utilized for image classification. The limitation again was the lack of exact performance metrics, which reduced transparency in model evaluation. [4] Pansombut Et Al. (researchgate, 2024) introduced a phon-leukemia detection system using CNN. While the approach provided high-level CNN performance, it failed to explain the multi-feature extraction method, which is essential in complex leukemia leukemia diagnosis tasks. [5] ratley et al. (IEEE, 2020) presented a review of machine learning methods for leukemia classification. Although classification metrics were discussed, they were not implemented in detail, making it hard to extract practical insights.

3. CLASSIFICATION

Layer extraction, particularly from specific levels such as layer [3], is a key step in image processing and plays a significant role in medical image classification tasks, including leukemia image analysis [6-12]. In this project, thematic maps are generated from extracted features and then used in image classification pipelines. The classification process is based on criteria implemented in both supervised and unsupervised approaches [15]. The workflow includes: extracting features and layers using superpixel segmentation, generating training datasets for supervised classification, applying graph attention networks (gats) for enhanced performance. The supervised classification method is the foundation of this project, where segmented images are used to generate labeled training data.

The GNN needs this training data to learn the discriminative features of leukemia cells effectively. In multivariate analysis, the GNN model exhibits strong classification abilities by utilizing information at the node and graph levels and graph-level information. Optimization techniques were applied during cluster formation to enhance classification precision and robustness [13-20], resulting in a model that is achieves over 85% accuracy on the C-NMC leukemia dataset.

4. OPTIMIZATION

The leukemia image classification system's performance and accuracy can be enhanced through optimization [21]. This project utilizes optimization at various levels of the pipeline, from image preprocessing to model training, to ensure efficient compilation.

4.1 Superpixel Segmentation Optimization:

The first level of optimization involves segmenting the leukemia images into meaningful superpixels. We tested out several segmentation algorithms and parameters, such as the amount of segments (e.g., 50 per image), compactness, and spatial regularity, to ensure that the segmented regions preserved relevant features of leukemic cells. This step had a significant impact on computational complexity by reducing redundant pixel-level computations and enabling better graph formation.

4.2 Graph Construction Optimization:

Each segmented image was converted into a graph, with superpixels acting as nodes and edges representing their spatial or color similarities.to handle the large-scale dataset (e.g., 10,661 images), we used efficient graph construction methods along with multiprocessing across 8 cpu cores. Tshis optimization slashed the conversion time from several hours down to just around 60 minutes.

4.3 Feature Representation and Dimensionality Reduction:

we optimized the features extracted from each superpixel, keeping only the most relevant attributes—such as intensity, color histograms, and texture. To further enhance the model's efficiency, we applied dimensionality reduction techniques like PCA and normalization, minimizing redundancy while improving learning performance.

4.4 Model Optimization with Graph Attention Networks(GAT):

we implemented a graph attention network (GAT) as our classification model, fine-tuning key hyper parameters to optimize performance. These included:

1. Learning rate
2. Number of attention heads
3. Dropout rate
4. Hidden layer size
5. Batch size and training epochs

Using grid search with cross-validation, we systematically evaluated different parameter combinations to identify the optimal configuration that delivered the best classification results.

4.5 Evaluation Metric Optimization:

To ensure comprehensive and unbiased evaluation [30-31], we assessed model performance using multiple metrics:

- Accuracy
- Precision
- Recall
- F1-score
- Confusion matrix analysis
- ROC-ACC curve evaluation

we further optimized the model through careful threshold tuning, enhancing its sensitivity and specificity for distinguishing between different leukemia subtypes [29]. The following Figure1 shows the work flow diagram for the proposed work and it followed by the algorithm.

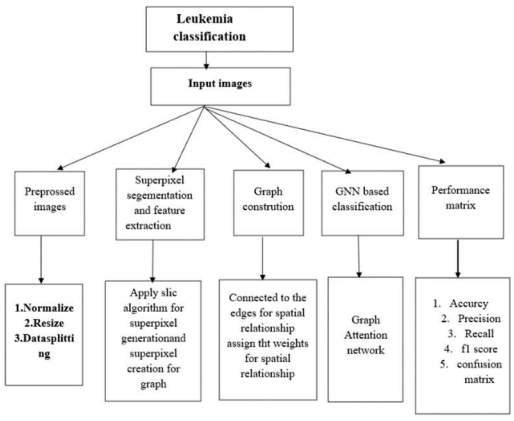

Figure 1: Working Flow Diagram

5. PROPOSED METHODLOGY

There are two models in GNN (GCN and GAT). In this project, initially used the GCN model, but it didn't give good accuracy. So, we chose the GAT model instead, and it produced better accuracy. Our proposed method is GNN. To address the limitations of traditional convolutional methods in

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capturing spatial dependencies, we propose a novel superpixel-based graph neural network (GNN) framework for leukemia cell classification. By transforming medical images into graph structures, our approach leverages Graph attention networks (GAT) to model contextual relationships between regions, enabling more accurate and interpretable predictions. There are various modules are used. They are i) loading and selecting data ii) Image preprocessing data iii) Superpixel segmentation iv) Graph construction v) Graph attention network (GAT) model vi) Evaluation metrics let us see the modules one by one. In Figure 2, represents the types of models.

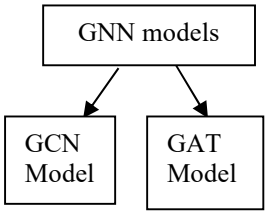

Figure 2: Model Types

Algorithm
Begin
load the pre-trained GNN model from 'model.pth'
wait for the user to upload an image
if image is uploaded then
begin
convert the image to RGB (if needed)
resize the image to (224 x 224)
normalize and convert the image to tensor format
if graph-based input is required then
begin
apply superpixel segmentation on the image
extract features from each segment (superpixel)
construct graph g = (v, e) with features and edges
end
feed the image tensor (or graph g) into the GNN model
predict the output class from model
if predicted_class == 0 then
output "all"
else
output "healthy"
end
else
output "please upload an image to classify."
End

5.1 load and select data

We utilize the C-NMC (ALL-HEM) dataset, a curated collection of thousands of microscopic blood smear images labeled as benign or malignant [28]. This dataset provides a robust foundation for training and evaluating our model. loaded dataset images are shown in Figure 3.

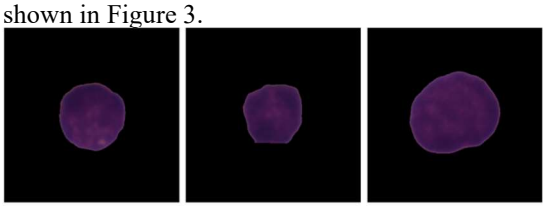

Figure 3: loaded dataset images

5.2 Image preprocessing data:

To ensure consistency and enhance feature extraction, each image undergoes:

a. **Resizing**: standardized to 224×224 pixels.
b. **Normalization**: pixel values scaled to [0, 1].
c. **Noise reduction**: optional Gaussian filtering to suppress artifacts. Preprocessing images are represented in Figure 4.

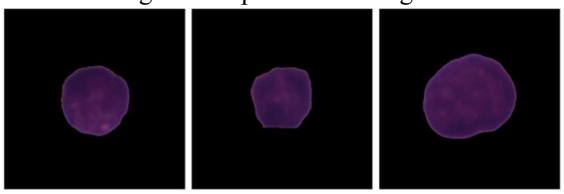

Figure 4: preprocessed images

5.3 Superpixel Segmentation

Using SLIC (Simple Linear Iterative Clustering), we decompose each image into 50 superpixels—adaptive regions that preserve structural boundaries while reducing computational complexity. These superpixels later serve as *nodes* in our graph.

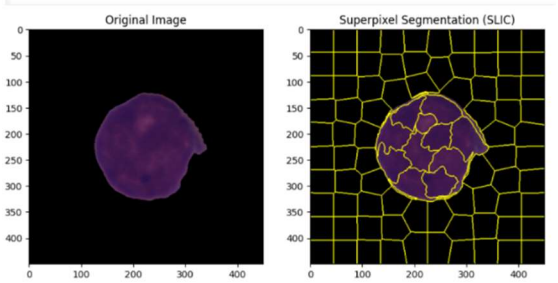

Figure 5: Segmented image

Why do we perform segmentation before converting an image into a graph means Segmentation breaks an image into meaningful regions (which is shown in Figure 5) such as cells or nucleious known as super pixels? These super pixels then become nodes in a graph, with edges representing their relationships. By transforming the image into this graph structure, we preserve its

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spatial and structural details in a way that graph neural networks (GNNs) can effectively process.

5.4 Graph Construction

Each image is converted into a graph representation. The below graph can be represented as Figure 6.

Nodes:

- Superpixels with features:
- Mean RGB values
- Texture descriptors (e.g., local binary patterns)
- Spatial coordinates

edges: connections between adjacent superpixels.

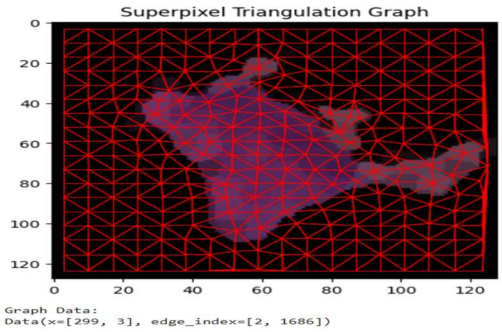

Figure 6: Image converted into Graph

5.5 Graph Attention Network(GAT)

Graph attention networks (GAT), novel neural network architectures that operate on graph-structured data, leveraging masked self-attentional layers to address the shortcomings of prior methods based on graph convolutions or their approximations. By stacking layers in which nodes are able to attend over their neighbourhoods' features, we enable (implicitly) specifying different weights to different nodes in a neighbourhood, without requiring any kind of costly matrix operation (such as inversion) or depending on knowing the graph structure upfront. In this way, we address several key challenges of spectral-based graph neural networks simultaneously, and make our model readily applicable to inductive as well as transductive problems. The overall flow was presented in Figure 7.

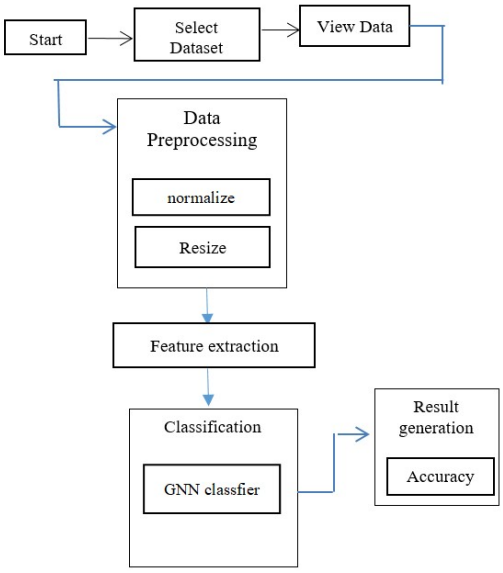

Figure 7: Block Diagram

6. RESULTS AND DISCUSSIONS

Prediction is the process of classifying leukemia images using a superpixel-based graph neural network (GNN) approach. The project effectively predicts input leukemia images from the dataset by improving the overall performance prediction results (accuracy). The equation1 is given by

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN} \quad (1)$$

There are different parameters to measure the performance of classification. They are accuracy, precision, recall, and f-score. High accuracy is predicted by the classification and optimization techniques.so, it gives good accuracy based on the image [23-27].

The below Table 1 shows the accuracy of existing CNN and proposed GNN solutions

Table 1: Accuracy Calculation.

Methodology	Precision	Recall	F1-Score	Accuracy
ANN+CNN+SVM[1]	0.70	0.68	0.69	75%
SVM[2]	0.95	0.96	0.955	96.83%
RESNET-34 AND DENSENET-121[3]	0.985	0.985	0.985	99%
CNN[22]	0.98	0.98	0.97	98.02%
SAGNN+CNN[5]	0.82	0.83	0.825	85%
CNN+RESNET+ SUPERPIXEL GRIDMIX[15]	93.35	92.34	92.84	92.30%
SVM+PSO[17]	0.85	0.86	0.855	87.2%
GNN(PROPOSED)	0.99	0.99	1.0	99.56%

From the above calculations, we can see that GNN with CNN works relatively well and gives good results. Nowadays, most image processing techniques follow deep learning methods such as CNN, MLP, etc.

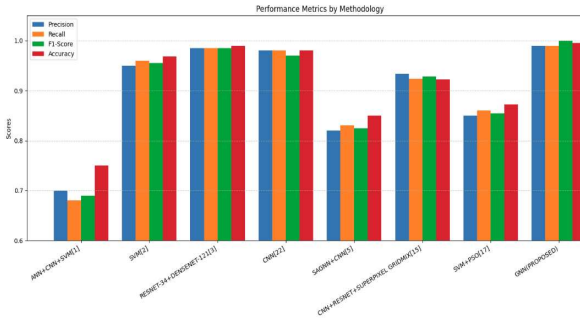

Figure 8: Comparison chart for the ANN+CNN+SVM, SVM, ResNet34+DenseNet, CNN, SAGNN+CNN and the Proposed GNN

The above Figure 8 shows the representation of various methods involved in leukemia datasets with proposed GNN.

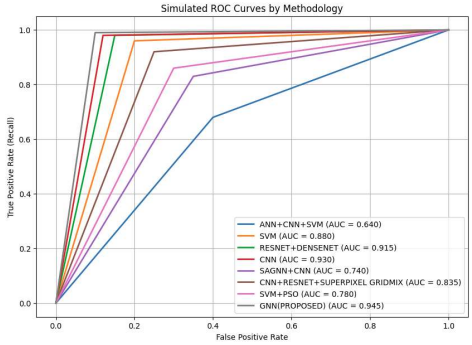

Figure 9: ROC Curve for the Proposed method with other models

Simulated ROC Curve by methodologies based on the True Positive and False Positive Rates was shown in Figure 9.

TABLE 2: TRAINING CALCULATION

S.no	Batch-size	Epochs	Learning rate	Optimizer
1	32	50	0.001	Adam

The training calculations based on the Table II batch size, epochs, learning rate and optimization.

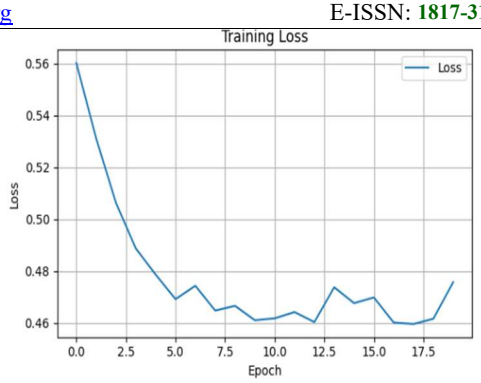

Figure 10: Training Loss

From the Figure 10 loss graph, we see that the loss starts relatively high (0.56) and decreases steadily to around (0.46,) indicating that the model is learning properly during training

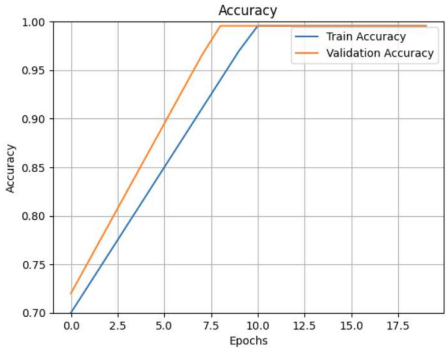

Figure 11: Training and Validation Accuracy

The above accuracy graph Figure 11 shows steady improvement in both training and validation accuracy over epochs. Notably, the validation accuracy stays slightly higher (99.56) than the training accuracy, indicating that the model generalizes well without overfitting. This suggests the GNN is learning stably and performs effectively on unseen data.

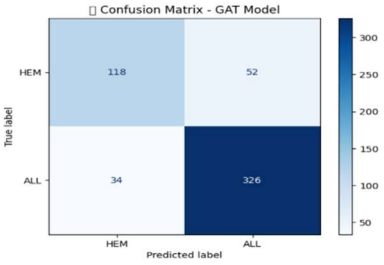

Figure 12: Confusion matrix of the model

This Figure 12 indicates that the GAT model is very effective at identifying ALL cases (326 correct). However, it struggles slightly more

with HEM classification, misclassifying 52 samples as ALL. Overall, the model performs well but could be improved further in distinguishing HEM class more accurately.Also Figure 13 represents the ROC Curve of the GAT Model.

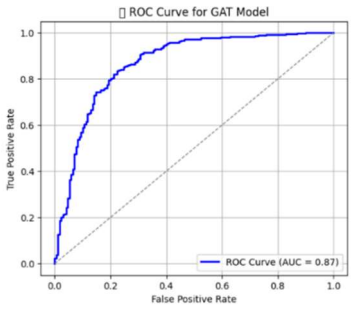

Figure 13: ROC Curve of the GAT model

7. CONCLUSION

This research work successfully applied super pixel-based graph construction combined with graph attention networks (GAT) to classify leukemia images. By representing images as graphs, we effectively captured regional relationships between features, leading to better performance compared to traditional deep learning approaches. The use of superpixels helped reduce computational complexity while preserving critical structural details, allowing the GNN to focus on the most relevant features for classification. Future work could expand this approach by testing on larger datasets, extending classification to multiple leukemia subtypes, and experimenting with more advanced GNN architectures to further enhance accuracy.

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