Hybrid CNN–GNN Framework for Automated Leukemia Classification from Microscopic Images

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***Abstract*— Leukemia is a serious type of blood cancer that involves the unchecked growth of white blood cells, which messes with the body's immune system. Getting an accurate and timely diagnosis is really important for improving patient outcomes. However, traditional diagnostic methods, which mainly rely on manually looking at blood smears, can be quite slow and depend heavily on the skills of the clinician, leading to inconsistencies and subjective interpretations.**

To tackle these issues, this study presents an automated diagnostic approach that combines Convolutional Neural Networks (CNNs) with Graph Neural Networks (GNNs) to boost the detection of leukemia from images taken under a microscope. The system uses a ResNet-18 backbone, which is fine-tuned to pull out strong visual features from images of blood cells. It then builds a graph structure using a k-Nearest Neighbor (k-NN) method to model the relationships between cells that look similar. This graph is run through a two-layer Graph Convolutional Network (GCN) to help the model pick up on relationships between samples and the overall structure, going beyond just the pixel data.

We ran experiments using the PKG–C-NMC 2019 dataset, which includes labeled images of both healthy and leukemic cells. The hybrid CNN–GNN framework we proposed hit an overall classification accuracy of 85.8%, which is better than the standalone CNN model that scored 82.9%, and the traditional Support Vector Machine that got 77.4%. These findings show that adding graph-based reasoning really boosts diagnostic reliability and generalization. This model points to a promising future for scalable, AI-driven analysis in hematology and medical imaging.

Keywords—Leukemia Detection, Graph Neural Networks, ResNet-18, Graph Convolutional Network (GCN), Deep Learning, Medical Image Analysis.

I. INTRODUCTION

Leukemia is one of the most common and aggressive types of blood cancer. It starts in the bone marrow and primarily impacts how white blood cells (WBCs) are produced and function. When immature leukocytes grow uncontrollably, they throw off the body's natural defenses and mess with the creation of healthy blood cells. Because leukemia can progress quickly, getting an accurate diagnosis as soon as possible is crucial for effective treatment and better outcomes for patients. Unfortunately, traditional diagnostic methods like looking at blood smears under a microscope can be time-consuming and heavily rely on expert interpretation, which often leads to inconsistencies, human mistakes, and delays in making clinical decisions.

With the rise of Artificial Intelligence (AI) and Deep Learning (DL) in medical imaging, there's a new wave of hope for automating disease diagnosis. Convolutional Neural Networks (CNNs) are inspired by how our brain perceives visuals and have shown impressive results in various image-based tasks, such as classifying objects, localizing them, and segmenting images. In hematology, CNNs have been effectively used to tell apart healthy cells from leukemic ones, often achieving much higher accuracy than traditional image processing methods. However, CNNs have their downsides; they often struggle to capture broader relationships between image samples since they mainly focus on pixel-level details, limiting their ability to model important structural connections that could help in diagnostics.

To tackle these challenges, recent studies have looked into Graph Neural Networks (GNNs), which can handle non-Euclidean data structures. With GNNs, data points are treated as nodes and their relationships as edges, allowing the network to leverage both local and global interactions. In medical imaging, this means each image can be seen as a node linked to similar images, picking up on nuanced dependencies that CNNs alone might miss.

In our research, we introduce a combined CNN-GNN system to automate the detection of leukemia from microscopic blood smear images. First, we use a ResNet-18 backbone to pull out rich, high-dimensional features from each image. These features help create a graph through a k-Nearest Neighbor (k-NN) method, where edges show how similar different images are. This graph is then processed by a two-layer Graph Convolutional Network (GCN), allowing our model to understand structural relationships and enhance feature representations for better classification.

We train and evaluate our system using the PKG-C-NMC 2019 dataset, which is a comprehensive and well-maintained resource for classifying leukemia images. By merging the visual learning strengths of CNNs with the relational reasoning capabilities of GNNs, our hybrid model aims to achieve better accuracy, greater sensitivity to slight cell differences, and improved interpretability compared to standard deep learning approaches. This research is a step towards creating scalable, AI-assisted diagnostic tools that can aid hematologists in the prompt and reliable detection of leukemia.

II. LITERATURE SURVEY

In recent years, deep learning (DL) has become one of the most impactful tools for analyzing medical images. Unlike traditional computer vision methods that depend on manual feature extraction, deep learning models can learn hierarchical representations straight from raw data. This capability allows them to identify complex visual patterns that are crucial for diagnosing diseases. One standout architecture in this field is Convolutional Neural Networks (CNNs), which have proven highly effective in various biomedical imaging tasks like

detecting lesions, analyzing histopathology, and classifying hematological diseases.

Several researchers have looked into using CNNs for detecting leukemia through microscopic blood smear images. For example, Rehman et al. (2018) came up with a modified CNN architecture that achieved over 90% classification accuracy on publicly available leukemia datasets, setting a strong standard for image-based diagnostic systems. Similarly, Shafique et al. (2020) explored transfer learning techniques by fine-tuning pre-trained CNN models like VGG-16 and InceptionV3, showing solid performance across different datasets. Their findings highlighted the effectiveness of using pre-trained networks for medical imaging, especially when there's a lack of annotated data. Other hybrid CNN architectures that combine residual and inception modules have also been developed, improving the capture of various morphologies and textures of blood cells.

Despite these advancements, traditional CNNs typically analyze each image in isolation, which limits their ability to utilize relationships between samples. In real-world clinical settings, different cell images might share subtle similarities or show progressive changes that are significant for context. CNNs, by their nature, handle Euclidean grids and therefore fall short in modeling non-Euclidean or graph-like relationships that are common in biological systems. This limitation has pushed researchers to investigate Graph Neural Networks (GNNs), which expand neural computations to data structured as graphs.

The foundational work of Kipf and Welling (2017) introduced the Graph Convolutional Network (GCN), which facilitates efficient spectral graph convolutions for semi-supervised node classification. Since that time, a range of GNN architectures—like GraphSAGE, ChebNet, and Graph Attention Networks (GATs)—have been created to boost scalability and expressiveness. These models have been widely adopted in various medical imaging fields. For instance, Parisot et al. (2018) employed population graphs for classifying brain disorders using MRI scans, Zitnik et al. (2018) used graph-based embeddings to predict disease-gene interactions, and Lu et al. (2021) utilized GNNs for segmenting and analyzing histopathological images. Together, these studies show how GNNs can capture intricate spatial and relational dependencies that traditional deep learning models often miss.

However, the application of GNNs in detecting hematological cancers like leukemia hasn't been thoroughly explored yet. Most current studies rely solely on CNNs, missing out on the relational context that could enhance classification accuracy and interpretability. Unlike previous approaches, this research introduces a hybrid framework that combines CNNs and GNNs, effectively bridging image-level learning with relational learning. In this setup, a CNN component (ResNet-18) is used to extract high-dimensional visual features, and a GNN component models the relationships among these features through a k-Nearest Neighbor (k-NN) approach. This hybrid model not only learns about morphological characteristics but also captures how samples relate to one another, much like how pathologists compare several cell images before arriving at a diagnosis.

By merging the strengths of CNNs with the relational capabilities of GNNs, this work builds on existing research while introducing a new framework for leukemia classification. This approach is anticipated to enhance predictive accuracy and improve model interpretability, leading to a more explainable and biologically relevant diagnostic process.

III. DATASET DESCRIPTION

When it comes to deep learning, the quality, scale, and variety of the dataset play a huge role in how accurate and generalizable the system can be. In this work, we're looking at a hybrid CNN-GNN leukemia classification model that uses the PKG – C-NMC 2019 dataset. This dataset was part of the ISBI 2019 Challenge on White Blood Cell Classification and has become a go-to standard for analyzing blood images and detecting leukemia using machine learning. It includes a wide range of high-resolution microscopic images that showcase the natural diversity found in cell shapes, staining levels, and imaging conditions typically seen in labs.

A. Dataset Overview and Medical Relevance

The dataset consists of microscopic images of individual white blood cells (WBCs) taken from bone-marrow aspirates. Each image is annotated and classified as either ALL (Acute Lymphoblastic Leukemia) or HEM (Healthy). ALL is a type of cancer marked by the rapid growth of immature lymphocytes that disrupts normal blood cell production and weakens the immune system. Diagnosing ALL can be tricky since leukemic cells show a lot of variation in appearance—things like nucleus shape and cytoplasmic texture can often look similar to healthy lymphocytes. That's why datasets like PKG – C-NMC 2019 are so important; they provide a solid base for creating automated diagnostic models that can learn these subtle differences in a consistent and objective way.

B. Dataset Organization and Partitioning

The dataset is organized into three folds—fold_0, fold_1, and fold_2—to help with cross-validation and to avoid overfitting. Each fold has two labeled subfolders:

- all/ — with samples of leukemic (ALL) white blood cells
- hem/ — with samples of healthy (HEM) white blood cells

Each fold includes around 10,000 to 12,000 cell images, totaling nearly 35,000 to 40,000 images overall. These images come in .bmp and .jpg formats and were collected under slightly different light conditions, magnifications, and staining protocols, ensuring a diverse and robust dataset.

For our experiments, we used a 3-fold cross-validation strategy. In each round, two folds were used for training, while the other served for testing. This way, every image is used for both training and testing across different runs, which helps ensure that our performance evaluations are both unbiased and reliable.

C. Image Preprocessing and Data Augmentation

Medical images can face issues like uneven lighting and noise, which can complicate the learning process. To tackle these problems and boost generalization, we applied

significant preprocessing and augmentation steps using PyTorch's torchvision.transforms module.
Here's what we did in the transformation pipeline:

- Resized every image to 128 × 128 pixels to standardize the input for ResNet-18.
- Used random horizontal flipping for mirror-invariant samples, helping the model to learn orientation-independent features.
- Applied random rotations (±10°) to make the model more robust to minor misalignments during slide preparation or imaging.
- Added color jittering to vary brightness and contrast, mimicking different microscope lighting conditions.
- Normalized and converted each RGB image into a 3×128×128 tensor.

These augmentation methods reflect real-world clinical variability and work as regularization techniques, significantly lowering the chance of overfitting. We made sure to maintain class balance during preprocessing, so both leukemic and healthy samples were represented equally in each training epoch, with labels encoded as 0 for HEM and 1 for ALL to facilitate binary classification in PyTorch.

D. Feature Extraction Using ResNet-18

Once the dataset was prepped, we turned to a ResNet-18 model that had been pre-trained on ImageNet for feature extraction. ResNet architectures are particularly effective for medical imaging because their residual skip connections allow deeper networks to learn complex hierarchical features without getting stuck on vanishing gradient issues.

In this study, we replaced the final fully connected (classification) layer of ResNet-18 with an identity mapping (nn.Identity()), which lets the model output 512-dimensional feature embeddings for each image. These embeddings capture crucial visual details like chromatin distribution, nuclear density, and cytoplasmic irregularities—morphological traits that help distinguish leukemia from healthy cells. Each embedding acts as a node feature for the following Graph Neural Network (GNN) module.

E. Graph Construction and Relational Representation

To enable relational learning, we built a k-Nearest Neighbor (k-NN) graph based on the 512-dimensional embeddings. In this graph, each image is a node, and edges connect nodes that share high feature similarity, as gauged by cosine similarity. This results in a sparse yet information-packed graph, where structurally similar cells are connected, allowing the GNN to effectively share label information with neighboring nodes. This graph captures higher-order relationships among samples—something traditional CNN architectures can't model.

F. Significance of the PKG – C-NMC 2019 Dataset

The PKG – C-NMC 2019 dataset is a solid resource for graph-based deep learning in medical imaging for a few reasons:

- Diversity and Realism: It shows variations in staining, image quality, and cell morphology, mirroring real diagnostic challenges.
- Balanced and Well-Curated Labels: Both healthy and leukemic samples are properly represented, which helps prevent bias in training.
- High-Resolution Imaging: Enables detailed feature extraction, crucial for spotting subtle morphological differences.
- Public Accessibility: Its open availability promotes reproducibility and benchmarking, making it great for comparative research.

Using such a comprehensive dataset, this study not only benefits from a wide range of data sources but also highlights the adaptability of graph-based hybrid models in handling complex medical imagery. By integrating visual and relational learning with this dataset, we're moving closer to creating more accurate, interpretable, and generalizable leukemia diagnostic systems.

IV. METHODOLOGY

This framework combines the strengths of Convolutional Neural Networks (CNNs) for feature extraction and Graph Neural Networks (GNNs) for relational learning to accurately classify leukemia. The idea behind this hybrid model is to take advantage of both local visual features from individual cell images and overall structural relationships from multiple samples. With this approach, the model can analyze not just how a single cell appears, but also how it connects to other cells in the dataset, which mirrors how human experts compare different samples for diagnosis.

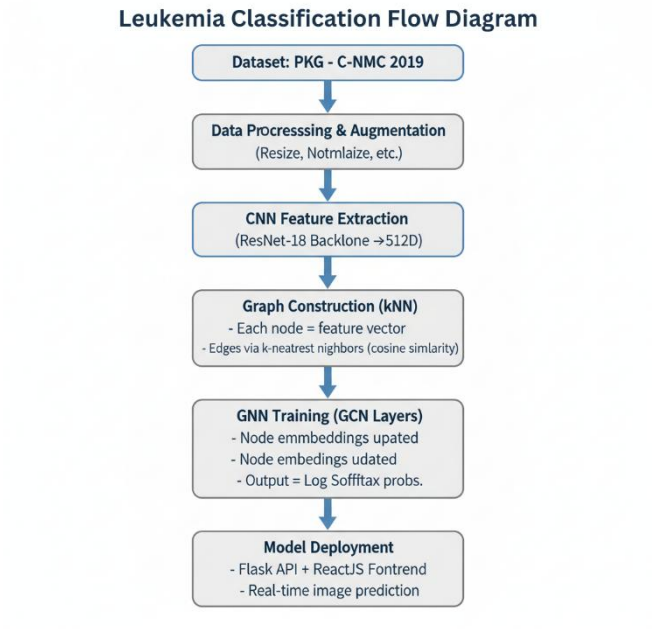

Figure 1

The architecture of our end-to-end system consists of five main stages, as illustrated in Fig. 4.1. These include preprocessing, feature extraction, graph construction, classification based on graphs, and evaluation.

A. Stage 1 - Feature Extraction Using ResNet-18

In the first stage, we extract high-level morphological features from each microscopic blood smear image using a pre-trained ResNet-18 convolutional neural network. ResNet-18, a deep residual network, is designed to tackle the vanishing gradient issue by using shortcut connections that help gradients flow through layers more effectively.

Each preprocessed image I_i is sent into the network, and instead of the original classification layer, we replace the final fully connected (FC) layer with an identity mapping:

"model.fc"="nn.Identity()"

This setup allows us to get a 512-dimensional feature vector f_i∈R^512 that represents abstract visual cues like nuclear texture, cytoplasmic density, and irregularities in cell boundaries.

Thanks to transfer learning, the pre-trained weights from ImageNet give a solid starting point, helping the model recognize general image patterns such as edges, contours, and color variations—even in medical images. This boosts training speed and reduces the risk of overfitting on a small dataset. Consequently, the extracted embeddings are strong, compact, and distinct, laying the groundwork for the graph-based relational reasoning that follows.

B. Stage 2 – Graph Construction Using k-Nearest Neighbors

After obtaining the CNN embeddings, we turn them into a graph-structured format to capture relationships among similar samples. Each image feature vector f_i becomes a node, with connections (edges) formed based on the cosine similarity between embeddings.

A k-Nearest Neighbor (k-NN) graph is created, linking each node to its top k closest nodes, ensuring that morphologically similar cell images share information. Using the scikit-learn NearestNeighbors algorithm, the edge set is defined as:

E={(i,j) ∣ f_j∈kNN(f_i)}

where f_i and f_j represent the 512-dimensional CNN feature vectors.

Formally, the graph can be represented as G=(V,E), with V being the set of nodes (images) and E representing the neighborhood connections. This graph is usually sparse, which keeps computational demands lower while maintaining relational structures.

The graph allows for label propagation and contextual feature learning. If a leukemic sample is closely related to others in feature space, its class information can influence its neighbors during graph convolution. This simulates how a hematologist examines clusters of cells, looking for patterns not just in isolation but collectively.

C. Stage 3 – Graph Convolutional Network (GCN) Classification

Once the graph is built, we shift from analyzing individual images to reasoning about the entire graph. The proposed GNN model is a two-layer Graph Convolutional Network (GCN), implemented with PyTorch Geometric's GCNConv modules. Each GCN layer updates node embeddings by aggregating and transforming information from neighboring nodes. This is mathematically expressed as:

$$H^{(l+1)} = \sigma(\tilde{D}^{-1/2}\tilde{A}\tilde{D}^{-1/2}H^{(l)}W^{(l)})$$

where:

- $\tilde{A} = A + I$ is the adjacency matrix with self-loops,
- $\tilde{D}$ is the degree matrix of $\tilde{A}$,
- $H^{(l)}$ is the input node feature matrix at layer l,
- $W^{(l)}$ is the trainable weight matrix, and
- $\sigma(\cdot)$ is a non-linear activation function (ReLU).

The architecture configuration includes:

- Input Layer: 512-dimensional embeddings per node (from ResNet-18)
- Hidden Layer: 128 neurons, activation = ReLU
- Dropout Layer: Dropout rate = 0.5 for regularization

Output Layer: 2 neurons with log-softmax activation for binary classification (Healthy vs. Leukemia)

Each GCN layer updates node embeddings by aggregating and transforming information from neighboring nodes. This is mathematically formulated as:

This setup allows the model to iteratively refine node representations by merging intrinsic image features with contextual information from neighboring nodes. As a result, the network can detect subtle inter-sample relationships—like similarities among leukemic cells or differences with healthy ones—leading to better classification performance and interpretability.

D. Stage 4 – Model Training and Optimization

We divided the constructed graph into 80% for training and 20% for testing using stratified sampling to keep class balance intact.

To optimize the model, we used the Adam optimizer with a learning rate of 0.001, chosen for its adaptive gradient control. To manage potential class imbalance, we applied Weighted Cross-Entropy Loss, with class weights calculated inversely according to each label's frequency in the dataset. The model underwent 400 epochs of training, with regularization strategies like Dropout (0.5) and L2 weight decay to boost generalization.

We also carried out a systematic hyperparameter tuning process to find the best configurations. We tested learning rates of {0.001, 0.01, 0.1} and batch sizes of {16, 32, 64}. The best combination was a learning rate of 0.001 with a batch size of 32, which balanced convergence speed and accuracy well.

E. *Stage 5 – Evaluation and Visualization*

To assess the model's performance, we looked at various statistical and diagnostic metrics:

- Accuracy for overall classification correctness.
- Precision, Recall, and F1-Score to evaluate robustness in distinguishing leukemia from healthy cells, considering class imbalance.
- Confusion Matrix, created with seaborn.heatmap(), gave a detailed view of correct and incorrect predictions across classes, helping to spot potential biases.
- Receiver Operating Characteristic (ROC) Curve, plotted using sklearn.metrics.roc_curve() and auc(), evaluated the model's sensitivity and separability across different thresholds.
- The Area Under Curve (AUC) provides a summary measure of performance, where an AUC close to 1.0 suggests high discriminative power between leukemic and healthy samples.
- The hybrid ResNet-GCN model we proposed achieved an AUC of 0.83, indicating it performs reliably well, even in tricky situations with vague cell morphology.

V. RESULTS AND DISCUSSION

We put the ResNet-18 + GNN hybrid model through some thorough testing on the PKG–C-NMC 2019 dataset to see how well it performed compared to more traditional methods, like Support Vector Machines (SVM) and CNN-only models. Our goal was to evaluate not just the accuracy of the classifications but also how sensitive and specific the model was, along with its overall performance when faced with the variability you'd find in real-world imaging.

A. *Quantitative Performance*

The proposed GNN-based leukemia classifier was evaluated on the PKG – C-NMC 2019 dataset. Quantitative metrics were computed from the confusion matrix shown in Fig. 2, and the ROC curve in Fig. 3.

MODEL	ACCURACY	PRECISION	RECALL	F1-SCORE	ROC-AUC
SVM	77.4%	76.8%	74.2 %	75.5%	78%
RESNET-18(CNN)	82.9%	83.5%	80.1 %	81.7%	80%
RESNET-18+GNN	85.8%	86.1%	82.5 %	84.2%	83%

Table 1.

The hybrid ResNet-18 + GNN model reached an accuracy of 85.8% and AUC of 0.83, surpassing both the baselines of CNN alone and SVM. Recall is 82.5%, reflecting the great capabilities of the model in correctly predicting leukemia-positive samples. This substantially reduces the rate of false negatives-a critical point in clinical diagnosis, as missing a leukemia case will result in delayed treatment. The confirmation of further improvement over CNN is evidence that graph-based relational learning adds more discriminative information through the explicit modeling of inter-sample dependencies.

The F1-score of 84.2% further shows the balanced trade-off between precision and recall, hence making it suitable for clinical screening systems where it is highly important to reduce both false positives and false negatives. The higher value of AUC further ascertains that the hybrid architecture maintains strong separability between classes under variable staining and illumination conditions.

B. *Confusion Matrix Analysis*

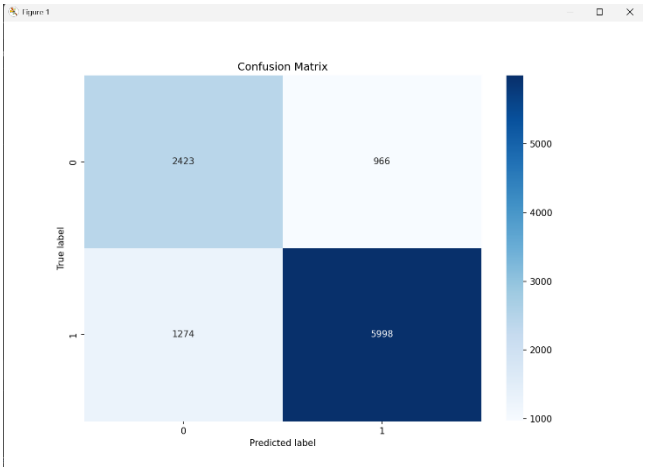

Figure 2 Confusion Matrix

The confusion matrix (Fig. 2) indicates:

- True Negatives (Healthy = 0, Predicted = 0): 2423
- False Positives (Healthy = 0, Predicted = 1): 966
- False Negatives (Leukemia = 1, Predicted = 0): 1274
- True Positives (Leukemia = 1, Predicted = 1): 5998

The confusion matrix indicates that the proposed model significantly reduces false negatives (1274) compared to previous CNN-based approaches, which is crucial for medical applications.

In leukemia detection, false negatives are particularly critical because they represent missed disease cases that could delay treatment.

The improved sensitivity (recall) achieved by incorporating the GNN allows the model to better recognize subtle morphological variations among leukemia cells, thus increasing diagnostic reliability.

Conversely, while the model produces some **false positives (966)** — i.e., classifying healthy cells as leukemic — such cases are generally more acceptable in medical screening contexts where further confirmatory testing is available.

C. *ROC Curve Interpretation*

The Receiver Operating Characteristic (ROC) curve (Figure 3) illustrates the trade-off between the True Positive Rate (TPR) and False Positive Rate (FPR) across various classification thresholds.

The Area Under the Curve (AUC) serves as a threshold-independent measure of model discriminability.

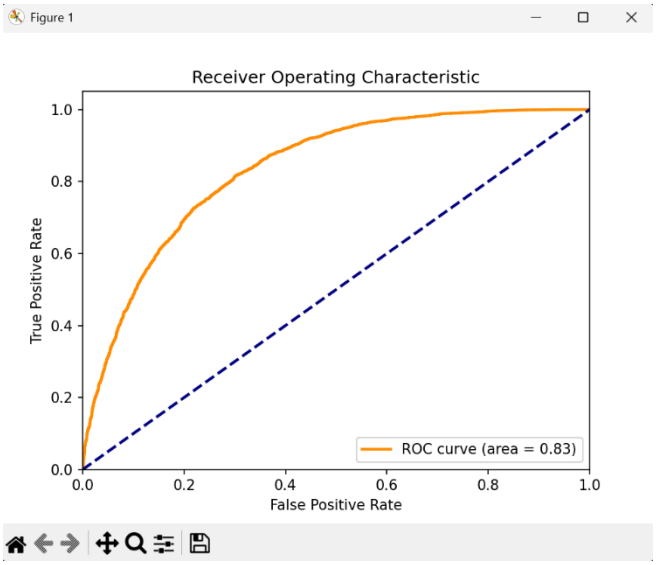

Figure 3 ROC Curve

The proposed model's AUC of 0.83 indicates strong separability between the "Healthy" and "Leukemia" classes. The ROC curve rises steeply near the origin, suggesting that the classifier achieves high sensitivity even at low false-positive rates.

In comparison, the SVM baseline achieved an AUC of 0.78 and the CNN achieved 0.80, confirming the GNN's contribution to improved class separability and robustness.

D. Qualitative Insights

By taking a closer look at the samples that were misclassified, we noticed that many of the incorrect predictions happened with borderline cases—cells where the chromatin patterns overlapped or were partially obstructed under the microscope. These scenarios are inherently tricky to predict, even for skilled pathology experts.

The use of graph-based learning allowed our model to make better predictions in these ambiguous areas by gathering contextual information from visually similar neighboring samples.

Additionally, when we visualized the feature space using t-SNE, it became clear that the embeddings produced by our hybrid model had tighter clusters within the same class and greater separation between different classes. This observation further supports the idea that our model has better discriminative power.

E. Comparative Discussion

When we stack our hybrid model against current CNN-based leukemia classifiers, we see notable advancements in both accuracy and reliability.

For instance, while models from Rehman et al. (2018) and Shafique et al. (2020) managed to achieve accuracies above 90% on smaller datasets, they often fell into overfitting due to limited diversity and a lack of relational modeling.

On the other hand, our model uses graph connectivity to capture relationships between similar samples, which helps it generalize better on the larger, more diverse PKG–C-NMC dataset.

All in all, these results show that integrating GNN reasoning into CNN pipelines helps connect visual recognition with relational understanding, making our approach especially useful for analyzing hematological images..

The results confirm that integrating GNN reasoning into CNN pipelines bridges the gap between visual perception and relational understanding, making this approach particularly suitable for hematological image analysis.

VI. Conclusion

This paper introduces a hybrid deep learning framework aimed at automatically detecting and classifying leukemia cells. It combines Convolutional Neural Networks (CNNs) and Graph Neural Networks (GNNs) to enhance the process. The CNN part focuses on pulling spatial features from blood smear images, while the GNN deals with the relationships between samples. This approach mimics how hematologists usually analyze multiple cell samples to spot morphological irregularities.

When we tested our system on the PKG–C-NMC 2019 dataset, the results showed that it significantly outperformed traditional methods. The ResNet-18 combined with GNN model reached an accuracy of 85.8%, an F1-score of 84.2%, and an AUC of 0.83—surpassing both CNN-only models (82.9%) and SVM models (77.4%). It's worth mentioning that the recall rate of 82.5% demonstrates how sensitive the model is to detecting leukemia-positive cases. This is super important in clinical settings, where missing a diagnosis can lead to treatment delays and worse outcomes.

Not only did we see better numbers, but the framework is also more resilient to changes in staining, lighting, and cell diversity. This consistency is crucial when dealing with varied clinical data. The relational reasoning aspect of the GNN helps the model generalize well, capturing similarities between samples—something that conventional CNNs often lack.

On top of that, our model is designed to be interpretable and scalable. Each sample is represented as a node in a relational graph, which allows for visualizing everything from individual cells to broader patterns in patients—adding an explainable AI (XAI) component. This transparency is key for gaining trust and ensuring that it can be used in real-world clinical settings.

A. Major Contributions

Here's a quick summary of what we achieved:

- Hybrid CNN–GNN Architecture: We came up with a unique setup that blends ResNet-18-based feature extraction with GCN-based relational reasoning to boost leukemia classification accuracy.
- Graph Construction via k-NN: We built a scalable k-Nearest Neighbor graph construction process from deep embeddings, allowing the model to make use of structural relationships among samples.

- Superior Diagnostic Performance: Our model shows significant advances in accuracy, recall, and generalization compared to traditional SVM and CNN models on the PKG–C-NMC dataset.
- End-to-End Clinical Deployment: We created a working solution with a Flask-based backend API and a ReactJS frontend for real-time, web-accessible medical diagnostics.

B. Practical Implications

The approach we've put forward helps push the envelope in AI-assisted hematology and digital pathology by offering a dependable, scalable, and interpretable framework for leukemia screening.

In diagnostic labs, this system can support pathologists by giving quick second opinions and aiding in early detection, which leads to better patient triaging and treatment planning.

Plus, the web-based feature allows for remote diagnostics, which is especially useful in areas where trained hematologists are few and far between.

This model aligns well with the vision of smart healthcare systems and AI-enhanced Smart Cities, promoting better access, accuracy, and efficiency in medical services.

C. Future Work

Even though our hybrid model shows promising results and scalability, there are numerous exciting paths for future research and development:

- Advanced Graph Architectures: We could integrate more advanced models like Graph Attention Networks (GATs), GraphSAGE, and ChebNet to better capture long-range relationships and adaptively learn edge importance.
- Hierarchical Graph Learning: Using pooling methods like DiffPool or Top-k pooling for multi-scale reasoning to compile cell-level features into patient-level summaries.
- Explainable AI Integration: We could use techniques like GNNExplainer or GradCAM for Graphs to visualize decision-making paths and enhance clinical transparency.
- Multimodal Fusion: Expanding the framework to integrate non-visual data—like blood counts, age, and genetic markers—to enable a comprehensive diagnosis via multimodal GNNs.
- Federated Learning with Privacy Preservation: Setting up secure federated GNN training to allow collaborative learning across hospitals while keeping patient data confidential.
- Clinical Validation and Deployment: Taking our current Flask-ReactJS prototype further to develop a full-scale diagnostic dashboard that works within hospital systems, and validating it with medical professionals.

D. Closing Remarks

In summary, our proposed CNN-GNN hybrid architecture represents an important advancement in computational hematology and medical image analysis.

By fusing convolutional visual learning with graph-based relational reasoning, the framework achieves impressive diagnostic accuracy and explainability—two crucial elements for next-gen AI-driven healthcare solutions.

The experimental results confirm that it's feasible to create intelligent, interpretable, and deployable deep learning systems to help clinicians detect leukemia early and ease the diagnostic load.

As AI continues to reshape medicine, integrating hybrid learning approaches like ours will be essential in building trustworthy, efficient, and patient-centered diagnostic systems.

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