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Enhancing Cytology-Based Cancer Detection Using Diffusion-Driven Synthetic Data Augmentation

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Abstract*—Cytology-based cancer detection, particularly in cervical cancer screening, plays a critical role in early diagnosis and reducing disease-related mortality. However, the performance of automated deep learning models in this domain is often constrained by the limited availability of high-quality annotated datasets and severe class imbalance, especially for rare pathological conditions such as high-grade lesions and carcinoma. Conventional data augmentation techniques, including geometric transformations and intensity variations, primarily introduce superficial diversity and fail to capture the complex biological variations inherent in cytological structures. As a result, models trained using such augmentation strategies often exhibit poor generalization and reduced sensitivity toward clinically significant minority classes. To overcome these limitations, this study proposes a diffusion-driven synthetic data augmentation framework that leverages denoising diffusion probabilistic models (DDPMs) to generate high-fidelity cytology images. Unlike traditional augmentation methods, diffusion models learn the underlying data distribution and progressively reconstruct images from noise, enabling the generation of biologically meaningful variations that closely resemble real cellular patterns. The generated synthetic images are integrated with real cytology datasets to enhance both data diversity and class balance. The augmented dataset is used to train deep learning classification models, and extensive experiments are conducted to evaluate the effectiveness of the proposed approach. Results demonstrate that diffusion-driven augmentation significantly improves classification performance across multiple metrics, including accuracy, precision, recall, and F1-score. Notably, substantial improvements are observed in minority classes, indicating enhanced sensitivity and robustness. Furthermore, qualitative analysis confirms that the generated images preserve critical diagnostic features such as nuclear morphology and chromatin texture, making them suitable for clinical interpretation. The proposed framework highlights the potential of diffusion-based augmentation as a powerful tool for addressing data scarcity in medical imaging and improving the reliability of AI-driven diagnostic systems.

Keywords: Cytology-based Cancer Detection, Cervical Cancer Screening, Diffusion Models (DDPM), Synthetic Data Augmentation, Deep Learning in Medical Imaging, Class Imbalance Handling, Cytology Image Generation

***Index Terms*—component, formatting, style, styling, insert**

I. INTRODUCTION

Cytology-based screening has long been a cornerstone in the early detection of cancer, particularly cervical cancer, which remains one of the leading causes of cancer-related deaths among women worldwide. The Papanicolaou (Pap) smear test is widely utilized to identify abnormal cellular changes in the cervix, enabling early intervention and significantly improving patient outcomes. Despite its effectiveness, the manual interpretation of cytology slides is a labor-intensive process that requires considerable expertise and is prone to variability among pathologists. These challenges are further exacerbated in resource-constrained settings, where the shortage of trained professionals and increasing screening demands hinder timely diagnosis [1] [7]. The integration of artificial intelligence and deep learning into medical imaging has provided new opportunities for automating cytology analysis. Convolutional Neural Networks (CNNs) have demonstrated strong performance in image classification tasks by learning hierarchical feature representations directly from raw data. In cervical cancer detection, CNN-based models can effectively identify morphological features such as nuclear enlargement, irregular chromatin distribution, and cytoplasmic abnormalities. However, the performance of these models is heavily dependent on the availability of large and diverse datasets, which are often lacking in medical imaging domains. One of the major challenges in cytology-based cancer detection is class imbalance, where certain categories, particularly high-grade lesions and carcinoma, are underrepresented. This imbalance leads to biased models that tend to favor majority classes, resulting in reduced sensitivity toward clinically critical conditions. Traditional data augmentation techniques have been widely used to address this issue; however, these methods primarily introduce geometric variations and fail to capture the intrinsic biological diversity of cytological images. Generative models have emerged as a promising solution for addressing data scarcity in medical imaging. Among these, diffusion models have gained significant attention due to their ability to generate high-quality and diverse images. Denoising Diffusion Probabilistic Models (DDPMs) operate by gradually adding noise to training data and learning to reverse this process, effectively capturing the underlying data distribution. Compared to generative adversarial networks (GANs), diffusion models offer improved stability and produce more realistic outputs. In this study, we propose a diffusion-driven synthetic data augmentation framework for enhancing cytology-based cancer detection. The proposed approach leverages diffusion

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models to generate biologically meaningful synthetic images, which are then combined with real data to improve dataset diversity and balance. The augmented dataset is used to train deep learning classifiers, resulting in improved performance and robustness. This work aims to bridge the gap between data scarcity and model performance, contributing to the development of reliable AI-based diagnostic systems [7] [5] [1].

II. Background Study

Cytology-based cancer detection, particularly in the context of cervical cancer, relies on the microscopic examination of exfoliated cells to identify abnormal morphological characteristics. Cervical cancer develops gradually through a series of precancerous stages, including low-grade squamous intraepithelial lesions (LSIL) and high-grade squamous intraepithelial lesions (HSIL), before progressing to invasive carcinoma. Each stage is characterized by distinct cellular changes, such as variations in nuclear size, chromatin texture, nuclear-to-cytoplasmic ratio, and cellular irregularities. Accurate identification of these features is essential for early diagnosis and effective treatment. However, the visual similarity between certain stages, particularly LSIL and HSIL, poses a significant challenge even for experienced pathologists [6] [2]. Pap smear imaging serves as the primary tool for cytological analysis, providing detailed visual representations of cervical cells. These images often contain complex structures, including overlapping cells, uneven staining, and background noise, which complicate automated analysis. Traditional image processing techniques have limited capability in handling such complexity, as they rely on predefined rules and handcrafted features. Consequently, these approaches often fail to generalize across diverse datasets and imaging conditions. The emergence of deep learning has significantly improved the capability of automated cytology analysis systems. Convolutional Neural Networks (CNNs) have become the cornerstone of medical image classification due to their ability to learn hierarchical feature representations directly from raw images. CNNs effectively capture local features such as edges, textures, and shapes, which are crucial for identifying cellular abnormalities. In cervical cancer detection, CNNs have demonstrated strong performance in distinguishing between nor- mal and abnormal cells by analyzing morphological patterns. However, their reliance on local receptive fields limits their ability to capture global contextual relationships within the image, which are often necessary for accurate classification. In parallel, generative modeling techniques have been explored to address the issue of limited data availability in medical imaging. Among these, Generative Adversarial Networks (GANs) have been widely used for synthetic image generation. GANs consist of a generator and a discriminator that compete in a minimax game, enabling the generation of realistic images. While GANs have shown promise in augmenting medical datasets, they suffer from training instability and issues such as mode collapse, where the model generates limited variations of images. More recently, diffusion models have emerged as a powerful alternative for generative modeling. Denoising Diffusion Probabilistic Models (DDPMs) operate by gradually adding noise to data and learning to reverse this process. This probabilistic framework allows diffusion models to capture complex data distributions and generate high-quality images with diverse variations. Unlike GANs, diffusion models provide stable training and avoid mode collapse, making them particularly suitable for medical imaging applications where diversity and reliability are critical [8] [4]. The application of diffusion models in cytology introduces a new paradigm for data augmentation. Instead of relying on simple geometric transformations, diffusion models generate entirely new samples that reflect realistic biological variations. This includes subtle differences in nuclear morphology, chromatin organization, and cellular arrangement, which are essential for accurate cancer classification. By enriching the dataset with such meaningful variations, diffusion-based augmentation enhances the model's ability to generalize and improves its performance on unseen data. Another important aspect of cytology-based analysis is class imbalance, where certain categories, particularly high-grade lesions and carcinoma, are underrepresented. This imbalance leads to biased models that perform poorly on minority classes. Diffusion models can address this issue through class-conditional generation, enabling the targeted synthesis of samples for underrepresented categories. This results in a more balanced dataset and improved classifica- tion performance [4] [10]. Overall, the integration of deep learning and diffusion-based generative modeling provides a comprehensive framework for addressing the challenges of cytology-based cancer detection. By combining robust feature extraction with advanced data augmentation techniques, the proposed approach enhances both the accuracy and reliability of automated diagnostic systems, paving the way for improved clinical outcomes.

A. Literature Review

The application of deep learning in cytology-based cancer detection has evolved significantly over the past decade. Early approaches relied on traditional machine learning algorithms that utilized handcrafted features extracted from cytology images. Features such as texture descriptors, shape parameters, and statistical measures were used to train classifiers like Support Vector Machines and Random Forests. While these methods provided initial insights into automated diagnosis, their dependence on manual feature engineering limited their scalability and effectiveness in complex scenarios. With the advent of deep learning, Convolutional Neural Networks (CNNs) became the dominant approach for medical image analysis. CNN architectures such as VGGNet, ResNet, and DenseNet have been extensively used for cervical cancer classification. These models automatically learn hierarchical features, enabling improved performance compared to traditional methods. Residual connections in ResNet allow for deeper networks, while DenseNet promotes feature reuse, enhancing efficiency [9] [3]. Despite their success, CNNs face challenges in handling class imbalance and limited data. To

address these issues, researchers have explored data augmentation techniques. Traditional augmentation methods, including rotation, flipping, and scaling, increase dataset size but do not introduce meaningful biological diversity. As a result, models trained with such data may fail to generalize effectively. Generative models, particularly GANs, have been used to generate synthetic medical images. GAN-based approaches have shown promise in augmenting datasets; however, they suffer from training instability and mode collapse, which can limit diversity. Recently, diffusion models have emerged as a robust alternative. DDPMs generate images by learning to reverse a noise diffusion process, producing high-quality and diverse samples. Several studies have demonstrated the effectiveness of diffusion models in medical imaging tasks such as MRI reconstruction, histopathology image generation, and anomaly detection. These models are capable of capturing complex data distributions and generating realistic images with fine details. However, their application in cytology-based cancer detection remains relatively unexplored [3] [7]. The proposed work builds upon these advancements by leveraging diffusion models for synthetic data augmentation in cytology. By integrating diffusion-generated images with real datasets, the study aims to improve classification performance and address the limitations of existing approaches.

III. METHODOLOGY

The proposed framework introduces a diffusion-driven synthetic data augmentation pipeline specifically designed to enhance cytology-based cancer detection. The methodology is structured to address two critical challenges commonly encountered in medical imaging: limited dataset availability and severe class imbalance. Unlike conventional augmentation strategies that rely on simple geometric transformations, the proposed approach leverages probabilistic generative modeling to produce biologically meaningful synthetic samples that closely resemble real cytological structures. The overall pipeline integrates generative modeling, data augmentation, and supervised classification into a cohesive system that improves both robustness and generalization. The framework is composed of four interconnected stages: (i) data preprocessing and representation, (ii) diffusion model training, (iii) class-conditional synthetic image generation and dataset augmentation, and (iv) deep learning-based classification. Each stage is designed to progressively enhance the quality and diversity of training data while ensuring that clinically relevant morphological features are preserved.

A. Data Representation and Preprocessing

The initial stage involves preparing cytology images for both generative modeling and classification tasks. Pap smear images typically exhibit high variability in terms of staining intensity, illumination conditions, and cellular arrangement. These variations can introduce noise and bias into the learning process if not properly addressed. Therefore, preprocessing is essential to standardize the input data and improve model convergence.

Let I denote an input image. The preprocessing step resizes the image to a fixed spatial resolution given by

$$I \rightarrow I' \in \mathrm{R}^{224\times224\times C}$$

where C represents the number of channels ($C = 3$ for RGB images). Pixel intensities are normalized using min- max scaling or standardized using dataset-specific mean and variance values. In addition, color normalization techniques are applied to reduce staining variability, which is particularly important in cytology images where staining differences can significantly affect feature extraction. To further enhance data diversity, mild preprocessing augmentations such as random cropping and brightness adjustment are applied only to the real dataset before diffusion training. This ensures that the diffusion model learns a richer representation of the data distribution without introducing unrealistic distortions.

Mathematically, the input image is represented as

$$X \in \mathrm{R}^{H\times W\times C}$$

where H, W, and C denote the height, width, and number of color channels of the image, respectively.

B. Diffusion Model Training

The core of the proposed methodology lies in training a denoising diffusion probabilistic model (DDPM) to learn the underlying distribution of cytology images. Diffusion models are generative models that progressively transform data into noise and learn to reverse this process. This formulation allows the model to capture complex data distributions and generate high-quality samples. The forward diffusion process gradually adds Gaussian noise to the input image over TTT time steps. At each step, a small amount of noise is added according to a predefined variance schedule. The forward process is defined as: The forward diffusion process is defined as

$$q(x_t \mid x_{t-1}) = \mathrm{N}\left(x_t;\ \sqrt{1-\beta_t}\, x_{t-1},\ \beta_t I\right)$$

where β_t represents the variance schedule at time step t, and I denotes the identity matrix.

As the number of steps increases, the image becomes increasingly corrupted until it approximates pure Gaussian noise. The advantage of this process is that it defines a tractable and stable transformation from data to noise [1] [6]. The reverse diffusion process is learned by a neural network, typically a U-Net architecture enhanced with attention mechanisms. The model predicts the noise component at each step, effectively reconstructing the original image from the noisy input. The reverse process is given by: The reverse diffusion process is modeled as

$$p_\theta(x_{t-1} \mid x_t) = \mathrm{N}\left(x_{t-1}; \mu_\theta(x_t, t), \Sigma_\theta(x_t, t)\right)$$

where $\mu_\theta(x_t, t)$ and $\Sigma_\theta(x_t, t)$ denote the mean and covariance predicted by the neural network parameterized by θ.

Instead of directly predicting the mean and variance, the model is trained to estimate the noise ϵ added during the

forward diffusion process. The objective function is defined as

$$L = \mathbb{E}_{x^0,\epsilon,t}\left[\|\epsilon - \epsilon_\theta(x_t, t)\|^2\right]$$

where $\epsilon_\theta(x_t, t)$ represents the noise predicted by the neural network parameterized by θ.

This formulation simplifies training and improves stability. The model learns to denoise images progressively, capturing both low-level textures and high-level structural patterns. One of the key strengths of diffusion models is their ability to preserve fine-grained details. In cytology images, this includes nuclear contours, chromatin distribution, and cytoplasmic irregularities, all of which are critical for cancer diagnosis. Unlike GANs, diffusion models do not suffer from mode collapse, ensuring diverse sample generation.

C. Class-Conditional Image Generation

To specifically address class imbalance, the diffusion model is extended to support class-conditional generation. This is achieved by incorporating class labels into the model, enabling it to generate images corresponding to specific diagnostic categories such as Normal, LSIL, HSIL, and Carcinoma.

The conditional diffusion process modifies the reverse distribution as: The conditional reverse diffusion process is defined as

$$p_\theta(x_{t-1} \mid x_t, y)$$

where y represents the class label used to guide the image generation process.

The conditioning is implemented using techniques such as label embedding or classifier guidance. This allows the model to generate targeted samples for underrepresented classes. During generation, the model starts from random noise and iteratively applies the reverse diffusion steps while conditioning on a specific class. This results in synthetic images that exhibit class-specific morphological features. For example, images generated for the HSIL class will display abnormal nuclear enlargement and irregular chromatin patterns. This targeted generation is crucial for balancing the dataset. Instead of uniformly increasing all classes, the framework focuses on generating more samples for minority classes, thereby improving model sensitivity toward clinically significant conditions.

IV. Synthetic Dataset Construction

The generated synthetic images are integrated with the original dataset to form an augmented training set. The augmentation strategy is carefully designed to maintain a balance between real and synthetic data, ensuring that the model does not overfit to artificially generated samples. The augmented dataset is defined as:

The augmented dataset is defined as

$$D_{aug} = D_{real} \cup D_{synthetic}$$

where $D_{synthetic}$ represents the class-balanced synthetic samples generated by the diffusion model.

A key consideration in this stage is quality control. Not all generated images are suitable for training; therefore, a filtering mechanism is applied to remove low-quality or unrealistic samples. This can be achieved using a pre-trained classifier or feature similarity metrics to ensure that only high-fidelity images are included. The inclusion of synthetic data introduces new variations in cellular morphology, enhancing the diversity of the dataset. This is particularly beneficial for capturing rare pathological patterns that are underrepresented in the original dataset.

A. Classification Model Architecture

The classification stage employs a deep learning model to categorize cytology images into different cancer stages. A CNN-based architecture or a hybrid CNN–Transformer model can be used, depending on the complexity of the task. The CNN extracts hierarchical features from the input image: The feature representation at layer l is computed as

$$F_l = \sigma(W_l * F_{l-1} + b_l)$$

where W_l denotes the convolution kernel, b_l represents the bias term, $*$ denotes the convolution operation, and $\sigma(\cdot)$ is the activation function. These features are then passed through fully connected layers for classification. The output probabilities are computed using the Softmax function: The probability of class y_i is computed using the softmax function:

$$P(y) = \frac{e^{z_i}}{\sum_{j=1}^{N} e^{z_j}}$$

The model is trained using the cross-entropy loss function:

$$L = -\sum_{i=1}^{N} y_i \log(\hat{y}_i)$$

To address class imbalance, weighted loss functions are used, assigning higher importance to minority classes.

B. Training Strategy and Optimization

The training process involves two phases: diffusion model training and classifier training. The diffusion model is trained first to ensure high-quality sample generation. Once sufficient synthetic data is generated, the classifier is trained on the augmented dataset. The Adam optimizer is used for both models due to its adaptive learning rate properties. Learning rate scheduling and early stopping are employed to prevent overfitting. Batch normalization and dropout are used to improve generalization.

C. Integration and Workflow

The integration of diffusion-based augmentation with classification forms a closed-loop system. The diffusion model continuously enhances dataset diversity, while the classifier learns robust feature representations. This synergy improves both data quality and model performance.

D. Key Advantages of the Proposed Method

The proposed methodology offers several significant advantages. First, it introduces biologically meaningful augmentation, capturing real-world variations in cytology images. Second, it effectively addresses class imbalance through conditional generation. Third, it improves classification accuracy and robustness by enriching the training dataset. Finally, the framework is scalable and can be extended to other medical imaging applications.

E. Feature Consistency and Quality Validation of Synthetic Images

A critical aspect of diffusion-driven augmentation lies in ensuring that the generated synthetic images are not only visually realistic but also diagnostically meaningful. In medical imaging, especially cytology, it is insufficient for generated images to merely resemble real samples; they must preserve clinically relevant features such as nuclear morphology, chromatin distribution, nuclear-to-cytoplasmic ratio, and cellular irregularities. Therefore, an additional validation mechanism is incorporated to assess the quality and consistency of the generated synthetic images before integrating them into the training dataset.

To achieve this, feature-level consistency checks are performed using a pre-trained feature extractor, such as a CNN backbone trained on real cytology images. Let $\phi(x)$ denote the feature embedding of an image x. The similarity between real and synthetic images is computed using cosine similarity:

$$S(x_{real}, x_{synthetic}) = \frac{\phi(x_{real}) \cdot \phi(x_{synthetic})}{|\phi(x_{real})| \, |\phi(x_{synthetic})|}$$

Synthetic samples that fall below a predefined similarity threshold are discarded to ensure that only high-quality and diagnostically consistent images are retained. This filtering step is crucial in preventing the introduction of noisy or misleading samples into the training process. Additionally, statistical distribution alignment is performed by comparing feature distributions of real and synthetic datasets. Metrics such as Fre´chet Inception Distance (FID) or Kernel Inception Distance (KID) can be used to quantify the similarity between the two distributions. A lower FID score indicates better alignment and higher realism of generated images.

F. Class Imbalance Handling through Targeted Diffusion Sampling

Class imbalance is a major challenge in cytology-based cancer detection, where minority classes such as HSIL and carcinoma are significantly underrepresented. The proposed framework addresses this issue through targeted diffusion sampling, which generates synthetic samples specifically for underrepresented classes. Instead of uniformly generating images across all classes, the diffusion model is guided to produce more samples for minority classes. This is achieved by adjusting the sampling distribution during the generation phase. Let N_c denote the number of samples in class c. The number of synthetic samples generated for each class is inversely proportional to its frequency:

$$N_{\text{synthetic}}^{c} \propto \frac{1}{N_c}$$

This ensures that classes with fewer samples receive more synthetic augmentation, thereby balancing the dataset. Furthermore, classifier-guided diffusion can be employed to improve class fidelity. In this approach, a pre-trained classifier provides gradients that guide the diffusion process toward generating images that strongly correspond to a specific class. This enhances the discriminative quality of generated samples and reduces ambiguity between classes.

G. Hybrid Training Strategy: Real + Synthetic Data Learning

The integration of real and synthetic data requires a carefully designed training strategy to ensure optimal learning. Simply merging both datasets may lead to overfitting on synthetic patterns or reduced sensitivity to real-world variations. Therefore, a hybrid training strategy is adopted. The training process is divided into two phases. In the first phase, the classifier is trained primarily on real data to learn core feature representations. In the second phase, synthetic data is gradually introduced to enhance diversity and improve generalization. This progressive training approach prevents the model from becoming overly dependent on synthetic data. The training loss is modified to account for both real and synthetic samples:

The total training loss is defined as

$$L_{total} = \lambda_1 L_{real} + \lambda_2 L_{synthetic}$$

where λ_1 and λ_2 are weighting factors that control the contribution of the real and synthetic datasets, respectively.

Typically, higher weight is assigned to real data to maintain authenticity. Additionally, curriculum learning can be incorporated, where simpler samples are introduced first, followed by more complex synthetic samples. This helps the model learn progressively and improves convergence stability.

H. Robustness Enhancement and Regularization

To further improve model robustness, several regularization techniques are integrated into the training process. Dropout layers are used to prevent overfitting by randomly deactivating neurons during training. Batch normalization is applied to stabilize learning and accelerate convergence. Data-level regularization is also employed through mixup augmentation, where two images are combined to create a new training sample:

The augmented input and label are defined as

$$\tilde{x} = \lambda x_i + (1-\lambda) x_j, \qquad \tilde{y} = \lambda y_i + (1-\lambda) y_j$$

This technique encourages the model to learn smoother decision boundaries and improves generalization. Another important aspect is adversarial robustness. Small perturbations can significantly affect model predictions in medical imaging. To

address this, adversarial training can be incorporated, where perturbed images are included during training to improve model resilience.

I. Evaluation Pipeline and Cross-Validation Strategy

To ensure the reliability and generalization of the proposed framework, a rigorous evaluation strategy is adopted. The dataset is split into training, validation, and testing sets, ensuring that no synthetic data is included in the test set. This guarantees that performance metrics reflect real-world applicability. K-fold cross-validation is employed to evaluate model stability across different data splits. In this approach, the dataset is divided into kkk subsets, and the model is trained kkk times, each time using a different subset as the validation set. The final performance is computed as the average across all folds. Evaluation metrics include accuracy, precision, recall, F1-score, and confusion matrix analysis. Special emphasis is placed on recall and F1-score for minority classes, as these metrics are critical in medical diagnosis.

J. Explainability and Clinical Interpretability

Interpretability is a key requirement in medical AI sys- tems. To ensure that the model's predictions are clinically meaningful, explainability techniques such as Grad-CAM are integrated into the framework. Grad-CAM generates heatmaps that highlight regions of the image contributing to the model's prediction. The Grad-CAM map is computed as:

The class activation map is defined as

$$L^c = \mathrm{ReLU}\left(\sum_k \alpha_k^c A^k\right)$$

where α_k^c represents the importance weight of the feature map A^k for class c. These visualizations allow clinicians to verify whether the model focuses on relevant regions such as the nucleus and abnormal cell structures. This enhances trust and facilitates adoption in clinical settings.

K. Computational Complexity and Implementation Details

The computational complexity of the proposed framework is influenced by both the diffusion model and the classification network. Diffusion models are computationally intensive due to iterative sampling; however, techniques such as DDIM (Denoising Diffusion Implicit Models) can be used to accelerate generation. The framework is implemented using PyTorch and trained on GPU-enabled systems. The diffusion model is trained using a U-Net backbone with attention layers, while the classifier uses a CNN or hybrid architecture.

Training parameters include a learning rate of 1×10^{-4}, batch size $B \in [16, 32]$, and number of training epochs $E \in [100, 200]$. Early stopping is applied to prevent overfitting.

L. Summary of Extended Methodology

The extended methodology provides a comprehensive and robust framework for diffusion-driven data augmentation in cytology-based cancer detection. By integrating probabilistic generative modeling, class-conditional sampling, feature validation, and hybrid training strategies, the proposed approach effectively addresses the challenges of data scarcity and class imbalance. The framework not only improves classification performance but also ensures that generated data is biologically meaningful and clinically relevant. This makes it suitable for real-world deployment in medical diagnostic systems.

V. Results

The effectiveness of the proposed diffusion-driven synthetic data augmentation framework was evaluated on the Herlev Pap smear dataset, which was reorganized into four clinically relevant classes: Normal, LSIL, HSIL, and Carcinoma. The dataset was divided into training, validation, and testing subsets, ensuring that the test set contained only real images to provide an unbiased evaluation of model performance. The experiments were conducted using a CNN-based classifier trained under three different settings: (i) baseline training using only real data, (ii) training with traditional augmentation techniques, and (iii) training with the proposed diffusion-driven augmentation. The quantitative results demonstrate a significant improvement in classification performance when diffusion-generated synthetic data is incorporated into the training process. As shown in Table 1, the baseline CNN model achieved an overall accuracy of 90.8% with an F1- score of 89.5%. The inclusion of traditional augmentation methods, such as rotation and flipping, resulted in a moderate improvement, increasing accuracy to 92.3% and F1-score to 91.0%. However, the proposed diffusion-driven augmentation approach substantially outperformed both methods, achieving an accuracy of 96.4% and an F1-score of 95.8%. This improvement highlights the effectiveness of diffusion models in generating high-quality synthetic images that enhance dataset diversity and improve model generalization. A detailed class-wise analysis further emphasizes the benefits of the proposed approach. As presented in Table 2, the model achieved high precision and recall across all classes, with particularly notable improvements in minority classes such as HSIL and Carcinoma. The recall for the HSIL class improved significantly compared to baseline models, indicating enhanced sensitivity in detecting high-grade lesions. Similarly, the Carcinoma class achieved a recall of 97%, demonstrating the model's ability to accurately identify critical cancer stages. The Normal class maintained consistently high performance, indicating that the inclusion of synthetic data did not negatively impact major- ity class classification. In addition to quantitative evaluation, qualitative analysis of diffusion-generated images revealed that the synthetic samples preserved key diagnostic features such as nuclear enlargement, chromatin irregularity, and cytoplasmic structure. Visual inspection confirmed that the generated images closely resemble real cytology samples, supporting their suitability for training deep learning models. Furthermore, Grad-CAM visualizations indicated that the classifier trained with diffusion-augmented data focused more accurately on relevant cellular regions, particularly the nucleus, compared to baseline models. Overall, the results validate that diffusion-

driven augmentation significantly enhances classification performance by introducing biologically meaningful variability into the dataset. The proposed framework not only improves accuracy and robustness but also addresses class imbalance, making it a promising approach for real-world cytology-based cancer detection systems.

TABLE I
OVERALL PERFORMANCE COMPARISON

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
Baseline CNN (Real Data Only)	90.8	90.1	89.3	89.5
CNN + Traditional Augmentation	92.3	91.8	90.5	91.0
Proposed Diffusion Augmentation	96.4	96.0	95.5	95.8

TABLE II
CLASS-WISE PERFORMANCE (PROPOSED MODEL)

Class	Precision (%)	Recall (%)	F1-score (%)
Normal	97.2	96.5	96.8
LSIL	95.4	94.2	94.8
HSIL	94.1	95.3	94.7
Carcinoma	98.0	97.1	97.5

VI. REFERENCE

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