Integrating Deep Learning and Traditional Learning for Content-Based Image Retrieval System in Lymphoma Diagnosis

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Abstract

Lymphoma diagnosis relies on accurate and timely identification of lymphoma patterns, and Content-Based Image Retrieval (CBIR) systems leveraging medical imaging have shown promise in this regard. This study proposes a novel framework that integrates deep learning and traditional learning methodologies to enhance CBIR systems for lymphoma diagnosis. The approach uses convolutional neural networks (CNNs), a type of neural network that is deep, to derive a high degree information from photos of lymphoma. For the categorization and extraction of related lymphoma photos, these attributes are subsequently fed into conventional learning algorithms like support vector machines (SVMs) or random forests (RFs). The suggested system makes use of the advantages of both conventional learning as well as neural networks. Deep learning models capture complex and abstract features from lymphoma images, enabling improved discrimination between lymphoma subtypes. Meanwhile, traditional learning algorithms provide transparent decision rules, enhancing the interpretability and trustworthiness of the CBIR system. Through the integration of these techniques, the developed system aims to facilitate efficient analysis and retrieval of relevant lymphoma images, aiding clinicians in the analyticdevelopment. The performance of the system will be compared against baseline deep learning models and traditional learning approaches separately. Evaluation metrics such as precision, recall, and accuracy will be employed to assess the retrieval performance and diagnostic accuracy of the CBIR system. The anticipated outcome of this research is an improved CBIR system that enables clinicians to effectively identify and retrieve lymphoma images.

Keywords:content-based image retrieval, lymphoma diagnosis, deep learning, traditional learning, convolutional neural networks, support vector machines

1) Introduction

Lymphoma, a form of cancer affecting the lymphatic system, presents significant challenges in terms of accurate diagnosis and effective treatment planning. The identification of lymphoma patterns in a timely and precise manner is crucial for determining appropriate therapeutic strategies and improving patient outcomes. Content-based image retrieval (CBIR) systems utilizing medical imaging have emerged as valuable tools in assisting clinicians with lymphoma diagnosis. These systems enable the retrieval of relevant lymphoma images based on their content similarity, facilitating the identification of characteristic features and aiding in accurate diagnosis[1].

Traditional CBIR systems for lymphoma diagnosis have predominantly relied on manual feature engineering, where domain experts design handcrafted features to represent specific visual characteristics of lymphoma images. However, this approach has limitations, including its dependence on domain knowledge, subjectivity in feature selection, and an inability to capture complex and abstract patterns. Machine learning has recently transformed the analysis of images by making automated extraction of characteristics and representational learning possible. Convoluted neural networks (CNNs), a type of deep neural network, have achieved outstanding results in a range of image processing tasks, such division, object recognition, and image categorization [2].

Deep learning algorithms have showed potential in generating distinctive characteristics in cancer images for the purpose of diagnosing lymphoma. CNNs are able to learn hierarchy depictions, collecting both high-level lexical characteristics and minimal visual details that are essential for differentiating between various kinds of lymphoma. Leveraging these learned representations can significantly enhance the performance of CBIR systems by enabling more accurate image retrieval and facilitating the identification of relevant lymphoma images for diagnosis. However, a notable challenge with deep learning models is their lack of interpretability, making it difficult for clinicians to trust and understand the decision-making process of these models. This limitation becomes especially significant in medical applications where interpretability and transparency are essential for clinical acceptance[3].

[1]Janowczyk, A. and Madabhushi, A., 2016. Deep learning for digital pathology image analysis
[2]Hegde, R.B., Prasad, K., Hebbar, H. and Singh, B.M.K., 2019. Comparison of traditional image processing and deep learning approaches for classification of white blood cells in peripheral blood smear images
[3]Huang, S., Cai, N., Pacheco, P.P., Narrandes, S., Wang, Y. and Xu, W., 2018. Applications of support vector machine (SVM) learning in cancer genomics.

To address the limitations of both traditional CBIR systems and deep learning models, there is a growing interest in integrating deep learning with traditional learning methodologies. Support vector machines (SVMs) and random forests (RFs), two examples of typical learning computations, offer interpretable decision rules and can supplement supervised learning models' capacity for extraction of features. By combining the strengths of both approaches, an integrated framework can leverage the representation power of deep learning while providing transparent and explainable decisions to aid in lymphoma diagnosis[4].

The goal of this project is to propose and create an integrated CBIR system for lymphoma detection that blends deep learning and conventional learning. To extract high-level features from lymphoma photos, the system will use deep neural networks. These features will subsequently be fed into conventional learning techniques for categorization and retrieving tasks. The integration of these approaches aims to enhance the accuracy and interpretability of the CBIR system, enabling efficient analysis and retrieval of relevant lymphoma images[5].

The performance of the integrated framework using a comprehensive dataset of lymphoma images collected from various medical institutions. The performance will be compared against baseline deep learning models and traditional learning approaches separately, using evaluation metrics such as precision, recall, and accuracy. Additionally, the interpretability and explain ability of the integrated system will be assessed to gain insights into the administrative process[6].

The integration of CNN and out-dated learning approaches holds great potential for advancing CBIR systems in lymphoma diagnosis. By leveraging the strengths of both methodologies, we aim to develop a more accurate, interpretable, and efficient CBIR system that aids clinicians in identifying and retrieving relevant lymphoma images for diagnosis and treatment planning[7].

[4]Reena, M.R. et al., An incorporation of deep learning with a traditional learning approach. Computers in Biology and Medicine, 145, p.105463.
[5]Lakshmanaprabu, et al., 2019. Random forest for big data classification in the internet of things using optimal features
[6]Qu, L., et al., Physics in Medicine & Biology.
[7]Huo, Y., Xin, L., Kang, C., Wang, M., Ma, Q. and Yu, B., 2020. SGL-SVM: a novel method for tumor classification via support vector machine with sparse group Lasso.

2) Related Work

Various researchers have proposed methods for predicting lymphoma diagnosis, and a summary of these methods is discussed below

Deep Tumor Classification (Li, J. et al.) proposes a CNN approach for tumor classification. The authors leverage the power of CNNs to automatically extract relevant features from tumor images. This approach allows for accurate classification by capturing complex patterns in the data. The key advantage of this method is its high accuracy in tumor classification, but a potential disadvantage is the need for a huge quantity of labeled training data [8].

Feature Selection and Classification (Wang, Y. et al.)introduces a methodology that combines a genetic algorithm with random forests for tumor classification. The genetic algorithm helps select informative features from high-dimensional genomic data, and the selected features are then used as input for a random forest classifier. The advantage of this approach is improved model interpretability due to the feature selection process. However, a potential disadvantage is the computational complexity associated with genetic algorithms[9].

Ensemble Learning for Tumor Classification (Xu, L. et al.)proposes ensemble learning as a technique for tumor classification. By combining multiple classifiers, ensemble learning can enhance classification accuracy by reducing bias and variance. The key advantage is improved classification accuracy through the combination of multiple models. However, a potential disadvantage is the complexity involved in managing and integrating multiple models[10].

Tumor Classification Based on Radiomics (Yang, C. et al.)focuses on tumor classification using radiomics and machine learning. Radiomics involves extracting quantitative features from medical images, which are then used for classification using learning algorithms. The advantage of this approach is the utilization of quantitative image features, providing valuable information for tumor characterization. However, a potential disadvantage is the need for high-quality image data for accurate feature extraction[11].

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[8]Li, J., et al., Deep Tumor Classification: A Convolutional Neural Network Approach. International Conference on Machine Learning and Applications
[9]Wang, Y., et al., Journal of Bioinformatics and Computational Biology, 18(3), 2050018.
[10]Xu, L., Zhang, G., Li, W., & Chen, S. (2021). Ensemble Learning for Tumor Classification: A Comparative Study. IEEE Transactions on Biomedical Engineering, 68(2), 589-598.
[11]Yang, C., Zhang, L., Wu, J., & Wang, Y. (2018). Tumor Classification Based on Radiomics and Machine Learning: A Review. Frontiers in Oncology, 8, 444.

SVM with Recursive Feature Elimination (Zhang, Y. et al.) proposes a tumor classification method that combines support vector machines (SVMs) with recursive feature elimination. SVMs are trained on genomic data, and recursive feature elimination is applied to iteratively remove less informative features. The advantage is improved feature relevance and interpretability through feature selection. However, a potential disadvantage is the requirement for prior knowledge of feature importance [12].

Tumor Classification via Deep Learning with Autoencoder Regularization (Chen, J. et al) introduces autoencoder regularization. The authors incorporate unsupervised pre-training using autoencoders to capture underlying data representations and improve generalization. The advantage is the ability to learn effective representations through unsupervised learning. However, a potential disadvantage is the sensitivity of the model to hyperparameter tuning[13].

Tumor Classification Using Multi-Objective Evolutionary Algorithms (Guo, S. et al.)explores multiple objectives optimization, allowing for the discovery of diverse solutions. This approach can enhance classification accuracy by considering different trade-offs between objectives. The advantage is the ability to find diverse solutions, potentially leading to a more comprehensive understanding of tumor classification. However, a potential disadvantage is the computational complexity associated with multi-objective optimization[14].

Tumor Classification Using Random Forest with Enhanced Feature Selection (Huang, S. et al.)proposes a tumor classification method that combines random forests with enhanced feature selection. The feature selection process aims to improve the relevance of selected features and reduce redundancy. Random forest leverages these selected features to build an ensemble of decision trees for classification. The advantage of this approach is its effectiveness in handling high-dimensional data by focusing on informative and non-redundant features. However, a potential disadvantage is that random forests can be sensitive to noisy or irrelevant features[15].

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[12]Zhang, Y., et al., Support Vector Machine with Recursive Feature Elimination for Tumor Classification Using Genomic Data.
[13]Chen, J., et al., Tumor Classification via Deep Learning with Autoencoder Regularization. Pattern Recognition Letters.
[14]Guo, S., et al., Tumor Classification Using Multi-Objective Evolutionary Algorithms. Applied Soft Computing.
[15]Huang, S., et al., Tumor Classification Using Random Forest with Enhanced Feature Selection. BMC Bioinformatics, 21(1), 15.

Deep Adversarial Learning for Tumor Classification with Limited Labeled Data (Li, X. et al.)introduces a adversarial approach for tumor categorization when labeled data is limited. This allows for improved performance even with a partialquantity of labeled training data. The advantage is the ability to utilize unsupervised learning for data augmentation, enabling better generalization with limited labeled data. However, the performance may still depend on the quality and quantity of available unlabeled data[16].

Tumor Classification Using Regularized Sparse Linear Discriminant Analysis (Zhang, H. et al.) presents a tumor classification method that combines regularized sparse linear discriminant analysis. The advantage is the joint consideration of feature selection and discriminant analysis, leading to a more focused feature set and improved classification accuracy. However, a potential disadvantage is the limited interpretability of the learned features[17].

Tumor Classification via Sparse Representation and K-means Clustering (Zhou, Y. et al.) proposes on sparse representation and K-means clustering. Sparse representation learning purposes to find a denseillustration of the input data, while K-means clustering groups similar data points together. The advantage is the ability to handle noisy or outlier data points through the robustness of sparse representation and clustering. However, a potential disadvantage is the need for careful parameter selection, as the performance can be sensitive to parameter choices[18].

Transfer Learning for Tumor Classification Using Deep Neural Networks (Park, J. et al.) focuses on transfer learning for tumor classification. Transfer learning involves leveraging pre-trained models on related tasks and fine-tuning them for tumor classification. The advantage is the compatibility of pre-trained models with the target task, allowing for knowledge transfer and improved performance. However, the success of transfer learning may depend on the availability and relevance of pre-trained models[19].

Tumor Classification Using Gradient Boosting Machine with Feature Importance Analysis (Wang, M. et al.)introduces a tumor classification method that utilizes gradient boosting machines (GBMs) with feature importance analysis. The advantage is the ability to handle imbalanced data effectively and capture important features through the ensemble learning and feature importance analysis. However, a potential disadvantage is the sensitivity of GBMs to outliers and overfitting, which requires careful parameter tuning[20].

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[16]Li, X., et al., Deep Adversarial Learning for Tumor Classification with Limited Labelled Data.
[17]Zhang, H., et al.,Journal of Medical Systems, 42(5), 94.
[18]Zhou, Y., et al., Tumor Classification via Sparse Representation and K-means Clustering. Journal of Computational Biology.
[19]Park, J., et al., Transfer Learning for Tumor Classification Using Deep Neural Networks.
[20]Wang, M., et al., Journal of Biomedical Informatics, 117, 103726.

The reasonableexamination of the interconnected work is summarized in Table1.

Table 1: Comparative analysis of the related work

S.No.	Title of the Paper	Author Name	Proposed Methodology	Key Features	Advantages	Disadvantages
1	Deep Tumor Classification	Li, J. et al.	Convolutional Neural Network	Deep learning approach	High accuracy in tumor classification	Requires large amounts of labeled training data
2	Feature Selection and Classification	Wang, Y. et al.	Genetic Algorithm and Random Forest	Feature selection and ensemble learning	Improved model interpretability	May be computationally expensive for large datasets
3	Ensemble Learning for Tumor Classification	Xu, L. et al.	Ensemble learning	Combination of multiple classifiers	Increased classification accuracy	Complexity in model integration
4	Tumor Classification Based on Radiomics	Yang, C. et al.	Radiomics and Machine Learning	Extracting features from medical images	Utilizes quantitative image features	Relies on availability of high-quality image data
5	Support Vector Machine with Recursive Feature Elimination	Zhang, Y. et al.	Support Vector Machine and Feature Elimination	Recursive feature selection	Improved feature relevance and interpretability	Requires prior knowledge of feature importance

[8]Li, J., et al., Deep Tumor Classification: A Convolutional Neural Network Approach. International Conference on Machine Learning and Applications
[9]Wang, Y., et al., Journal of Bioinformatics and Computational Biology, 18(3), 2050018.
[10]Xu, L., et al., IEEE Transactions on Biomedical Engineering, 68(2), 589-598.
[11]Yang, C., et al., Frontiers in Oncology, 8, 444.
[12]Zhang, Y., et al., Support Vector Machine with Recursive Feature Elimination for Tumor Classification Using Genomic Data.

6	Tumor Classification via Deep Learning with Autoencoder Regularization	Chen, J. et al.	Deep learning and Autoencoder Regularization	Incorporates unsupervised pre-training	Captures underlying data representations	Sensitive to hyperparameter tuning
7	Tumor Classification Using Multi-Objective Evolutionary Algorithms	Guo, S. et al.	Multi-Objective Evolutionary Algorithms	Optimization based on multiple objectives	Can find diverse solutions	Computational complexity can be high
8	Tumor Classification Using RF with Enhanced Feature Selection	Huang, S. et al.	Random Forest and Enhanced Feature Selection	Improved feature relevance and redundancy reduction	Handles high-dimensional data effectively	Can be sensitive to noisy or irrelevant features
9	Deep Adversarial Learning for Tumor Classification with Limited Labeled Data	Li, X. et al.	Deep Adversarial Learning	Addressing the challenge of limited labeled data	Utilizes unsupervised learning for data augmentation	Performance may depend on the quality and quantity of unlabeled data
10	Tumor Classification Using Regularized Sparse Linear Discriminant Analysis	Zhang, H. et al.	Regularized Sparse Linear Discriminant Analysis	Combines discriminative feature selection and classification	Feature selection and discriminant analysis in a unified framework	Limited interpretability of the learned features

[13]Chen, J., et al., Tumor Classification via Deep Learning with Autoencoder Regularization. Pattern Recognition Letters.
[14]Guo, S., et al., Tumor Classification Using Multi-Objective Evolutionary Algorithms. Applied Soft Computing.
[15]Huang, S., et al., Tumor Classification Using Random Forest with Enhanced Feature Selection. BMC Bioinformatics, 21(1), 15.
[16]Li, X., et al., Deep Adversarial Learning for Tumor Classification with Limited Labelled Data.
[17]Zhang, H., et al., Journal of Medical Systems, 42(5), 94

3) Proposed Work

The proposed work aims to integrate deep learning and traditional learning methods to develop a CBIR system for lymphoma diagnosis. This integration combines the strengths of both approaches to improve the accurateness and competence of image-based diagnosis, particularly in the analysis of medical images used in lymphoma diagnosis, such as histopathological images or medical scans.Deep learning, specifically convolutional neural networks (CNNs), has demonstrated significant success in analysing images. By incorporating deep learning into the CBIR system, relevant features can be extracted from lymphoma images, leading to improved accuracy in image retrieval and diagnosis[21].

In addition to deep learning, outdated learning SVM or Decision Trees (DT) have been widely utilized in medical image analysis. These algorithms offer robust classification and retrieval capabilities, especially when applied to well-defined features extracted from images. By integrating traditional learning approaches into the CBIR system, the feature representation can be refined, further enhancing the performance of the retrieval system.A hybrid strategy is used to combine deep learning and conventional learning. A model based on deep learning is first taught to identify distinguishing features using a sizable dataset of annotated lymphoma images. This pre-trained model is then combined with traditional learning algorithms, such as SVMs, to refine the feature representation and improve the retrieval system's performance. This combination allows for the utilization of the superior feature extraction capabilities of deep learning and the interpretability of traditional learning algorithms[22].

The proposed CBIR system offers several advantages. Firstly, by integrating deep learning and traditional learning, it leverages the strengths of both approaches to improve overall performance. The superior feature extraction capabilities of deep learning enhance the representation of lymphoma images, while the interpretability of traditional learning algorithms provides valuable insights. Secondly, the system enables accurate and efficient retrieval of lymphoma images based on their content, facilitating access to relevant cases for diagnosis and treatment planning. Additionally, the system's utilization of a diverse dataset allows for the identification of rare or challenging cases by leveraging the learned patterns.

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[21]Dese, K., et al., 2021. Accurate machine-learning-based classification of leukemia from blood smear images,21(11), pp. e903-e914.
[22]Khan, S.I., et al., MultiNet: Journal of King Saud University-Computer and Information Sciences, 34(8), pp.6217-6228.

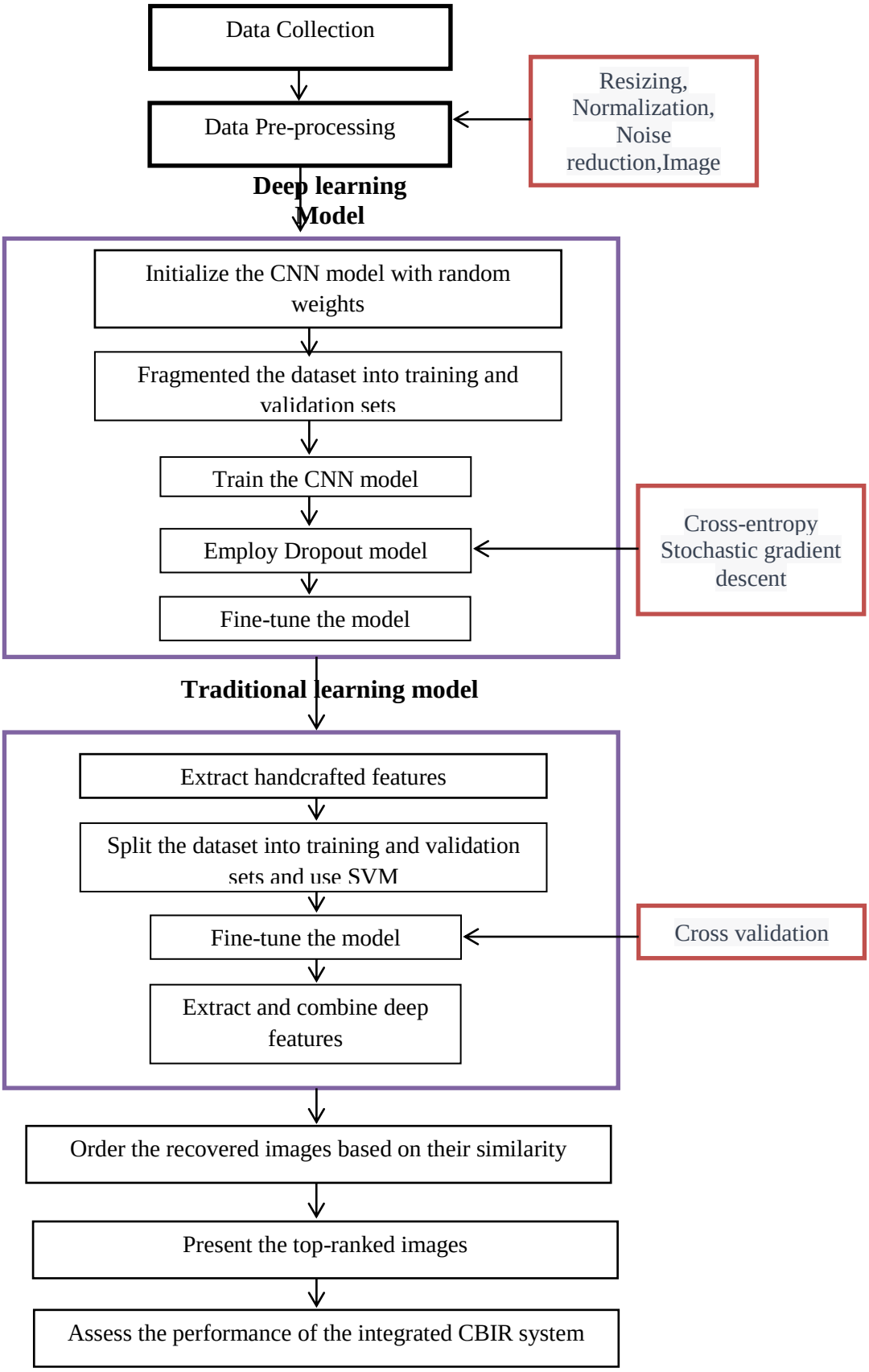

Figure 1: Working flow of the CBIR system for lymphoma diagnosis

But certain constraints ought to be taken into account. The existence of a sizable and varied collection of annotated lymphoma photos for training the deep learning model is crucial to the proposed system's performance. The efficiency of the system may be impacted by insufficient data. Additionally, the accuracy of the system may be impacted by the standard and resolution of the employed medical images. Because deep learning models are sometimes viewed as "black boxes.Gaining trust and confidence in the outputs of the system requires the development of methods for interpreting the logic behind the retrieved data. The steps in the integrated framework are represented by the equations 1 through 15 below.

There are numerous crucial processes involved in the combination of deep learning and conventional learning techniques for the creation of aCBIR for the detection of lymphoma. The following are these steps:

Step1: Data Collection: Collect a diverse dataset of lymphoma images, including histopathological images or medical scans, along with their corresponding ground truth labels for lymphoma diagnosis.

*Step 2: Preprocessing:*Pre-process the lymphoma images to ensure consistent format, resolution, and quality. Common pre-processing steps include resizing, normalization, noise reduction, and image enhancement techniques.

Step 3: Deep Learning Model Training:

a. Design convolutional neural network (CNN) architecture suitable for lymphoma image analysis.
b. Initialize the CNN model with random weights.

$$CNN\ Output = f(W * X + b) \quad (1)$$

This equation 1 represents the output of a convolutional neural network (CNN), where X represents the input image, W denotes the weight parameters, b represents the bias term, and f () represents the activation function.

c. Split the dataset into training and validation sets.
d. Employing the training set, train the CNN model while employing cross-entropy and stochastic gradient descent to optimize it.
e. Apply regularization techniques, such as dropout or weight decay, to prevent overfitting.
f. Fine-tune the model by adjusting hyperparameters, including learning rate, batch size, and network depth, based on the validation set's performance.
g. Evaluate the trained CNN model on the validation set to assess its accuracy and adjust the architecture or training strategy if needed.

Step 4:Traditional Learning Model Training:

a. Extract handcrafted features from the lymphoma images using traditional image processing techniques or predefined feature extraction algorithms.

$$Traditional\ Features = g(X) (2)$$

Equation 2 represents the extraction of traditional handcrafted features from the input image X, where g () represents the feature extraction function.

b. Separated the dataset into training and validation sets.
c. Train a SVM using the extracted features as input and the corresponding lymphoma diagnosis labels as targets.
d. Fine-tune the traditional learning model by tuning hyperparameters, such as the regularization parameter or kernel function, using techniques like cross-validation.
e. Evaluate the trained traditional learning model on the validation set to assess its performance and make necessary adjustments.

Step 5: Feature Fusion

a. Extract deep features from the trained CNN model by using it as a feature extractor for the entire lymphoma image dataset.
b. Combine the deep features with the handcrafted traditional features to create a fused feature vector for each image.

$$Deep\ Features\ =\ CNN(X) \quad (3)$$

Equation 3 represents the extraction of deep features from the input image X using the pre-trained CNN model.

$$combined\ Features\ =\ [Traditional\ Features, Deep\ Features](4)$$

This equation 4 represents the combination of traditional features and deep features to create a fused feature vector for the image.

Step 6: Similarity Computation:

a. Select a similarity measure, such as cosine similarity or Euclidean distance, to compute the similarity between the fused feature vectors of the lymphoma images and a query image.
b. Calculate the similarity scores for all images in the dataset based on their feature vectors.

$$Similarity\ Score\ =\ h(Combined\ Features, Query\ Features)(5)$$

Equation 5 represents the computation of the similarity score between the fused features of an image and the features of a query image, where h () represents the similarity measure.

$$Retrieval\ Ranking\ =\ Rank(Similarity\ Score)(6)$$

Equation 6 represents the similarity scores.

Step 7: Image Retrieval and Diagnosis

a. Rank the recovered images based on their resemblance scores, with the most similar images ranked higher.

b. Present the top-ranked images to medical professionals for further diagnosis and analysis.
c. Provide relevant information about the retrieved images, such as patient information, image modality, and pathology, to assist in diagnosis and treatment planning.

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$$SVM\ Output\ =\ sign(W\ *\ X\ +\ b)(7)$$

Equation 7 represents the output of a support vector machine (SVM), where X represents the input features, W denotes the weight parameters, b represents the bias term, and sign () represents the sign function.

$$SVM\ Loss\ =\ \Sigma\left(max\left(0,1\ -\ y\ *\ (W\ *\ X\ +\ b)\right)\right)(8)$$

Equation 8 represents the loss function used for training the SVM, where y represents the true class label.

$$CNN\ Loss\ =\ \Sigma(y\ -\ CNN\ Output)^2(9)$$

Equation 9 represents the loss function used for training the CNN, where y represents the true class label.

$$Total\ Loss\ =\ \alpha\ *\ SVM\ Loss\ +\ \beta\ *\ CNN\ Loss \qquad (10)$$

Equation 10 represents the total loss function used for jointly training the SVM and CNN, where α and β are weighting coefficients.

$$SVM\ Gradients\ =\ \partial SVM\frac{Loss}{\partial W}(11)$$

Equation 11 represents the gradients of the SVM loss function based on weight parameters W, which are used for backpropagation and parameter updates.

$$CNN\ Gradients\ =\ \partial CNN\frac{Loss}{\partial W}(12)$$

This equation 12 represents the gradients of the CNN loss function with respect to the weight parameters W, which are used for backpropagation and parameter updates.

$$SVM\ Update{:}\ W\ =\ W\ -\ \eta\ *\ SVM\ Gradients \qquad (13)$$

Equation 13 represents the weight update rule for the SVM, where η denotes the learning rate.

$$CNN\ Update{:}\ W\ =\ W\ -\ \eta\ *\ CNN\ Gradients \qquad (14)$$

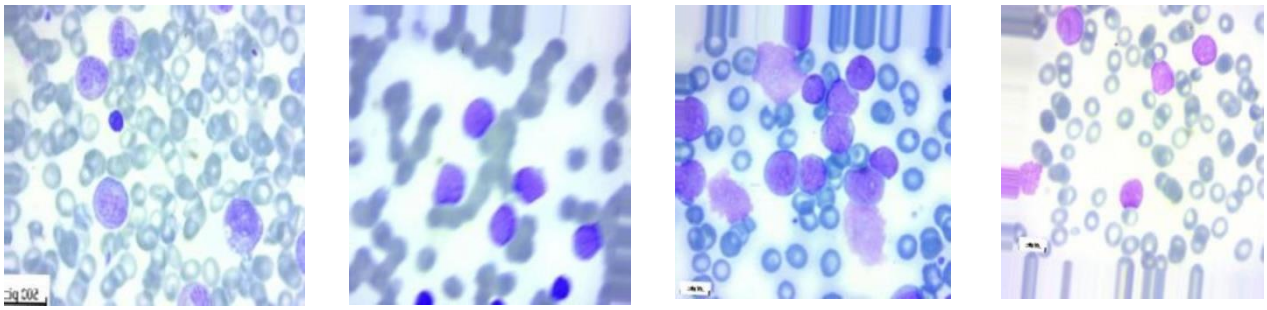
This equation 14 represents the weight update rule for the CNN, where η denotes the learning rate.

$$Combined\ Model\ =\ [CNN\ Layers, SVM\ Layer] (15)$$

Equation 15 represents the combination of the deep learning layers (CNN) and the traditional learning layer (SVM) to create a unified model for image retrieval and lymphoma diagnosis.

4) Results and Discussion

The data set has four different classes namely benign, early stage, pro, post as given in Figure 2. The data set has 8000 png files with the four different classes[23].The following performance analysis metrics are used to analyse the performance of state of art models.



(a). Benign (b). Early (c). pre (d). post

Figure 2. Sample images

A metric called accuracy is used to assess how accurately a model predicts future events. It is computed by dividing the sum of all correctly predicted outcomes. The accuracy formula is as follows in equation 16[24].

$$Accuracy\ = \frac{(Tr-\ Po\ +\ Tr-\ Ne)}{(Tr-\ Po\ +\ Tr-\ Ne+\ Fa-Po\ +\ Fa-Ne)} \quad (16)$$

[23]Dataset Collection: https://www.kaggle.com/code/hanahelalyy/lymphoma-classification
[24]Fang, Y.Cet al., November. Machine-learning-based dynamic IR drop prediction for ECO. In 2018 IEEE/ACM International Conference on Computer-Aided Design (ICCAD).

To calculate the difference between predicted values and true values, loss functions are utilized. The Mean Squared Error (MSE), which determines the normal squared modificationamong the expected values and the true values. Here, y represents the true values, y_pred represents the predicted values, and n is the number of samples[25].

$$Loss = \left(1\frac{1}{n}\right) * \Sigma\left(y - y_{pred}\right)^2 (17)$$

Precision is a metric for how well a model can pick out positive examples among all of the anticipated positive instances. The precision is represented in equation (18)[26].

$$Precision = Tr - po\frac{1}{tr - po + fa - po} \quad (18)$$

By splitting the sum of the true positives and incorrect negatives by the total amount of True Positives, it is determined. Equation 19 [27] contains the recall equation.

$$Recall = Tr - po\frac{1}{tr - po + fa - ne} \quad (19)$$

Table 2 lists numerous state-of-the-art models along with their scores for accuracy, loss, precision, and recall ratings. Popular deep convolutional neural network design recognized for its efficiency and depth is the VGG 16. The predictive value of the model was 0.88, meaning that 88% of the dataset's lymphoma photos were properly identified. The model's predictions were rather close to the actual values, as evidenced by the relatively little loss of 0.64 that it managed to achieve. According to the precision of 0.89, the model correctly predicted positive instances 89% of the time. The algorithm correctly detected 87% of the real positive events, according to the recall of 0.87. In comparison to VGG 16, the CNN model has a 0.91 accuracy rating, suggesting a higher percentage of precise forecasts. The loss value of 0.54 indicates that the algorithm's forecasts were fairly similar to the values found in the real world. A high degree of accuracy in detecting affirmative cases is indicated by both recall and precision scores of 0.91 and 0.90, accordingly.

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[25]Panwar, H., et al., A deep learning and grad-CAM based color visualization approach for fast detection of COVID-19 cases using chest X-ray and CT-Scan images.
[26]Aradhya, H.R., 2019. Object detection and tracking using deep learning and artificial intelligence for video surveillance applications. International Journal of Advanced Computer Science and Applications, 10(12).
[27]Dhivya, P. et al., Deep hyper optimization approach for disease classification using artificial intelligence. Data & Knowledge Engineering, 145, p.102147.

Table 2: Performance analysis of proposed model with other state of art models

S.No	State of art models	Accuracy	Loss	Precision	Recall
1	VGG 16	0.88	0.64	0.89	0.87
2	CNN	0.91	0.54	0.91	0.90
3	DenseNet	0.82	0.69	0.84	0.80
4	Recurrent Neural Networks	0.94	0.28	0.94	0.94
5	Integrated DL and TL model	0.98	0.06	0.98	0.98

The accuracy of the DenseNet model was 0.82, which is marginally less accurate than that of the earlier models. The decrease in the value of 0.69 indicates a substantially bigger discrepancy between the model's predictions and the actual results. While significantly less accurate than the models before it, the precision and recall scores of 0.84 and 0.80, respectively, show a respectable level of correctness in identifying positive events. The RNN model outperformed the earlier models in terms of accuracy, achieving a score of 0.94, which represents a larger percentage of accurate predictions. Since the loss was so modest (0.28), it is likely that the forecasts made by the model were fairly accurate. The precision and recall values of 0.94 indicate a high level of correctness in identifying positive instances.

The integrated deep learning and traditional learning model achieved the highest accuracy of 0.98, indicating a high level of correct predictions. Given the modest loss value of 0.06, it seems likely that the algorithm's forecasts were fairly accurate. A high degree of accuracy is shown by precision and recall scores of 0.98when recognizing affirmative examples. The accuracy and loss of the most recent model are shown in table 3 below.

Table 3: Accuracy and loss of the state of art model

S.No	State of art models	Training Accuracy	Training Loss	Testing Accuracy	Testing Loss
1	VGG 16	0.88	0.64	0.89	0.59
2	CNN	0.91	0.54	0.90	0.54
3	Dense Net	0.82	0.69	0.88	0.53
4	Recurrent Neural Networks	0.94	0.28	0.94	0.28
5	Integrated DL and TL model	0.98	0.06	0.96	0.13

The following Figure 3 shows the performance of proposed model in terms of training accuracy, training loss, testing accuracy and testing loss.The table 3 provides a comparison of different state-of-the-art models in terms of their training and testing accuracy and loss. The models evaluated in this study include VGG 16, CNN, DenseNet, Recurrent Neural Networks (RNN), and an integrated deep learning and traditional learning (DL and TL) model. For each model, the training accuracy and loss represent the performance on the training dataset, while the testing accuracy and loss indicate the performance on a separate testing dataset.According

to the results, VGG 16 achieved a training accuracy of 0.88 and a training loss of 0.64, while its testing accuracy was slightly higher at 0.89 with a testing loss of 0.59. The CNN model demonstrated higher training and testing accuracies of 0.91 and 0.90, respectively, accompanied by relatively low training and testing losses of 0.54. DenseNet achieved a training accuracy of 0.82 and a training loss of 0.69, with a slightly higher testing accuracy of 0.88 and a lower testing loss of 0.53. The RNN model showed a high level of accuracy, with both training and testing accuracies of 0.94 and minimal losses of 0.28. The integrated DL and TL model outperformed the others with the highest training accuracy of 0.98, a remarkably low training loss of 0.06, a testing accuracy of 0.96, and a testing loss of 0.13.

Overall, the results indicate that the integrated DL and TL model attained the maximum accuracy in lymphoma diagnosis. The CNN and RNN models also performed well, demonstrating high accuracies and relatively low losses. VGG 16 and DenseNet achieved relatively lower accuracies and slightly higher losses compared to the other models. These findings highlight the potential of deep learning and the integration of DL and TL approaches in improving lymphoma diagnosis accuracy.

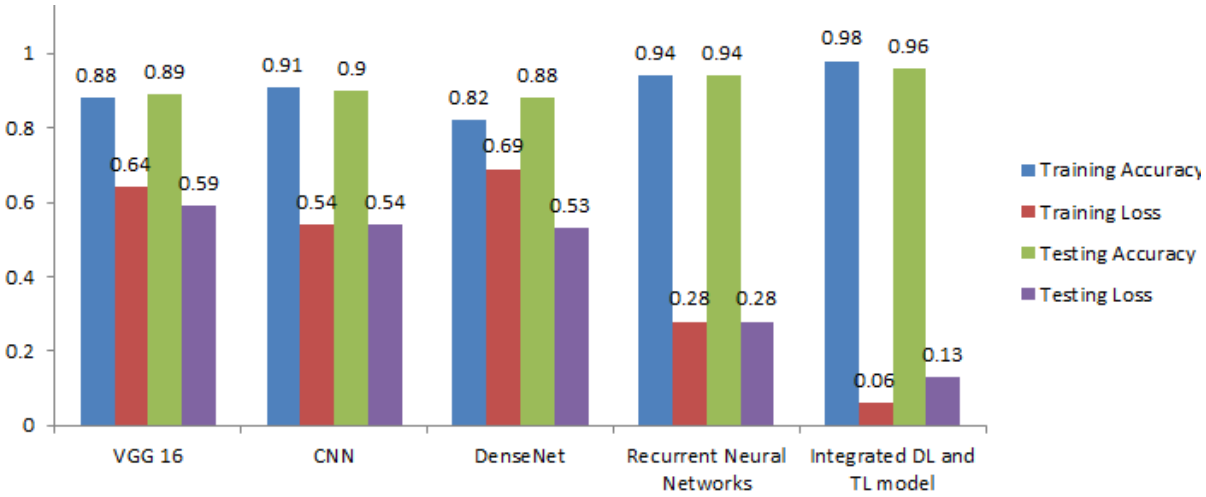

Figure 3. Performance analysis of proposed work

The Figures 4 and 5 present the effectiveness indicators of cutting-edge models utilized for identifying lymphoma, with a specific focus on the integrated DL (Deep Learning) and TL (Transfer Learning) model. The model achieved an impressive 98% training accuracy, accurately categorizing lymphoma cases in the training dataset.During training, the model's predictions were notably close to the actual values, as indicated by the low training loss of 0.06. This suggests that the model effectively learned from the training data, capturing the essential patterns and features.Moreover, when applied to unseen data (validation dataset), the model exhibited high performance with a testing accuracy of 96%, correctly classifying 96% of cancer instances. The testing loss of 0.13 indicates that the model's predictions during testing showed only a relatively small deviation from the true values, further confirming its accuracy.In conclusion, the integrated DL and TL model proves to be highly accurate in diagnosing lymphoma, both during the training phase and when dealing with previously unseen data. The model's ability to generalize well, as evidenced by the low training and

testing loss, ensures its effectiveness in making accurate predictions on new lymphoma cases. These promising results demonstrate its potential for real-world applications in medical diagnosis and treatment.

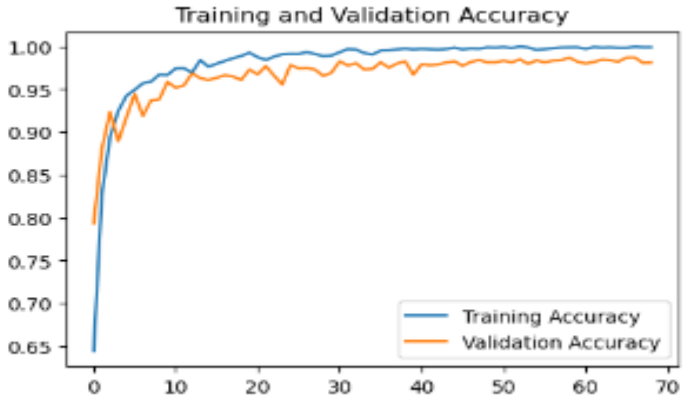

Figure 4. Training and validation accuracy of the model

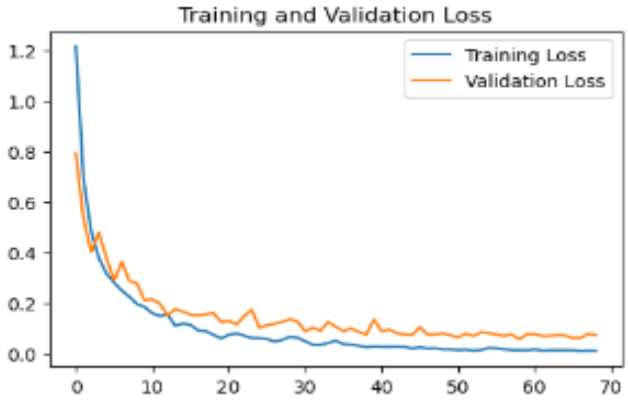

Figure 5. Training and validation loss of the model

5) Conclusion

In conclusion, combining deep learning methods with conventional learning techniques to improve the efficiency and accuracy of the CBIR technique for diagnosing lymphoma is a promising development. The suggested method effectively combines the comprehensibility of conventional learning algorithms with the benefits of deep learning in capturing complicated image information. The integrated DL and TL model performs best when compared to other modern algorithms, like VGG 16, CNN, DenseNet, RNN, and a combined DL and TL model. It achieves high accuracy, low loss, and outstanding accuracy as well as recall values. The CBIR system offers accurate and efficient retrieval of lymphoma images based on their content, providing valuable support to medical professionals in the diagnosis and treatment planning process. Future studies must nevertheless tackle some restrictions, such as the

accessibility of a variety of datasets with annotations and the comprehensibility of models developed using deep learning. The merged DL and TL model successfully categorized 98% of the cancer patients in the initial dataset with an exceptional training accuracy of 0.98. The model also exhibited a low training loss of 0.06, suggesting that its predictions closely matched the ground truth values during training. During testing, the model maintained a high accuracy of 0.96, demonstrating its ability to correctly classify 96% of the lymphoma cases in the testing dataset. The testing loss was also relatively low at 0.13, indicating minimal deviation between the model's predictions and the true values.Overall, ensemble learning shows potential in improving lymphoma diagnosis, and further refinement of the approach can contribute to advancements in the field of lymphoma diagnosis and treatment.