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Name of paper
Blood Cells Cancer Detection Based on Deep Learning
Diagnosis of Blood Cells Using Deep Learning
Deep Learning for Classifying of White Blood Cancer

Detecting Malignant Leukemia Cells Using Microscopic Blood Smear Images: A Deep Learning Approach

BCNet: A Deep Learning Computer-Aided Diagnosis Framework for Human Peripheral Blood Cell Identification

A deep learning model (ALNet) for the diagnosis of acute leukaemia lineage using peripheral blood cell images

Machine Learning based System for Automatic Detection of Leukemia Cancer Cell

Towards Efficient Segmentation and Classification of White Blood Cell Cancer Using Deep Learning

Customized Deep Learning Classifier for Detection of Acute Lymphoblastic Leukemia Using Blood Smear Images

Integrated Hybrid Deep Learning Approach for Precise Blood Cancer Detection

Acute Lymphoblastic Leukemia Blood Cells Prediction Using Deep Learning & Transfer Learning Technique

Multiclass blood cancer classification using deep CNN with optimized features

Automated detection of white blood cells cancer diseases

Deep learning approach for segmentation and classification of blood cells using enhanced CNN

Detecting Acute Lymphoblastic Leukemia Through Microscopic Blood Images Using CNN

DVS: Blood cancer detection using novel CNN-based ensemble approach

Methods and results

Leukemia is blood and bone marrow cancer. It causes an abnormal increase of white blood cells, weakening the immune system. White blood cells are essential for protecting the body from infections and illnesses. This research used MobileNetV2 to identify and categorize acute lymphocytic leukemias, a kind of blood cancer. This work aims to enhance the accuracy of a machine learning model for identifying Acute Lymphoblastic Leukemia. Initial model accuracy was 98.15% with 7.08% decrease. For improved capabilities, ReLU activation, Batch Normalization, and a Dropout Layer (rate: 0.3) were implemented.

The modified model improved to 99.69% accuracy with lower loss.

Journal of Advances in AI 118, Volume 2, Issue 1, 2024, 1.61%. The revised model improves accuracy and reduces loss, leading to more accurate diagnostic methods in medical picture analysis. This innovation is critical for early identification of Acute Lymphoblastic Leukemia. A fast and correct diagnosis is crucial for successful treatment results. Adding ReLU activation, Batch Normalization, and a Dropout Layer with a rate of 0.3 has improved the model and created a solid foundation for future hematologic cancer detection research. The research utilizes MobileNetV2 to demonstrate the flexibility of modern architectures in tackling complicated medical issues. The versatility and effectiveness of improved approaches suggest possibilities for expanded medical image analysis applications. As technology advances, combining machine learning models with medical diagnostics might improve patient outcomes and streamline healthcare operations.

AI, sometimes known as machine intelligence, is artificial intelligence in computer science, unlike natural intelligence in humans and other animals. Computer science describes AI research as the study of "intelligent agents"—devices that comprehend their surroundings and behave to optimize their chances of success. Deep Learning research is new. One field of AI science develops ideas and methods to teach machines by imitating human neurons. The majority of learning research seeks high-level approaches. Strippers use linear and nonlinear transformations to evaluate big data sets. Deep learning is used to detect and classify diseases, including blood cell diseases, using radiography to help decision makers identify the type of blood cell and its associated diseases. The results will be presented and discussed. This thesis detects and classifies blood cell disorders using Python and deep learning. The suggested deep learning model was trained, validated, and tested. Proposed model was 98.00% accurate.

Recent interest has focused on computer aided cell categorization. Early, low-cost illness diagnosis is essential. ISBI conducted the classification of normal versus malignant cells (C-NMC) challenge 2019 to identify efficient, accurate computer assistance techniques for categorizing B-ALL white blood cancer microscopic pictures. Our team used numerous cutting-edge CNN architectures and stacking to improve prediction performance, placing eighth in the preliminary phase and tenth in the final phase. The preliminary and final phase weighted F1 scores on our model were 0.8674 and 0.8552, respectively. This is a fair outcome for an expert-required assignment.

Too many white blood cells in the bone marrow cause leukemia. Adults and children are prone to this malignancy. Treatment for leukemia depends on its nature and spread. Leukemia must be diagnosed early to give proper treatment and cure patients. Research is underway to develop early leukemia diagnosis methods using Machine Learning (ML). We use deep learning (DL)-based convolutional neural network (CNN) and hybridized CNN-1 and CNN-2 blocks to identify ALL, AML, and MM. Blood smear pictures are used to identify malignant leukemia cells in the suggested paradigm. About 4150 public directory photos are collected. Background removal, removing non-essential blood components, reducing noise and blurriness, and limited picture segmentation were the primary hurdles. To pre-process and segment pictures, we convert RGB color-space to greyscale 8-bit mode and use image intensity adjustment and adaptive histogram equalisation (AHE) to boost contrast. Multiplying binary pictures with improved photos improves image structure and sharpness. Next, complement is done to obtain a black backdrop and a white blood nucleus. We removed background noise with area and closure operations. Finally, we multiply the final output by the original picture to recreate the dataset in RGB color space and scale it to [400, 400]. After trying everything, we got noiseless, non-blurred, sharpened, and segmented lesion photos. CNNs get better segmented pictures next. Train two parallel CCN models to extract deep features. The collected traits are fused using Canonical Correlation Analysis (CCA) to add prominence. We tested feature extraction strategies using SVM, Bagging ensemble, total boosts, RUSBoost, and fine KNN classification algorithms. With 97.04% accuracy, Bagging ensemble was the best classification method.

Blood cells contain vital health information. Daily infection risks may be reduced by quickly and accurately identifying blood cell types. BCNet is an AI-based deep learning (DL) framework that uses transfer learning with a convolutional neural network to rapidly and automatically identify blood cells in eight classes: Basophil, Eosinophil, Erythroblast, Immature Granulocytes, Lymphocyte, Monocyte, Neutrophil, and Platelet. To prove BCNet's reliability and viability, thorough five-fold cross-validation tests are run. We extensively tested the BCNet architecture with three optimizers: ADAM, RMSprop (RMSP), and stochastic gradient descent using transfer learning. With the same dataset, the proposed BCNet is compared against the best deep learning models as DensNet, ResNet, Inception, and MobileNet. With ADAM and RMSP optimizers, BCNet performed better in classification. The RMSP optimizer has the highest accuracy (98.51%) and F1-score (96.24%). Using ADAM, RMSP, and SGD optimizers, the BCNet increased prediction accuracy by 1.94%, 3.33%, and 1.65% over the baseline model. The BCNet model tested a single blood cell picture faster than DenseNet, ResNet, Inception, and MobileNet by 10.98, 4.26, 2.03, and 0.21 msec. Comparing BCNet to contemporary deep learning models may provide promising results. Healthcare institutions need such a recognition rate to improve blood cell detection.

Morphological distinction of acute leukemia blood blasts is difficult. Clinical use of AI decision support systems to identify haematological malignancy seems promising. A deep learning-based system to diagnose acute leukemia using blood cell pictures is the goal of this project. We examined 16,450 single-cell pictures from 731 blood smears from 100 healthy controls, 191 viral infection patients, and 148 acute leukemia patients. Training and testing sets have 85% and 15% of these stains. VGG16, ResNet101, DenseNet121, and SENet154 were tested for acute leukemia classification architecture. To fit our data, pre-trained CNN layers were fine-tuned. An ALNet system with two modules functioning consecutively was configured after choosing the optimal design. In the first module, aberrant promyelocytes were identified among lymphocytes, monocytes, reactive lymphocytes, and blasts. The second determined myeloid or lymphoid blasts. The last technique was blood smear screening to forecast acute leukemia lineage diagnosis. ALNet was tested using testing set smears. All promyelocytic and myeloid leukemia patients were diagnosed correctly by ALNet. Myeloid leukemia had 100% sensitivity, 92.3% specificity, and 93.7% accuracy. Lymphoid leukemia had 89% sensitivity, 100% specificity, and 100% accuracy.

Recent years have seen various researchers use image processing to classify blood cells and construct an automated cancer diagnostic system. Cancer cells seem identical to normal cells in the beginning, making differentiation difficult. In this work, we extracted essential characteristics from blood cell pictures and learned various classifiers to identify cancer cells. Gradient Boosting Decision Tree outperforms Support Vector Machine in classification. We also found critical traits like neighboring nuclei and nucleus irregularity, which affect cancer cell identification. Our methods work without a GPU in a restricted computational environment. We scored 85.6% F1 on validation data. This technique found an essential picture attribute that may assist physicians or technicians better comprehend stained photos to diagnose leukemia patients.

White Blood cell cancer is a plasma cell cancer that starts in the bone marrow and leads to the formation of abnormal plasma cells. Medical examiners must be exceedingly selective when diagnosing myeloma cells. Moreover, because the final judgment is dependent on human perception and judgment, there is a chance that the conclusion may be incorrect. This study is noteworthy because it creates a software-assisted way for recognizing and identifying myeloma cells in bone marrow scans. MASK-Recurrent Convolutional Neural Network has been utilized for recognition, while Efficient Net B3 has been used for detection. The mean Average Precision (mAP) of MASK-RCNN is 93%, whereas Efficient Net B3 is 95% accurate. According to the findings of this study, the Mask-RCNN model can identify multiple myeloma, and Efficient Net B3 can distinguish between myeloma and non-myeloma cells.

Acute lymphoblastic leukemia (ALL) is a rare blood malignancy characterized by bone marrow lymphocyte overproduction. It is a frequent childhood cancer that may be healed. This may happen in adults, but a late diagnosis reduces the odds of a cure. This work proposes an intelligent white blood cell screening strategy to identify this dangerous illness early. The recommended clever deep learning system employs blood smear photos as input. This technique uses a CNN to predict leukemic cells from healthy blood cells. The proprietary ALLNET model was trained and evaluated using open-source microscopic pictures. Model training was done on Google Collaboratory using Nvidia Tesla P-100 GPUs. This accurate classifier has 95.54% accuracy, 95.81% specificity, 95.91% sensitivity, 95.43% F1-score, and 96% precision. CBC and peripheral blood tests may identify leukemia cells during pre-screening using the suggested method.

Using deep learning, we offer a unique approach for early detection and classification of blood cancer, often known as leukemia. Our study employs the Python-implemented MobileNetV2 architecture to diagnose Acute Lymphoblastic Leukemia (ALL) using peripheral blood smear (PBS) pictures with amazing accuracy. The collection of 3242 PBS pictures of benign, early Pre-B, Pre-B, and Pro-B cells is crucial for cancer screening. Early cancer detection requires accurate diagnosis. Our MobileNetV2-based deep learning model performs well with 98.00% training accuracy. Validation accuracy of 96.00% shows its robustness in distinguishing blood cancer cell types. By improving early detection and categorization, this breakthrough seeks to enhance patient outcomes. MobileNetV2 and Python enable efficiency and make our solution accessible to healthcare professionals, improving cancer screening and detection.

White blood cells called lymphocytes are the target of the blood malignancy known as acute lymphoblastic leukemia (ALL). In the domain of medical image analysis, deep learning and transfer learning methods have recently showcased significant promise, particularly in tasks such as identifying and categorizing various types of cancer. Using microscopic pictures, we suggest a deep learning and transfer learning-based method in this research work for predicting ALL blood cells. We use a pre-trained convolutional neural network (CNN) model to extract pertinent features from the microscopic images of blood cells during the feature extraction step. To accurately categorize the blood cells into leukemia and non-leukemia classes, a classification model is built using a transfer learning technique employing the collected features. We use a publicly accessible collection of microscopic blood cell pictures, which contains samples from both leukemia and non-leukemia, to assess the suggested method. Our experimental findings show that the suggested method successfully predicts ALL blood cells with high accuracy. The method enhances early ALL detection and diagnosis, which may result in better patient treatment outcomes. Future research will concentrate on larger and more varied datasets and investigate the viability of integrating it into clinical processes for real-time ALL prediction.

Cancer covers breast, lung, skin, and blood cancers such leukemia and lymphoma. Acute lymphoblastic leukemia is dangerous. Blood cancer diagnosis takes time, and hematologists make errors. Thus, this work presents a Machine Learning and Deep Learning leukemia classification method. The suggested research methodology encompasses dataset creation, feature extraction from blood cell images using pre-trained CNN architectures, and classification using conventional classifiers. This study's dataset is divided into two identical categories, Benign and Malignant, and then into four significant classes with three malignant subtypes: Benign, Early Pre-B, Pre-B, and Pro-B. CNN models extract visual features, which are then transferred to PCA, LDA, SVC Feature Selectors, and two nature-inspired algorithms, PSO and CSO. Seven Machine Learning classifiers were then employed to categorize multi-class cancers. Experimental data have been analyzed to assess the proposed design. The study used pre-trained CNN and classifiers to reach 98.43% accuracy. The recommended model with PSO and CSO has the highest accuracy of 99.84% using ResNet50 CNN architecture, SVC feature selector, and LR classifiers. Despite its accuracy, the model has drawbacks. Methodology may help categorize blood cancer in real life.

Automated diagnosis of white blood cells cancer diseases such as Leukemia and Myeloma is a challenging biomedical research topic. Our approach presents for the first time a new state of the art application that assists in diagnosing the white blood cells diseases. we divide these diseases into two categories, each category includes similar symptoms diseases that may confuse in diagnosing. Based on the doctor's selection, one of two approaches is implemented. Each approach is applied on one of the two diseases category by computing different features. Finally, Random Forest classifier is applied for final decision. The proposed approach aims to early discovery of white blood cells cancer, reduce the misdiagnosis cases in addition to improve the system learning methodology. Moreover, allowing the experts only to have the final tuning on the result obtained from the system. The proposed approach achieved an accuracy of 93% in the first category and 95% in the second category.

Our suggested study uses K means method and image processing to segment and categorize blood cells. A comprehensive blood cell count is crucial for medical examination of the body's health. Traditionally, blood cells were counted manually using a hem cytometer, lab equipment, and reagents. Time-consuming and difficult procedure. Deep Learning (DL) is an AI subset of machine learning that analyzes unsupervised data. Blood contains many dark red red blood cells, or RBCs. Leukocytes, white blood cells, fight infection. White blood cells are distinguished by their area, perimeter, and statistical factors like mean and standard deviation, which are calculated using MATLAB. In this work, Enhanced CNN can classify and recognize normal and abnormal blood cell pictures due to its accuracy. Higher accuracy and precision than CNN at 95% and 0.93, respectively.

Bone marrow produces too many aberrant blood cells, causing leukemia. These aberrant blood cells develop quickly, disrupting normal cell function. Thus, the body loses its capacity to resist viruses, bacteria, fungus, and other external organisms, lowering immunity. Lack of treatment for leukemia may kill. Adults and toddlers get this sickness. Thus, early illness diagnosis aids therapy. This condition requires blood tests and biopsy for manual diagnosis, which is arduous and time-consuming. This research describes a deep-learning-based computer-aided automated diagnostic system for acute lymphoblastic leukemia (ALL) to address these issues. This job uses a pretrained AlexNet model. Experiment uses tiny blood cell imaging. This architecture helps identify cancer cells quickly. The experimental findings show that this suggested approach achieves 98% accuracy without picture segmentation or feature extraction. Thus, the article would help pathologists diagnose acute lymphoblastic leukemia promptly and reliably.

Blood cancer can only be diagnosed properly if it is detected early. Each year, more than 1.24 million new cases of blood cancer are reported worldwide. There are about 6,000 cancers worldwide due to this disease. The importance of cancer detection and classification has prompted researchers to evaluate Deep Convolutional Neural Networks for the purpose of classifying blood cancers. The objective of this research is to conduct an in-depth investigation of the efficacy and suitability of modern Convolutional Neural Network (CNN) architectures for the detection and classification of blood malignancies. The study focuses on investigating the potential of Deep Convolutional Neural Networks (D-CNNs), comprising not only the foundational CNN models but also those improved through transfer learning methods and incorporated into ensemble strategies, to detect diverse forms of blood cancer with a high degree of accuracy. This paper provides a comprehensive investigation into five deep learning architectures derived from CNNs. These models, namely VGG19, ResNet152v2, SEresNet152, ResNet101, and DenseNet201, integrate ensemble learning techniques with transfer learning strategies. A comparison of DenseNet201 (98.08%), VGG19 (96.94%), and SEresNet152 (90.93%) shows that DVS outperforms CNN. With transfer learning, DenseNet201 had 95.00% accuracy, VGG19 had 72.29%, and SEresNet152 had 94.16%. In the study, the ensemble DVS model achieved 98.76% accuracy. Based on our study, the ensemble DVS model is the best for detecting and classifying blood cancers.

Why Different ViT Project
<p>Uses MobileNetV2 and specific optimizations, while my project uses ViT with Entropy Filtering and Region Growing Segmentation for potentially enhanced spatial analysis.</p>
<p>Focuses on traditional deep learning with Python, whereas my project uses ViT, which incorporates self-attention for potentially superior feature extraction.</p>
<p>Relies on CNN stacking; my project explores ViT's attention mechanisms, possibly providing higher precision in microscopic image analysis.</p>

My project employs ViT combined with Entropy Filtering, a novel approach, unlike the hybrid CNN and ensemble methods used here.

My project focuses on ViT's capacity for detailed cellular recognition, contrasting with BCNet's reliance on transfer learning CNN methods.

ALNet uses CNN-based architecture, while my project explores ViT's self-attention mechanism, potentially improving focus on leukemia-specific features.

Focuses on traditional machine learning classifiers rather than a ViT-based approach that utilizes self-attention for feature extraction.

Utilizes a hybrid architecture (MASK-RCNN and EfficientNet) instead of ViT; my project emphasizes ViT's self-attention mechanism for feature extraction.

Focuses on CNN architecture while my project explores ViT, which may improve detailed cellular recognition through its self-attention mechanism.

Uses MobileNetV2 instead of ViT, focusing on traditional CNN architectures, while my project leverages ViT for enhanced feature extraction.

Emphasizes transfer learning with CNNs, whereas my project focuses on using ViT with specific preprocessing techniques for better spatial analysis.

Relies on multiple CNN architectures and traditional classifiers instead of the ViT architecture, which utilizes self-attention for improved focus on specific features.

Utilizes traditional machine learning classifiers rather than a ViT-based method, which may enhance feature extraction through its self-attention mechanism.

Uses an enhanced CNN architecture, whereas my project focuses on ViT, which may provide more sophisticated feature extraction capabilities through self-attention.

Focuses on CNN without image segmentation or feature extraction; my project leverages ViT with advanced preprocessing techniques for detailed analysis.

Employs an ensemble of CNN architectures, while my project focuses on a single ViT architecture with specific preprocessing for potentially improved feature extraction.