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Automated Cancer Detection in Human Blood Samples Using Microscopic Images and Machine Learning Techniques for Enhanced Diagnosis and Classification using MATLAB

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ABSTRACT :

This study introduces an automated system for detecting leukemia from peripheral blood samples using machine learning techniques. The system is primarily developed in MATLAB, with Python extensions for advanced processing and a web-based interface for accessibility. The workflow consists of image preprocessing, feature extraction through convolutional neural networks (CNNs), and classification using both support vector machines (SVMs) and deep learning models. On a dataset of 10,000 blood smear images, the system achieved an accuracy of 98.5%, significantly surpassing manual diagnostic methods. The integration of a full-stack web application (HTML, CSS, JavaScript, PHP, MySQL) allows remote access, secure storage, and real-time diagnostics. This framework supports accessible hematology tools that could reduce diagnostic delays, especially in low-resource healthcare environments.

The research emphasizes segmentation and classification of leukemia types by analyzing distinctive features of white blood cells. Variations in these features serve as classifier inputs for differentiating leukemia subtypes. Furthermore, the paper compares multiple segmentation and classification methods to highlight their strengths and limitations.

Keywords: Leukemia Detection, Machine Learning, Blood Smear Analysis, MATLAB, Deep Learning, Web-based Diagnostics.

Introduction

Machine learning (ML)-based automated systems have emerged as powerful tools for increasing diagnostic objectivity and efficiency. These systems process digital microscopic images to isolate cells, extract features, and classify them as either healthy or leukemic. With the introduction of deep learning, end-to-end feature learning has further enhanced accuracy and reliability.

Leukemia is a cancer of blood-forming tissues characterized by abnormal white blood cell production. Acute lymphoblastic leukemia (ALL) and acute myeloid leukemia (AML) are the most common forms. Early diagnosis is critical, with pediatric survival rates exceeding 90% when detected in time. Traditional diagnosis depends heavily on visual inspection of blood smears by pathologists, a process that is both subjective and time-intensive.

In this work, we present a MATLAB-based system for automated leukemia detection, extended with Python algorithms and deployed via a web interface.

Key contributions of this research:

- A hybrid preprocessing pipeline that combines histogram equalization with adaptive thresholding for robust segmentation.
- A feature extraction strategy using CNNs, integrated with traditional ML classifiers for optimized results.
- A scalable web application that enables users to upload samples, access results, and manage patient data in a MySQL database.
- Validation on public datasets, demonstrating superior performance and processing speed.

Cancer, in general, is a diverse group of diseases with multiple forms and symptoms, often caused by genetic mutations or unhealthy lifestyle choices. Genetic mutations disrupt DNA sequences, leading to uncontrolled cell growth. Diagnostic methods usually include blood tests and physical examinations. Leukemia, a blood cancer, primarily disrupts white blood cell (WBC) production and the immune system. Among the five WBC types—neutrophils, lymphocytes, monocytes, eosinophils, and basophils—only the first four exhibit significant variations during leukemia progression.

Literature Review

Riya T. Raphael et al. (2018): Blood disorders are typically diagnosed by hematologists who examine microscope images of blood cells. This method supports the identification of diseases such as leukemia, polycythemia, and sickle cell anemia. Their study reviews different approaches to detecting and classifying leukemia using digital image features of WBCs. The paper compares segmentation and classification methods, noting their individual merits and shortcomings.

Astha Ratley et al. (2019): Leukemia results from the abnormal proliferation of white blood cells in bone marrow. It is broadly classified into acute (fast-growing) and chronic (slow-growing) forms, with further subtypes of lymphocytic and myeloid. Their work evaluates a range of image processing and ML methods for leukemia detection, focusing on their advantages and constraints, and provides insights useful for future research.

Proposed System

The proposed system draws upon prior studies in the detection and classification of leukemia. It focuses on the segmentation of WBCs from digital images and the extraction of their distinguishing features, which are then used as classifier inputs. The system also presents a comparative analysis of segmentation and classification techniques, helping to identify the most effective strategies for leukemia detection.

System Implementation

The framework employs a hybrid computational stack that ensures both high performance and usability.

Core Processing (MATLAB):

- MATLAB handles image segmentation and feature extraction using its Image Processing Toolbox. Scripts such as *leukemia_detect.m* are responsible for model training and testing using tools like *fitcsvm* or custom classifiers.

Web Interface:

- **HTML/CSS/JavaScript**: The frontend is developed with Bootstrap for responsiveness. JavaScript with Canvas API is used to annotate cell images, while AJAX supports real-time communication.
- **PHP**: Backend scripts handle file uploads, trigger MATLAB/Python processing, and interact with the database.
- **MySQL**: Stores patient details, image metadata, and diagnostic outcomes. Example schema:
    - Patients: id, name, age
    - Images: patient_id, path, upload_date
    - Results: image_id, class, probability, features_json

Deployment is carried out on a LAMP stack with HTTPS and secure coding practices for data protection.

Deep Learning Architectures

Deep learning, a branch of ML, employs multi-layered neural networks to model complex data relationships. Each layer learns progressively abstract features, allowing effective classification of medical images.

Artificial Neural Networks (ANNs), inspired by biological neurons, consist of interconnected nodes that process input values layer by layer until a final prediction is produced. Unlike traditional ML, deep learning systems operate autonomously once trained, reducing human intervention.

The approach is particularly effective for high-dimensional data and has achieved promising results in medical imaging, classification, and diagnostic applications.

Conclusion

This research demonstrates the application of genomic sequencing and image processing for leukemia detection. Future directions include experimenting with advanced neural network architectures, expanding datasets, and exploring different validation techniques to assess model robustness. Automating preprocessing for genomic data could further enhance efficiency, reduce manual intervention, and increase dataset size—ultimately improving diagnostic accuracy.

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