

Malaria Diagnosis Using CNNs

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Introduction

This project focuses on developing a deep learning model for malaria diagnosis using convolutional neural networks (CNNs). The architecture is inspired by recent advancements in medical image analysis, particularly in the detection of malaria parasites from blood smear images. Particularly, inspiration is drawn from a 2025 Nature article^[1], which provides a framework for the data preprocessing and CNN architecture.

Architecture

The CNN architecture used in this project is based on a multi-layered structure designed to effectively classify malaria-infected cells from uninfected ones. The model consists of several convolutional layers followed by fully connected layers. Here's a brief overview:

- **Convolutional Layers:** These layers are responsible for extracting features from the input images. The architecture includes multiple convolutional layers with varying filter sizes and numbers, allowing the model to capture both local and global features.
- **Pooling Layers:** Max pooling layers are used to reduce the spatial dimensions of the feature maps, thereby decreasing the number of parameters and computations required.
- **Fully Connected Layers:** After flattening the output of the convolutional and pooling layers, fully connected layers are used to classify the images into infected or uninfected categories.

The specific architecture used in this project includes:

- **Convolutional Blocks:** Multiple convolutional layers with batch normalization and ReLU activation.
- **Pooling Layers:** Max pooling layers to reduce spatial dimensions.
- **Fully Connected Layers:** Two dense layers with dropout for regularization.

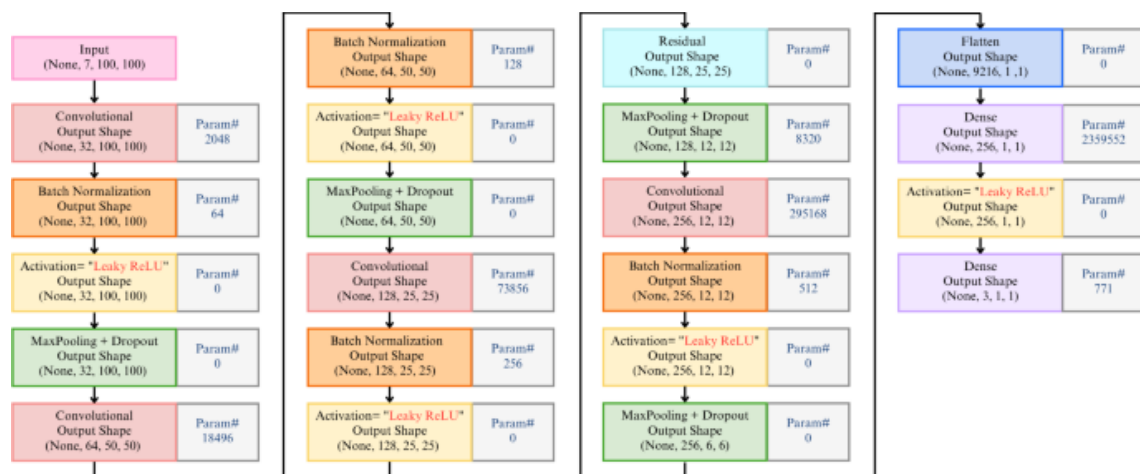


Figure 1: Architecture of CNN in Ramos-Briceno, et al (2025), Nature

Process

1. **Data Preprocessing:** The dataset consists of images of blood smears. Preprocessing involves resizing images to a uniform size and applying enhancements such as CLAHE (Contrast Limited Adaptive Histogram Equalization) to improve contrast.
2. **Model Training:** The model is trained on the preprocessed dataset using a binary cross-entropy loss function and an Adam optimizer. Training involves splitting the dataset into training and validation sets to monitor performance and prevent overfitting.
3. **Model Evaluation:** The trained model is evaluated on a test dataset to assess its accuracy, precision, recall, and F1-score.
4. **Embeddings Visualization:** To visualize the learned features, embeddings from the convolutional layers are extracted and reduced in dimensionality using t-SNE (t-distributed Stochastic Neighbor Embedding). This allows for the visualization of how the model separates infected and uninfected cells in a lower-dimensional space.

Embeddings Visualization

The embeddings visualization is crucial for understanding how the model distinguishes between infected and uninfected cells. By applying t-SNE to the high-dimensional embeddings, we can observe patterns and clusters that indicate the model's ability to differentiate between classes.

- **t-SNE Plot:** The plot shows points representing individual images, colored based on their predicted labels. Clusters or distinct patterns in the plot suggest that the model has learned meaningful features for classification.

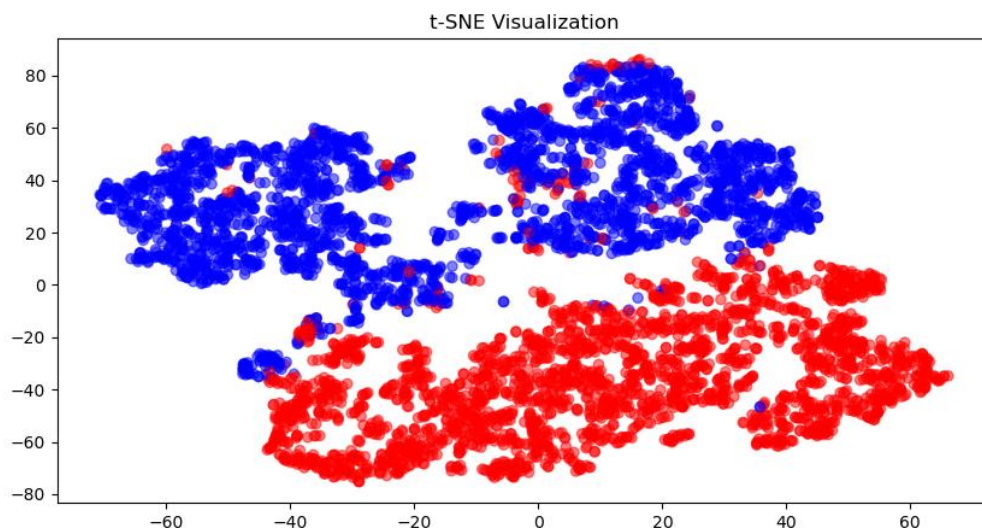


Figure 2: t-SNE Visualization of CNN Embeddings in 2D Space

Results

The best model achieved an F1 accuracy of >96% over 30 epochs on the training data, and a similar F1 accuracy of >96% on the test data in Kaggle. This indicates that the model trained was robust and generalizes well. Moreover, the visualization of the embeddings using t-SNE indicates a model that has learned the distinction between uninfected and parasitized cells well in the embedding space.

Conclusion

This project demonstrates the effectiveness of CNNs in malaria diagnosis by leveraging advanced image processing techniques and deep learning architectures. The model's performance is evaluated through metrics such as accuracy, precision, and recall, providing insights into its reliability for clinical applications. The embeddings visualization offers a deeper understanding of how the model categorizes images, highlighting its potential for improving diagnostic accuracy in resource-limited settings.

Future Directions

1. **Multiclass Classification:** Extending the model to classify different *Plasmodium* species could enhance diagnostic capabilities.
2. **Real-World Deployment:** Developing a user-friendly interface for healthcare professionals to input images and receive diagnoses could facilitate widespread adoption.
3. **Data Augmentation:** Applying additional data augmentation techniques could improve the model's robustness to variations in image quality.

By addressing these areas, the model can become a valuable tool for improving malaria diagnosis and treatment outcomes globally.

Citations and Further Reading:

1. <https://www.nature.com/articles/s41598-025-87979-5>
2. <https://pmc.ncbi.nlm.nih.gov/articles/PMC11846849/>
3. <https://arxiv.org/pdf/1909.13101.pdf>
4. <https://www.nature.com/articles/s41598-024-63831-0>
5. <https://www.nature.com/articles/s41598-025-90851-1>
6. <https://pubmed.ncbi.nlm.nih.gov/36772541/>