

Malaria Detection Report

Introduction

Malaria is a life-threatening disease caused by parasites that are transmitted through the bites of infected mosquitoes. Early and accurate detection of malaria is crucial for effective treatment and prevention. In this report, we present an approach to detect malaria-infected cells using deep learning and visualize the model's predictions to provide explanations for its decisions.

Dataset

The dataset used for training and evaluation consists of images of cells infected with malaria (parasitized) and uninfected cells. The dataset is balanced, with an equal number of images for each class. The images are initially of different sizes, and we preprocess them by resizing them to a consistent size of 256x256 pixels.

Data Preparation

We split the dataset into training and validation sets, with 80% of the data used for training and 20% for validation. We use data loaders to efficiently load and process the images during training. The images are transformed into tensors and normalized before being fed into the model.

Model Architecture

For malaria detection, we employ a convolutional neural network (CNN) based on the ResNet architecture. ResNet models have shown remarkable performance in computer vision tasks, especially for deep networks. The model consists of several convolutional blocks, with each block containing convolutional layers followed by batch normalization and ReLU activation. The output of the convolutional blocks is then passed through a classifier to predict the class labels.

Training and Evaluation

During training, we use the cross-entropy loss function to measure the difference between the predicted and actual class labels. We optimize the model's parameters using gradient descent with a suitable learning rate. The training progress is monitored, and the model with the best performance on the validation set is saved.

After each epoch, we evaluate the model's performance on the validation set by calculating the loss and accuracy. This allows us to monitor the model's progress and detect any overfitting or underfitting issues. We also track the learning rate used during training to analyze its impact on the model's performance.

Model Evaluation and Visualization

Once the model is trained, we can evaluate its performance on unseen images. We use the trained model to classify individual cells as either infected or uninfected. Additionally, we generate a visualization of the model's predictions, which highlights the areas in the image that highly influence the classification decision. This visualization provides an explanation for the model's prediction and helps in understanding its reasoning.

Streamlit App

To provide a user-friendly interface for malaria detection, we deploy the model in a Streamlit app. The app allows users to upload an image of a cell and obtain the model's prediction along with the hotspot visualization. The hotspot visualization overlays the areas of the image that significantly contribute to the model's decision, aiding in the interpretation of the prediction.

Results and Discussion

The model achieved promising results in detecting malaria-infected cells. During training, the model's loss decreased, and the accuracy increased, indicating effective learning. On the validation set, the model achieved an accuracy of 96.4%. The hotspot visualization provided valuable insights into the model's decision-making process, allowing us to identify the regions of the image that influenced the classification.

Conclusion

In this project, we developed a deep learning model for malaria detection and deployed it in a Streamlit app for easy access and interpretation. The model showed promising results in classifying infected and uninfected cells. The hotspot visualization provided valuable insights into the model's predictions, making it explainable and trustworthy for practical applications. Further improvements can be explored, such as using more advanced architectures.

References

<https://jovian.com/aakashns/05b-cifar10-resnet>