Deep Neural Network for Malaria Infected Cell Recognition

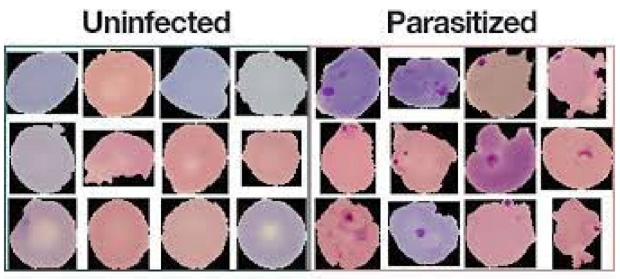
AIM

To develop a deep neural network for Malaria infected cell recognition and to analyze the performance.

Problem Statement and Dataset

Aims to create an algorithm that can detect malaria-infected cells in blood samples using deep learning techniques. The goal is to develop a model that can accurately identify infected cells and distinguish them from healthy ones. The performance of the model will be evaluated based on its accuracy, precision, recall, and F1 score. This problem statement is important because it can help improve the diagnosis of malaria and reduce the time and cost associated with manual diagnosis.

Malaria dataset of 27,558 cell images with an equal number of parasitized and uninfected cells. A level-set based algorithm was applied to detect and segment the red blood cells. The images were collected and annotated by medical professionals.Here we build a convolutional neural network model that is able to classify the cells.



DESIGN STEPS

STEP-1:

Import tensorflow and preprocessing libraries

STEP 2:

Download and load the dataset folder

STEP-3:

Split the training and testing folders.

STEP 4:

Perform image data generation methods.

STEP-5:

Build the convolutional neural network model

STEP-6:

Train the model with the training data

STEP-7:

Plot the performance plot

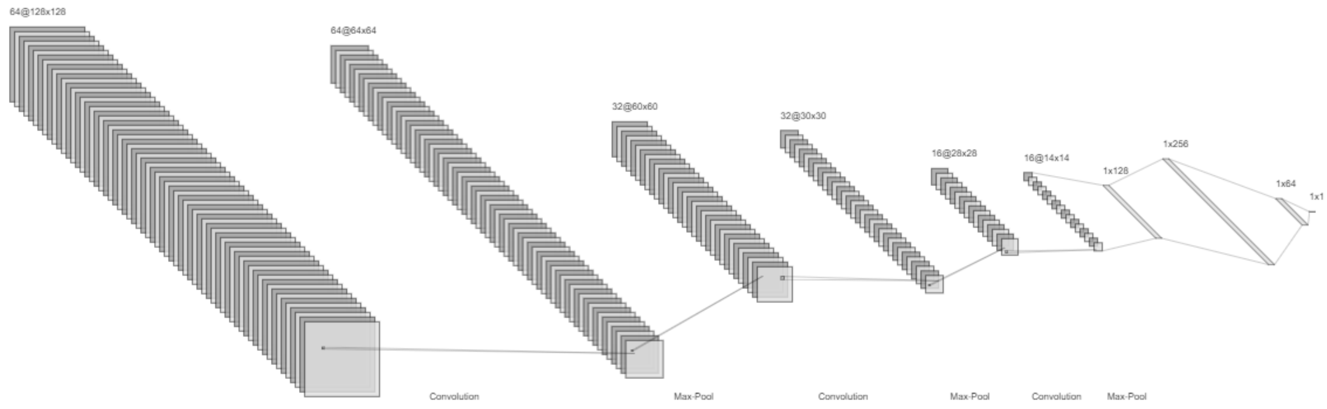
STEP-8:

Evaluate the model with the testing data using probability prediction(uninfected-> prob>0.5,parasitized-> <=0.5)

STEP-9:

Fit the model and predict the sample input.

Network model



PROGRAM

Import required libraries

```
import os
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from matplotlib.image import imread
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow import keras
from tensorflow.keras import layers
from tensorflow.keras import utils
from tensorflow.keras import models
from sklearn.metrics import classification_report,confusion_matrix
import tensorflow as tf


#this is share the GPU space

from tensorflow.compat.v1.keras.backend import set_session
config = tf.compat.v1.ConfigProto()
config.gpu_options.allow_growth = True # dynamically grow the memory used on the GPU
config.log_device_placement = True # to log device placement (on which device the operation ran)
sess = tf.compat.v1.Session(config=config)
set_session(sess)

%matplotlib inline
```

Acess the dataset from directory which contains training and testing folder, and show some sample data

```
my_data_dir = 'dataset/cell_images'

os.listdir(my_data_dir)

test_path = my_data_dir+'/test/'
train_path = my_data_dir+'/train/'

os.listdir(train_path)

len(os.listdir(train_path+'/uninfected/'))
len(os.listdir(train_path+'/parasitized/'))
os.listdir(train_path+'/parasitized')[5604]
para_img= imread(train_path+
                 '/parasitized/'+
                 os.listdir(train_path+'/parasitized')[5604])
plt.imshow(para_img)
uninfe_img= imread(train_path+
                 '/uninfected/'+
                 os.listdir(train_path+'/uninfected')[5604])
plt.imshow(uninfe_img)
```

Checking the image dimensions and find the common image length, and reshaping all images to common dimension, before feeding the model

```
dim1 = []
dim2 = []
for image_filename in os.listdir(test_path+'/uninfected'):
    img = imread(test_path+'/uninfected'+'/'+image_filename)
    d1,d2,colors = img.shape
    dim1.append(d1)
    dim2.append(d2)
sns.jointplot(x=dim1,y=dim2)

image_shape = (130,130,3)
```

Creating model,compile and summarize it

```
model = models.Sequential()

model.add(layers.Conv2D(filters=64, kernel_size=(3,3),input_shape=image_shape, activation='relu',))
model.add(layers.MaxPooling2D(pool_size=(2, 2)))

model.add(layers.Conv2D(filters=32, kernel_size=(5,5), activation='relu',))
model.add(layers.MaxPooling2D(pool_size=(2, 2)))

model.add(layers.Conv2D(filters=16, kernel_size=(3,3), activation='relu',))
model.add(layers.MaxPooling2D(pool_size=(2, 2)))


model.add(layers.Flatten())


model.add(layers.Dense(128))
model.add(layers.Activation('relu'))
model.add(layers.Dropout(0.5))

model.add(layers.Dense(256))
model.add(layers.Activation('relu'))



model.add(layers.Dense(64))
model.add(layers.Activation('relu'))

model.add(layers.Dense(1))
model.add(layers.Activation('sigmoid'))

model.compile(loss='binary_crossentropy',
              optimizer='adam',
              metrics=['accuracy'])

model.summary()
```

Performing data augmentation to increase the size of dataset

```
image_gen = ImageDataGenerator(rotation_range=40, # rotate the image 20 degrees
                               width_shift_range=0.10, # Shift the pic width by a max of 5%
                               height_shift_range=0.10, # Shift the pic height by a max of 5%
```

```
                              rescale=1/255, # Rescale the image by normalzing it.
                              shear_range=0.1, # Shear means cutting away part of the image (max 10%)
                              zoom_range=0.1, # Zoom in by 10% max
                              horizontal_flip=True, # Allo horizontal flipping
                              fill_mode='nearest' # Fill in missing pixels with the nearest filled
value
                             )

batch_size = 32
train_image_gen = image_gen.flow_from_directory(train_path,
                                               target_size=image_shape[:2],
                                                color_mode='rgb',
                                               batch_size=batch_size,
                                               class_mode='binary')

len(train_image_gen.classes)

test_image_gen = image_gen.flow_from_directory(test_path,
                                               target_size=image_shape[:2],
                                               color_mode='rgb',
                                               batch_size=batch_size,
                                               class_mode='binary',shuffle=False)

train_image_gen.class_indices
```

Fitting the model

```
results = model.fit(train_image_gen,epochs=4,
validation_data=test_image_gen )
```

Ploting graphs nd creating confusion matrix and classification report

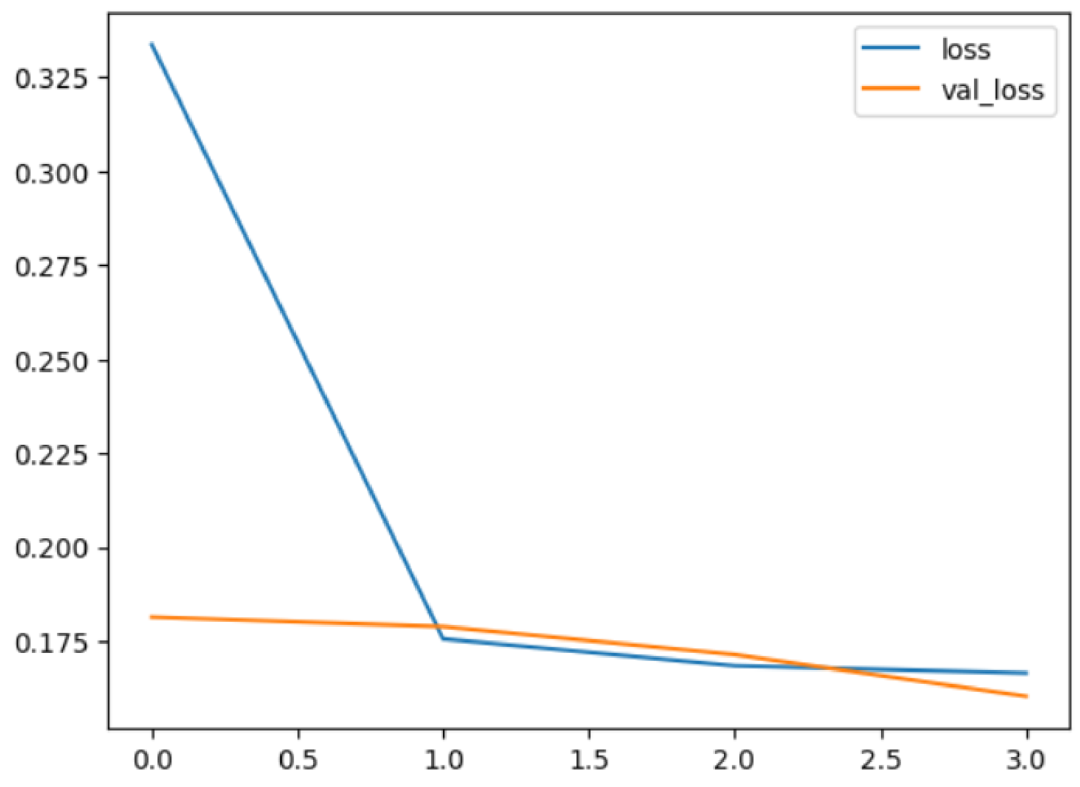
```
losses = pd.DataFrame(model.history.history)
losses[['loss','val_loss']].plot()
model.evaluate(test_image_gen)

pred_probabilities = model.predict(test_image_gen)
test_image_gen.classes
predictions = pred_probabilities > 0.5

print(classification_report(test_image_gen.classes,predictions))

print(confusion_matrix(test_image_gen.classes,predictions))
```

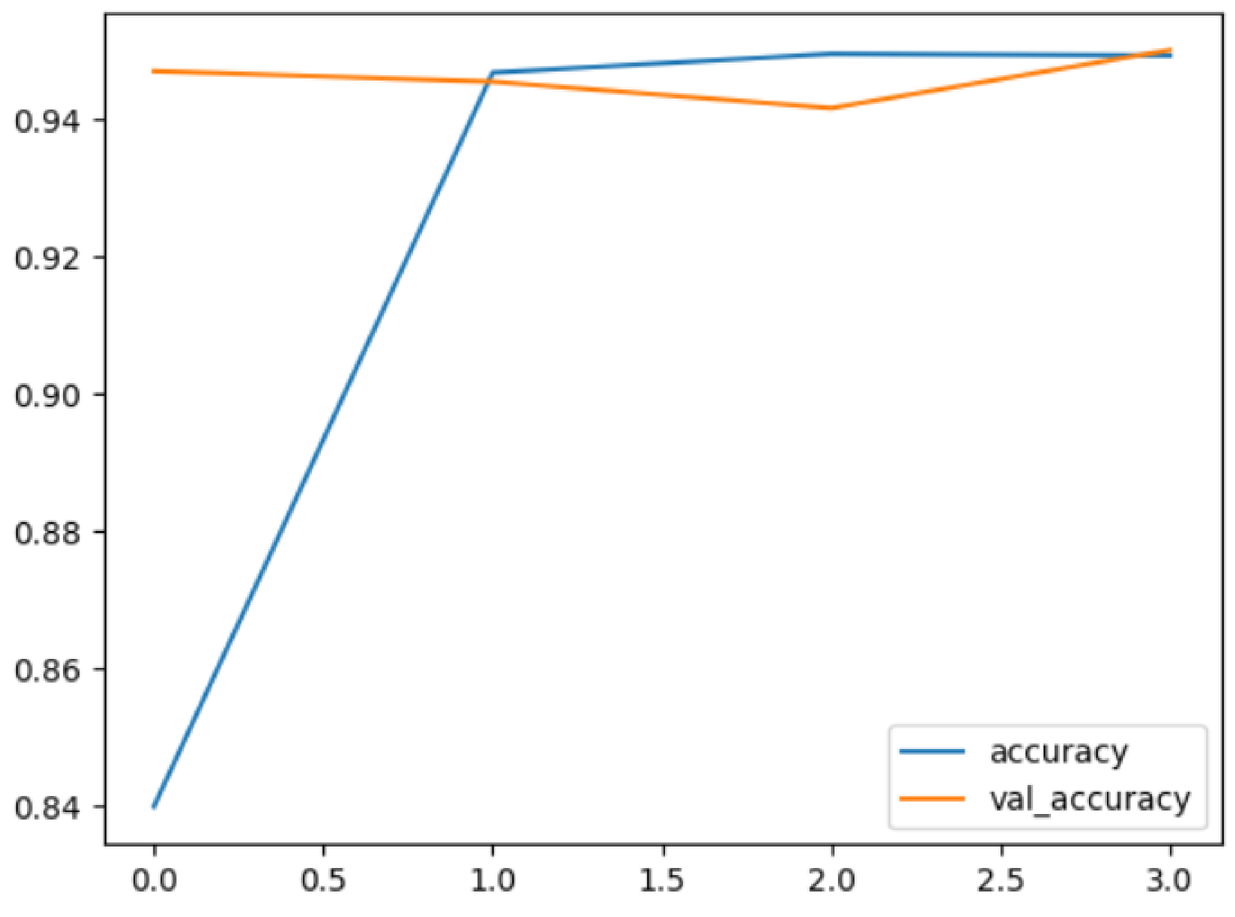
Sample data prediction

```
import random
import tensorflow as tf
list_dir=["uninfected","parasitized"]
dir_=(random.choice(list_dir))
para_img= imread(train_path+
                 '/'+dir_+'/'+
                 os.listdir(train_path+'/'+dir_)[random.randint(0,100)])
img  = tf.convert_to_tensor(np.asarray(para_img))
img = tf.image.resize(img,(130,130))
img=img.numpy()
pred=bool(model.predict(img.reshape(1,130,130,3))<0.5 )
plt.title("Model prediction: "+("Parasitized" if pred  else "Uninfected")+"\nActual Value: "+str(dir_))
plt.axis("off")
plt.imshow(img)
plt.show()
```

OUTPUT

Training Loss, Validation Loss Vs Iteration Plot





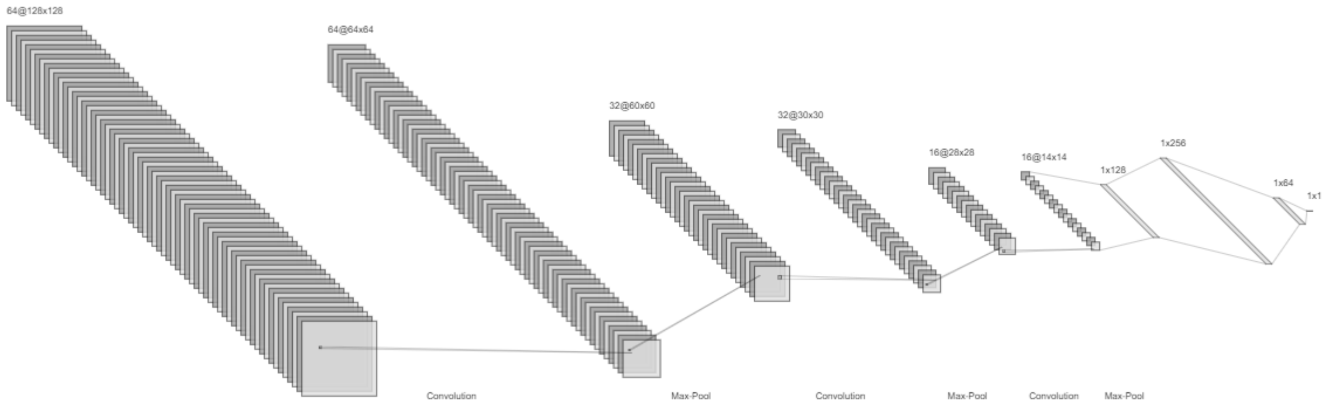
Classification Report

```
array([[1231,   69],
       [  58, 1242]])
```

Confusion Matrix

```
              precision    recall  f1-score   support

           0       0.96      0.95      0.95      1300
           1       0.95      0.96      0.95      1300

    accuracy                           0.95      2600
   macro avg       0.95      0.95      0.95      2600
weighted avg       0.95      0.95      0.95      2600
```

New Sample Data Prediction



RESULT

Thus, a deep neural network for Malaria infected cell recognition is developed and the performance is analyzed.