

Model for classifying whether a blood smear is uninfected or parasitized

CEMA internship shortlisting assignment - computer science track

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Introduction

Advanced technology and AI are playing a crucial role in combating malaria, a disease affecting millions annually. This deep learning model with a high accuracy rate is a notable advancement, potentially improving malaria detection and accelerating treatment, potentially saving lives worldwide.

BASIC LIBRARY IMPORTS

```
In [8]: # pip install tensorflow_datasets==4.9.2
```

```
In [4]: # Basic imports
# pip install tensorflow
import tensorflow as tf
import numpy as np
import matplotlib.pyplot as plt
import tensorflow_datasets as tfds
import os

from tensorflow.keras.layers import Dense , InputLayer , Conv2D , MaxPool2D , F1
from tensorflow.keras.models import Sequential
from tensorflow.keras.optimizers import Adam
from tensorflow.keras.losses import BinaryCrossentropy
from PIL import Image
```

```
C:\Users\Dell Latitude E6410\Documents\python projects\tfenv\lib\site-packages\tqdm\auto.py:21: TqdmWarning: IPProgress not found. Please update jupyter and ipywidgets. See https://ipywidgets.readthedocs.io/en/stable/user_install.html
from .autonotebook import tqdm as notebook_tqdm
```

IMPORTING THE DATASET

```
In [134... dataset , dataset_info = tfds.load('malaria' , with_info=True , as_supervised =
dataset_info

Out[134... tfds.core.DatasetInfo(
    name='malaria',
    full_name='malaria/1.0.0',
    description="""
The Malaria dataset contains a total of 27,558 cell images with equal insta
nces
of parasitized and uninfected cells from the thin blood smear slide images
of
segmented cells.
""",
    homepage='https://lhncbc.nlm.nih.gov/publication/pub9932',
    data_path='C:\\Users\\Dell Latitude E6410\\tensorflow_datasets\\malaria\\1.
0.0',
    file_format=tfrecord,
    download_size=337.08 MiB,
    dataset_size=317.62 MiB,
    features=FeaturesDict({
        'image': Image(shape=(None, None, 3), dtype=uint8),
        'label': ClassLabel(shape=(), dtype=int64, num_classes=2),
    }),
    supervised_keys=('image', 'label'),
    disable_shuffling=False,
    splits={
        'train': <SplitInfo num_examples=27558, num_shards=4>,
    },
    citation="""@article{rajaraman2018pre,
        title={Pre-trained convolutional neural networks as feature extractors to
ward
improved malaria parasite detection in thin blood smear images},
        author={Rajaraman, Sivaramakrishnan and Antani, Sameer K and Poostchi, Ma
hdieh
and Silamut, Kamolrat and Hossain, Md A and Maude, Richard J and Jaeger,
Stefan and Thoma, George R},
        journal={PeerJ},
        volume={6},
        pages={e4568},
        year={2018},
        publisher={PeerJ Inc.}
    }""",
)
```

DISPLAYING THE CLASS NAMES

```
In [135... class_names = dataset_info.features['label'].names
class_names
```

```
Out[135... ['parasitized', 'uninfected']
```

DATA SPLITTING

```
In [11]: def splits(dataset , TRAIN_RATIO , VAL_RATIO , TEST_RATIO):
DATASET_SIZE = len(dataset)
```

```
train_dataset = dataset.take(int(TRAIN_RATIO * DATASET_SIZE))

val_dataset = dataset.skip(int(TRAIN_RATIO * DATASET_SIZE))
val_dataset = dataset.take(int(VAL_RATIO * DATASET_SIZE))

test_dataset = dataset.skip(int(TRAIN_RATIO * DATASET_SIZE))
test_dataset = dataset.skip(int(VAL_RATIO * DATASET_SIZE))
test_dataset = dataset.take(int(TEST_RATIO * DATASET_SIZE))

return train_dataset , val_dataset , test_dataset

train_dataset , val_dataset , test_dataset = splits(dataset[0] , 0.6 , 0.2 , 0.2
```

DATA VISUALIZATION

```
In [12]: for i , (image,label) in enumerate(train_dataset.take(16)):
          ax = plt.subplot(4,4 ,i+1)
          plt.imshow(image)
          plt.axis("off")
          plt.title(dataset_info.features['label'].int2str(label))
          plt.subplots_adjust(top=2)
```

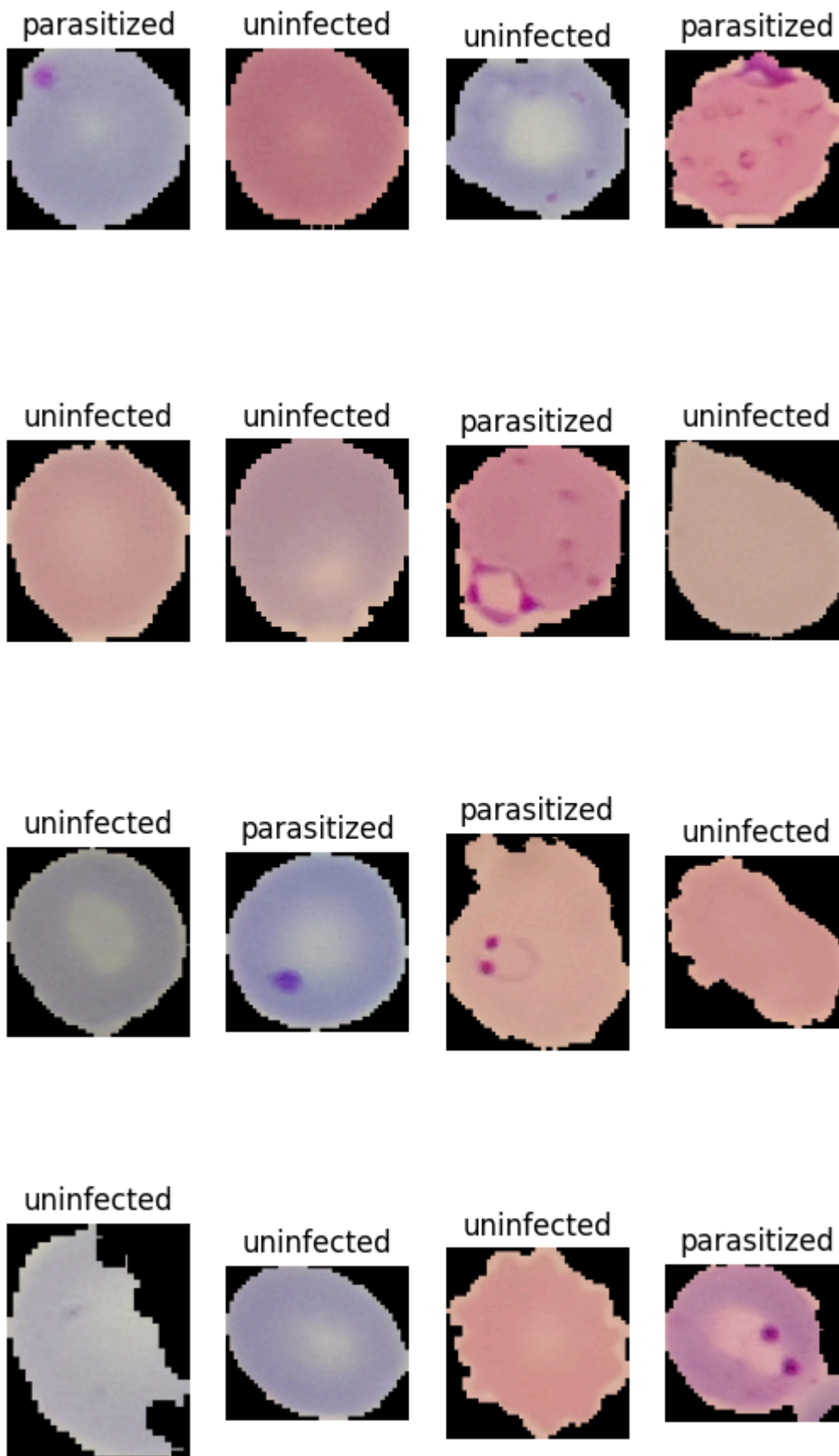


IMAGE / DATA PREPROCESSING

```
In [13]: IMG_SIZE = 224
def resize_rescale(image , label):
    return tf.image.resize(image , (IMG_SIZE,IMG_SIZE))/255.0 , label
```

```
train_dataset = train_dataset.map(resize_rescale)
val_dataset = val_dataset.map(resize_rescale)
test_dataset = test_dataset.map(resize_rescale)

train_dataset = train_dataset.shuffle(buffer_size = 8 , reshuffle_each_iteration
val_dataset = val_dataset.shuffle(buffer_size = 8 , reshuffle_each_iteration = 1
test_dataset = test_dataset.batch(1)
```

MODEL BUILDING

```
In [14]: model = Sequential([

    InputLayer(input_shape=(IMG_SIZE,IMG_SIZE,3)),

    Conv2D(filters=6 , kernel_size=5 , strides=1 ,padding = 'valid' , activation=
    BatchNormalization(),
    MaxPool2D(pool_size=2 , strides =2 ),

    Conv2D(filters=16 , kernel_size=5 , strides=1 ,padding = 'valid' , activation
    MaxPool2D(pool_size=2 , strides =2 ),

    Flatten(),

    Dense(100 , activation='relu'),
    BatchNormalization(),
    Dense(10 , activation='relu'),
    Dense(1 , activation='sigmoid')

])
```

MODEL COMPILATION , TRAINING AND EVALUATION

```
In [15]: # Compilation

model.compile(optimizer=Adam(learning_rate=0.01) , loss = BinaryCrossentropy(),

# Training

history = model.fit(train_dataset , validation_data = val_dataset, epochs = 30,

# Evaluation
model.evaluate(test_dataset)
```

Epoch 1/30
517/517 [=====] - 2000s 4s/step - loss: 0.4406 - accuracy: 0.7949 - val_loss: 0.9967 - val_accuracy: 0.4859

Epoch 2/30
517/517 [=====] - 1724s 3s/step - loss: 0.2206 - accuracy: 0.9245 - val_loss: 0.1798 - val_accuracy: 0.9354

Epoch 3/30
517/517 [=====] - 1880s 4s/step - loss: 0.1812 - accuracy: 0.9413 - val_loss: 0.1392 - val_accuracy: 0.9555

Epoch 4/30
517/517 [=====] - 2895s 6s/step - loss: 0.1573 - accuracy: 0.9491 - val_loss: 0.1907 - val_accuracy: 0.9354

Epoch 5/30
517/517 [=====] - 2450s 5s/step - loss: 0.1367 - accuracy: 0.9550 - val_loss: 0.1492 - val_accuracy: 0.9421

Epoch 6/30
517/517 [=====] - 1945s 4s/step - loss: 0.1211 - accuracy: 0.9584 - val_loss: 0.1500 - val_accuracy: 0.9510

Epoch 7/30
517/517 [=====] - 3013s 6s/step - loss: 0.1093 - accuracy: 0.9610 - val_loss: 0.1096 - val_accuracy: 0.9615

Epoch 8/30
517/517 [=====] - 2394s 5s/step - loss: 0.1001 - accuracy: 0.9660 - val_loss: 0.0904 - val_accuracy: 0.9682

Epoch 9/30
517/517 [=====] - 1824s 4s/step - loss: 0.0866 - accuracy: 0.9708 - val_loss: 0.1110 - val_accuracy: 0.9561

Epoch 10/30
517/517 [=====] - 1913s 4s/step - loss: 0.0777 - accuracy: 0.9741 - val_loss: 0.1727 - val_accuracy: 0.9490

Epoch 11/30
517/517 [=====] - 1635s 3s/step - loss: 0.0667 - accuracy: 0.9768 - val_loss: 0.0943 - val_accuracy: 0.9679

Epoch 12/30
517/517 [=====] - 1579s 3s/step - loss: 0.0619 - accuracy: 0.9790 - val_loss: 0.0827 - val_accuracy: 0.9744

Epoch 13/30
517/517 [=====] - 2650s 5s/step - loss: 0.0616 - accuracy: 0.9796 - val_loss: 0.1079 - val_accuracy: 0.9659

Epoch 14/30
517/517 [=====] - 1713s 3s/step - loss: 0.0553 - accuracy: 0.9813 - val_loss: 0.0615 - val_accuracy: 0.9782

Epoch 15/30
517/517 [=====] - 1619s 3s/step - loss: 0.0514 - accuracy: 0.9823 - val_loss: 0.0466 - val_accuracy: 0.9833

Epoch 16/30
517/517 [=====] - 2104s 4s/step - loss: 0.0421 - accuracy: 0.9857 - val_loss: 0.0948 - val_accuracy: 0.9719

Epoch 17/30
517/517 [=====] - 2185s 4s/step - loss: 0.0385 - accuracy: 0.9871 - val_loss: 0.0542 - val_accuracy: 0.9828

Epoch 18/30
517/517 [=====] - 2182s 4s/step - loss: 0.0412 - accuracy: 0.9847 - val_loss: 0.2102 - val_accuracy: 0.9559

Epoch 19/30
517/517 [=====] - 2146s 4s/step - loss: 0.0349 - accuracy: 0.9877 - val_loss: 0.1310 - val_accuracy: 0.9668

Epoch 20/30
517/517 [=====] - 2033s 4s/step - loss: 0.0360 - accuracy: 0.9880 - val_loss: 0.0408 - val_accuracy: 0.9893

```

Epoch 21/30
517/517 [=====] - 1533s 3s/step - loss: 0.0277 - accuracy: 0.9898 - val_loss: 0.0297 - val_accuracy: 0.9902
Epoch 22/30
517/517 [=====] - 1314s 3s/step - loss: 0.0188 - accuracy: 0.9927 - val_loss: 0.0238 - val_accuracy: 0.9918
Epoch 23/30
517/517 [=====] - 1293s 3s/step - loss: 0.0326 - accuracy: 0.9891 - val_loss: 0.0362 - val_accuracy: 0.9882
Epoch 24/30
517/517 [=====] - 1266s 2s/step - loss: 0.0232 - accuracy: 0.9918 - val_loss: 0.0448 - val_accuracy: 0.9887
Epoch 25/30
517/517 [=====] - 1255s 2s/step - loss: 0.0255 - accuracy: 0.9920 - val_loss: 0.0704 - val_accuracy: 0.9819
Epoch 26/30
517/517 [=====] - 1260s 2s/step - loss: 0.0216 - accuracy: 0.9925 - val_loss: 0.0344 - val_accuracy: 0.9884
Epoch 27/30
517/517 [=====] - 1271s 2s/step - loss: 0.0253 - accuracy: 0.9910 - val_loss: 0.0660 - val_accuracy: 0.9804
Epoch 28/30
517/517 [=====] - 1257s 2s/step - loss: 0.0159 - accuracy: 0.9944 - val_loss: 0.0836 - val_accuracy: 0.9877
Epoch 29/30
517/517 [=====] - 1249s 2s/step - loss: 0.0225 - accuracy: 0.9921 - val_loss: 0.0273 - val_accuracy: 0.9911
Epoch 30/30
517/517 [=====] - 1254s 2s/step - loss: 0.0351 - accuracy: 0.9889 - val_loss: 0.0585 - val_accuracy: 0.9786
5511/5511 [=====] - 217s 39ms/step - loss: 0.0586 - accuracy: 0.9784

```

```
Out[15]: [0.058616239577531815, 0.9784068465232849]
```

VISUALIZING ACCURACY AND LOSSES

```

In [22]: # Create subplots
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(12, 6))

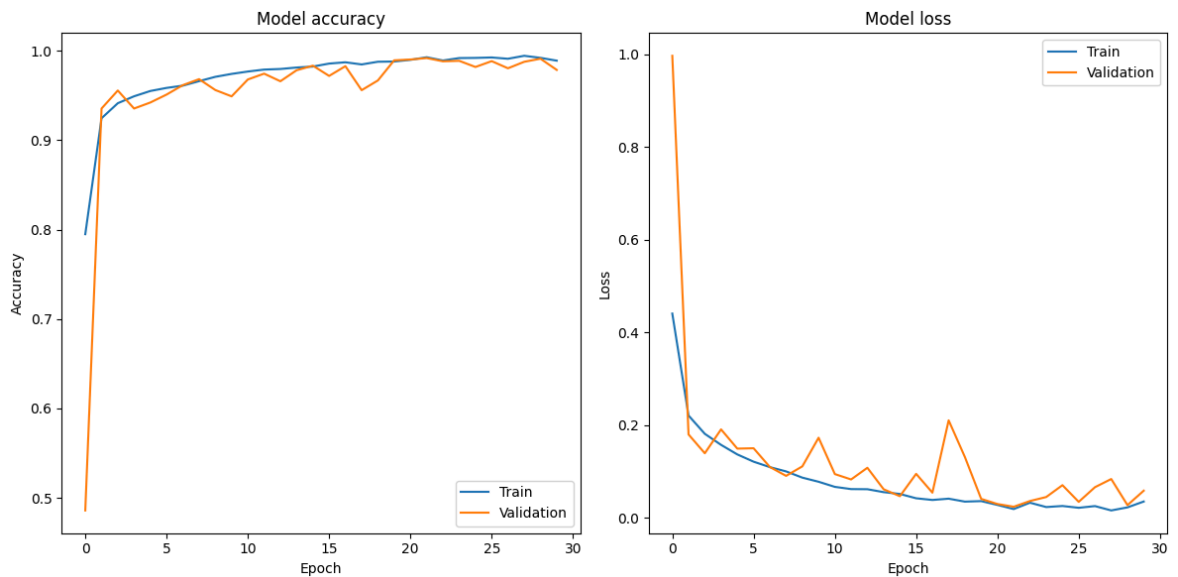
# Plot training & validation accuracy values
ax1.plot(history.history['accuracy'])
ax1.plot(history.history['val_accuracy'])
ax1.set_title('Model accuracy')
ax1.set_ylabel('Accuracy')
ax1.set_xlabel('Epoch')
ax1.legend(['Train', 'Validation'], loc='lower right')

# Plot training & validation loss values
ax2.plot(history.history['loss'])
ax2.plot(history.history['val_loss'])
ax2.set_title('Model loss')
ax2.set_ylabel('Loss')
ax2.set_xlabel('Epoch')
ax2.legend(['Train', 'Validation'], loc='upper right')

# Show plot

```

```
plt.tight_layout()
plt.show()
```



SAVING THE MODEL

```
In [19]: folder_path = r'\\.model'

# Save the model in .h5 format
model.save(os.path.join(folder_path, "malaria_model.h5"))
```

```
In [20]: # Save the model in .keras format

model.save(os.path.join(folder_path, "malaria_model.keras"))
```

MAKING PREDICTIONS ON AN IMAGE

```
In [51]: def predict(model, img):
    img_array = tf.keras.preprocessing.image.img_to_array(images[i].numpy())
    img_array = tf.expand_dims(img_array, 0)

    predictions = model.predict(img_array)

    predicted_class = class_names[np.argmax(predictions[0])]
    confidence = round(100 * (np.max(predictions[0])), 2)
    return predicted_class, confidence
```

```
In [65]: plt.figure(figsize=(15,15))
for images, labels in test_dataset.take(9):
    for i in range(1):
        ax = plt.subplot(3,3, i+1)
        plt.imshow(images[i].numpy())

        predicted_class, confidence = predict(model, images[i].numpy())
        actual_class = class_names[labels[i]]

        plt.title(f"Actual: {actual_class}, \n Predicted: {predicted_class}")
        plt.axis("off")
```

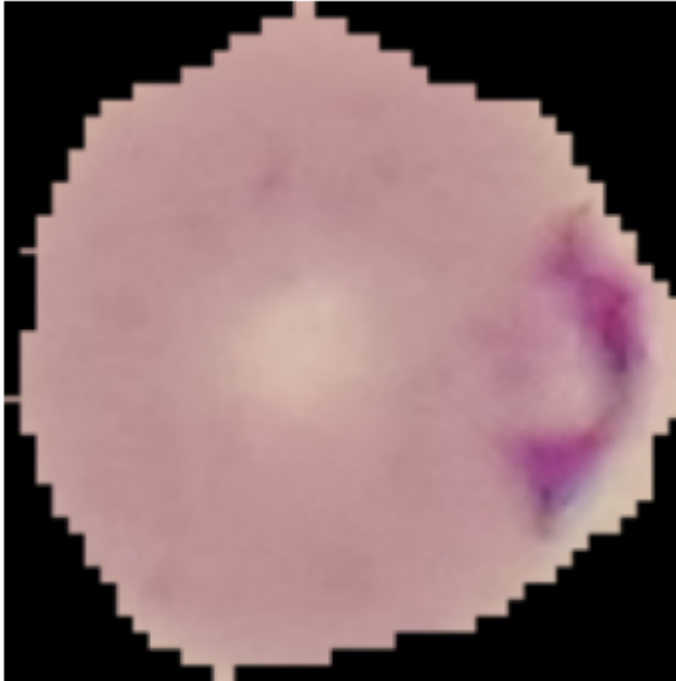


```

1/1 [=====] - 0s 125ms/step
1/1 [=====] - 0s 90ms/step
1/1 [=====] - 0s 60ms/step
1/1 [=====] - 0s 61ms/step
1/1 [=====] - 0s 61ms/step
1/1 [=====] - 0s 74ms/step
1/1 [=====] - 0s 91ms/step
1/1 [=====] - 0s 65ms/step
1/1 [=====] - 0s 62ms/step

```

Actual: parasitized,
Predicted: parasitized



RUNNING PREDICTIONS ON IMAGES WITH THE SAVED MODEL

```

In [6]: # Load the model
        malaria_model = tf.keras.models.load_model(r".\model\malaria_model.h5")

        image_path = r".\test_image"

        # Get a list of image files in the folder
        images = [f for f in os.listdir(image_path) if f.endswith(".jpg") or f.endswith(

        # Iterate over the images
        for image_file in images:
            # Load the image
            img = Image.open(os.path.join(image_path, image_file))

            # Convert to RGB mode
            img = img.convert("RGB")

            # Resize the image
            desired_size = (224, 224)
            img = img.resize(desired_size)

```

```
# Convert the image to numpy array and preprocess
img_array = tf.keras.preprocessing.image.img_to_array(img)
img_array = img_array / 255.0 # Normalize pixel values

# Expand dimensions to match model input shape
img_array = tf.expand_dims(img_array, axis=0)

# Make predictions using the model
predictions = malaria_model.predict(img_array)
predicted_class = "Uninfected" if predictions[0][0] > 0.5 else "Parasitized"

# Display the image along with the prediction
plt.imshow(img)
plt.title(f"Predicted: {predicted_class}")
plt.axis("off")
plt.show()
```

1/1 [=====] - 0s 305ms/step

Predicted: Parasitized



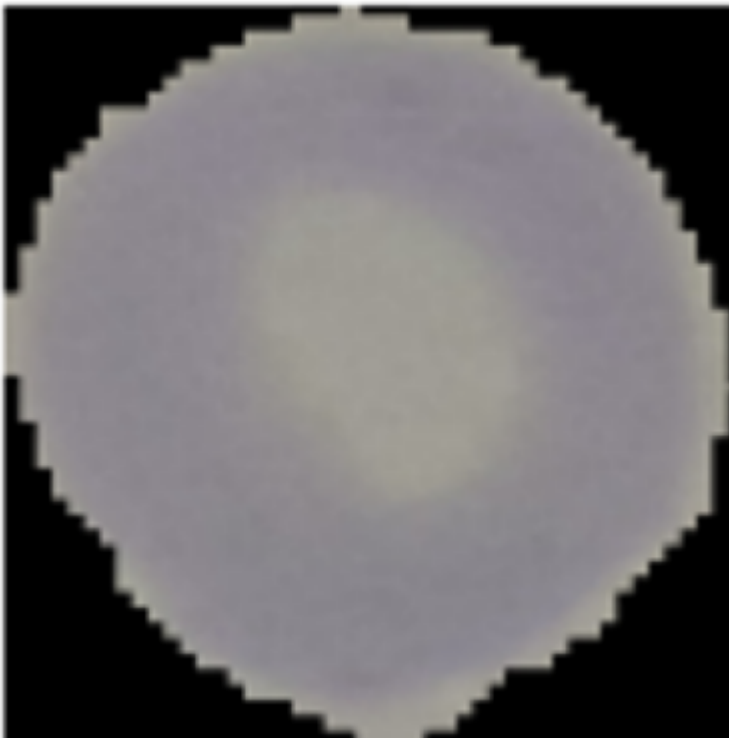
1/1 [=====] - 0s 58ms/step

Predicted: Parasitized



1/1 [=====] - 0s 58ms/step

Predicted: Uninfected



End

In []: