

```
from google.colab import drive  
drive.mount("/content/drive")
```

↳ Go to this URL in a browser: https://accounts.google.com/o/oauth2/auth?client_id=947318989803

```
Enter your authorization code:  
.....  
Mounted at /content/drive
```

```
!mkdir /root/.kaggle
```

```
!cp /content/drive/'My Drive'/'Colab Notebooks'/kaggle.json /root/.kaggle/
```

```
!pip install -q kaggle  
!kaggle datasets download -d iarunava/cell-images-for-detecting-malaria
```

↳ Downloading cell-images-for-detecting-malaria.zip to /content
98% 661M/675M [00:07<00:00, 109MB/s]
100% 675M/675M [00:07<00:00, 90.4MB/s]

```
!unzip cell-images-for-detecting-malaria.zip
```

```
!git clone https://github.com/mjkvaak/ImageDataAugmentor.git
```

↳ Cloning into 'ImageDataAugmentor'...
remote: Enumerating objects: 141, done.
remote: Counting objects: 100% (141/141), done.
remote: Compressing objects: 100% (111/111), done.
remote: Total 306 (delta 72), reused 70 (delta 23), pack-reused 165
Receiving objects: 100% (306/306), 146.55 KiB | 10.47 MiB/s, done.
Resolving deltas: 100% (171/171), done.

```
pip install git+https://github.com/mjkvaak/ImageDataAugmentor
```

↳

```
Collecting git+https://github.com/mjkvaak/ImageDataAugmentor
  Cloning https://github.com/mjkvaak/ImageDataAugmentor to /tmp/pip-req-build-07_uh1i3
    Running command git clone -q https://github.com/mjkvaak/ImageDataAugmentor /tmp/pip-req-build-07_uh1i3
Collecting opencv-python>=4.2
  Downloading https://files.pythonhosted.org/packages/46/16/e49e5abd27d988e687634f58b0aa329fe7
    |██████████| 49.4MB 54kB/s
Requirement already satisfied: matplotlib in /usr/local/lib/python3.6/dist-packages (from ImageDataAugmentor)
Requirement already satisfied: Pillow in /usr/local/lib/python3.6/dist-packages (from ImageDataAugmentor)
```

```
pip install twine
```

```
↳
```

```
Collecting twine
  Downloading https://files.pythonhosted.org/packages/ad/db/b2c65078b783c6694bdfa0911bbbe0e2be
```

```
pip install efficientnet
```

```
↳ Collecting efficientnet
  Downloading https://files.pythonhosted.org/packages/28/91/67848a143b54c331605bfba5fd31cf4e9d
Collecting keras-applications<=1.0.8,>=1.0.7
  Downloading https://files.pythonhosted.org/packages/71/e3/19762fdfc62877ae9102edf6342d71b28f | [██████████] 51kB 3.7MB/s
Requirement already satisfied: scikit-image in /usr/local/lib/python3.6/dist-packages (from ef
Requirement already satisfied: numpy>=1.9.1 in /usr/local/lib/python3.6/dist-packages (from ke
Requirement already satisfied: h5py in /usr/local/lib/python3.6/dist-packages (from keras-app
Requirement already satisfied: networkx>=2.0 in /usr/local/lib/python3.6/dist-packages (from s
Requirement already satisfied: imageio>=2.3.0 in /usr/local/lib/python3.6/dist-packages (from
Requirement already satisfied: matplotlib!=3.0.0,>=2.0.0 in /usr/local/lib/python3.6/dist-pac
Requirement already satisfied: scipy>=0.19.0 in /usr/local/lib/python3.6/dist-packages (from s
Requirement already satisfied: PyWavelets>=0.4.0 in /usr/local/lib/python3.6/dist-packages (fr
Requirement already satisfied: pillow>=4.3.0 in /usr/local/lib/python3.6/dist-packages (from s
Requirement already satisfied: six in /usr/local/lib/python3.6/dist-packages (from h5py->keras
Requirement already satisfied: decorator>=4.3.0 in /usr/local/lib/python3.6/dist-packages (fro
Requirement already satisfied: python-dateutil>=2.1 in /usr/local/lib/python3.6/dist-packages
Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.6/dist-packages (from ma
Requirement already satisfied: pyparsing!=2.0.4,!>=2.1.2,!>=2.1.6,>=2.0.1 in /usr/local/lib/pyt
Requirement already satisfied: kiwisolver>=1.0.1 in /usr/local/lib/python3.6/dist-packages (fr
Installing collected packages: keras-applications, efficientnet
Successfully installed efficientnet-1.1.0 keras-applications-1.0.8
```

```
Requirement already satisfied: chardet<4,>=3.0.2 in /usr/local/lib/python3.6/dist-packages (tr
```

```
from ImageDataAugmentor.image_data_augmentor import *
import glob
import pandas as pd
import os
import numpy as np
from sklearn.model_selection import train_test_split
```

```
parasitized=os.listdir('cell_images/Parasitized')
uninfected=os.listdir('cell_images/Uninfected')
par=list(zip(parasitized,['parasitized']*(len(parasitized))))
parasitized_df = pd.DataFrame(par,columns=['file','label'])
parasitized_df.head()
```

```
↳
```

	file	label
0	C66P27N_ThinF_IMG_20150818_164008_cell_154.png	parasitized
1	C51AP12thinF_IMG_20150724_155046_cell_102.png	parasitized
2	C145P106ThinF_IMG_20151016_154719_cell_151.png	parasitized
3	C184P145ThinF_IMG_20151203_102543_cell_147.png	parasitized
4	C51AP12thinF_IMG_20150724_153313_cell_102.png	parasitized

```
uninf=list(zip(uninfected,['uninfected']*(len(uninfected))))
uninfected_df = pd.DataFrame(uninf,columns=['file','label'])
uninfected_df.head()
```

```
↳
```

```
          file      label
0  C149P110ThinF_IMG_20151115_114729_cell_8.png  uninfected
1  C78P39ThinF_IMG_20150606_104426_cell_24.png  uninfected
2  C67P28N_ThinF_IMG_20150819_133000_cell_23.png  uninfected
3  C33P1thinF_IMG_20150619_121102a_cell_176.png  uninfected

parasitized_df, parasitized_df1 = train_test_split(parasitized_df,
                                                    test_size=0.2,
                                                    random_state=0)

uninfected_df, uninfected_df1 = train_test_split(uninfected_df,
                                                test_size=0.2,
                                                random_state=0)

dataframe=pd.concat([parasitized_df, uninfected_df])
dataframe.head()
```

```
→          file      label
309  C144P105ThinF_IMG_20151015_160529_cell_271.png  parasitized
785  C132P93ThinF_IMG_20151004_151733_cell_150.png  parasitized
6887  C179P140ThinF_IMG_20151127_153521_cell_172.png  parasitized
7926  C175P136NThinF_IMG_20151127_141253_cell_249.png  parasitized
13767  C39P4thinF_original_IMG_20150622_110900_cell_1...  parasitized
```

```
dataframe1=pd.concat([parasitized_df1, uninfected_df1])
dataframe1.head()
```

```
→          file      label
1238  C51AP12thinF_IMG_20150724_153313_cell_99.png  parasitized
9320  C39P4thinF_original_IMG_20150622_111942_cell_1...  parasitized
8919  C179P140ThinF_IMG_20151127_153436_cell_174.png  parasitized
221   C39P4thinF_original_IMG_20150622_114804_cell_1...  parasitized
643   C126P87ThinF_IMG_20151004_104408_cell_168.png  parasitized
```

```
df = pd.get_dummies(dataframe['label'])
df.head()
```

```
→
```

```

import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from albumentations import *

aug=Compose([
    RandomRotate90(),
    Flip(),
    Transpose(),
    OneOf([
        IAAAdditiveGaussianNoise(),
        GaussNoise(),], p=0.2),
    OneOf([
        MotionBlur(p=.2),
        MedianBlur(blur_limit=3, p=.1),
        Blur(blur_limit=3, p=.1),], p=0.3),
    ShiftScaleRotate(shift_limit=0.0625,
                      scale_limit=0.2,
                      rotate_limit=45, p=.2),
    OneOf([
        OpticalDistortion(p=0.3),
        GridDistortion(p=.1),
        IAAPiecewiseAffine(p=0.3),], p=0.3),
    OneOf([
        CLAHE(clip_limit=2),
        IAASharpen(),
        IAAEmboss(),
        RandomContrast(),
        RandomBrightness(),], p=0.3),
    #HueSaturationValue(p=0.3),
    ], p=1)

from ImageDataAugmentor.image_data_augmentor import *

data_gen= ImageDataAugmentor(rescale=1/255, augment=aug)

img_shape=224
batch_size=16

from tensorflow.keras.models import Sequential,Model
from tensorflow.keras.layers import Activation, Dropout, Flatten, Dense, \
                                    Conv2D, MaxPool2D, BatchNormalization, \
                                    Input, MaxPooling2D, GlobalMaxPooling2D, \
                                    concatenate
from tensorflow.keras.layers import GlobalAveragePooling2D
from tensorflow.keras.applications.resnet50 import ResNet50
from tensorflow.keras.callbacks import ModelCheckpoint,ReduceLROnPlateau
from tensorflow.keras.optimizers import Adam
import tensorflow.keras.backend as K
import tensorflow as tf
import random
from sklearn.metrics import confusion_matrix

random.seed(1234)
from sklearn.model_selection import KFold
from sklearn.model_selection import StratifiedKFold
import gc
import seaborn as sns
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score

```

```
parasitized uninfected
```

```
df1 = pd.get_dummies(dataframe1['label'])  
df1.head()
```

```
↳      parasitized uninfected
```

	parasitized	uninfected
1238	1	0
9320	1	0
8919	1	0
221	1	0
643	1	0

```
df = pd.concat([dataframe, df], axis=1)  
df.head()
```

```
↳      file      label  parasitized  uninfected
```

	file	label	parasitized	uninfected
309	C144P105ThinF_IMG_20151015_160529_cell_271.png	parasitized	1	0
785	C132P93ThinF_IMG_20151004_151733_cell_150.png	parasitized	1	0
6887	C179P140ThinF_IMG_20151127_153521_cell_172.png	parasitized	1	0
7926	C175P136NThinF_IMG_20151127_141253_cell_249.png	parasitized	1	0
13767	C39P4thinF_original_IMG_20150622_110900_cell_1...	parasitized	1	0

```
df1 = pd.concat([dataframe1, df1], axis=1)  
df1.head()
```

```
↳      file      label  parasitized  uninfected
```

	file	label	parasitized	uninfected
1238	C51AP12thinF_IMG_20150724_153313_cell_99.png	parasitized	1	0
9320	C39P4thinF_original_IMG_20150622_111942_cell_1...	parasitized	1	0
8919	C179P140ThinF_IMG_20151127_153436_cell_174.png	parasitized	1	0
221	C39P4thinF_original_IMG_20150622_114804_cell_1...	parasitized	1	0
643	C126P87ThinF_IMG_20151004_104408_cell_168.png	parasitized	1	0

```
df.shape
```

```
↳  (22048, 4)
```

```
df1.shape
```

```
↳  (5512, 4)
```

```
!mkdir data  
!cp -r cell_images/Parasitized/* data  
!cp -r cell_images/Uninfected/* data
```



```

        monitor='val_loss',
        mode='min')
    ])
model.load_weights('model_{}.hdf5'.format(fold))
model.save('final_model_{}'.format(fold))
val_generator.reset()
y_pred=model.predict(val_generator,
                      steps=val_generator.n/batch_size,
                      verbose=1)
y_pred=y_pred.round().astype(int)
y_true=val.iloc[:,2::]
y_true = y_true[0:len(y_pred)]
classification_reports.append(classification_report(y_true,
                                                      y_pred,
                                                      target_names=['parasitized',
                                                                     'uninfected'],
                                                      digits=6))
accuracy.append(accuracy_score(y_true,y_pred))
f1=f1_score(y_true,y_pred,average='macro')
print('f1 score is ', f1)
f1_scores.append(f1)
fold+=1
cm=confusion_matrix(y_true.values.argmax(axis=1), y_pred.argmax(axis=1))
plt.figure(figsize=(5.5,4))
sns.heatmap(cm, annot=True)
plt.title('Malaria Classifier \nAccuracy:{0:.4f}'.format(
            accuracy_score(y_true, y_pred)))
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()
plt.plot(results.history['accuracy'])
plt.plot(results.history['val_accuracy'])
plt.title('model accuracy')
plt.ylabel('accuracy')
plt.xlabel('epoch')
plt.legend(['train', 'test'], loc='upper left')
plt.show()
plt.plot(results.history['loss'])
plt.plot(results.history['val_loss'])
plt.title('model loss')
plt.ylabel('loss')
plt.xlabel('epoch')
plt.legend(['train', 'test'], loc='upper left')
plt.show()
from itertools import cycle
plt.style.use('ggplot')
fpr = dict()
tpr = dict()
roc_auc = dict()
n_classes=2

for i in range(n_classes):
    fpr[i], tpr[i], _ = roc_curve(y_true.values[:, i], y_pred[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i])

```

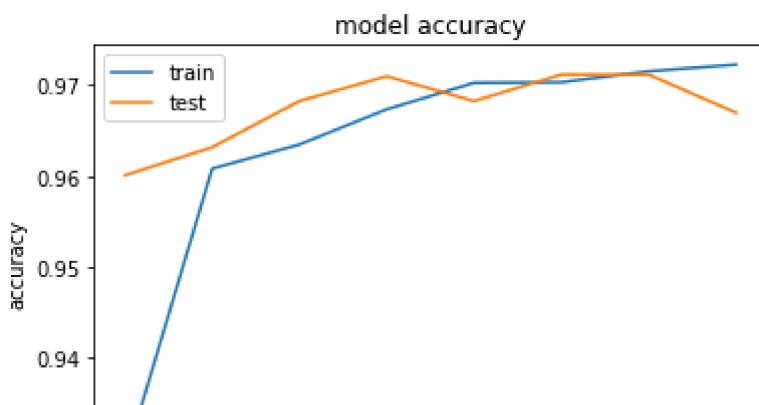
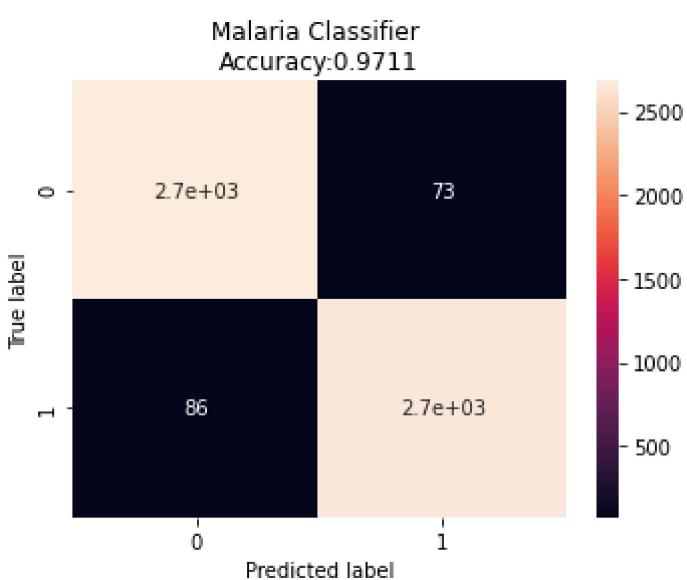
```
colors = cycle(['blue', 'red'])
for i, color in zip(range(n_classes), colors):
    plt.plot(fpr[i], tpr[i], color=color, lw=1.5,
              label='ROC curve of class {0} (area = {1:0.2f})'.format(i+1,
                                                                        roc_auc[i]))
plt.plot([0, 1], [0, 1], 'k-', lw=1.5)
plt.xlim([-0.05, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver operating characteristic for binary-class data')
plt.legend(loc="lower right")
plt.show()
del model
tf.keras.backend.clear_session()
gc.collect()
```

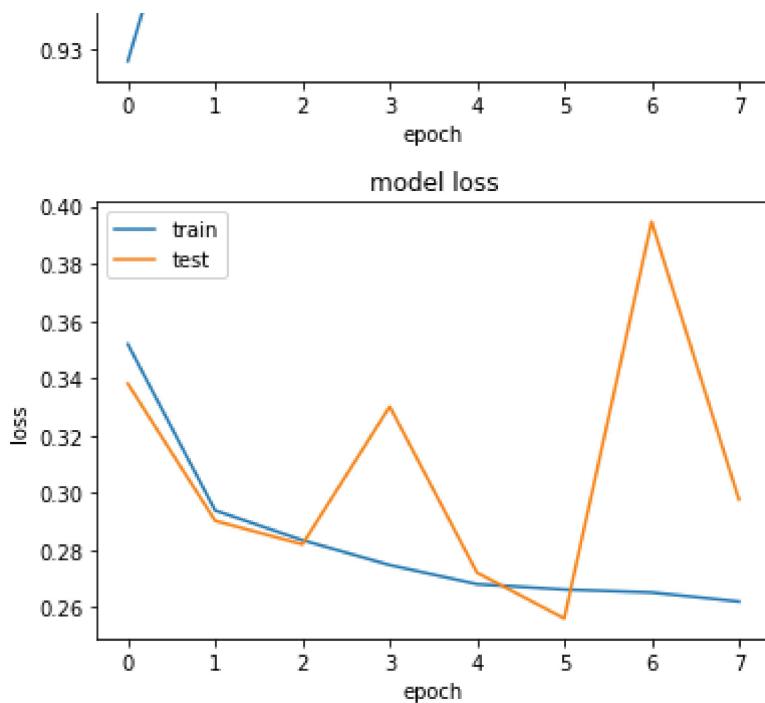
➡

```

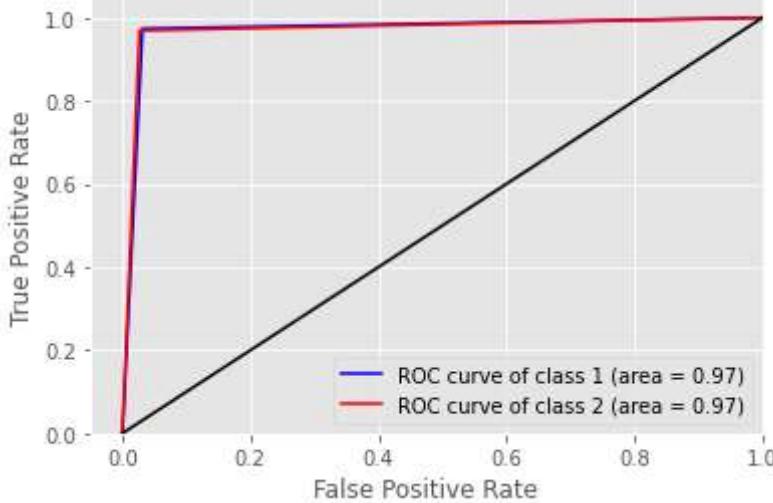
/usr/local/lib/python3.6/dist-packages/statsmodels/tools/_testing.py:19: FutureWarning: pandas
    import pandas.util.testing as tm
/usr/local/lib/python3.6/dist-packages/ImageDataAugmentor/dataframe_iterator.py:276: UserWarning
    .format(n_invalid, x_col)
-----fold 0-----
Found 16535 validated image filenames.
Found 5511 validated image filenames.
Downloading data from https://github.com/qubvel/efficientnet/releases/download/v0.0.1/efficientnet-b0-71680000/71678424 [=====] - 2s 0us/step
Epoch 1/8
1034/1033 [=====] - 541s 523ms/step - loss: 0.3519 - accuracy: 0.9286
Epoch 2/8
1034/1033 [=====] - 537s 520ms/step - loss: 0.2939 - accuracy: 0.9608
Epoch 3/8
1034/1033 [=====] - 518s 501ms/step - loss: 0.2835 - accuracy: 0.9635
Epoch 4/8
1034/1033 [=====] - 520s 503ms/step - loss: 0.2748 - accuracy: 0.9673
Epoch 5/8
1034/1033 [=====] - 512s 495ms/step - loss: 0.2681 - accuracy: 0.9702
Epoch 6/8
1034/1033 [=====] - 515s 498ms/step - loss: 0.2663 - accuracy: 0.9703
Epoch 7/8
1034/1033 [=====] - 509s 492ms/step - loss: 0.2652 - accuracy: 0.9715
Epoch 8/8
1034/1033 [=====] - 510s 493ms/step - loss: 0.2621 - accuracy: 0.9722
WARNING:tensorflow:From /usr/local/lib/python3.6/dist-packages/tensorflow/python/training/trac
Instructions for updating:
This property should not be used in TensorFlow 2.0, as updates are applied automatically.
WARNING:tensorflow:From /usr/local/lib/python3.6/dist-packages/tensorflow/python/training/trac
Instructions for updating:
This property should not be used in TensorFlow 2.0, as updates are applied automatically.
INFO:tensorflow:Assets written to: final_model_0/assets
345/344 [=====] - 88s 255ms/step
f1 score is 0.9711484256735678

```





Receiver operating characteristic for binary-class data



-----fold 1-----

Found 16534 validated image filenames.

Found 5512 validated image filenames.

```
/usr/local/lib/python3.6/dist-packages/ImageDataAugmentor/dataframe_iterator.py:276: UserWarning
    .format(n_invalid, x_col)
```

Epoch 1/8

```
1034/1033 [=====] - 519s 501ms/step - loss: 0.3588 - accuracy: 0.9210
```

Epoch 2/8

```
1034/1033 [=====] - 510s 493ms/step - loss: 0.2985 - accuracy: 0.9597
```

Epoch 3/8

```
1034/1033 [=====] - 512s 495ms/step - loss: 0.2871 - accuracy: 0.9623
```

Epoch 4/8

```
1034/1033 [=====] - 514s 497ms/step - loss: 0.2808 - accuracy: 0.9649
```

Epoch 5/8

```
1034/1033 [=====] - 515s 498ms/step - loss: 0.2749 - accuracy: 0.9677
```

Epoch 6/8

```
1034/1033 [=====] - 513s 496ms/step - loss: 0.2696 - accuracy: 0.9697
```

Epoch 7/8

```
1034/1033 [=====] - 510s 493ms/step - loss: 0.2672 - accuracy: 0.9712
```

Epoch 8/8

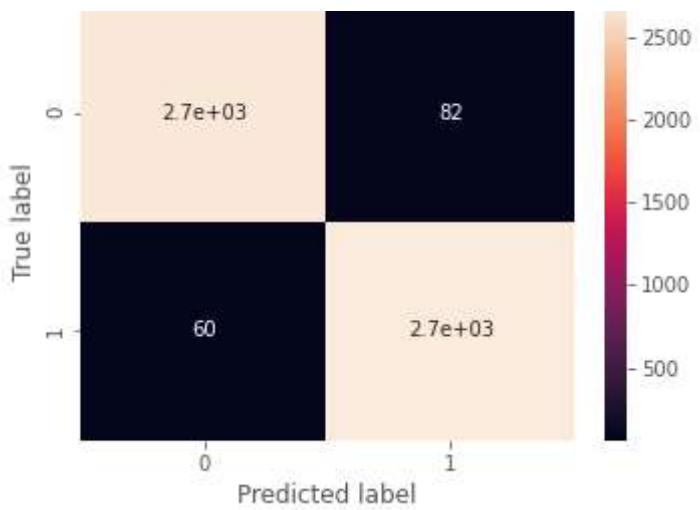
```
1034/1033 [=====] - 510s 493ms/step - loss: 0.2578 - accuracy: 0.9748
```

INFO:tensorflow:Assets written to: final_model_1/assets

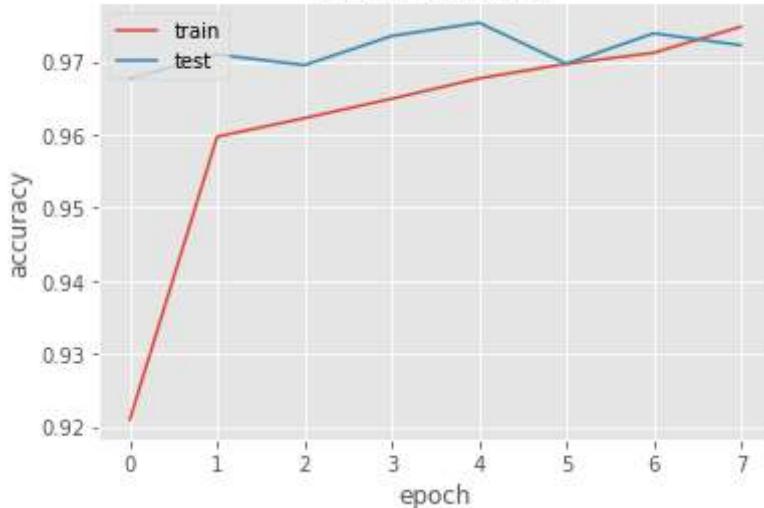
345/344 [=====] - 92s 266ms/step

f1 score is 0.9742376157194834

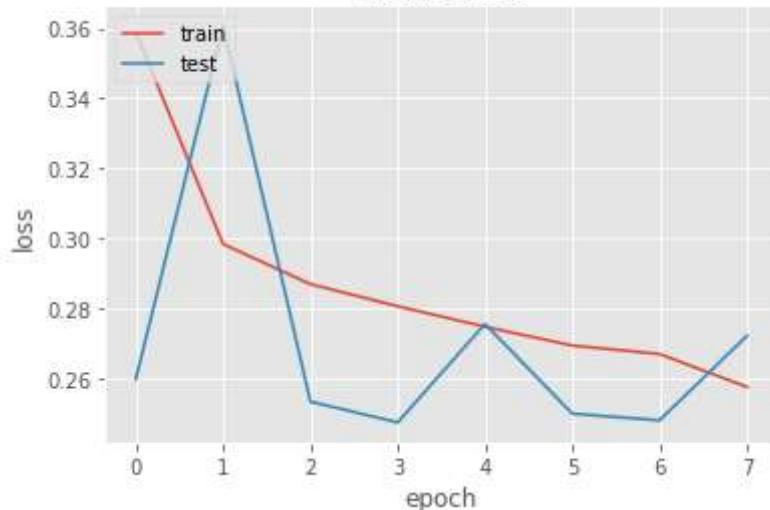
Malaria Classifier
Accuracy:0.9742



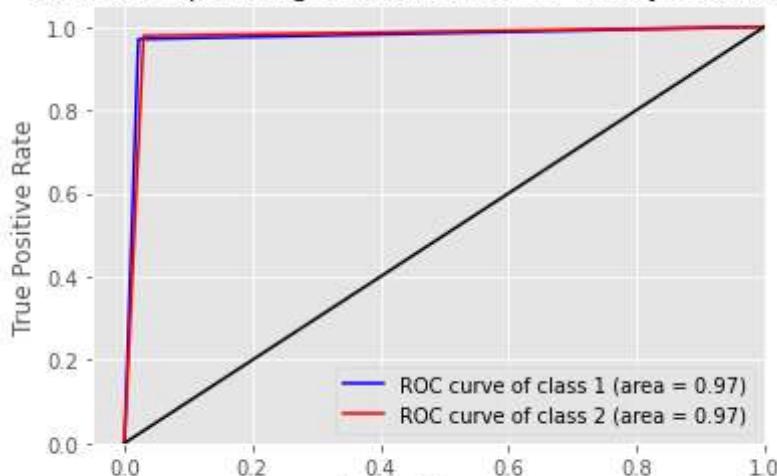
model accuracy



model loss



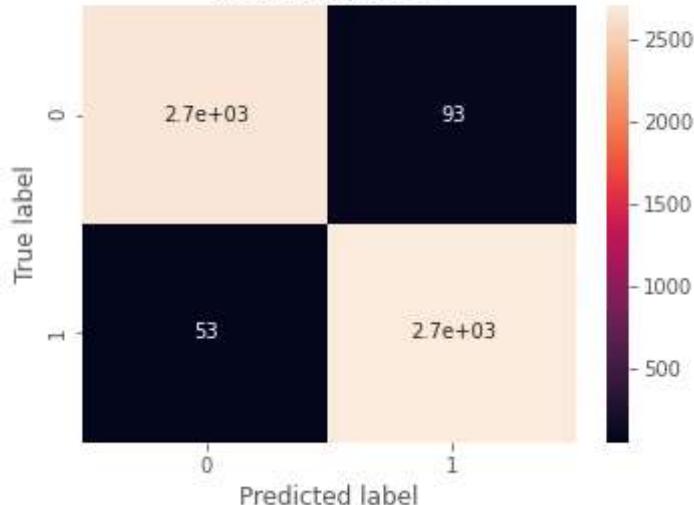
Receiver operating characteristic for binary-class data



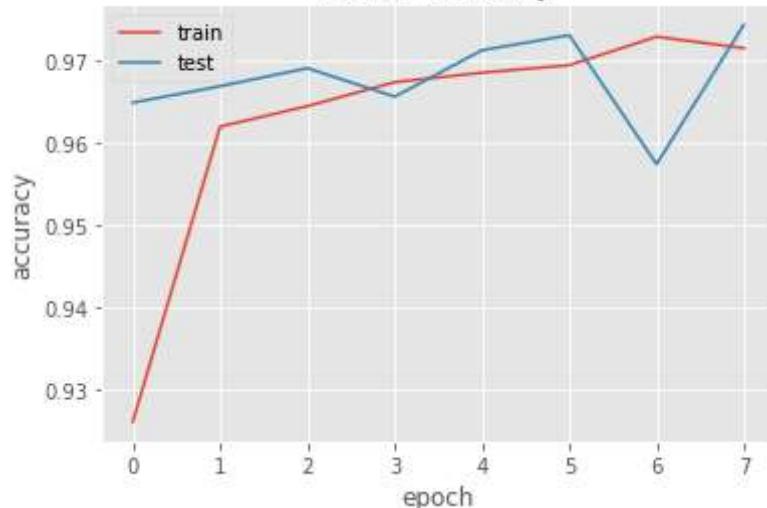
False Positive Rate

```
-----fold 2-----  
Found 16535 validated image filenames.  
Found 5511 validated image filenames.  
/usr/local/lib/python3.6/dist-packages/ImageDataAugmentor/dataframe_iterator.py:276: UserWarning  
    .format(n_invalid, x_col)  
Epoch 1/8  
1034/1033 [=====] - 518s 501ms/step - loss: 0.3516 - accuracy: 0.9262  
Epoch 2/8  
1034/1033 [=====] - 513s 496ms/step - loss: 0.2948 - accuracy: 0.9619  
Epoch 3/8  
1034/1033 [=====] - 507s 490ms/step - loss: 0.2833 - accuracy: 0.9644  
Epoch 4/8  
1034/1033 [=====] - 514s 497ms/step - loss: 0.2760 - accuracy: 0.9673  
Epoch 5/8  
1034/1033 [=====] - 515s 498ms/step - loss: 0.2722 - accuracy: 0.9684  
Epoch 6/8  
1034/1033 [=====] - 524s 507ms/step - loss: 0.2688 - accuracy: 0.9693  
Epoch 7/8  
1034/1033 [=====] - 515s 498ms/step - loss: 0.2641 - accuracy: 0.9728  
Epoch 8/8  
1034/1033 [=====] - 525s 507ms/step - loss: 0.2652 - accuracy: 0.9714  
INFO:tensorflow:Assets written to: final_model_2/assets  
345/344 [=====] - 93s 271ms/step  
f1 score is 0.973506203571993
```

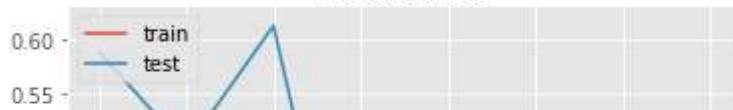
Malaria Classifier
Accuracy:0.9735

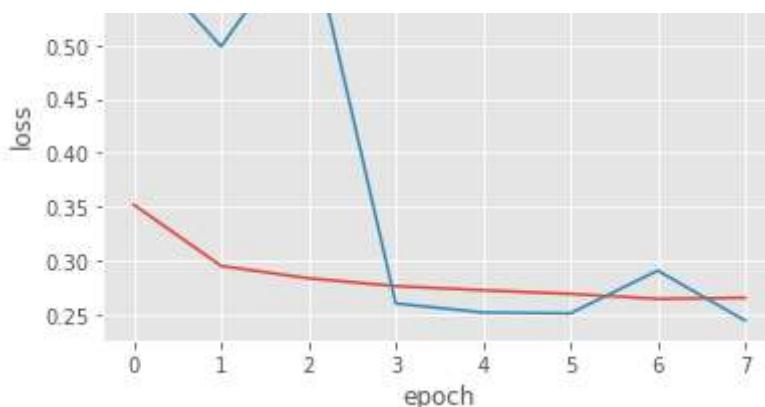


model accuracy

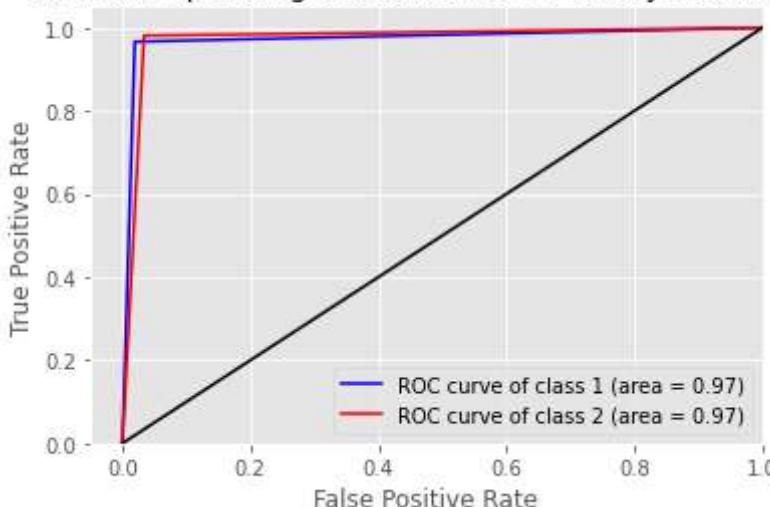


model loss





Receiver operating characteristic for binary-class data



-----fold 3-----

Found 16534 validated image filenames.

Found 5512 validated image filenames.

```
/usr/local/lib/python3.6/dist-packages/ImageDataAugmentor/dataframe_iterator.py:276: UserWarning
    .format(n_invalid, x_col)
```

Epoch 1/8

1034/1033 [=====] - 524s 507ms/step - loss: 0.3627 - accuracy: 0.9158

Epoch 2/8

1034/1033 [=====] - 530s 513ms/step - loss: 0.2951 - accuracy: 0.9600

Epoch 3/8

1034/1033 [=====] - 532s 514ms/step - loss: 0.2807 - accuracy: 0.9664

Epoch 4/8

1034/1033 [=====] - 533s 516ms/step - loss: 0.2754 - accuracy: 0.9676

Epoch 5/8

1034/1033 [=====] - 538s 521ms/step - loss: 0.2708 - accuracy: 0.9691

Epoch 6/8

1034/1033 [=====] - 543s 525ms/step - loss: 0.2640 - accuracy: 0.9719

Epoch 7/8

1034/1033 [=====] - 543s 525ms/step - loss: 0.2639 - accuracy: 0.9716

Epoch 8/8

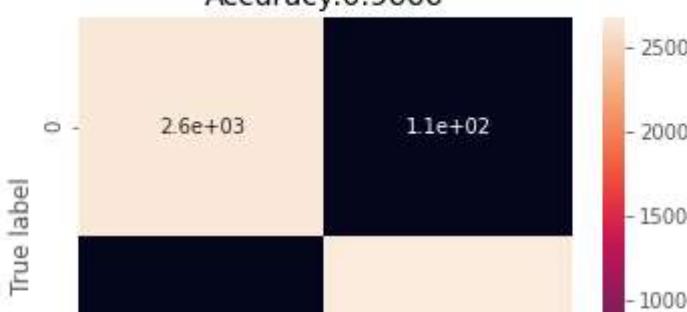
1034/1033 [=====] - 546s 528ms/step - loss: 0.2582 - accuracy: 0.9734

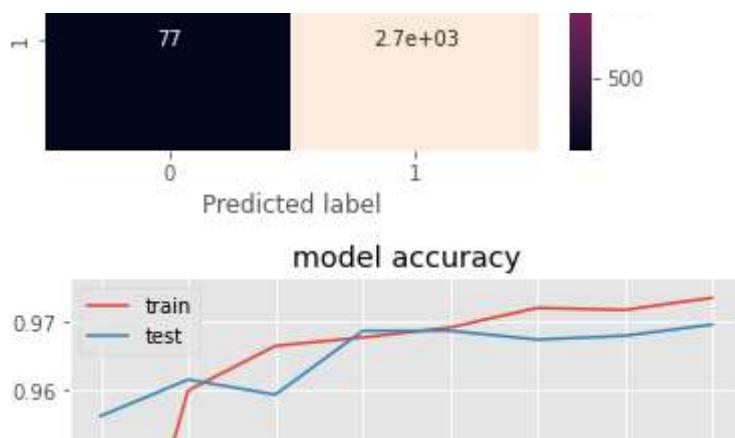
INFO:tensorflow:Assets written to: final_model_3/assets

345/344 [=====] - 99s 286ms/step

f1 score is 0.9666172984885016

Malaria Classifier
Accuracy:0.9666





accuracy

```
↳ [0.9711486118671747,  
 0.9742380261248186,  
 0.9735075303937579,  
 0.9666182873730044]
```



```
print(np.mean(accuracy))
```

```
↳ 0.971378113939689
```



f1_scores

```
↳ [0.9711484256735678, 0.9742376157194834, 0.973506203571993, 0.9666172984885016]
```



```
np.mean(f1_scores)
```

```
↳ 0.9713773858633865
```



```
for i in range(4):  
    print('-----FOLD {}-----'.format(i))  
    print(classification_reports[i])
```

```
↳
```

```

-----FOLD 0-----
      precision    recall   f1-score   support
parasitized    0.968942   0.973512   0.971222     2756
uninfected     0.973377   0.968784   0.971075     2755

   micro avg    0.971149   0.971149   0.971149     5511
   macro avg    0.971159   0.971148   0.971148     5511
weighted avg    0.971159   0.971149   0.971148     5511
samples avg    0.971149   0.971149   0.971149     5511

```

```

-----FOLD 1-----
      precision    recall   f1-score   support
parasitized    0.978054   0.970247   0.974135     2756
uninfected     0.970482   0.978229   0.974340     2756

   micro avg    0.974238   0.974238   0.974238     5512
   macro avg    0.974268   0.974238   0.974238     5512
weighted avg    0.974268   0.974238   0.974238     5512
samples avg    0.974238   0.974238   0.974238     5512

```

```

val=df1.iloc[:, :]
va_generator=data_gen.flow_from_dataframe(val,directory='data',
                                             target_size=(img_shape,img_shape),
                                             x_col="file",
                                             y_col=['parasitized','uninfected'],
                                             class_mode='raw',
                                             shuffle=False,
                                             batch_size=batch_size)

```

→ Found 5512 validated image filenames.

```

-----FOLD 3-----
import tensorflow as tf

model=tf.keras.models.load_model("final_model_3",compile=False)

y_pred=model.predict(va_generator,
                     steps=va_generator.n/batch_size,
                     verbose=1)

y_pred=y_pred.round().astype(int)
y_true=val.iloc[:,2::]
y_true = y_true[0:len(y_pred)]
print(classification_report(y_true, y_pred,
                            target_names=['parasitized','uninfected'], digits=6))
accuracy.append(accuracy_score(y_true,y_pred))
f1=f1_score(y_true,y_pred,average='macro')
print('f1 score is ', f1)
cm=confusion_matrix(y_true.values.argmax(axis=1), y_pred.argmax(axis=1))
plt.figure(figsize=(5.5,4))
sns.heatmap(cm, annot=True)
plt.title('Malaria Classifier \nAccuracy:{0:.4f}'.format(accuracy_score(y_true,
                                                                     y_pred)))
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()
from itertools import cycle
plt.style.use('ggplot')
```

```

plt.roc_curve(y_true, y_pred)
fpr = dict()
tpr = dict()
roc_auc = dict()
n_classes=2
for i in range(n_classes):
    fpr[i], tpr[i], _ = roc_curve(y_true.values[:, i], y_pred[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i])
colors = cycle(['blue', 'red'])
for i, color in zip(range(n_classes), colors):
    plt.plot(fpr[i], tpr[i], color=color, lw=1.5,
              label='ROC curve of class {0} (area = {1:0.2f})'.format(i+1,
                                                                        roc_auc[i]))
plt.plot([0, 1], [0, 1], 'k-', lw=1.5)
plt.xlim([-0.05, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver operating characteristic for binary-class data')
plt.legend(loc="lower right")
plt.show()
del model
tf.keras.backend.clear_session()
gc.collect()

```

➡

345/344 [=====] - 100s 291ms/step

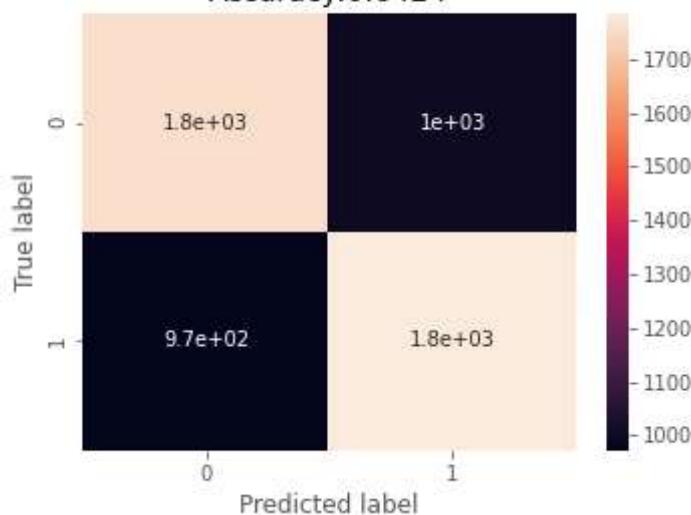
precision recall f1-score support

parasitized	0.643826	0.637518	0.640656	2756
uninfected	0.641035	0.647315	0.644160	2756
micro avg	0.642417	0.642417	0.642417	5512
macro avg	0.642430	0.642417	0.642408	5512
weighted avg	0.642430	0.642417	0.642408	5512
samples avg	0.642417	0.642417	0.642417	5512

f1 score is 0.6424079655276096

Malaria Classifier

Accuracy:0.6424



Receiver operating characteristic for binary-class data

