Malaria Bounding Boxes

Final Notebook

In [0]:

```
#Mouning Google Drive
from google.colab import drive
drive.mount('/content/drive',force_remount=True)
```

```
Go to this URL in a browser: https://accounts.google.com/o/oauth2/auth?client_id=947318989803-6bn6
qk8qdgf4n4g3pfee6491hc0brc4i.apps.googleusercontent.com&redirect_uri=urn%3aietf%3awg%3aoauth%3a2.0%
b&response_type=code&scope=email%20https%3a%2f%2fwww.googleapis.com%2fauth%2fdocs.test%20https%3a%2
www.googleapis.com%2fauth%2fdrive%20https%3a%2f%2fwww.googleapis.com%2fauth%2fdrive.photos.readonly
ttps%3a%2f%2fwww.googleapis.com%2fauth%2fpeopleapi.readonly

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

In [0]:

```
import cv2
import numpy as np
import pandas as pd
from sklearn.metrics import average_precision_score
from tqdm import tqdm
import pandas as pd
import matplotlib.pyplot as plt
from matplotlib import patches
import numpy as np
from os import path
import pandas as pd
import matplotlib.pyplot as plt
from matplotlib import patches
import numpy as np
from os import path
from tqdm import tqdm
import tensorflow.python.keras
from tensorflow.python.keras import models, layers
from tensorflow.python.keras.layers import SeparableConv2D, DepthwiseConv2D
from tensorflow.python.keras.models import Model, load_model
from tensorflow.python.keras.layers import BatchNormalization, Activation, Flatten
from tensorflow.python.keras.optimizers import Adam
from keras.preprocessing.image import ImageDataGenerator
```

```
The default version of TensorFlow in Colab will soon switch to TensorFlow 2.x.
We recommend you upgrade now or ensure your notebook will continue to use TensorFlow 1.x via the %tensorflow_version 1.x magic: more info.
```

```
Using TensorFlow backend.
```

Mean Average Precision

In [0]:

```
def map_value(annotate_path, result_df_path):
 """
  This Function takes annotations file path and path of result dataframe which genereates after ec
aluating test images
 """

 def get_data(input_path):
  """
   This Function takes annotations file path and gives a dictionory of ground truth labels and bou
nding boxes coordinates
```

```
  """

  img_data = []

  with open(input_path,'r') as f:
   for line in f:
    line_split = line.strip().split(',')
    (filename,x1,y1,x2,y2,class_name) = line_split

    img_data.append({'class': class_name, 'x1': int(x1), 'x2': int(x2), 'y1': int(y1), 'y2': int(y2
)})

  return img_data
 def union(au, bu, area_intersection):
  """
   This function gives the area of union for intersection over union calculation
  """
  area_a = (au[2] - au[0]) * (au[3] - au[1])
  area_b = (bu[2] - bu[0]) * (bu[3] - bu[1])
  area_union = area_a + area_b - area_intersection
  return area_union


 def intersection(ai, bi):
  """
   This function gives the area of intersection for intersection over union calculation

  """
  x = max(ai[0], bi[0])
  y = max(ai[1], bi[1])
  w = min(ai[2], bi[2]) - x
  h = min(ai[3], bi[3]) - y
  if w < 0 or h < 0:
   return 0
  return w*h

 def iou(a, b):
  # a and b should be (x1,y1,x2,y2)
  """
   This function takes two boxes cordinates(ground truth and predicted) and gives intersection ove
r union of 2 boxes

  """

  if a[0] >= a[2] or a[1] >= a[3] or b[0] >= b[2] or b[1] >= b[3]:
   return 0.0

  area_i = intersection(a, b)
  area_u = union(a, b, area_i)

  return float(area_i) / float(area_u + 1e-6)

 gt = get_data(annotate_path)
 pred = pd.read_csv(result_df_path)
 pred.columns = ["name", "class", "x1","y1","x2","y2", "prob"]
 Truth = {}
 Predicted = {}


 for bbox in gt:
  bbox['bbox_matched'] = False

 pred_probs = np.array(pred["prob"])
 box_idx_sorted_by_prob = np.argsort(pred_probs)[::-1]
 # we compare each predicted bounding box with ground truth bounding box
 for box_idx in tqdm(box_idx_sorted_by_prob):
  pred_box = pred.loc[box_idx]
  pred_class = pred_box['class']
  pred_x1 = pred_box['x1']
  pred_x2 = pred_box['x2']
  pred_y1 = pred_box['y1']
  pred_y2 = pred_box['y2']
  pred_prob = pred_box['prob']
  if pred_class not in Predicted:
   Predicted[pred_class] = []
   Truth[pred_class] = []
```

```
  Predicted[pred_class].append(pred_prob)
  found_match = False
  for gt_box in gt:
   gt_class = gt_box['class']
   gt_x1 = gt_box['x1']
   gt_x2 = gt_box['x2']
   gt_y1 = gt_box['y1']
   gt_y2 = gt_box['y2']
   gt_seen = gt_box['bbox_matched']
   if gt_class != pred_class:
    continue
   if gt_seen:
    continue
   iou1 = iou((pred_x1, pred_y1, pred_x2, pred_y2), (gt_x1, gt_y1, gt_x2, gt_y2))
  # taking 0.5 as threshold i.e. if iou is greater than 0.5 then only it will consider as correct
matching
   if iou1 >= 0.5:
    found_match = True
    gt_box['bbox_matched'] = True
    break
   else:
    continue


  Truth[pred_class].append(int(found_match))

 for gt_box in gt:
  if not gt_box['bbox_matched']:
   if gt_box['class'] not in Predicted:
    Predicted[gt_box['class']] = []
    Truth[gt_box['class']] = []

   Truth[gt_box['class']].append(1)
   Predicted[gt_box['class']].append(0)
 t = {}
 p = {}
 for key in Truth.keys():
   if key not in t:
    t[key] = []
    p[key] = []
   t[key].extend(Truth[key])
   p[key].extend(Predicted[key])

 all_aps = []
 for key in t.keys():
  ap = average_precision_score(t[key], p[key])
  print('{} AP: {}'.format(key, ap))
  all_aps.append(ap)
 print('mAP = {}'.format(np.mean(np.array(all_aps))))
```

loading second level classifier best weights

In [0]:

```
def denseblock(input, num_filter = 12, dropout_rate = 0.5):
    global compression
    temp = input
    for _ in range(l):
        BatchNorm = layers.BatchNormalization()(temp)
        relu = layers.Activation('relu')(BatchNorm)
        Conv2D_3_3 = layers.SeparableConv2D(int(num_filter*compression), (5,5), use_bias=False ,pad
ding='same')(relu)
        if dropout_rate>0:
            Conv2D_3_3 = layers.Dropout(dropout_rate)(Conv2D_3_3)
        concat = layers.Concatenate(axis=-1)([temp,Conv2D_3_3])

        temp = concat

    return temp

## transition Blosck
def transition(input, num_filter = 12, dropout_rate = 0.5):
    global compression
    BatchNorm = layers.BatchNormalization()(input)
```

```
    relu = layers.Activation('relu')(BatchNorm)
    Conv2D_BottleNeck = layers.SeparableConv2D(int(num_filter*compression), (7,7), use_bias=False,p
adding='same')(relu)
    if dropout_rate>0:
         Conv2D_BottleNeck = layers.Dropout(dropout_rate)(Conv2D_BottleNeck)
    avg = layers.AveragePooling2D(pool_size=(2,2))(Conv2D_BottleNeck)
    return avg

#output layer
def output_layer(input):
    global compression
    BatchNorm = layers.BatchNormalization()(input)
    relu = layers.Activation('relu')(BatchNorm)
    AvgPooling = layers.AveragePooling2D(pool_size=(2,2))(relu)
    flat = layers.Flatten()(AvgPooling)
    output = layers.Dense(num_classes, activation='softmax')(flat)
    return output
num_filter = 64
batch_size = 32
num_classes = 6
epochs = 100
l = 10
compression = 0.45
dropout_rate = 0
input = layers.Input(shape=(32, 32, 3,))
First_Conv2D = layers.SeparableConv2D(num_filter, (5,5), use_bias=False, padding='same')(input)

First_Block = denseblock(First_Conv2D, num_filter, dropout_rate)
First_Transition = transition(First_Block, num_filter, dropout_rate)

Second_Block = denseblock(First_Transition, num_filter, dropout_rate)
Second_Transition = transition(Second_Block, num_filter, dropout_rate)

Third_Block = denseblock(Second_Transition, num_filter, dropout_rate)
Third_Transition = transition(Third_Block, num_filter, dropout_rate)

Last_Block = denseblock(Third_Transition,  num_filter, dropout_rate)
output = output_layer(Last_Block)
model = Model(inputs=[input], outputs=[output])
model.load_weights("/content/drive/My Drive/rcnn/second_classifier_checkpoint/epochs:030-
val_acc:0.715.hdf5")
```

```
WARNING:tensorflow:From /usr/local/lib/python3.6/dist-
packages/tensorflow_core/python/ops/resource_variable_ops.py:1630: calling
BaseResourceVariable.__init__ (from tensorflow.python.ops.resource_variable_ops) with constraint i
s deprecated and will be removed in a future version.
Instructions for updating:
If using Keras pass *_constraint arguments to layers.
```

Function to print images

In [0]:

```
def predicted(image_name):

   """
   This function takes imag name and prints original image, predicted images of first lavel classi
fier and second level classifier

   """
  #print("Original Image with ground truth bounding boxes and labels")

   fig = plt.figure(figsize=(12,6))
   ax = fig.add_axes([0,0,1,1])
   ax.set_title("Original Image with ground truth bounding boxes and labels")

  # read and plot the image
   image = plt.imread('/content/drive/My Drive/rcnn/test_images/'+image_name)
   plt.imshow(image)
   edgecolor = 'r'
   test_df = pd.read_csv("/content/drive/My Drive/rcnn/test_df.csv")
  # iterating over the image for different objects
   for _,row in test_df[test_df["image"]=="/images/"+image_name].iterrows():
        xmin = row.x_min
```

```
        xmin = row.x_min
        #print(xmin)
        xmax = row.x_max
        ymin = row.y_min
        ymax = row.y_max
        width = xmax - xmin
        height = ymax - ymin
       # assign different color to different classes of objects
        if row.class_label == 'red blood cell':
            edgecolor = 'r'

            ax.annotate('RBC', xy=(xmax-40,ymin+20))

        elif row.class_label == 'trophozoite':
            edgecolor = 'b'
            ax.annotate('trophozoite', xy=(xmax-40,ymin+20))
        elif row.class_label == 'difficult':
            edgecolor = 'b'
            ax.annotate('difficult', xy=(xmax-40,ymin+20))
        elif row.class_label == 'ring':
            edgecolor = 'b'
            ax.annotate('ring', xy=(xmax-40,ymin+20))
        elif row.class_label == 'schizont':
            edgecolor = 'b'
            ax.annotate('schizont', xy=(xmax-40,ymin+20))
        elif row.class_label == 'gametocyte':
            edgecolor = 'b'
            ax.annotate('gametocyte', xy=(xmax-40,ymin+20))
        elif row.class_label == 'leukocyte':
            edgecolor = 'b'
            ax.annotate('leukocyte', xy=(xmax-40,ymin+20))

       # add bounding boxes to the image
        rect = patches.Rectangle((xmin,ymin), width, height, edgecolor = edgecolor, facecolor = 'non
e')

        ax.add_patch(rect)

   #print("Prediction after first classifier(which classifies RBC and OTHER)")
   fig = plt.figure(figsize=(12,6))
   ax = fig.add_axes([0,0,1,1])
   ax.set_title("Prediction after first classifier(which classifies RBC and OTHER)")

   # read and plot the image
   image = plt.imread('/content/drive/My Drive/rcnn/test_images/' + image_name)
   plt.imshow(image)
   result_df_2class = pd.read_csv("/content/drive/My Drive/rcnn/Data_model_2/result_df_2class.csv"
)


  # iterating over the image for different objects
   for _,row in result_df_2class.loc[result_df_2class["name"]==image_name].iterrows():
        xmin = row.x1
        #print(xmin)
        xmax = row.x2
        ymin = row.y1
        ymax = row.y2

        width = xmax - xmin
        height = ymax - ymin
        # assign different color to different classes of objects
        if row.label == 'other':
            edgecolor = 'b'
            ax.annotate('other', xy=(xmax-40,ymin+20))

        elif row.label == 'RBC':
            edgecolor = 'r'
            ax.annotate('RBC', xy=(xmax-40,ymin+20))

        # add bounding boxes to the image

        rect = patches.Rectangle((xmin,ymin), width, height, edgecolor = edgecolor, facecolor = 'non
e')
        ax.add_patch(rect)
   testing_image = result_df_2class[result_df_2class["label"]=="other"][result_df_2class["name"]==i
mage_name]
   testing_image.reset_index(inplace=True)
   if (testing_image.shape[0] != 0):
```

```
    if (testing_image.shape[0] != 0):

      import cv2
      from tqdm import tqdm
      testing_img_arrays = []
      y = []
      WIDTH = 32
      HEIGHT = 32

      for i in range(testing_image.shape[0]):
        image = plt.imread('/content/drive/My Drive/rcnn/test_images/'+image_name)
        image_crop = image[testing_image["y1"][i]:testing_image["y2"][i],testing_image["x1"][i]:test
ing_image["x2"][i]]
        testing_img_arrays.append(cv2.resize(image_crop, (WIDTH,HEIGHT), interpolation=cv2.INTER_CUB
IC))
      testing_img_arrays_final = np.array(testing_img_arrays)
      model.load_weights("/content/drive/My Drive/rcnn/second_classifier_checkpoint/epochs:030-
val_acc:0.715.hdf5")
      model_prediction = model.predict(testing_img_arrays_final)
      result_label = np.argmax(model_prediction, axis=1)
      feature_names = ['difficult', 'gametocyte', 'leukocyte', 'ring', 'schizont', 'trophozoite']
      fig = plt.figure(figsize=(12,6))
      ax = fig.add_axes([0,0,1,1])

     # read and plot the image
      image = plt.imread('/content/drive/My Drive/rcnn/test_images/'+image_name)
      plt.imshow(image)
      ax.set_title("prediction after second classifier(final prediction)")
      i=0

     # iterating over the image for different objects
      for _,row in result_df_2class[result_df_2class["name"]==image_name].iterrows():
          xmin = row.x1
          #print(xmin)
          xmax = row.x2
          ymin = row.y1
          ymax = row.y2

          width = xmax - xmin
          height = ymax - ymin
          # assign different color to different classes of objects
          if row.label == 'other':
              edgecolor = 'b'
              ax.annotate(feature_names[result_label[i]], xy=(xmax-40,ymin+20))
              i = i+1
          elif row.label == 'RBC':
              edgecolor = 'r'
              ax.annotate('RBC', xy=(xmax-40,ymin+20))

         # add bounding boxes to the image
          rect = patches.Rectangle((xmin,ymin), width, height, edgecolor = edgecolor, facecolor = 'n
one')

          ax.add_patch(rect)
```

Final Results

map of Test Data

In [0]:

```
print("MAP of test DATA:")
map_value("/content/drive/My Drive/rcnn/annotate_test_2class.txt","/content/drive/My
Drive/rcnn/Data_model_2/result_df_2class.csv")
```

```
MAP of test DATA:

100%|██████████| 9195/9195 [01:22<00:00, 111.75it/s]

other AP: 0.960051090010949
RBC AP: 0.998090609353597
mAP = 0.979070849682273
```

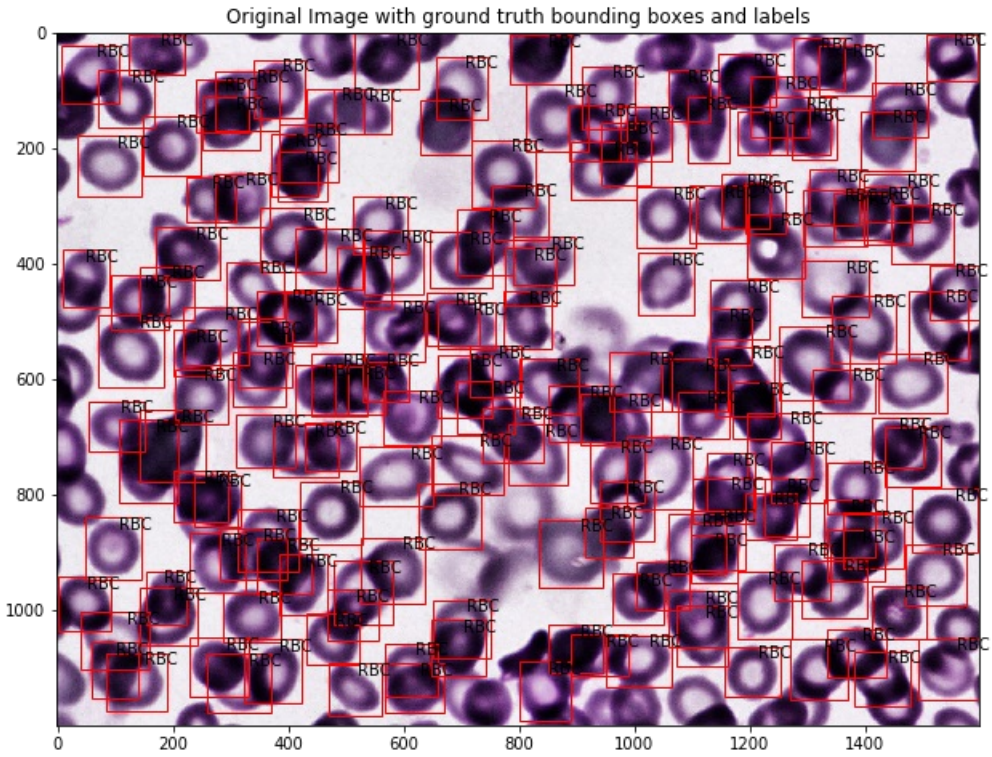
Image Predictions

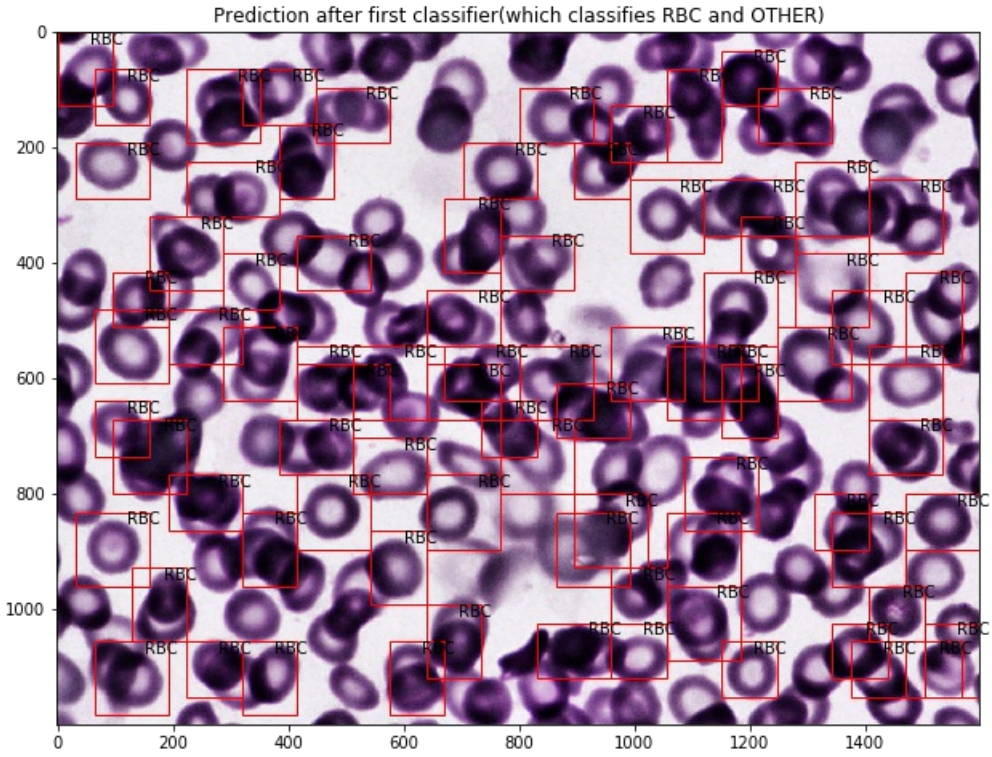
- sample_image:1 ***Image with more nubmer of cells***

In [0]:

```
predicted("46a2d369-4bea-4405-ac78-91bbe130b9a7.png")
```

```
/usr/local/lib/python3.6/dist-packages/ipykernel_launcher.py:85: UserWarning: Boolean Series key w
ill be reindexed to match DataFrame index.
```



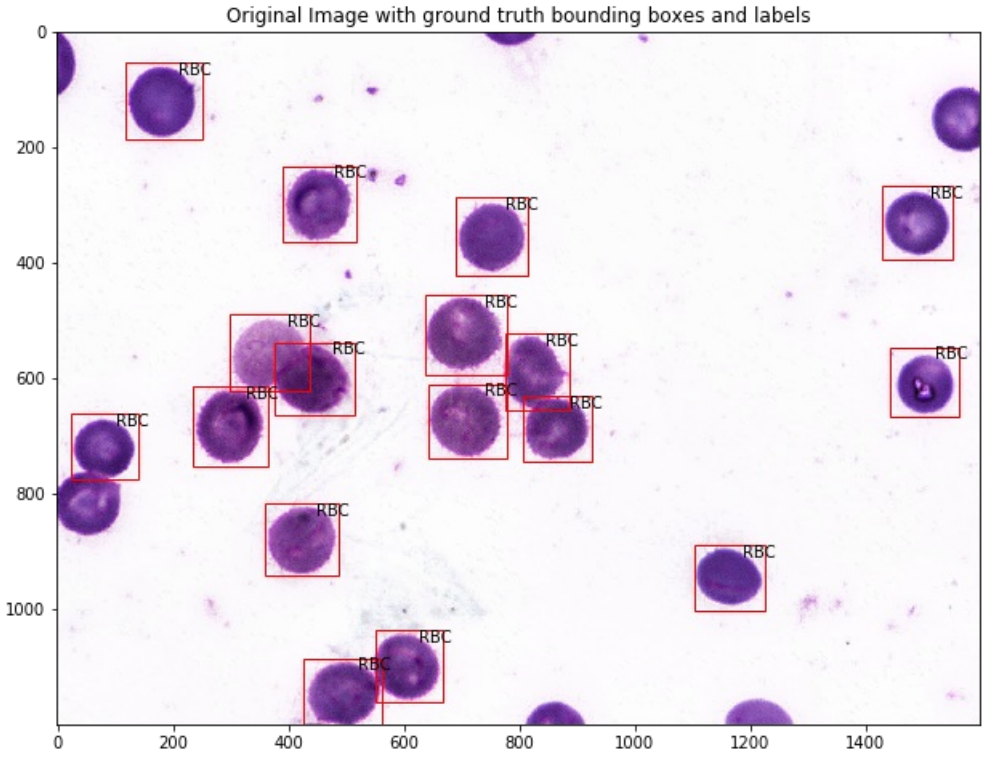


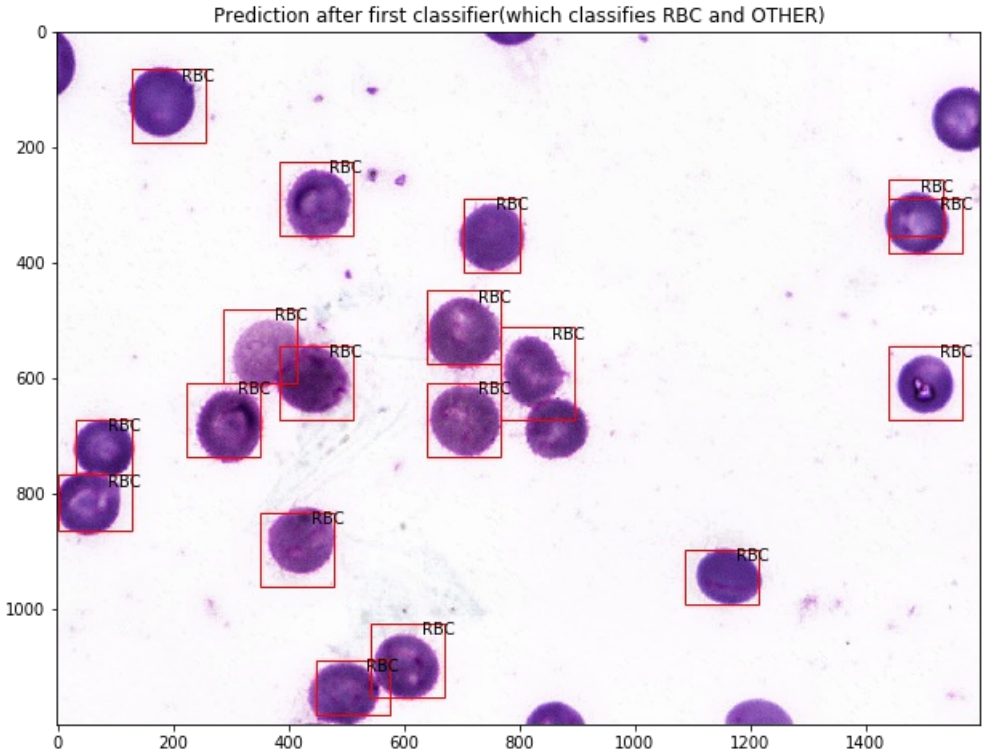
- sample_image:2 ***Image with very few cells***

In [0]:

```
predicted("c3209548-7f7c-4afd-b47c-b42a72b1ebf7.png")
```

```
/usr/local/lib/python3.6/dist-packages/ipykernel_launcher.py:85: UserWarning: Boolean Series key w
ill be reindexed to match DataFrame index.
```



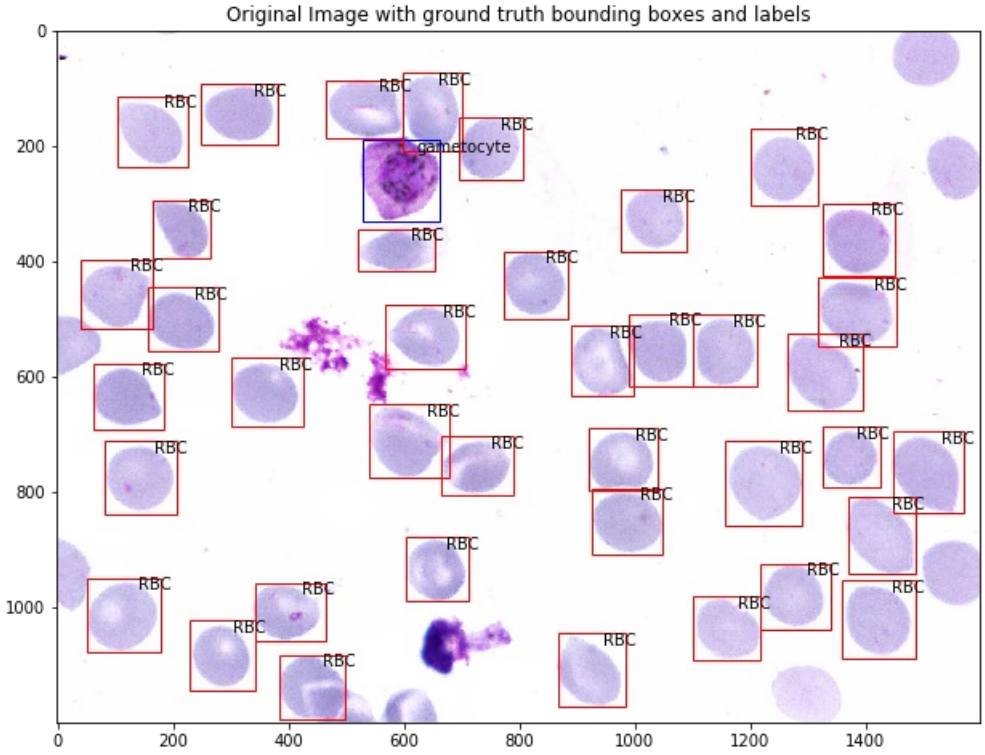


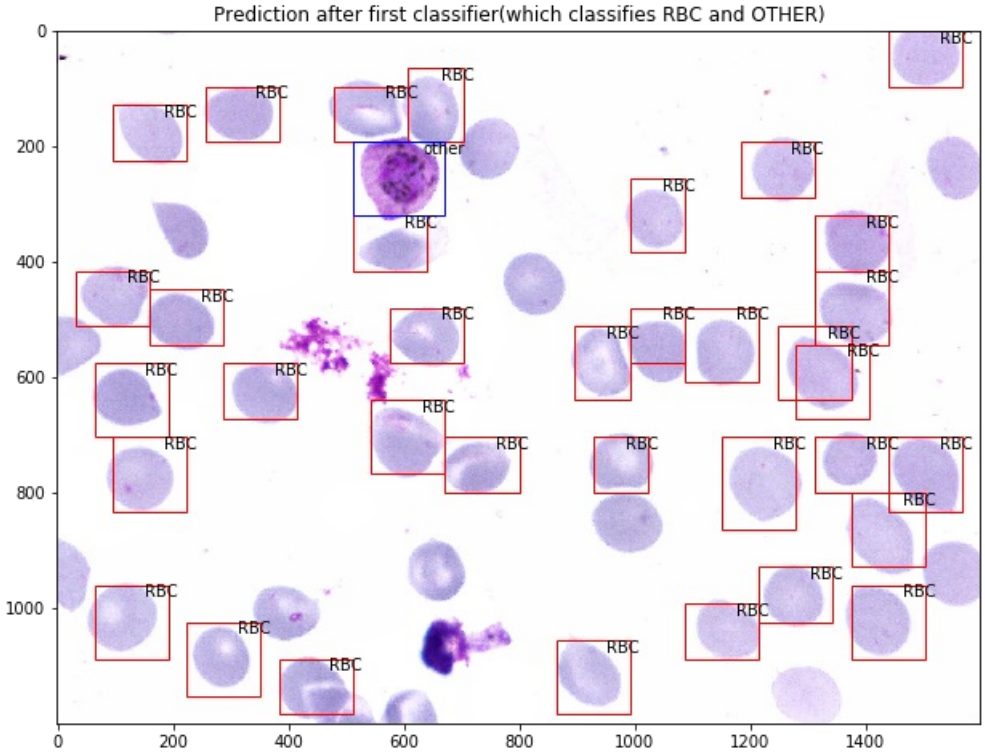
- sample_image:3

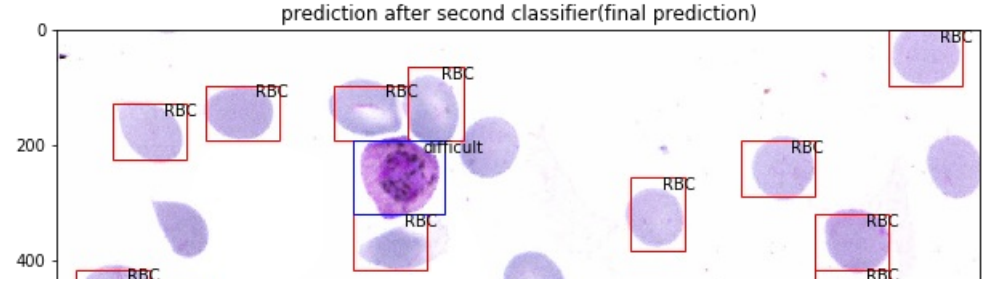
In [0]:

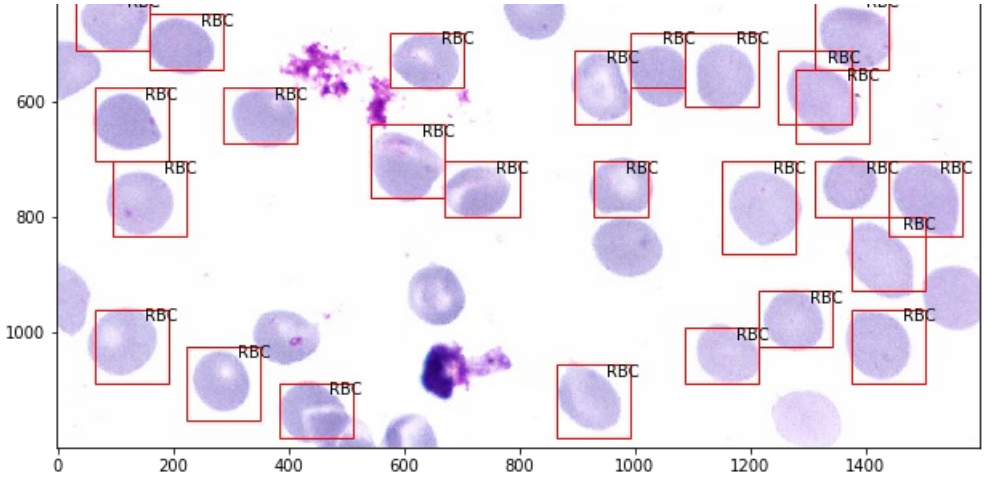
```
predicted("04de27ff-0d36-4da3-a829-e93851d76981.png")
```

```
/usr/local/lib/python3.6/dist-packages/ipykernel_launcher.py:85: UserWarning: Boolean Series key w
ill be reindexed to match DataFrame index.
```









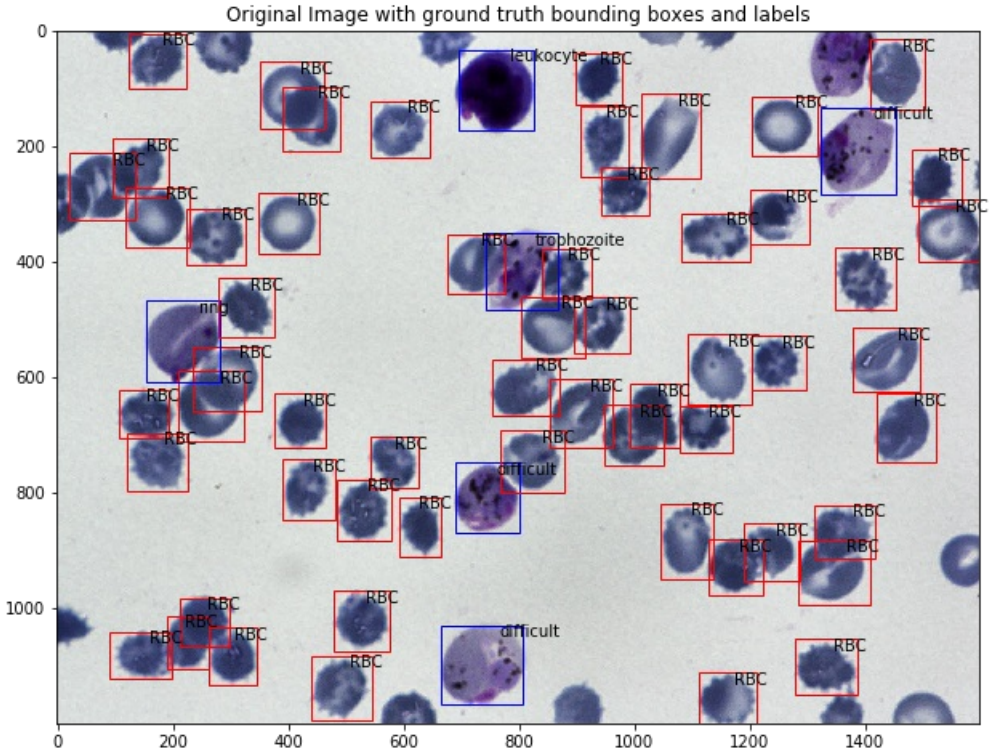
- First level classifier predicting correctly and in this image we have "gametocyte" but our model is predicting as difficult, but difficult class consists of the cells which are difficult to classify. So if our model predict class as difficult we have to manually classify the cell.

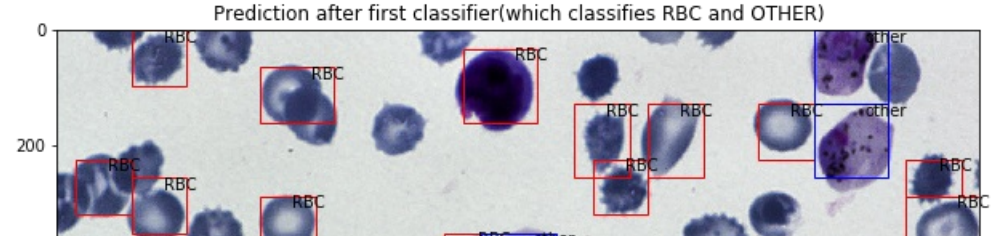
- sample_image:4

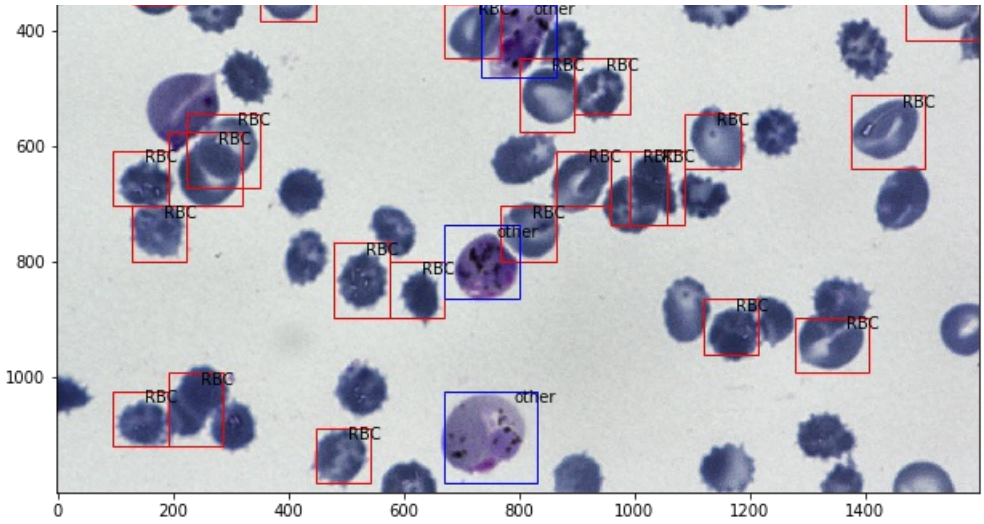
In [0]:

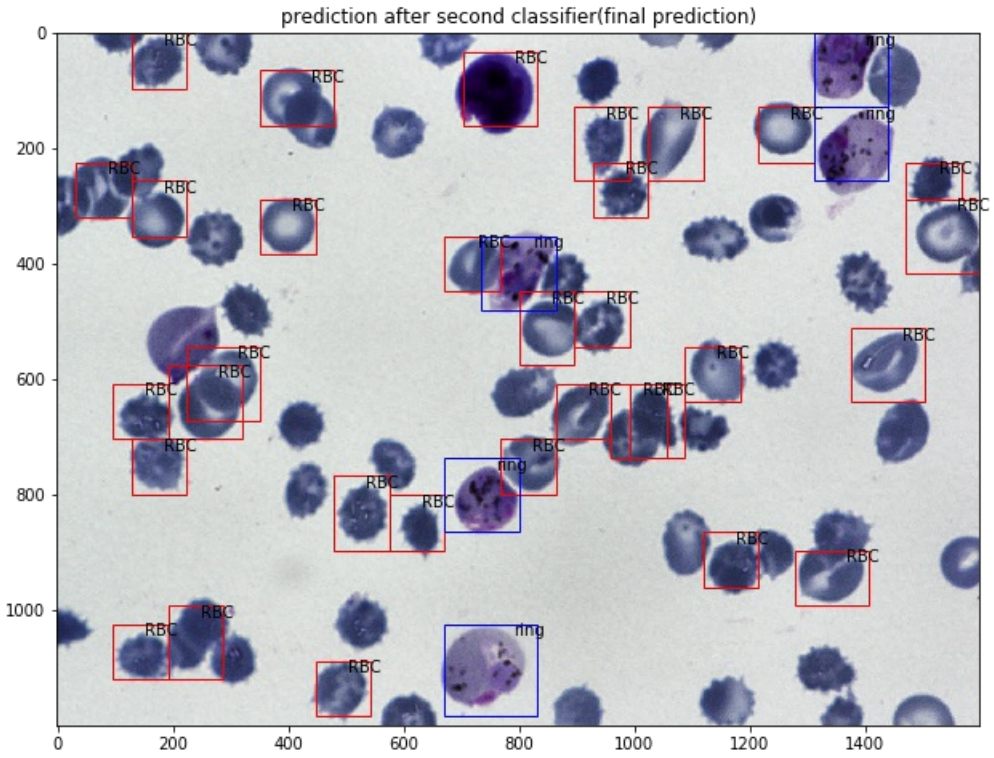
```
predicted("be6fe358-dee1-4dcf-9b0d-5d8612aba577.png")
```

```
/usr/local/lib/python3.6/dist-packages/ipykernel_launcher.py:85: UserWarning: Boolean Series key w
ill be reindexed to match DataFrame index.
```









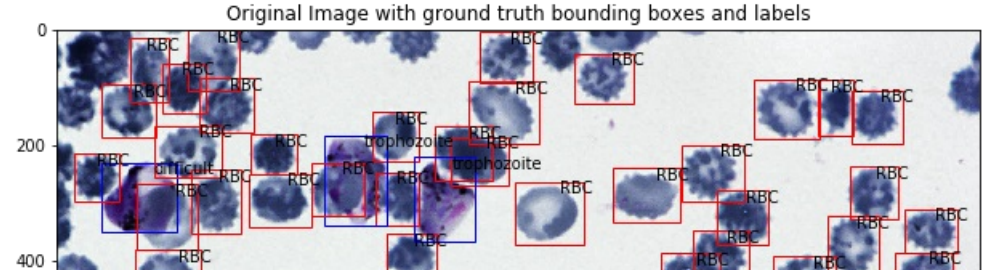
- in the Actual image we have class difficult but our model predict them as ring. This may be correct prediction.
- Model could not able to predict the uninfected cell "Leuckocyte". This is the failure of first level classifier.

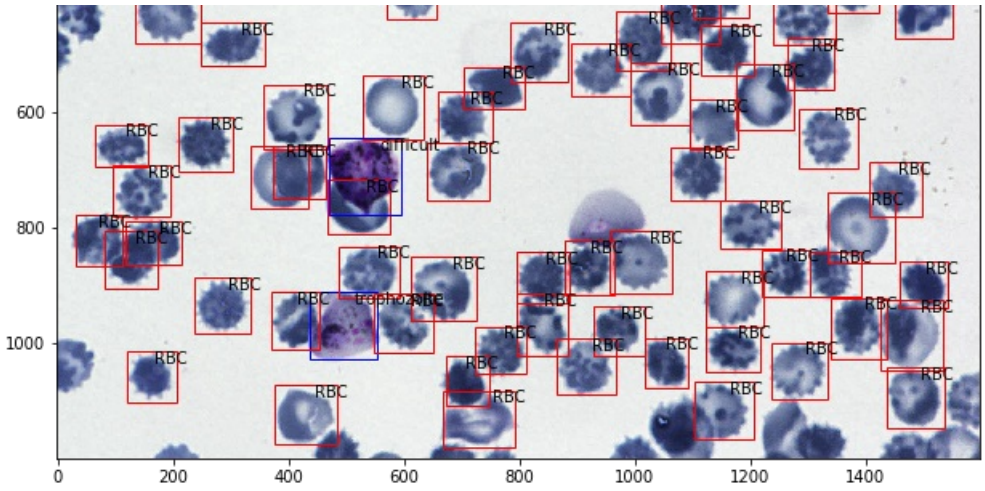
- sample_image:5

In [17]:

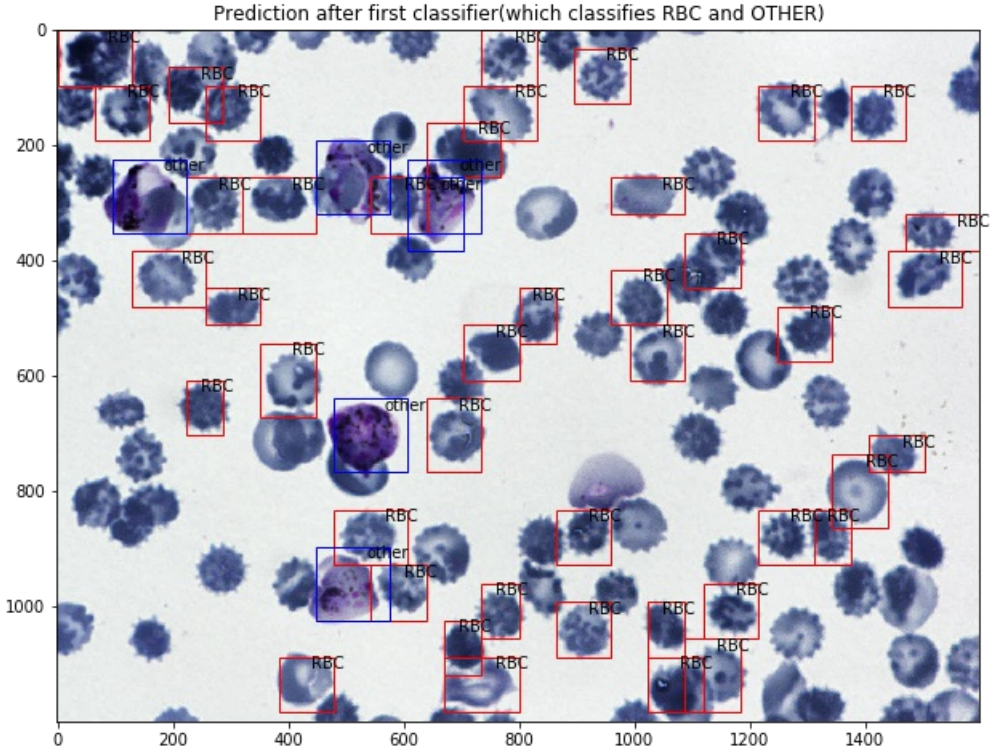
```
predicted("11b72c7b-5c52-44b7-adb7-21eacc25e441.png")
```

```
/usr/local/lib/python3.6/dist-packages/ipykernel_launcher.py:91: UserWarning: Boolean Series key w
ill be reindexed to match DataFrame index.
```

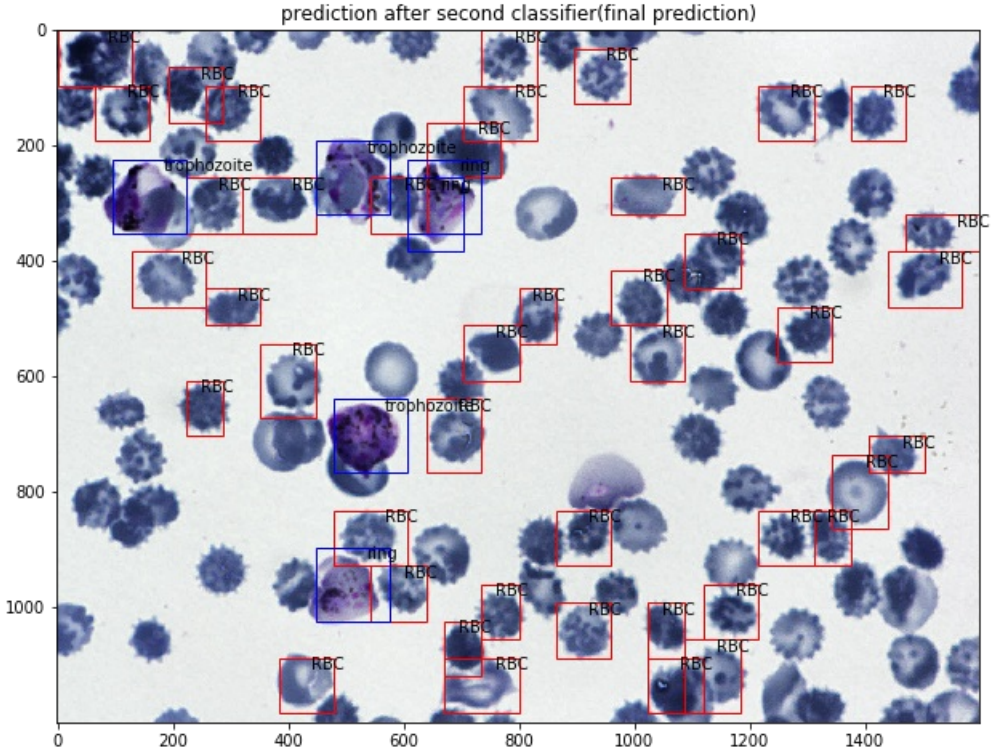




Prediction after first classifier(which classifies RBC and OTHER)



prediction after second classifier(final prediction)



Conclusion

- Our First level Classifier is doing decent job in classifying the infected and and uninfected cells but not so well in classifying uninfected cells(RBC and Lueckocyte)
- Our second level classifier also working nice but i have taken very less resolution of cropped images due to memory issues. If we take good resolution we can get still more good results.
- our model is slightly confusing with "difficult" class, since actually it is not an infected cell type,it is just given because we could not able to classify few cells into any of 6 categories. So our model will predict correct class instead of difficult.

Future Work

- Instead of taking two different classifiers, we could balance the dataset by creating duplicate images of minor class for example we can use GAN(Generative Adversarial Network) as a data augmentation technique.